Package 'VarEff'

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Type Package

Title Variation of effective population size

Version 1.0

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Description Functions for estimate the changes of effective population size with coalescent approach.

License GPL (>= 2)

LazyLoad yes

Depends mcmc, graphics, grDevices

URL https://qgp.jouy.inra.fr

R topics documented:

VarEff-package	*Overview: Estimation of effective sizes from present to ancestral time*

Description

This package is a model called `VarEff` to estimate the evolution of effective population size with coalescent approach.

The estimation is done on simulated demographies modelled by steps of constant size for which the posterior probabilities are derived using an approximation of likelihood.

Details

Package:	VarEff
Type:	Package
Version:	1.0
Date:	2012-02-07
License:	GPL (>= 2)
LazyLoad:	yes
Depends:	mcmc
URL:	URL: https://qgp.jouy.inra.fr

Overview

This package depends on package MCMC (C.J. Geyer, 2009, version 0.7-3), so you have to load the library mcmc: library(mcmc).

To use this package and explore the results go through four steps:

1. Data preparation
2. Variable input
3. Output files
4. Explore the results

1. Data preparation

The data file describes the genotypes of a population at microsatellite markers.

The model assumes alleles defined by their lengths (number of microsatellite repeats).

The format of the file is close to MSVAR infile (Beaumont 1999). To convert a MSVAR file in `VarEff` file go to the Web site: https://qgp.jouy.inra.fr

Infile:

Each markers is described by 2 lines.

The first line gives the number of alleles (allelic classes) at the locus.

The second line gives the numbers of alleles at each corresponding length of the locus.

Caution:

You have to specify all potential alleles between those of minimum and maximum lengths.

It means that if you have a locus with 2 types of alleles at the lengths 10 and 12 (number of repeat motifs), you have to mention the unobserved allele with 11 motifs.

So if the alleles 10 and 12 have observed at the frequencies 24 and 6 respectively, you have to describe the locus by:

3

24 0 6

In this package the infile test is called `InputTest`.

2. Variable input

Because this model follows a Bayesian approach, you have to give priors on effective sizes (current and ancestral) and age of the population, specifying means and variances on the logarithmic scale.

Estimations are concerned with reduced population sizes (on the Theta = 4 * N * u scale) and reduced time (product of generation times (T) and mutation rate (u)).

The mutation rate is not estimated in this package. The package used the mutation rate as a scale parameter to recover actual census size and actual times (generation numbers) from the results.

In the case that you want estimation not in Theta (4*Ne*u) but in effective size Ne), you have to estimate previously the mutation rate (u) with existing method (Ex: MSVAR (Beaumont 1999).

The other parameters use in the package to visualize results concern the time (generations) that you want to go back and the times you want to watch.

Call the package `VarEff` then answer the questions:

- parafile (Name that you give to the job and to the output files created by the model).

- infile (Name of the data file).

- NBLOC (Number of Loci).

- JMAX (Number of times when the effective size has changed, used to generate step functions simulating the past demography. Ex: JMAX=2, if you think that the population took 3 different effective sizes in the past).

- MODEL (choose one mutation model in: S = Single Step Model, T = Two Phase Model, G = Geometric Model, and provide an additional coefficient (C) for T and G models).

- MUTAT (Mutation rate, assumed the same for all loci).

- NBAR (Global prior mean of effective size).

- VARP1 (Variance of the prior log-distribution of effective sizes. Ex: VARP1=3 allows for searches with 20- to 40-fold relative variations of effective size).

- RHOCORN (Coefficient of correlation between effective sizes in successive intervals).

- GBAR (Number of generations since the assumed origin of the population).

- VARP2 (Variance of the prior log-distribution of time intervals during which the population is assumed of constant size).

- DMAXPLUS = DMAX+1 (DMAX is the maximal distance between alleles (number of microsatellite motifs) that is used in the estimation algorithm).

- Diagonale (A smoothing parameter to balance the observed covariance structure with a theoretical diagonal variance matrix and avoid numerical instability. Diagonale = 0.5 is a robust choice).

- NumberBatch (number of batch (nbatch) for metrop in MCMC).

- LengthBatch (length of batch (blen) for metrop in MCMC).

- SpaceBatch (space of batch (nspac) for metrop in MCMC).

You can also directly give the parameters into R console.

Exemple with data `InputTest`:

VarEff(infile=system.file("data/InputTest.txt", package = "VarEff"), parafile = 'job', NBLOC=20, JMAX=3, MODEL = 'S', MUTAT=0.01, NBAR=1000, VARP1=3, RHOCORN=0, GBAR=5000, VARP2=3, DMAXPLUS=12, Diagonale=0.5, NumberBatch = 2, LengthBatch = 1, SpaceBatch = 1)

3. Output files

At the end of the calculations, VarEff() returns global theta values, the summaries of adjustment criteria of data to model, and the distribution of posterior probabilities, which are added to the .Theta file.

