

Package ‘APIS’

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Type Package

Title Auto-Adaptive Parentage Inference Software Tolerant to Missing Parents

Version 2.0.2

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

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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 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)

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	<i>Example dam genotypes</i>
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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	<i>Example offspring genotypes</i>
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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	<i>Example offspring 3n genotypes</i>
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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	<i>Example sire genotypes</i>
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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	<i>Assignment power</i>
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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	<i>Import from Plink .ped</i>
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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	<i>Plot deltas</i>
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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	<i>Plot mismatches</i>
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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 ploid 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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