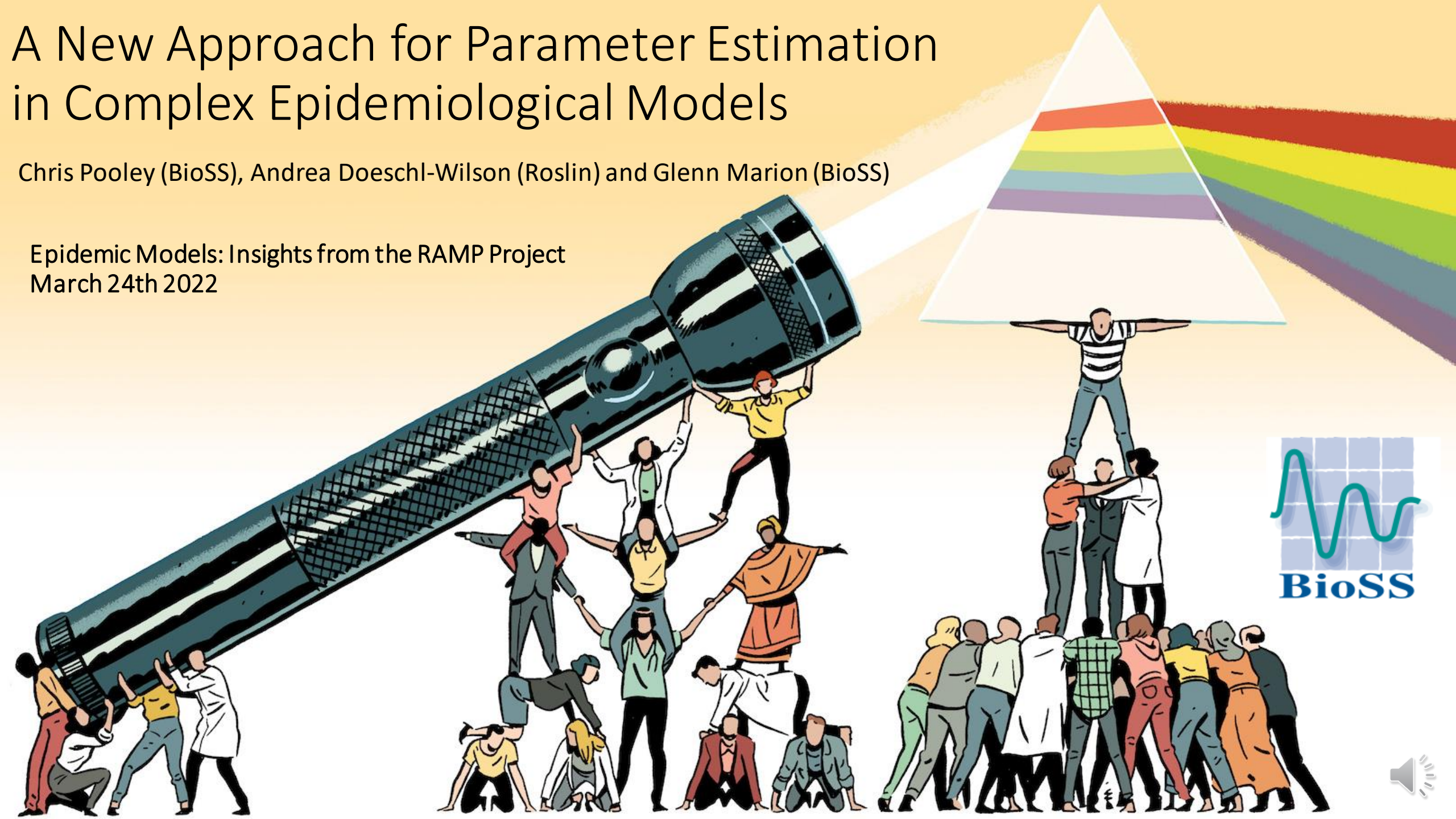


A New Approach for Parameter Estimation in Complex Epidemiological Models

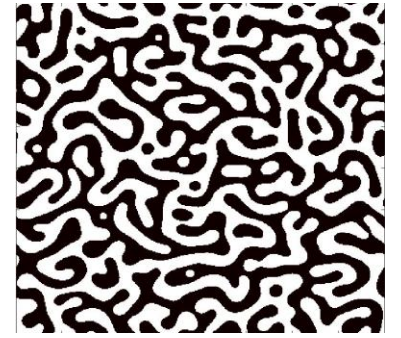
Chris Pooley (BioSS), Andrea Doeschl-Wilson (Roslin) and Glenn Marion (BioSS)

Epidemic Models: Insights from the RAMP Project
March 24th 2022



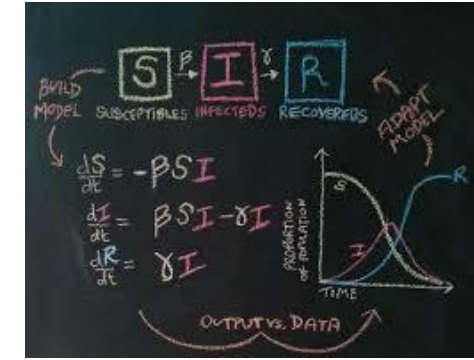
My background

- Physics → Genetics → Epidemiology
- Understanding genetics of disease spread in animals
 - Selective breeding programs to help combat disease
- Bayesian methods for disease transmission experiments
 - Typically data from 100s of animals/fish
 - Individual-based models

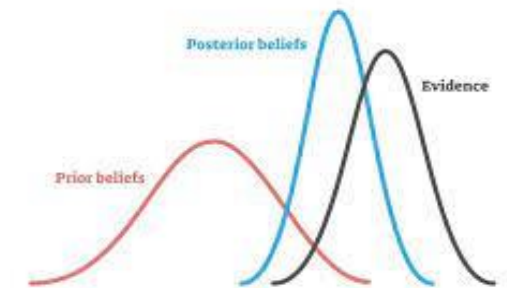


Motivation

- Develop mathematical models for COVID-19
 - Understanding
 - Looking into the future
 - Test control strategies before applying them in reality
- Models only useful if well parameterised
- Bayesian inference
 - Accounts for uncertainty in prior and data
 - Output model parameters and system behaviour INCLUDING uncertainty
 - Provides best evidence-based advice for policy



BAYESIAN ANALYSIS



Aim

- Develop models and Bayesian methods to analyse publically available COVID-19 data
- Ideally account for:
 - Differences in disease severity
 - Spatial variation
 - Demographic variation (*e.g.* age, sex)
 - Time variation in external force of infection
 - Government interventions
 - Human behavioural change
 - Different virus variants
 - Vaccination effects
 - Biases in the data





Start of
RAMP

①
Individual
based

③
PMCMC

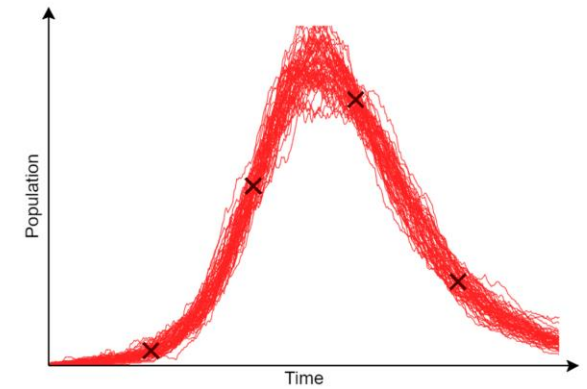
④
ABC-MBP

⑤
Diffusion
Approx.

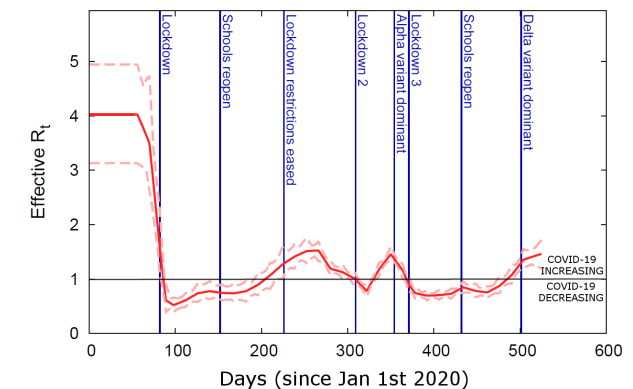
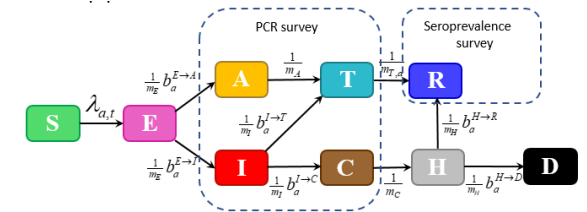
②
ABC

Overview

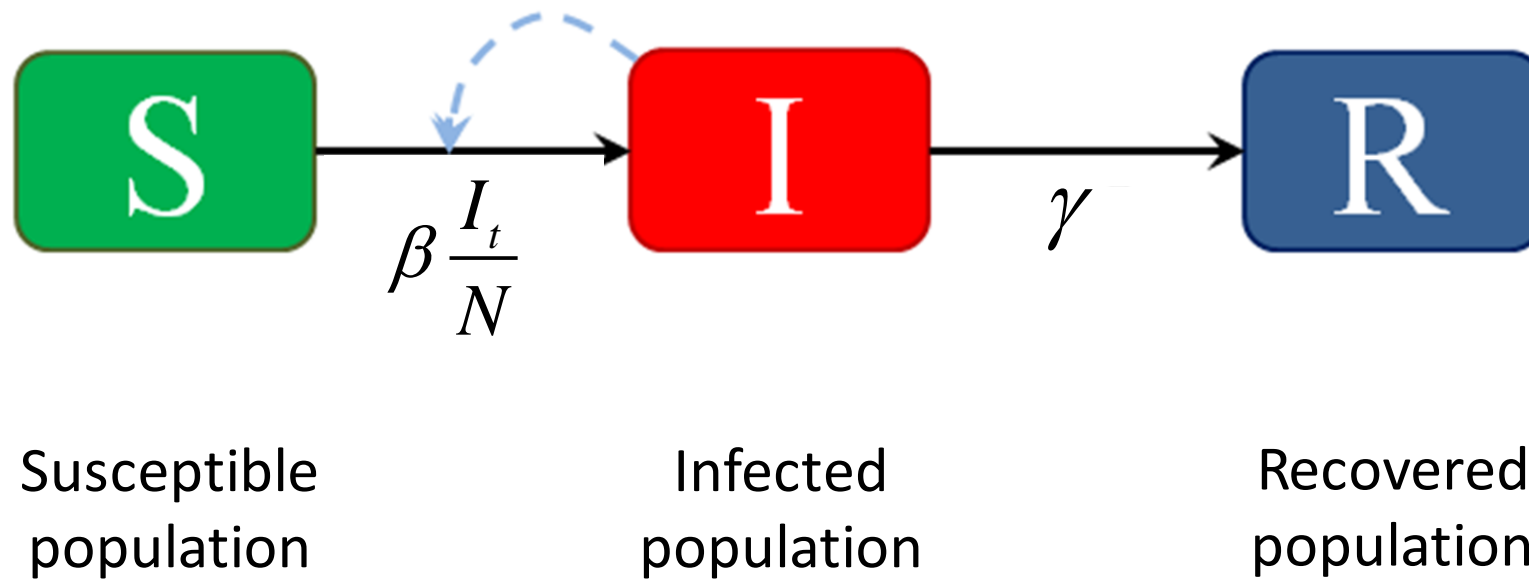
- Outline existing methods:
 - ABC rejection sampling and ABC-SMC
- Introduce new inference methodology:
 - ABC-MBP
- BEEPmbp software
 - Speed comparison between different approaches
- Application to age-structured model of Covid-19



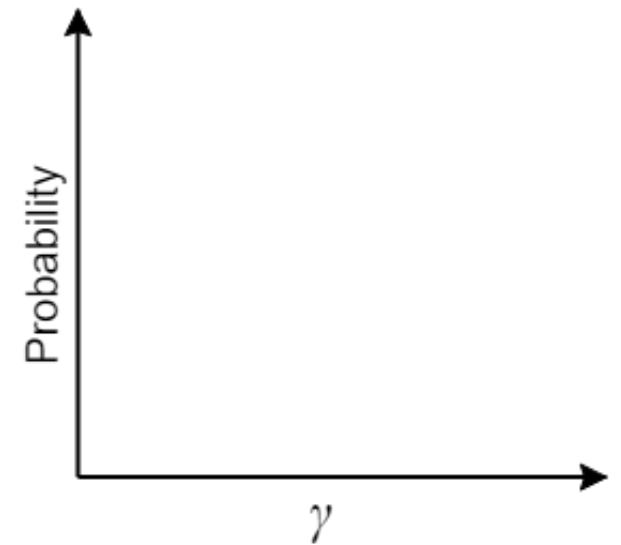
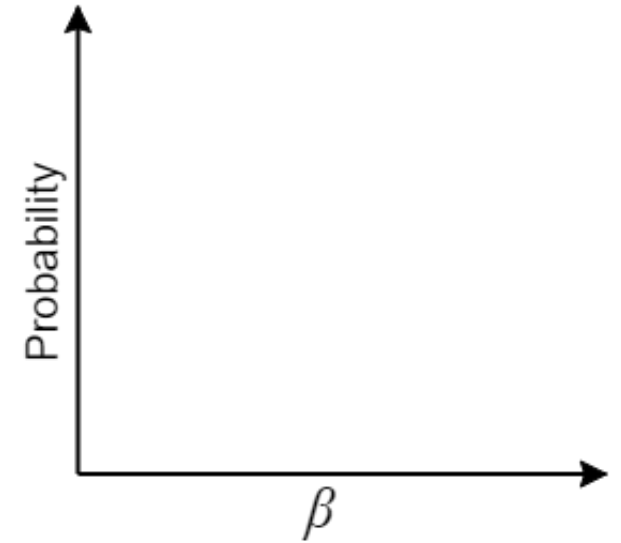
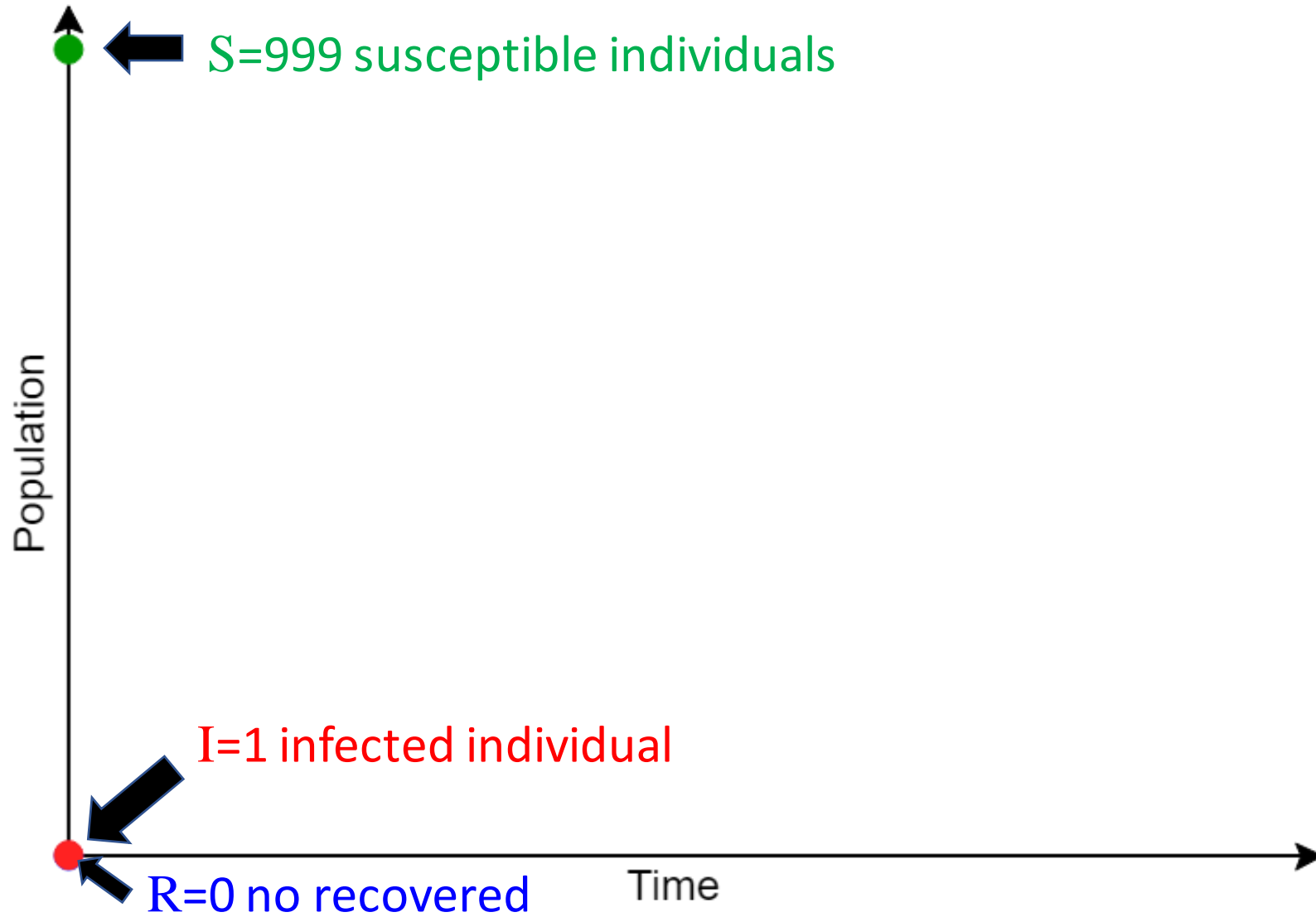
BEEPmbp



