Package ‘forensim’

June 2, 2009

Type Package

Title Statistical tools for the interpretation of forensic DNA mixtures

Version 1.0-0

Date 2009-01-19

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Depends methods

Description Statistical methods and simulation tools for the interpretation of forensic DNA mixtures

License (>=2)

LazyLoad yes


R topics documented:

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forensim-package

The forensim package

Description

forensim is dedicated to the interpretation of forensic DNA mixtures through statistical methods. It relies on three S4 classes that facilitate the manipulation and the storage of genetic data produced in forensic casework: tabfreq, simugeno and simumix. 

tabfreq objects are used to store allele frequencies, simugeno objects are used to store genotypes and simumix objects are used to store DNA mixtures.

For more information about these classes type `class ?tabfreq`, `class ?simugeno` and `class ?simumix`.

Author(s)

Hinda Haned <haned@biomserv.univ-lyon1.fr>

Accessors for forensim objects

Description

Accessors for forensim objects: simugen, simumix and tabfreq. "$" and "$<-" are used to access the slots of an object, they are equivalent to "@" and "@<-".

Value

A simugeno, a simumix or a tabfreq object.

Author(s)

Hinda Haned (<haned@biomserv.univ-lyon1.fr)>
changepop

Examples

data(strusa)
class(strusa)

strusa@pop.names
#equivalent
strusa$pop.names

data(strveneto)
tabi <- simugen ostrveneto, n=100)
tab2 <- changepop(tabi, "Veneto", "VENE")
tabi$pop.names
tab2$pop.names

changepop  Function to change population related information in forensim objects

Description

The changepop function changes population related information in tabfreq, simugen or simumix objects

Usage

cangepop(obj, oldpop, newpop)

Arguments

obj  a forensim object, either a tabfreq, a simugen or a simumix object
oldpop  a character vector giving the population names to be changed
newpop  a character vector giving the new population names

Value

a forensim object where the slots containing population related information have been modified

Author(s)

Hinda Haned  haned@biomserv.univ-lyon1.fr

Examples

data(strveneto)
tabi <- simugen ostrveneto, n=100)
tab2 <- changepop(tabi, "Veneto", "VENE")
tabi$pop.names
tab2$pop.names
The number of all possible combinations of $m$ elements among $n$ with repetitions.

**Description**

The number of all possible combinations of $m$ elements among $n$ with repetitions.

**Usage**

\[ Cmn(m, n) \]

**Arguments**

- $m$: the $m$ elements to combine among $n$
- $n$: the $n$ elements from which to combine $m$ elements with repetitions

**Details**

There are \((n+m-1)!/(m!(n-1)!))\ ways to combine $m$ elements among $n$ with repetitions.

**Note**

$Cmn$ was implemented as an auxiliary function for the $dataL$ function which computes the likelihood of a mixture alleles conditional on the number of contributors.

**Author(s)**

Hinda Haned <haned@biomserv.univ-lyon1.fr>

**See Also**

- $comb$ for all possible combinations of $m$ elements among $n$ with repetitions

**Examples**

\[ Cmn(2, 3) \]
\[ comb(2, 3) \]
**comb**

Generate all possible combinations of \( m \) elements among \( n \) with repetitions.

**Description**

Generate all possible combinations of \( m \) elements among \( n \) with repetitions.

**Usage**

\[
\text{comb}(m, n)
\]

**Arguments**

- \( m \) the number of elements to combine
- \( n \) the number of elements from which to combine the \( m \) elements

**Details**

There are \((n+m-1)!/(m!(n-1)!))\) ways to combine \( m \) elements among \( n \) with repetitions, `combn` generates all these possible combinations.

**Value**

A matrix of \((n+m-1)!/(m!(n-1)!))\) rows, and \( n \) columns, each row is a possible combination of \( m \) elements among \( n \).

**Author(s)**

Hinda Haned \(<\text{haned@biomserv.univ-lyon1.fr}>\)

**See Also**

`Cmn` for the calculation of the number of all possible combinations of \( m \) elements among \( n \) with repetitions

**Examples**

```r
#combine 2 objects among 3 with repetitions
Cmn(2, 3)
comb(2, 3)
```
The function `dataL` gives the likelihood of a set of alleles observed at a specific locus conditional on the number of contributors that gave these alleles. Calculation is based upon the frequencies of the observed alleles.

