Package ‘aroma.affymetrix’

February 18, 2024

Version 3.2.2

Depends R (>= 3.2.0), R.utils (>= 2.9.0), aroma.core (>= 3.2.0)

Imports methods, R.methodsS3 (>= 1.7.1), R.oo (>= 1.23.0), R.cache (>= 0.14.0), R.devices (>= 2.16.1), R.filesets (>= 2.13.0), aroma.apd (>= 0.6.0), MASS, splines, matrixStats (>= 0.55.0), listenv, future

Suggests DBI (>= 1.0.0), gsmoothr (>= 0.1.7), RColorBrewer (>= 1.1-2), Biobase (>= 2.28.0), BiocGenerics (>= 0.14.0), affxparser (>= 1.40.0), affy (>= 1.46.0), affyPLM (>= 1.44.0), aroma.light (>= 2.4.0), gcrma (>= 2.40.0), limma (>= 3.24.1), oligo (>= 1.32.0), oligoClasses (>= 1.30.0), pdInfoBuilder (>= 1.32.0), preprocessCore (>= 1.28.0), AffymetrixDataTestFiles, dChipIO (>= 0.1.1)

SuggestsNote BioC (>= 3.0), Recommended: preprocessCore, affyPLM, aroma.light, affxparser, DNAcopy

Title Analysis of Large Affymetrix Microarray Data Sets

Description A cross-platform R framework that facilitates processing of any number of Affymetrix microarray samples regardless of computer system. The only parameter that limits the number of chips that can be processed is the amount of available disk space. The Aroma Framework has successfully been used in studies to process tens of thousands of arrays. This package has actively been used since 2006.

License LGPL (>= 2.1)

URL `https://www.aroma-project.org/`, `https://github.com/HenrikBengtsson/aroma.affymetrix`

BugReports `https://github.com/HenrikBengtsson/aroma.affymetrix/issues`

LazyLoad TRUE

biocViews Infrastructure, ProprietaryPlatforms, ExonArray, Microarray, OneChannel, GUI, DataImport, DataRepresentation, Preprocessing, QualityControl, Visualization, ReportWriting, aCGH, CopyNumberVariants, DifferentialExpression, GeneExpression, SNP, Transcription

NeedsCompilation no

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R topics documented:

`aroma.affymetrix-package`

Package aroma.affymetrix

Description

A cross-platform R framework that facilitates processing of any number of Affymetrix microarray samples regardless of computer system. The only parameter that limits the number of chips that can be processed is the amount of available disk space. The Aroma Framework has successfully been used in studies to process tens of thousands of arrays. This package has actively been used since 2006.

Installation and updates

The preferred way to install this package is:

```
source("https://callr.org/install#aroma.affymetrix")
```

To get started

To get started, see the online user guides and the vignettes `https://www.aroma-project.org/`.

How to cite this package

In order to keep improving and providing support for this project, please cite references [1], [2], or any applicable publication listed on `https://aroma-project.org/publications/`, whenever you publish work that have been used any of the Aroma Framework.

License

The releases of this package is licensed under LGPL version 2.1 or newer.

The development code of the packages is under a private license (where applicable) and patches sent to the author fall under the latter license, but will be, if incorporated, released under the "release" license above.

Author(s)

Henrik Bengtsson, James Bullard, Kasper Hansen, Pierre Neuvial, Elizabeth Purdom, Mark Robinson, Ken Simpson

References

[1] H. Bengtsson, K. Simpson, J. Bullard, and K. Hansen, *aroma.affymetrix: A generic framework in R for analyzing small to very large Affymetrix data sets in bounded memory*, Tech Report #745, Department of Statistics, University of California, Berkeley, February 2008.
[2] H. Bengtsson, R. Irizarry, B. Carvalho, and T. Speed, *Estimation and assessment of raw copy numbers at the single locus level*, Bioinformatics, 2008.
[3] H. Bengtsson, *The R.oo package - Object-Oriented Programming with References Using Standard R Code*, In Kurt Hornik, Friedrich Leisch and Achim Zeileis, editors, Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003), March 20-22, Vienna, Austria. `https://www.r-project.org/conferences/DSC-2003/Proceedings/`

For a complete list, see `https://aroma-project.org/publications/`.

`AbstractProbeSequenceNormalization`

The AbstractProbeSequenceNormalization class

Description

Package: aroma.affymetrix
Class AbstractProbeSequenceNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelTransform3
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AbstractProbeSequenceNormalization
```

Directly known subclasses:
BaseCountNormalization, *BasePositionNormalization*, *LinearModelProbeSequenceNormalization*, MatNormalization

public abstract static class **AbstractProbeSequenceNormalization**
extends *ProbeLevelTransform3*

This abstract class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in probe sequences.

Usage

```
AbstractProbeSequenceNormalization(..., target=NULL)
```

Arguments

`...`	Arguments passed to the constructor of `ProbeLevelTransform3`.
`target`	A `character` string specifying type of "target" used. If `"zero"`, all arrays are normalized to have no effects. If `NULL`, all arrays a normalized to have the same effect as the average array has.

Fields and Methods

Methods:

```
getTargetFile  -
process        -
```

Methods inherited from ProbeLevelTransform3:
getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Requirements

This class requires that an `AromaCellSequenceFile` is available for the chip type.

Author(s)

Henrik Bengtsson

`AdditiveCovariatesNormalization`

The AdditiveCovariatesNormalization class

Description

Package: aroma.affymetrix
Class AdditiveCovariatesNormalization

```
Object
~~|
```

```
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ChipEffectTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AdditiveCovariatesNormalization
```

Directly known subclasses:
GcContentNormalization2

public abstract static class **AdditiveCovariatesNormalization**
extends *ChipEffectTransform*

This class represents a normalization method that corrects for GC-content effects on copy-number chip-effect estimates.

Usage

```
AdditiveCovariatesNormalization(dataSet=NULL, ..., target=NULL, subsetToFit="-XY",
  shift=0, onMissing=c("median", "ignore"))
```

Arguments

`dataSet`	A `SnpChipEffectSet`.
`...`	Additional arguments passed to the constructor of `ChipEffectTransform`.
`target`	(Optional) A `character` string or a `function` specifying what to normalize toward.
`subsetToFit`	The units from which the normalization curve should be estimated. If `NULL`, all are considered.
`onMissing`	Specifies how to normalize units for which the GC contents are unknown.
`shift`	An optional amount the data points should be shifted (translated).

Details

For SNPs, the normalization function is estimated based on the total chip effects, i.e. the sum of the allele signals. The normalizing is done by rescale the chip effects on the intensity scale such that the mean of the total chip effects are the same across samples for any given GC content. For allele-specific estimates, both alleles are always rescaled by the same amount. Thus, when normalizing allele-specific chip effects, the total chip effects is change, but not the relative allele signal, e.g. the allele B frequency.

Fields and Methods

Methods:

`getCdf`	-
`process`	-

Methods inherited from ChipEffectTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AffineCnPlm` *The AffineCnPlm class*

Description

Package: aroma.affymetrix
Class AffineCnPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffinePlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffineSnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CnPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffineCnPlm
```

Directly known subclasses:

public abstract static class **AffineCnPlm**
extends CnPlm

Usage

```
AffineCnPlm(..., combineAlleles=FALSE)
```

Arguments

`...`	Arguments passed to `AffineSnpPlm`.
`combineAlleles`	If `FALSE`, allele A and allele B are treated separately, otherwise together.

Fields and Methods

Methods:
No methods defined.

Methods inherited from CnPlm:
getCellIndices, getChipEffectSet, getCombineAlleles, getParameters, getProbeAffinityFile, setCombineAlleles

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from AffineSnpPlm:
getAsteriskTags

Methods inherited from AffinePlm:
getAsteriskTags, getFitUnitGroupFunction, getProbeAffinityFile

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AffinePlm` *The AffinePlm class*

Description

Package: aroma.affymetrix
Class AffinePlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffinePlm
```

Directly known subclasses:
AffineCnPlm, *AffineSnpPlm*

public abstract static class **AffinePlm**
extends *ProbeLevelModel*

This class represents affine model in Bengtsson & Hossjer (2006).

Usage

```
AffinePlm(..., background=TRUE)
```

Arguments

`...`	Arguments passed to `ProbeLevelModel`.
`background`	If `TRUE`, background is estimate for each unit group, otherwise not. That is, if `FALSE`, a *linear* (proportional) model without offset is fitted, resulting in very similar results as obtained by the `MbeiPlm`.

Fields and Methods

Methods:

`getProbeAffinityFile`	-

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Model

For a single unit group, the affine model is:

$$y_{ik} = a + \theta_i \phi_k + \varepsilon_{ik}$$

where a is an offset common to all probe signals, θ_i are the chip effects for arrays $i = 1, ..., I$, and ϕ_k are the probe affinities for probes $k = 1, ..., K$. The ε_{ik} are zero-mean noise with equal variance. The model is constrained such that $\prod_k \phi_k = 1$.

Note that with the additional constraint $a = 0$ (see arguments above), the above model is very similar to `MbeiPlm`. The differences in parameter estimates is due to difference is assumptions about the error structure, which in turn affects how the model is estimated.

Author(s)

Henrik Bengtsson

References

Bengtsson & Hossjer (2006).

`AffineSnpPlm` *The AffineSnpPlm class*

Description

Package: aroma.affymetrix
Class AffineSnpPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffinePlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffineSnpPlm
```

Directly known subclasses:
AffineCnPlm

public abstract static class **AffineSnpPlm**
extends SnpPlm

Usage

```
AffineSnpPlm(..., mergeStrands=FALSE)
```

Arguments

`...`	Arguments passed to `AffinePlm`.
`mergeStrands`	If `TRUE`, the sense and the anti-sense strands are fitted together, otherwise separately.

Fields and Methods

Methods:
No methods defined.

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from AffinePlm:
getAsteriskTags, getFitUnitGroupFunction, getProbeAffinityFile

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AffymetrixCdfFile` *The AffymetrixCdfFile class*

Description

Package: aroma.affymetrix
Class AffymetrixCdfFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaChipTypeAnnotationFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitAnnotationDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitTypesFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitNamesFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCdfFile
```

Directly known subclasses:

public abstract static class **AffymetrixCdfFile**
extends *UnitNamesFile*

An AffymetrixCdfFile object represents a generic Affymetrix CDF file.

Usage

```
AffymetrixCdfFile(...)
```

Arguments

`...`	Arguments passed to `AromaChipTypeAnnotationFile`.

Fields and Methods

Methods:

`convert`	-
`createExonByTranscriptCdf`	-
`getACSFile`	-
`getAromaCellSequenceFile`	-
`getCellIndices`	-
`getChipType`	-
`getDimension`	-
`getFileFormat`	-
`getGenomeInformation`	-
`getImage`	-
`getPlatform`	-
`getUnitNames`	-
`getUnitTypes`	-
`hasUnitTypes`	-
`isMonocellCdf`	-
`isPm`	-
`isUniqueCdf`	-
`nbrOfCells`	-
`nbrOfColumns`	-
`nbrOfQcUnits`	-
`nbrOfRows`	-
`nbrOfUnits`	-
`readDataFrame`	-
`readUnits`	-

Methods inherited from UnitNamesFile:
getUnitNames, indexOf, nbrOfUnits

Methods inherited from UnitTypesFile:
getUnitTypes, nbrOfUnits

Methods inherited from UnitAnnotationDataFile:
byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaChipTypeAnnotationFile:
as.character, byChipType, byName, findByChipType, fromFile, getChipType, getDefaultExtension, getHeader, getPlatform

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson, Ken Simpson

`AffymetrixCelFile` *The AffymetrixCelFile class*

Description

Package: aroma.affymetrix
Class AffymetrixCelFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
```

Directly known subclasses:
ChipEffectFile, *CnChipEffectFile*, *CnProbeAffinityFile*, *ExonChipEffectFile*, *ExonProbeAffinityFile*, *FirmaFile*, *ParameterCelFile*, *ProbeAffinityFile*, *QualityAssessmentFile*, *ResidualFile*, *SnpChipEffectFile*, *SnpProbeAffinityFile*, *WeightsFile*

public abstract static class **AffymetrixCelFile**
extends *AffymetrixFile*

An AffymetrixCelFile object represents a single Affymetrix CEL file.

Usage

```
AffymetrixCelFile(..., cdf=NULL)
```

Arguments

`...`	Arguments passed to `AromaMicroarrayDataFile`.
`cdf`	An optional `AffymetrixCdfFile` making it possible to override the default CDF file as specified by the CEL file header. The requirement is that its number of cells must match that of the CEL file. If `NULL`, the CDF structure is inferred from the the chip type as specified in the CEL file header.

Fields and Methods

Methods:

```
extractMatrix      -
getAm              -
getCdf             -
getFileFormat      -
getImage           -
getUnitNamesFile   -
getUnitTypesFile   -
image270           -
nbrOfCells         -
plotDensity        -
plotImage          -
```

`plotMvsA`	-
`plotMvsX`	-
`setCdf`	-
`smoothScatterMvsA`	-
`writeImage`	-

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

For developers

If you subclass this class, please make sure to query the `AffymetrixCdfFile` object (see `*getCdf()`) whenever querying CDF information. Do not use the CDF file inferred from the chip type in CEL header, unless you really want it to be hardwired that way, otherwise you will break to possibility to override the CDF structure.

Author(s)

Henrik Bengtsson

See Also

An object of this class is typically part of an `AffymetrixCelSet`.

`AffymetrixCelSet` *The AffymetrixCelSet class*

Description

Package: aroma.affymetrix
Class AffymetrixCelSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
```

Directly known subclasses:
ChipEffectSet, CnChipEffectSet, ExonChipEffectSet, FirmaSet, ParameterCelSet, QualityAssessmentSet, ResidualSet, SnpChipEffectSet, WeightsSet

public static class **AffymetrixCelSet**
extends *AffymetrixFileSet*

An AffymetrixCelSet object represents a set of Affymetrix CEL files with *identical* chip types.

Usage

```
AffymetrixCelSet(files=NULL, ...)
```

Arguments

`files`	A `list` of `AffymetrixCelFile`:s.
`...`	Not used.

Fields and Methods

Methods:

`as` -
`as.AffymetrixCelSet` -
`byName` -
`doCRMAv1` -
`doCRMAv2` -
`doFIRMA` -
`doGCRMA` -
`doRMA` -
`extractAffyBatch` -
`extractFeatureSet` -
`extractMatrix` -
`getAverage` -
`getAverageAsinh` -
`getAverageFile` -
`getAverageLog` -
`getCdf` -
`getChipType` -
`getData` -
`getIntensities` -
`getPlatform` -
`getTimestamps` -
`getUnitGroupCellMap` -
`getUnitIntensities` -
`getUnitNamesFile` -
`getUnitTypesFile` -
`justSNPRMA` -
`plotDensity` -
`readUnits` -
`setCdf` -
`writeSgr` -

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNames-

TranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

`AffymetrixCelFile`.

Examples

```
## Not run:
  for (zzz in 0) {

# Find any dataset
path <- NULL
if (is.null(path))
  break

# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Define a dataset object based on all CEL files in a directory
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
ds <- AffymetrixCelSet$fromFiles(path)
print(ds)

# Keep at most three arrays for this example
ds <- ds[1:min(3,nbrOfArrays(ds))]
print(ds)
```

```
} # for (zzz in 0)
rm(zzz)


## End(Not run)
```

`AffymetrixCelSetReporter`

The AffymetrixCelSetReporter class

Description

Package: aroma.affymetrix
Class AffymetrixCelSetReporter

```
Object
~~|
~~+--GenericReporter
~~~~~~~|
~~~~~~~+--AffymetrixFileSetReporter
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AffymetrixCelSetReporter
```

Directly known subclasses:
SpatialReporter

public abstract static class **AffymetrixCelSetReporter**
extends *AffymetrixFileSetReporter*

Usage

```
AffymetrixCelSetReporter(..., .setClass="AffymetrixCelSet")
```

Arguments

`...`	Arguments passed to `AffymetrixFileSetReporter`.
`.setClass`	The name of the class of the input set.

Fields and Methods

Methods:

`getDataSet` -

Methods inherited from AffymetrixFileSetReporter:
getFileSet, getInputName, getInputTags

Methods inherited from GenericReporter:
as.character, getAlias, getAsteriskTags, getFullName, getInputName, getInputTags, getMainPath, getName, getPath, getReportSet, getRootPath, getTags, process, setAlias, setup

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AffymetrixCelSetTuple` *The AffymetrixCelSetTuple class*

Description

Package: aroma.affymetrix
Class AffymetrixCelSetTuple

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSetList
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSetTuple
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AffymetrixCelSetTuple
```

Directly known subclasses:
ChipEffectSetTuple, CnChipEffectSetTuple

public static class **AffymetrixCelSetTuple**
extends *AromaMicroarrayDataSetTuple*

Usage

```
AffymetrixCelSetTuple(..., .setClass="AffymetrixCelSet")
```

Arguments

`...`	Arguments passed to the constructor of `AromaMicroarrayDataSetTuple`.
`.setClass`	The name of the class of the input set.

