

## HELP function BTlike

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

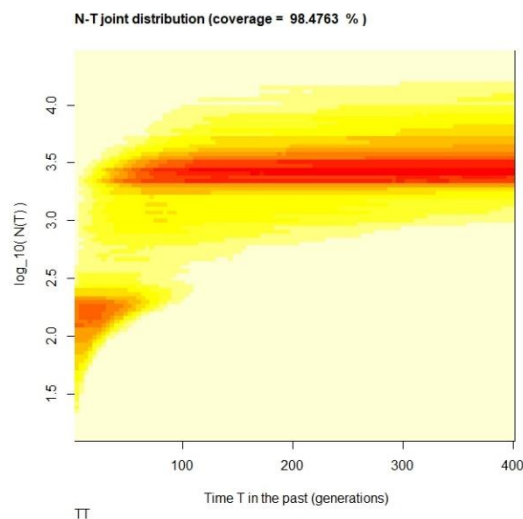
This function (BTlike) uses the file.Batch (produced by the package VarEff) and works with R software. The function BTlike estimates the likelihood frequency of a bottleneck detected from previous analyses (NTdist and TMRCA functions from VarEff package).

The function calculates the probability or likelihood frequency of a bottleneck at the time  $t_1$  and  $t_2$  in the past ( $t_2 > t_1$ ), from the demographic patterns estimated by VarEff algorithm.

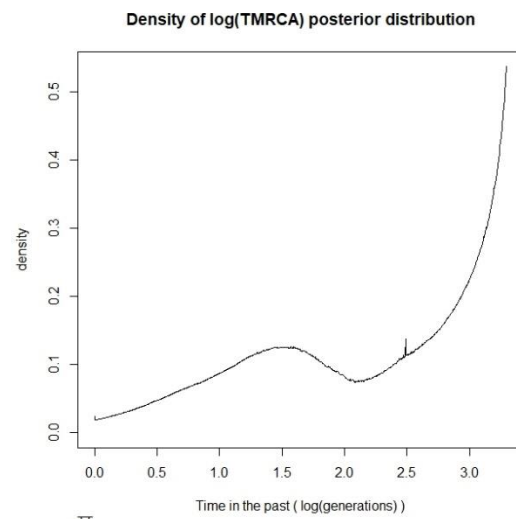
Please refer to the manual for VarEff to use R package VarEff and to obtain the necessary file (.Batch) used by BTlike function.

### 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 ( $\text{Log}_{10}(30) \approx 1.5$ ) 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  $\text{Log}_{10}(\text{generation time})$ .

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 ( $t_1 = 15$  and  $30$ ,  $t_2 = 70$ ,  $100$  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:

	<b>t2=70</b>	<b>t2=100</b>	<b>t2=200</b>
<b>t1 =15</b>	0.6423.	<b>0.7483</b>	0.8332
<b>t1=30</b>	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.