**Usage**

```r
dataL(x = 1, p, theta = 0)
```

**Arguments**

- `x`: an integer giving the number of contributors
- `p`: a numeric vector giving the frequencies of the observed alleles in the mixture
- `theta`: a float in [0,1]. `theta` is equivalent to Wright’s Fst. In case of population subdivision, it allows a correction of the allele frequencies in the subpopulation of interest

**Note**

`dataL` function has several similarities with the `Pevid.gen` function of the `forensic` package which computes the probability of the DNA evidence. `dataL` implements a particular case of this probability. Please see [http://cran.r-project.org/web/packages/forensic/](http://cran.r-project.org/web/packages/forensic/)

**Author(s)**

Hinda Haned ⟨haned@biomserv.univ-lyon1.fr⟩

**References**


**See Also**

`lik.loc` and `lik` for calculating the likelihood of a given `simumix` object

**Examples**

```r
# likelihood of observing two alleles at frequencies 0.1 and 0.01 when the number of contributors is 2, in two cases: theta=0 and theta=0.03
dataL(x=2, p=c(0.1,0.01), theta=0)
dataL(x=2, p=c(0.1,0.01), theta=0.03)
```
##### findfreq

*findfreq*  
*Finds the frequencies of the alleles of a mixture from a tabfreq object*

**Description**

The `findfreq` function finds the frequencies of the alleles of a mixture stored in a simumix object, from a given tabfreq object. If the tabfreq object contains multiple populations, a reference population from which to extract the frequencies must be specified.

**Usage**

```r
findfreq(mix, freq, refpop = NULL)
```

**Arguments**

- `mix`: a `simumix` object  
- `freq`: a `tabfreq` object from which to extract the allele frequencies of the mixture  
- `refpop`: a factor giving the reference population in `tabfreq` from which to extract the allele frequencies

**Value**

A list giving the allele frequencies for each locus.

**Author(s)**

Hinda Haned <haned@biomserv.univ-lyon1.fr>

**See Also**

- `simumix`

**Examples**

```r
data(strusa)
s2<-simumix(simugeno(strusa,n=c(0,2000,0)),ncontri=c(0,2,0))
findfreq(s2,strusa,refpop="Cauc")
```

---

##### findmax

*findmax*  
*Function to find the maximum of a vector and its position*

**Description**

The `findmax` function finds the maximum of a vector and its position.

**Usage**

```r
findmax(vec)
```
Arguments

vec a numeric vector

Details

findmax finds the maximum value of a vector and its position.

Value

A matrix of two rows:

max the position of the maximum in vec

maxval the maximum

Note

findmax is an auxiliary function for the dataL function, used to compute the likelihood of a mixture alleles given the number of contributors.

Author(s)

Hinda Haned <haned@biomserv.univ-lyon1.fr>

Examples

findmax(1:10)

lik Likelihood of the alleles observed at different loci in a DNA mixture conditional on the number of contributors to the mixture

Description

The lik function computes the likelihood of the observed alleles in a forensic DNA mixture, for a set of loci, conditional on the number of contributors to the mixture. The overall likelihood is computed as the product of loci likelihoods.

Usage

lik(x = 1, mix, freq, refpop = NULL, theta = NULL, loc=NULL)

Arguments

x the number of contributors to the DNA mixture, default is 1
mix a simumix object which contains the mixture to be analyzed
freq a tabfreq object from which to extract the allele frequencies
refpop a factor giving the reference population in tabfreq from which to extract the mixture allele frequencies. This argument is used only if freq contains allele frequencies for multiple populations, otherwise it is by default set to NULL
theta a float from [0,1] giving Wright’s Fst coefficient. theta accounts for population subdivision while computing the likelihood of the data
loc loci for which the overall likelihood shall be computed. Default (NULL) corresponds to all loci
lik.loc

Details

lik computes the likelihood of the alleles observed at all loci conditional on the number of contributors. This function implements a particular case of the general formula of the match probability in the case of subdivided populations (Curran et al, 1999), in the particular case where all contributors are unknown.

