

Package ‘rforensicbatwing’

March 21, 2018

Type Package

Title BATWING for Calculating Forensic Trace-Suspect Match Probabilities

Version 1.3.1

Date 2018-03-21

Author Mikkel Meyer Andersen and Ian J. Wilson

Maintainer Mikkel Meyer Andersen <mik1@math.aau.dk>

Description A modified version (with great help from Ian J. Wilson) of Ian J. Wilson's program BATWING for calculating forensic trace-suspect match probabilities.

License GPL

LinkingTo Rcpp

Imports Rcpp (>= 0.12.16)

NeedsCompilation yes

Repository CRAN

Date/Publication 2018-03-21 22:21:24 UTC

R topics documented:

rforensicbatwing-package	1
Inference from STR data using coalescent theory	2

Index	6
--------------	----------

rforensicbatwing-package
BATWING for calculating forensic trace-suspect match probabilities

Description

A modified version (with great help from Ian J. Wilson) of Ian J. Wilson's program BATWING for calculating forensic trace-suspect match probabilities.

Details

Please see the documentation of [coalmatchprob](#) for an usage example.

Author(s)

Mikkel Meyer Andersen and Ian J. Wilson

Maintainer: Mikkel Meyer Andersen <mikl@math.aau.dk>

References**The BATWING manual**

I.J. Wilson, D.J. Balding, *Genealogical inference from microsatellite data*, Genetics 150 (1998) 499-510.

I.J. Wilson, M.E. Weale, D.J. Balding, *Inferences from DNA data: population histories, evolutionary processes and forensic match probabilities*, J. R. Stat. Soc. Ser. A 166 (2003) 155-201.

M.M. Andersen, A. Caliebe, A. Jochens, S. Willuweit, M. Krawczak, *Estimating trace-suspect match probabilities for singleton Y-STR haplotypes using coalescent theory*, Forensic Sci. Int. Genet. (In Press, Corrected Proof [10.1016/j.fsigen.2012.11.004](#)).

See Also

[batwing coalmatchprob](#)

Inference from STR data using coalescent theory

Inference from STR data using coalescent theory (e.g. calculating forensic trace-suspect match probability)

Description

Estimates the trace-suspect match probability for a lineage haplotype of STR markers using coalescent theory.

Usage

```
coalmatchprob(database, haplotype,
  reps = 10, burnin = 0, treebetN = 10, Nbetsamp = 10,
  muprior = "constant(0.003)", Nprior = "lognormal(9, 1)", alphaprior = NULL,
  progress = TRUE, trace = FALSE)
batwing(database,
  reps = 10, burnin = 0, treebetN = 10, Nbetsamp = 10,
  muprior = "constant(0.003)", Nprior = "lognormal(9, 1)", alphaprior = NULL,
  progress = TRUE, trace = FALSE)
## S3 method for class 'batwing'
print(x, ...)
## S3 method for class 'forensicbatwing'
plot(x, ...)
```

Arguments

database	Reference STR database.
haplotype	Haplotype of the suspect.
reps	Number of output lines.
burnin	Number of reps to take before starting recording data.
treebetN	The number of times that changes to the genealogical tree are attempted before any changes to the hyperparameters are attempted. Thus BATWING outputs are separated by treebetN * Nbetsamp attempted tree updates.
Nbetsamp	The number of times that changes to hyperparameters are attempted between outputs.
muprior	Either a single prior distribution for the mutation rate or a vector of prior distributions (one for each locus). If only one prior is supplied, the same mutation rate is used for all loci. If one prior per locus is supplied, each locus has its own chain of mutation rates.
Nprior	Prior distribution of the effective population size.
alphaprior	If NULL, there is no growth (constant population size). If a prior distribution is specified, this gives exponential growth at rate alpha at all times.
progress	Whether to print progress or not.
trace	Whether to print extra trace information or not.
x	A batwing or forensicbatwing object.
...	Not used

Details

Note that the batwing function runs a standard coalescent inference as described in I.J. Wilson (1999, 2003).

Note that, in contrast to the original BATWING program, migration is not supported. Neither is BATWING's sizemode1=2 (constant-sized population up to a time from where there is exponential growth).