The 4 lines includes in .Theta file contain:

Line 1: global Theta0, Theta1 and Theta2 estimates.

Line 2: imbalance indices ln(Theta1/Theta0) and ln(Theta2/Theta0).

Line 3: expected range of Ne values, from the minimum and maximum global Theta estimates.

Line 4: means and standard deviations over simulations of the quadratic deviations of data from simulated state and of natural logarithm of the prior probabilities of the simulated states.

The main result of VarEff() is the .Batch file, which reports a list of demographic evolutions described by step functions. Each line includes:

Column 1: the number i of the simulated state (from 1 to Numberbatch).

Column 2: quadratic deviation of data from the i-th simulated state.

Column 3: natural logarithm of the prior probability the i-th state.

Columns 4 to JMAX+4: the JMAX+1 population sizes in the i-th state.

Columns JMAX+5 to 2 JMAX+4: times of size changes in the i-th state.

Columns 2 JMAX + 5: value of the C parameter of the mutation model.

Results are kept in the .Batch files in reduced scales:

Theta's for population sizes, products of generation numbers times mutation rate for times of size changes.

The additional C parameter is set to 0 for the Single Step Mutation Model, positive for geometrical model or negative for the Two Phase Model.

NatSizeDist

To obtain the distributions of effective size at a number of generations in the past, from the time of sampling to an ancestral time, use the function called NatSizeDist().

This function provides 2 files with the results in the Ne scale:

-job.Nstat

-job.Ndist

Format of Nstat or Lstat file

Column 1: Time in generations (if MUTAT is not 0) or the corresponding reduced time.

Columns 2: Arithmetic Mean of Ne or Log(Ne).

Columns 3: Harmonic means of Ne (not provided for Log(Ne), set to 0 in .Lstat file).

Columns 4: Mode of Ne or Log(Ne).

Columns 5: Median of Ne or Log(Ne).

Columns 6: Quantile 5 percent of Ne or Log(Ne).

Columns 7: Quantile 95 percent of Ne or Log(Ne).

LogSizeDist

To obtain the distributions of logarithm of effective size at a number of generations in the past, from the time of sampling to an ancestral time, use the function called LogSizeDist().

This function provides 2 files with the results in the Log(Ne) scale:

-job.Lstat

-job.Ldist

Format of Ndist or Ldist file:

Posterior densities of Ne or Log(Ne) at past times (fitted distribution using the density R function).

File with (Nbinstants+1) lines and 514 or 1025 columns.

Lines: Instants when the distribution of N(T(i-1)) was calculated (1<i<Nbinstants+1; 0<T(i-1)<Tempsmax).

File Ndist:

Columns in line i :

Column 1 : Value of T(i-1).

Columns 2 : Size of each of the intervals (=TMAX/511) in the abcsissa (Ne scale).

Columns 3 to 514 : Ordinates (densities of Ne at 512 points).

File Ldist:

Columns in line i :

Column 1 : Value of T(i-1).

Columns 2 to 513 : Abscissa (Log(Ne) values).

Columns 514 to 1025 : Ordinates (densities of these Log(Ne)).

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Maintainer: Who to complain to <documents_57@hotmail.com> Natacha Nikolic

References

Nikolic N, Chevalet C. 2011. Detecting the evolution of coalescent effective population size. In preparation.

Chevalet C & Nikolic N. 2010. Distribution of coalescent times and distances between microsatellite alleles with changing effective population size. Theoretical Population Biology, 77(3): 152-163.

See Also

Summary: `VarEff`
Exemple: `InputTest`
HelpData: `HelpData`
Functions to built output files: `NatSizeDist`
or `LogSizeDist`
Functions to visualize and plot the results: `plotNdistrib`
and `NTdist`
Web site: `https://qgp.jouy.inra.fr`

`HelpData`	*Help: Infile to test the model*

Description

The infile called InputTest provides an example used to give an overview of possible results.

It is a simulation of a population that underwent a huge bottleneck 200 generations ago. The past effective population was 1000 and the present size is 100.

Usage

```
data(InputTest)
```

Format

The format is:

num [1:240] 9 4 12 2 0 14 21 15 3 9 ...

Details

The data file `InputTest.txt` is an example which can be used directly in the R console.

How to use the example

Read the parts `VarEff-package`
and `VarEff`

Meaning of input variables

The variables to run one of the two functions (Theta or VarEff) correspond to the input arguments:

- parafile (Name that you give to the job and to the output files created by the model).

- infile (Name of the data file).

- NBLOC (Number of Loci).

- JMAX (Number of times when the effective size has changed, used to generate step functions simulating the past demography.

Ex: JMAX=2, if you think that the population took 3 different effective sizes in the past).

- MODEL (choose a mutation model in: S = Single Step Model, T = Two Phase Model, G = Geometric Model, and provide an additional coefficient (C) for T and G models).

- MUTAT (Mutation rate, assumed the same for all loci).

