Package 'RCALI'

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Title Calculation of the Integrated Flow of Particles Between Polygons

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Description Calculate the flow of particles between polygons by two integration methods: integration by a cubature method and integration on a grid of points.
Annie Bouvier, Kien Kieu, Kasia Adamczyk and Herve Monod (2009) <doi:10.1016/j.envsoft.2008.11.006>.

License GPL-3

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Contents

RCALI-package *Calculation of the Integrated Flow of Particles Between Polygons*

Description

Calculate the flow of particles between polygons by two integration methods: integration by a cubature method and integration on a grid of points.

Details

Depends:	splancs
License:	GPL version 2 or later
This package is an interface between R and the programme CaliFloPP: http://genome.jouy.inra.fr/logiciels/califlopp/	
News	`file.show(system.file("NEWS", package="RCAL`
Main function:	`califlopp`

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as.poly *Create an object of class 'poly'*

Description

Create an object of class "poly" from two vectors or from a matrix.

Usage

```
as.poly(x, y=NULL)
```

Arguments

x	vector of x-coordinates or two-columns matrix
y	vector of y-coordinates when 'x' is a vector.

Value

An object of class "poly", i.e a two-columns matrix labelled "xcoord", "ycoord".

See Also

crpoly

Examples

```
# A triangle
a <- as.poly(matrix(c(2,2,2,3,3,3), ncol=2, byrow=TRUE))
```

califlopp *Calculation of the Integrated Flow of Particles between Polygons*

Description

Calculation of the flow of particles between polygons by two integration methods: integration by a cubature method and integration on a grid of points.

Usage

```
califlopp(file, dispf=c(1,2), param=NULL, resfile = NULL)
```

Arguments

`file`	Pathname of the polygons-file. See details.
`dispf`	The required dispersion functions. Vector of integers or vector of R functions. The maximum length of this vector is 5. • If vector of integers, the dispersion functions are then compiled. Five are provided. To modify them, see Details. By default, 1 is for dispersal of oilseed rape pollen, 2 for dispersal of oilseed rape seed (dispersals of oilseed rape are the ones defined in *GeneSys* - see References), 3 for the constant function, 4 for an anisotropic version of the dispersal of yellow rust of wheat defined in *Soubeyrand and all*, 5 for a discontinuous function. These functions are viewable in the C file `src/functions.cc`. To modify them, see Details. • If vector of functions, the dispersion functions are coded in R (more time consuming than compiled version). Two R dispersal functions are provided, `fpollen` and `fseed`, the functions used in Genesys. To specify your own function, see details.
`param`	Optional list of parameters. Valid components are `input`, `output`, `verbose`, `warn.poly`, `warn.conv`,`delim`, `poly`, `send.and.receive`, `method`, `dz`, `dp`. In addition, when `method` is "`cub`": `maxpts`, `reler`, `abser`, `tz`. When `method` is "`grid`": `seed`, `step`, `nr`. See details.
`resfile`	Optional pathname of a result-file. When set, the results are written on it. This file can be read by using function `getRes` or `read.table`. See details, as to the content of the file.

Details

The polygons-file

The coordinates of the polygons should be provided in an ASCII file, denoted here "polygons-file". The unit is the meter. The vertices should be ordered clockwise. The polygons can be closed or not, but without holes. The first line contains the number of polygons. The following lines depend of the `input` parameter:

`input=1` Two lines per polygon: on the first one, an identifier (a positive integer), followed by the x-coordinates, on the second one, the same identifier followed by the y-coordinates. The function export.listpoly generates such a file from R structures

`input=2` Three lines per polygon: on the first one, an identifier (a positive integer), followed by a name for the polygon and by the number of its vertices, on the second one, the x-coordinates, and on the third one, the y-coordinates.

The individual dispersion functions

The individual dispersion functions can either be compiled or R functions.

Compiled function: Five compiled dispersal functions are provided (see argument `dispf`). To replace them by yours, you have to download the source of `RCALI`, modify and compile it.