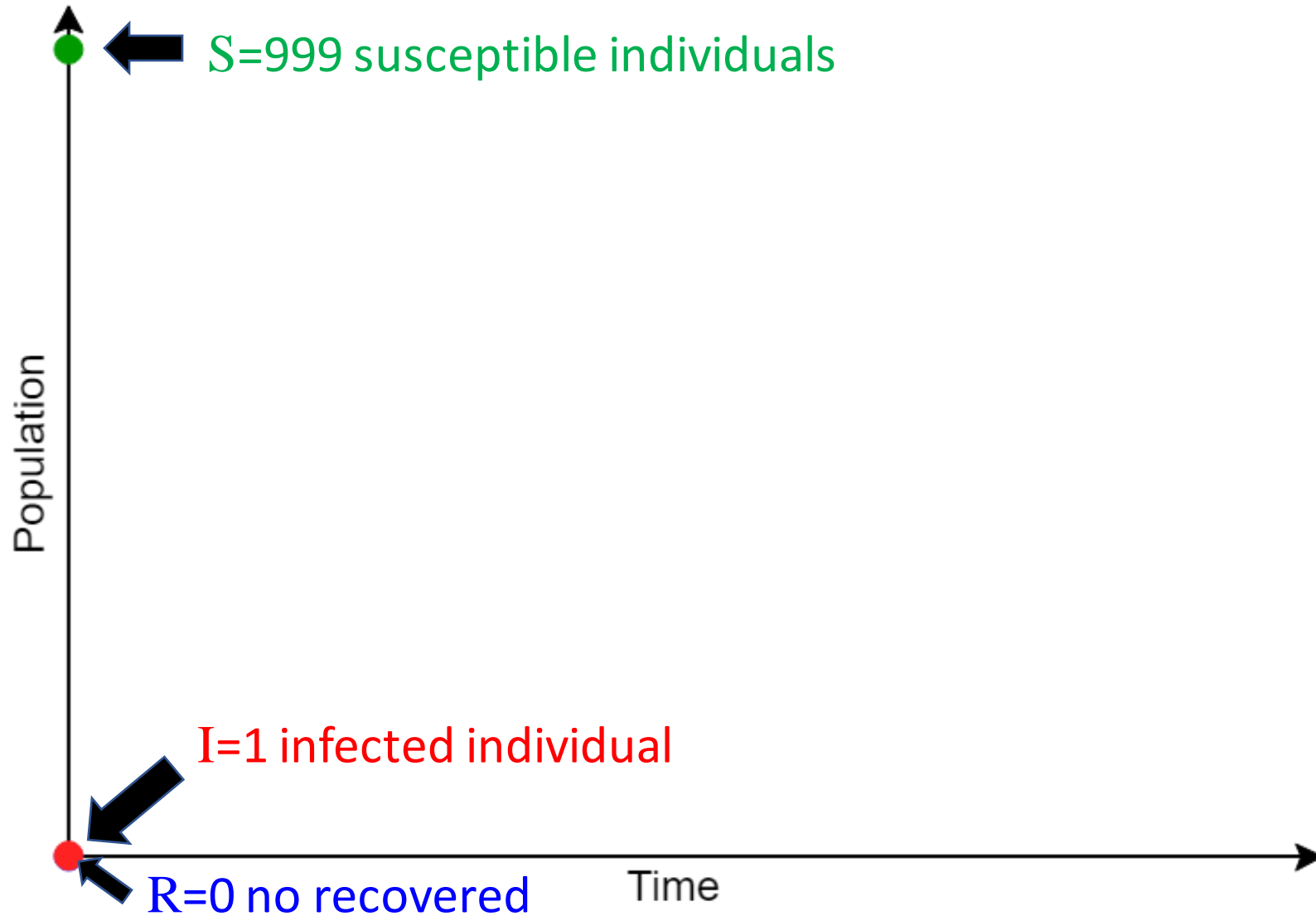
SIR compartmental model



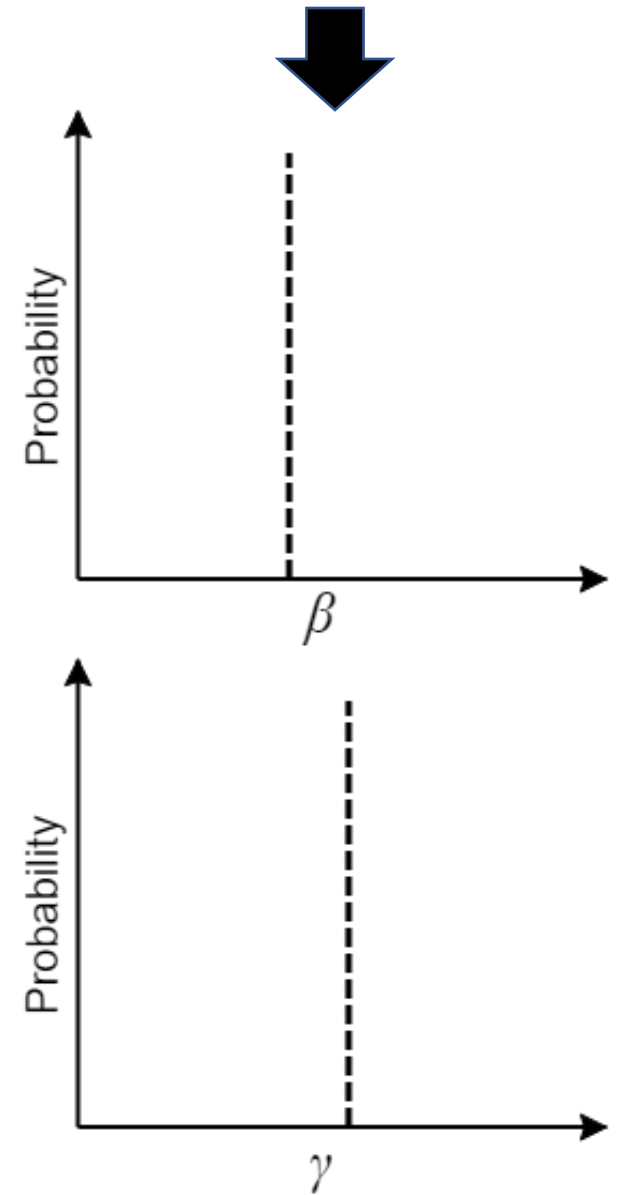
Simulation



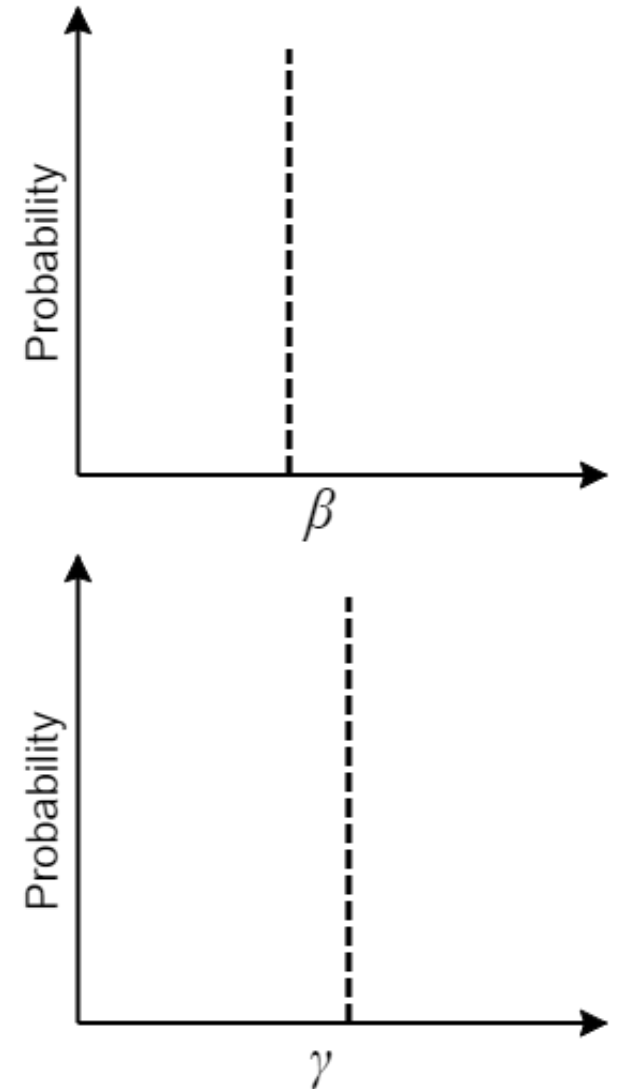
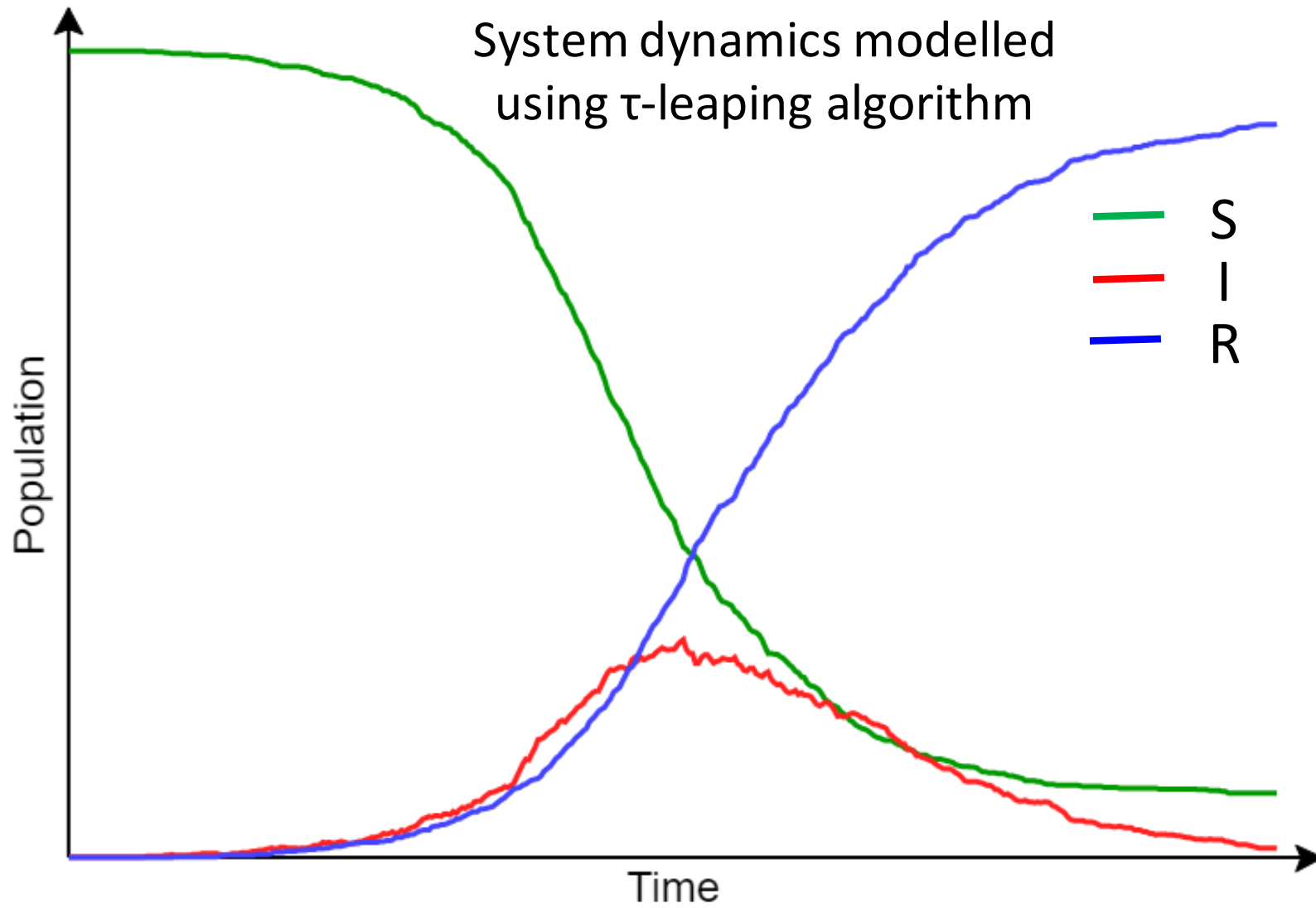
Simulation



We select a set of suitable model parameters

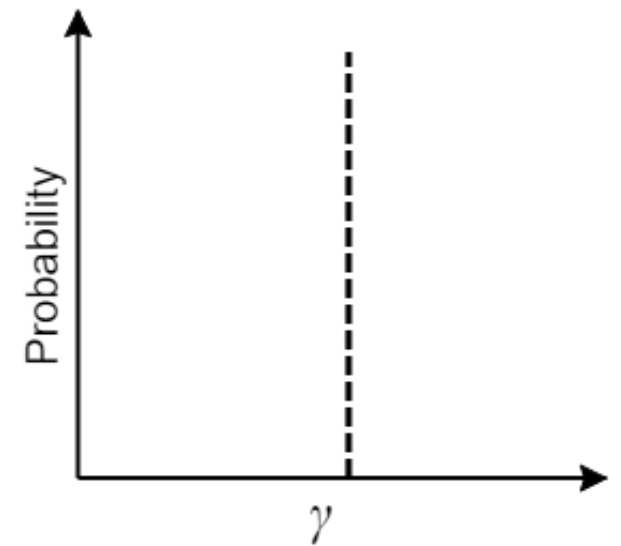
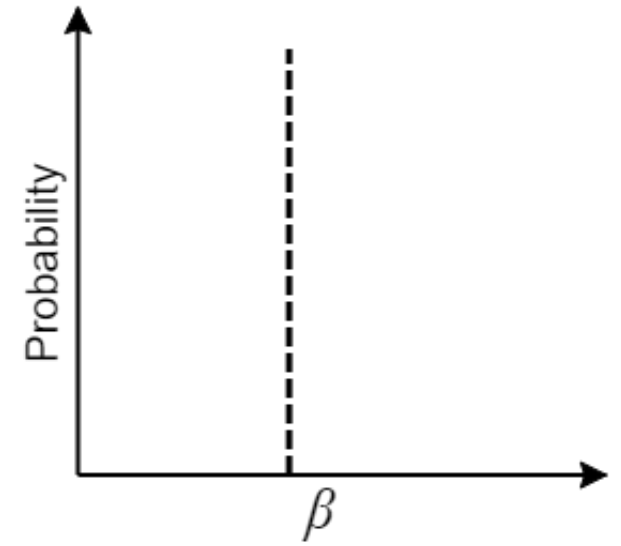
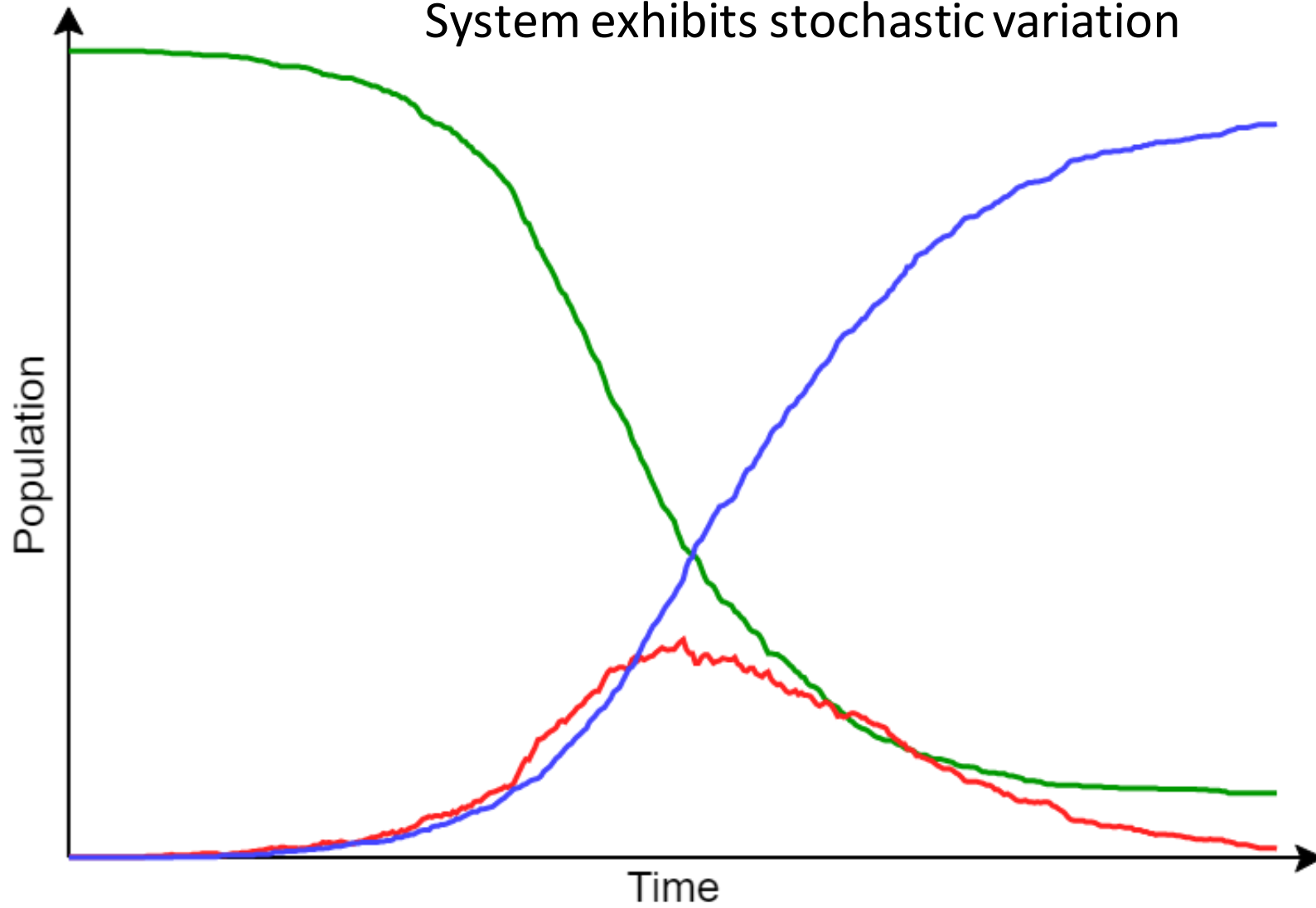


Simulation

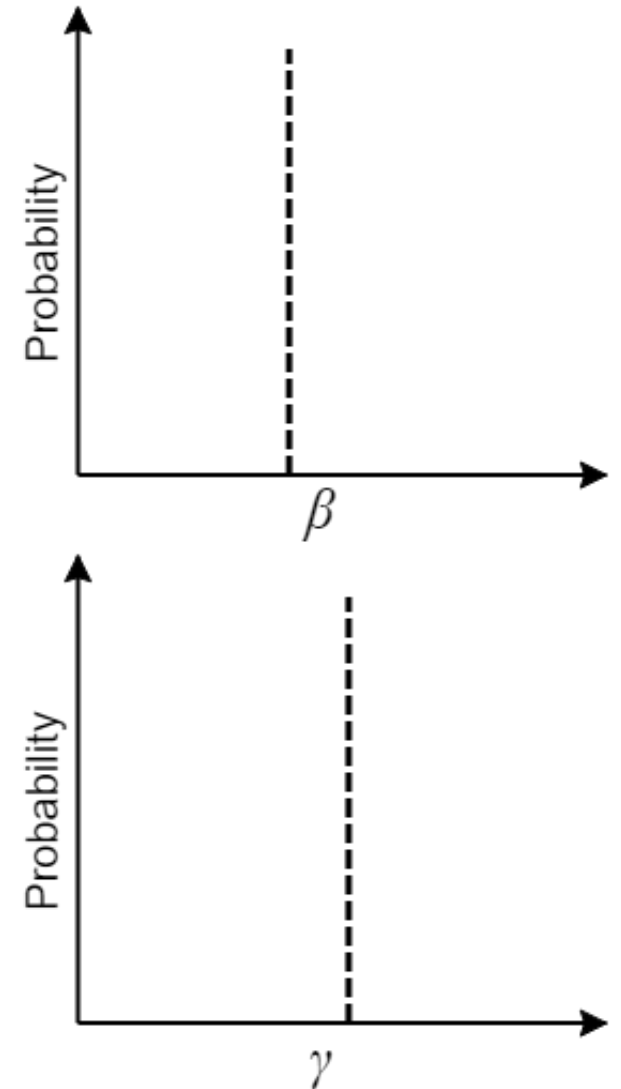
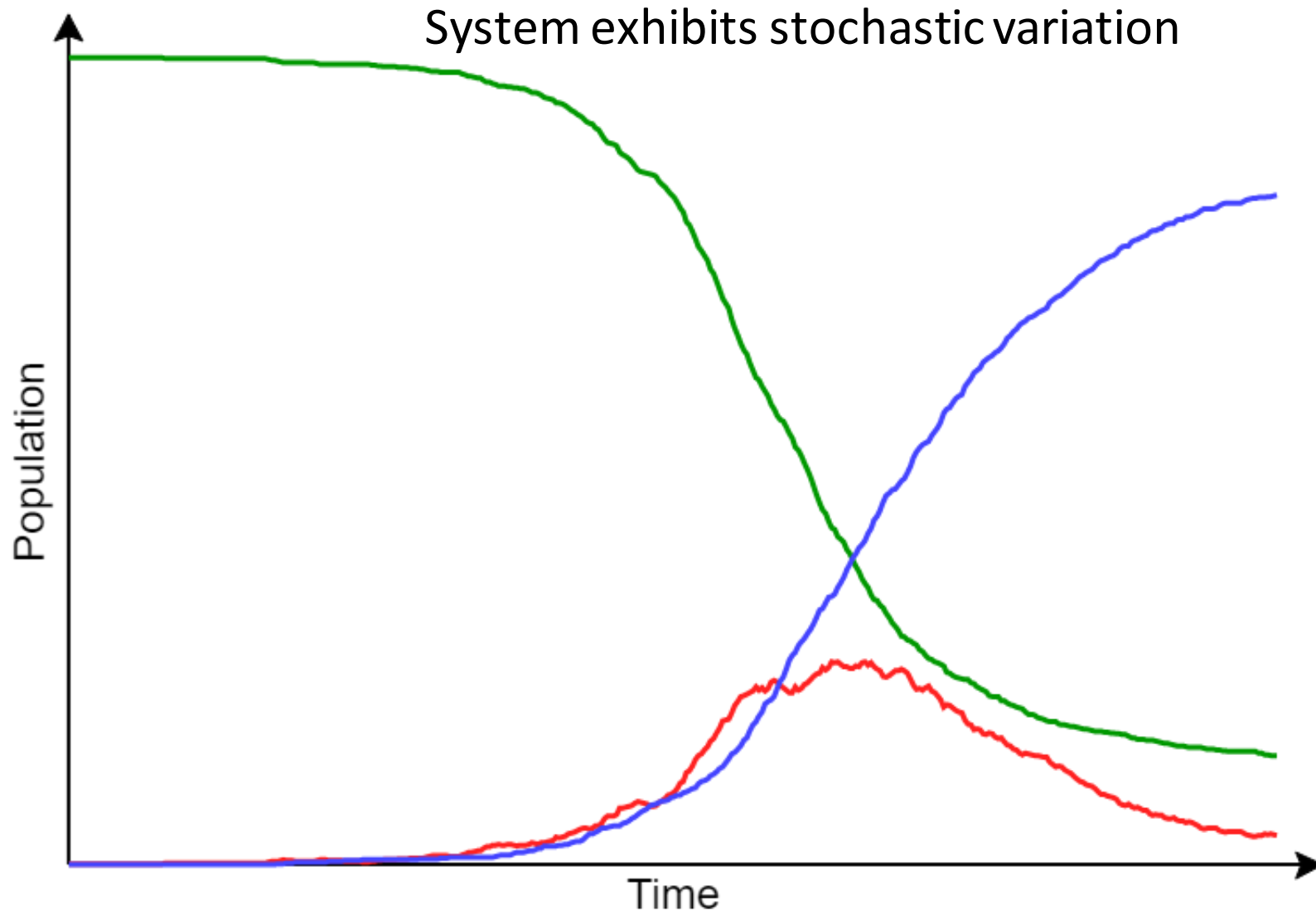


Simulation

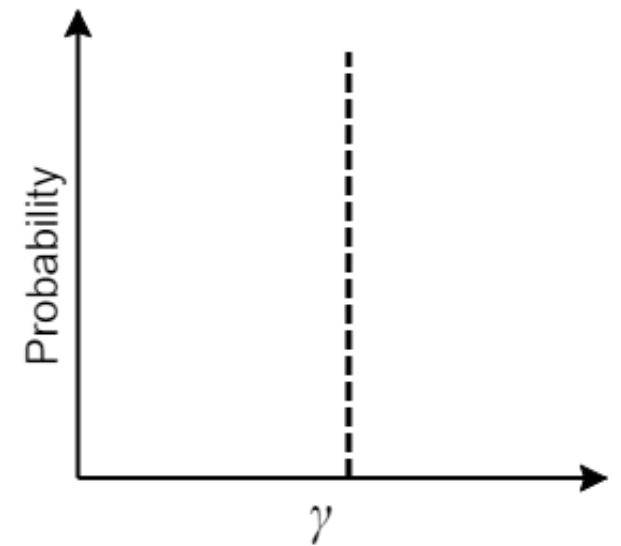
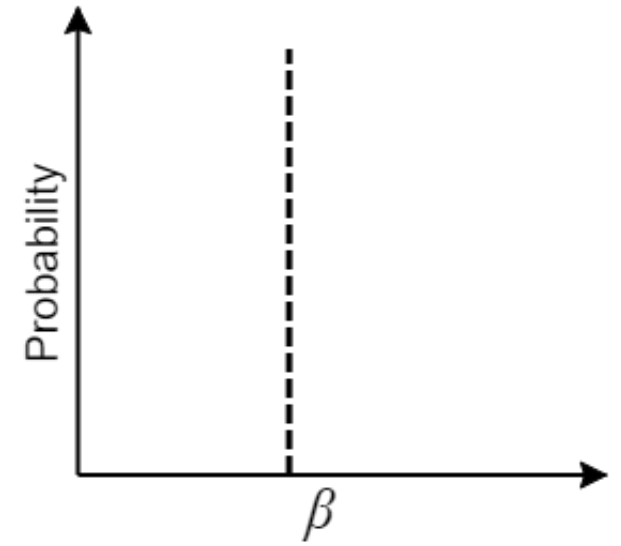
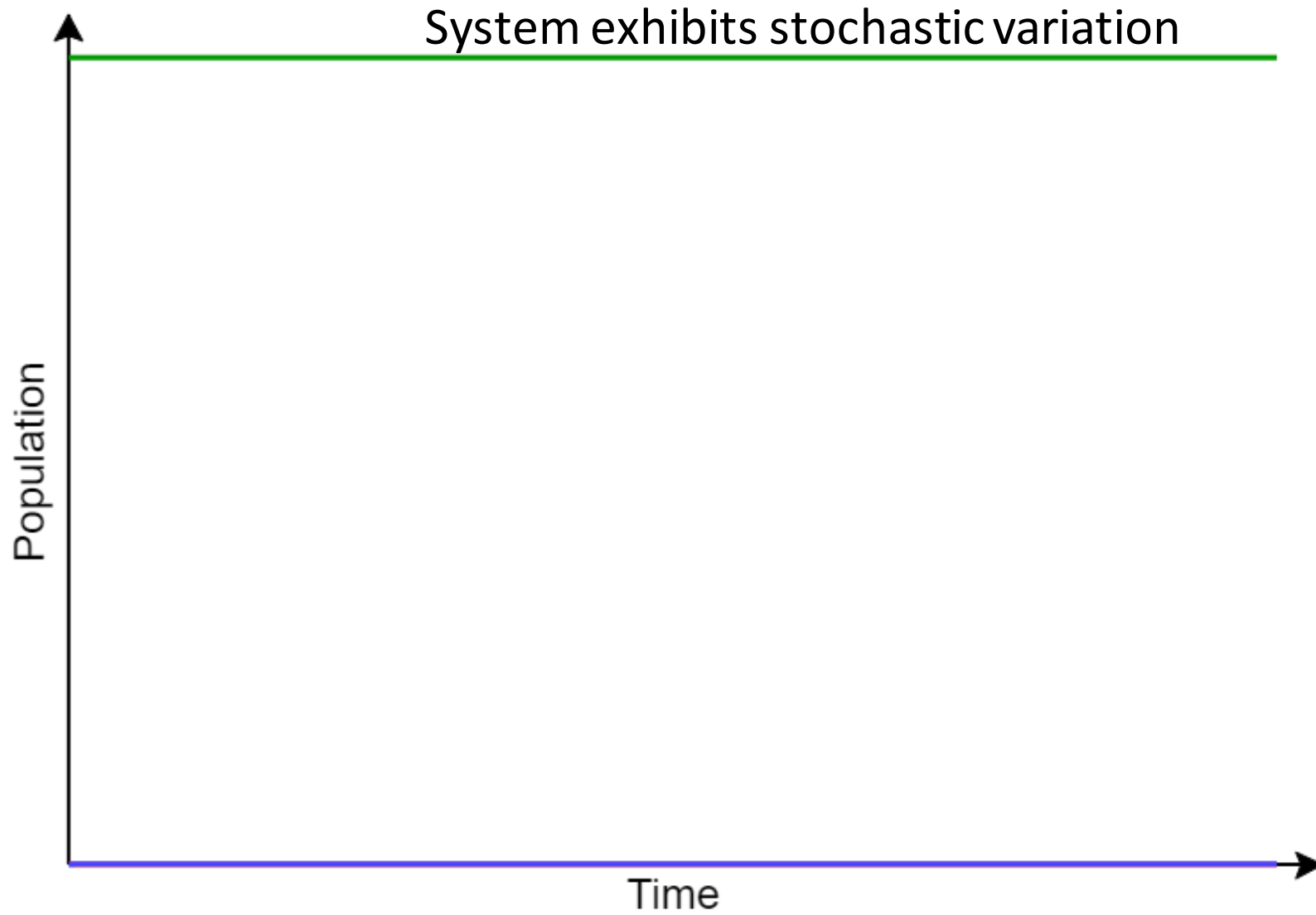
System exhibits stochastic variation



