



Demographic inference using skyline plots on approximate bayesian computation

Miguel Navascués, Concetta Burgarella

► To cite this version:

Miguel Navascués, Concetta Burgarella. Demographic inference using skyline plots on approximate bayesian computation. Annual Meeting of the Society for Molecular biology et Evolution, Jun 2012, Dublin, Ireland. 2012, Posters abstracts. hal-01267944

HAL Id: hal-01267944


<https://hal.science/hal-01267944>

Submitted on 3 Mar 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

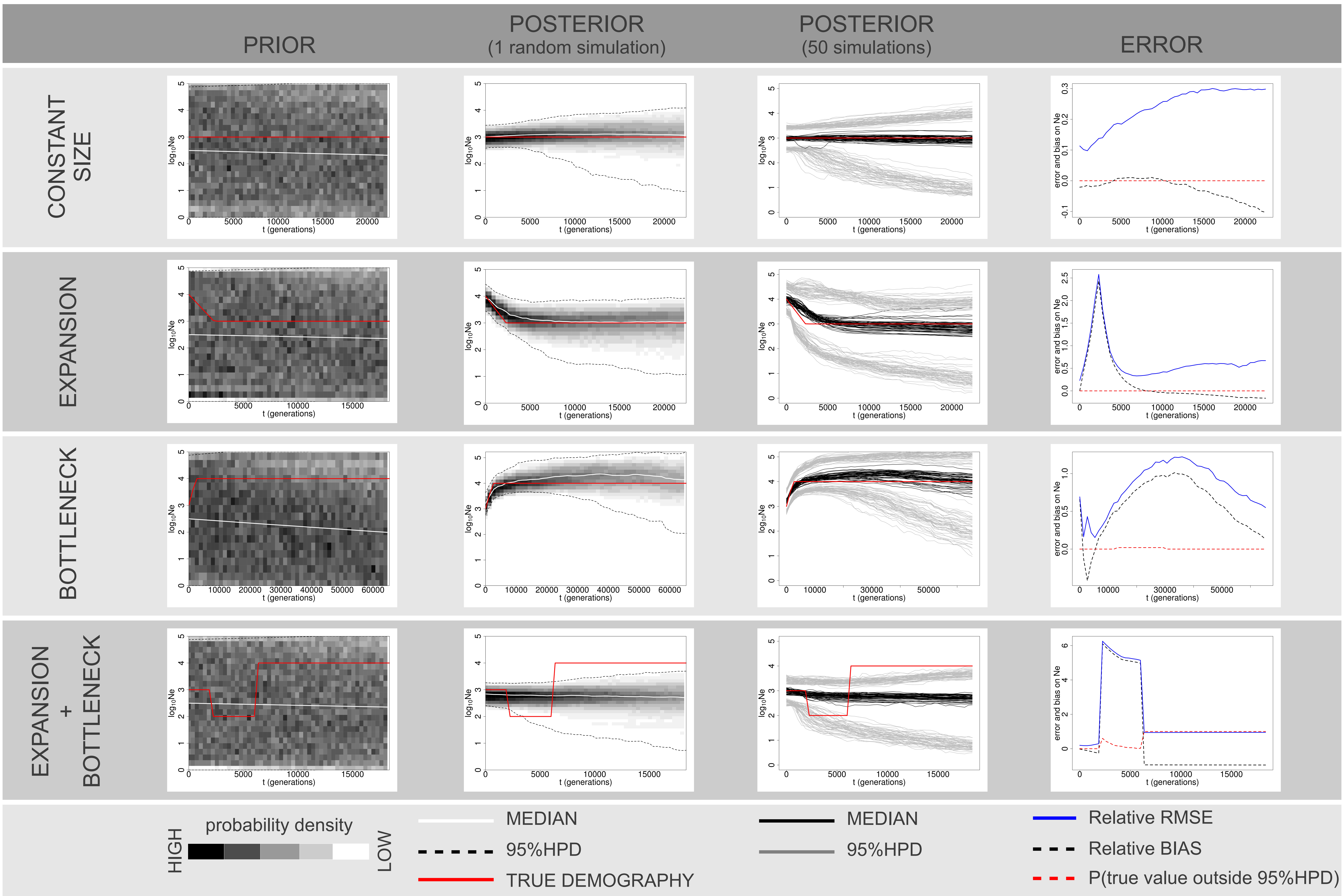
L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Demographic Inference Using Skyline Plots on Approximate Bayesian Computation

Miguel Navascués & Concetta Burgarella  UMR CBGP, INRA Montpellier, navascues@supagro.inra.fr
UMR AGAP, INRA Montpellier, burgarella@supagro.inra.fr

Bayesian Skyline Plots are representations of the posterior probability density of the effective population size in function of time. A model with several periods of constant population size is used to explore the demographics that best explain the data. Instead of estimating the posterior probability density for parameters of the model (i.e. size at each interval) the probability density of population size in function of time (i.e. size at each generation) is estimated. This method is currently implemented in BEAST (Drummond & Rambaut 2007 BMC Evol Biol), which uses an MCMC estimation of likelihood under the coalescent.

We have implemented the same approach under an **Approximate Bayesian Computation** analysis. The purpose of this is to facilitate analysis of dataset where the MCMC approach is inappropriate, such as analysis of DNA sequences with intragenic recombination. The performance of the method has been evaluated with simulated datasets (see table). Simulations for the ABC procedure were performed with FASTSIMCOAL (Excoffier & Foll 2011 Bioinformatics), using a model with 10 periods of constant size. Sample size of 50 diploid individuals typed at 100 microsatellite loci. Summary statistics were calculated with ARLSUMSTATS (from Arlequin). Relative root of mean squared error, relative bias and proportion of times the true value fall outside the 95%HPD interval were estimated from 50 simulations of target data.



Application to European Yew (*Taxus baccata*)

Burgarella *et al.* (2012) Mol Ecol 21:3006–21