Wright’s Fst coefficient given in the theta argument allows accounting for population subdivision when all contributors belong to the same subpopulation.

The likelihood for multiple loci is computed as the product of loci likelihoods.

Author(s)

Hinda Haned <haned@biomserv.univ-lyon1.fr>

References


See Also

lik.loc for the likelihood per locus, likestim and likestim.loc for the estimation of the number of contributors to a DNA mixture through likelihood maximization

Examples

data(strusa)
#simulation of 1000 genotypes from the African American allele frequencies
gen<-simugeno(strusa,n=c(1000,0,0))
#3-person mixture
mix3<-simumix(gen,ncontri=c(3,0,0))
sapply(1:3, function(i) lik(x=i,mix3, strusa, refpop="Afri"))

lik.loc

Likelihood per locus of the alleles observed in a DNA mixture conditional on the number of contributors to the mixture

Description

The lik.loc function computes the likelihood of the observed data in a forensic DNA mixture, for each of the loci involved, conditional on the number of contributors to the mixture.

Usage

lik.loc(x = 1, mix, freq, refpop = NULL, theta = NULL, loc=NULL)
Arguments

\( x \)  the number of contributors to the DNA mixture

\( \text{mix} \)  a simumix object which contains the mixture to be analyzed

\( \text{freq} \)  a tabfreq object from which to extract the mixture allele frequencies

\( \text{refpop} \)  a factor giving the reference population in tabfreq from which to extract the mixture allele frequencies

\( \theta \)  a float from \([0,1]\) giving Wright’s Fst coefficient. \( \theta \) counts for population subdivision while computing the likelihood of the data.

\( \text{loc} \)  the loci for which the likelihood shall be computed. Default (set to NULL) corresponds to all loci.

Details

\text{lik.loc} \) computes the likelihood per locus of the observed alleles. This function implements a particular case of the general formula of the match probability in the case of subdivided populations (Curran et al., 1999), in the particular case where all contributors are unknown. The Fst coefficient given in the \( \theta \) argument allows accounting for population subdivision when all contributors belong to the same subpopulation.

Value

The function \text{lik.loc} returns a vector, of length the number of loci in \( \text{loc} \), giving the likelihood of the data for each locus.

Author(s)

Hinda Haned <haned@biomserv.univ-lyon1.fr>

References


See Also

\text{lik} for the overall loci likelihood, \text{likestim} and \text{likestim.loc} for the estimation of the number of contributors to a DNA mixture through likelihood maximization

Examples

data(strusa)
# simulation of 1000 genotypes from the Caucasian allele frequencies
gen<-simugen0(strusa,n=c(0,100,0))

# 4-person mixture
mix4<-simumix(gen,ncontri=c(0,4,0))
lik.loc(x=2,mix4,strusa,refpop="Cauc")
likestim

Maximum of likelihood estimation of the number of contributors to a forensic DNA mixture for a set of loci

Description

The likestim function gives multiloci estimation of the number of contributors to a forensic DNA mixture using likelihood maximization.

Usage

likestim(mix, freq, refpop = NULL, theta = NULL, loc=NULL)

Arguments

mix  
a simumix object
freq  
a tabfreq object containing the allele frequencies to use for the likelihood calculation
refpop  
the reference population from which to extract the allele frequencies used in the likelihood calculation. If tabfreq contains more than one population, refpop must be specified, otherwise, refpop is set to default (NULL).
theta  
a float from [0,1] giving Wright’s Fst coefficient. theta accounts for population subdivision while computing the likelihood of the data.
loc  
loci to be considered in the estimation. Default (set to NULL) corresponds to all loci.

Details

The number of contributors which maximizes the likelihood of the data observed in the mixture is searched in the discrete interval [1,6]. In most cases this interval is a plausible range for the number of contributors.

Value

A matrix, the first row, max, gives the maximum likelihood estimation of the number of contributors, the second row gives the corresponding likelihood value maxvalue.