Simulation

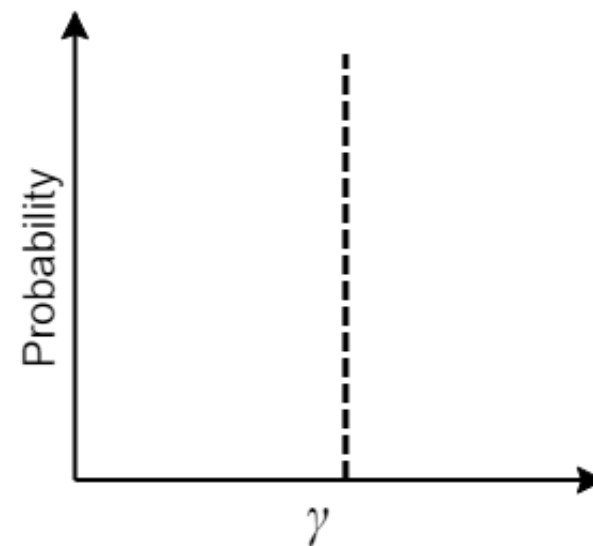
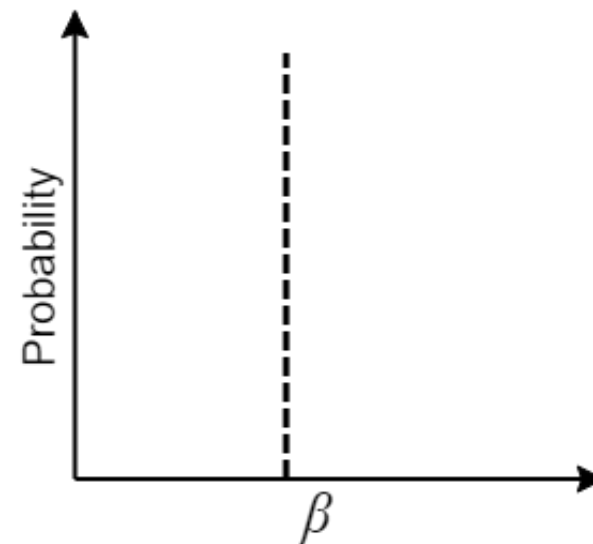
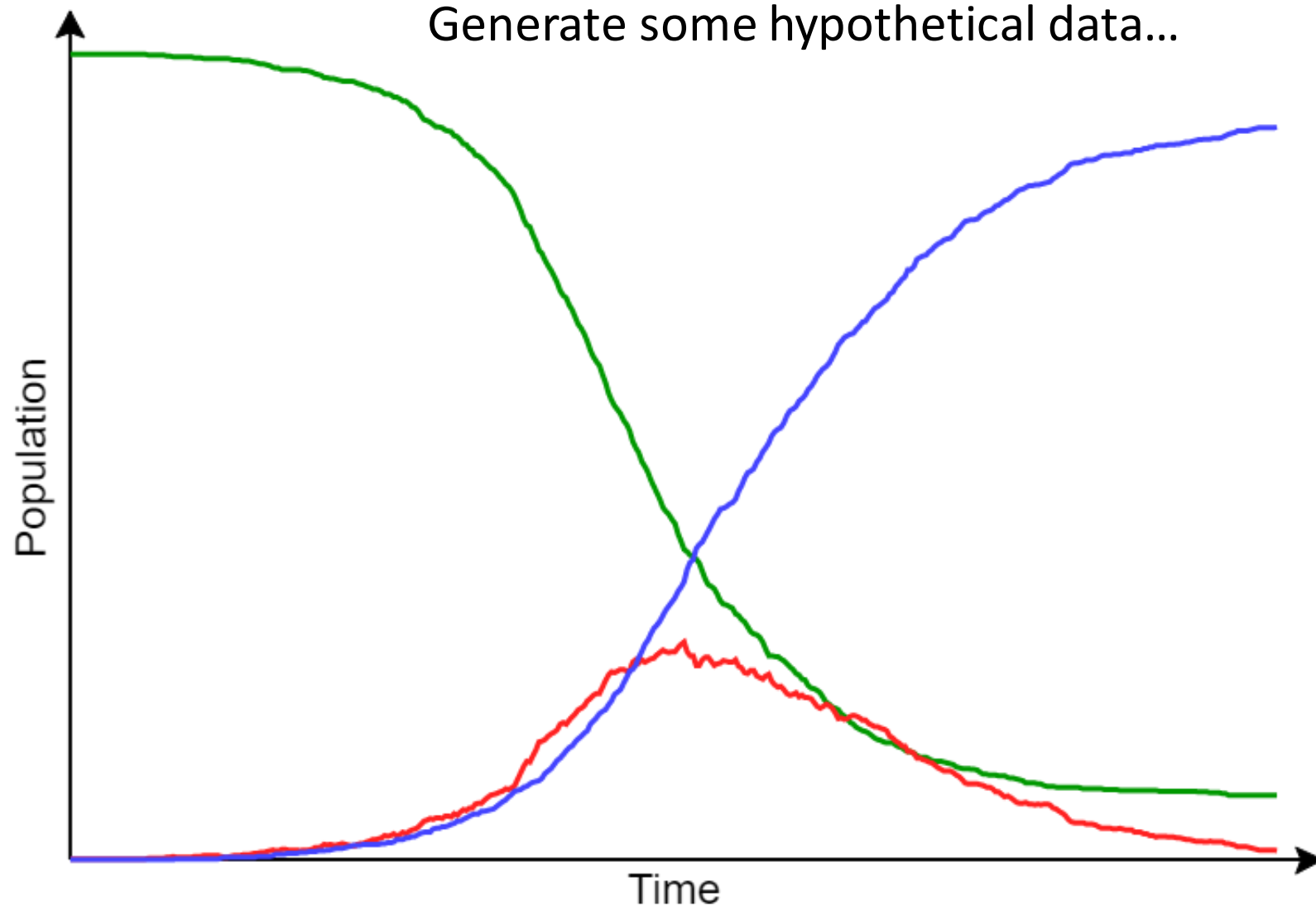


Simulation

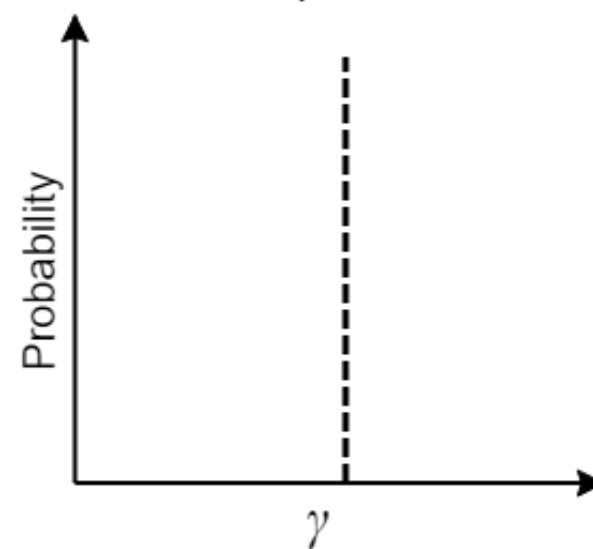
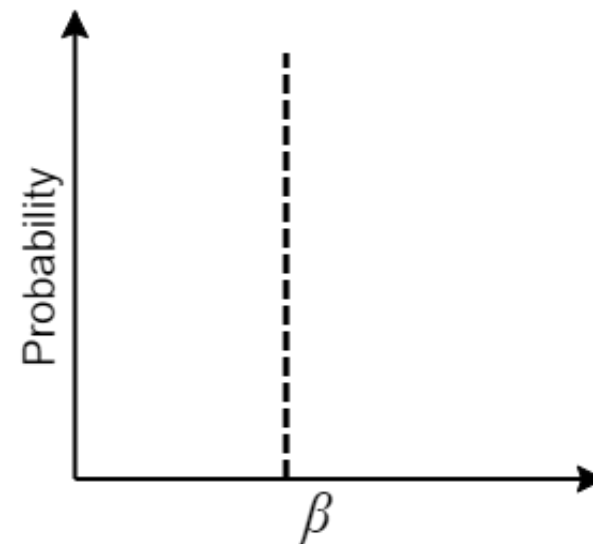
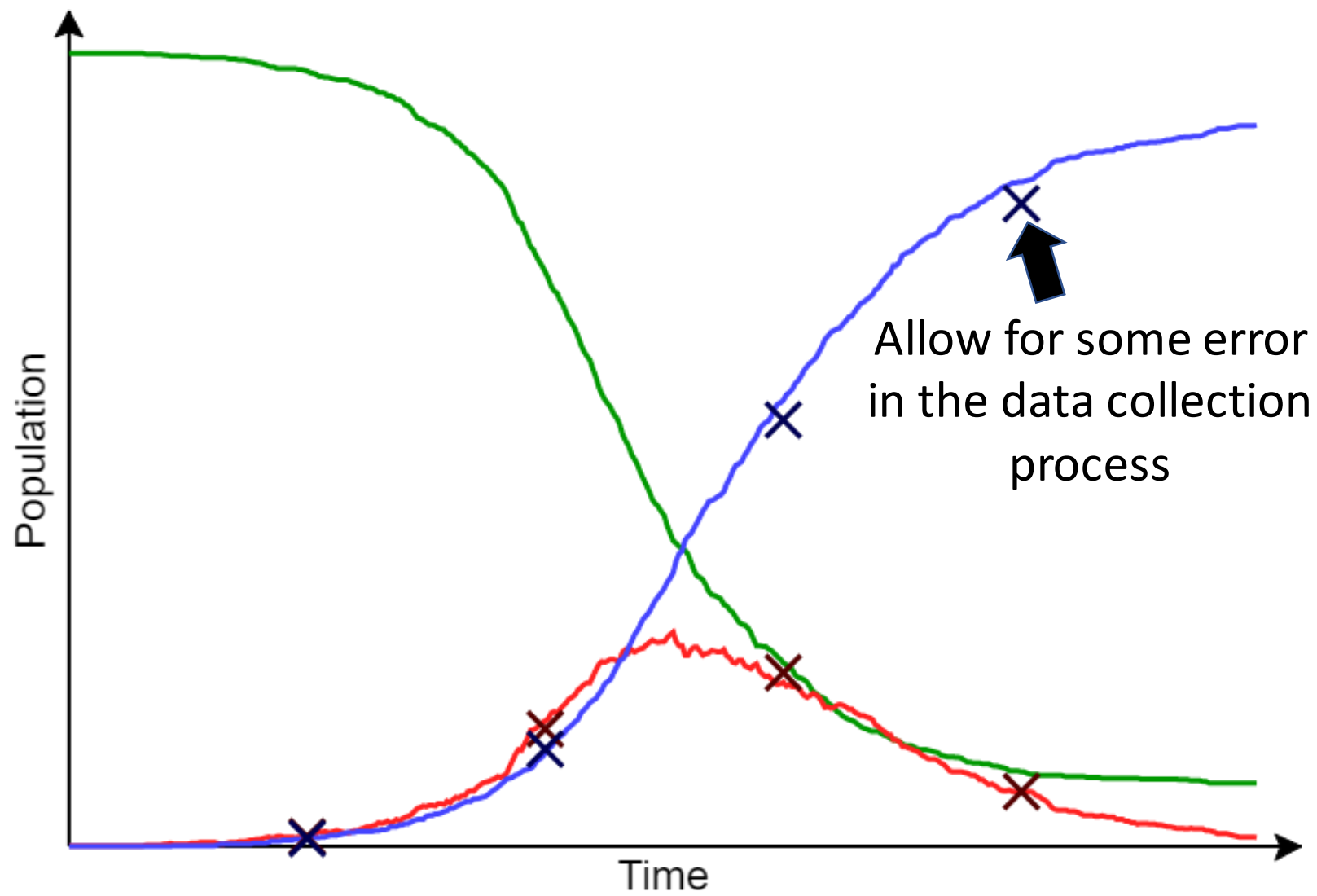


Data

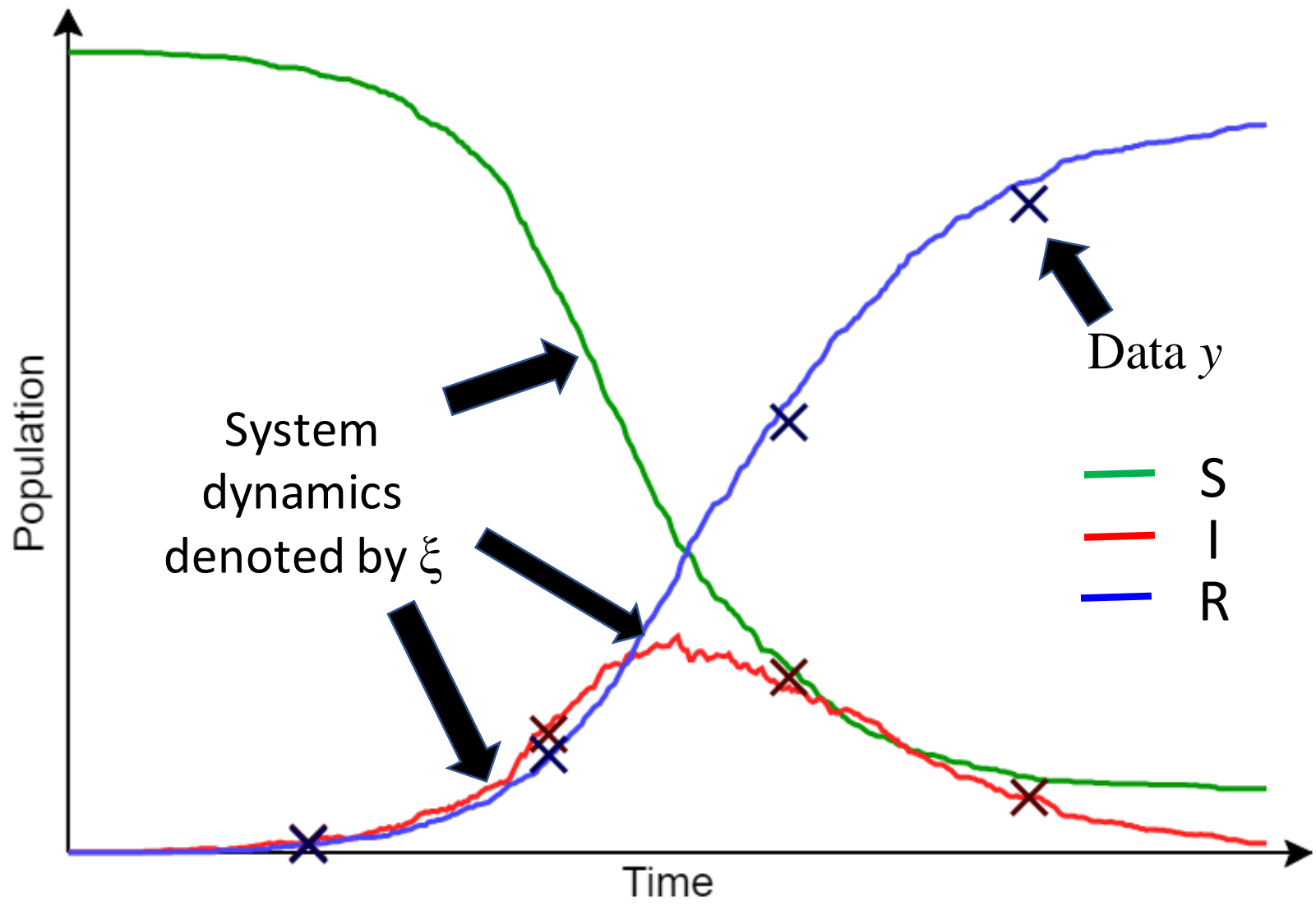
Generate some hypothetical data...



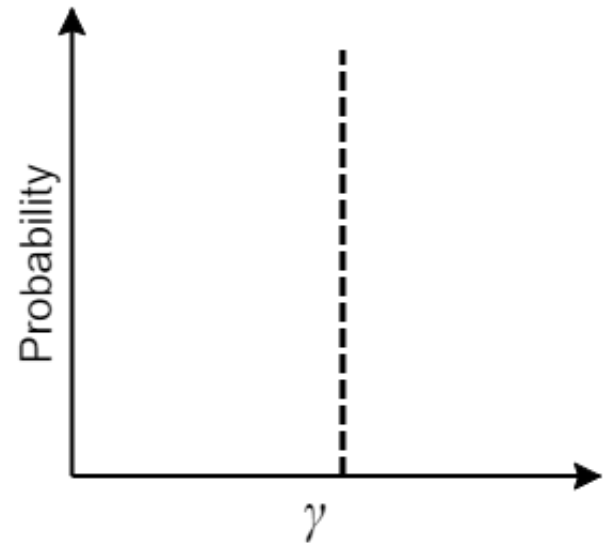
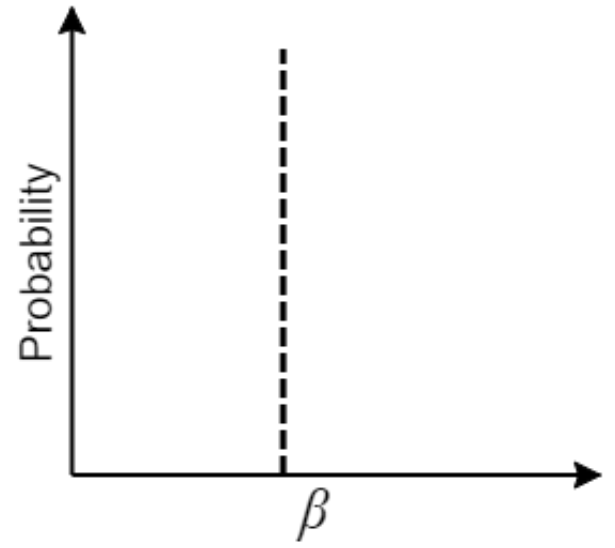
Data



