Simulation-based inference of epidemic and phylodynamic models via Neural Posterior Estimation (NPE)

Francesco Pinotti¹, Julien Thézé², Xavier Bailly² and Guillaume Fournié^{1,2,3}

- ¹ Université de Lyon, INRAE, VetAgro Sup, UMR EPIA, France
- ² Université Clermont Auvergne, INRAE, VetAgro Sup, UMR EPIA, France
- ³ Department of Pathobiology and Population Sciences, Royal Veterinary College, UK







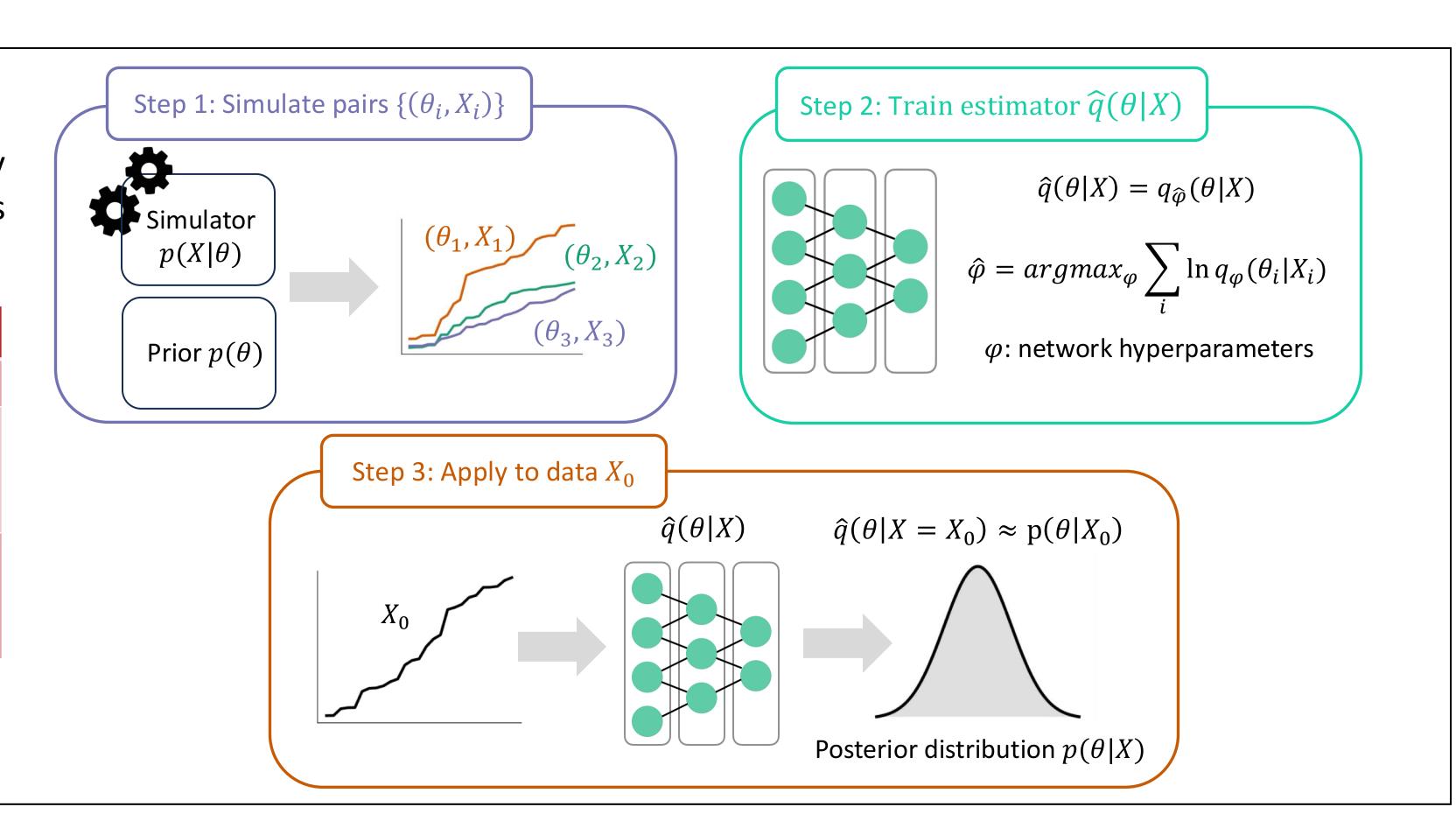
francesco.pinotti@inrae.fr

Background

Bayesian inference of transmission models can be made difficult by complicated likelihood functions. Simulation-based inference (SBI) methods use simulations to perform inference^a.