Author(s)

Hinda Haned <haned@biomserv.univ-lyon1.fr>
References


See Also

likestim.loc for maximum of likelihood estimations per locus

Examples

data(strusa)
#simulation of 1000 genotypes from the Hispanic allele frequencies
gen<-simugen(strusa,n=c(0,0,100))
#4-person mixture
mix4 <- simumix(gen,ncontri=c(0,0,4))
likestim(mix4,strusa,refpop="Hisp")

###

likestim.loc  Maximum of likelihood estimation per locus of the number of contributors to forensic DNA mixtures.

Description

The likestim.loc function returns the estimation of the number of contributors, at each locus, obtained by maximizing the likelihood.

Usage

likestim.loc(mix, freq, refpop = NULL, theta = NULL, loc = NULL)

Arguments

mix  a simumix object
freq  a tabfreq object containing the allele frequencies to use for the likelihood calculation
refpop  the reference population from which to extract the allele frequencies used in the likelihood calculation. Default set to NULL, if tabfreq contains more than one population, refpop must be specified
theta  a float from [0,1] giving Wright's Fst coefficient. theta accounts for population subdivision while computing the likelihood of the data.
loc  loci to be considered in the estimation. Default (set to NULL) corresponds to all loci.
Details

The number of contributors which maximizes the likelihood of the data observed in the mixture is searched in the discrete interval $[1,6]$. In most cases this interval is a plausible range for the number of contributors.

Value

A matrix of dimension $2 \times \text{loc}$. The first row, $\max$, gives the maximum likelihood estimation of the number of contributors for each locus in column. The second row, $\maxvalue$, gives the corresponding likelihood value.

Author(s)

Hinda Haned <haned@biomserv.univ-lyon1.fr>

References

Haned H, Pontier D, Lobry J R, Pene L, Dufour AB. Estimating the number of contributors to forensic DNA mixtures: does maximizing the likelihood performs better than the maximum allele count? In prep., 2009.


See Also

`likestim` for multiloci estimations

Examples

data(strusa)
# simulation of 1000 genotypes from the Hispanic allele frequencies
gen<-simugen(strusa,n=c(0,0,100))
# 4-person mixture
mix4 <- simumix(gen,ncontri=c(0,0,4))
likestim.loc(mix4,strusa,refpop="Hisp")

`mincontri` gives the minimum number of contributors required to explain a forensic DNA mixture. This method is also known as the maximum allele count as it relies on the maximum number of alleles showed through all available loci.
Usage

\[ \text{mincontri}(\text{mix, loc = NULL}) \]

Arguments

- **mix**: a `simumix` object
- **loc**: the loci to consider for the calculation of the minimum of contributors, default (NULL) corresponds to all loci

Author(s)

Hinda Haned ⟨haned@biomserv.univ-lyon1.fr⟩

See Also

`likestim` for the estimation of the number of contributors through likelihood maximization

Examples

```r
data(strusa)
# simulation of 1000 genotypes from the African American allele frequencies
gen<-simugeno(strusa,n=c(1000,0,0))
# 5-person mixture
mix5<-simumix(gen,ncontri=c(5,0,0))
# compare
likestim(mix5, strusa, refpop="Afri")
mincontri(mix5)
```

---

**naomitab**

Handling of missing values in a data frame

Description

`naomitab` handles missing values (NA) in a data frame: it returns a list of the columns where NAs have been removed.

Usage

```
naomitab(tab)
```

Arguments

- **tab**: a data frame

Value

Returns a list of length the number of columns in `tab` where each component is a column of `tab`, and the values are the corresponding rows where NAs have been removed.
Note
This function was designed to handle missing values in data frames in the format of the Journal of Forensic Sciences for population genetic data: allele names are given in the first column, and frequencies for a given allele are read in rows for different loci. When a given allele is not observed, the value is coded NA (originally coded "-" in the journal).

Author(s)
Hinda Haned <haned@biomserv.univ-lyon1.fr>

See Also
tabfreq

Examples
data(Tu)
naomitab(Tu)

| nball | Number of alleles in a mixture |

Description
nball gives the number of alleles of a simumix object.