Fields and Methods

Methods:

`byPath` -

Methods inherited from AromaMicroarrayDataSetTuple:
as, as.AromaMicroarrayDataSetTuple, byPath, getAsteriskTags, getChipTypes, getFullNames, getSets, getTags, indexOf, nbrOfChipTypes

Methods inherited from GenericDataFileSetList:
as, as.GenericDataFileSetList, as.character, as.data.frame, as.list, assertDuplicates, clone, extract, getAsteriskTags, getDefaultFullName, getFileList, getFileListClass, getFullNames, getNames, getSet, getSets, getTags, indexOf, length, nbrOfFiles, nbrOfSets, setTags

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AffymetrixCnChpSet` *The AffymetrixCnChpSet class*

Description

Package: aroma.affymetrix
Class AffymetrixCnChpSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCnChpSet
```

Directly known subclasses:

public abstract static class **AffymetrixCnChpSet**
extends *AffymetrixFileSet*

A AffymetrixCnChpSet object represents a set of AffymetrixCnChpFile:s with *identical* chip types.

Usage

```
AffymetrixCnChpSet(files=NULL, ...)
```

Arguments

`files`	A `list` of `AffymetrixCnChpFile`:s.
`...`	Not used.

Fields and Methods

Methods:

`as`	-
`as.AffymetrixCnChpSet`	-
`exportTotalCnRatioSet`	-
`extractLogRatios`	-
`findByName`	-
`getCdf`	-
`setCdf`	-

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAt-

tributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

`AffymetrixCnChpFile`.

`AffymetrixFile` *The abstract AffymetrixFile class*

Description

Package: aroma.affymetrix
Class AffymetrixFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
```

```
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
```

Directly known subclasses:
AffymetrixCdfFile, *AffymetrixCelFile*, *AffymetrixCnChpFile*, *AffymetrixPgfFile*, *AffymetrixTsvFile*, *AromaChipTypeAnnotationFile*, *ChipEffectFile*, *CnChipEffectFile*, *CnProbeAffinityFile*, *CnagCfhFile*, *DChipCdfBinFile*, *DChipDcpFile*, *ExonChipEffectFile*, *ExonProbeAffinityFile*, *FirmaFile*, *ParameterCelFile*, *ProbeAffinityFile*, *QualityAssessmentFile*, *ResidualFile*, *SnpChipEffectFile*, *SnpProbeAffinityFile*, *WeightsFile*

public abstract static class **AffymetrixFile**
extends *AromaPlatformInterface*

An AffymetrixFile object represents a single Affymetrix file, e.g. an Affymetrix CEL file or an Affymetrix CDF file. Note that this class is abstract and can not be instanciated, but instead you have to use one of the subclasses or the generic `fromFile()` method.

Usage

```
AffymetrixFile(...)
```

Arguments

`...`	Arguments passed to `GenericDataFile`.

Fields and Methods

Methods:
No methods defined.

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

An object of this class is typically part of an `AffymetrixFileSet`.

`AffymetrixFileSet` *The AffymetrixFileSet class*

Description

Package: aroma.affymetrix
Class AffymetrixFileSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
```

```
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
```

Directly known subclasses:
AffymetrixCelSet, *AffymetrixCnChpSet*, ChipEffectSet, CnChipEffectSet, *DChipDcpSet*, ExonChipEffectSet, FirmaSet, ParameterCelSet, QualityAssessmentSet, ResidualSet, SnpChipEffectSet, WeightsSet

public abstract static class **AffymetrixFileSet**
extends *AromaPlatformInterface*

An AffymetrixFileSet object represents a set of `AffymetrixFile`s with *identical* chip types.

Usage

```
AffymetrixFileSet(files=NULL, ...)
```

Arguments

`files`	A `list` of `AffymetrixFile`:s.
`...`	Arguments passed to `GenericDataFileSet`.

Fields and Methods

Methods:

`as`	-
`as.AffymetrixFileSet`	-
`byPath`	-

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, get-

Pathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AffymetrixFileSetReporter` *The AffymetrixFileSetReporter class*

Description

Package: aroma.affymetrix
Class AffymetrixFileSetReporter

```
Object
~~|
~~+--GenericReporter
~~~~~~~|
~~~~~~~+--AffymetrixFileSetReporter
```

Directly known subclasses:
AffymetrixCelSetReporter, *SpatialReporter*

public abstract static class **AffymetrixFileSetReporter**
extends *GenericReporter*

Usage

```
AffymetrixFileSetReporter(set=NULL, ..., .setClass="AffymetrixFileSet")
```

Arguments

`set`	An `AffymetrixFileSet` object.
`...`	Arguments passed to `GenericReporter`.
`.setClass`	The name of the class of the input set.

Fields and Methods

Methods:

```
getInputName  -
getInputTags  -
```

Methods inherited from GenericReporter:
as.character, getAlias, getAsteriskTags, getFullName, getInputName, getInputTags, getMainPath, getName, getPath, getReportSet, getRootPath, getTags, process, setAlias, setup

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AffymetrixPgfFile` *The AffymetrixPgfFile class*

Description

Package: aroma.affymetrix
Class AffymetrixPgfFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaChipTypeAnnotationFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitAnnotationDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitTypesFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitNamesFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixPgfFile
```

Directly known subclasses:

public abstract static class **AffymetrixPgfFile**
extends *UnitNamesFile*

An AffymetrixPgfFile object represents a generic Affymetrix Probe Group File (PGF). A PGF file "provides information about what probes are contained within a probeset and information about the nature of the probes necessary for analysis. The current PGF file format (version 1) is only specified for expression style probesets." [1]

Usage

```
AffymetrixPgfFile(...)
```

Arguments

`...`	Arguments passed to `AromaChipTypeAnnotationFile`.

Fields and Methods

Methods:

`getChipType`	-
`getDimension`	-
`getPlatform`	-
`getUnitNames`	-
`nbrOfCells`	-
`nbrOfColumns`	-
`nbrOfRows`	-
`nbrOfUnits`	-

Methods inherited from UnitNamesFile:
getUnitNames, indexOf, nbrOfUnits

Methods inherited from UnitTypesFile:
getUnitTypes, nbrOfUnits

Methods inherited from UnitAnnotationDataFile:
byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaChipTypeAnnotationFile:
as.character, byChipType, byName, findByChipType, fromFile, getChipType, getDefaultExtension, getHeader, getPlatform

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

References

[1] ...

`AlleleSummation` *The AlleleSummation class*

Description

Package: aroma.affymetrix
Class AlleleSummation

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AlleleSummation
```

Directly known subclasses:

public abstract static class **AlleleSummation**
extends *UnitModel*

This class takes allele-specific chip effect estimates of a SnpChipEffectSet and returns a CnChipEffectSet holding the summed allele estimates.

Usage

```
AlleleSummation(dataSet=NULL, ignoreNAs=TRUE, ...)
```

Arguments

`dataSet`	A `SnpChipEffectSet`.
`ignoreNAs`	If `TRUE`, missing values are excluded when summing the signals from the two alleles.
`...`	Arguments passed to `UnitModel`.

Fields and Methods

Methods:

```
findUnitsTodo     -
getChipEffectSet  -
process           -
```

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AllelicCrosstalkCalibration`

The AllelicCrosstalkCalibration class

Description

Package: aroma.affymetrix
Class AllelicCrosstalkCalibration

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AllelicCrosstalkCalibration
```

Directly known subclasses:

public static class **AllelicCrosstalkCalibration**
extends *ProbeLevelTransform*

This class represents a calibration function that transforms the probe-level signals such that the signals from the two alleles are orthogonal. The method fits and calibrates PM signals only. MM signals will not affect the model fitting and are unaffected.

Usage

```
AllelicCrosstalkCalibration(dataSet=NULL, ..., model=c("asis", "auto", "CRMA", "CRMAv2"),
  rescaleBy=c("auto", "groups", "all", "none"), targetAvg=c(2200, 2200),
  subsetToAvg="-XY", mergeShifts=TRUE, B=1, flavor=c("sfit", "expectile"),
  alpha=c(0.1, 0.075, 0.05, 0.03, 0.01), q=2, Q=98, lambda=2,
  pairBy=c("CDF", "sequence"))
```

Arguments

`dataSet`	An `AffymetrixCelSet`.
`...`	Arguments passed to the constructor of `ProbeLevelTransform`.
`model`	A `character` string for quickly specifying default parameter settings.
`rescaleBy`	A `character` string specifying what sets of cells should be rescaled towards a target average, if any. Default is to rescale all cells together. If `"none"`, no rescaling is done.
`targetAvg`	The signal(s) that either the average of the sum (if one target value) or the average of each of the alleles (if two target values) should have after calibration. Only used if `rescaleBy != "none"`.
`subsetToAvg`	The indices of the cells (taken as the intersect of existing indices) used to calculate average in order to rescale to the target average. If `NULL`, all probes are considered.
`mergeShifts`	If `TRUE`, the shift of the probe sequence relative to the SNP position is ignored, otherwise not.
`B`	An `integer` specifying by how many nucleotides the allelic groups should be stratified by. If zero, all SNPs are put in one group.
`flavor`	A `character` string specifying what algorithm is used to fit the crosstalk calibration.
`alpha, q, Q, lambda`	Model fitting parameters.
`pairBy`	A `character` string specifying how allele probe pairs are identified.

What probe signals are updated?

Calibration for crosstalk between allele signals applies by definition only SNP units. Furthermore, it is only SNP units with two or four unit groups that are calibrated. For instance, in at least on custom SNP CDFs we know of, there is a small number of SNP units that have six groups. *Currently these units are not calibrated (at all).* It is only PM probes that will be calibrated. Note that, non-calibrated signals will be saved in the output files.

What probe signals are used to fit model?

All PM probe pairs are used to fit the crosstalk model. In the second step where signals are rescaled to a target average, it is possible to specify the set of cells that should be included when estimating the target average.

Important about rescaling towards target average

Rescaling each allele-pair group (e.g. AC, AG, AT, CG, CT, GC) towards a target average (`rescaleBy="groups"`) *must not* be used for multi-enzyme chip types, e.g. GenomeWideSNP_6. If still done, due to confounded effects of non-perfect enzyme mixtures etc, there will be a significant bias between raw CNs for SNPs and CN probes. Instead, for such chip types *all probe signals* should be rescale together towards the target average (`rescaleBy="all"`).

Fields and Methods

Methods:

`process` -

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AromaChipTypeAnnotationFile`

The AromaChipTypeAnnotationFile class

Description

Package: aroma.affymetrix
Class AromaChipTypeAnnotationFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaChipTypeAnnotationFile
```

Directly known subclasses:
AffymetrixCdfFile, *AffymetrixPgfFile*

public abstract static class **AromaChipTypeAnnotationFile**
extends *AffymetrixFile*

An AromaChipTypeAnnotationFile object represents an annotation file for a specific chip type.

Usage

```
AromaChipTypeAnnotationFile(...)
```

Arguments

`...`	Arguments passed to `AffymetrixFile`.

Fields and Methods

Methods:

`byChipType`	-
`getChipType`	-
`getHeader`	-
`getPlatform`	-

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`ArrayExplorer` *The ArrayExplorer class*

Description

Package: aroma.affymetrix
Class ArrayExplorer

```
Object
~~|
```

```
~~+--Explorer
~~~~~~~|
~~~~~~~+--ArrayExplorer
```

Directly known subclasses:

public abstract static class **ArrayExplorer**
extends *Explorer*

Usage

```
ArrayExplorer(csTuple=NULL, ...)
```

Arguments

`csTuple`	An `AffymetrixCelSet` object.
`...`	Not used.

Fields and Methods

Methods:

`addColorMap`	-
`getColorMaps`	-
`getDataSet`	-
`getSetTuple`	-
`nbrOfChipTypes`	-
`process`	-
`setArrays`	-
`setColorMaps`	-

Methods inherited from Explorer:
addIncludes, addIndexFile, as.character, display, getAlias, getArraysOfInput, getAsteriskTags, getFullName, getIncludePath, getMainPath, getName, getNameOfInput, getNames, getPath, getReportPathPattern, getRootPath, getSampleLayerPrefix, getSubname, getTags, getTagsOfInput, getTemplatePath, getVersion, nbrOfArrays, process, setAlias, setArrays, setReportPathPattern, setSubname, setup, splitByReportPathPattern, updateSetupExplorerFile

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AvgCnPlm` *The AvgCnPlm class*

Description

Package: aroma.affymetrix
Class AvgCnPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AvgPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AvgSnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CnPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AvgCnPlm
```

Directly known subclasses:

public abstract static class **AvgCnPlm**
extends CnPlm

Usage

```
AvgCnPlm(..., combineAlleles=FALSE)
```

Arguments

`...`	Arguments passed to `AvgSnpPlm`.
`combineAlleles`	If `FALSE`, allele A and allele B are treated separately, otherwise together.

Fields and Methods

Methods:
No methods defined.

Methods inherited from CnPlm:
getCellIndices, getChipEffectSet, getCombineAlleles, getParameters, getProbeAffinityFile, setCombineAlleles

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from AvgSnpPlm:
getAsteriskTags

Methods inherited from AvgPlm:
getAsteriskTags, getCalculateResidualsFunction, getParameters, validate

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`AvgPlm` *The AvgPlm class*

Description

Package: aroma.affymetrix
Class AvgPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AvgPlm
```

Directly known subclasses:
AvgCnPlm, *AvgSnpPlm*

public abstract static class **AvgPlm**
extends *ProbeLevelModel*

This class represents a PLM where the probe intensities are averaged assuming identical probe affinities. For instance, one may assume that replicated probes with identical sequences have the same probe affinities, cf. the GenomeWideSNP_6 chip type.

Usage

```
AvgPlm(..., flavor=c("median", "mean"))
```

Arguments

`...`	Arguments passed to `ProbeLevelModel`.
`flavor`	A `character` string specifying what model fitting algorithm to be used. This makes it possible to get identical estimates as other packages.

Fields and Methods

Methods:
No methods defined.

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Model

For a single unit group, the averaging PLM of K probes is:

$$y_{ik} = \theta_i + \varepsilon_{ik}$$

where θ_i are the chip effects for arrays $i = 1, ..., I$. The ε_{ik} are zero-mean noise with equal variance.

Different flavors of model fitting

The above model can be fitted in two ways, either robustly or non-robustly. Use argument `flavor="mean"` to fit the model non-robustly, i.e.

$$\hat{\theta}_i = 1/K \sum_k y_{ik}$$

.

Use argument `flavor="median"` to fit the model robustly, i.e.

$$\hat{\theta}_i = median_k y_{ik}$$

.

Missing values are always excluded.

Author(s)

Henrik Bengtsson

`AvgSnpPlm` *The AvgSnpPlm class*

Description

Package: aroma.affymetrix
Class AvgSnpPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AvgPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AvgSnpPlm
```

Directly known subclasses:
AvgCnPlm

public abstract static class **AvgSnpPlm**
extends SnpPlm

Usage

```
AvgSnpPlm(..., mergeStrands=FALSE)
```

Arguments

`...`	Arguments passed to `AvgPlm`.
`mergeStrands`	If `TRUE`, the sense and the anti-sense strands are fitted together, otherwise separately.

Fields and Methods

Methods:
No methods defined.

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from AvgPlm:
getAsteriskTags, getCalculateResidualsFunction, getParameters, validate

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`BackgroundCorrection` *The BackgroundCorrection class*

Description

Package: aroma.affymetrix
Class BackgroundCorrection

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--BackgroundCorrection
```

Directly known subclasses:
GcRmaBackgroundCorrection, LimmaBackgroundCorrection, NormExpBackgroundCorrection, OpticalBackgroundCorrection, RmaBackgroundCorrection

public abstract static class **BackgroundCorrection**
extends *ProbeLevelTransform*

This class represents a background adjustment function.

Usage

```
BackgroundCorrection(..., subsetToUpdate=NULL, typesToUpdate=NULL)
```

Arguments

`...`	Arguments passed to the constructor of `ProbeLevelTransform`.
`subsetToUpdate`	The probes to be updated. If `NULL`, all probes are updated.
`typesToUpdate`	Types of probes to be updated.

Fields and Methods

Methods:

`process` -

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach,

equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

`BaseCountNormalization`

The BaseCountNormalization class

Description

Package: aroma.affymetrix
Class BaseCountNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelTransform3
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AbstractProbeSequenceNormalization
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--BaseCountNormalization
```

Directly known subclasses:

public static class **BaseCountNormalization**
extends *AbstractProbeSequenceNormalization*

This class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in the number of A, C, G, and T:s in the probe sequences.

Usage

```
BaseCountNormalization(..., model=c("robustSmoothSpline", "lm"), bootstrap=FALSE)
```

Arguments

`...`	Arguments passed to the constructor of `AbstractProbeSequenceNormalization`.
`model`	A `character` string specifying the model used to fit the base-count effects.
`bootstrap`	If `TRUE`, the model fitting is done by bootstrap in order to save memory.

Fields and Methods

Methods:
No methods defined.

Methods inherited from AbstractProbeSequenceNormalization:
fitOne, getAromaCellSequenceFile, getParameters, getTargetFile, indexOfMissingSequences, predictOne, process

Methods inherited from ProbeLevelTransform3:
getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Requirements

This class requires that an aroma probe sequence file is available for the chip type.

Author(s)

Henrik Bengtsson

`BasePositionNormalization`

The BasePositionNormalization class

Description

Package: aroma.affymetrix
Class BasePositionNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelTransform3
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AbstractProbeSequenceNormalization
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--LinearModelProbeSequenceNormalization
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--BasePositionNormalization
```

Directly known subclasses:

public abstract static class **BasePositionNormalization**
extends *LinearModelProbeSequenceNormalization*

This class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in positioning of A, C, G, and T:s in the probe sequences.

Usage

```
BasePositionNormalization(..., model=c("smooth.spline"), df=5)
```

Arguments

`...`	Arguments passed to the constructor of `LinearModelProbeSequenceNormalization`.
`model`	A `character` string specifying the model used to fit the base-count effects.
`df`	The degrees of freedom of the model.

Fields and Methods

Methods:
No methods defined.

Methods inherited from LinearModelProbeSequenceNormalization:
fitOne, getDesignMatrix, getNormalEquations, getSignalTransform, predictOne

Methods inherited from AbstractProbeSequenceNormalization:
fitOne, getAromaCellSequenceFile, getParameters, getTargetFile, indexOfMissingSequences, predictOne, process

Methods inherited from ProbeLevelTransform3:
getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson, Mark Robinson

`ChipEffectFile` *The ChipEffectFile class*

Description

Package: aroma.affymetrix
Class ChipEffectFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
```

```
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ChipEffectFile
```

Directly known subclasses:
CnChipEffectFile, *ExonChipEffectFile*, *SnpChipEffectFile*

public abstract static class **ChipEffectFile**
extends *ParameterCelFile*

This class represents estimates of chip effects in the probe-level models.

Usage

```
ChipEffectFile(..., probeModel=c("pm"))
```

Arguments

`...`	Arguments passed to `ParameterCelFile`.
`probeModel`	The specific type of model, e.g. `"pm"`.

Fields and Methods

Methods:

`extractMatrix`	-
`extractTheta`	-
`findUnitsTodo`	-
`getAM`	-
`readUnits`	-

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

An object of this class is typically obtained through the `getChipEffectSet()` method for the `ProbeLevelModel` class. An object of this class is typically part of a `ChipEffectSet`.