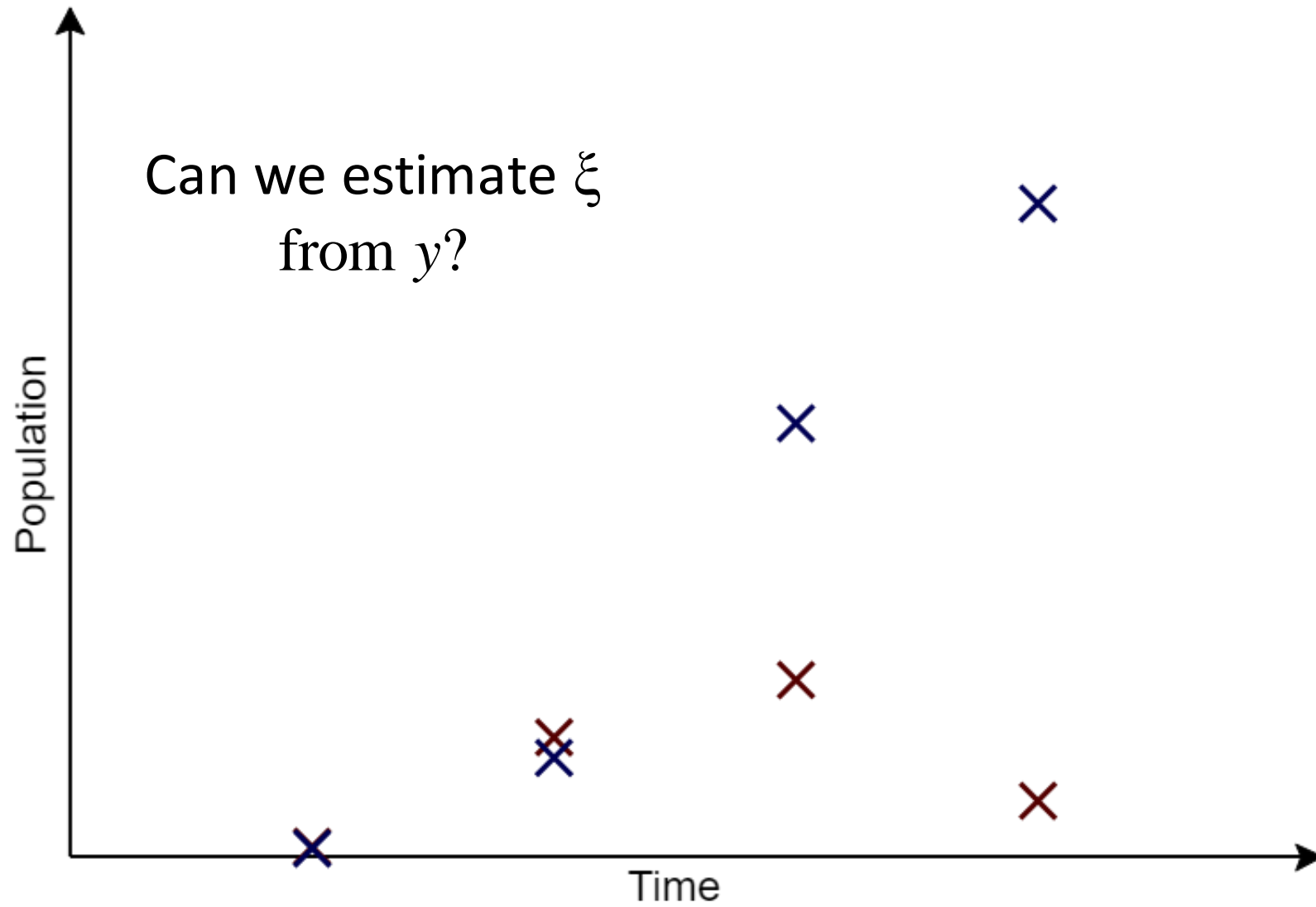
Terminology



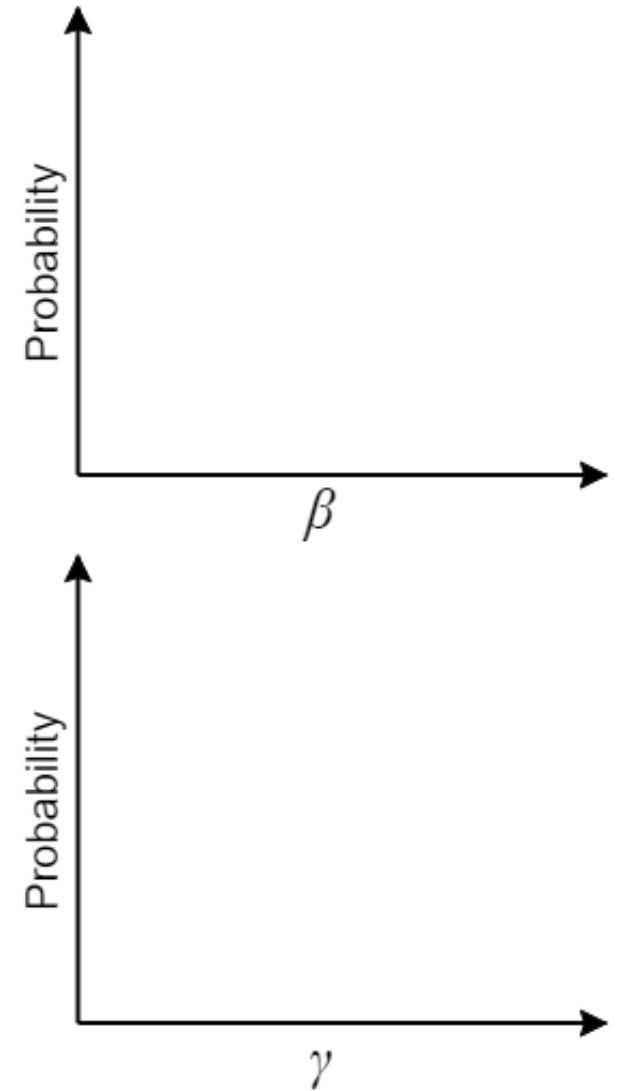
Model parameters
 $\theta = \{\beta, \gamma\}$



Inference



Can we estimate θ from y ?



Bayesian inference



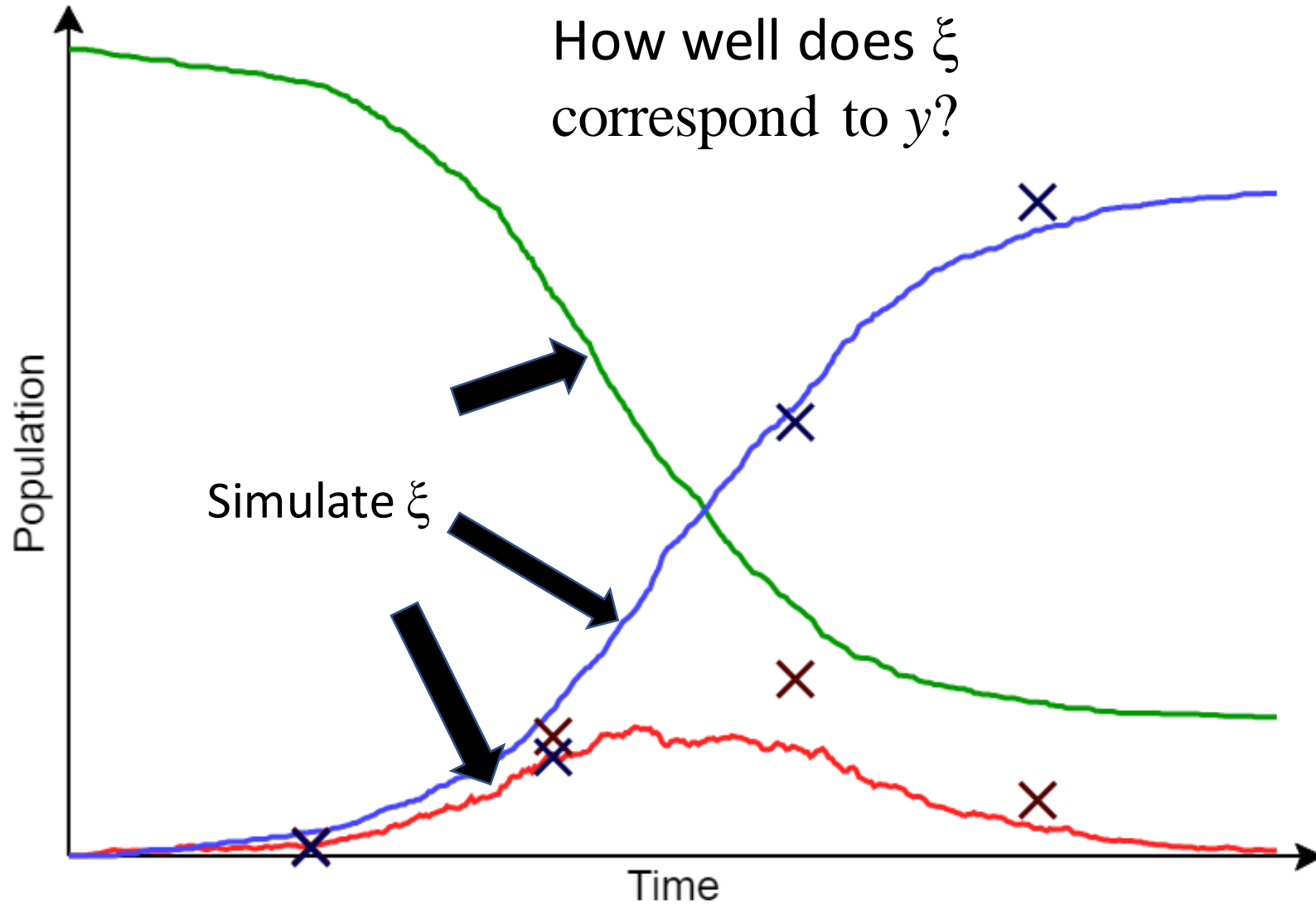
Parameters Dynamic state Data

↓ ↓ ↓

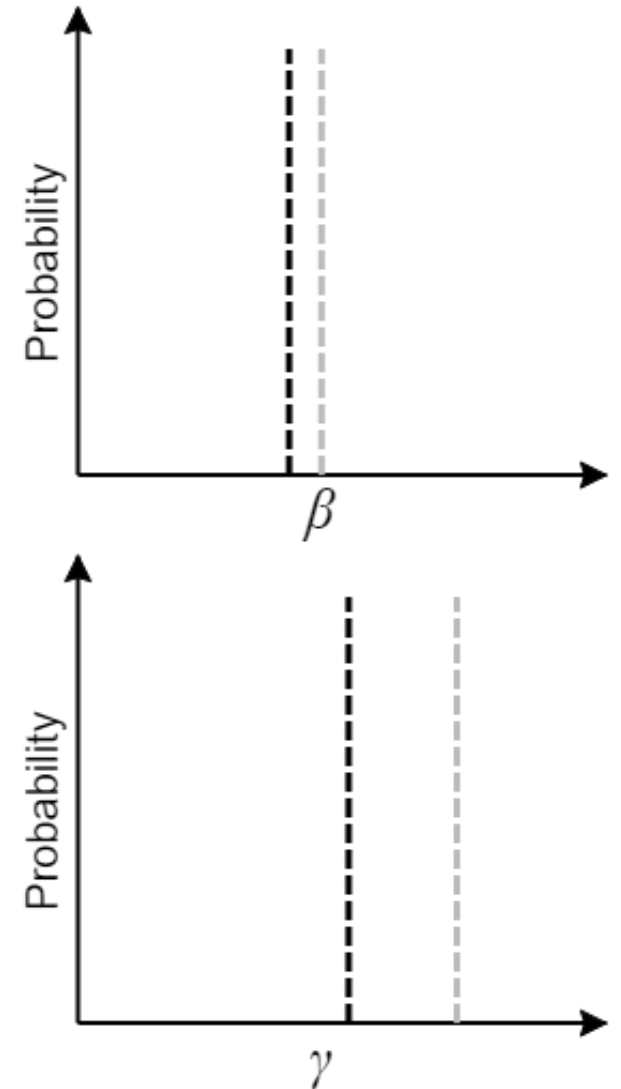
$$\pi(\theta, \xi | y) \propto \pi(y | \xi) \times \pi(\xi | \theta) \times \pi(\theta)$$

Posterior Observation model Latent process likelihood Prior

Observation model

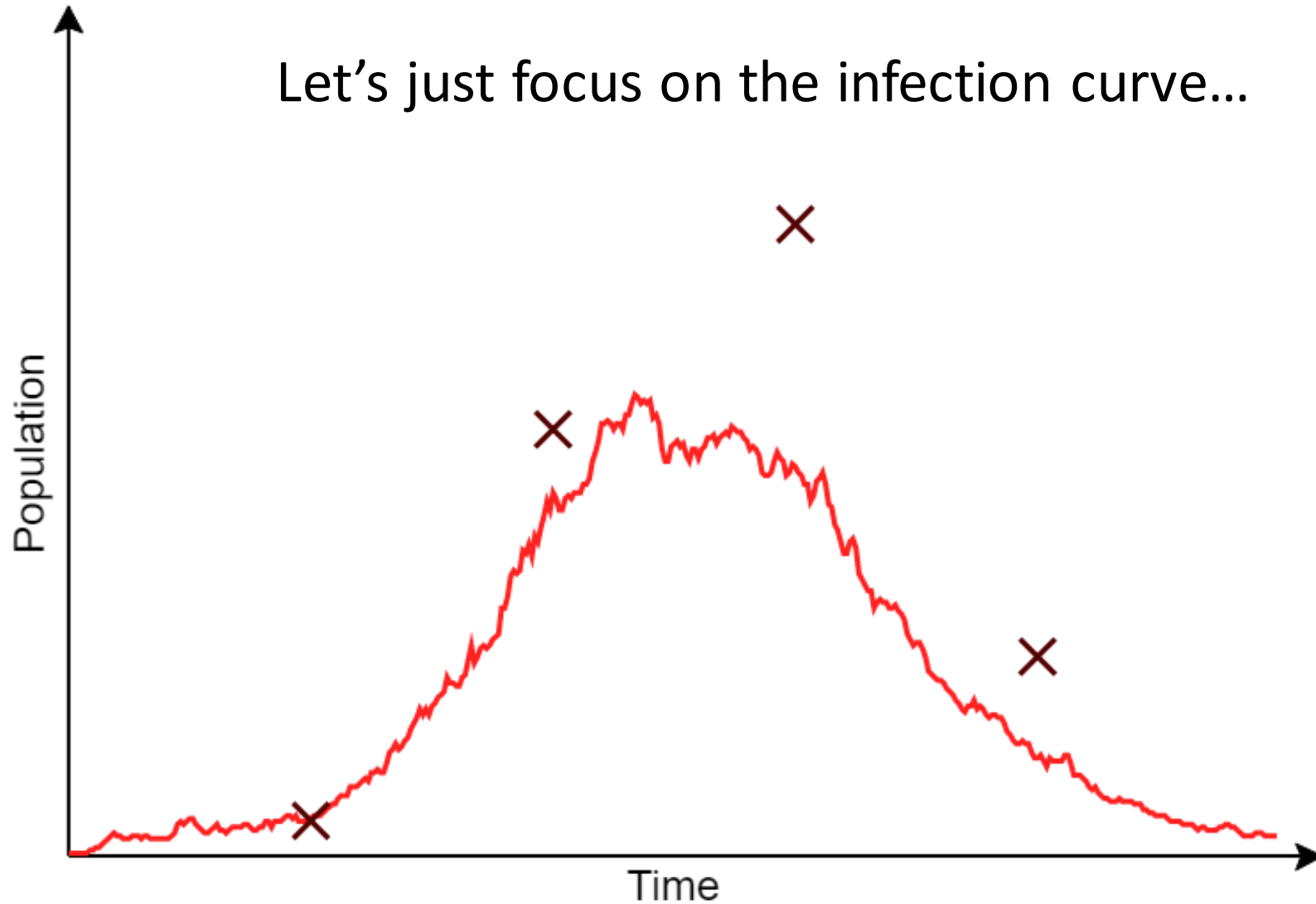


We use some θ
(not correct value)

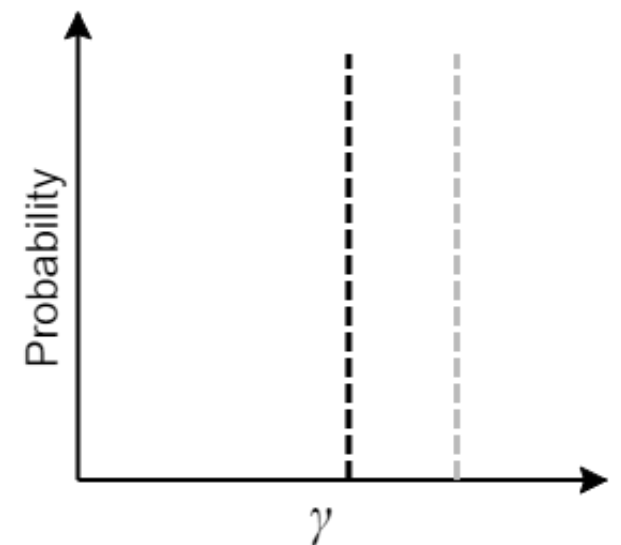
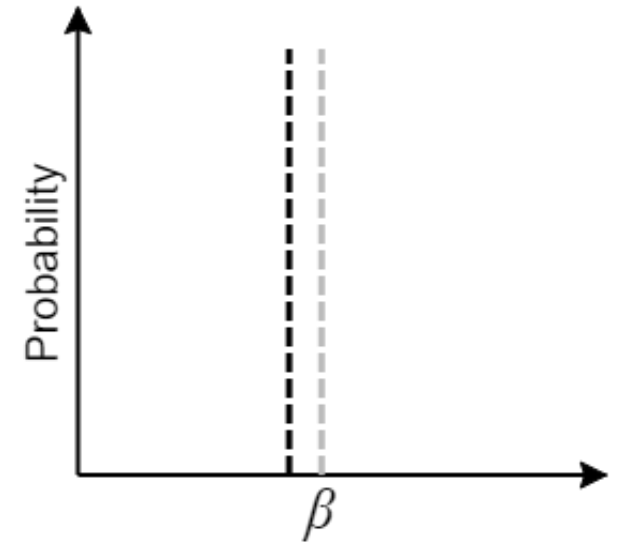


Observation model

Let's just focus on the infection curve...

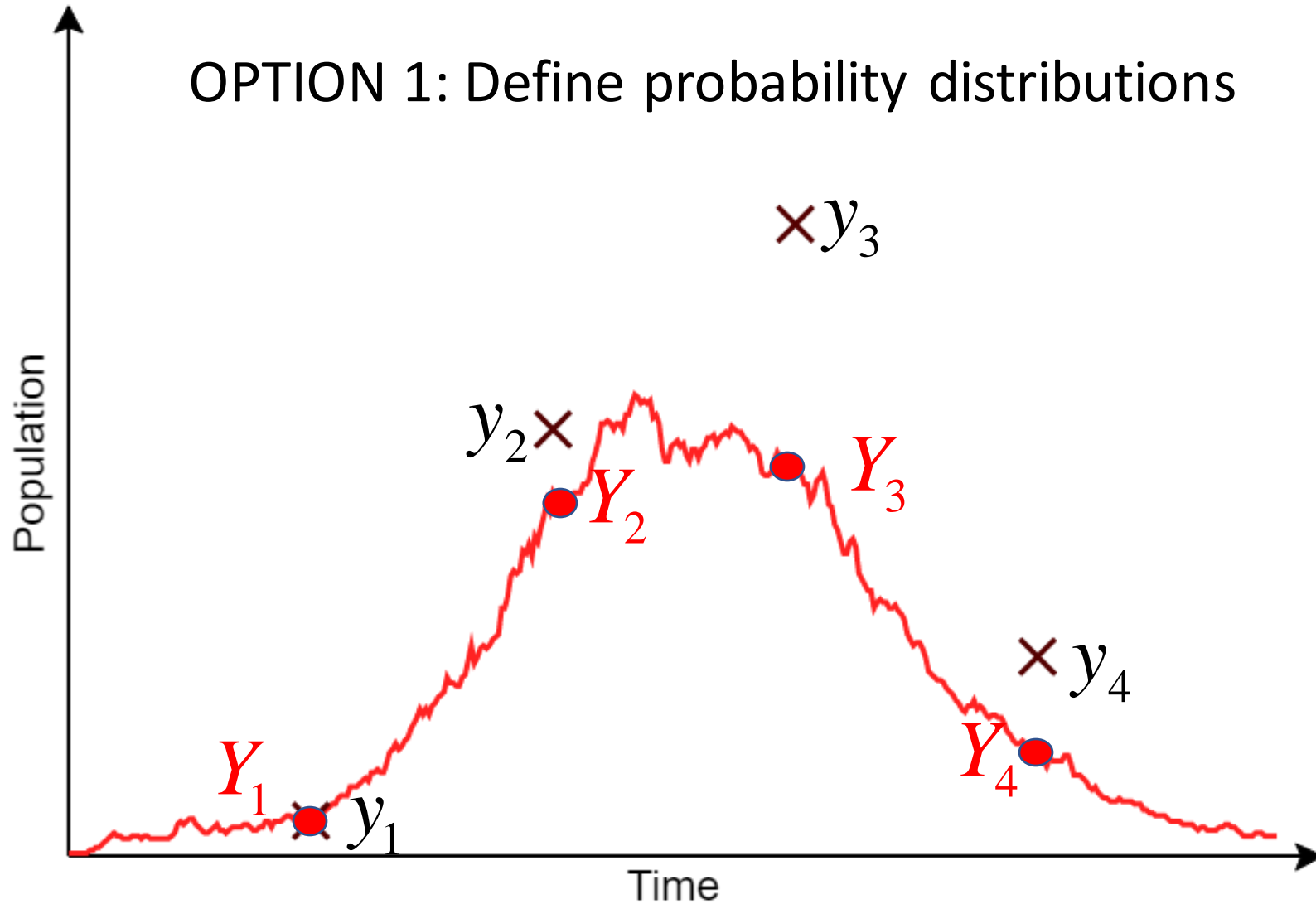


We use some θ
(not correct value)

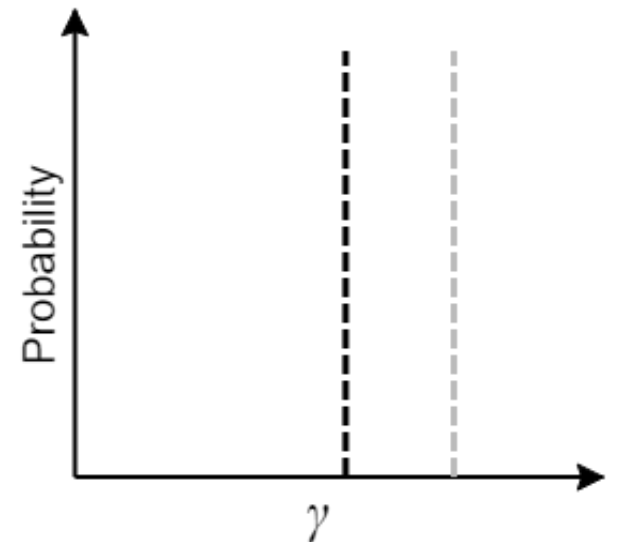
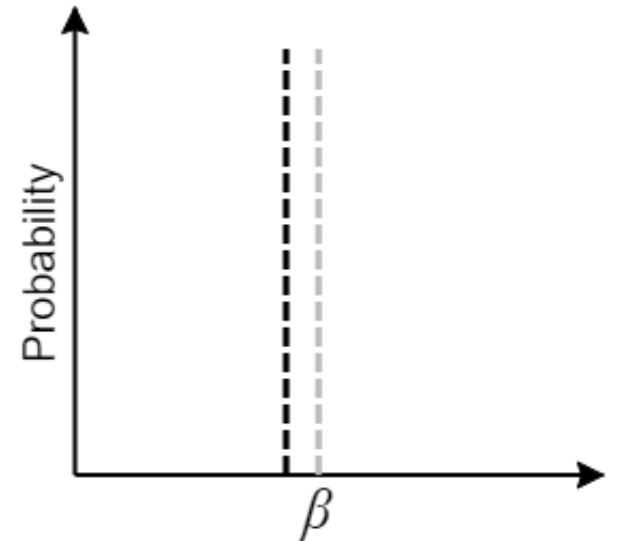