- NBAR (Prior value for the effective size).

- VARP1 (Variance of the prior log-distribution of effective sizes. Ex: VARP1=3 allows for searches with 20- to 40-fold relative variations of effective size).

- RHOCORN (Coefficient of correlation between effective sizes in successive intervals).

- GBAR (Number of generations since the assumed origin of the population).

- VARP2 (Variance of the prior log-distribution of time intervals during which the population is assumed of constant size).

- DMAXPLUS = DMAX+1 (DMAX is the maximal distance between alleles (number of microsatellite motifs) that is used in the estimation algorithm).

- Diagonale (A smoothing parameter to balance the observed covariance structure with a theoretical diagonal variance matrix and avoid numerical instability. Diagonale = 0.5 is a robust choice).

- NumberBatch (number of batch (nbatch) for metrop in MCMC).

- LengthBatch (length of batch (blen) for metrop in MCMC).

- SpaceBatch (space of batch (nspac) for metrop in MCMC).

The input example corresponds to a population genotyped with 20 microsatellite markers (NBLOC):

We supposed 3 huge events (JMAX) which have affected this population. JMAX has no impact on the present effective size but it can affect the distribution of past effective size. Hence check different JMAX (from 1 to 10) and keep the one in which the mean, median and mode are the nearest.

Generally the mutation rate (MUTAT) is around 0.01 to 0.0001. 0.01 was used in the simulation which built the data.

Concerning the other priors, we set the priors of actual effective size (NBAR) at 1000 with a large variance (VARP1=3).

We also assumed no correlation (RHOCORN=0) between the successive effective sizes from present to ancestral time.

We supposed a time since the ancestral population (GBAR) of 5000 generations with a large variance (VARP2=3).

Even if the range of alleles length differences (number of repeat motifs) in InputTest is equal at 18, we restricted DMAXPLUS to 12 because it is representative of more than 95 percent of data (above

the red line in graph Fk).

Here, the metrop (method of Monte Carlo Markov Chain) parameters are 1000 for the number of batches (NumberBatch), 10 for the length of batches (LengthBatch) and 10 for the space between batches (SpaceBatch) for a quick run. Recommended parameters are 10000 (NumberBatch), 10 (LengthBatch) and 10 (SpaceBatch) i.e. 1 million of iterations.

From the core file (.Batch) use the function `NatSizeDist`
or `LogSizeDist`
to estimate the effective size (Ne) (or Log(Ne)) at a number of times from 0 to a certain time ago (given by the user).

To visualize the results use the functions: `NTdist`
and `plotNdistrib`

Source

This data is a simulated set obtained by the model DemoDivMs from Nikolic and Chevalet `https://qgp.jouy.inra.fr`.

References

Nikolic N., Butler J., Bagliniere JL., Laughton R., McMyn I.A.G, Chevalet C. 2009. An examination of genetic diversity and effective population size in Atlantic salmon populations, and applications for conservation and management. Genetics Research. 91: 1-18.

InputTest   *Infile: Population simulated*

Description

This dataset corresponds to a population simulated with a size of 1000 individuals that underwent a bottleneck 200 generations ago to become a population with effective size 100.

The genetic data of this population are samples at 20 markers microsatellites.

Format

The format is:

num [1:240] 9 4 12 2 0 14 21 15 3 9 ...

Details

The infile is called InputTest and it provides the microsatellite data at 20 markers of one population.

Infile format

Each markers is describe by 2 lines and the alleles not present are mentionned by zero:

9 (number of alleles at the first locus)

4 12 2 0 14 21 15 3 9 (counts of number of alleles with the same length)

12 (number of alleles at second locus)

.

.

.

14 (number of alleles at last locus)

1 4 0 0 0 38 18 7 9 1 0 0 1 1

It means that if you have a locus with 2 types of alleles of lengths 10 and 12 (number of motifs) you have to mention the unobserved allele the 11 repeat motifs!

So if the alleles 10 and 12 have frequencies 24 and 6 respectively, you have to describe the locus by:

3

24 0 6

This file is close to MSVAR file and you can convert a MSVAR file to VarEff file at the website https://qgp.jouy.inra.fr

Source

This data is a simulated set obtained by the model DemoDivMs from Nikolic and Chevalet. https://qgp.jouy.inra.fr

References

Nikolic N., Butler J., Bagliniere JL., Laughton R., McMyn I.A.G, Chevalet C. 2009. An examination of genetic diversity and effective population size in Atlantic salmon populations, and applications for conservation and management. Genetics Research. 91: 1-18.

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job.Batch *File created by the functions*

Description

The first job created by the core function VarEff is a job.Batch

Format

Core of estimation by the model VarEff

Details

This infile created by the function VarEff is used by the others functions: NatSizeDist, LogSizeDist, NTDist.

Source

See SUMMARY Manual for VAREFF package: R software from Nikolic and Chevalet. https://qgp.jouy.inra.fr

References

Nikolic N., Chevalet C. 2012. SUMMARY Manual for VAREFF package: R software.