Suppose that you have download the tar-archive in the directory `MyDir`. The steps to customize the dispersion functions are:

1/ Replace one or several functions in `MyDir/RCALI/src/functions.cc` by yours: The dispersion function has one argument, the current point, `p`, of class `Point`. You can use `p.getX()` and `p.getY()` to get the coordinates of the current point (in meters*`SCALE`, where `SCALE` is the rescaling parameter defined in the file `src/calicinfig.h`), `p.dist0()`, the distance of `p` from the origin (in meters*`SCALE`) and `p.angle0()`, the angle (in degrees, in $[-\pi, +\pi]$) between the line (0,p) and the horizontal line.

2/ Create a directory `MyDir/RCALI/libs`, place you in `MyDir/RCALI/src` and type in:

```
R CMD SHLIB -o ../libs/RCALI.so  *.cc
```

to create the compiled shared library.

3/ To use in a R-session:

```
source("MyDir/RCALI/R/sourceDir.R")
sourceDir("MyDir/RCALI/R")
dyn.load("MyDir/RCALI/libs/RCALI.so")
```

The help-files are viewable by opening in a browser `MyDir/RCALI/inst/doc/html/00Index.html`

You can also build the tar.gz file again, after modifications, and install it as a library by using the standard R commands `R CMD build` and `R CMD INSTALL --html`.

R function: Two R dispersal functions are provided, `fpollen` and `fseed`, the functions used in Genesys.

You can define your own R dispersal function: it should have one vector argument, the localization of the current point, `p`. The first element of this vector is the distance of `p` from the origin (in meters) and the second one is the angle (in degrees, in $[-\pi, +\pi]$) between the line (0,p) and the horizontal line (i.e, stating `x` and `y` are the coordinates of `p`, the angle is $atan2(y, x) * \frac{180}{\pi}$)

The parameters

The argument `param` is a list which valid components are:

`input` format of the polygons-file. 1 or 2 (see above). Default 2

`output` output required on the screen: 0 nothing, 1: all results, 2: progression numbers, 3: the integrated flows and their means per squared meter. Default 1

`verbose` TRUE, if output is required about polygons convexity and landscape translation. Default FALSE

`warn.poly` TRUE, if output is required about polygons simplification. Default FALSE

`warn.conv` TRUE, if output is required when cubature convergence is not reached. Default TRUE

`delim` separator character between values in the polygons-file. Default: tabulate

`send.and.receive` TRUE, if results are required from sending polygons to target polygons and from target polygons to sending polygons (case of anisotropic functions). Default FALSE

`poly` required pairs of polygons. List of vectors of length 2, or two-columns matrix. If only one pair is required, it may be a vector of length 2. Default: all pairs of polygons.

`method` string equal to `cub` for cubature method, `grid` for the grid method. Default: `cub`

`dz` integer vector, whose length is greater or equal to the number of required dispersion functions. `dz[i]` is the distance in meters beyond which the `i`st dispersion function is considered as nul. Default in a standard configuration: 0,21,0,1000,0 for functions number 1 to 5, respectively.

`dp` integer vector, whose length is greater or equal to the number of required dispersion functions. `dp[i]` is the distance in meters beyond which the `i`st dispersion function is calculated between centroids only. Default in a standard configuration: 100, 0, 0, 500, 0 for functions number 1 to 5, respectively.

In addition, when `method` is `cub`:

`maxpts` maximal number of evaluation points required for each function. Vector of length equal to the number of required functions. Default in a standard configuration: 100000

`reler` relative error required for each function. Vector of length equal to the number of required functions. Should be positive when method is cubature. Default in a standard configuration: 1.0e-3

`abser` absolute error required for each function. Vector of length equal to the number of required functions. Should be positive when method is cubature. Default in a standard configuration: 1.0e-3

`tz` integer vector, whose length is greater or equal to the number of required dispersion functions. Mode of triangulation for the cubature method. `tz[i]` should be 1, if, for the `i`st dispersion function, triangulation from (0,0) has to be done when (0,0) is included in the integration area and, 0 if not. 1 is recommended when the dispersion function is very "sharp" at the origin. Default in a standard configuration: 0,1,0,0,0 for functions number 1 to 5, respectively.