Usage
nball(mix, byloc = FALSE)

Arguments

mix 
a simumix object

byloc 
a logical indicating whether the number of alleles must be calculated by locus or for all loci (default)

Author(s)
Hinda Haned <haned@biomserv.univ-lyon1.fr>

See Also
simumix

Examples
data(strusa)
# simulating 100 genotypes with allele frequencies from the African American population
gaa<-simugen0(strusa,n=c(100,0,0))
# simulating a 4-person mixture
maa4<-simumix(gaa,ncontri=c(4,0,0))
nball(maa4,byloc=TRUE)
Description

Computes the exclusion probability of a mixture stored in a simumix object.

Usage

PE(mix, freq, refpop = NULL, theta = 0, byloc = FALSE)

Arguments

- **mix**: a simumix object
- **freq**: a tabfreq object giving the allele frequencies from which to compute the exclusion probability
- **refpop**: character giving the reference population, used only if freq contains allele frequencies for multiple populations
- **theta**: a float from [0,1] giving Wright’s Fst coefficient. theta accounts for population subdivision while computing the likelihood of the data.
- **byloc**: logical, if TRUE, than the exclusion probability is computed per locus, if FALSE (default), the calculations are done for all loci simultaneously

Details

PE gives the exclusion probability at a locus, or at several loci when conditions for Hardy Weinberg are met. If this condition is not met in the population, than a value for theta must be supplied to take into account dependencies between alleles. The formula of the exclusion probability that allows taking into account departure from Hardy Weinberg proportions due to population subdivision was provided by Bruce Weir, please see the references section.

Author(s)

Hinda Haned <haned@biomserv.univ-lyon1.fr>

References


Examples

data(strusa)
gen1<-simugen(strusa,n=c(0,0,100))
mix2 <-simumix(gen1,ncontri=c(0,0,2))
PE(mix2,strusa,"Hisp",byloc=TRUE)
Function to simulate allele frequencies for independent loci from a Dirichlet model

Description

The `simufreqD` function simulates single population allele frequencies for independent loci. Allele frequencies are generated as random deviates from a Dirichlet distribution, the parameters of which control the mean and the variance of the simulated allele frequencies.

Usage

```
simufreqD(nloc = 1, nal = 2, alpha = 1)
```

Arguments

- `nloc` the number of loci to simulate
- `nal` the numbers of alleles per locus. Either an integer, if the loci have the same number of alleles, or an integer vector, if the number of alleles differ between loci
- `alpha` the parameter used to simulate allele frequencies from the Dirichlet distribution. If the `nloc` loci have the same allele number, `alpha` can either be the same for all alleles (default is one: uniform distribution), in this case `alpha` is an integer, or `alpha` can be different between alleles at a given locus, in this case, `alpha` is a matrix of dimension `nal x nloc`.
  When the number of alleles differ between loci, `alpha` can either be the same or differ between alleles at a given locus. In the first case `alpha` is a vector of length `nloc`, in the second case, `alpha` is a matrix of dimensions `nal x nloc` where NAs are introduced for alleles not seen at a given locus.

Details

Allele frequencies for independent loci are simulated using a Dirichlet distribution with parameter `alpha`. At a given locus `L` with `n` alleles, the allele frequencies are modeled as a vector of random variables `p=(p1, ..., pn)`, following a Dirichlet distribution with parameters:

```
alpha = (alpha1, ..., alphan)
```

where `p1+...+pn=1` and `alpha1,..., alphan > 0`.

Value

A matrix containing the simulated allele frequencies. The data is presented in the format of the Journal of Forensic Sciences for genetic data: allele names are given in the first column, and frequencies for a given allele are read in rows for the different markers in columns. When an allele is not observed for a given locus, the value is coded NA (instead of "-" in the original format).

Note

The code used here for the generation of random Dirichlet deviates was previously implemented in the gtools library.

Author(s)

Hinda Haned ⟨haned@biomserv.univ-lyon1.fr⟩
References


See Also

simupopD

Examples

# simulate alleles frequencies for 5 markers with respectively 2, 3, 4, 5, and 6 alleles
simufreqD(nloc=5,na=c(2,3,4,5,6), alpha=1)

Description

The S4 simugen class is used to store existing or simulated genotypes.