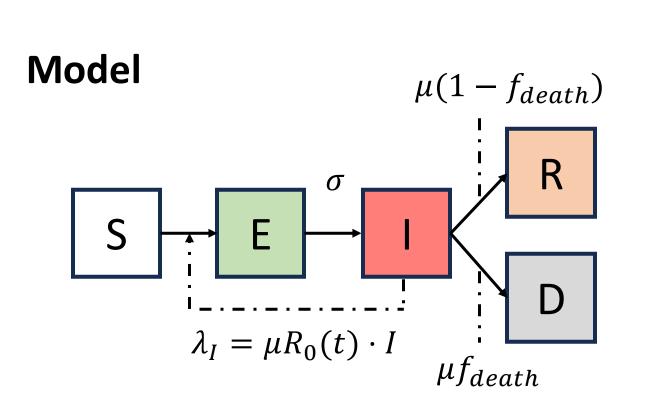
Traditional SBI methods	NPE
Target approximate posterior	Flow-based learning of exact posterior ^{c,d}
Ad-hoc selection of summary statistics ^b	Automatic detection of summary statistics from raw data via dedicated neural network
Potentially expensive to run and to calibrate	Training is costly but sampling is extremely fast. Inference is amortized , enabling powerfule calibration checks

This study aims to assess the effectiveness of flow-based NPE in two case studies of epidemiological relevance.



SEIRD model

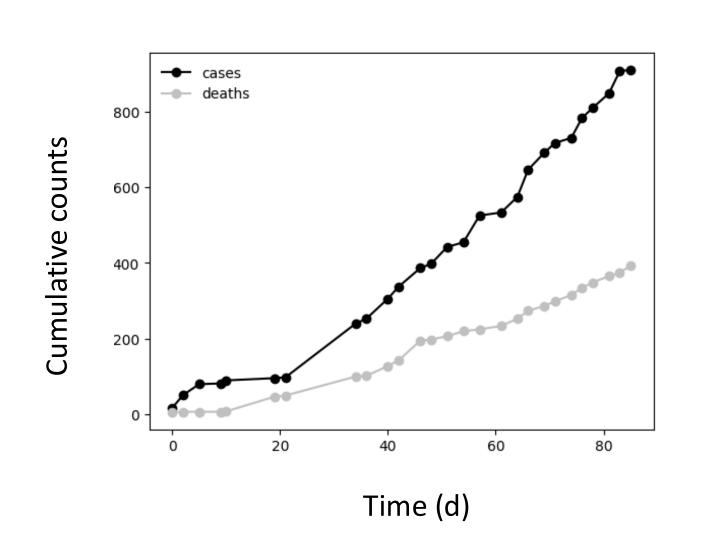
Data: Time series of reported cases C_t and deaths D_t during the 2014 Ebola virus outbreak in Sierra Leone^e.



 $R_0(t) = R_0 e^{-k\beta t}$

Reported cases/deaths follow a Negative Binomial distribution with expected counts set by the model:

$$C_t, D_t \sim NegBin(\langle C_t, D_t \rangle, s)$$

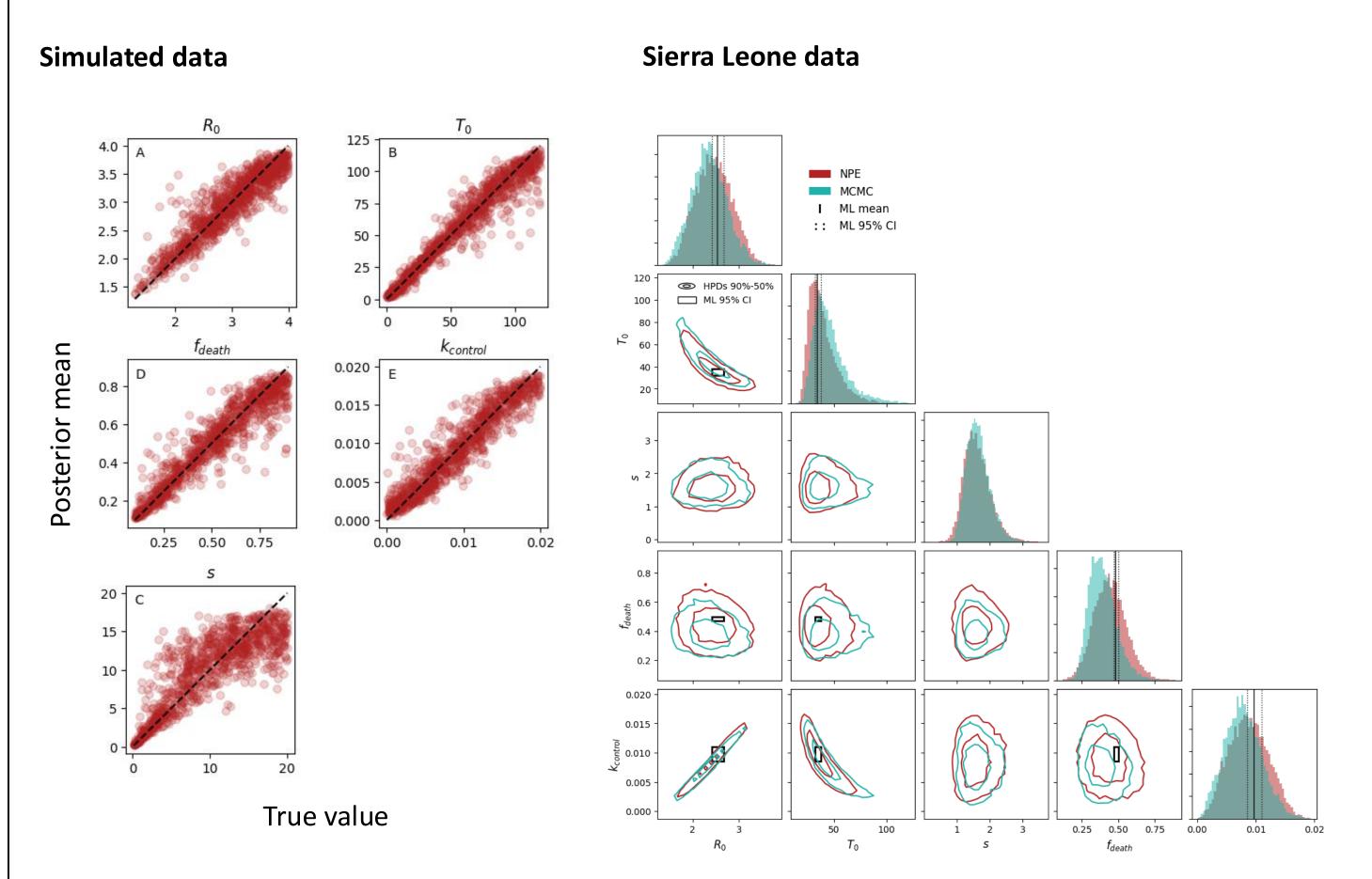


Inferred parameters:

- R_0 : basic reproduction number
- T_0 : time to first reporting
- s: reporting distribution shape
- f_{death} : infection fatality rate
- k_{β} : effectiveness of interventions

c_t

Results

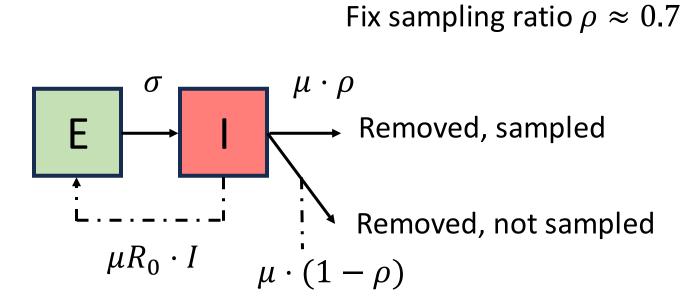


NPE retrieves the correct posterior.

Phylodynamics model

Data: 72 early genetic sequences from the 2014 Ebola virus outbreak in Sierra Leone. Model is fitted to estimated phylogenies, g,h.