`ChipEffectSet` *The ChipEffectSet class*

Description

Package: aroma.affymetrix
Class ChipEffectSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ChipEffectSet
```

Directly known subclasses:
CnChipEffectSet, ExonChipEffectSet, SnpChipEffectSet

public static class **ChipEffectSet**
extends ParameterCelSet

This class represents estimates of chip effects in the probe-level models.

Usage

```
ChipEffectSet(..., probeModel=c("pm"))
```

Arguments

`...`	Arguments passed to `AffymetrixCelSet`.
`probeModel`	The specific type of model, e.g. `"pm"`.

Fields and Methods

Methods:

`boxplotStats`	-
`extractExpressionSet`	-
`extractMatrix`	-
`extractTheta`	-
`findUnitsTodo`	-
`getAM`	-
`getAverageFile`	-
`getCellIndices`	-
`plotBoxplot`	-
`readUnits`	-

Methods inherited from ParameterCelSet:
extractDataFrame, extractMatrix

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelSet:
append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorBy-

function, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

An object of this class is typically obtained through the `getChipEffectSet()` method for the `ProbeLevelModel` class.

`ChipEffectTransform` *The ChipEffectTransform class*

Description

Package: aroma.affymetrix
Class ChipEffectTransform

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~~~~~~+--ChipEffectTransform
```

Directly known subclasses:
AdditiveCovariatesNormalization, ChipEffectGroupMerge, FragmentEquivalentClassNormalization, FragmentLengthNormalization, GcContentNormalization, GcContentNormalization2, SnpChipEffectGroupMerge

public abstract static class **ChipEffectTransform**
extends *Transform*

This abstract class represents a transform that transforms chip-effect estimates obtained from probe-level modeling.

Usage

```
ChipEffectTransform(dataSet=NULL, ...)
```

Arguments

`dataSet`	The input data set as an `ChipEffectSet`.
`...`	Arguments passed to the constructor of `Transform`.

Details

Subclasses must implement the `process()` method.

Fields and Methods

Methods:
No methods defined.

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`CnagCfhFile` *The CnagCfhFile class*

Description

Package: aroma.affymetrix
Class CnagCfhFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CnagCfhFile
```

Directly known subclasses:

public abstract static class **CnagCfhFile**
extends *AffymetrixFile*

A CnagCfhFile object represents a single CNAG CFH file.

Usage

```
CnagCfhFile(..., cdf=NULL)
```

Arguments

`...`	Arguments passed to `AromaMicroarrayDataFile`.
`cdf`	An optional `AffymetrixCdfFile`

Fields and Methods

Methods:

`getCdf`	-
`nbrOfCells`	-
`nbrOfSnps`	-
`setCdf`	-

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

An object of this class is typically part of an `CnagCfhSet`.

`CnagCfhSet` *The CnagCfhSet class*

Description

Package: aroma.affymetrix
Class CnagCfhSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CnagCfhSet
```

Directly known subclasses:

public static class **CnagCfhSet**
extends GenericDataFileSet

An CnagCfhSet object represents a set of CNAG CFH files with *identical* chip types.

Usage

```
CnagCfhSet(files=NULL, ...)
```

Arguments

`files`	A `list` of `CnagCfhFile`:s.
`...`	Not used.

Fields and Methods

Methods:

```
as                 -
as.CnagCfhSet      -
byName             -
getAverage         -
getAverageAsinh    -
getAverageFile     -
getAverageLog      -
getCdf             -
```

```
getData         -
getTimestamps   -
readUnits       -
setCdf          -
```

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

`CnagCfhFile`.

`CnChipEffectFile` *The CnChipEffectFile class*

Description

Package: aroma.affymetrix
Class CnChipEffectFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ChipEffectFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpChipEffectFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CopyNumberDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CnChipEffectFile
```

Directly known subclasses:

public abstract static class **CnChipEffectFile**
extends *CopyNumberDataFile*

This class represents estimates of chip effects in a copy-number probe-level models.

Usage

```
CnChipEffectFile(..., combineAlleles=FALSE)
```

Arguments

`...`	Arguments passed to `SnpChipEffectFile`.
`combineAlleles`	A `logical` indicating if the signals from allele A and allele B are combined or not.

Fields and Methods

Methods:

`exportTotalAndFracB`	-
`extractTheta`	-
`extractTotalAndFreqB`	-
`hasAlleleBFractions`	-
`hasStrandiness`	-
`mergeStrands`	-
`readUnits`	-

Methods inherited from CopyNumberDataFile:
as, as.CopyNumberDataFile, getNumberOfFilesAveraged, hasAlleleBFractions, hasStrandiness

Methods inherited from SnpChipEffectFile:
exportTotalAndFracB, extractCNT, extractTheta, extractTotalAndFracB, getCellIndices, getExpandedCellMap, getParameters, mergeStrands, readUnits, writeCNT

Methods inherited from ChipEffectFile:
as.character, extractChromosomalDataFrame, extractMatrix, extractTheta, findUnitsTodo, getAM, getAsFullCelFile, getCellIndices, getCellMapForMainCdf, getExpandedCellMap, getParameters, getUnitGroupCellArrayMap, getUnitGroupCellMatrixMap, getXAM, mergeGroups, readUnits, writeAsFullCelFile

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

An object of this class is typically part of a `CnChipEffectSet`.

`CnChipEffectSet` *The CnChipEffectSet class*

Description

Package: aroma.affymetrix
Class CnChipEffectSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
```

```
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ChipEffectSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpChipEffectSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CopyNumberDataSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CnChipEffectSet
```

Directly known subclasses:

public static class **CnChipEffectSet**
extends CopyNumberDataSet

This class represents estimates of chip effects in the probe-level models.

Usage

```
CnChipEffectSet(..., combineAlleles="byFirstFile")
```

Arguments

`...`	Arguments passed to `SnpChipEffectSet`.
`combineAlleles`	A `logical` indicating if the signals from allele A and allele B are combined or not.

Fields and Methods

Methods:

`as.CopyNumberDataSetTuple`	-
`exportTotalAndFracB`	-
`extractTheta`	-
`extractTotalAndFreqB`	-
`getAverageFile`	-
`getCombineAlleles`	-

```
hasAlleleBFractions       -
hasStrandiness            -
setCombineAlleles         -
writeWig                  -
```

Methods inherited from CopyNumberDataSet:
as, as.CopyNumberDataSet, doCBS, hasAlleleBFractions, hasStrandiness

Methods inherited from SnpChipEffectSet:
byPath, exportTotalAndFracB, extractAlleleSet, extractCNT, extractSnpCnvQSet, extractSnpQSet, extractTheta, extractTotalAndFreqB, getAverageFile, getBaseline, getMergeStrands, setMergeStrands, writeCNT

Methods inherited from ChipEffectSet:
as.character, boxplotStats, byPath, calculateBaseline, calculateFieldBoxplotStats, calculateNuseBoxplotStats, calculateRleBoxplotStats, extractAffyBatch, extractChromosomalDataFrame, extractExpressionSet, extractMatrix, extractTheta, findByName, findUnitsTodo, fromDataSet, getAM, getAsFullCelSet, getAverageFile, getBaseline, getCellIndices, getXAM, plotBoxplot, readUnits, updateUnits

Methods inherited from ParameterCelSet:
extractDataFrame, extractMatrix

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelSet:
append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName,

findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`CnPlm` *The CnPlm class*

Description

Package: aroma.affymetrix
Class CnPlm

```
Interface
~~|
~~+--SnpPlm
~~~~~~~|
~~~~~~~+--CnPlm
```

Directly known subclasses:
AffineCnPlm, *AvgCnPlm*, *HetLogAddCnPlm*, *MbeiCnPlm*, *RmaCnPlm*

public class **CnPlm**
extends SnpPlm

This support class represents a `SnpPlm` specially designed for copy-number analysis.

Usage

```
CnPlm(...)
```

Arguments

`...`	Arguments passed to `SnpPlm`.

Details

Models implementing this copy-number PLM, provides either allele-specific or total copy-number estimates. For allele-specific CNs the underlying `SnpPlm` model is fitted as is, i.e. for each allele separately with or without the strands first being merged.

For total CNs the probe signals for the two alleles are combined (=summed; not averaged) on the intensity scale before fitting underlying `SnpPlm` model, again with or without the strands first being merged.

Methods

Methods:

`getCellIndices`	-
`getChipEffectSet`	-
`getCombineAlleles`	-
`getProbeAffinityFile`	-
`setCombineAlleles`	-

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from Interface:
extend, print, uses

Requirements

Classes inheriting from this `Interface` must provide the following fields, in addition to the ones according to `SnpPlm`:

combineAlleles A `logical` indicating if total or allele-specific copy numbers should be estimated according to the above averaging.

Author(s)

Henrik Bengtsson

`CnProbeAffinityFile` *The CnProbeAffinityFile class*

Description

Package: aroma.affymetrix
Class CnProbeAffinityFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ProbeAffinityFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpProbeAffinityFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CnProbeAffinityFile
```

Directly known subclasses:

public abstract static class **CnProbeAffinityFile**
extends *SnpProbeAffinityFile*

This class represents estimates of probe affinities in SNP probe-level models.

Usage

```
CnProbeAffinityFile(..., combineAlleles=FALSE)
```

Arguments

`...`	Arguments passed to `SnpProbeAffinityFile`.
`combineAlleles`	If `FALSE`, allele A and allele B are treated separately, otherwise together.

Fields and Methods

Methods:
No methods defined.

Methods inherited from SnpProbeAffinityFile:
getCellIndices, setMergeStrands

Methods inherited from ProbeAffinityFile:
as.character, getCellIndices, getParameters, readUnits

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`CrlmmParametersFile` *The CrlmmParametersFile class*

Description

Package: aroma.affymetrix
Class CrlmmParametersFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--ColumnNamesInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--GenericTabularFile
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaTabularBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinaryFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CrlmmParametersFile
```

Directly known subclasses:

public static class **CrlmmParametersFile**
extends AromaUnitSignalBinaryFile

An CrlmmParametersFile is a `AromaUnitSignalBinaryFile`.

Usage

```
CrlmmParametersFile(...)
```

Arguments

`...`	Arguments passed to `AromaUnitSignalBinaryFile`.

Fields and Methods

Methods:

`allocate`	-
`findUnitsTodo`	-
`readParameter`	-
`updateParameter`	-

Methods inherited from AromaUnitSignalBinaryFile:
allocate, allocateFromUnitAnnotationDataFile, allocateFromUnitNamesFile, as.character, extractMatrix, extractRawGenomicSignals, fromFile, getChipType, getExtensionPattern, getFilenameExtension, getNumberOfFilesAveraged, getPlatform, isAverageFile, nbrOfUnits, readDataFrame, writeDataFrame

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaTabularBinaryFile:
[, [<-, [[, allocate, as.character, colApply, colMeans, colStats, colSums, dimnames<-, getBytesPerColumn, getColClasses, getDefaultColumnNames, getRootName, importFrom, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, readFooter, readHeader, readRawFooter, setAttributesByTags, subset, summary, updateData, updateDataColumn, writeFooter, writeRawFooter

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericTabularFile:
[, as.character, dim, extractMatrix, head, nbrOfColumns, nbrOfRows, readColumns, readDataFrame, tail, writeColumnsToFiles

Methods inherited from ColumnNamesInterface:
appendColumnNamesTranslator, appendColumnNamesTranslatorByNULL, appendColumnNamesTranslatorBycharacter, appendColumnNamesTranslatorByfunction, appendColumnNamesTranslatorBylist, clearColumnNamesTranslator, clearListOfColumnNamesTranslators, getColumnNames, getColumnNamesTranslator, getDefaultColumnNames, getListOfColumnNamesTranslators, nbrOfColumns, setColumnNames, setColumnNamesTranslator, setListOfColumnNamesTranslators, updateColumnNames

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`CrlmmParametersSet` *The CrlmmParametersSet class*

Description

Package: aroma.affymetrix
Class CrlmmParametersSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~+--GenericTabularFileSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaTabularBinarySet
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaUnitSignalBinarySet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CrlmmParametersSet
```

Directly known subclasses:

public static class **CrlmmParametersSet**
extends AromaUnitSignalBinarySet

An CrlmmParametersSet object represents a set of `CrlmmParametersFile`s with *identical* chip types.

Usage

```
CrlmmParametersSet(...)
```

Arguments

`...`	Arguments passed to `AromaUnitSignalBinarySet`.

Fields and Methods

Methods:

`byName`	-
`byPath`	-
`findUnitsTodo`	-

Methods inherited from AromaUnitSignalBinarySet:
byName, findByName, getAromaFullNameTranslatorSet, getAromaUgpFile, getChipType, getPlatform, validate, writeDataFrame

Methods inherited from AromaTabularBinarySet:
getDefaultFullName, getRootName, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, setAttributesByTags

Methods inherited from GenericTabularFileSet:
extractMatrix, calculateAverageColumnAcrossFiles

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorBy-

function, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`DChipCdfBinFile` *The DChipCdfBinFile class*

Description

Package: aroma.affymetrix
Class DChipCdfBinFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitAnnotationDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitNamesFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--DChipCdfBinFile
```

Directly known subclasses:

public abstract static class **DChipCdfBinFile**
extends *UnitNamesFile*

A DChipCdfBinFile object represents a DChip CDF.bin file.

Usage

```
DChipCdfBinFile(...)
```

Arguments

`...`	Arguments passed to `AffymetrixFile`.

Fields and Methods

Methods:

`byChipType`	-
`getChipType`	-
`getFileFormat`	-
`getHeader`	-
`getPlatform`	-
`getUnitNames`	-
`getUnitSizes`	-
`nbrOfCells`	-
`nbrOfUnits`	-
`readDataFrame`	-

Methods inherited from UnitNamesFile:
getUnitNames, indexOf, nbrOfUnits

Methods inherited from UnitAnnotationDataFile:
byChipType, getAromaUflFile, getAromaUgpFile, getChipType, getDefaultExtension, getPlatform, nbrOfUnits

Methods inherited from AromaPlatformInterface:

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`DChipDcpFile` *The DChipDcpFile class*

Description

Package: aroma.affymetrix
Class DChipDcpFile

```
Object
~~|
~~+--FullNameInterface
```

```
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--DChipDcpFile
```

Directly known subclasses:

public abstract static class **DChipDcpFile**
extends *AffymetrixFile*

A DChipDcpFile object represents a DChip DCP file.

Usage

```
DChipDcpFile(...)
```

Arguments

`...`	Arguments passed to `AffymetrixFile`.

Fields and Methods

Methods:

`dim`	-
`extractTheta`	-
`getCalls`	-
`getExcludes`	-
`getFileFormat`	-
`getHeader`	-
`getNormalizedIntensities`	-
`getRawIntensities`	-
`getThetaStds`	-
`getThetas`	-
`getThetasAB`	-
`hasMbeiData`	-
`hasNormalizedData`	-

`nbrOfCells`	-
`nbrOfUnits`	-

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

`DChipDcpSet`.

`DChipDcpSet` *The DChipDcpSet class*

Description

Package: aroma.affymetrix
Class DChipDcpSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--DChipDcpSet
```

Directly known subclasses:

public abstract static class **DChipDcpSet**
extends *AffymetrixFileSet*

A DChipDcpSet object represents a set of DChip DCP files for *identical* chip types.

Usage

```
DChipDcpSet(files=NULL, ...)
```

Arguments

`files`	A `list` of `DChipDcpFile`:s.
`...`	Not used.

Fields and Methods

Methods:

`as`	-
`as.DChipDcpSet`	-

`byName`	-
`exportTotalAndFracB`	-
`extractTheta`	-
`getCdfBin`	-
`getChipType`	-

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

`DChipDcpFile`.

`DChipGenomeInformation` *The DChipGenomeInformation class*

Description

Package: aroma.affymetrix
Class DChipGenomeInformation

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--GenomeInformation
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--DChipGenomeInformation
```

Directly known subclasses:

public abstract static class **DChipGenomeInformation**
extends *GenomeInformation*

This class represents dChip genome information files, which typically contains information about chromosomal locations of the units.

Usage

```
DChipGenomeInformation(...)
```

Arguments

`...`	Arguments passed to `GenomeInformation`.

Details

The dChip genome information files for various chip types can be downloaded from `https://sites.google.com/site/dchipsoft/`. Put each file in a directory named identically as the corresponding chip type under the *annotations/* directory, e.g. *annotations/Mapping50K_Hind240/50k hind genome info AfAm june 05 hg17.xls*. Note that dChip changes the filename and file format slightly between chip types, but currently the `*byChipType()` basically searches for files with names consisting of `"genome info"` or `"genome_info"`. At least for the most common chip types, there is no need to rename the files in order for this class to recognize them.