Slots

tab.freq: a list giving allele frequencies for each locus. If there are several populations, tab.freq gives allele frequencies in each population

nind: integer vector giving the number of individuals. If there are several populations, nind gives the numbers of individuals per population

pop.names: factor of populations names

pop.ind: factor giving the population of each individual

which.loc: character vector giving the locus names

tab.geno: matrix giving the genotypes (in rows) for each locus (in columns). The genotype of a homozygous individual carrying the allele "12" is coded "12/12". A heterozygous individual carrying alleles "12" and "13" is coded "12/13" or "13/12".

indID: character vector giving the individuals ID

Methods

names signature(x = "simugen"): gives the names of the attributes of a simugen object

show signature(object = "simugen"): shows a simugen object

print signature(object = "simugen"): prints a simugen object

Author(s)

Hinda Haned ⟨haned@biomserv.univ-lyon1.fr⟩
**simugeno constructor**

**See Also**

*as.simugeno* for the simugeno class constructor, *is.simugeno*, *simumix* and *tabfreq*

**Examples**

```
showClass("simugeno")
```

---

**Description**

Constructor for *simugeno* objects.

The function *simugeno* creates a *simugeno* object from a *tabfreq* object.

The function *as.simugeno* is an alias for *simugeno* function.

*is.simugeno* tests if an object is a valid simugeno object.

Note: to get the manpage about *simugeno*, please type ‘class ? simugeno’.

**Usage**

```
simugeno(tab, which.loc=NULL, n=1)
as.simugeno(tab, which.loc=NULL, n=1)
is.simugeno(x)
```

**Arguments**

- **tab**: a tabfreq object created with constructor *tabfreq*
- **which.loc**: a character vector giving the chosen loci for the genotypes simulation. The default is set to NULL, which corresponds to all the loci of the *tabfreq* object given in argument
- **n**: integer vector giving the number of individuals. If there are several populations, *n* gives the numbers of individuals to simulate per population. For a single population, default is 1.
- **x**: an object

**Value**

For *simugeno* and *as.simugeno*, a *simugeno* object. For *is.simugeno*, a logical.

**Author(s)**

Hinda Haned ⟨haned@biomserv.univ-lyon1.fr⟩
See Also

"simugenoc", and tabfreq for creating a tabfreq object from a data file.

Examples

```r
data(Tu)
tab<-tabfreq(Tu)
#simulation of 3 individual genotypes for the STR marker FGA
gen1 <- simugenoc(tab,which.loc='FGA', n =1000)
gen1@tab.geno
```

---

**simumix**

*forensic class for DNA mixtures*

**Description**

The S4 simumix class is used to store DNA mixtures of individual genotypes along with informations about the individuals populations and the loci used to simulate the genotypes.

**Slots**

- **ncontri**: integer vector giving the number of contributors to the DNA mixture. If there are several populations, ncontri gives the number of contributors per population
- **mix.prof**: matrix giving the contributors genotypes (in rows) for each locus (in columns). The genotype of a homozygous individual carrying the allele "12" is coded "12/12". A heterozygous individual carrying alleles "12" and "13" is coded "12/13" or "13/12".
- **mix.all**: list giving the alleles present in the mixture for each locus
- **which.loc**: character vector giving the locus names
- **popinfo**: factor giving the population of each contributor

**Methods**

- **names** signature(x = "simumix"): gives the names of the attributes of a simumix object
- **show** signature(object = "simumix"): shows a simumix object
- **print** signature(object = "simumix"): prints a simumix object

**Author(s)**

Hinda Haned ⟨haned@biomserv.univ-lyon1.fr⟩

**See Also**

simugenoc, as.simumix, is.simumix, simugenoc and tabfreq

**Examples**

```r
showClass("simumix")
data(strusa)
```
Description

Constructor for simumix objects. The function simumix creates a simumix object from a tabfreq object.

The function as.simumix is an alias for simumix function.

is.simumix tests if an object is a valid simumix object.

Note: to get the manpage about simumix, please type ’class ? simumix’.

Usage

```r
simumix(tab,which.loc=NULL,ncontri=1)
as.simumix(tab,which.loc=NULL,ncontri=1)
is.simumix(x)
```

Arguments

- `tab` a simugen object created with constructor simugen
- `which.loc` a character vector giving the chosen loci for the genotypes simulation. The default is set to NULL, which corresponds to all the loci of the simugen object given in argument
- `ncontri` integer vector giving the number of individuals. If there are several populations, ncontri gives the numbers of individuals to simulate per population. Default is one.
- `x` an object

Value

For simumix and as.simumix, a simumix object. For is.simumix, a logical.