Observation model

OPTION 1: Define probability distributions



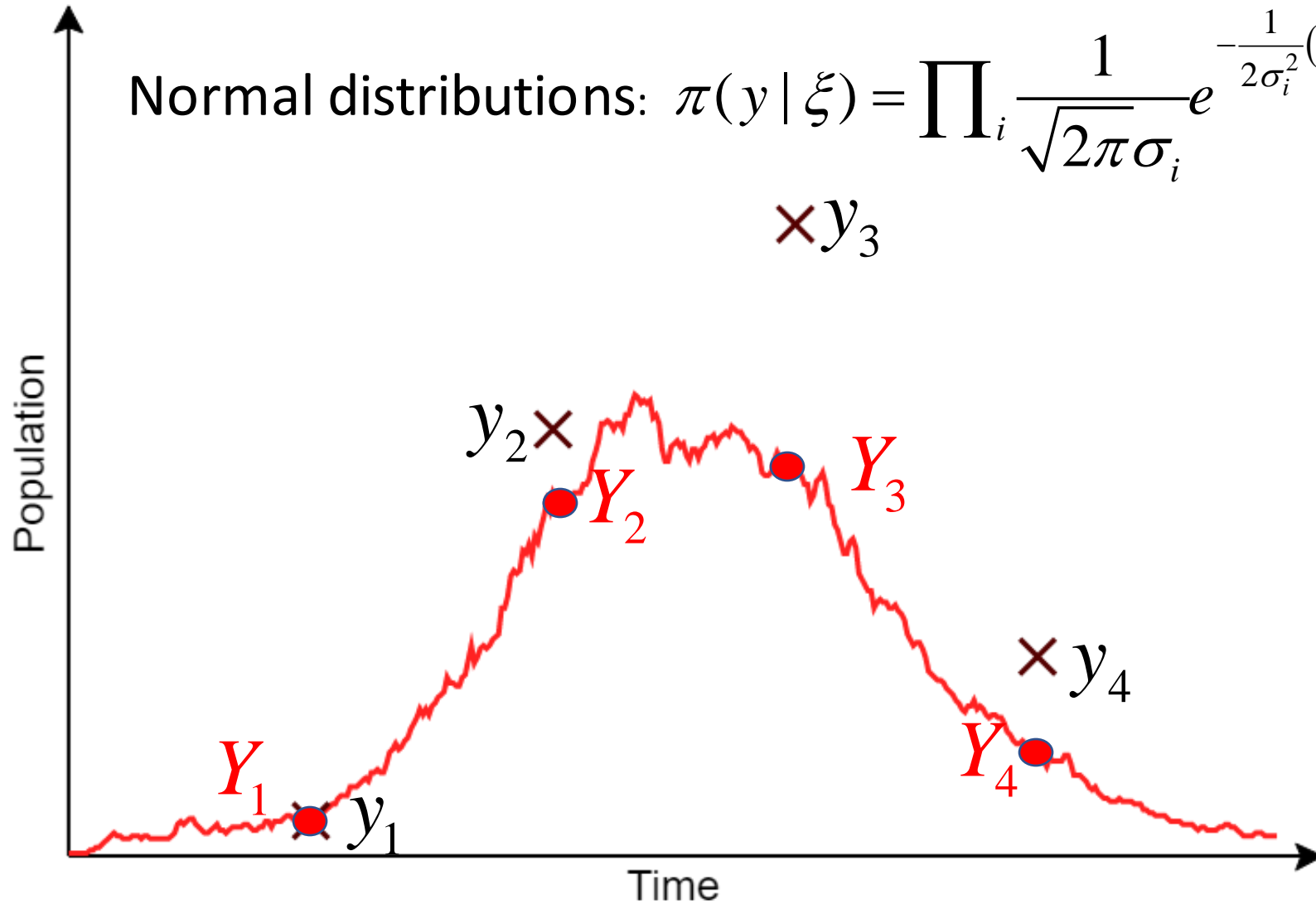
We use some θ
(not correct value)



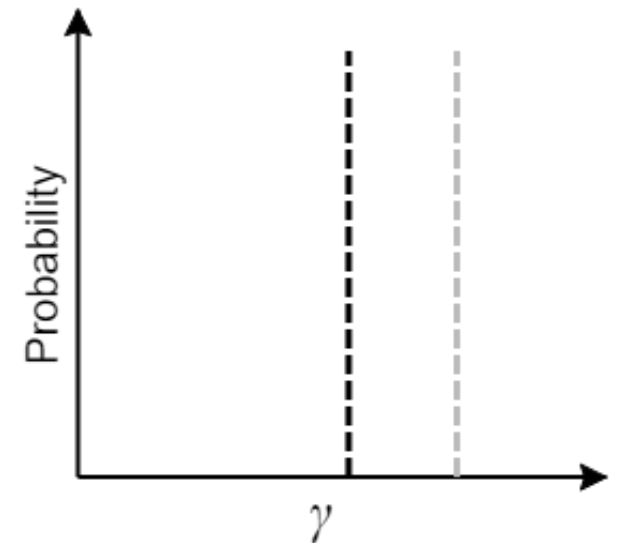
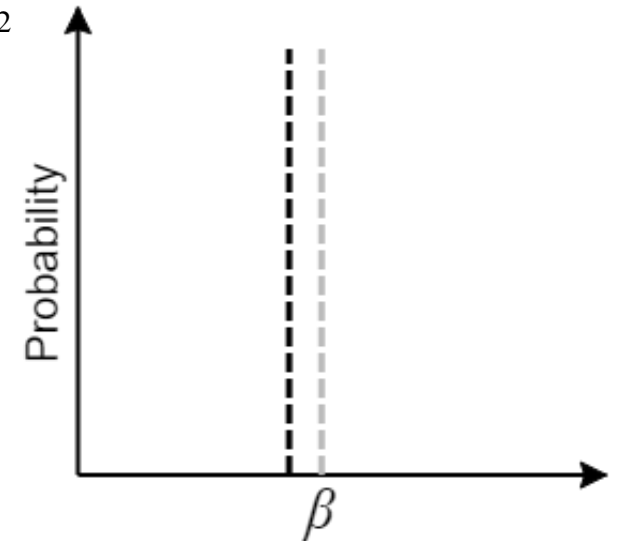
Observation model

Normal distributions: $\pi(y | \xi) = \prod_i \frac{1}{\sqrt{2\pi\sigma_i}} e^{-\frac{1}{2\sigma_i^2}(y_i - Y_i)^2}$

$\times y_3$

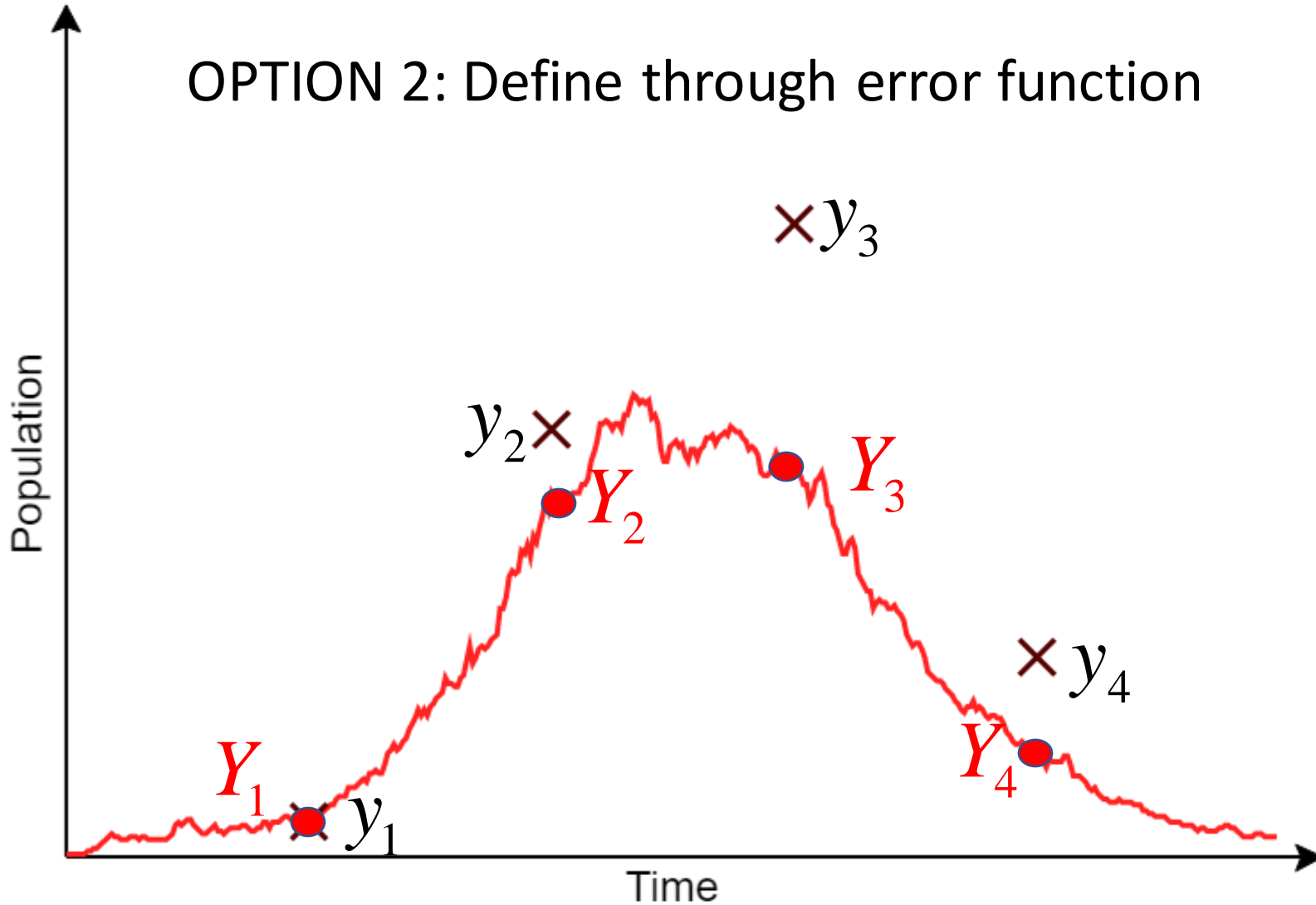


We use some θ
(not correct value)

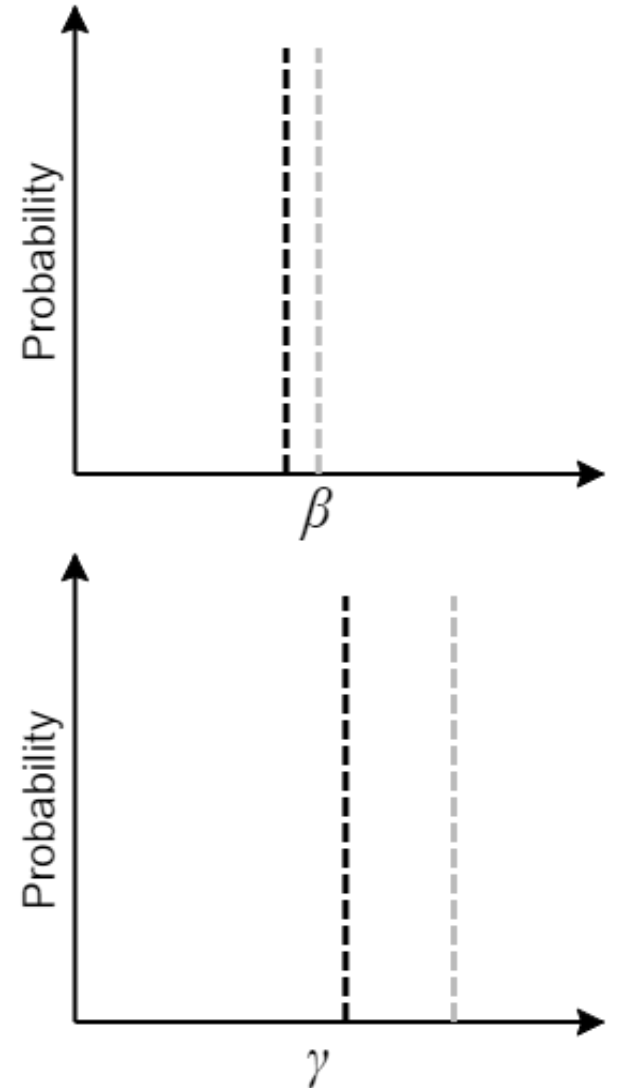


Observation model

OPTION 2: Define through error function

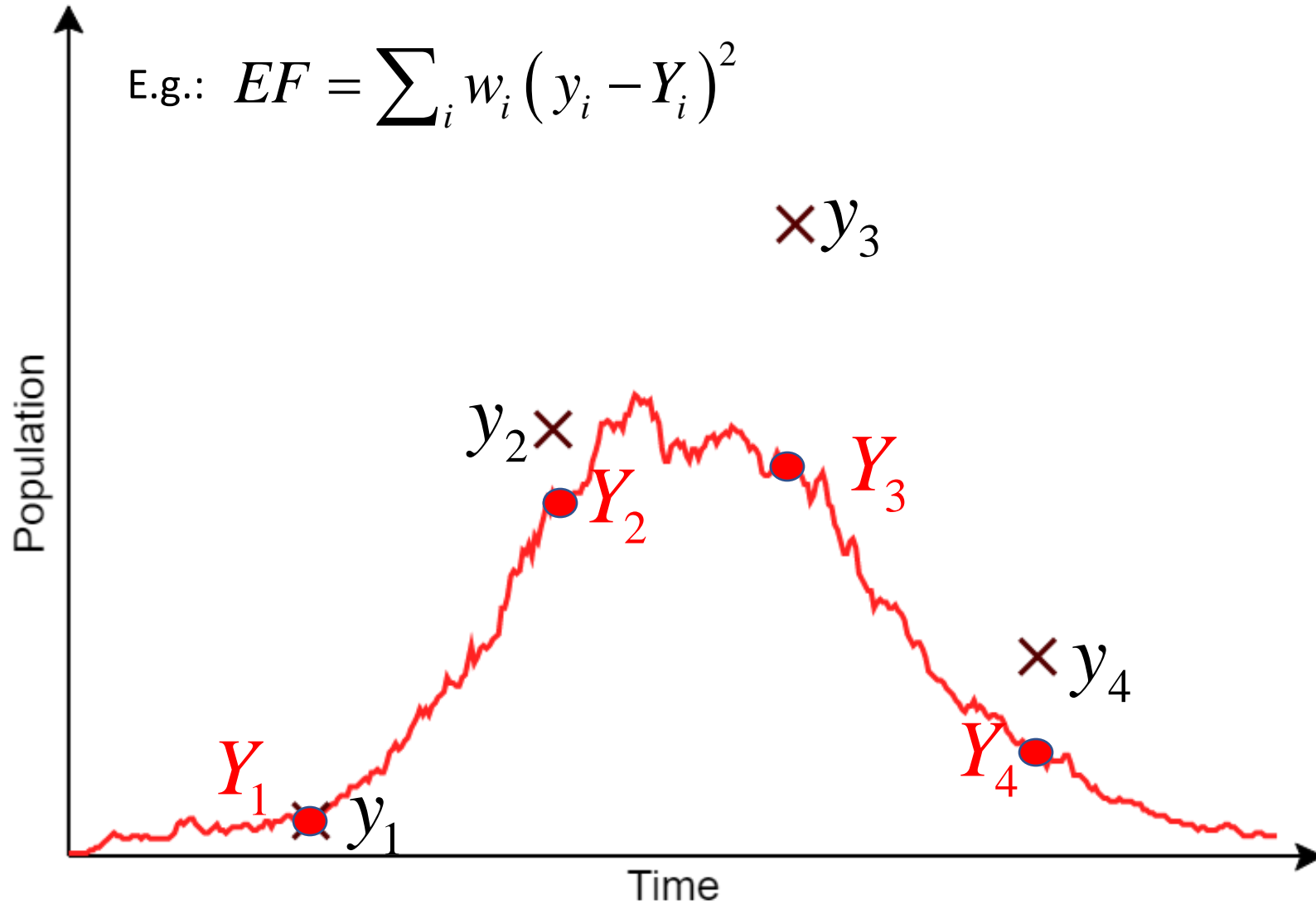


We use some θ
(not correct value)

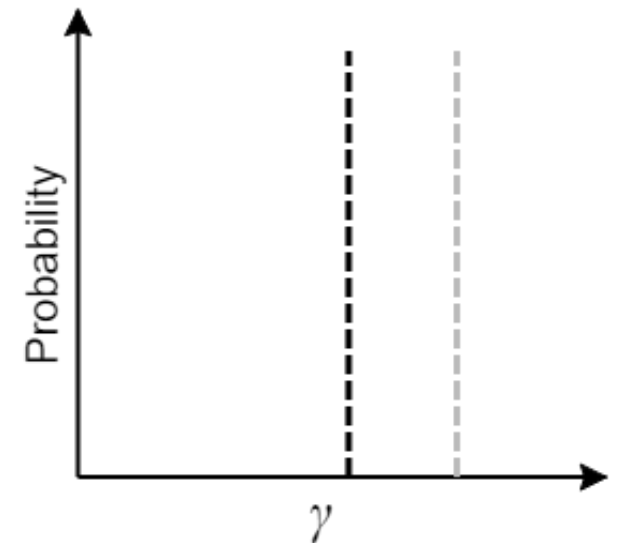
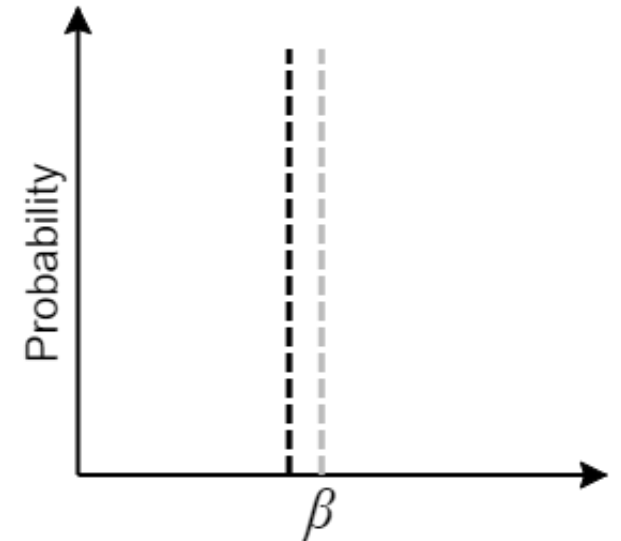


Observation model

E.g.: $EF = \sum_i w_i (y_i - Y_i)^2$



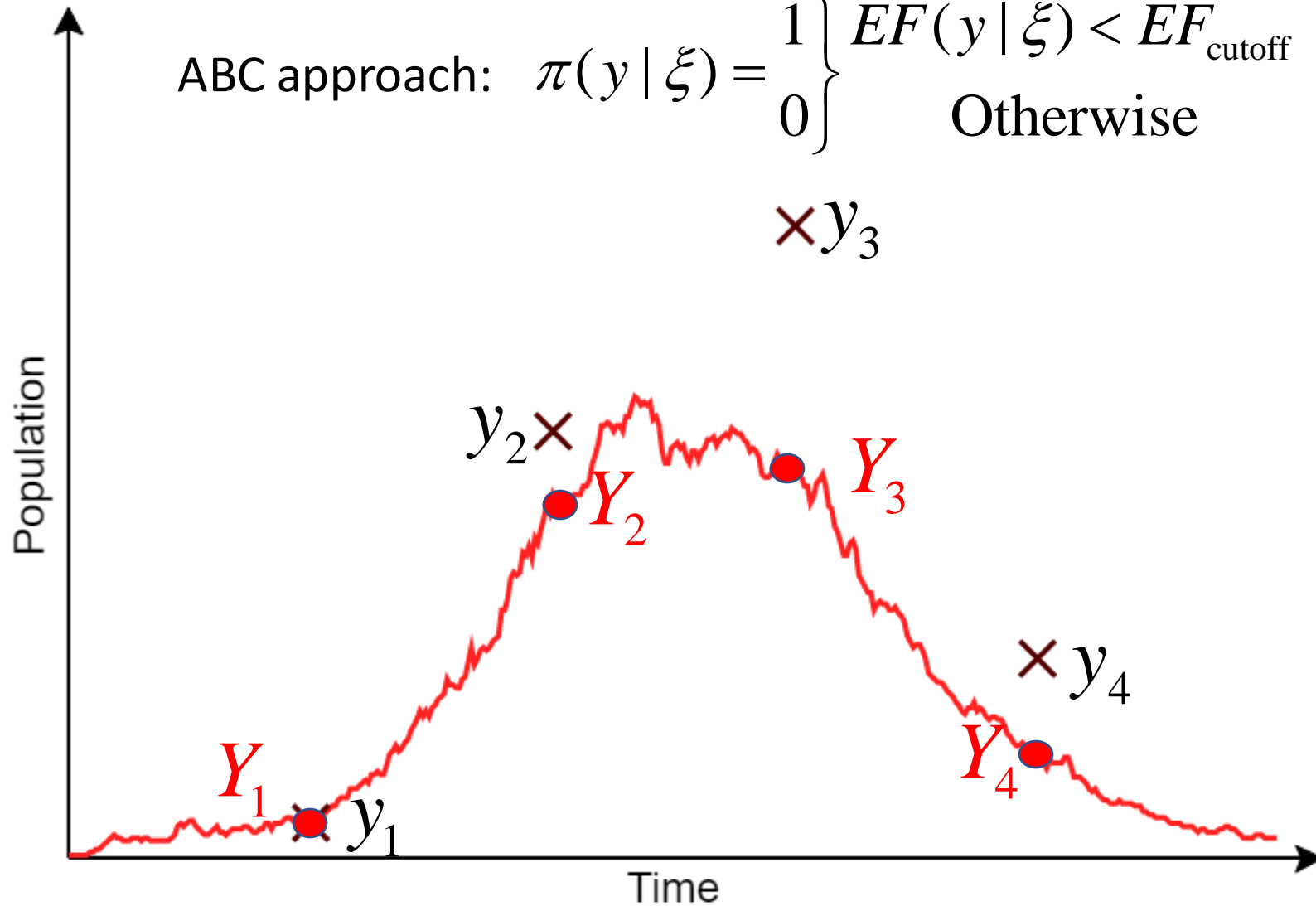
We use some θ
(not correct value)