Fields and Methods

Methods:

`byChipType`	-
`readDataFrame`	-

Methods inherited from GenomeInformation:
as.character, byChipType, fromCdf, fromDataSet, getChipType, getChromosomeStats, getChromosomes, getData, getPositions, getUnitIndices, getUnitsOnChromosome, getUnitsOnChromosomes, isCompatibleWithCdf, nbrOfUnits, plotDensity, readDataFrame, verify

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`DChipQuantileNormalization`

The DChipQuantileNormalization class

Description

Package: aroma.affymetrix
Class DChipQuantileNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--QuantileNormalization
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--DChipQuantileNormalization
```

Directly known subclasses:

public static class **DChipQuantileNormalization**
extends QuantileNormalization

This class represents a special `QuantileNormalization` using smooth-splines.

Usage

```
DChipQuantileNormalization(..., robust=FALSE)
```

Arguments

`...`	Arguments passed to the constructor of `QuantileNormalization`.
`robust`	If `TRUE`, the normalization function is estimated robustly, otherwise not.

Details

This normalization method implements the two-pass algorithm described in Bengtsson et al. (2008).

Fields and Methods

Methods:

`process`	-

Methods inherited from QuantileNormalization:
findTargetDistributionFile, getParameters, process

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

References

[1] H. Bengtsson, R. Irizarry, B. Carvalho, & T.P. Speed. Estimation and assessment of raw copy numbers at the single locus level, Bioinformatics, 2008.

`DChipSnpInformation` *The DChipSnpInformation class*

Description

Package: aroma.affymetrix
Class DChipSnpInformation

```
Object
~~|
~~+--FullNameInterface
```

```
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--SnpInformation
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--DChipSnpInformation
```

Directly known subclasses:

public abstract static class **DChipSnpInformation**
extends *SnpInformation*

This class represents dChip genome information files, which typically contains information on nucleotide sequences and fragment lengths of the units.

Usage

`DChipSnpInformation(...)`

Arguments

`...`	Arguments passed to `SnpInformation`.

Details

The dChip SNP information files for various chip types can be downloaded from `https://sites.google.com/site/dchipsoft/`. Put each file in a directory named identically as the corresponding chip type under the *annotations/* directory, e.g. *annotations/Mapping50K_Hind240/50k hind snp info AfAm june 05 hg17.xls*. Note that dChip changes the filename and file format slightly between chip types, but currently the `*byChipType()` basically searches for files with names consisting of `"snp info"` or `"snp_info"`. At least for the most common chip types, there is no need to rename the files in order for this class to recognize them.

Fields and Methods

Methods:

`byChipType`	-
`readDataFrame`	-

Methods inherited from SnpInformation:

as.character, byChipType, fromCdf, fromDataSet, getChipType, getData, getFields, getFragmentLengths, getFragmentStarts, getFragmentStops, isCompatibleWithCdf, nbrOfEnzymes, nbrOfUnits, readDataFrame, verify

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`doCRMAv1` *Estimation and assessment of raw copy numbers at the single locus level (CRMA v1)*

Description

Estimation and assessment of raw copy numbers at the single locus level (CRMA v1) based on [1]. The algorithm is processed in bounded memory, meaning virtually any number of arrays can be analyzed on also very limited computer systems.

Usage

```
  ## S3 method for class 'AffymetrixCelSet'
doCRMAv1(csR, shift=+300, combineAlleles=TRUE, lengthRange=NULL, arrays=NULL, drop=TRUE,
  verbose=FALSE, ...)
  ## Default S3 method:
doCRMAv1(dataSet, ..., verbose=FALSE)
  ## Default S3 method:
doASCRMAv1(...)
```

Arguments

`csR, dataSet`	An `AffymetrixCelSet` (or the name of an `AffymetrixCelSet`).
`shift`	An tuning parameter specifying how much to shift the probe signals before probe summarization.
`combineAlleles`	A `logical` specifying whether allele probe pairs should be summed before modeling or not.
`lengthRange`	An optional `numeric` vector of length two passed to `FragmentLengthNormalization`.
`arrays`	A `integer` `vector` specifying the subset of arrays to process. If `NULL`, all arrays are considered.
`drop`	If `TRUE`, the summaries are returned, otherwise a named `list` of all intermediate and final results.
`verbose`	See `Verbose`.
`...`	Additional arguments used to set up `AffymetrixCelSet` (when argument `dataSet` is specified).

Value

Returns a named `list`, iff `drop == FALSE`, otherwise only `ChipEffectSet` object.

Allele-specific or only total-SNP signals

If you wish to obtain allele-specific estimates for SNPs, which are needed to call genotypes or infer parent-specific copy numbers, then use argument `combineAlleles=FALSE`. Total copy number signals are still available. If you know for certain that you will not use allele-specific estimates, you will get slightly less noisy signals (very small difference) if you use `combineAlleles=TRUE`.

`doASCRMAv1(...)` is a wrapper for `doCRMAv1(..., combineAlleles=FALSE)`.

Author(s)

Henrik Bengtsson

References

[1] H. Bengtsson, R. Irizarry, B. Carvalho & T.P. Speed. *Estimation and assessment of raw copy numbers at the single locus level*, Bioinformatics, 2008.

See Also

For CRMA v2 (recommended by authors), which is a single-array improvement over CRMA v1, see `doCRMAv2`().

---

doCRMAv2 *A single-array preprocessing method for estimating full-resolution raw copy numbers from all Affymetrix genotyping arrays (CRMA v2)*

Description

A single-array preprocessing method for estimating full-resolution raw copy numbers from all Affymetrix genotyping arrays (CRMA v2) based on [1]. The algorithm is processed in bounded memory, meaning virtually any number of arrays can be analyzed on also very limited computer systems.

We recommend CRMA v2 for estimating allele-specific as well total SNP signals from Affymetrix SNP chips.

Usage

```
  ## S3 method for class 'AffymetrixCelSet'
doCRMAv2(csR, combineAlleles=TRUE, lengthRange=NULL, arrays=NULL,
  plm=c("AvgCnPlm", "RmaCnPlm"), drop=TRUE, verbose=FALSE, ...)
  ## Default S3 method:
doCRMAv2(dataSet, ..., verbose=FALSE)
  ## Default S3 method:
doASCRMAv2(...)
```

Arguments

`csR, dataSet`	An `AffymetrixCelSet` (or the name of an `AffymetrixCelSet`).
`combineAlleles`	A `logical` specifying whether allele probe pairs should be summed before modeling or not.
`lengthRange`	An optional `numeric` vector of length two passed to `FragmentLengthNormalization`.
`arrays`	A `integer` `vector` specifying the subset of arrays to process. If `NULL`, all arrays are considered.
`plm`	A `character` string specifying which type of probe-summarization model to used.
`drop`	If `TRUE`, the summaries are returned, otherwise a named `list` of all intermediate and final results.
`verbose`	See `Verbose`.
`...`	Additional arguments used to set up `AffymetrixCelSet` (when argument `dataSet` is specified).

Value

Returns a named `list`, iff `drop == FALSE`, otherwise only `ChipEffectSet` object.

Allele-specific or only total-SNP signals

If you wish to obtain allele-specific estimates for SNPs, which are needed to call genotypes or infer parent-specific copy numbers, then use argument `combineAlleles=FALSE`. Total copy number signals are still available. If you know for certain that you will not use allele-specific estimates, you will get slightly less noisy signals (very small difference) if you use `combineAlleles=TRUE`.

`doASCRMAv2(...)` is a wrapper for `doCRMAv2(..., combineAlleles=FALSE)`.

Author(s)

Henrik Bengtsson

References

[1] H. Bengtsson, P. Wirapati & T.P. Speed. *A single-array preprocessing method for estimating full-resolution raw copy numbers from all Affymetrix genotyping arrays including GenomeWideSNP 5 & 6*, Bioinformatics, 2009.

See Also

For CRMA v1, which is a multi-array methods that precedes CRMA v2, see `doCRMAv1`().

`doFIRMA` *Finding Isoforms using Robust Multichip Analysis (FIRMA)*

Description

Finding Isoforms using Robust Multichip Analysis (FIRMA) based on [1].

Usage

```
  ## S3 method for class 'AffymetrixCelSet'
doFIRMA(csR, ..., flavor=c("v1b", "v1a"), drop=TRUE, verbose=FALSE)
  ## Default S3 method:
doFIRMA(dataSet, ..., verbose=FALSE)
```

Arguments

`csR, dataSet`	An `AffymetrixCelSet` (or the name of an `AffymetrixCelSet`).
`...`	Additional arguments passed to `FirmaModel`, and to set up `AffymetrixCelSet` (when argument `dataSet` is specified).
`flavor`	A `character` string specifying the flavor of FIRMA to use.

`drop`	If `TRUE`, the FIRMA scores are returned, otherwise a named `list` of all intermediate and final results.
`verbose`	See `Verbose`.

Value

Returns a named `list`, iff `drop == FALSE`, otherwise only `FirmaSet` object (containing the FIRMA scores).

Using a custom exon-by-transcript CDF

It is strongly recommended to use a custom CDF, e.g. "core", "extended" or "full" [1]. To use a custom CDF, set it before calling this method, i.e. `setCdf(csR, cdf)`. Do not set the standard "non-supported" Affymetrix CDF (see also Section 'Flavors').

Flavors

If `flavor == "v1b"` (default), then the standard "non-supported" Affymetrix CDF is used for background correction and the quantile normalization steps, and the custom CDF is used for the probe summarization and everything that follows. The advantage of this flavor is that those two first preprocessing steps will remain the same if one later changes to a different custom CDF.

If `flavor == "v1a"`, then the custom CDF is used throughout all steps of FIRMA, which means that if one changes the custom CDF all steps will be redone.

Author(s)

Henrik Bengtsson

References

[1] E. Purdom, K. Simpson, M. Robinson, J. Conboy, A. Lapuk & T.P. Speed, *FIRMA: a method for detection of alternative splicing from exon array data*, Bioinformatics, 2008.

`doGCRMA` *Robust Multichip Analysis (GCRMA)*

Description

Robust Multichip Analysis (GCRMA) based on [1]. The algorithm is processed in bounded memory, meaning virtually any number of arrays can be analyzed on also very limited computer systems. The method replicates the results of `gcrma` (package **gcrma**) with great precision.

Usage

```
  ## S3 method for class 'AffymetrixCelSet'
doGCRMA(csR, arrays=NULL, type=c("fullmodel", "affinities"), uniquePlm=FALSE, drop=TRUE,
  verbose=FALSE, ...)
  ## Default S3 method:
doGCRMA(dataSet, ..., verbose=FALSE)
```

Arguments

`csR, dataSet`	An `AffymetrixCelSet` (or the name of an `AffymetrixCelSet`).
`arrays`	A `integer` `vector` specifying the subset of arrays to process. If `NULL`, all arrays are considered.
`type`	A `character` string specifying what type of model to use for the GCRMA background correction. For more details, see `GcRmaBackgroundCorrection`.
`uniquePlm`	If `TRUE`, the log-additive probe-summarization model is done on probeset with *unique* sets of probes. If `FALSE`, the summarization is done on "as-is" probesets as specified by the CDF.
`drop`	If `TRUE`, the summaries are returned, otherwise a named `list` of all intermediate and final results.
`verbose`	See `Verbose`.
`...`	Additional arguments used to set up `AffymetrixCelSet` (when argument `dataSet` is specified).

Value

Returns a named `list`, iff `drop` == `FALSE`, otherwise only `ChipEffectSet` object.

Author(s)

Henrik Bengtsson

References

[1] Z. Wu, R. Irizarry, R. Gentleman, F.M. Murillo & F. Spencer. *A Model Based Background Adjustment for Oligonucleotide Expression Arrays*, JASA, 2004.

`doRMA` *Robust Multichip Analysis (RMA)*

Description

Robust Multichip Analysis (RMA) based on [1]. The algorithm is processed in bounded memory, meaning virtually any number of arrays can be analyzed on also very limited computer systems. The method replicates the results of `fitPLM` (package **affyPLM**) with great precision.

Usage

```
  ## S3 method for class 'AffymetrixCelSet'
doRMA(csR, arrays=NULL, flavor=c("affyPLM", "oligo"), uniquePlm=FALSE, drop=TRUE,
  verbose=FALSE, ...)
  ## Default S3 method:
doRMA(dataSet, ..., verbose=FALSE)
```

Arguments

`csR, dataSet`	An `AffymetrixCelSet` (or the name of an `AffymetrixCelSet`).
`arrays`	A `integer` `vector` specifying the subset of arrays to process. If `NULL`, all arrays are considered.
`flavor`	A character string specifying what model fitting algorithm to be used, cf. `RmaPlm`.
`uniquePlm`	If `TRUE`, the log-additive probe-summarization model is done on probeset with *unique* sets of probes. If `FALSE`, the summarization is done on "as-is" probesets as specified by the CDF.
`drop`	If `TRUE`, the summaries are returned, otherwise a named `list` of all intermediate and final results.
`verbose`	See `Verbose`.
`...`	Additional arguments used to set up `AffymetrixCelSet` (when argument `dataSet` is specified).

Value

Returns a named `list`, iff `drop` == `FALSE`, otherwise only `ChipEffectSet` object.

Author(s)

Henrik Bengtsson

References

[1] Irizarry et al. *Summaries of Affymetrix GeneChip probe level data.* NAR, 2003, 31, e15.

`ExonChipEffectFile` *The ExonChipEffectFile class*

Description

Package: aroma.affymetrix
Class ExonChipEffectFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ChipEffectFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ExonChipEffectFile
```

Directly known subclasses:

public abstract static class **ExonChipEffectFile**
extends *ChipEffectFile*

This class represents estimates of chip effects in the probe-level models.

Usage

```
ExonChipEffectFile(..., mergeGroups=FALSE)
```

Arguments

`...`	Arguments passed to `ChipEffectFile`.
`mergeGroups`	Specifies if the groups are merged or not for these estimates.

Fields and Methods

Methods:

```
readUnits  -
```

Methods inherited from ChipEffectFile:
as.character, extractChromosomalDataFrame, extractMatrix, extractTheta, findUnitsTodo, getAM, getAsFullCelFile, getCellIndices, getCellMapForMainCdf, getExpandedCellMap, getParameters, getUnitGroupCellArrayMap, getUnitGroupCellMatrixMap, getXAM, mergeGroups, readUnits, writeAsFullCelFile

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags,

hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

See Also

An object of this class is typically part of a `ExonChipEffectSet`.

`ExonChipEffectSet` *The ExonChipEffectSet class*

Description

Package: aroma.affymetrix
Class ExonChipEffectSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ChipEffectSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ExonChipEffectSet
```

Directly known subclasses:

public static class **ExonChipEffectSet**
extends ChipEffectSet

This class represents estimates of chip effects in the probe-level models.

Usage

```
ExonChipEffectSet(..., mergeGroups=TRUE)
```

Arguments

`...`	Arguments passed to `ChipEffectSet`.
`mergeGroups`	Specifies if groups (individual exons in a CDF file) are merged or not for these estimates, i.e. whether transcript-level expression is to be estimated.

Fields and Methods

Methods:

`findUnitsTodo`	-
`getAverageFile`	-
`getMergeGroups`	-
`setMergeGroups`	-

Methods inherited from ChipEffectSet:
as.character, boxplotStats, byPath, calculateBaseline, calculateFieldBoxplotStats, calculateNuseBoxplotStats, calculateRleBoxplotStats, extractAffyBatch, extractChromosomalDataFrame, extractExpressionSet, extractMatrix, extractTheta, findByName, findUnitsTodo, fromDataSet, getAM, getAsFullCelSet, getAverageFile, getBaseline, getCellIndices, getXAM, plotBoxplot, readUnits, updateUnits

Methods inherited from ParameterCelSet:
extractDataFrame, extractMatrix

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelSet:
append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

`ExonProbeAffinityFile` *The ExonProbeAffinityFile class*

Description

Package: aroma.affymetrix
Class ExonProbeAffinityFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ProbeAffinityFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ExonProbeAffinityFile
```

Directly known subclasses:

public abstract static class **ExonProbeAffinityFile**
extends *ProbeAffinityFile*

This class represents estimates of probe affinities in exon array probe-level models.

Usage

```
ExonProbeAffinityFile(..., mergeGroups=FALSE)
```

Arguments

`...`	Arguments passed to `ProbeAffinityFile`.
`mergeGroups`	Specifies if the groups (exons) are merged or not for these estimates.

Fields and Methods

Methods:
No methods defined.

Methods inherited from ProbeAffinityFile:
as.character, getCellIndices, getParameters, readUnits

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

`ExonRmaPlm` *The ExonRmaPlm class*

Description

Package: aroma.affymetrix
Class ExonRmaPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ExonRmaPlm
```

Directly known subclasses:

public abstract static class **ExonRmaPlm**
extends *RmaPlm*

This class represents the log-additive model part of the Robust Multichip Analysis (RMA) method described in Irizarry et al (2003), as implemented for exon arrays. The model may be fitted with exons merged into transcripts (all probes fitted together) or on an individual exon basis (probes within an exon treated as a group, but exons fitted separately).

Usage

```
ExonRmaPlm(..., mergeGroups=TRUE)
```

Arguments

`...`	Arguments passed to `RmaPlm`.
`mergeGroups`	A `logical` flag specifying whether to merge exons into transcripts.

Fields and Methods

Methods:

`getCellIndices`	-
`getChipEffectSet`	-
`getProbeAffinityFile`	-
`setMergeGroups`	-

Methods inherited from RmaPlm:
getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Model

`RmaPlm`.

Author(s)

Ken Simpson, Henrik Bengtsson, Elizabeth Purdom

References

Irizarry et al. *Summaries of Affymetrix GeneChip probe level data*. NAR, 2003, 31, e15.

`FirmaFile` *The FirmaFile class*

Description

Package: aroma.affymetrix
Class FirmaFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FirmaFile
```

Directly known subclasses:

public abstract static class **FirmaFile**
extends *ParameterCelFile*

This class represents scores calculated by the FIRMA algorithm.

Usage

```
FirmaFile(...)
```

Arguments

`...`	Arguments passed to `AffymetrixCelFile`.

Fields and Methods

Methods:

`extractMatrix`	-
`findUnitsTodo`	-
`readUnits`	-

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

See Also

An object of this class is typically part of a `FirmaSet`.

`FirmaModel` *The FirmaModel class*

Description

Package: aroma.affymetrix
Class FirmaModel

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FirmaModel
```

Directly known subclasses:

public abstract static class **FirmaModel**
extends *UnitModel*

This class represents the FIRMA (Finding Isoforms using RMA) alternative splicing model.

Usage

```
FirmaModel(rmaPlm=NULL, summaryMethod=c("median", "upperQuartile", "max"),
  operateOn=c("residuals", "weights"), ...)
```

Arguments

`rmaPlm`	An @RmaPlm object.
`summaryMethod`	A `character` specifying what summarization method should be used.
`operateOn`	A `character` specifying what statistic to operate on.
`...`	Arguments passed to constructor of `UnitModel`.

Fields and Methods

Methods:

`fit`	-
`getCdf`	-
`getDataSet`	-
`getFirmaSet`	-
`getName`	-
`getPlm`	-
`getTags`	-

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

`FirmaSet` *The FirmaSet class*

Description

Package: aroma.affymetrix
Class FirmaSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--FirmaSet
```

Directly known subclasses:

public static class **FirmaSet**
extends ParameterCelSet

Usage

```
FirmaSet(...)
```

Arguments

`...`	Arguments passed to constructor of `AffymetrixCelSet`.

