



EasyABC: performing efficient approximate Bayesian computation sampling schemes using R

Franck Jabot, Thierry Faure, N. Dumoulin

► To cite this version:

Franck Jabot, Thierry Faure, N. Dumoulin. EasyABC: performing efficient approximate Bayesian computation sampling schemes using R. ABC (Approximate Bayesian Computation), May 2013, Rome, Italy. 2013. hal-02599551

HAL Id: hal-02599551

<https://hal.inrae.fr/hal-02599551>

Submitted on 16 May 2020

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.



EasyABC

performing efficient approximate Bayesian computation sampling schemes using 


Franck Jabot, Thierry Faure & Nicolas Dumoulin

JOIN US ! franck.jabot@irstea.fr thierry.faure@irstea.fr nicolas.dumoulin@irstea.fr


LISC – Laboratoire d'Ingénierie pour les Systèmes Complexes

IRSTEA – Clermont-Ferrand, France

Context

- A number of efficient ABC schemes have been developed (Marin *et al.* 2012, Lenormand *et al.* 2012)
- Available ABC tools: ABCtoolbox (Wegmann *et al.* 2010), ABC-SysBio (Liepe *et al.* 2010) but they have not benefited from recent improvements
- The community of  users has grown tremendously
- To better keep track of on-going improvements, a collaborative toolbox seems advantageous.

Objectives

- Diffusing recent improvements in sequential ABC methodologies: 4 sequential schemes, 3 MCMC schemes.
- Using the  platform to ease diffusion, ergonomics and collaborative improvements.
- Easy to pipeline with the package « abc » (Csilléry *et al.* 2012)
- Making use of multicore computing

The package EasyABC: how to use it?

