

# Package: APIS (via r-universe)

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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.

**License** GPL

**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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**Config/pak/sysreqs** cmake make libicu-dev libuv1-dev libssl-dev zlib1g-dev

**Repository** <https://julienrocheigepp.r-universe.dev>

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APIS\_2n

*APIS for diploids*

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### 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)

```

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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)

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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)

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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)
```

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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	<i>Import from .vcf</i>
-----------------	-------------------------

---

**Description**

Import from .vcf

**Usage**

```
import_from_vcf(vcf_file)
```

**Arguments**

vcf_file	name of the vcf file
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**Value**

matrix of genotypes for APIS

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launch_APIshiny	<i>Shiny App for interactive session of APIS</i>
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**Description**

Launch the shiny interface to use APIS interactively

**Usage**

```
launch_APIshiny()
```

**Value**

void : most results are automatically saved

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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

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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 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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