Fields and Methods

Methods:

`extractMatrix`	-
`findUnitsTodo`	-
`getCellIndices`	-
`readUnits`	-

Methods inherited from ParameterCelSet:
extractDataFrame, extractMatrix

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelSet:
append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

`FragmentEquivalentClassNormalization`

The FragmentEquivalentClassNormalization class

Description

Package: aroma.affymetrix
Class FragmentEquivalentClassNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ChipEffectTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--FragmentEquivalentClassNormalization
```

Directly known subclasses:

public static class **FragmentEquivalentClassNormalization**
extends *ChipEffectTransform*

This class represents a normalization method that corrects for systematic effects between loci of different equivalent classes of pairs of sequences that are recognized by the restriction enzymes that cut the DNA studies.

Usage

```
FragmentEquivalentClassNormalization(dataSet=NULL, ..., targetAvgs=NULL,
  subsetToFit="-XY")
```

Arguments

`dataSet`	A `CnChipEffectSet`.
`...`	Additional arguments passed to the constructor of `ChipEffectTransform`.
`targetAvgs`	An optional list of `function`s. For each enzyme there is one target averages to which all arrays should be normalized to.
`subsetToFit`	The units from which the normalization curve should be estimated. If `NULL`, all are considered.

Fields and Methods

Methods:

`getAromaUfcFile`	-
`getCdf`	-
`process`	-

Methods inherited from ChipEffectTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Requirements

This class requires an UFC (Unit Fragment Class) annotation file.

Acknowledgments

The idea of normalization signals stratified on enzyme recognition sequences is credited to Jim Veitch and Ben Bolstad at Affymetrix Inc. (2008) who have designed a similar method for copy number estimation in the Affymetrix' Genotype Console v2.

Author(s)

Henrik Bengtsson

`FragmentLengthNormalization`

The FragmentLengthNormalization class

Description

Package: aroma.affymetrix
Class FragmentLengthNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ChipEffectTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--FragmentLengthNormalization
```

Directly known subclasses:

public static class **FragmentLengthNormalization**
extends *ChipEffectTransform*

This class represents a normalization method that corrects for PCR fragment length effects on copy-number chip-effect estimates.

Usage

```
FragmentLengthNormalization(dataSet=NULL, ..., target=targetFunctions, subsetToFit="-XY",
  lengthRange=NULL, onMissing=c("median", "ignore"), shift=0, targetFunctions=NULL)
```

Arguments

`dataSet`	A `SnpChipEffectSet`.
`...`	Additional arguments passed to the constructor of `ChipEffectTransform`.
`target`	(Optional) A `character` string or a list of `functions` specifying what to normalize toward. For each enzyme there is one target function to which all arrays should be normalized to.
`subsetToFit`	The units from which the normalization curve should be estimated. If `NULL`, all are considered.
`lengthRange`	If given, a `numeric` `vector` of length 2 specifying the range of fragment lengths considered. All fragments with lengths outside this range are treated as if they were missing.
`onMissing`	Specifies how to normalize units for which the fragment lengths are unknown.
`shift`	An optional amount the data points should be shifted (translated).
`targetFunctions`	Deprecated.

Details

For SNPs, the normalization function is estimated based on the total chip effects, i.e. the sum of the allele signals. The normalizing is done by rescale the chip effects on the intensity scale such that the mean of the total chip effects are the same across samples for any given fragment length. For allele-specific estimates, both alleles are always rescaled by the same amount. Thus, when normalizing allele-specific chip effects, the total chip effects is change, but not the relative allele signal, e.g. the allele B frequency.

Fields and Methods

Methods:

`getCdf`	-
`process`	-

Methods inherited from ChipEffectTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Requirements

This class requires a SNP information annotation file for the chip type to be normalized.

Author(s)

Henrik Bengtsson

`GcContentNormalization`

The GcContentNormalization class

Description

Package: aroma.affymetrix
Class GcContentNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ChipEffectTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--GcContentNormalization
```

Directly known subclasses:

public static class **GcContentNormalization**
extends *ChipEffectTransform*

Usage

```
GcContentNormalization(dataSet=NULL, ..., targetFunction=NULL, subsetToFit=NULL)
```

Arguments

`dataSet`	A `CnChipEffectSet`.
`...`	Additional arguments passed to the constructor of `ChipEffectTransform`.
`targetFunction`	A `function`. The target function to which all arrays should be normalized to.
`subsetToFit`	The units from which the normalization curve should be estimated. If `NULL`, all are considered.

Fields and Methods

Methods:

`getCdf`	-
`process`	-

Methods inherited from ChipEffectTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Requirements

This class requires an Aroma unit GC-content (UGC) file.

Author(s)

Henrik Bengtsson

`GcContentNormalization2`

The GcContentNormalization2 class

Description

Package: aroma.affymetrix
Class GcContentNormalization2

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ChipEffectTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AdditiveCovariatesNormalization
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--GcContentNormalization2
```

Directly known subclasses:

public static class **GcContentNormalization2**
extends *AdditiveCovariatesNormalization*

This class represents a normalization method that corrects for annotation-data covariate effects on copy-number chip-effect estimates.

Usage

```
GcContentNormalization2(...)
```

Arguments

`...`	Arguments passed to the constructor of `AdditiveCovariatesNormalization`.

Fields and Methods

Methods:

`plotCovariateEffects`	-

Methods inherited from AdditiveCovariatesNormalization:
getAsteriskTags, getCdf, getCovariates, getOutputDataSet00, getParameters, process

Methods inherited from ChipEffectTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`GcRmaBackgroundCorrection`

The GcRmaBackgroundCorrection class

Description

Package: aroma.affymetrix
Class GcRmaBackgroundCorrection

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--BackgroundCorrection
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--GcRmaBackgroundCorrection
```

Directly known subclasses:

public static class **GcRmaBackgroundCorrection**
extends *BackgroundCorrection*

This class represents the GCRMA background adjustment function.

Usage

```
GcRmaBackgroundCorrection(..., indicesNegativeControl=NULL, affinities=NULL,
  type=c("fullmodel", "affinities"), opticalAdjust=TRUE, gsbAdjust=TRUE,
  gsbParameters=NULL, seed=NULL)
```

Arguments

`...`	Arguments passed to the constructor of `ProbeLevelTransform`.
`indicesNegativeControl`	Locations of any negative control probes (e.g., the anti-genomic controls on the human exon array). If `NULL` and `type == "affinities"`, then all non-PM probes are used as the negative controls.

`affinities`	A `numeric` `vector` of probe affinities, usually as calculated by `computeAffinities()` of the `AffymetrixCdfFile` class.
`type`	Type (flavor) of background correction, which can be either `"fullmodel"` (uses MMs; requires that the chip type has PM/MM pairs) or `"affinities"` (uses probe sequence only).
`gsbAdjust`	If `TRUE`, adjustment for specific binding is done, otherwise not.
`opticalAdjust`	If `TRUE`, correction for optical effect is done first, utilizing `OpticalBackgroundCorrection`.
`gsbParameters`	Additional argument passed to the internal `bgAdjustGcrma()` method.
`seed`	An (optional) `integer` specifying a temporary random seed to be used during processing. The random seed is set to its original state when done. If `NULL`, it is not set.

Fields and Methods

Methods:

`process` -

Methods inherited from BackgroundCorrection:
getParameters, process

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

References

[1] Z. Wu, R. Irizarry, R. Gentleman, F.M. Murillo & F. Spencer. *A Model Based Background Adjustment for Oligonucleotide Expression Arrays*, JASA, 2004.

`GenericReporter` *The GenericReporter class*

Description

Package: aroma.affymetrix
Class GenericReporter

```
Object
~~|
~~+--GenericReporter
```

Directly known subclasses:
AffymetrixCelSetReporter, *AffymetrixFileSetReporter*, *SpatialReporter*

public abstract static class **GenericReporter**
extends Object

Usage

```
GenericReporter(tags="*", ...)
```

Arguments

`tags`	A `character` `vector` of tags to be added to the output path.
`...`	Not used.

Fields and Methods

Methods:

`getFullName`	-
`getName`	-
`getPath`	-
`getTags`	-
`process`	-
`setup`	-

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`GenomeInformation` *The GenomeInformation class*

Description

Package: aroma.affymetrix
Class GenomeInformation

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--GenomeInformation
```

Directly known subclasses:
AffymetrixCsvGenomeInformation, *DChipGenomeInformation*, *UgpGenomeInformation*

public abstract static class **GenomeInformation**
extends FileCacheKeyInterface

Usage

```
GenomeInformation(..., .verify=TRUE)
```

Arguments

`...`	Arguments passed to `GenericDataFile`.
`.verify`	For internal use only.

Fields and Methods

Methods:

`byChipType`	-
`getChipType`	-

`getChromosomeStats`	-
`getChromosomes`	-
`getData`	-
`getPositions`	-
`getUnitsOnChromosome`	-
`getUnitsOnChromosomes`	-
`nbrOfUnits`	-
`plotDensity`	-

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`HetLogAddCnPlm` *The HetLogAddCnPlm class*

Description

Package: aroma.affymetrix
Class HetLogAddCnPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--HetLogAddPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--HetLogAddSnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CnPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--HetLogAddCnPlm
```

Directly known subclasses:

public abstract static class **HetLogAddCnPlm**
extends CnPlm

Usage

```
HetLogAddCnPlm(..., combineAlleles=FALSE)
```

Arguments

`...`	Arguments passed to `HetLogAddCnPlm`.
`combineAlleles`	If `FALSE`, allele A and allele B are treated separately, otherwise together.

Fields and Methods

Methods:
No methods defined.

Methods inherited from CnPlm:
getCellIndices, getChipEffectSet, getCombineAlleles, getParameters, getProbeAffinityFile, setCombineAlleles

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from HetLogAddSnpPlm:
getAsteriskTags

Methods inherited from HetLogAddPlm:
getAsteriskTags, getFitUnitGroupFunction

Methods inherited from RmaPlm:
getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Model

TO DO.

Author(s)

Henrik Bengtsson

`HetLogAddPlm` *The HetLogAddPlm class*

Description

Package: aroma.affymetrix
Class HetLogAddPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--HetLogAddPlm
```

Directly known subclasses:
HetLogAddCnPlm, *HetLogAddSnpPlm*

public abstract static class **HetLogAddPlm**
extends *RmaPlm*

This class represents a log-additive model similar to the one described in Irizarry et al (2003), except that the errors may have different variances for different probes.

Usage

```
HetLogAddPlm(...)
```

Arguments

`...`	Arguments passed to `RmaPlm`.

Fields and Methods

Methods:
No methods defined.

Methods inherited from RmaPlm:
getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

`RmaPlm`.

`HetLogAddSnpPlm` *The HetLogAddSnpPlm class*

Description

Package: aroma.affymetrix
Class HetLogAddSnpPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--HetLogAddPlm
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--HetLogAddSnpPlm
```

Directly known subclasses:
HetLogAddCnPlm

public abstract static class **HetLogAddSnpPlm**
extends SnpPlm

Usage

```
HetLogAddSnpPlm(..., mergeStrands=FALSE)
```

Arguments

`...`	Arguments passed to `HetLogAddPlm`.
`mergeStrands`	If `TRUE`, the sense and the anti-sense strands are fitted together, otherwise separately.

Fields and Methods

Methods:
No methods defined.

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from HetLogAddPlm:
getAsteriskTags, getFitUnitGroupFunction

Methods inherited from RmaPlm:
getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`justRMA` *Robust Multichip Analysis (RMA) reproducing the affy package*

Description

Robust Multichip Analysis (RMA) reproducing the affy package as far as possible. The RMA method is described in [1].

The algorithm is processed in bounded memory, meaning a very large number of arrays can be analyzed on also very limited computer systems. The only limitation is the amount of memory required to load the final chip-effect estimates into memory (as a `ExpressionSet`).

Usage

```
  ## S3 method for class 'AffymetrixCelSet'
justRMA(csR, flavor=c("oligo", "affyPLM"), ..., verbose=FALSE)
  ## Default S3 method:
justRMA(...)
```

Arguments

`csR`	An `AffymetrixCelSet`.
`flavor`	A `character` string specifying the estimators used in the RMA summarization step.
`...`	Additional arguments passed to `doRMA`() used internally.
`verbose`	See `Verbose`.

Value

Returns an annotated `ExpressionSet`.

Reproducibility of affy

This implementation of the RMA method reproduces `justRMA` in **affy** package quite well. It does so by still using a constant memory profile, i.e. it is possible to use this implementation to run RMA on a much large data set than what is possible with **affy**. At least 20-50 *times* more samples should be doable, if not more.

Author(s)

Henrik Bengtsson

References

[1] Irizarry et al. *Summaries of Affymetrix GeneChip probe level data*. NAR, 2003, 31, e15.

See Also

`doRMA`().

`LimmaBackgroundCorrection` *The LimmaBackgroundCorrection class*

Description

Package: aroma.affymetrix
Class LimmaBackgroundCorrection

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--BackgroundCorrection
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--LimmaBackgroundCorrection
```

Directly known subclasses:
NormExpBackgroundCorrection

public static class **LimmaBackgroundCorrection**
extends *BackgroundCorrection*

This class represents the various "background" correction methods implemented in the **limma** package.

Usage

```
LimmaBackgroundCorrection(..., args=NULL, addJitter=FALSE, jitterSd=0.2, seed=6022007)
```

Arguments

`...`	Arguments passed to the constructor of `BackgroundCorrection`.
`args`	A `list` of additional arguments passed to the correction algorithm.
`addJitter`	If `TRUE`, Zero-mean gaussian noise is added to the signals before being background corrected.
`jitterSd`	Standard deviation of the jitter noise added.
`seed`	An (optional) `integer` specifying a temporary random seed to be used for generating the (optional) jitter. The random seed is set to its original state when done. If `NULL`, it is not set.

Details

By default, only PM signals are background corrected and MMs are left unchanged.

Fields and Methods

Methods:

`process` -

Methods inherited from BackgroundCorrection:
getParameters, process

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Jitter noise

The fitting algorithm of the normal+exponential background correction model may not converge if there too many small and discrete signals. To overcome this problem, a small amount of noise may be added to the signals before fitting the model. This is an ad hoc solution that seems to work. However, adding Gaussian noise may generate non-positive signals.

Author(s)

Henrik Bengtsson. Adopted from RmaBackgroundCorrection by Ken Simpson.

See Also

Internally, `backgroundCorrect` is used.

`LinearModelProbeSequenceNormalization` *The LinearModelProbeSequenceNormalization class*

Description

Package: aroma.affymetrix
Class LinearModelProbeSequenceNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelTransform3
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AbstractProbeSequenceNormalization
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--LinearModelProbeSequenceNormalization
```

Directly known subclasses:
BasePositionNormalization

public abstract static class **LinearModelProbeSequenceNormalization**
extends *AbstractProbeSequenceNormalization*

This abstract class represents a normalization method that corrects for systematic effects in the probe intensities due to probe-sequence dependent effects that can be modeled using a linear model.

Usage

```
LinearModelProbeSequenceNormalization(...)
```

Arguments

`...`	Arguments passed to the constructor of `AbstractProbeSequenceNormalization`.

Fields and Methods

Methods:
No methods defined.

Methods inherited from AbstractProbeSequenceNormalization:
fitOne, getAromaCellSequenceFile, getParameters, getTargetFile, indexOfMissingSequences, predictOne, process

Methods inherited from ProbeLevelTransform3:
getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Requirements

This class requires that an aroma probe sequence file is available for the chip type.

Memory usage

The model fitting methods of this class are bounded in memory. This is done by first building up the normal equations incrementally in chunks of cells. The generation of normal equations is otherwise the step that consumes the most memory. When the normal equations are available, the `solve`() method is used to solve the equations. Note that this algorithm is still exact.

Author(s)

Henrik Bengtsson

`MatNormalization` *The MatNormalization class*

Description

Package: aroma.affymetrix
Class MatNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelTransform3
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AbstractProbeSequenceNormalization
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--MatNormalization
```

Directly known subclasses:

public static class **MatNormalization**
extends *AbstractProbeSequenceNormalization*

This class represents a normalization method that corrects for systematic effects in the probe intensities due to differences in the number of A, C, G, and T:s and the match scores according to MAT [1].

Usage

```
MatNormalization(..., unitsToFit=NULL, model=c("lm"), nbrOfBins=200)
```

Arguments

`...`	Arguments passed to the constructor of `AbstractProbeSequenceNormalization`.
`unitsToFit`	The units from which the normalization curve should be estimated. If `NULL`, all are considered.
`model`	A `character` string specifying the model used to fit the base-count effects.
`nbrOfBins`	The number of bins to use for the variance smoothing step.

Fields and Methods

Methods:

`process` -

Methods inherited from AbstractProbeSequenceNormalization:
fitOne, getAromaCellSequenceFile, getParameters, getTargetFile, indexOfMissingSequences, predictOne, process

Methods inherited from ProbeLevelTransform3:
getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Requirements

This class requires that an aroma probe sequence file and aroma match scores file is available for the chip type.

Author(s)

Mark Robinson

References

[1] Johnson WE, Li W, Meyer CA, Gottardo R, Carroll JS, Brown M, Liu XS. *Model-based analysis of tiling-arrays for ChIP-chip*, PNAS, 2006.

`MatSmoothing` *The MatSmoothing class*

Description

Package: aroma.affymetrix
Class MatSmoothing

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--MatSmoothing
```

Directly known subclasses:

public static class **MatSmoothing**
extends *ProbeLevelTransform*

This class represents a function for smoothing data with a trimmed mean.

Usage

```
MatSmoothing(..., design=NULL, probeWindow=300, nProbes=10, meanTrim=0.1)
```

Arguments

`...`	Arguments passed to `ProbeLevelTransform`.
`design`	A design `matrix`.
`probeWindow`	Bandwidth to use. Effectively the width is 2*probeWindow since it looks probeWindow bases in either direction.
`nProbes`	The minimum number of probes to calculate a MAT score for.
`meanTrim`	The amount of trimming of the mean in [0,0.5].

Fields and Methods

Methods:

```
process  -
```

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Mark Robinson, Henrik Bengtsson

`MbeiCnPlm` *The MbeiCnPlm class*

Description

Package: aroma.affymetrix
Class MbeiCnPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--MbeiPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--MbeiSnpPlm
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CnPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--MbeiCnPlm
```

Directly known subclasses:

public abstract static class **MbeiCnPlm**
extends CnPlm

Usage

```
MbeiCnPlm(..., combineAlleles=FALSE)
```

Arguments

`...`	Arguments passed to `MbeiSnpPlm`.
`combineAlleles`	If `FALSE`, allele A and allele B are treated separately, otherwise together.