When `method` is `grid`:

`seed` seed of the random generator.

`step` step of the grid on the x-axis and on the y-axis in meter. Vector of length 2.

`nr` maximal number of replications or grids.

The result-file

When the argument `resfile` is set, a file is created. On this file, the values are separated by tabulates.

Its contains, when the method is `cub`,

on the first line: "npoly:", "input-file:", "nfunc:", "method:", each of these identifiers followed by the actual values.

on each of the following lines, the results for a couple of polygons: the identifiers of both polygons; the integrated flow divided by the area of the second polygon, for each dispersal function; the areas of both polygons; then, for each dispersal function, the integrated flow, the lower and upper bounds of the confidence interval, the absolute error, and the number of evaluations.

Its contains, when the method is `grid`,

on the first line: "npoly:", "input-file:", "nfunc:", "method:", "stepx:", "stepy:", each of these identifiers followed by the actual values.

on each of the following lines, the results for a couple of polygons: the identifiers of both polygons; the integrated flow divided by the area of the second polygon, for each dispersal function; the areas of both polygons; then, for each dispersal function, the integrated flow, and the standard deviation.

This file can be read in a R-session by using the function `getRes` or `read.table`, with option `skip=1`.

Value

Nothing. To store the results, set the argument `resfile`, then use the function `getRes` or `read.table`, with option `skip=1`

Side effect

This function creates a temporary file to store the parameters, usually in the directory `tmp` of the user. This file is destroyed at the end of execution.

Author(s)

A. Bouvier

References

- The CaliFloPP software: http://genome.jouy.inra.fr/logiciels/califlopp/
- Main reference paper: A. Bouvier, K. Kieu, K. Adamczyk, and H. Monod. Computation of integrated flow of particles between polygons. Environmental Modelling & Software, 24:843–849, 2009.
- N. Colbach, and all.Genesys: a model of the influence of cropping system on gene escape from herbicide tolerant rapeseed crops to rape volunteers. Agriculture, Ecosystems and Environnement, 83:235–270, 2001.

See Also

`getRes`

Examples

```
# Grid method with compiled constant and seed dispersion functions:
param <- list(method="grid",  grid=list(step=c(50,50)))
## Not run: califlopp("MyPolygonsFile",dispf=c(3,1), param=param)

# Cubature method with a R dispersion function:
param <- list( output=1, input=2, dz=0, dp=100, tz=0)
## Not run: califlopp("MyPolygonsFile", dispf=fpollen, param=param)
```

---

crlistpoly *Create an object of class 'listpoly' from objects of class 'poly'*

Description

Create an object of class "`listpoly`" from objects of class "`poly`"

Usage

```
crlistpoly(...)
```

Arguments

...	objetcs of class "poly"

Value

An object of class "listpoly" : a list where each component is a 'poly' object (see poly-class).

See Also

poly-class

Examples

```
# A triangle:
a <- as.poly(matrix(c(2,2,2,3,3,3), ncol=2, byrow=TRUE))
# A square:
b <- as.poly(matrix(c(2.5,2,2.5,2.5,3,2.5,3,2), ncol=2, byrow=TRUE))
# The both:
 z <- crlistpoly(a,b)
```

---

crpoly *Create un object of class 'poly' by clicking on points*

Description

Create un object of class "poly" by clicking on a graphic: the locations of the clicks will be the vertices of the polygon.

Usage

```
crpoly()
```

Details

The system prompts the user to enter points on the current graphic using the mouse or other pointing device. The points are joined on the screen with the current line symbol. A polygon of the points entered is drawn on the current graphics device and returned as a 'poly' object.

Value

An object of class "poly" i.e a two-columns matrix with the coordinates.

Warning

A plot should be drawn on the current graphics device before.

See Also

as.poly, getpoly of the package splancs

Examples

```
## Not run: plot(x=c(1,10), y=c(1,10), type='n')
## Not run: a<-crpoly()
#    Enter points with button 1
#    Finish with button 2
```

`export` *Generic for 'export'*

Description

Generic function for 'export'

Usage

```
export(x, filename)
```

Arguments

`x`	object to export
`filename`	target filename

Value

None.

