Package 'APIS'

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Type Package

Title Auto-Adaptive Parentage Inference Software Tolerant to Missing Parents

Version 2.0.8

Description Parentage assignment package.
Parentage assignment is performed based on observed average Mendelian transmission probability distributions or Exclusion.
The main functions of this package are the function APIS_2n(), APIS_3n() and launch_APIShiny(), which perform parentage assignment.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Imports cowplot, data.table, doParallel, dplyr, DT, foreach, ggplot2, gridExtra, htmltools, methods, plotly, rlang, shiny, shinythemes

Depends R (>= 3.5.0), shinyBS

NeedsCompilation yes

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Contents

`APIS_2n` *APIS for diploids*

Description

APIS for diploids

Usage

```
APIS_2n(
  offspring_genotype,
  sire_genotype,
  dam_genotype,
  method = "mendel",
  exclusion_threshold = NULL,
  error = 0.05,
  simulation_if_small = FALSE,
  number_offspring_simulated = max(0, 500 - nrow(offspring_genotype)),
  number_cores = 2,
  verbose = FALSE
)
```

Arguments

`offspring_genotype`	matrix of the offspring genotypes
`sire_genotype`	matrix of the sire genotypes
`dam_genotype`	matrix of the offspring genotypes

`method`	method : "mendel" i.e. likelihood or "exclusion" (default : "mendel"). Can also be "" to select the method a posteriori.
`exclusion_threshold`	threshold for "exclusion" method (default : NULL). Override the error parameter if not NULL
`error`	error accepted (default : 0.05)
`simulation_if_small`	simulate individuals (TRUE or FALSE)
`number_offspring_simulated`	number of offspring simulated (default : 500)
`number_cores`	number of cores
`verbose`	verbose

Value

list of 2 elements : a pedigree file and the log file

Examples

```
data("APIS_offspring")
data("APIS_sire")
data("APIS_dam")

assignment <- APIS_2n(offspring_genotype = APIS_offspring[1:35,1:50],
                      sire_genotype = APIS_sire[ ,1:50],
                      dam_genotype = APIS_dam[ ,1:50],
                      simulation_if_small = FALSE)
```

`APIS_3n` *APIS for triploids*

Description

APIS for triploids

Usage

```
APIS_3n(
  offspring_genotype,
  sire_genotype,
  dam_genotype,
  method = "mendel",
  exclusion_threshold = NULL,
  error = 0.05,
  simulation_if_small = FALSE,
  number_offspring_simulated = max(0, 500 - nrow(offspring_genotype)),
```

```
  number_cores = 2,
  verbose = FALSE,
  t_recom = 0.5
)
```

Arguments

`offspring_genotype`	matrix of the offspring genotypes
`sire_genotype`	matrix of the sire genotypes
`dam_genotype`	matrix of the dam genotypes
`method`	method : "mendel" i.e. likelihood or "exclusion" (default : "mendel"). Can also be "" to select the method a posteriori.
`exclusion_threshold`	threshold for "exclusion" method (default : NULL). Override the error parameter if not NULL
`error`	error accepted (default : 0.05)
`simulation_if_small`	simulate individuals (TRUE or FALSE) (default : TRUE)
`number_offspring_simulated`	number of offspring simulated (default : 500)
`number_cores`	number of cores
`verbose`	verbose
`t_recom`	recombination rate

Value

list of 2 elements : a pedigree file and the log file

Examples

```
data("APIS_offspring3n")
data("APIS_sire")
data("APIS_dam")
assignment <- APIS_3n(offspring_genotype = APIS_offspring3n[1:35,1:50],
                      sire_genotype = APIS_sire[ ,1:50],
                      dam_genotype = APIS_dam[ ,1:50],
                      simulation_if_small = FALSE)
```

`APIS_dam` *Example dam genotypes*

Description

Example dam genotypes

Usage

```
APIS_dam
```

Format

A matrix with 14 rows (one row = one dam) and 100 columns (one column = one marker)

`APIS_offspring` *Example offspring genotypes*

Description

Example offspring genotypes

Usage

```
APIS_offspring
```

Format

A matrix with 500 rows (one row = one offspring) and 100 columns (one column = one marker)

`APIS_offspring3n` *Example offspring 3n genotypes*

Description

Example offspring 3n genotypes

Usage

```
APIS_offspring3n
```

Format

A matrix with 50 rows (one row = one offspring) and 100 columns (one column = one marker)