Fields and Methods

Methods:
No methods defined.

Methods inherited from CnPlm:
getCellIndices, getChipEffectSet, getCombineAlleles, getParameters, getProbeAffinityFile, setCombineAlleles

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from MbeiSnpPlm:
getAsteriskTags

Methods inherited from MbeiPlm:
getAsteriskTags, getFitUnitGroupFunction

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`MbeiPlm` *The MbeiPlm class*

Description

Package: aroma.affymetrix
Class MbeiPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--MbeiPlm
```

Directly known subclasses:
MbeiCnPlm, *MbeiSnpPlm*

public abstract static class **MbeiPlm**
extends *ProbeLevelModel*

This class represents the *model-based expression indexes* (MBEI) multiplicative model in Li & Wong (2001).

Usage

```
MbeiPlm(...)
```

Arguments

`...`	Arguments passed to `ProbeLevelModel`.

Fields and Methods

Methods:
No methods defined.

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Model

For a single unit group, the multiplicative model is:

$$y_{ik} = \theta_i \phi_k + \varepsilon_{ik}$$

where θ_i are the chip effects for arrays $i = 1, ..., I$, and ϕ_k are the probe affinities for probes $k = 1, ..., K$. The ε_{ik} are zero-mean noise with equal variance. To make to parameters identifiable, the constraint $\prod_k \phi_k = 1$ is added.

Author(s)

Henrik Bengtsson

References

Li, C. and Wong, W.H. (2001), Genome Biology 2, 1-11.
Li, C. and Wong, W.H. (2001), Proc. Natl. Acad. Sci USA 98, 31-36.

See Also

Internally `fit.li.wong` is used.

`MbeiSnpPlm` *The MbeiSnpPlm class*

Description

Package: aroma.affymetrix
Class MbeiSnpPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--MbeiPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--MbeiSnpPlm
```

Directly known subclasses:
MbeiCnPlm

public abstract static class **MbeiSnpPlm**
extends SnpPlm

Usage

```
MbeiSnpPlm(..., mergeStrands=FALSE)
```

Arguments

`...`	Arguments passed to `MbeiPlm`.
`mergeStrands`	If `TRUE`, the sense and the anti-sense strands are fitted together, otherwise separately.

Fields and Methods

Methods:
No methods defined.

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from MbeiPlm:
getAsteriskTags, getFitUnitGroupFunction

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`Model` *The Model class*

Description

Package: aroma.affymetrix
Class Model

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
```

Directly known subclasses:
AffineCnPlm, *AffinePlm*, *AffineSnpPlm*, *AlleleSummation*, *AvgCnPlm*, *AvgPlm*, *AvgSnpPlm*, CrlmmModel, *ExonRmaPlm*, *FirmaModel*, *HetLogAddCnPlm*, *HetLogAddPlm*, *HetLogAddSnpPlm*, *MbeiCnPlm*, *MbeiPlm*, *MbeiSnpPlm*, *MultiArrayUnitModel*, *ProbeLevelModel*, *RmaCnPlm*, *RmaPlm*, *RmaSnpPlm*, *SingleArrayUnitModel*, *UnitModel*

public abstract static class **Model**
extends ParametersInterface

This class is abstract and represents a generic model that applies to a data set.

Usage

```
Model(dataSet=NULL, tags="*", ..., .onUnknownArgs=c("error", "warning", "ignore"))
```

Arguments

`dataSet`	The data set to which this model should be fitted.
`tags`	A `character` `vector` of tags to be appended to the tags of the input data set.
`...`	Not used.
`.onUnknownArgs`	A `character` string specifying what should occur if there are unknown arguments in `...`.

Fields and Methods

Methods:

`fit`	-
`getAsteriskTags`	-
`getDataSet`	-
`getFullName`	-
`getName`	-
`getPath`	-
`getTags`	-
`setTags`	-

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`MultiArrayUnitModel` *The MultiArrayUnitModel class*

Description

Package: aroma.affymetrix
Class MultiArrayUnitModel

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
```

Directly known subclasses:
AffineCnPlm, *AffinePlm*, *AffineSnpPlm*, *AvgCnPlm*, *AvgPlm*, *AvgSnpPlm*, *ExonRmaPlm*, *HetLogAddCnPlm*, *HetLogAddPlm*, *HetLogAddSnpPlm*, *MbeiCnPlm*, *MbeiPlm*, *MbeiSnpPlm*, *ProbeLevelModel*, *RmaCnPlm*, *RmaPlm*, *RmaSnpPlm*

public abstract static class **MultiArrayUnitModel**
extends *UnitModel*

This abstract class represents a unit model that fits one model per unit based on signals for all arrays in the data set. The nature of a multi-array unit model is that all arrays must be available at the time of the fit and the estimated parameters will depend on the data from all arrays. Thus, if the signals in one array changes the model has to be refitted.

Usage

```
MultiArrayUnitModel(..., listOfPriors=NULL)
```

Arguments

`...`	Arguments passed to `UnitModel`.
`listOfPriors`	A `list` of priors to be used when fitting the model.

Fields and Methods

Methods:

`getListOfPriors`	-
`setListOfPriors`	-

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`NormExpBackgroundCorrection`

The NormExpBackgroundCorrection class

Description

Package: aroma.affymetrix
Class NormExpBackgroundCorrection

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--BackgroundCorrection
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--LimmaBackgroundCorrection
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--NormExpBackgroundCorrection
```

Directly known subclasses:

public static class **NormExpBackgroundCorrection**
extends LimmaBackgroundCorrection

This class represents the normal exponential background correction model. Estimators of the **limma** package is used.

Usage

```
NormExpBackgroundCorrection(..., method=c("rma", "saddle", "mle"))
```

Arguments

`...`	Arguments passed to the constructor of `LimmaBackgroundCorrection`.
`method`	The estimator used, cf. argument `normexp.method` of `backgroundCorrect` in **limma** for more details.

Fields and Methods

Methods:
No methods defined.

Methods inherited from LimmaBackgroundCorrection:
getAsteriskTags, getParameters, process

Methods inherited from BackgroundCorrection:
getParameters, process

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

Internally, `backgroundCorrect` is used.

`OpticalBackgroundCorrection`

The OpticalBackgroundCorrection class

Description

Package: aroma.affymetrix
Class OpticalBackgroundCorrection

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--BackgroundCorrection
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--OpticalBackgroundCorrection
```

Directly known subclasses:

public static class **OpticalBackgroundCorrection**
extends *BackgroundCorrection*

This class represents "optical" background adjustment.

Usage

```
OpticalBackgroundCorrection(..., minimum=1)
```

Arguments

`...`	Arguments passed to the constructor of `ProbeLevelTransform`.
`minimum`	The minimum signal allowed after adjustment.

Fields and Methods

Methods:

```
process   -
```

Methods inherited from BackgroundCorrection:
getParameters, process

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson

`ParameterCelFile` *The ParameterCelFile class*

Description

Package: aroma.affymetrix
Class ParameterCelFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
```

Directly known subclasses:
ChipEffectFile, *CnChipEffectFile*, *CnProbeAffinityFile*, *ExonChipEffectFile*, *ExonProbeAffinityFile*, *FirmaFile*, *ProbeAffinityFile*, *ResidualFile*, *SnpChipEffectFile*, *SnpProbeAffinityFile*, *WeightsFile*

public abstract static class **ParameterCelFile**
extends ParametersInterface

A ParameterCelFile object represents parameter estimates.

Usage

```
ParameterCelFile(..., encodeFunction=NULL, decodeFunction=NULL)
```

Arguments

`...`	Arguments passed to `AffymetrixCelFile`.
`encodeFunction`	A `function` taking a single `list` structure as its argument.
`decodeFunction`	A `function` taking a single `list` structure as its argument.

Fields and Methods

Methods:

`extractDataFrame`	-
`extractMatrix`	-
`readUnits`	-

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:

getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

File format

The idea behind this class is store data fields which by nature have one value per probe (per field) in CEL files. A perfect example is to store probe-affinity estimates and their standard deviations. There is one probe affinity per probe so the structure of a CEL file (and its coupled CDF file) is well suited to read/write such information.

Consider a unit group with L probes. A CEL file stores `intensities` (L floats), `stdvs` (L floats), and `pixels` (L integers). Thus, for each probe l=1,...,L, a (float, float, integer) tuple is stored. We can use this for any information we want. If we want a slightly different structure, we can choose to encode/decode our structure/information to fit the structure of the CEL file. This abstract class provides transparent methods for encoding and decoding such information through methods `encodeUnitGroup()` and `decodeUnitGroup()`. By subclassing you can implement different types of data structures.

Author(s)

Henrik Bengtsson

`ParameterCelSet` *The ParameterCelSet class*

Description

Package: aroma.affymetrix
Class ParameterCelSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelSet
```

Directly known subclasses:
ChipEffectSet, CnChipEffectSet, ExonChipEffectSet, FirmaSet, SnpChipEffectSet

public static class **ParameterCelSet**
extends ParametersInterface

A ParameterCelSet object represents a set of `ParameterCelFile`:s.

Usage

```
ParameterCelSet(...)
```

Arguments

`...`	Arguments passed to `AffymetrixCelSet`.

Fields and Methods

Methods:

```
extractDataFrame  -
extractMatrix     -
```

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelSet:
append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`ProbeAffinityFile` *The ProbeAffinityFile class*

Description

Package: aroma.affymetrix
Class ProbeAffinityFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ProbeAffinityFile
```

Directly known subclasses:
CnProbeAffinityFile, *ExonProbeAffinityFile*, *SnpProbeAffinityFile*

public abstract static class **ProbeAffinityFile**
extends *ParameterCelFile*

This class represents estimates of probe affinities in probe-level models.

Usage

```
ProbeAffinityFile(..., probeModel=c("pm", "mm", "pm-mm", "min1(pm-mm)", "pm+mm"))
```

Arguments

`...`	Arguments passed to `ParameterCelFile`.
`probeModel`	The specific type of probe model.

Fields and Methods

Methods:

`readUnits` -

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags,

hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

An object of this class is typically obtained through the `getProbeAffinityFile()` method for the `ProbeLevelModel` class.

`ProbeLevelModel` *The ProbeLevelModel class*

Description

Package: aroma.affymetrix
Class ProbeLevelModel

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
```

Directly known subclasses:
AffineCnPlm, *AffinePlm*, *AffineSnpPlm*, *AvgCnPlm*, *AvgPlm*, *AvgSnpPlm*, *ExonRmaPlm*, *HetLogAddCnPlm*, *HetLogAddPlm*, *HetLogAddSnpPlm*, *MbeiCnPlm*, *MbeiPlm*, *MbeiSnpPlm*, *RmaCnPlm*, *RmaPlm*, *RmaSnpPlm*

public abstract static class **ProbeLevelModel**
extends *MultiArrayUnitModel*

This abstract class represents a probe-level model (PLM) as defined by the **affyPLM** package: "A [...] PLM is a model that is fit to probe-intensity data. More specifically, it is where we fit a model with probe level and chip level parameters on a probeset by probeset basis", where the more general case for a probeset is a *unit group* in Affymetrix CDF terms.

Usage

```
ProbeLevelModel(..., standardize=TRUE)
```

Arguments

`...`	Arguments passed to `MultiArrayUnitModel`.
`standardize`	If `TRUE`, chip-effect and probe-affinity estimates are rescaled such that the product of the probe affinities is one.

Details

In order to minimize the risk for mistakes, but also to be able compare results from different PLMs, all PLM subclasses must meet the following criteria:

1. All parameter estimates must be (stored and returned) on the intensity scale, e.g. log-additive models such as `RmaPlm` have to transform the parameters on the log-scale to the intensity scale.
2. The probe-affinity estimates ϕ_k for a unit group must be constrained such that $\prod_k \phi_k = 1$, or equivalently if $\phi_k > 0, \sum_k \log(\phi_k) = 0$.

Note that the above probe-affinity constraint guarantees that the estimated chip effects across models are on the same scale.

Fields and Methods

Methods:

`fit`	-
`getChipEffectSet`	-
`getProbeAffinityFile`	-
`getResidualSet`	-
`getWeightsSet`	-

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:

$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

For more details on probe-level models, please see the **preprocessCore** package.

`ProbeLevelTransform` *The ProbeLevelTransform class*

Description

Package: aroma.affymetrix
Class ProbeLevelTransform

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
```

Directly known subclasses:
AbstractProbeSequenceNormalization, AllelicCrosstalkCalibration, *BackgroundCorrection*, BaseCountNormalization, *BasePositionNormalization*, DChipQuantileNormalization, GcRmaBackgroundCorrection, LimmaBackgroundCorrection, *LinearModelProbeSequenceNormalization*, MatNormalization, MatSmoothing, NormExpBackgroundCorrection, OpticalBackgroundCorrection, *ProbeLevelTransform3*, QuantileNormalization, ReseqCrosstalkCalibration, RmaBackgroundCorrection, ScaleNormalization, ScaleNormalization3, SpatialRowColumnNormalization, UnitTypeScaleNormalization

public abstract static class **ProbeLevelTransform**
extends *Transform*

This abstract class represents a transformation methods that transforms probe-level signals, typically intensities.

Usage

```
ProbeLevelTransform(...)
```

Arguments

`...`	Arguments passed to the constructor of `Transform`.

Details

Subclasses must implement the `process()` method.

Fields and Methods

Methods:
No methods defined.

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`ProbeLevelTransform3` *The ProbeLevelTransform3 class*

Description

Package: aroma.affymetrix
Class ProbeLevelTransform3

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
```

```
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelTransform3
```

Directly known subclasses:
AbstractProbeSequenceNormalization, BaseCountNormalization, *BasePositionNormalization*, *LinearModelProbeSequenceNormalization*, MatNormalization, ScaleNormalization3, UnitTypeScaleNormalization

public abstract static class **ProbeLevelTransform3**
extends *ProbeLevelTransform*

This abstract class is specialized from `ProbeLevelTransform` and provides methods to identify subsets and types of probes that are used for fitting and/or updating the signals.

Usage

```
ProbeLevelTransform3(dataSet=NULL, ..., unitsToFit="-XY", typesToFit=typesToUpdate,
  unitsToUpdate=NULL, typesToUpdate="pm", shift=0)
```

Arguments

`dataSet`	A `AffymetrixCelSet`.
`...`	Arguments passed to the constructor of `ProbeLevelTransform`.
`unitsToFit`	The units from which the normalization curve should be estimated. If `NULL`, all are considered.
`typesToFit`	Types of probes to be used when fitting the model.
`unitsToUpdate`	The units to be updated. If `NULL`, all are considered.
`typesToUpdate`	Types of probes to be updated.
`shift`	An optional amount to shift data before fitting and updating.

Fields and Methods

Methods:
No methods defined.

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`QualityAssessmentFile` *The QualityAssessmentFile class*

Description

Package: aroma.affymetrix
Class QualityAssessmentFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--QualityAssessmentFile
```

Directly known subclasses:

public abstract static class **QualityAssessmentFile**
extends *AffymetrixCelFile*

This class represents probe-level QC information (residuals, weights, etc.)

Usage

```
QualityAssessmentFile(...)
```

Arguments

`...`	Arguments passed to `AffymetrixCelFile`.

Fields and Methods

Methods:

`findUnitsTodo`	-

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson

See Also

An object of this class is typically part of a `QualityAssessmentSet`.

`QualityAssessmentModel`

The QualityAssessmentModel class

Description

Package: aroma.affymetrix
Class QualityAssessmentModel

```
Object
~~|
~~+--QualityAssessmentModel
```

Directly known subclasses:

public static class **QualityAssessmentModel**
extends Object

Usage

```
QualityAssessmentModel(plm=NULL, tags="*", ...)
```

Arguments

`plm`	A `ProbeLevelModel`.
`tags`	A `character vector` of tags.
`...`	Not used.

Fields and Methods

Methods:

`getChipEffectSet`	-
`getDataSet`	-
`getFullName`	-
`getName`	-
`getPath`	-
`getPlm`	-
`getResiduals`	-
`getTags`	-
`getWeights`	-
`nbrOfArrays`	-
`plotNuse`	-
`plotRle`	-

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

`QualityAssessmentSet` *The QualityAssessmentSet class*

Description

Package: aroma.affymetrix
Class QualityAssessmentSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--QualityAssessmentSet
```

Directly known subclasses:

public static class **QualityAssessmentSet**
extends AffymetrixCelSet

Usage

```
QualityAssessmentSet(...)
```

Arguments

`...`	Arguments passed to constructor of `AffymetrixCelSet`.

Fields and Methods

Methods:
No methods defined.

Methods inherited from AffymetrixCelSet:
append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName,

getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson

`QuantileNormalization` *The QuantileNormalization class*

Description

Package: aroma.affymetrix
Class QuantileNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--QuantileNormalization
```

Directly known subclasses:
DChipQuantileNormalization

public static class **QuantileNormalization**
extends *ProbeLevelTransform*

This class represents a normalization function that transforms the probe-level signals towards the same empirical distribution.

Usage

```
QuantileNormalization(..., subsetToUpdate=NULL, typesToUpdate=NULL,
  targetDistribution=NULL, subsetToAvg=subsetToUpdate, typesToAvg=typesToUpdate)
```

Arguments

`...`	Arguments passed to the constructor of `ProbeLevelTransform`.
`subsetToUpdate`	The probes to be updated. If `NULL`, all probes are updated.
`typesToUpdate`	Types of probes to be updated.
`targetDistribution`	A `numeric` `vector`. The empirical distribution to which all arrays should be normalized to.
`subsetToAvg`	The probes to calculate average empirical distribution over. If a single `numeric` in (0,1), then this fraction of all probes will be used. If `NULL`, all probes are considered.
`typesToAvg`	Types of probes to be used when calculating the average empirical distribution. If `"pm"` and `"mm"` only perfect-match and mismatch probes are used, respectively. If `"pmmm"` both types are used.

Fields and Methods

Methods:

`process` -

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach,

equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

Examples

```
## Not run:
  for (zzz in 0) {

# Setup verbose output
verbose <- Arguments$getVerbose(-2)
timestampOn(verbose)

# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Define an example dataset
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Find any dataset
path <- NULL
if (is.null(path))
  break

ds <- AffymetrixCelSet$fromFiles(path)
print(ds)

# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Normalization
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
norm <- QuantileNormalization(ds, subsetToAvg=1/3)
dsQN <- process(norm, verbose=verbose)
print(dsQN)

} # for (zzz in 0)
rm(zzz)


## End(Not run)
```

`ReseqCrosstalkCalibration`

The ReseqCrosstalkCalibration class

Description

Package: aroma.affymetrix
Class ReseqCrosstalkCalibration

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ReseqCrosstalkCalibration
```

Directly known subclasses:

public static class **ReseqCrosstalkCalibration**
extends *ProbeLevelTransform*

This class represents a calibration function that transforms the probe-level signals such that the signals from the four nucleotides (A, C, G, T) are orthogonal.

