HELP function BTlike

Authors contact: Claude Chevalet (claude.chevalet@wanadoo.fr)
Natacha Nikolic (natachanikolic@hotmail.com)

This function (BTlike) uses file .Batch (product with the package VarEff) and works with R software. The function BTlike estimates the likelihood frequency of a bottleneck detected from previous analyses (NTdist and TMRCA functions from VarEff package). The function calculates the frequency with which the estimated population size at time t1 in the past is smaller than the size estimated at time t2 in the past (t2 > t1), from the set of simulated demographic patterns generated by the MCMC VarEff algorithm.

Please refer to the manual for VarEff to use VarEff package working with R software and to obtain the necessary file (.Batch) for BTlike function.

Example:

Salmon data showed a recent bottleneck that occurred in the 100 last generations, as seen in the two-dimensional T – N(T) distribution (Figure 1, T is the generation time), with a clear separation between the current effective size (N) around 100 and the past size around 2500. The TMRCA distribution (Figure 2) also suggests that recent coalescence events occurred recently around the 30th generation (Log10(30)≈1.5) in the past.
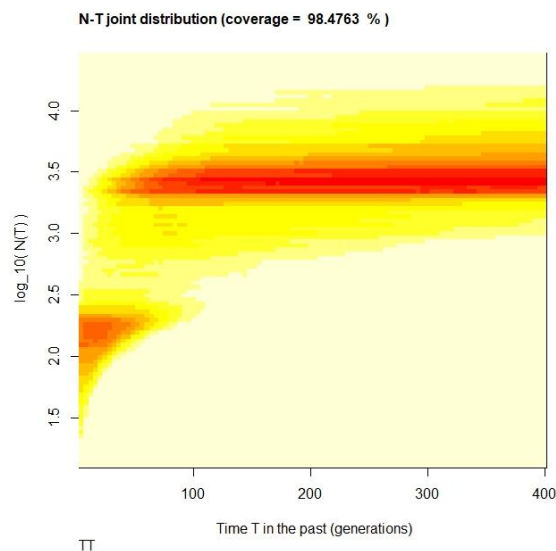

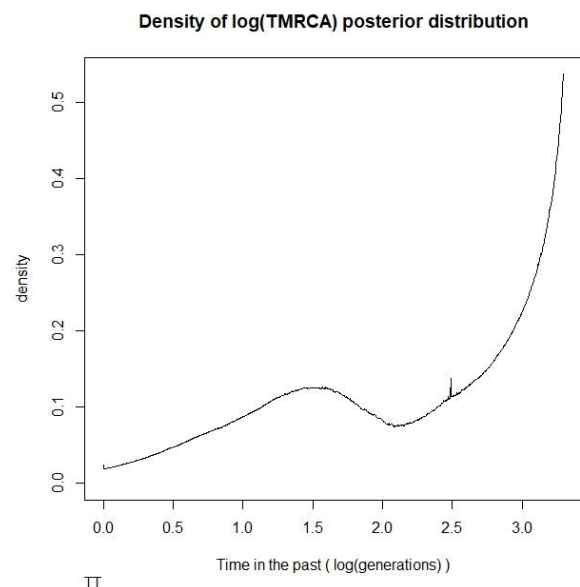**Figure 1.** Joint distribution of T and N(T) in the past. T is the generation time.

Figure 2. Distribution of the Time to the Most Recent Common Ancestor (TMRCA), in the recent past. X-axis equals to Log10(generation time).

So we used the function BTlike by entering times in generation (but you can also use the reduced time = g*u if you do not know the mutation rate by entering the value 0) that frame

the bottleneck (t1 = 15 and 30, t2 = 70, 100 and 200), to check when most likely the sharp decrease of population size occurred.

R command to use the function BTlike:

> Library(VarEff)
#Source the script BTlike
> BTlike()
[1] Read the data .batch
 Name of the batch file= TT.batch
[1] Mutation rate: Enter 0 to use reduced scales Theta's and G*u
 Mutation rate = 0.005
 Number of t1 instants= 2
[1] " enter t1 times :"
1: 15 30
Read 2 items
 Number of t2 instants= 3
[1] " enter t2 times :"
1: 70 100 200
Read 3 items
[1] 0.6423 0.7483 0.8332
[1] 0.4135 0.5338 0.6468
NULL
>

These results are presented as a pairwise matrix:

	t2=70	t2=100	t2=200
t1 =15	0.6423.	0.7483	0.8332
t1=30	0.4135	0.5338	0.6468

They show that the bottleneck occurred very likely between times 100 and 15 in the past, with a posterior probability of about .75 (i.e. 75% of probability or likelihood frequency).

Cited package VarEff and associated publications when you use this function:

Nikolic N, Chevalet C (2014). Detecting past changes of effective population size. Evolutionary Applications, 7(6), 663–681.

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