Author(s)

Hinda Haned ⟨haned@biomserv.univ-lyon1.fr⟩

See Also

"simumix", simugen for creating a simugen object.

Examples

```r
data(Tu)
tab<-simugen(tabfreq(Tu),n=1200)
#simulation of a 3-person mixture characterized with markers FGA, TH01 and TPOX
simumix(tab,which.loc=c('FGA','TH01', 'TPOX') , n =3)
```
simupopD  

Simulate multi-population allele frequencies for independent loci from  
a reference population, following a Dirichlet model

Description

Simulate multi-population allele frequencies for independent loci, from a given reference population, following a Dirichlet model. Allele frequencies in the populations are generated as random deviates from a Dirichlet distribution, the parameters of which control the deviation of allele frequencies from the values in the reference population.

Usage

simupopD(npop = 1, nloc = 1, na = 2, globalfreq = NULL, which.loc = NULL, alpha1, alpha2 = 1)

Arguments

- `npop` the number of populations
- `nloc` the number of loci
- `na` an integer vector giving the numbers of alleles per locus
- `globalfreq` matrix of allele frequencies in the reference population. Data must be given in the format of the Journal of Forensic Sciences for genetic data. Default corresponds to allele frequencies generated form a Dirichlet distribution with parameter \( \alpha_2 \) for all allele frequencies.
- `which.loc` which loci to simulate from the `globalfreq` matrix, default considers all loci
- `alpha1` a positive float vector of length `npop` giving the variance parameter of the Dirichlet distribution used to generate allele frequencies in the `npop` independent populations
- `alpha2` a positive float giving the parameter to be used to in the Dirichlet distribution to generate allele frequencies for the reference population

Details

In the reference population, allele frequencies for independent loci are simulated using a Dirichlet distribution with parameter \( \alpha_2 \).

At a given locus L with \( n \) alleles, the allele frequencies are modeled as a vector of random variables \( p=(p_1, ..., p_n) \) following a Dirichlet distribution with a parameter vector of length \( n \), where each component is equal to \( \alpha_2 \), \( p_1+...+p_n=1 \) and \( \alpha_2 > 0 \).

Note that a more sophisticated generation of global allele frequencies is possible using the `simufreqD` function. Similarly, allele frequencies in the independent populations are simulated using a Dirichlet Distribution. For example, for the first population to simulate, at a given locus L with \( n \) alleles, the allele frequencies are modeled as a vector of random variables \( p=(p_1, ..., p_n) \) following a Dirichlet distribution with a parameter vector of length \( n \):

\( (p_1(1-\alpha_1/\alpha_1[1]), ..., p_n(1-\alpha_1[1]/\alpha_1[1])), \) where \( p_1+...+p_n=1 \) and \( \alpha_1[1] > 0 \).

\( \alpha_1[1] \) is the variance parameter for population 1 and is equivalent to Wright’s Fst. The closest this parameter is to one, the more the population allele frequencies are different from the values of the reference population.
Value

The result is stored in a list with two elements:

- `globfreq`: a tabfreq object giving the allele frequencies of the chosen reference population, with the chosen loci.
- `popfreq`: a tabfreq object giving the allele frequencies of the simulated populations.

Note

The code used here for the generation of random Dirichlet deviates was previously implemented in the gtools library.

Author(s)

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References


See Also

- `simufreqD`

Examples

```r
# simulate allele frequencies for two populations
data(Tu)
simupopD(npop=2,globalfreq=Tu, which.loc=c("FGA","TH01","TPOX"),
alph1=c(0.2,0.3),alpha2=1)
```

---

strusa

Allele frequencies for 15 autosomal short tandem repeats core loci on U.S. Caucasian, African American, and Hispanic populations.