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job.Ndist	*File created by the function NatSizeDist*

Description

Posterior distribution of effective size (Ne).

Format

Big file containing the detailed densities of the posterior distributions of Ne, with 512 points.

Details

This infile created by the function VarEff is used by the function: plotNdistrib.

Source

See SUMMARY Manual for VAREFF package: R software from Nikolic and Chevalet. https://qgp.jouy.inra.fr

References

Nikolic N., Chevalet C. 2012. SUMMARY Manual for VAREFF package: R software.

LogSizeDist	*Reveal the estimates of Log(Ne)*

Description

Calculates estimates of effective size in Logarithm (Log(Ne)), at a number of times from 0 to a certain time ago (given by the user), plots and saves results on files.

Usage

```
LogSizeDist(NameBATCH = NULL, MUTAT = NULL, TMAX = NULL, NBT = NULL)
```

Arguments

`NameBATCH`	[matrix]:File .Batch created by the function VarEff.
`MUTAT`	[numeric]:Mutation rate.
`TMAX`	[integer]:Length of the period for which the distributions of Log(Ne) in the past are generated.
`NBT`	[integer]:Number of time intervals.
	Example: If TMAX=1000 generations, and NBT=100, the estimates are calculated every 10th generation until 1000 generations ago.

Details

To obtain the distribution of Log(Ne) at a number of generations in the past, run the function LogSizeDist().

The function uses the job.Batch file created by VarEff(). Results can be shown in natural census values of population sizes, or in reduced theta scale if mutation rate is set to 0 in this function.

Lstat file:

Column 1: Time in generations (if MUTAT is not 0) or the corresponding reduced time.

Columns 2: Arithmetic Mean of Log(Ne).

Columns 3: None (value set to 0).

Columns 4: Mode of Log(Ne).

Columns 5: Median of Log(Ne).

Columns 6: Quantile 5 percent of Log(Ne).

Columns 7: Quantile 95 percent of Log(Ne).

Ldist file:

Posterior densities of Log(Ne) at past times (fitted distribution using the density R function).

File with (Nbinstants+1) lines and 514 or 1025 columns.

Lines: Instants when the distribution of N(T(i-1)) was calculated: 1<i<NBT+1; 0<T(i-1)<TMAX.

TMAX corresponds to the length of the period for which the distributions of Log(Ne) in the past are generated)

NBT corresponds to the number of time intervals. Example: If TMAX=1000 generations, and NBT=100, estimates are calculated every 10th generation until 1000 generations ago)

Columns in line i :

Column 1 : Values of T(i-1)

Columns 2 to 513 : Abscissa (Log(Ne) values)

Columns 514 to 1025 : Ordinates (densities of these Log(Ne))

Value

`job.Lstat`	Summary statistics of posterior effective population size in logarithm (Log(Ne)). Matrix(ncol=7,nrow=NBT+1): Time in generations or in in reduced scale (Theta) (if MUTAT set to 0), Arithmetic mean of Log(Ne), Mode of Log(Ne), Median of Log(Ne), Quantile 5 percent of Log(Ne), Quantile 95 percent of Log(Ne).
`job.Ldist`	Densities of the posterior distributions of Ne (Matrix(ncol=1025,nrow=NBT+1).

Note

More details on the model can be found on the website: <https://qgp.jouy.inra.fr>

Author(s)

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References

Nikolic N., Chevalet C. 2011. Detecting past changes of effective population size.

Chevalet C., Nikolic N. 2010. Distribution of coalescent times and distances between microsatellite alleles with changing effective population size. Theoretical Population Biology, 77(3): 152-163.

See Also

Overview: `VarEff-package`
Exemple: `InputTest`
HelpData: `HelpData`

Examples

```
LogSizeDist (NameBATCH = system.file("extdata/job.Batch", package = "VarEff") , MUTAT = 0
TMAX = 200, NBT = 10)
```

`NatSizeDist`   *Reveal the estimates of Ne*

Description

Calculates estimates of effective size (Ne), at a number of times from 0 to a certain time ago (given by the user), plots and saves results on files.

Usage

```
NatSizeDist(NameBATCH = NULL, MUTAT = NULL, TMAX = NULL, NBT = NULL)
```

Arguments

`NameBATCH`	[matrix]:File .Batch create by the function VarEff.
`MUTAT`	[numeric]:Mutation rate.
`TMAX`	[integer]:Length of the period for which the distributions of Ne in the past are generated.
`NBT`	[integer]:Number of time intervals.
	Example: If TMAX=1000 generations, and NBT=100, the estimates are calculated every 10th generation until 1000 generations ago.

Details

To obtain the distribution of effective size (Ne) at a number of generations in the past, run the function NatSizeDist().

The function makes use of the job.Batch file created by VarEff(). Results can be shown in natural census values of population sizes, or in reduced theta scale if mutation rate is set to 0 in these functions.