Usage

```
ReseqCrosstalkCalibration(dataSet=NULL, ..., targetAvg=2200, subsetToAvg=NULL,
  mergeGroups=FALSE, flavor=c("sfit", "expectile"), alpha=c(0.1, 0.075, 0.05, 0.03,
   0.01), q=2, Q=98)
```

Arguments

`dataSet`	An `AffymetrixCelSet`.
`...`	Arguments passed to the constructor of `ProbeLevelTransform`.
`targetAvg`	The signal(s) that the average of the sum of the probe quartets should have after calibration.
`subsetToAvg`	The indices of the cells (taken as the intersect of existing indices) used to calculate average in order to rescale to the target average. If `NULL`, all probes are considered.
`mergeGroups`	A `logical` ...
`flavor`	A `character` string specifying what algorithm is used to fit the crosstalk calibration.
`alpha, q, Q`	Additional arguments passed to `fitMultiDimensionalCone()`.

Fields and Methods

Methods:

`process` -

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`ResidualFile` *The ResidualFile class*

Description

Package: aroma.affymetrix
Class ResidualFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ResidualFile
```

Directly known subclasses:

public abstract static class **ResidualFile**
extends *ParameterCelFile*

This class represents estimates of residuals in the probe-level models.

Usage

```
ResidualFile(..., probeModel=c("pm"))
```

Arguments

`...`	Arguments passed to `ParameterCelFile`.
`probeModel`	The specific type of model, e.g. `"pm"`.

Fields and Methods

Methods:

`findUnitsTodo`	-
`getImage`	-
`readUnits`	-
`writeImage`	-

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

See Also

An object of this class is typically obtained through the `getResidualSet()` method for the `ProbeLevelModel` class. An object of this class is typically part of a `ResidualSet`.

`ResidualSet` *The ResidualSet class*

Description

Package: aroma.affymetrix
Class ResidualSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ResidualSet
```

Directly known subclasses:

public static class **ResidualSet**
extends ParametersInterface

This class represents probe-level residuals from probe-level models.

Usage

```
ResidualSet(..., probeModel=c("pm"))
```

Arguments

`...`	Arguments passed to `AffymetrixCelSet`.
`probeModel`	The specific type of model, e.g. `"pm"`.

Fields and Methods

Methods:

`findUnitsTodo`	-
`getAverageFile`	-
`getCellIndices`	-
`readUnits`	-

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelSet:
append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Ken Simpson, Henrik Bengtsson

See Also

An object of this class is typically obtained through the `getResidualSet()` method for the `ProbeLevelModel` class.

`RmaBackgroundCorrection` *The RmaBackgroundCorrection class*

Description

Package: aroma.affymetrix
Class RmaBackgroundCorrection

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--BackgroundCorrection
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaBackgroundCorrection
```

Directly known subclasses:

public static class **RmaBackgroundCorrection**
extends *BackgroundCorrection*

This class represents the RMA background adjustment function.

Usage

```
RmaBackgroundCorrection(..., addJitter=FALSE, jitterSd=0.2, seed=6022007)
```

Arguments

`...`	Arguments passed to the constructor of `BackgroundCorrection`.
`addJitter`	If `TRUE`, Zero-mean gaussian noise is added to the signals before being background corrected.
`jitterSd`	Standard deviation of the jitter noise added.

`seed`	An (optional) `integer` specifying a temporary random seed to be used for generating the (optional) jitter. The random seed is set to its original state when done. If `NULL`, it is not set.

Details

Internally `bg.adjust` is used to background correct the probe signals. The default is to background correct PM signals only.

Fields and Methods

Methods:

`process` -

Methods inherited from BackgroundCorrection:
getParameters, process

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Jitter noise

The fitting algorithm of the RMA background correction model may not converge if there too many small and discrete signals. To overcome this problem, a small amount of noise may be added to the signals before fitting the model. This is an ad hoc solution that seems to work. However, add Gaussian noise may generate non-positive signals.

Author(s)

Ken Simpson, Henrik Bengtsson

`RmaCnPlm` *The RmaCnPlm class*

Description

Package: aroma.affymetrix
Class RmaCnPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaSnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--CnPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaCnPlm
```

Directly known subclasses:

public abstract static class **RmaCnPlm**
extends CnPlm

Usage

```
RmaCnPlm(..., combineAlleles=FALSE)
```

Arguments

`...`	Arguments passed to `RmaSnpPlm`.
`combineAlleles`	If `FALSE`, allele A and allele B are treated separately, otherwise together.

Fields and Methods

Methods:
No methods defined.

Methods inherited from CnPlm:
getCellIndices, getChipEffectSet, getCombineAlleles, getParameters, getProbeAffinityFile, setCombineAlleles

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from RmaSnpPlm:
getAsteriskTags

Methods inherited from RmaPlm:
getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Model

TO DO.

Author(s)

Henrik Bengtsson

`RmaPlm` *The RmaPlm class*

Description

Package: aroma.affymetrix
Class RmaPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaPlm
```

Directly known subclasses:
ExonRmaPlm, *HetLogAddCnPlm*, *HetLogAddPlm*, *HetLogAddSnpPlm*, *RmaCnPlm*, *RmaSnpPlm*

public abstract static class **RmaPlm**
extends *ProbeLevelModel*

This class represents the log-additive model part of the Robust Multichip Analysis (RMA) method described in Irizarry et al (2003).

Usage

```
RmaPlm(..., flavor=c("affyPLM", "oligo"))
```

Arguments

`...`	Arguments passed to `ProbeLevelModel`.
`flavor`	A `character` string specifying what model fitting algorithm to be used. This makes it possible to get identical estimates as other packages.

Fields and Methods

Methods:
No methods defined.

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Model

For a single unit group, the log-additive model of RMA is:

$$log_2(y_{ik}) = \beta_i + \alpha_k + \varepsilon_{ik}$$

where β_i are the chip effects for arrays $i = 1, ..., I$, and α_k are the probe affinities for probes $k = 1, ..., K$. The ε_{ik} are zero-mean noise with equal variance. The model is constrained such that $\sum_k \alpha_k = 0$.

Note that all PLM classes must return parameters on the intensity scale. For this class that means that $\theta_i = 2^{\beta}_{i}$ and $\phi_k = 2^{\alpha}_{k}$ are returned.

Different flavors of model fitting

There are a few differ algorithms available for fitting the same probe-level model. The default and recommended method (`flavor="affyPLM"`) uses the implementation in the **preprocessCore** package which fits the model parameters robustly using an M-estimator (the method used to be in **affyPLM**).

Alternatively, other model-fitting algorithms are available. The algorithm (`flavor="oligo"`) used by the **oligo** package, which originates from the **affy** packages, fits the model using median polish, which is a non-robust estimator. Note that this algorithm does not constraint the probe-effect parameters to multiply to one on the intensity scale. Since the internal function does not return these estimates, we can neither rescale them.

Author(s)

Henrik Bengtsson, Ken Simpson

References

Irizarry et al. *Summaries of Affymetrix GeneChip probe level data*. NAR, 2003, 31, e15.

`RmaSnpPlm` *The RmaSnpPlm class*

Description

Package: aroma.affymetrix
Class RmaSnpPlm

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--MultiArrayUnitModel
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelModel
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpPlm
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--RmaSnpPlm
```

Directly known subclasses:
RmaCnPlm

public abstract static class **RmaSnpPlm**
extends SnpPlm

Usage

```
RmaSnpPlm(..., mergeStrands=FALSE)
```

Arguments

`...`	Arguments passed to `RmaPlm`.
`mergeStrands`	If `TRUE`, the sense and the anti-sense strands are fitted together, otherwise separately.

Fields and Methods

Methods:
No methods defined.

Methods inherited from SnpPlm:
getCellIndices, getChipEffectSet, getMergeStrands, getParameters, getProbeAffinityFile, setMergeStrands

Methods inherited from RmaPlm:
getAsteriskTags, getCalculateResidualsFunction, getParameters, getRlmFitFunctions

Methods inherited from ProbeLevelModel:
calculateResidualSet, calculateWeights, fit, getAsteriskTags, getCalculateResidualsFunction, getChipEffectSet, getProbeAffinityFile, getResidualSet, getRootPath, getWeightsSet

Methods inherited from MultiArrayUnitModel:
getListOfPriors, setListOfPriors, validate

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`ScaleNormalization` *The ScaleNormalization class*

Description

Package: aroma.affymetrix
Class ScaleNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
```

```
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ScaleNormalization
```

Directly known subclasses:

public static class **ScaleNormalization**
extends *ProbeLevelTransform*

This class represents a normalization function that transforms the probe-level signals towards the same scale.

Usage

```
ScaleNormalization(dataSet=NULL, ..., targetAvg=4400, subsetToUpdate=NULL,
  typesToUpdate=NULL, subsetToAvg="-XY", typesToAvg=typesToUpdate, shift=0)
```

Arguments

`dataSet`	`AffymetrixCelSet` to be normalized.
`...`	Arguments passed to the constructor of `ProbeLevelTransform`.
`targetAvg`	A `numeric` value.
`subsetToUpdate`	The probes to be updated. If `NULL`, all probes are updated.
`typesToUpdate`	Types of probes to be updated.
`subsetToAvg`	The probes to calculate average signal over. If a single `numeric` in (0,1), then this fraction of all probes will be used. If `NULL`, all probes are considered.
`typesToAvg`	Types of probes to be used when calculating the average signal. If `"pm"` and `"mm"` only perfect-match and mismatch probes are used, respectively. If `"pmmm"` both types are used.
`shift`	Optional amount of shift if data before fitting/normalizing.

Fields and Methods

Methods:

`process` -

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`ScaleNormalization3` *The ScaleNormalization3 class*

Description

Package: aroma.affymetrix
Class ScaleNormalization3

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelTransform3
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ScaleNormalization3
```

Directly known subclasses:

public static class **ScaleNormalization3**
extends *ProbeLevelTransform3*

This class represents a normalization function that transforms the probe-level signals towards the same scale.

Usage

```
ScaleNormalization3(..., targetAvg=4400)
```

Arguments

`...`	Arguments passed to the constructor of `ProbeLevelTransform3`.
`targetAvg`	A `numeric` value.

Fields and Methods

Methods:

`process` -

Methods inherited from ProbeLevelTransform3:
getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`SingleArrayUnitModel` *The SingleArrayUnitModel class*

Description

Package: aroma.affymetrix
Class SingleArrayUnitModel

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--SingleArrayUnitModel
```

Directly known subclasses:

public abstract static class **SingleArrayUnitModel**
extends *UnitModel*

This abstract class represents a unit model that fits one model per unit based on signals from a single arrays. The nature of a single-array unit model is that each array can be fitted independently of the others.

Usage

```
SingleArrayUnitModel(...)
```

Arguments

`...`	Arguments passed to `UnitModel`.

Fields and Methods

Methods:

`fit` -

Methods inherited from UnitModel:
findUnitsTodo, getAsteriskTags, getFitSingleCellUnitFunction, getParameters

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`SmoothMultiarrayModel` *The SmoothMultiarrayModel class*

Description

Package: aroma.affymetrix
Class SmoothMultiarrayModel

```
Object
~~|
~~+--ChromosomalModel
~~~~~~~|
~~~~~~~+--SmoothMultiarrayModel
```

Directly known subclasses:
SmoothRmaModel, *SmoothSaModel*

public abstract static class **SmoothMultiarrayModel**
extends *ChromosomalModel*

This abstract class represents a chromosomal smoothing method done chromosome by chromosome.

Usage

```
SmoothMultiarrayModel(..., typoOfWeights=c("none", "1/s2"), bandwidth=10000, tags="*")
```

Arguments

`...`	Arguments passed to the constructor of `ChromosomalModel`.
`typoOfWeights`	A `character` string.
`bandwidth`	A single `numeric` specifying the smoothing bandwidth in units of nucleotides.
`tags`	A `character` `vector` of tags to be added.

Fields and Methods

Methods:

```
getBandwidth    -
getOutputTuple  -
setBandwidth    -
```

Methods inherited from ChromosomalModel:
as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome, getListOfGenomeInformations, getPcuTheta, getPositionChipTypeUnit

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

`CopyNumberSegmentationModel`.

`SmoothRmaModel` *The SmoothRmaModel class*

Description

Package: aroma.affymetrix
Class SmoothRmaModel

```
Object
~~|
~~+--ChromosomalModel
~~~~~~~|
~~~~~~~+--SmoothMultiarrayModel
~~~~~~~~~~~~|
~~~~~~~~~~~~+--SmoothRmaModel
```

Directly known subclasses:

public abstract static class **SmoothRmaModel**
extends *SmoothMultiarrayModel*

This class represents the Chromosomal Smoothing Robust Multichip Analysis method.

Usage

```
SmoothRmaModel(...)
```

Arguments

`...`	Arguments passed to the constructor of `SmoothMultiarrayModel`.

Fields and Methods

Methods:
No methods defined.

Methods inherited from SmoothMultiarrayModel:
as.character, createOutputTuple, fitOneChromosome, getAsteriskTags, getBandwidth, getFitUnitGroupFunction, getOutputTuple, getRootPath, setBandwidth

Methods inherited from ChromosomalModel:
as.character, fit, getAlias, getAromaGenomeTextFile, getAsteriskTags, getChipType, getChipTypes, getChromosomes, getFullName, getFullNames, getGenome, getGenomeData, getGenomeFile, getListOfAromaUgpFiles, getName, getNames, getParentPath, getPath, getReportPath, getRootPath, getSetTuple, getSets, getTags, indexOf, nbrOfArrays, nbrOfChipTypes, setChromosomes, setGenome, getListOfGenomeInformations, getPcuTheta, getPositionChipTypeUnit

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`SnpChipEffectFile` *The SnpChipEffectFile class*

Description

Package: aroma.affymetrix
Class SnpChipEffectFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ChipEffectFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpChipEffectFile
```

Directly known subclasses:
CnChipEffectFile

public abstract static class **SnpChipEffectFile**
extends *ChipEffectFile*

This class represents estimates of chip effects in the probe-level models.

Usage

```
SnpChipEffectFile(..., mergeStrands=FALSE)
```

Arguments

`...`	Arguments passed to `ChipEffectFile`.
`mergeStrands`	Specifies if the strands are merged or not for these estimates.

Fields and Methods

Methods:

`extractTheta`	-
`extractTotalAndFracB`	-
`readUnits`	-

Methods inherited from ChipEffectFile:
as.character, extractChromosomalDataFrame, extractMatrix, extractTheta, findUnitsTodo, getAM, getAsFullCelFile, getCellIndices, getCellMapForMainCdf, getExpandedCellMap, getParameters,

getUnitGroupCellArrayMap, getUnitGroupCellMatrixMap, getXAM, mergeGroups, readUnits, writeAsFullCelFile

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

See Also

An object of this class is typically part of a `SnpChipEffectSet`.

`SnpChipEffectSet` *The SnpChipEffectSet class*

Description

Package: aroma.affymetrix
Class SnpChipEffectSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ChipEffectSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpChipEffectSet
```

Directly known subclasses:
CnChipEffectSet

public static class **SnpChipEffectSet**
extends ChipEffectSet

This class represents estimates of chip effects in the probe-level models.

Usage

```
SnpChipEffectSet(..., mergeStrands="byFirstFile")
```

Arguments

`...`	Arguments passed to `ChipEffectSet`.
`mergeStrands`	Specifies if the strands are merged or not for these estimates.

Fields and Methods

Methods:

`extractAlleleSet`	-
`extractSnpCnvQSet`	-
`extractSnpQSet`	-
`extractTheta`	-
`extractTotalAndFreqB`	-
`getAverageFile`	-
`getMergeStrands`	-
`setMergeStrands`	-

Methods inherited from ChipEffectSet:
as.character, boxplotStats, byPath, calculateBaseline, calculateFieldBoxplotStats, calculateNuseBoxplotStats, calculateRleBoxplotStats, extractAffyBatch, extractChromosomalDataFrame, extractExpressionSet, extractMatrix, extractTheta, findByName, findUnitsTodo, fromDataSet, getAM, getAsFullCelSet, getAverageFile, getBaseline, getCellIndices, getXAM, plotBoxplot, readUnits, updateUnits

Methods inherited from ParameterCelSet:
extractDataFrame, extractMatrix

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelSet:
append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`SnpInformation` *The SnpInformation class*

Description

Package: aroma.affymetrix
Class SnpInformation

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~~~~~~~~~~~+--SnpInformation
```

Directly known subclasses:
DChipSnpInformation, *UflSnpInformation*

public abstract static class **SnpInformation**
extends FileCacheKeyInterface

Usage

```
SnpInformation(...)
```

Arguments

`...`	Arguments passed to `GenericDataFile`.