Valid prior distributions:

- `uniform(v1, v2)` uniform on the interval (v1, v2).
- `constant(v1)` constant value v1.
- `normal(v1, v2)` Normal distribution with mean = v1 and sd = v2.
- `lognormal(v1, v2)` If X has this distribution then log(X) has the normal(v1, v2) distribution.
- `gamma(v1, v2)` Gamma distribution with shape v1 and rate v2 giving mode = (v1-1)/v2 and mean = v1/v2.
- `beta(v1, v2)` Beta distribution with shape parameters v1 and v2 giving mean = v1/(v1 + v2) and the variance is (v1*v2)/((v1 + v2)^2 * (v1 + v2 + 1))

Value

coalmatchprob	An object of type forensicbatwing and batwing (for now, forensicbatwing just means that there is a p column in the result matrix).
batwing	An object of type batwing
batwing-object	parameters The parameters used priors The priors used result Matrix with information about the iterations (forensic match probability (if coalmatchprob), current value of N, mu's, tree height T, total branch length L, population growth alpha, and loglikelihoods for times, mutations and priors). proposals_tree The number of new tree proposals. accepted_tree The number of new trees accepted. proposals_hyperparameters The number of new hyperparameters proposals. accepted_hyperparameters The number of new hyperparameters accepted.

Author(s)

Mikkel Meyer Andersen and Ian Wilson

Source

[BATWING at Ian Wilson's homepage](#)

References

[The BATWING manual](#)

I.J. Wilson, D.J. Balding, *Genealogical inference from microsatellite data*, Genetics 150 (1998) 499-510.

I.J. Wilson, M.E. Weale, D.J. Balding, *Inferences from DNA data: population histories, evolutionary processes and forensic match probabilities*, J. R. Stat. Soc. Ser. A 166 (2003) 155-201.

M.M. Andersen, A. Caliebe, A. Jochens, S. Willuweit, M. Krawczak, *Estimating trace-suspect match probabilities for singleton Y-STR haplotypes using coalescent theory*, Forensic Sci. Int. Genet. (In Press, Corrected Proof [10.1016/j.fsigen.2012.11.004](#)).

Examples

```
## Not run:
database <- matrix(c(1, 1, 2, 2, 1, 3), 3, 2)
haplotype <- c(1, 1)

# coalmatchprob:
coalmp <- coalmatchprob(database, haplotype,
  reps = 1000, burnin = 0, treebetN = 10, Nbetsamp = 10,
  muprior = c("normal(0.003, 0.001)", "normal(0.005, 0.001)"),
  Nprior = "lognormal(9, 1)",
  alphaprior = NULL,
  progress = TRUE, trace = FALSE)
```

```
coalmp

murange <- range(c(coalmp$result$mu1, coalmp$result$mu2))

par(mfrow = c(2, 2))
plot(coalmp)
plot(coalmp$result$N, type = "l", ylab = "N")

plot(coalmp$result$mu1, type = "l", col = "red", ylim = murange, ylab = "mu")
points(coalmp$result$mu2, type = "l", col = "blue")

hist(coalmp$result$mu1, col = "#FF000066",
     xlim = murange, ylim = c(0, 250), main = NULL, xlab = "mu")
hist(coalmp$result$mu2, add = TRUE, col = "#0000FF66")
par(mfrow = c(1, 1))

# batwing:
bw <- batwing(database,
  reps = 10000, burnin = 1000, treebetN = 10, Nbetsamp = 10,
  muprior = "normal(0.003, 0.001)",
  Nprior = "lognormal(9, 1)",
  alphaprior = NULL,
  progress = TRUE, trace = FALSE)
bw

## End(Not run)
```

Index

*Topic **coalescence**

Inference from STR data using
coalescent theory, [2](#)

*Topic **coalescent**

Inference from STR data using
coalescent theory, [2](#)

*Topic **package**

rforensicbatwing-package, [1](#)

batwing, [2](#)

batwing(Inference from STR data using
coalescent theory), [2](#)

coalmatchprob, [2](#)

coalmatchprob(Inference from STR data
using coalescent theory), [2](#)

Inference from STR data using
coalescent theory, [2](#)

plot.forensicbatwing(Inference from
STR data using coalescent
theory), [2](#)

print.batwing(Inference from STR data
using coalescent theory), [2](#)

rforensicbatwing
(rforensicbatwing-package), [1](#)
rforensicbatwing-package, [1](#)