Nstat file:

Column 1: Time in generations (if MUTAT is not 0) or the corresponding reduced time.

Columns 2: Arithmetic Mean of Ne.

Columns 3: Harmonic means of Ne.

Columns 4: Mode of Ne.

Columns 5: Median of Ne.

Columns 6: Quantile 5 percent of Ne.

Columns 7: Quantile 95 percent of Ne.

Ndist file:

Posterior densities of Ne or Log(Ne) at past times (fitted distribution using the density R function).

File with (Nbinstants+1) lines and 514 columns.

Lines: Instants when the distribution of N(T(i-1)) was calculated: 1<i<NBT+1; 0<T(i-1)<TMAX. TMAX corresponds to the length of the period for which the distributions of Log(Ne) in the past are generated). NBT corresponds to the number of time intervals. Example: If TMAX=1000 generations, and NBT=100, estimates are calculated every 10th generation until 1000 generations ago).

Columns in line i :

Column 1 : Values of T(i-1).

Columns 2 : Size of each of the intervals (=TMAX/511) in the abcsissa (Ne scale).

Columns 3 to 514 : Ordinates (densities of Ne at 512 points).

Value

job.Nstat	Summary statistics of posterior effective population size. Matrix(ncol=7,nrow=NBT+1): Time in generations (or reduced time (Theta) if MUTAT was set to 0), Arithmetic mean of Ne, Harmonic mean of Ne, Mode of Ne, Median of Ne, Quantile 5 percent of Ne, Quantile 95 percent of Ne.
job.Ndist	Containing the detailed densities of the posterior distributions of Ne.

Note

More details on the model can be found on the website: https://qgp.jouy.inra.fr

Author(s)

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References

Nikolic N., Chevalet C. 2011. Detecting past changes of effective population size.

Chevalet C., Nikolic N. 2010. Distribution of coalescent times and distances between microsatellite alleles with changing effective population size. Theoretical Population Biology, 77(3): 152-163.

See Also

Overview: VarEff-package
Exemple: InputTest
HelpData: HelpData

Examples

```
NatSizeDist (NameBATCH = system.file("extdata/job.Batch", package = "VarEff") , MUTAT = 0
TMAX = 200, NBT = 10)
```

NTdist   *Graphical summary*

Description

Graphical summary of the posterior distribution of estimates of Log(Ne) in the past (a 2D plot).

Usage

```
NTdist(NameBATCH = NULL, MUTAT = NULL, TMAX = NULL)
```

Arguments

NameBATCH	[matrix]: File .Batch create by the function VarEff.
MUTAT	[numeric]:Mutation rate.
TMAX	[integer]:Length of the period for which the distributions of Log(Ne) in the past are generated.

Details

The function NTdist() uses the job.Batch file and makes a figure to summarise the posterior distribution of Log(Ne) in a certain period (TMAX) given by the user.

The given mutation rate is used to choose natural scales (census size and generations), or reduced scales (theta and generations times mutation rate) if the mutation rate is set to 0.

The graph is plotted and saved in a text file job.2D of 101 lines:

Line 1, column 1: rate of coverage of the plotted distributions.

Line 1, columns 2 to 101: abscissa (times from 0 to TMAX when the Log(Ne) distribution is estimated).

Lines 2 to 101, column 1: ordinates (values of Log(Ne) in the selected range).

Lines 2 to 101, columns 2 to 101: densities of Log(Ne) (integer values).

Value

`R plot`	In R console: Graphical summary of the posterior distribution of estimates of Log(Ne) in the past.
`job.2D`	Text file, 101 lines and 101 columns.

Note

More details on the model can be found on the website: <https://qgp.jouy.inra.fr>

Author(s)

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References

Nikolic N., Chevalet C. 2011. Detecting past changes of effective population size.

Chevalet C., Nikolic N. 2010. Distribution of coalescent times and distances between microsatellite alleles with changing effective population size. Theoretical Population Biology, 77(3): 152-163.

See Also

Overview: `VarEff-package`
Exemple: `InputTest`
HelpData: `HelpData`

Examples

```
NTdist (NameBATCH = system.file("extdata/job.Batch", package = "VarEff") , MUTAT = 0.01,
TMAX = 200)
```

| plotNdistrib | *Plots the posterior distributions of Ne or Log(Ne))* |

Description

Plots the posterior distributions of the estimates of Ne (or Log(Ne)) at a number of times in the past.

Usage

```
plotNdistrib(infile = NULL, nbcases=NULL)
```

Arguments

infile	[matrix]:job.Ndist created by the function NatSizeDist or job.Ldist created by the function LogSizeDist.
nbcases	[integer]: number of times (suggestion: <=5) you wish to plot the distribution.

Details

The function plotNdistrib() makes use of files .Ndist or .Ldist previously built by NatSizeDist() or LogSizeDist().

It allows the user to exhibit the density of the posterior distribution of Ne (or of Log(Ne)) at several times in the past.