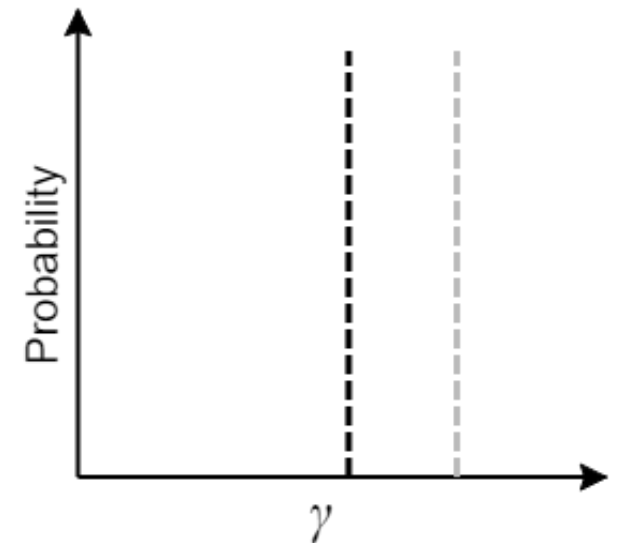
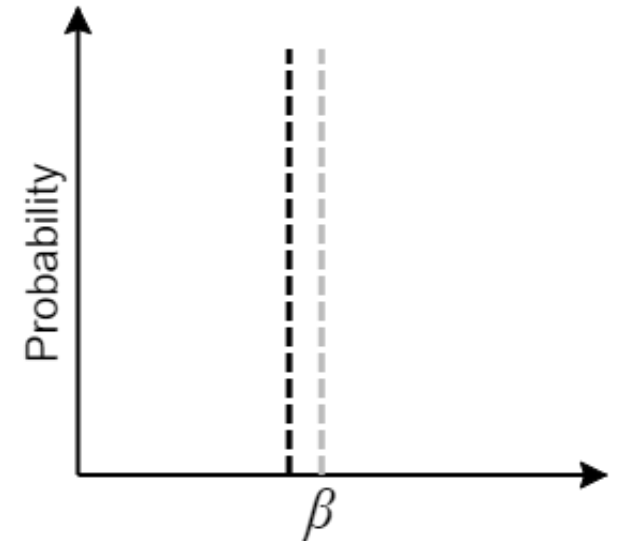
Observation model

ABC approach: $\pi(y | \xi) = \begin{cases} 1 & EF(y | \xi) < EF_{\text{cutoff}} \\ 0 & \text{Otherwise} \end{cases}$

$\times y_3$



We use some θ
(not correct value)



Inference algorithms

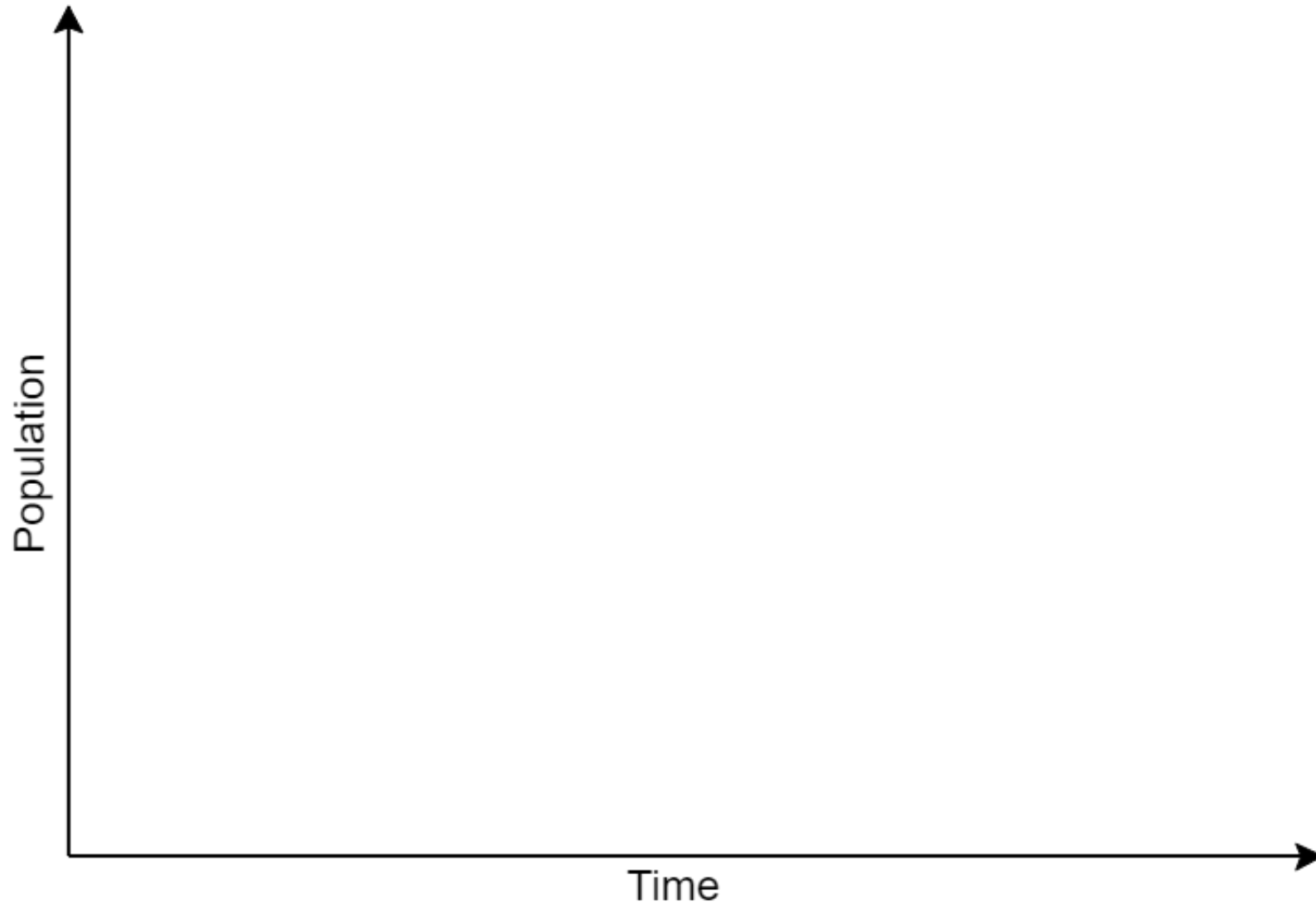
OPTION 1: Observation model with probability distributions

- Data augmentation Markov chain Monte Carlo (DA-MCMC)
- Particle MCMC (PMCMC)
- Metropolis coupled MCMC (MC³)

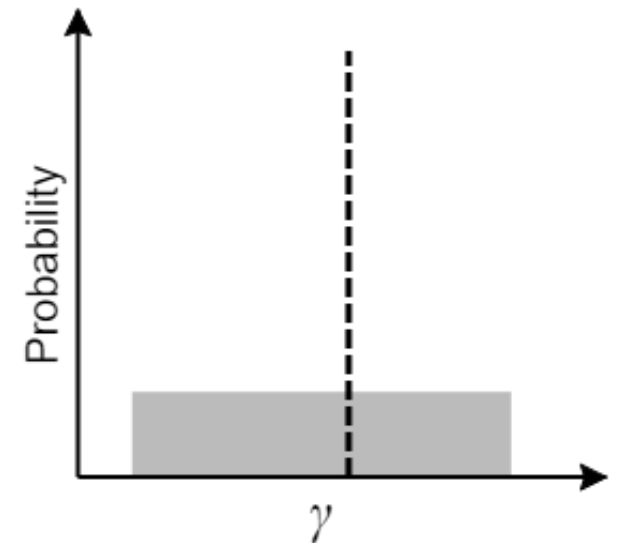
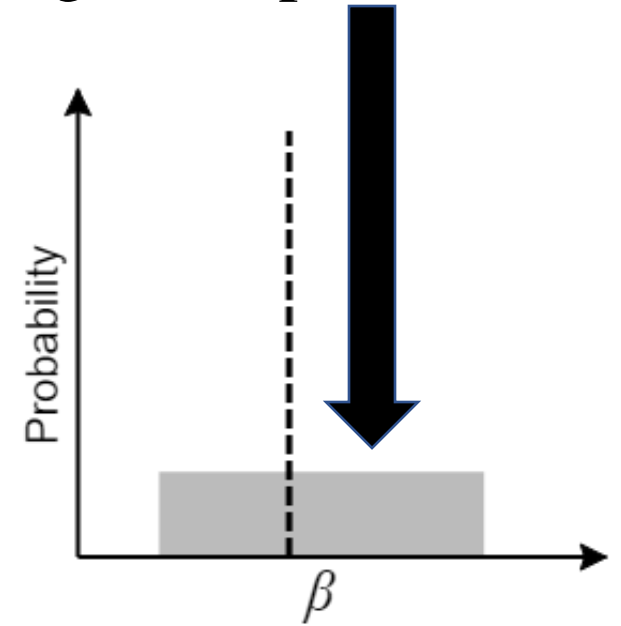
OPTION 2: Error functions

- Approximate Bayesian computation rejection sampling (ABC)
- ABC sequential Monte Carlo (ABC-SMC)
- ABC with model-based proposals (ABC-MBP)

ABC rejection sampling

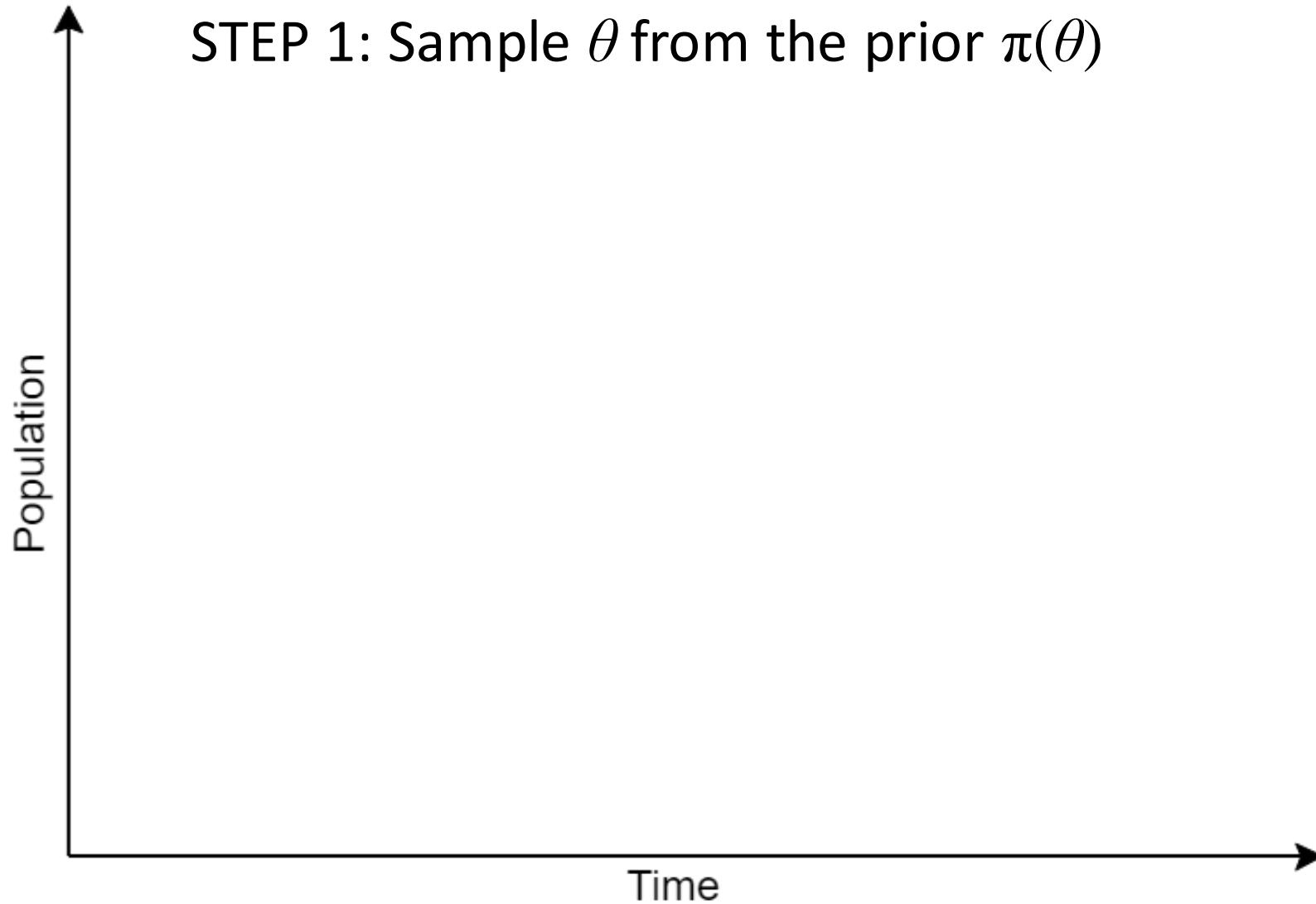


Prior $\pi(\theta)$ defines plausible ranges for parameters

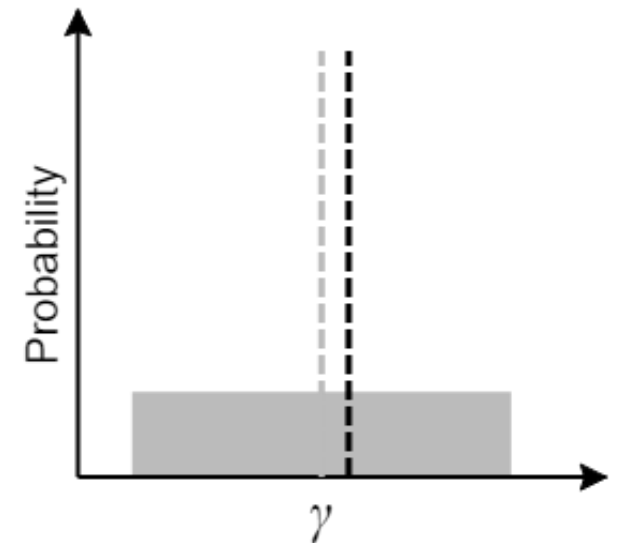
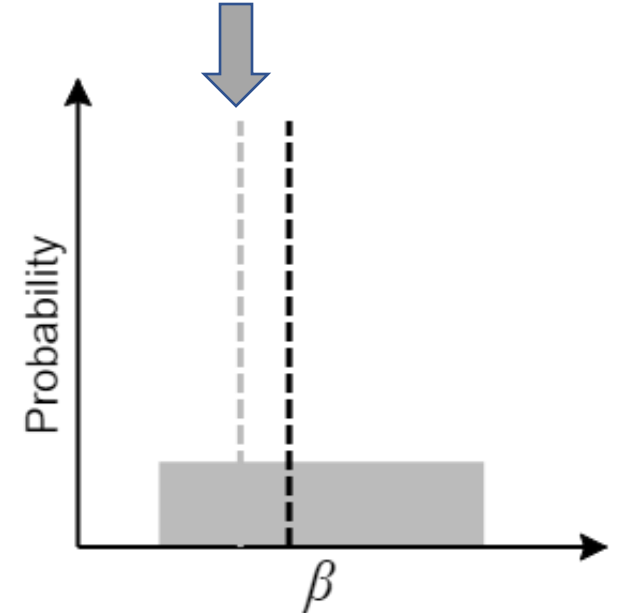


ABC rejection sampling

STEP 1: Sample θ from the prior $\pi(\theta)$

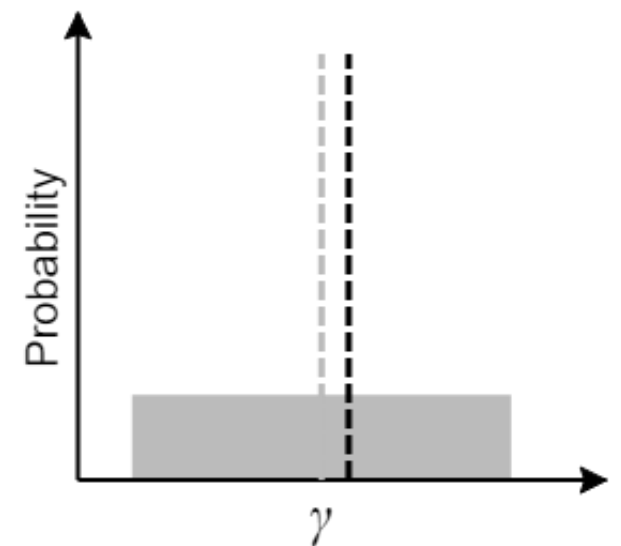
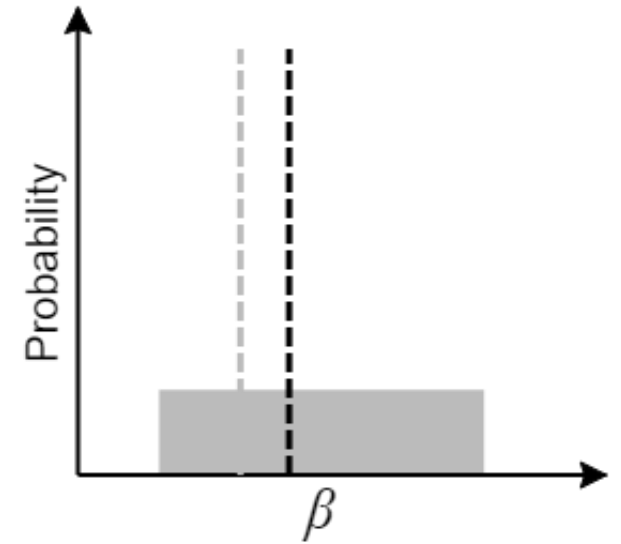
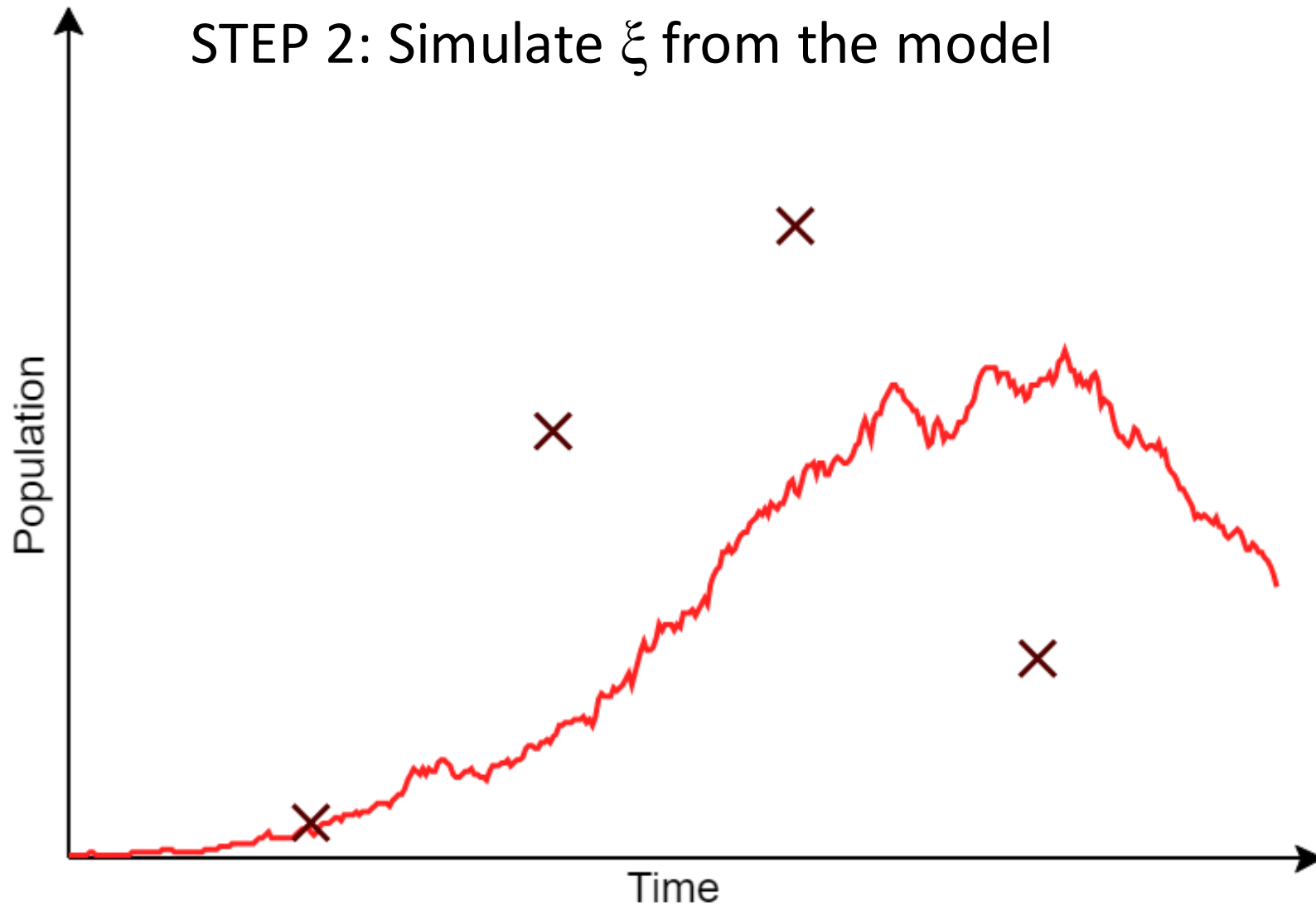


Values sampled (grey)