Model



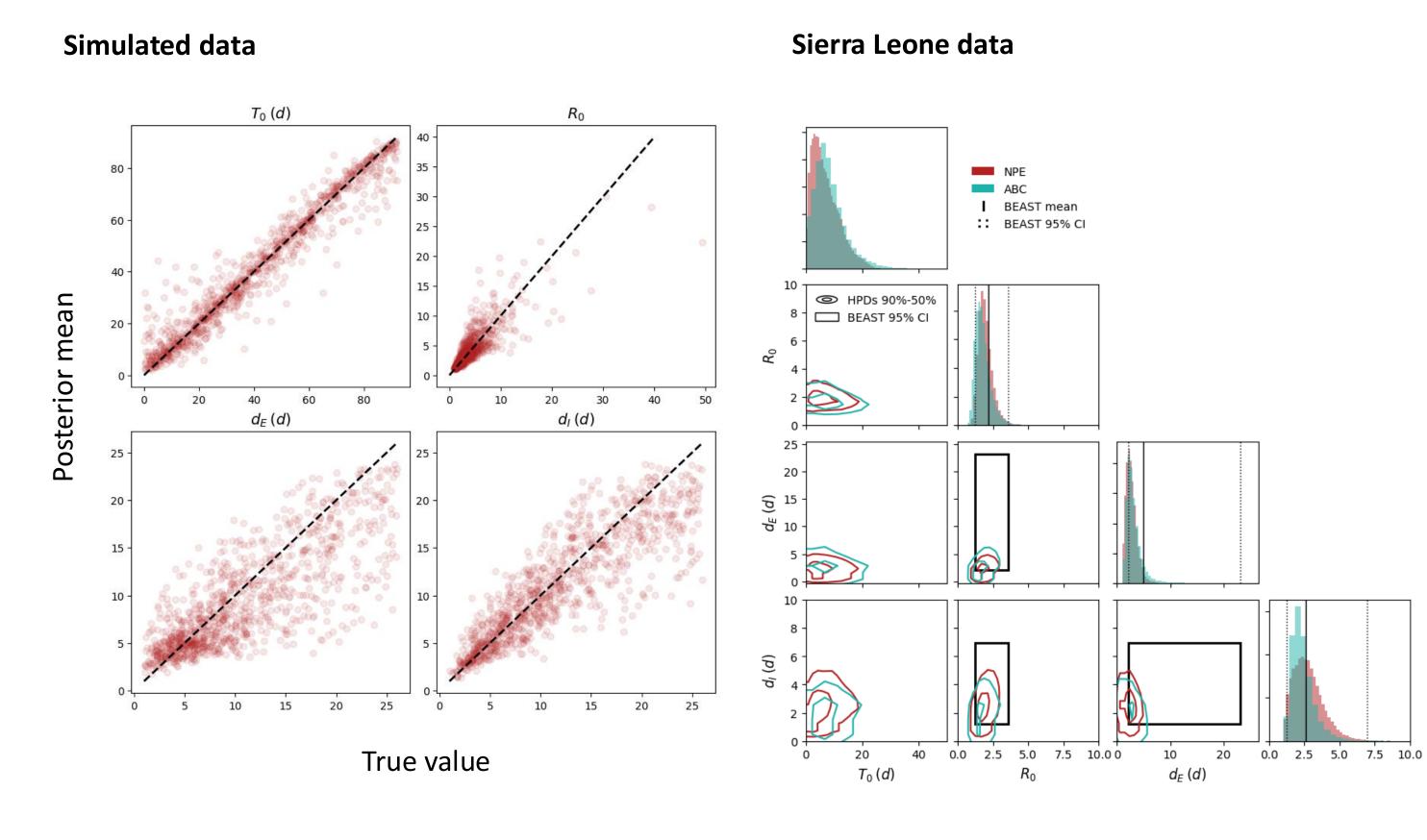
Observed and simulated trees are formatted into Compact Bijective Ladderized Vectors (CBLV)ⁱ.

