Package 'APIS'

October 2, 2024

Type Package

Title Auto-Adaptive Parentage Inference Software Tolerant to Missing
Parents

Version 2.0.7

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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Date/Publication 2024-10-02 12:10:06 UTC

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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