See Also

`export.listpoly`

`export.default` *export.default method*

Description

Default method `export`

Usage

```
  ## Default S3 method:
export(x, filename)
```

Arguments

`x`	object to export
`filename`	target filename

Value

None.

See Also

export.listpoly

`export.listpoly` *Create a polygons file in format 1.*

Description

From an object of class "listpoly", create a polygons file for input to the software CaliFloPP or to the function califlopp. The format of this file corresponds to the format 1 of them, i.e you should set the param input to 1 when used as input to califlopp.

Usage

```
  ## S3 method for class 'listpoly'
export(x, filename)
```

Arguments

x	Object of class "listpoly"
filename	Name of the file to be created.

Value

None.

`fpollen` *Individual pollen dispersion function*

Description

From a vector of distances, calculate the individual pollen dispersion function used in *Genesys*

Usage

```
fpollen(point)
```

Arguments

point	scalar or vector of length 2, whose first element is a distance expressed in meter.

Value

The calculated dispersions.

References

Colbach, N. and Clermont-Dauphin, C. and Meynard, J.M. *Genesys: a model of the influence of cropping system on gene escape from herbicide tolerant rapeseed crops to rape volunteers. i. temporal evolution of a population of rapeseed volunteers in a field.* Agriculture, Ecosystems and Environnement, 83:235-253, 2001.

See Also

fseed

Examples

```
distance = seq(1,1.5, by=0.05)
a=matrix(distance, ncol=1)
b= apply(a,1,fpollen)
par(pty="s")
plot(x=distance, y =b)
lines(x=distance, y = apply(a,1,fseed))
```

---

fseed *Individual seed dispersion function*

Description

From a vector of distances, calculate the individual seed dispersion function used in *Genesys*

Usage

```
fseed(point)
```

Arguments

point	scalar or vector of length 2, whose first element is a distance expressed in meter.

Value

The calculated dispersions.

References

Colbach, N. and Clermont-Dauphin, C. and Meynard, J.M. *Genesys: a model of the influence of cropping system on gene escape from herbicide tolerant rapeseed crops to rape volunteers. i. temporal evolution of a population of rapeseed volunteers in a field.* Agriculture, Ecosystems and Environnement, 83:235-253, 2001.

See Also

fpollen

Examples

```
distance = seq(1,1.5, by=0.05)
a=matrix(distance, ncol=1)
b= apply(a,1,fseed)
par(pty="s")
plot(x=distance, y =b)
```

---

generPoly *Generate a regular grid of polygons*

Description

Generate a regular grid of polygons and optionally write them on a file for input to `califlopp`

Usage

```
generPoly(step = 5, np = 10, file = "data", plot = TRUE)
```

Arguments

`step`	Step of grid, in meter.
`np`	Number of polygons on each axis.
`file`	Pathname of the polygons file to be created. If NULL, no file created.
`plot`	If TRUE, plot of the polygons.

Details

When `file` is not NULL, a polygons file is created. It is in the format 2 of `califlopp` and the values separator is tabulate.

Value

An object of class `"listpoly"`

Note

The polygons are numbered from 1, from the left to the right, then from bottom to top.

See Also

`"listpoly-class"`, `plot.listpoly`

Examples

```
a <- generPoly(np=3, file=NULL)
```

generVois *Generate the neighbors of each polygon of a regular grid*

Description

For each polygon of a regular grid, generate the indexes of its neighbour polygons

Usage

```
generVois(np = 10, nvois = 1)
```

Arguments

np	Number of polygons on each axis of the grid.
nvois	Number of polygons required in the neighbourhood, on each direction, for each polygon

Details

For each polygon P of a regular grid made of np polygons along each axis, the indexes of its neighbours are generated: the neighbours are the polygons included in the square made of nvois polygons below, above, at the right and left sides of P, in the limit of the grid bounds.

Value

A two-columns matrix, of all pairs of neighbourgs.