- Design a simulation code in R or a binary code

function arguments = model parameters

function values = an array of summary statistics

- Use the built-in ABC schemes

defining the model

```
> toy_model<-function(x){2 * x + 1 + rnorm(1)}
```

defining the prior distribution

```
> toy_prior=list(c("unif",0,10))
```

defining the target summary statistics

```
> sum_stat_obs=5
```

defining the sequence of tolerance levels

```
> tolerance=c(1,0.1,0.01)
```

performing a sequential ABC scheme

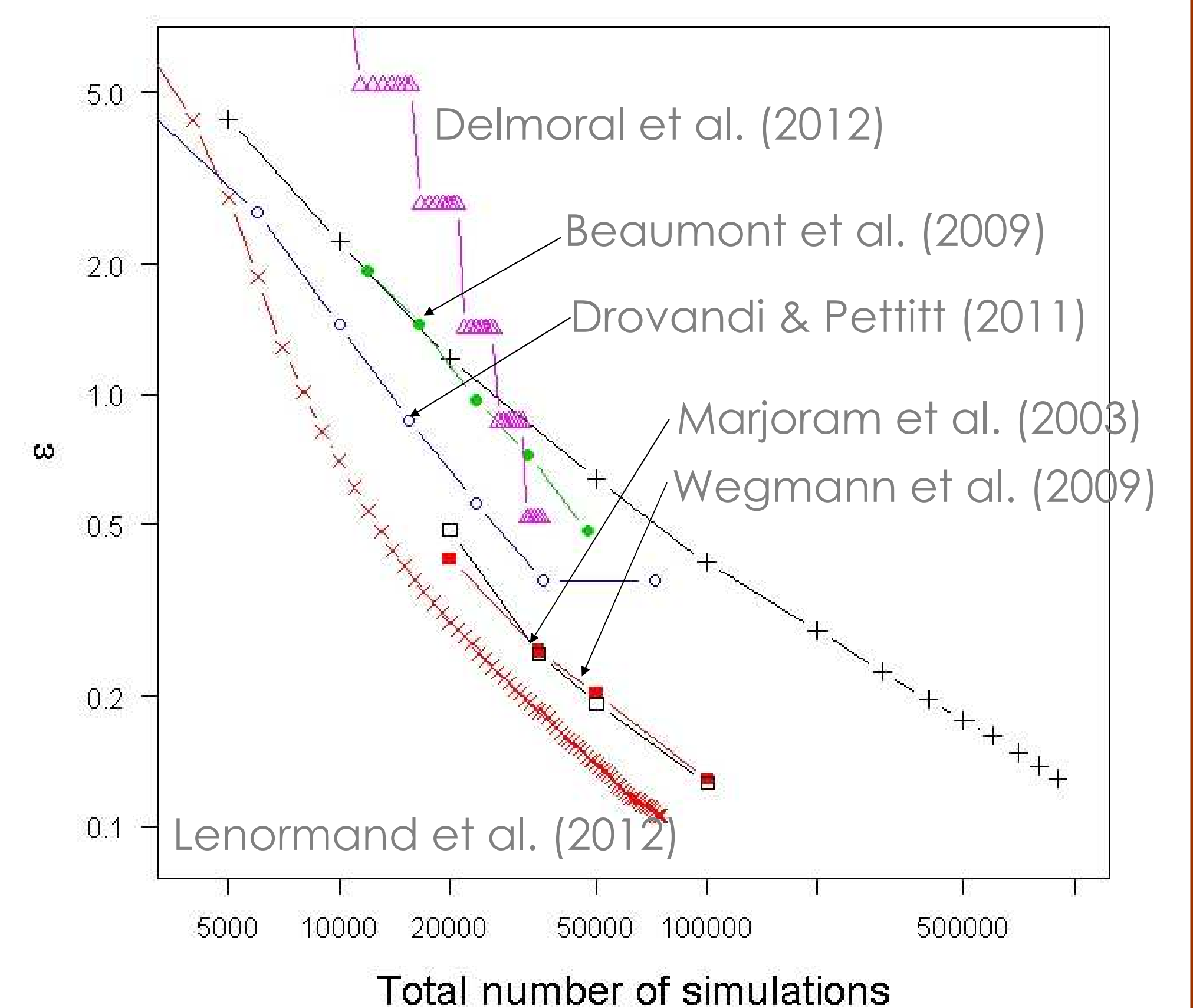
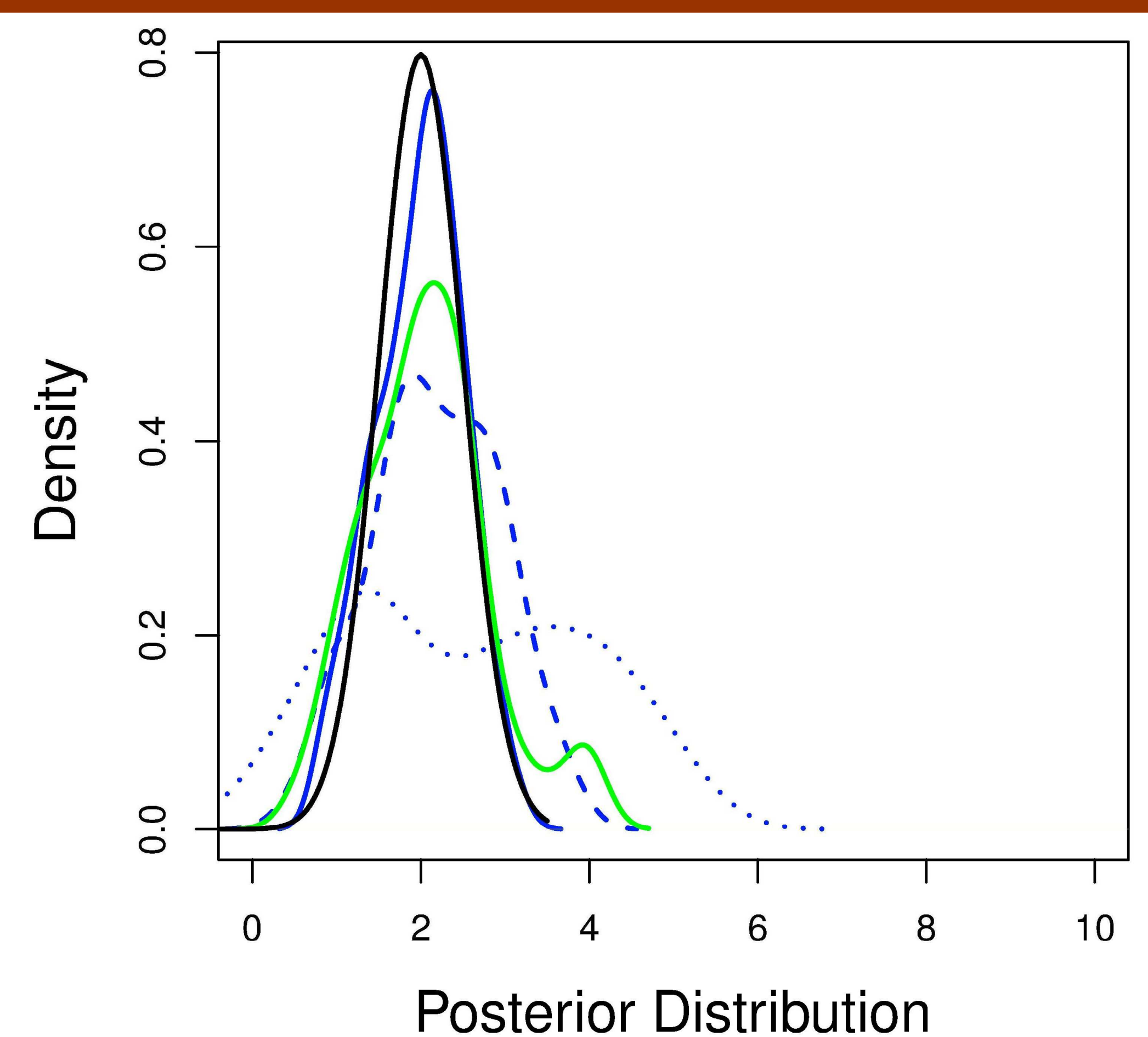
```
> post<-ABC_sequential(method="Beaumont",  
model=toy_model, prior=toy_prior,nb_simul=100,  
summary_stat_target=sum_stat_obs,  
tolerance_tab=tolerance)
```

plotting the results

```
> d=density(post$param,weights=post$weights)
```

```
> plot(d,type="l",col="blue")
```

ALL CONTRIBUTIONS / SUGGESTIONS ARE WELCOME !



References

- Csilléry, François & Blum (2012) *Methods in Ecology & Evolution*, 3, 475-479.
- Jabot, Faure & Dumoulin (2013) *Methods in Ecology & Evolution*, *Online Early*.
- Lenormand, Jabot & Deffuant (2012) Available on ArXiv: <http://arxiv.org/pdf/1111.1308.pdf>.
- Liepe *et al.* (2010) *Bioinformatics*, 26, 1797-1799.
- Marin *et al.* (2012) *Statistics and Computing*, 22, 1167-1180.
- Wegmann *et al.* (2010) *BMC Bioinformatics*, 11, 116.