Compared to NTdist() that gives a rough but global view of these densities, plotNdistrib() gives a precise view of these densities at a small number of times.

The global 2D plot given by NTdist() may help choosing the times when plotNdistrib() is used.

Caution! In the example below, we used nbcases=0 to get out. It allowed to built the package because the function is interactive.

If you want to use it just call the function

plotNdistrib ()

Value

job_Ndist	Figure of the posterior distributions of Ne at R console.
job_Ldist	Figure of the posterior distributions of Log(Ne) at R console.

Note

More details on the model can be found on the website: https://qgp.jouy.inra.fr

Author(s)

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References

Nikolic N., Chevalet C. 2011. Detecting past changes of effective population size.

Chevalet C., Nikolic N. 2010. Distribution of coalescent times and distances between microsatellite alleles with changing effective population size. Theoretical Population Biology, 77(3): 152-163.

See Also

Overview: `VarEff-package`
Exemple: `InputTest`
HelpData: `HelpData`

Examples

```
plotNdistrib (NameBATCH = system.file("extdata/job.Ndist", package = "VarEff") , nbcases=
plotNdistrib (infile = "../VarEff/extdata/job.Ndist",nbcases=0)
```

Theta	*Preliminary analysis of data to choose Theta priors and DMAX from microsatellites data*

Description

This function allows to get Theta (4*Ne*u) using 3 estimators correlated to the mean of Present (Theta_0), Intermediate (Theta_1) and Ancestral (Theta_2) population size.

The results are written to a .Theta file.

It also provides Imbalance indices ln(Theta_1/Theta_0) and ln(Theta_2/Theta_0), the minimum of census Ne (Ne0=Theta_0/4*u) and the maximum Ne (Ne_2=Theta_2/4*u).

Values of .Theta file:

- Theta_0, Theta_1, Theta_2.

- Imbalance indices ln(Theta_1/Theta_0) and ln(Theta_2/Theta_0).

- MinNe, MaxNe.

- Means and standard deviations of the quadratic deviations of data.

These results provide an overview of priors necessary for VarEff function.

The programm also allows to built a file .R to process the model VarEff with the function VarEff()

Usage

```
Theta(infile = NULL, parafile = NULL, NBLOC = NULL, MUTAT = NULL,
JMAX = NULL, MODEL = NULL, NBAR = NULL, VARP1 = NULL, RHOCORN = NULL,
GBAR = NULL, VARP2 = NULL, DMAXPLUS = NULL, Diagonale = NULL,
NumberBatch = NULL, LengthBatch = NULL, SpaceBatch = NULL)
```

Arguments

`parafile`	[matrix]:Output data.
`infile`	[matrix]:Input data.
`NBLOC`	[integer]:Number of markers.
`JMAX`	[integer]:Number of time that the effective size has changed.
`MODEL`	[numeric]:Mutation model.
`MUTAT`	[numeric]:Mutation rate.
`NBAR`	[integer]:Global mean of effective size.
`VARP1`	[integer]:Logarithmic variance of effective size.
`RHOCORN`	[numeric]:Coefficient of correlation between successive effective size.
`GBAR`	[integer]:Number of generations since the origin of the population.
`VARP2`	[integer]:Logarithmic variance of time interval.
`Diagonale`	[numeric]:Smoothing parameter.
`DMAXPLUS`	[integer]:Range of allele distances to be analysed.
`NumberBatch`	[integer]:Number of batch.
`LengthBatch`	[integer]:Length of batch.
`SpaceBatch`	[integer]:Space of batch.

Details

It provides three global theta: Theta0 (linked to current effective size N0, Theta=4*N0*u), Theta1 (linked to intermediate size), Theta2 (linked to ancestral size), imbalance indices, and a range of population size.

It also builds a script to run VarEff (job.R) and a plot showing the distribution of allele distances in the sample.

Value

`job.Theta`	File with the first 3 lines: the 3 theta values, the 2 imbalances indices, the minimal and maximal suggested population sizes.
`job.R`	A file containing a script to run the VarEff function.
`R.plot`	Figure showing the distribution of allele distances in the sample.

Note

More details on the model can be found on the website: <https://qgp.jouy.inra.fr> The example is done with few batches to test the model. The minimum is NumberBatch =10000, Length-Batch=10, SpaceBatch=10.

Author(s)

Natacha Nikolic <documents_57@hotmail.com> and Claude Chevalet <claude.chevalet@toulouse.inra.fr>

References

Nikolic N., Chevalet C. 2011. Detecting past changes of effective population size.

Chevalet C., Nikolic N. 2010. Distribution of coalescent times and distances between microsatellite alleles with changing effective population size. Theoretical Population Biology, 77(3): 152-163.