See Also

generPoly, califlopp

Examples

```
generVois(np=3)
```

getRes *Read a result-file of 'califlopp'*

Description

Return the results stored on a file created by califlopp.

Usage

```
getRes(ficres)
```

Arguments

ficres	Pathname of a result-file created by califlopp.

Value

A data.frame with as many rows as pairs of polygons on the file. The columns are:

poly1, poly2	Identifiers of the polygons.
mean.flow/area	Integrated flow divided by the area of the second polygon. If several dispersion functions have been studied, as many columns as functions. The columns labels are then mean.flow.f1/area, mean.flow.f2/area, etc...
area1, area2	Areas of the polygons in squared meters.
mean.flow, conf.int.lower, conf.int.upper, abs.err, n.eval	when the method is "cubature", only: integrated flow, lower and upper bounds of the confidence interval, absolute error, number of evaluations. If several dispersion functions have been studied, the columns labels are suffixed with ".f1", "f2", etc...
mean.flow, std	when the method is "grid", only: mean of the integrated flow, standard deviation. If several dispersion functions have been studied, the columns labels are suffixed with ".f1", "f2", etc...

Note

This function works when RCALI has been configured with OUTPUT_FILE_FORMAT = LIGHT only (this is the default; see the file src/caliconfig.h to be sure your configuration is compatible).

Details about the returned values can be found in the Reference Manual.

See Also

califlopp

---

listpoly-class *Class 'listpoly'*

Description

A class to store a suite of polygons and its methods.

Objects from the Class

Objects can be created by calls of the function crlistpoly and generPoly

Slots

list List where each component is an object of poly-class

Methods

plot.listpoly, range.listpoly, export.listpoly

See Also

poly-class

---

plot.listpoly *Plot of an object of class 'listpoly'*

Description

Plot all the polygons of an object of class "listpoly", optionnaly with colors.

Usage

```
## S3 method for class 'listpoly'
plot(x, add = F, color = T, ...)
```

Arguments

x	Object of class "listpoly".
add	TRUE, to add to a previous plot, for example after a zoom.
color	TRUE, to fill each polygon in a different color.
...	List of arguments passed as-is to plot.poly

Value

None.

Note

To make a zoom, type in: zoom() (see 'splancs') then use this function with argument "add=TRUE".

plot.poly *Plot of an object of class 'poly'*

Description

Plot an object of class "poly" via the function polymap of the library splancs.

Usage

```
## S3 method for class 'poly'
plot(x, ...)
```

Arguments

x	Object of class "poly".
...	Arguments passed as-it to 'polymap'.

Value

None.

poly-class *Class 'poly'*

Description

A class to store the coordinates of a polygons and its methods.

Objects from the Class

Objects can be created by calls of the functions as.poly and crpoly

Slots

m Matrix with two columns xcoord and ycoord

Methods

plot.poly

See Also

listpoly-class

range.listpoly *Range of the coordinates of an object of class 'listpoly'*

Description

Return the minimum and maximum coordinates over all the polygones of an object of class "listpoly".

Usage

```
## S3 method for class 'listpoly'
range(x, ...)
```

Arguments

x	an object of class "listpoly"
...	arguments passed as-it to the R function range

Value

Matrix ; its two columns are "xrange" and "yrange" and its two lines are "lower" and "upper".

readpoly1 *Read a polygons file in format 1*

Description

Create an object of class "listpoly" from the values read on a polygons file in format 1.

Usage

```
readpoly1(filename, delim=" ")
```

Arguments

filename	Name of the polygons file
delim	Separator character on the file.

Value

An object of class "listpoly", i.e a list, each component of which is an object of class "poly"

See Also

readpoly2

`readpoly2` *Read a polygons file in format 2*

Description

Create an object of class "`listpoly`" from the values read on a polygons file in format 2.

Usage

```
readpoly2(filename, delim="\t")
```

Arguments

`filename`	Name of the polygons file
`delim`	Separator character on the file.

Value

An object of class "`listpoly`", i.e a list, each component of which is an object of class "`poly`"

See Also

readpoly1

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