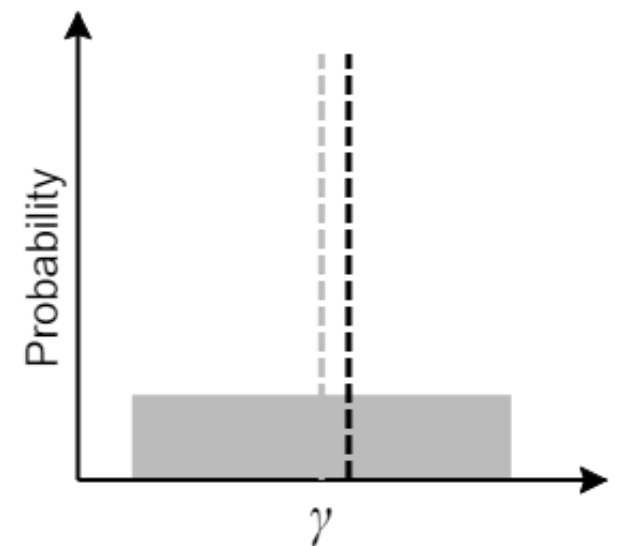
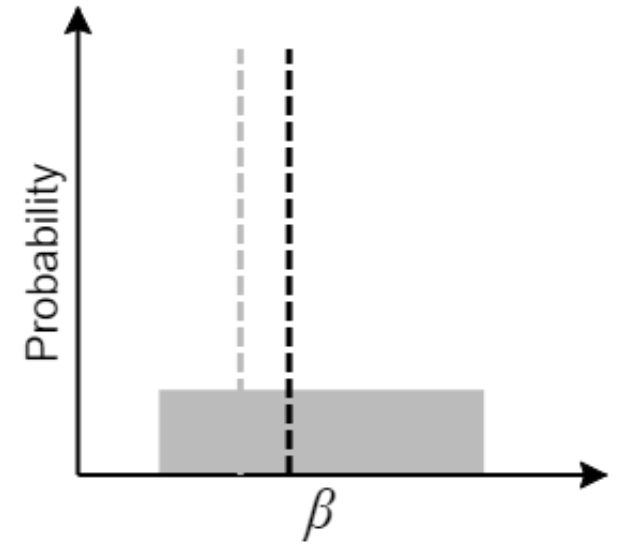
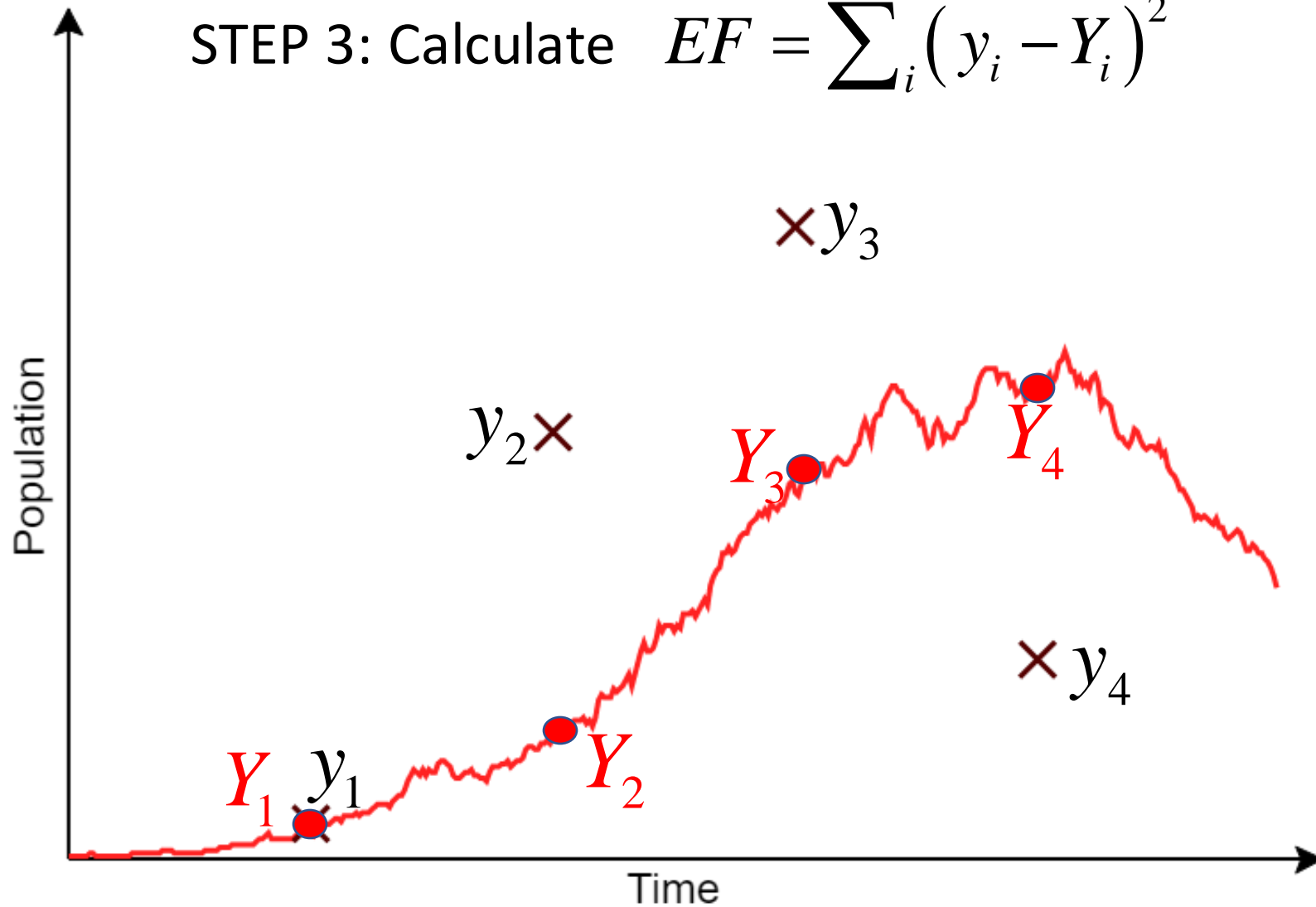
ABC rejection sampling

STEP 2: Simulate ξ from the model



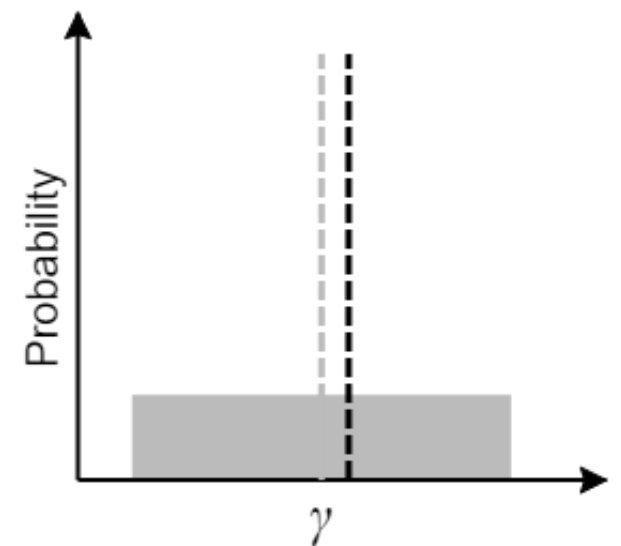
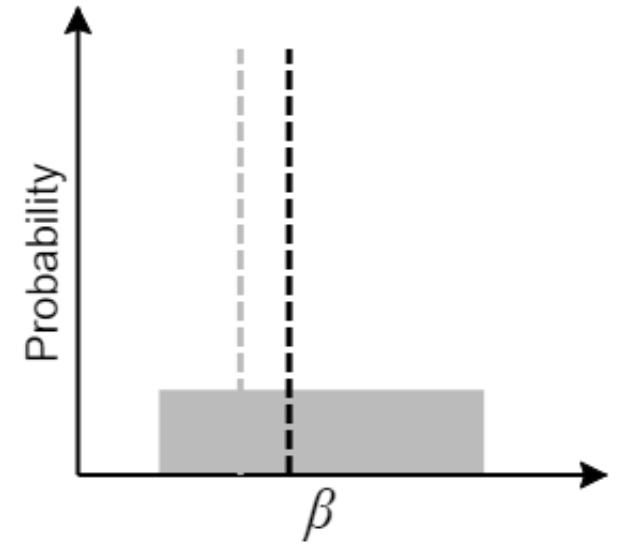
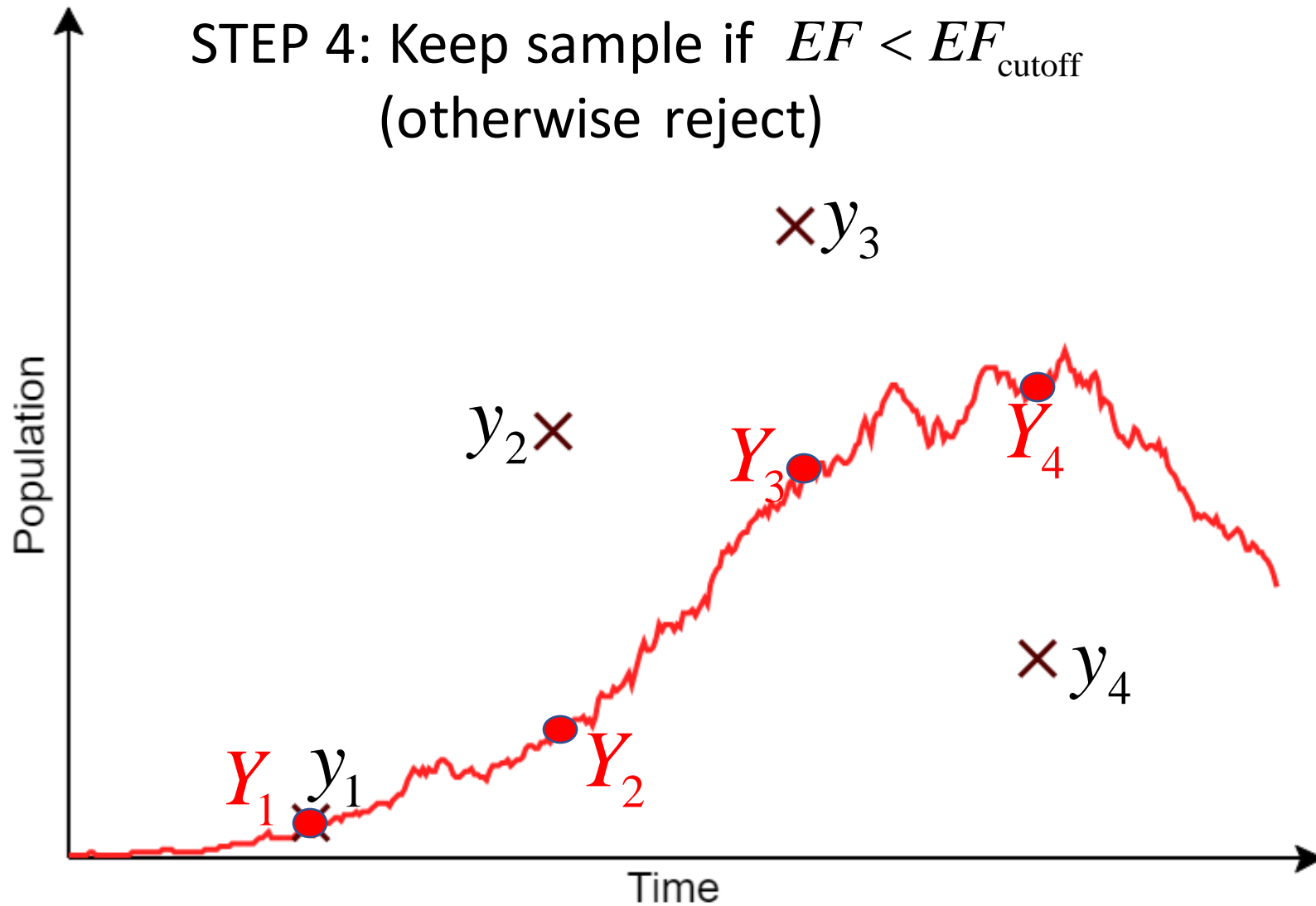
ABC rejection sampling

STEP 3: Calculate $EF = \sum_i (y_i - Y_i)^2$



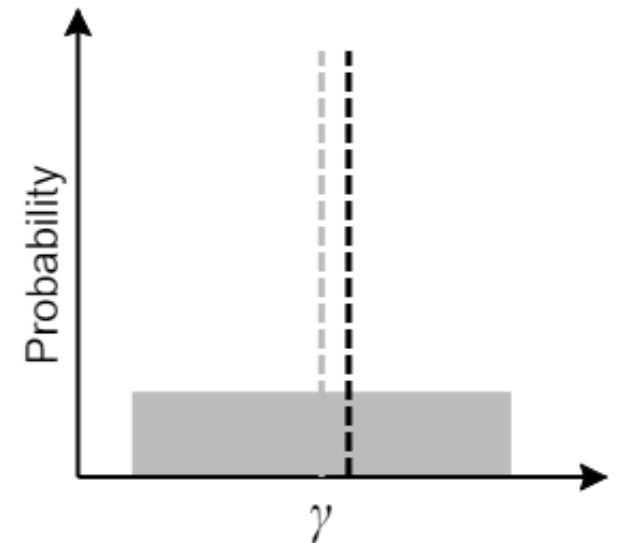
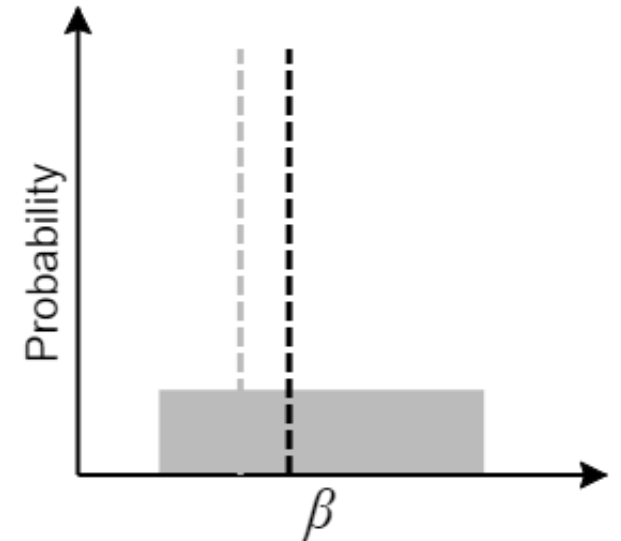
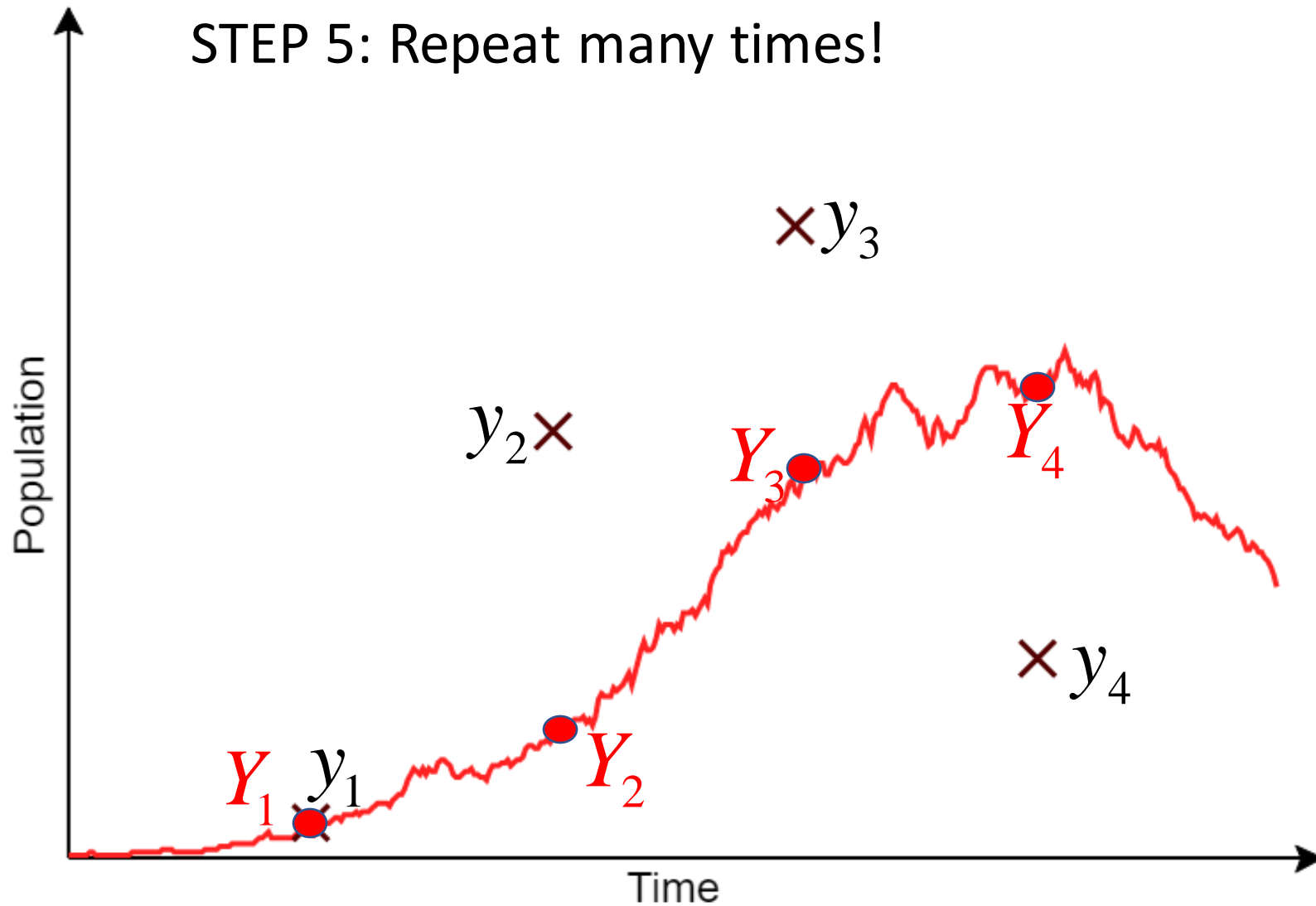
ABC rejection sampling

STEP 4: Keep sample if $EF < EF_{\text{cutoff}}$
(otherwise reject)



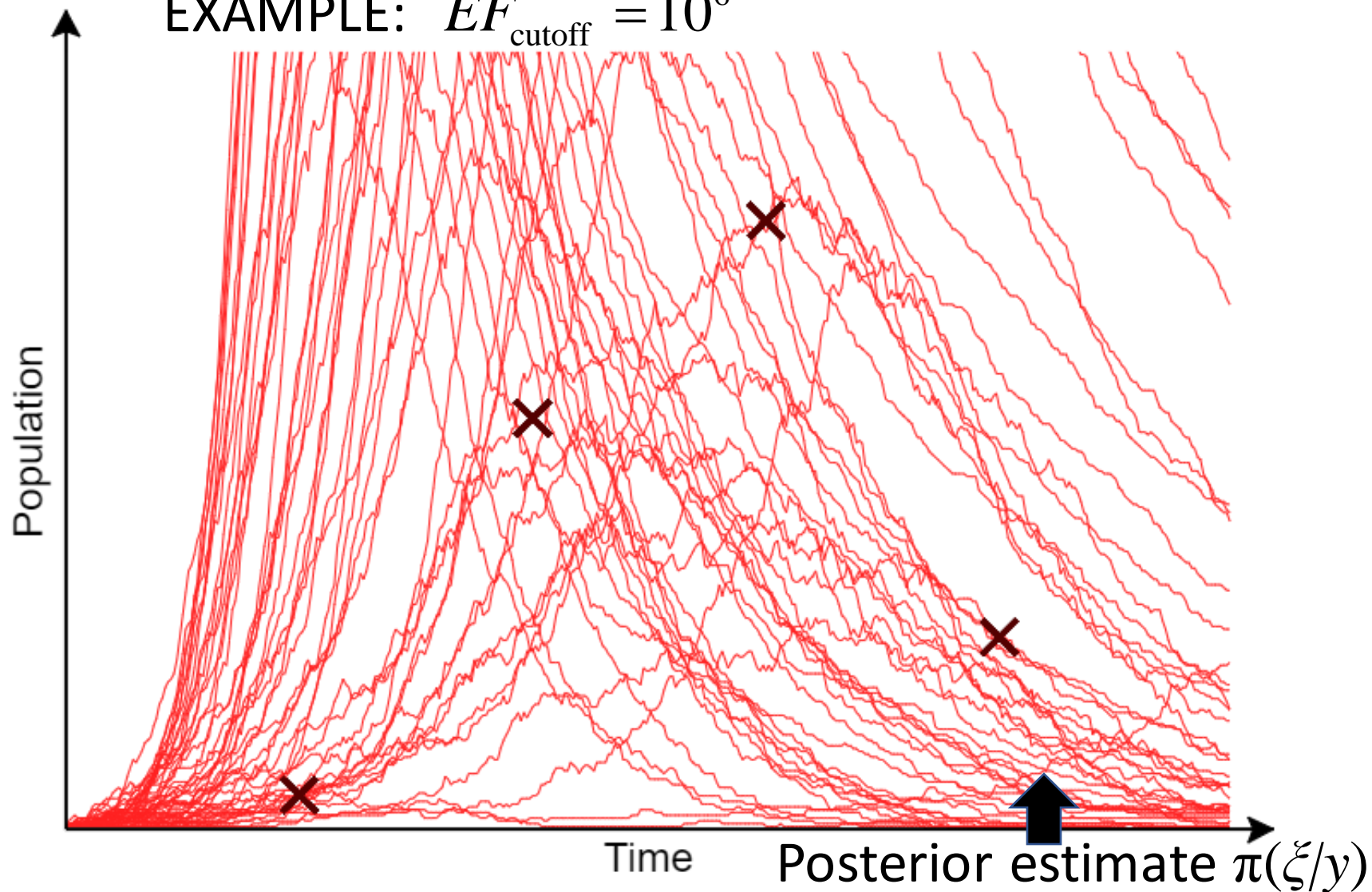
ABC rejection sampling

STEP 5: Repeat many times!