See Also

Overview: `VarEff-package`
Exemple: `InputTest`
HelpData: `HelpData`

Examples

```
Theta (infile=system.file("data/InputTest.txt", package = "VarEff"),
                         parafile = 'job',
                         NBLOC=20,
                         MUTAT=0.01,
                         JMAX=3,
                         MODEL = 'S',
                         NBAR=1000,
                         VARP1=3,
                         RHOCORN=0,
                         GBAR=5000,
                         VARP2=3,
                         DMAXPLUS=12,
                         Diagonale=0.5,
                         NumberBatch = 100,
                         LengthBatch = 10,
                         SpaceBatch = 10)
```

VarEff   *Function VarEff from the package called also VarEff*

Description

`VarEff` (Variation of effective size) is a model to estimate the evolution of effective population size with coalescent approach. The estimation is done on simulated demographies modelled by steps of constant size for which the posterior probabilities are derived using an approximation of likelihood.

The user is asked the number of different steps he wishes to use to model the variation of effective size in the past.

Here, the function VarEff is given with all parameters to solve the model `VarEff`.

It produces 2 output files: summary statistics (.Theta) and the list of detailed states simulated by the MCMC chain (.Batch).

Further, files are produced by the additional functions that allows results to be visualized.

For an overview of the package, see VarEff-package.

Caution: Source the MCMC package of C.J. Geyer (2009): version 0.7-3.

Usage

```
VarEff(infile = NULL, parafile =NULL, NBLOC = NULL, JMAX = NULL,
MODEL = NULL, MUTAT = NULL, NBAR = NULL, VARP1 = NULL, RHOCORN = NULL,
GBAR = NULL, VARP2 = NULL, DMAXPLUS = NULL, Diagonale = NULL,
NumberBatch = NULL, LengthBatch = NULL, SpaceBatch = NULL)
```

Arguments

`parafile`	[matrix]:Output data.
`infile`	[matrix]:Input data.
`NBLOC`	[integer]:Number of markers.
`JMAX`	[integer]:Number of times when the effective size has changed.
`MODEL`	[numeric]:Mutation model.
`MUTAT`	[numeric]:Mutation rate.
`NBAR`	[integer]:Global prior mean of effective size.
`VARP1`	[integer]:Logarithmic variance of effective size.
`RHOCORN`	[numeric]:Coefficient of correlation between effective sizes in successive steps.
`GBAR`	[integer]:Number of generations since the origin of the population.
`VARP2`	[integer]:Logarithmic variance of time interval.
`Diagonale`	[numeric]:Smoothing parameter.
`DMAXPLUS`	[integer]:Range of allele distances to be analysed.
`NumberBatch`	[integer]:Number of batch.
`LengthBatch`	[integer]:Length of batch.
`SpaceBatch`	[integer]:Space of batch

Details

The package named `VarEff` works with the main function called VarEff.

This function is the corpus of coalescent estimation of effective sizes from the time of sampling to ancestor population size.

The user can get the posterior distribution of effective population size at any time in the past, as asked in further functions.

Value

`job.Theta`	Summary statistics
`job.Batch`	Core of program to produce all files .Nstat, Ndist, etc.

Summary

To summarize the main part of this package go thought these four section:

1. INFILE
2. INPUT
3. BATCH FILE
4. OUTPUTS
5. PLOT

1. INFILE

The infile is the microsatellite data of a population. It is near of MSVAR (Beaumont 1999) infile. Go to https://qgp.jouy.inra.fr to convert a MSVAR file in VarEff file.

In this package an exemple can be found in the directory data called InputTest.

2. INPUT

- parafile (Name that you give to the job and to the output files created by the model).

- infile (Name of the data file).

- NBLOC (Number of Loci).

- JMAX (Number of times when the effective size has changed, used to generate step functions simulating the past demography. Ex: JMAX=2, if you think that the population took 3 different effective sizes in the past).

- MODEL (choose one mutation model in: S = Single Step Model, T = Two Phase Model, G = Geometric Model, and provide an additional coefficient (C) for T and G models).

- MUTAT (Mutation rate, assumed the same for all loci).

- NBAR (Prior value for the effective size).

- VARP1 (Variance of the prior log-distribution of effective sizes. Ex: VARP1=3 allows for searches with 20- to 40-fold relative variations of effective size).

- RHOCORN (Coefficient of correlation between effective sizes in successive intervals).

- GBAR (Number of generations since the assumed origin of the population).

- VARP2 (Variance of the prior log-distribution of time intervals during which the population is assumed of constant size).

- DMAXPLUS = DMAX+1 (DMAX is the maximal distance between alleles (number of microsatellite motifs) that is used in the estimation algorithm).

- Diagonale (A smoothing parameter to balance the observed covariance structure with a theoretical diagonal variance matrix and avoid numerical instability. Diagonale = 0.5 is a robust choice).

- NumberBatch (number of batch (nbatch) for metrop in MCMC).

- LengthBatch (length of batch (blen) for metrop in MCMC).

- SpaceBatch (space of batch (nspac) for metrop in MCMC).