`APIS_sire` *Example sire genotypes*

Description

Example sire genotypes

Usage

```
APIS_sire
```

Format

A matrix with 39 rows (one row = one sire) and 100 columns (one column = one marker)

`assignment_power` *Assignment power*

Description

Assignment power

Usage

```
assignment_power(
  sire_genotype,
  dam_genotype,
  ploidy_level = 2,
  verbose = FALSE
)
```

Arguments

`sire_genotype`	matrix of the sire genotypes
`dam_genotype`	matrix of the dam genotypes
`ploidy_level`	ploidy level of the parents
`verbose`	verbose

Value

the theoretical assignment power calculated with the formula proposed in Vandeputte (2012)

Examples

```
data("APIS_sire")
data("APIS_dam")

P = assignment_power(sire_genotype = APIS_sire, dam_genotype = APIS_dam)
```

`import_from_ped` *Import from Plink .ped*

Description

Import from Plink .ped

Usage

```
import_from_ped(
  ped_file,
  no_fid = FALSE,
  no_parents = FALSE,
  no_sex = FALSE,
  no_pheno = FALSE,
  marker_names = NULL
)
```

Arguments

`ped_file`	name of the ped file (from Plink)
`no_fid`	if "no_fid" parameter was used in plink (default : FALSE)
`no_parents`	if "no_parents" parameter was used in plink (default : FALSE)
`no_sex`	if "no_sex" parameter was used in plink (default : FALSE)
`no_pheno`	if "no_pheno" parameter was used in plink (default : FALSE)
`marker_names`	list of marker names (default : NULL)

Value

matrix of genotypes for APIS

`import_from_vcf` *Import from .vcf*

Description

Import from .vcf

Usage

```
import_from_vcf(vcf_file)
```

Arguments

`vcf_file`	name of the vcf file

Value

matrix of genotypes for APIS

`launch_APIShiny` *Shiny App for interactive session of APIS*

Description

Launch the shiny interface to use APIS interactively

Usage

```
launch_APIShiny()
```

Value

void : most results are automatically saved

`plot_delta` *Plot deltas*

Description

Plot deltas

Usage

```
plot_delta(log_file, threshold = NULL, simulated_individuals = NULL)
```

Arguments

`log_file`	log file from the APIS_2n() or APIS_3n function
`threshold`	threshold
`simulated_individuals`	names of the simulated individuals

Value

plot of the distribution of delta

`plot_mismatches` *Plot mismatches*

Description

Plot mismatches

Usage

```
plot_mismatches(log_file, threshold = NULL, simulated_individuals = NULL)
```

Arguments

`log_file`	log file from the APIS_2n() or APIS_3n function
`threshold`	threshold
`simulated_individuals`	names of the simulated individuals

Value

plot of the distribution of mismatches

`plot_probabilities` *Plot probabilities*

Description

Plot probabilities

Usage

```
plot_probabilities(log_file, threshold = NULL, simulated_individuals = NULL)
```

Arguments

`log_file`	log file from the APIS_2n() or APIS_3n function
`threshold`	threshold
`simulated_individuals`	names of the simulated individuals

Value

plot of the distribution of probabilities

`simulate_offspring` *Simulate offspring*

Description

Simulate offspring

Usage

```
simulate_offspring(
  sire_genotype,
  dam_genotype,
  number_offspring,
  ploidy_level = 2,
  sire_contribution = 1,
  dam_contribution = 1,
  recombination_rate = 0.5,
  genotyping_error = 0.01
)
```

Arguments

`sire_genotype`	sire genotype
`dam_genotype`	dam genotype
`number_offspring`	number of offspring to simulate
`ploidy_level`	ploidy level of offspring
`sire_contribution`	sire contribution
`dam_contribution`	dam contribution
`recombination_rate`	recombination rate (only important for tri/tetra ploids offspring)
`genotyping_error`	genotyping error

Value

list with matrix with simulated offspring and pedigree

Examples

```
data("APIS_sire")
data("APIS_dam")

# For diploide offspring
simulate_offspring(sire_genotype=APIS_sire, dam_genotype=APIS_dam,
                   number_offspring=10,
                   ploidy_level = 2,
                   sire_contribution = 1, dam_contribution = 1,
                   recombination_rate = 0.5,
                   genotyping_error = 0.01)

# For triploide offspring
simulate_offspring(sire_genotype=APIS_sire, dam_genotype=APIS_dam,
                   number_offspring=10,
                   ploidy_level = 3,
                   sire_contribution = 1, dam_contribution = 2,
                   recombination_rate = 0.5,
                   genotyping_error = 0.01)
```

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