Description

Allele frequencies for 15 autosomal short tandem repeats loci on three American populations: Caucasians, African Americans and Hispanics. Among the 15 loci, 13 belong to the core Combined DNA Index System (CODIS) loci used by the Federal Bureau of Investigation (USA), in forensic DNA analysis, and two supplementary loci are more commonly used in Europe, see details.
Usage

data(strusa)

Format

strusa is a tabfreq object giving allele frequencies of 15 loci in three American populations.

Details

CSF1PO, FGA, TH01, TPOX, vWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51 and D21S11, belong to the core CODIS loci used in the US, whereas D2S1338 and D19S433 belong to the European core loci.

References


Examples

data(strusa)
strusa
#genotypes simulations from each population
geno<- simugen(strusa,n=c(100,100,100))
geno
#3-person mixture simulation with the contributors from the 3 populations
mix3<- simumix(geno,ncontri=c(1,1,1))
mix3

strveneto

Population study of three miniSTR loci in Veneto (Italy)

Description

Allele frequencies for three short tandem repeats loci D10S1248, D2S441 and D22S1045 in a sample of 198 individuals born in Veneto, Italy. These loci are commonly used in forensic DNA characterization.

Usage

data(strveneto)

Format

strveneto is a tabfreq object
tabfreq

References


Examples

data(strveneto)
#allele frequencies
strveneto@tab

tabfreq  forensim class for population allele frequencies

Description

The S4 tabfreq class is used to store allele frequencies, from either one or several populations.

Slots

tab: a list giving allele frequencies for each locus. If there are several populations, tab gives allele frequencies in each population

which.loc: character vector giving the names of the loci

pop.names: factor of populations names (optional)

Methods

names signature(x = "tabfreq"): gives the names of the attributes of a tabfreq object

show signature(object = "tabfreq"): shows a tabfreq object

print signature(object="tabfreq"): prints a tabfreq object

Author(s)

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See Also

as.tabfreq, is.tabfreq and simugen for genotypes simulation from allele frequencies stored in a tabfreq object

Examples

showClass("tabfreq")
Description

Constructor for `tabfreq` objects.

The function `tabfreq` creates a `tabfreq` object from a data frame or a matrix giving allele frequencies for a single population in the Journal of Forensic Sciences (JFS) format for population genetic data. When multiple populations are considered, data shall be given as a list, where each element is either a matrix or a data frame in the JFS format, and the populations names must be specified.

The function `as.tabfreq` is an alias for the `tabfreq` function.

`is.tabfreq` tests if an object is a valid `tabfreq` object.

Note: to get the manpage about `tabfreq`, please type `class ? tabfreq`.

Usage

```r
tabfreq(tab, pop.names=NULL)
as.tabfreq(tab, pop.names=NULL)
is.tabfreq(x)
```

Arguments

- `tab`: either a matrix or a data.frame of markers allele frequencies given in the Journal of Forensic Sciences format for population genetic data.
- `pop.names`: (optional) a factor giving the populations names. For a single population in `tab`, default is set to `NULL`.
- `x`: an object

Value

For `tabfreq` and `as.tabfreq`, a `tabfreq` object. For `is.tabfreq`, a logical.

Author(s)

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See Also

"`tabfreq`, `simugenon` for creating a simugenon object from a tabfreq object.

Examples

```r
data(Tu)
tabfreq(Tu, pop.names=factor("Tu"))
```
**Tu**

*Allele frequencies of 15 autosomal short tandem repeats loci on Chinese Tu ethnic minority group*

**Description**

Population genetic analysis of 15 STR loci of Chinese Tu ethnic minority group.

**Usage**

```r
data(Tu)
```

**Format**

A data frame presented in the format of the Journal of Forensic Sciences for genetic data: allele names are given in the first column, and frequencies for a given allele are read in rows for the different markers. When a given allele is not observed, value is coded NA (rather than "-" in the original format).

**Details**

CSF1PO, FGA, TH01, TPOX, vWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51 and D21S11, belong to the core CODIS loci used in the US, whereas D2S1338 and D19S433 belong to the European core loci.

**References**


**Examples**

```r
data(Tu)
tabfreq(Tu)
```

**virtualClasses**

*Virtual classes for forensim*

**Description**

Virtual classes that are only for internal use in forensim

**Objects from the Class**

A virtual Class: programming tool, not intended for objects creation.

**Author(s)**

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