Data atggagaacatagtacatggagaaaatagtgcatggagagaaaatagtgcatggagaaaatagtgcatggagagaaatagtgcatggagagaaaatagtgcatggagagaaaatagtgcatggagagaaatagtgcatggagagaaatagtgcatggagagaaatagtgcatggagagaaatagtgcatggagagaaatagtgcatggagagaaatagtgcatggagaaaatagtgcatggagaaaatagtgcatggagaaaatagtgcatggagaaaatagtgcatggagaaatagtgcatggagaaaatagtgcatggagaaaatagtgcatggagaaaatagtgcatggagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtgcatgagaaaatagtg

Inferred parameters:

- R_0 : basic reproduction number
- $d_E = \sigma^{-1}$: incubation period
- T_0 : time to first reported cases
- $d_I = \mu^{-1}$: infectious period

Results



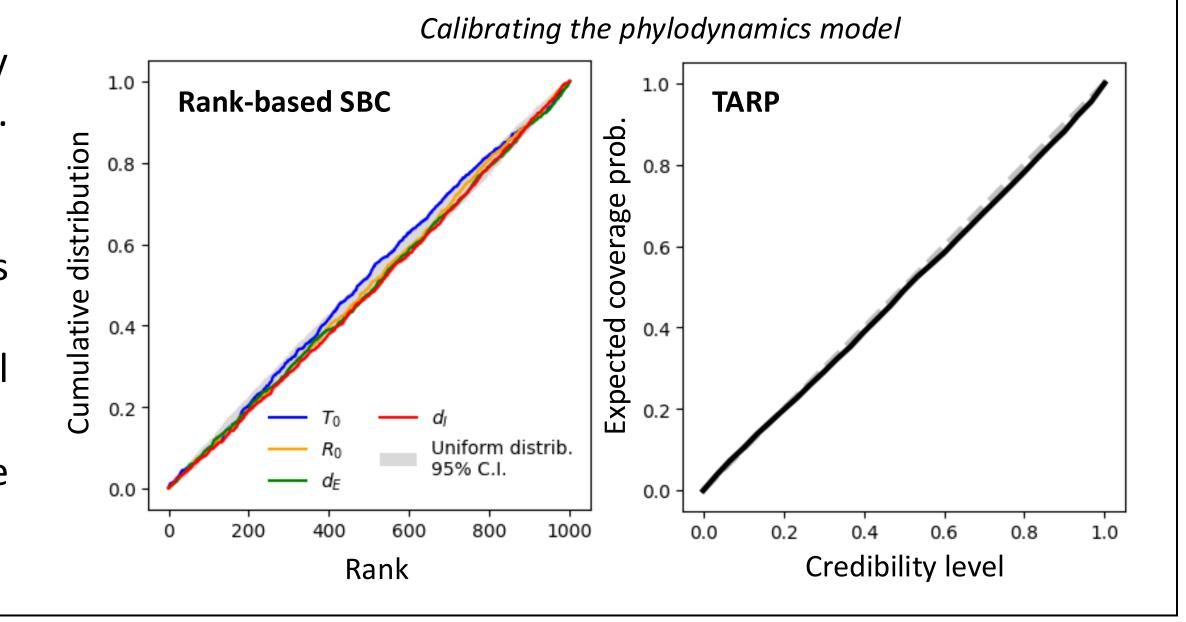
NPE yields posterior estimates that agree with ABC ones without calculating tree summary statistics.

Amortized inference & posterior calibration

Amortization refers to the NPE estimator being instantly applicable to new data without further training.

Posterior calibration methods

- Rank-based simulation-based calibration^j (SBC): checks global accuracy of marginal distributions.
- Test of Accuracy with Random Points^k (TARP): checks global accuracy of entire posterior distribution.
- Local Classifier 2-Samples Test¹: checks accuracy of entire posterior distribution on particular data.



References

aCranmer et al, PNAS, 2020
bSisson et al, Chapman & Hall, 2018
cPapamakarios et al, NEURIPS, 2016
dLueckmann et al, NEURIPS, 2017
eAlthaus, PLoS Curr, 2014
fGire et al, Science, 2014
gStadler et al, PLoS Curr, 2014
hSaulnier et al, PLoS Comp Biol, 2017
iVoznica et al, Nat Comms, 2022
jTalts et al, ArXiv, 2020
kLemos et al, ICML, 2023
Linhart et al, NEURIPS, 2023