Fields and Methods

Methods:

`byChipType`	-
`getChipType`	-
`getData`	-
`getFragmentLengths`	-
`getFragmentStarts`	-
`getFragmentStops`	-
`nbrOfEnzymes`	-
`nbrOfUnits`	-
`readDataFrame`	-

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTab-

ularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`SnpPlm` *The SnpPlm interface class*

Description

Package: aroma.affymetrix
Class SnpPlm

```
Interface
~~|
~~+--SnpPlm
```

Directly known subclasses:
AffineCnPlm, *AffineSnpPlm*, *AvgCnPlm*, *AvgSnpPlm*, CnPlm, *HetLogAddCnPlm*, *HetLogAddSnpPlm*, *MbeiCnPlm*, *MbeiSnpPlm*, *RmaCnPlm*, *RmaSnpPlm*

public class **SnpPlm**
extends Interface

An `Interface` implementing methods special for `ProbeLevelModel`s specific to SNP arrays.

Usage

```
SnpPlm(...)
```

Arguments

`...`	Not used.

Methods

Methods:

```
getCellIndices        -
getChipEffectSet      -
getMergeStrands       -
getProbeAffinityFile  -
setMergeStrands       -
```

Methods inherited from Interface:
extend, print, uses

Requirements

Classes inheriting from this `Interface` must provide the following fields:

mergeStrands A `logical` value indicating if strands should be merged or not.

Author(s)

Henrik Bengtsson

Examples

```
for (zzz in 0) {

# Setup verbose output
verbose <- Arguments$getVerbose(-2)
timestampOn(verbose)

# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Define an example dataset using this path
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Find any SNP dataset
path <- NULL
if (is.null(path))
  break

if (!exists("ds")) {
  ds <- AffymetrixCelSet$fromFiles(path)
}
print(ds)

# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Create a set of various PLMs for this dataset
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
if (!exists("models", mode="list")) {
  mergeStrands <- TRUE
  models <- list(
    rma = RmaSnpPlm(ds, mergeStrands=mergeStrands),
    mbei = MbeiSnpPlm(ds, mergeStrands=mergeStrands)
#   affine = AffineSnpPlm(ds, background=FALSE, mergeStrands=mergeStrands)
  )
```

```
}
print(models)


# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# For each model, fit a few units
#
# Note, by fitting the same set of units across models, the internal
# caching mechanisms of aroma.affymetrix makes sure that the data is
# only read into memory once. See log for reading speed.
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
units <- 55+1:100

for (model in models) {
  ruler(verbose)
  fit(model, units=units, force=TRUE, verbose=verbose)
}

# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# For each unit, plot the estimated (thetaB,thetaA) for all models
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# Should we plot the on the log scale?
log <- TRUE

# Do only user to press ENTER if more than one unit is plotted
opar <- par(ask=(length(units) > 1))

Alab <- expression(theta[A])
Blab <- expression(theta[B])
if (log) {
  lim <- c(6, 16)
} else {
  lim <- c(0, 2^15)
}

# For each unit...
for (unit in units) {
  # For all models...
  for (kk in seq_along(models)) {
    ces <- getChipEffects(models[[kk]])
    ceUnit <- ces[unit]
    snpName <- names(ceUnit)[1]
    theta <- ceUnit[[1]]
    thetaA <- theta[[1]]$theta
    thetaB <- theta[[2]]$theta
    if (log) {
      thetaA <- log(thetaA, base=2)
      thetaB <- log(thetaB, base=2)
    }

    # Create the plot?
    if (kk == 1) {
      plot(NA, xlim=lim, ylim=lim, xlab=Blab, ylab=Alab, main=snpName)
```

```
      abline(a=0, b=1, lty=2)
    }

    # Plot the estimated parameters
    points(thetaB, thetaA, col=kk, pch=19)
  }
} # for (unit ...)

# Reset graphical parameter settings
par(opar)

} # for (zzz in 0)
rm(zzz)
```

`SnpProbeAffinityFile` *The SnpProbeAffinityFile class*

Description

Package: aroma.affymetrix
Class SnpProbeAffinityFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ProbeAffinityFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--SnpProbeAffinityFile
```

Directly known subclasses:
CnProbeAffinityFile

public abstract static class **SnpProbeAffinityFile**
extends *ProbeAffinityFile*

This class represents estimates of probe affinities in SNP probe-level models.

Usage

```
SnpProbeAffinityFile(..., mergeStrands=FALSE)
```

Arguments

`...`	Arguments passed to `ProbeAffinityFile`.
`mergeStrands`	Specifies if the strands are merged or not for these estimates.

Fields and Methods

Methods:
No methods defined.

Methods inherited from ProbeAffinityFile:
as.character, getCellIndices, getParameters, readUnits

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern,

getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`SpatialReporter` *The SpatialReporter class*

Description

Package: aroma.affymetrix
Class SpatialReporter

```
Object
~~|
~~+--GenericReporter
~~~~~~~|
~~~~~~~+--AffymetrixFileSetReporter
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AffymetrixCelSetReporter
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--SpatialReporter
```

Directly known subclasses:

public abstract static class **SpatialReporter**
extends *AffymetrixCelSetReporter*

A SpatialReporter generates image files of spatial representations of cell signals for each of the arrays in the input set.

Usage

```
SpatialReporter(..., reference=NULL)
```

Arguments

`...`	Arguments passed to `AffymetrixCelSetReporter`.
`reference`	An optional reference `AffymetrixCelFile`.

Fields and Methods

Methods:

```
addColorMap   -
getColorMaps  -
plotMargins   -
process       -
setColorMaps  -
```

Methods inherited from AffymetrixCelSetReporter:
as.character, getChipType, getDataSet, getPath, nbrOfArrays

Methods inherited from AffymetrixFileSetReporter:
getFileSet, getInputName, getInputTags

Methods inherited from GenericReporter:
as.character, getAlias, getAsteriskTags, getFullName, getInputName, getInputTags, getMainPath, getName, getPath, getReportSet, getRootPath, getTags, process, setAlias, setup

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`TransformReport` *The TransformReport class*

Description

Package: aroma.affymetrix
Class TransformReport

```
Object
~~|
~~+--TransformReport
```

Directly known subclasses:

public static class **TransformReport**
extends Object

Usage

```
TransformReport(inSet=NULL, outSet=NULL, ...)
```

Arguments

`inSet`	The input data set as an `AffymetrixCelSet`.
`outSet`	The output data set as an `AffymetrixCelSet`.
`...`	Not used.

Fields and Methods

Methods:

`getCdf`	-
`getFullName`	-
`getInputDataSet`	-
`getName`	-
`getOutputDataSet`	-
`getPath`	-
`getTags`	-
`getUnitNamesFile`	-
`getUnitTypesFile`	-
`getYY`	-
`nbrOfArrays`	-
`plotXYCurve`	-
`plotXYCurveLog2`	-
`seq`	-
`writeImageCombined`	-
`writeImages`	-

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`UgpGenomeInformation` *The UgpGenomeInformation class*

Description

Package: aroma.affymetrix
Class UgpGenomeInformation

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--GenomeInformation
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UgpGenomeInformation
```

Directly known subclasses:

public abstract static class **UgpGenomeInformation**
extends *GenomeInformation*

This class represents Aroma UGP genome information files.

Usage

```
UgpGenomeInformation(..., .ugp=NULL, .verify=TRUE)
```

Arguments

`...`	Arguments passed to `GenomeInformation`.
`.ugp`	For internal use only.
`.verify`	For internal use only.

Fields and Methods

Methods:

`byChipType` -
`getChipType` -
`getChromosomes` -
`getData` -
`getUnitsOnChromosome` -
`isCompatibleWithCdf` -
`nbrOfUnits` -
`readDataFrame` -

Methods inherited from GenomeInformation:
as.character, byChipType, fromCdf, fromDataSet, getChipType, getChromosomeStats, getChromosomes, getData, getPositions, getUnitIndices, getUnitsOnChromosome, getUnitsOnChromosomes, isCompatibleWithCdf, nbrOfUnits, plotDensity, readDataFrame, verify

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach,

equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`UnitModel` *The UnitModel class*

Description

Package: aroma.affymetrix
Class UnitModel

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--Model
~~~~~~~~~~~~|
~~~~~~~~~~~~+--UnitModel
```

Directly known subclasses:
AffineCnPlm, *AffinePlm*, *AffineSnpPlm*, *AlleleSummation*, *AvgCnPlm*, *AvgPlm*, *AvgSnpPlm*, *ExonRmaPlm*, *FirmaModel*, *HetLogAddCnPlm*, *HetLogAddPlm*, *HetLogAddSnpPlm*, *MbeiCnPlm*, *MbeiPlm*, *MbeiSnpPlm*, *MultiArrayUnitModel*, *ProbeLevelModel*, *RmaCnPlm*, *RmaPlm*, *RmaSnpPlm*, *SingleArrayUnitModel*

public abstract static class **UnitModel**
extends *Model*

This class is abstract and represents a generic unit model, i.e. a model that is applied to each unit separately.

Usage

```
UnitModel(dataSet=NULL, probeModel=c("pm", "mm", "pm-mm", "min1(pm-mm)", "pm+mm"),
  shift=0, ...)
```

Arguments

`dataSet`	An `AffymetrixCelSet` to which this model should be fitted.
`probeModel`	A `character` string specifying how PM and MM values should be modeled. By default only PM signals are used.

`shift`	An optional amount the signals should be shifted (translated) before fitting the model.
`...`	Arguments passed to the constructor of `Model`.

Fields and Methods

Methods:

`findUnitsTodo`	-

Methods inherited from Model:
as.character, fit, getAlias, getAsteriskTags, getDataSet, getFullName, getName, getPath, getRootPath, getTags, setAlias, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`UnitTypeScaleNormalization`

The UnitTypeScaleNormalization class

Description

Package: aroma.affymetrix
Class UnitTypeScaleNormalization

```
Object
~~|
~~+--ParametersInterface
~~~~~~~|
~~~~~~~+--AromaTransform
~~~~~~~~~~~~|
~~~~~~~~~~~~+--Transform
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--ProbeLevelTransform
~~~~~~~~~~~~~~~~~~~~~~|
```

```
~~~~~~~~~~~~~~~~~~~~~~+--ProbeLevelTransform3
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--UnitTypeScaleNormalization
```

Directly known subclasses:

public static class **UnitTypeScaleNormalization**
extends *ProbeLevelTransform3*

This class represents a normalization function that transforms the probe signals such that each unit type gets the same average.

Usage

```
UnitTypeScaleNormalization(..., targetAvg=4400)
```

Arguments

`...`	Arguments passed to the constructor of `ProbeLevelTransform3`.
`targetAvg`	A `numeric` value.

Fields and Methods

Methods:

`process` -

Methods inherited from ProbeLevelTransform3:
getAsteriskTags, getCellsTo, getCellsToFit, getCellsToUpdate, getParameters, getUnitsTo, getUnitsToFit, getUnitsToUpdate, writeSignals

Methods inherited from ProbeLevelTransform:
getRootPath

Methods inherited from Transform:
getOutputDataSet, getOutputFiles

Methods inherited from AromaTransform:
as.character, findFilesTodo, getAsteriskTags, getExpectedOutputFiles, getExpectedOutputFullnames, getFullName, getInputDataSet, getName, getOutputDataSet, getOutputDataSet0, getOutputFiles, getPath, getRootPath, getTags, isDone, process, setTags

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson

`WeightsFile` *The WeightsFile class*

Description

Package: aroma.affymetrix
Class WeightsFile

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFile
~~~~~~~~~~~~|
~~~~~~~~~~~~+--CacheKeyInterface
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--FileCacheKeyInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AromaMicroarrayDataFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParameterCelFile
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--WeightsFile
```

Directly known subclasses:

public abstract static class **WeightsFile**
extends *ParameterCelFile*

This class represents weights calculated from residuals of probe-level models.

Usage

```
WeightsFile(..., probeModel=c("pm"))
```

Arguments

`...`	Arguments passed to `ParameterCelFile`.
`probeModel`	The specific type of model, e.g. `"pm"`.

Fields and Methods

Methods:

`findUnitsTodo`	-
`getImage`	-
`readUnits`	-
`writeImage`	-

Methods inherited from ParameterCelFile:
extractDataFrame, extractMatrix, readUnits

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelFile:
allocateFromCdf, as.character, clone, createFrom, extractMatrix, fromFile, getAm, getCdf, getExtensionPattern, getFileFormat, getImage, getUnitNamesFile, getUnitTypesFile, highlight, image270, nbrOfCells, plotDensity, plotImage, plotMvsA, plotMvsX, range, setCdf, smoothScatterMvsA, writeImage

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataFile:
getAttributeXY, getChipType, getPlatform, getPloidy, getXAM, hasAttributeXY, isAverageFile, setAttributeXY, setAttributesByTags

Methods inherited from FileCacheKeyInterface:
getCacheKey

Methods inherited from CacheKeyInterface:
getCacheKey

Methods inherited from GenericDataFile:
as.character, clone, compareChecksum, copyTo, equals, fromFile, getAttribute, getAttributes, getChecksum, getChecksumFile, getCreatedOn, getDefaultFullName, getExtension, getExtensionPattern, getFileSize, getFileType, getFilename, getFilenameExtension, getLastAccessedOn, getLastModifiedOn, getOutputExtension, getPath, getPathname, gunzip, gzip, hasBeenModified, is.na, isFile, isGzipped, linkTo, readChecksum, renameTo, renameToUpperCaseExt, setAttribute, setAttributes, setAttributesBy, setAttributesByTags, setExtensionPattern, testAttributes, validate, validateChecksum, writeChecksum, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBychar-

acter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson, Ken Simpson

See Also

An object of this class is typically obtained through the `getWeightsSet()` method for the `ProbeLevelModel` class. An object of this class is typically part of a `WeightsSet`.

`WeightsSet` *The WeightsSet class*

Description

Package: aroma.affymetrix
Class WeightsSet

```
Object
~~|
~~+--FullNameInterface
~~~~~~~|
~~~~~~~+--GenericDataFileSet
~~~~~~~~~~~~|
~~~~~~~~~~~~+--AromaMicroarrayDataSet
~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~+--AromaPlatformInterface
~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixFileSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~+--AffymetrixCelSet
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--ParametersInterface
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~|
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~+--WeightsSet
```

Directly known subclasses:

public static class **WeightsSet**
extends ParametersInterface

This class represents probe-level weights.

Usage

```
WeightsSet(..., probeModel=c("pm"))
```

Arguments

`...`	Arguments passed to `AffymetrixCelSet`.
`probeModel`	The specific type of model, e.g. `"pm"`.

Fields and Methods

Methods:

`findUnitsTodo`	-
`getAverageFile`	-
`getCellIndices`	-
`readUnits`	-

Methods inherited from ParametersInterface:
getParameterSets, getParameters, getParametersAsString

Methods inherited from AffymetrixCelSet:
append, as, as.AffymetrixCelSet, as.character, averageQuantile, byName, byPath, clone, convertToUnique, doCRMAv1, doCRMAv2, doFIRMA, doGCRMA, doRMA, extractAffyBatch, extractFeatureSet, extractMatrix, extractSnpFeatureSet, findByName, getAverage, getAverageAsinh, getAverageFile, getAverageLog, getCdf, getChipType, getData, getIntensities, getPlatform, getTimestamps, getUnitGroupCellMap, getUnitIntensities, getUnitNamesFile, getUnitTypesFile, isDuplicated, justRMA, justSNPRMA, nbrOfArrays, normalizeQuantile, plotDensity, range, readUnits, setCdf, update2, writeSgr

Methods inherited from AffymetrixFileSet:
as, as.AffymetrixFileSet, byPath, getDefaultFullName

Methods inherited from AromaPlatformInterface:
getAromaPlatform, getAromaUflFile, getAromaUgpFile, getChipType, getPlatform, getUnitAnnotationDataFile, getUnitNamesFile, getUnitTypesFile, isCompatibleWith

Methods inherited from AromaMicroarrayDataSet:
as.AromaMicroarrayDataSetList, as.AromaMicroarrayDataSetTuple, getAromaFullNameTranslatorSet, getAverageFile, getChipType, getDefaultFullName, getPlatform, setAttributesBy, setAttributesBySampleAnnotationFile, setAttributesBySampleAnnotationSet, validate

Methods inherited from GenericDataFileSet:
[, [[, anyDuplicated, anyNA, append, appendFiles, appendFullNamesTranslator, appendFullNamesTranslatorByNULL, appendFullNamesTranslatorByTabularTextFile, appendFullNamesTranslatorByTabularTextFileSet, appendFullNamesTranslatorBydata.frame, appendFullNamesTranslatorByfunction, appendFullNamesTranslatorBylist, as.character, as.list, byName, byPath, c, clearCache, clearFullNamesTranslator, clone, copyTo, dsApplyInPairs, duplicated, equals, extract, findByName, findDuplicated, getChecksum, getChecksumFileSet, getChecksumObjects, getDefaultFullName, getFile, getFileClass, getFileSize, getFiles, getFullNames, getNames, getOneFile, getPath, getPathnames, getSubdirs, gunzip, gzip, hasFile, indexOf, is.na, names, nbrOfFiles, rep, resetFullNames, setFullNamesTranslator, sortBy, unique, update2, updateFullName, updateFullNames, validate, getFullNameTranslatorSet, getParentName

Methods inherited from FullNameInterface:
appendFullNameTranslator, appendFullNameTranslatorByNULL, appendFullNameTranslatorByTabularTextFile, appendFullNameTranslatorByTabularTextFileSet, appendFullNameTranslatorBycharacter, appendFullNameTranslatorBydata.frame, appendFullNameTranslatorByfunction, appendFullNameTranslatorBylist, clearFullNameTranslator, clearListOfFullNameTranslators, getDefaultFullName, getFullName, getFullNameTranslator, getListOfFullNameTranslators, getName, getTags, hasTag, hasTags, resetFullName, setFullName, setFullNameTranslator, setListOfFullNameTranslators, setName, setTags, updateFullName

Methods inherited from Object:
$, $<-, [[, [[<-, as.character, attach, attachLocally, clearCache, clearLookupCache, clone, detach, equals, extend, finalize, getEnvironment, getFieldModifier, getFieldModifiers, getFields, getInstantiationTime, getStaticInstance, hasField, hashCode, ll, load, names, objectSize, print, save, asThis

Author(s)

Henrik Bengtsson, Ken Simpson

See Also

An object of this class is typically obtained through the `getWeightsSet()` method for the `ProbeLevelModel` class.

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