3. BATCH FILE

Two files are produced by the model `VarEff`:

-job.Theta provides summary statistics (see below).

-job.Batch which is the core of the estimate.

It reports a list of demographic evolutions described by step functions. Each line includes:

Column 1: the number i of the simulated state (from 1 to Numberbatch).

Column 2: quadratic deviation of data from the i-th simulated state.

Column 3: natural logarithm of the prior probability the i-th state.

Columns 4 to JMAX+4: the JMAX+1 population sizes in the i-th state.

Columns JMAX+5 to 2 JMAX+4: the JMAX times when the size changed in the i-th state.

Columns 2 JMAX + 5: value of the C parameter of the mutation model.

Results are kept in the job.Batch file in reduced scales:

Theta's for population sizes, products of generation numbers times mutation rate for times of size changes.

The additional C parameter is a constant set to 0 for the Single Step Mutation Model, to a positive value for geometrical model or a negative value for the Two Phase Model.

4. OUTPUTS

Firstly, the VarEff() function produces summary statistics in a file job.Theta.

The first 3 lines are the same as produces by the Theta() function:

Line 1: global Theta0, Theta1 and Theta2 estimates.

Line 2: imbalance indices ln(Theta1/Theta0) and ln(Theta2/Theta0).

Line 3: expected range of Ne values, from the minimum and maximum global Theta estimates.

An the 4th line provides means and standard deviations over simulations of the quadratic deviations of data from simulated state and of natural logarithm of the prior probabilities of the simulated states.

To obtain the distributions of effective size at a number of generations in the past, from the time of sampling to an ancestral time, use the function called NatSizeDist().

This function provides 2 files with the results in the Ne scale:

-job.Nstat

-job.Ndist

To obtain the distributions of logarithm of effective size at a number of generations in the past, from the time of sampling to an ancestral time, use the function called LogSizeDist().

This function provide 2 files with the results given in the Log(Ne) scale:

-job.Lstat

-job.Ldist

Format of Nstat or Lstat file:

Column 1: Time in generations (if MUTAT is not 0) or the corresponding reduced time.

Columns 2: Arithmetic Mean of Ne or Log(Ne).

Columns 3: Harmonic means of Ne (not provided for Log(Ne)).

Columns 4: Mode of Ne or Log(Ne).

Columns 5: Median of Ne or Log(Ne).

Columns 6: Quantile 5 percent of Ne or Log(Ne).

Columns 7: Quantile 95 percent of Ne or Log(Ne.

Format of Ndist or Ldist file:

Posterior densities of Ne or Log(Ne) at past times (fitted distribution using the density R function).

File with (Nbinstants+1) lines and 514 (Ndist) or 1025 (Ldist) columns.

Lines: Instants when the distribution of N(T(i-1)) was calculated.

File Ndist:

Columns in line i :

Column 1 : Values of T(i-1).

Columns 2 : Size of each of the intervals (=TMAX/511) in the abcsissa (Ne scale).

Columns 3 to 514 : Ordinates (densities of Ne at 512 points).

File Ldist:

Columns in line i :

Column 1 : Values of T(i-1).

Columns 2 to 513 : Abscissa (Log(Ne) values).

Columns 514 to 1025 : Ordinates (densities of these Log(Ne)).

5. PLOT

- Two functions are provided to plot posterior distributions:

1) NTdist(): Graphical summary of the posterior distribution of estimates of Log(Ne) in the past (a 2D plot), using the job.Batch file and the length of time during which distributions are retrieved.

2) plotNdistrib(): Plots the posterior distributions of the estimates of Ne (or Log(Ne)) at a number of times in the past, using a job.Ndist or job.Ldist file as previously calculated with NatSizeDist() or LogSizeDist().

- Plot Harmonic Mean from the .Nstat file. In addition to the proposed functions, we illustrate how to plot specific results from a file produced by NatSizeDist():

dat2=read.table("job.Nstat")

x2=dat2[,1]

y2=dat2[,3]

x2=as.numeric(x2)

y2=as.numeric(y2)

maxX2=max(x2)

maxY2=max(y2)

plot(x2,y2,type='l', lwd="2",ylim=c(0,maxY2),xlab="Time T in the past (generations)",ylab="Ne(T)")

Note

More details on the model can be found on the website: https://qgp.jouy.inra.fr This package needs mcmc package. The example is done with few batches to test the model. The minimum is NumberBatch =10000, LengthBatch=10, SpaceBatch=10.

Author(s)

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References

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See Also

Overview: `VarEff-package`
Exemple: `InputTest`
HelpData: `HelpData`

Examples

```
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                        parafile = 'job',
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                        JMAX=3,
                        MODEL = 'S',
                        MUTAT=0.01,
                        NBAR=1000,
                        VARP1=3,
                        RHOCORN=0,
                        GBAR=5000,
                        VARP2=3,
                        DMAXPLUS=12,
                        Diagonale=0.5,
                        NumberBatch = 100,
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```

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