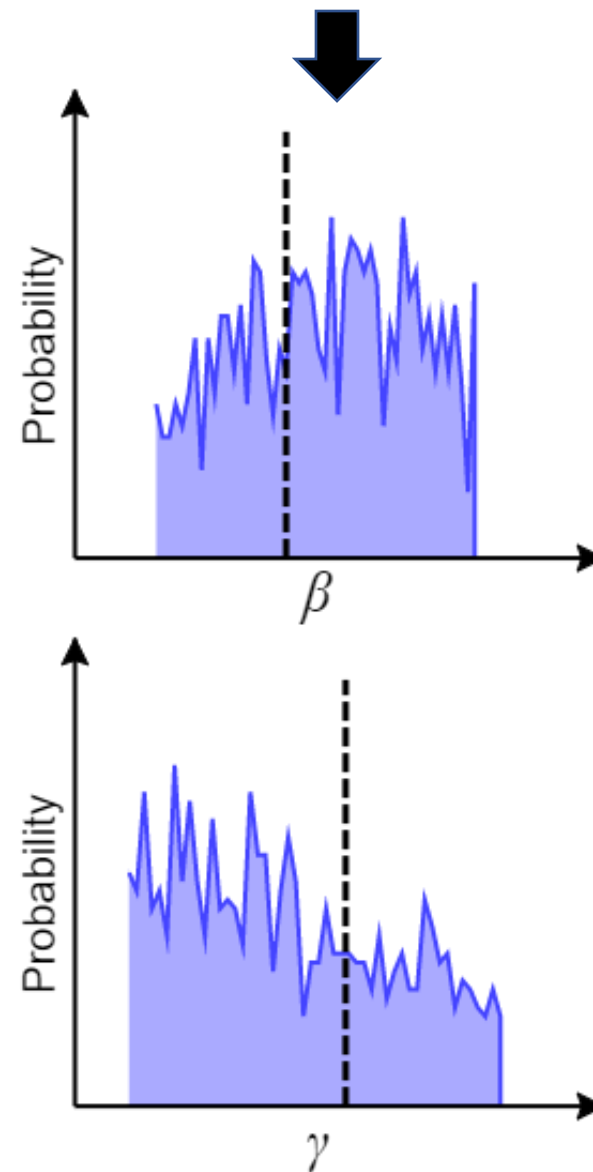


ABC rejection sampling

EXAMPLE: $EF_{\text{cutoff}} = 10^6$

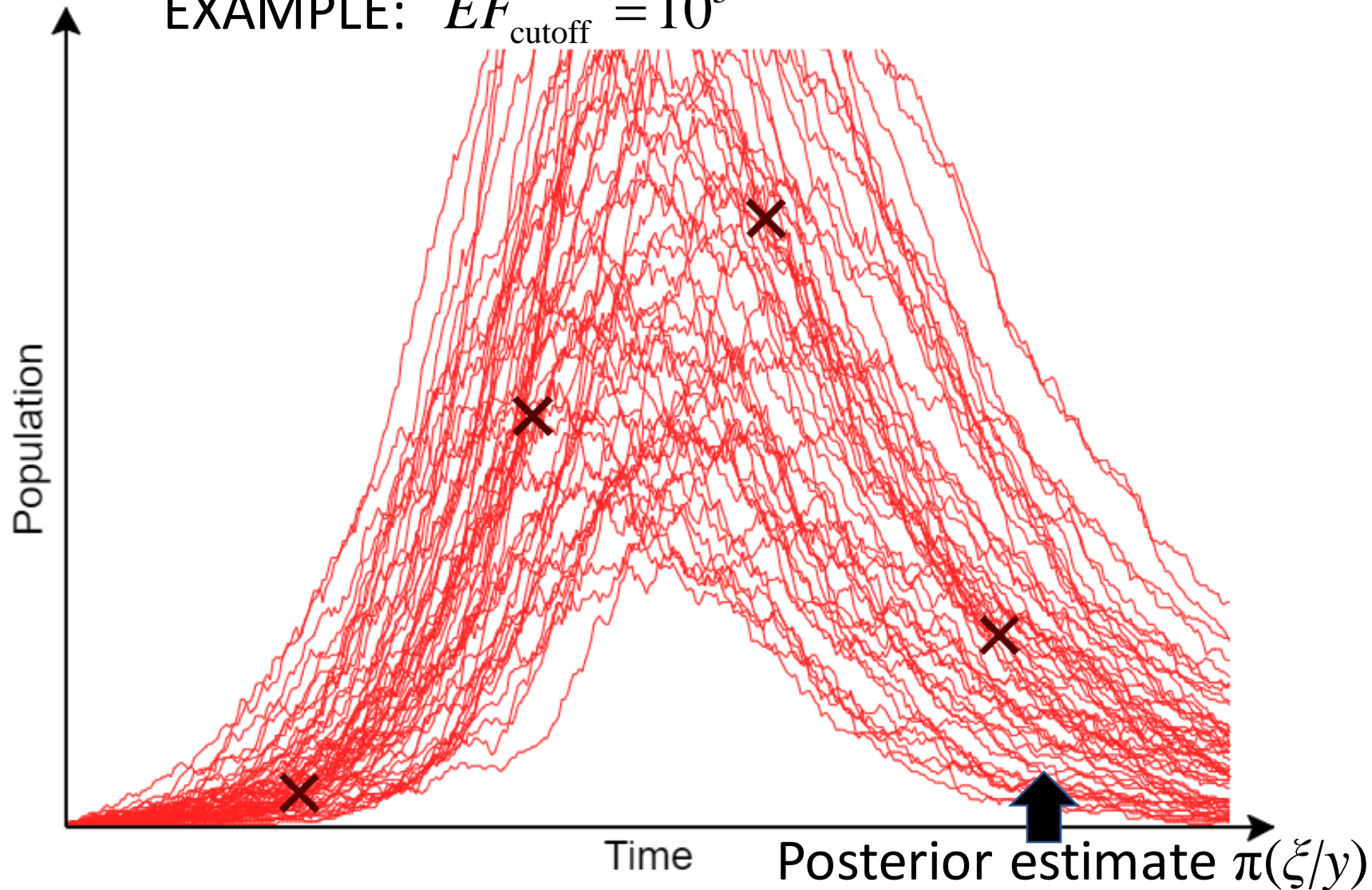


Posterior estimate $\pi(\theta/y)$

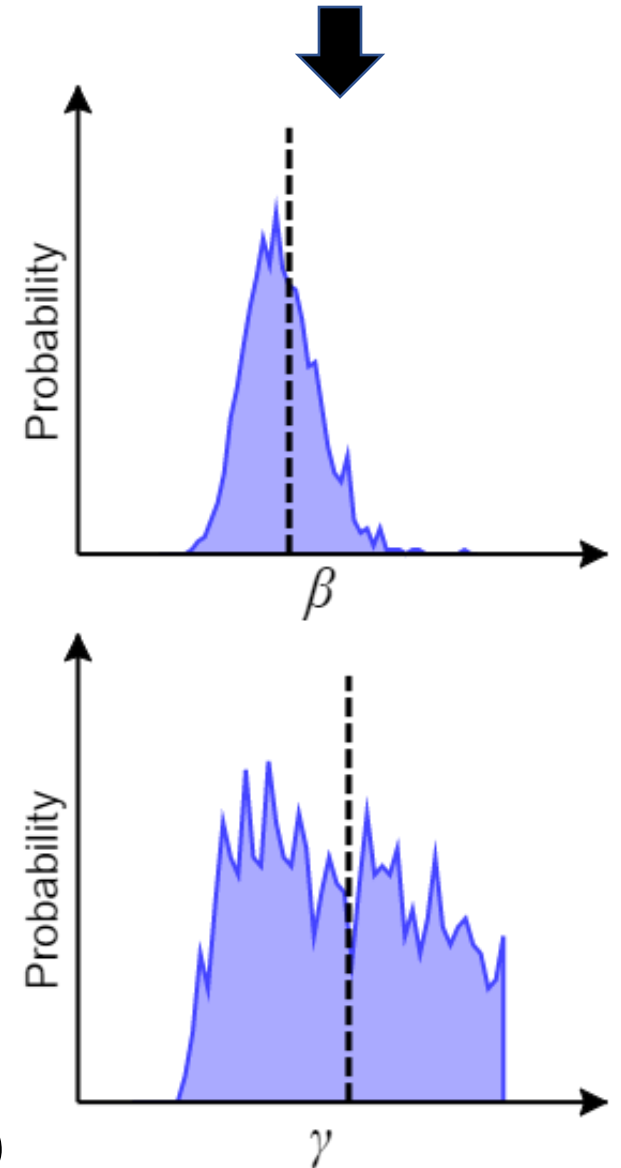


ABC rejection sampling

EXAMPLE: $EF_{\text{cutoff}} = 10^5$

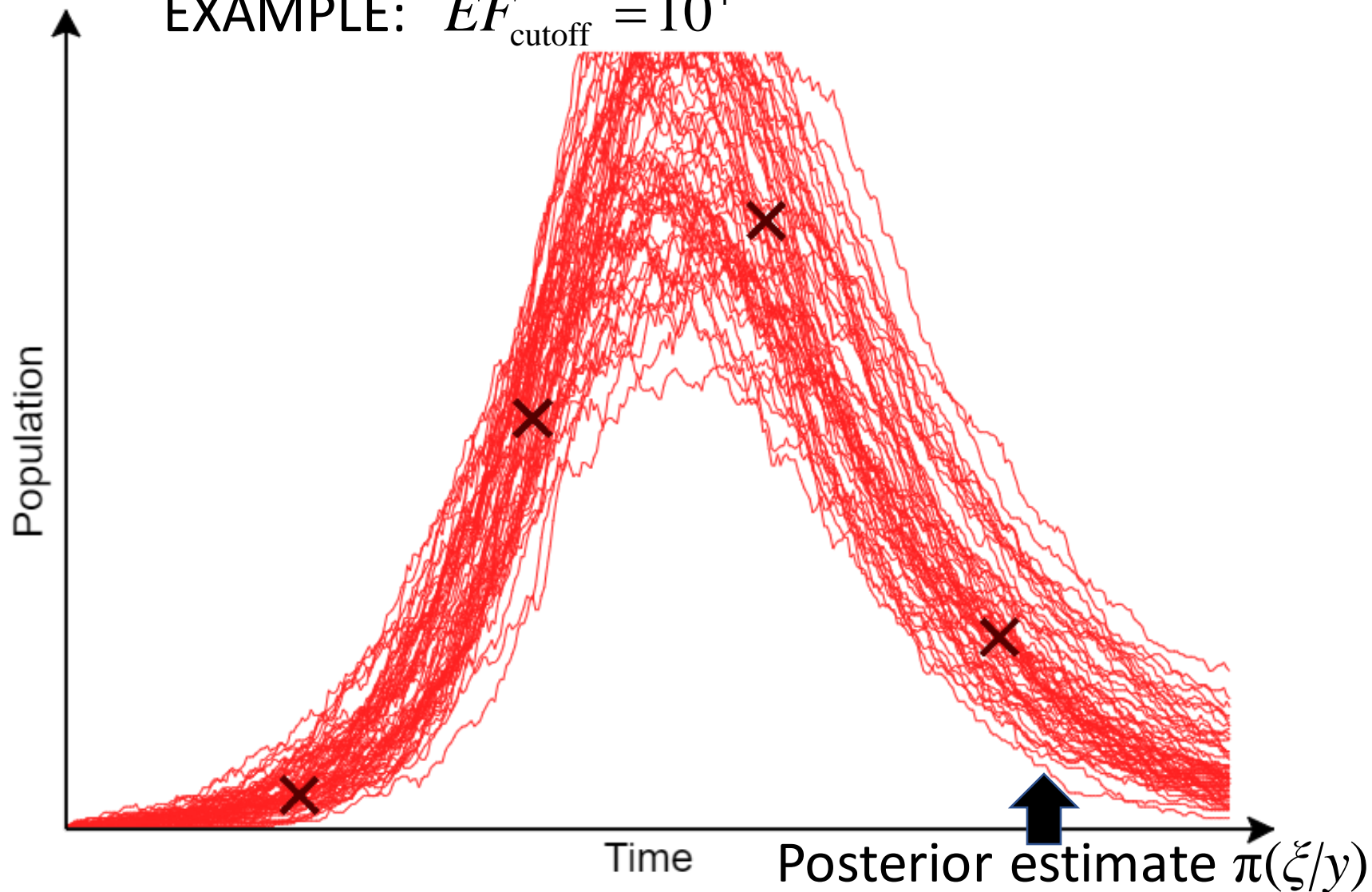


Posterior estimate $\pi(\theta/y)$

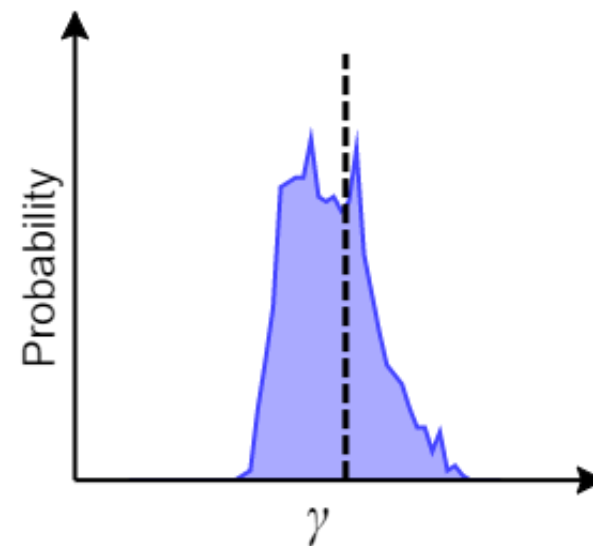
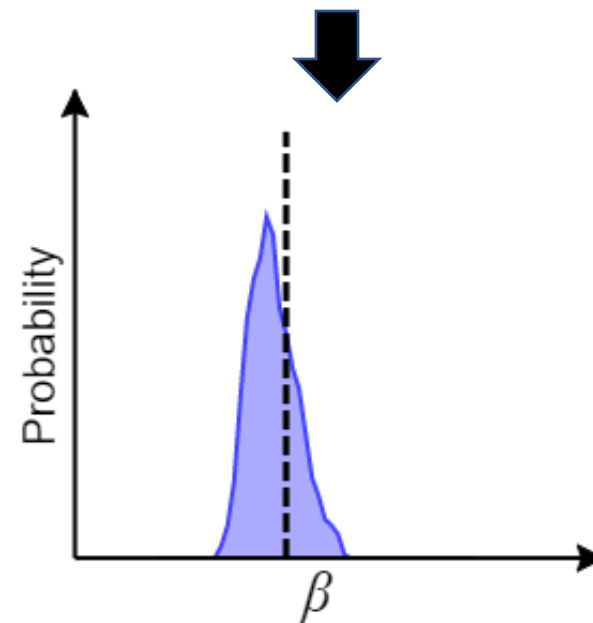


ABC rejection sampling

EXAMPLE: $EF_{\text{cutoff}} = 10^4$

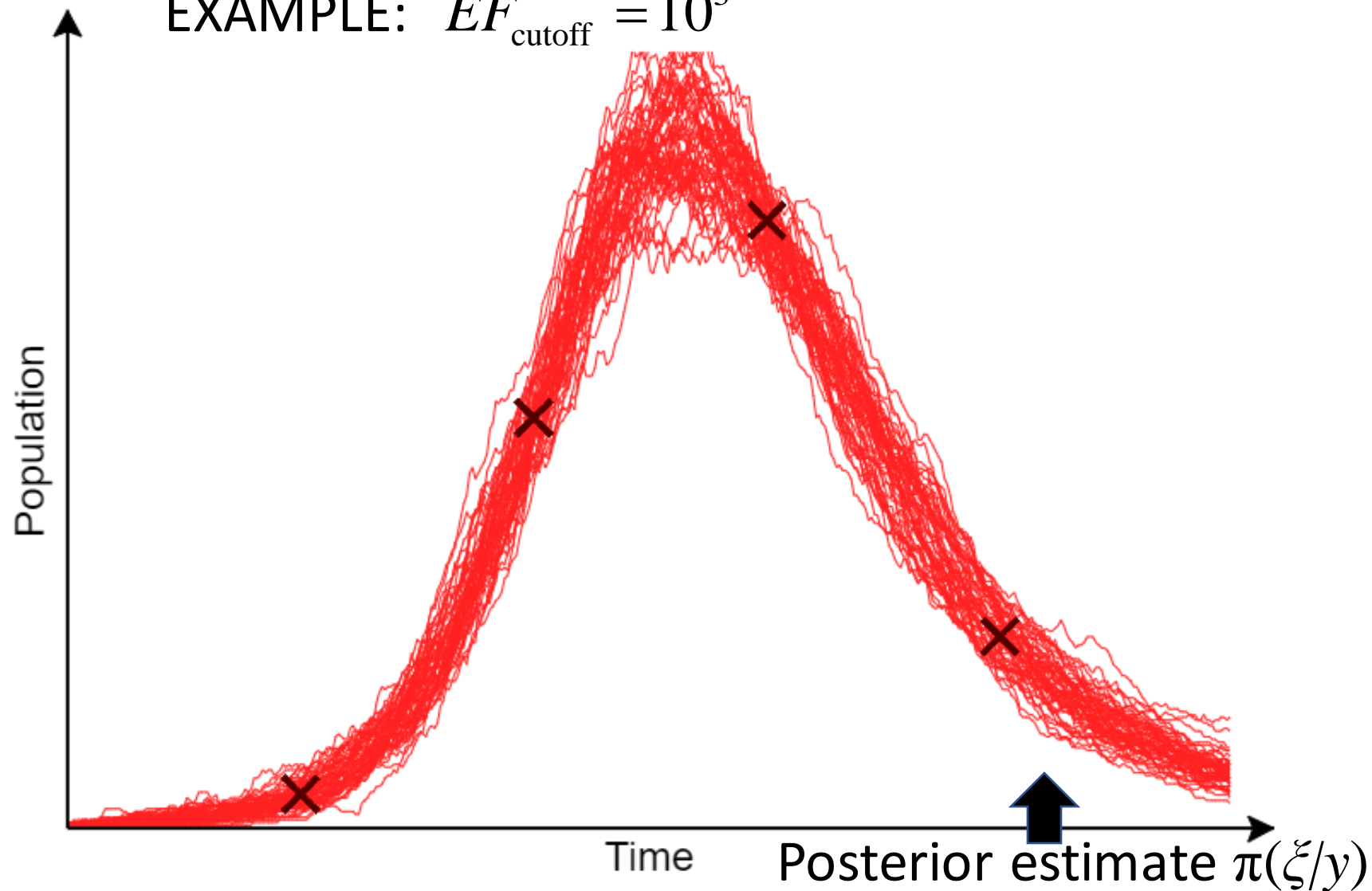


Posterior estimate $\pi(\theta/y)$

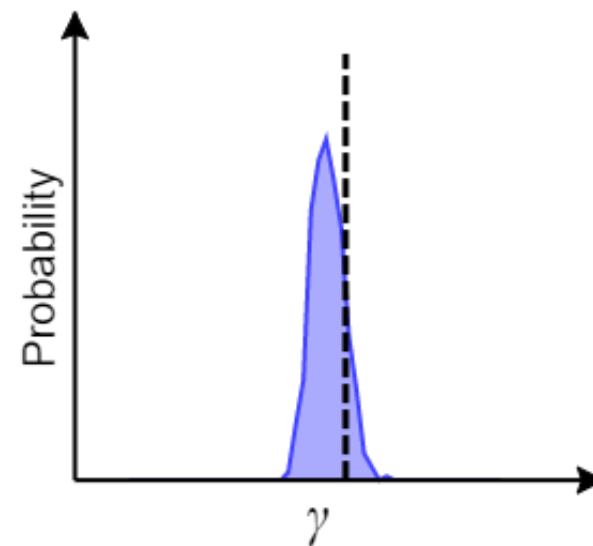
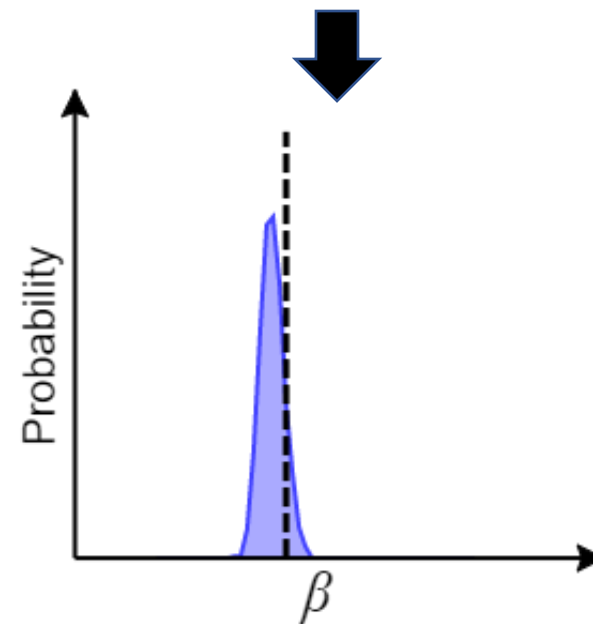


ABC rejection sampling

EXAMPLE: $EF_{\text{cutoff}} = 10^3$

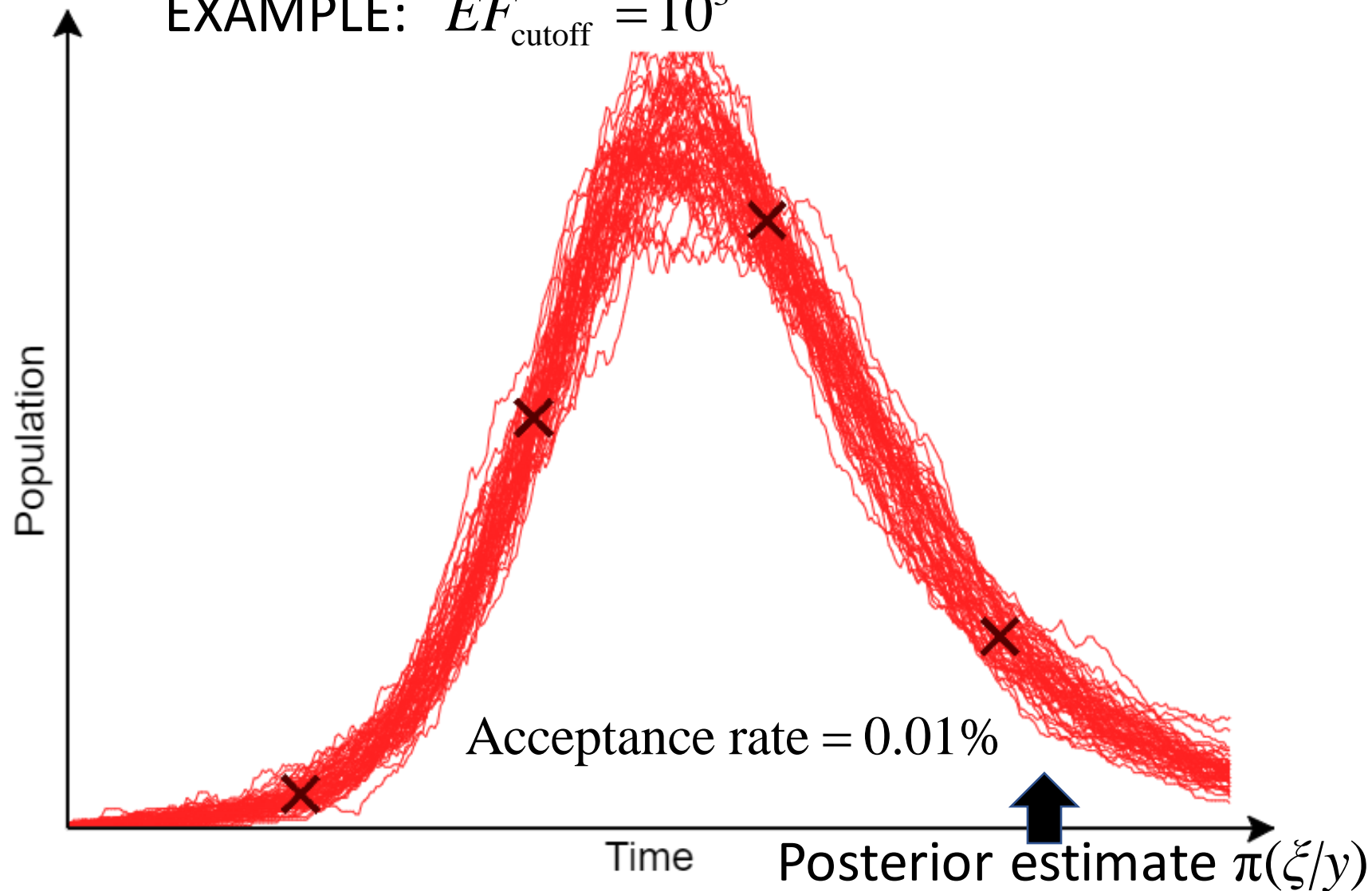


Posterior estimate $\pi(\theta/y)$

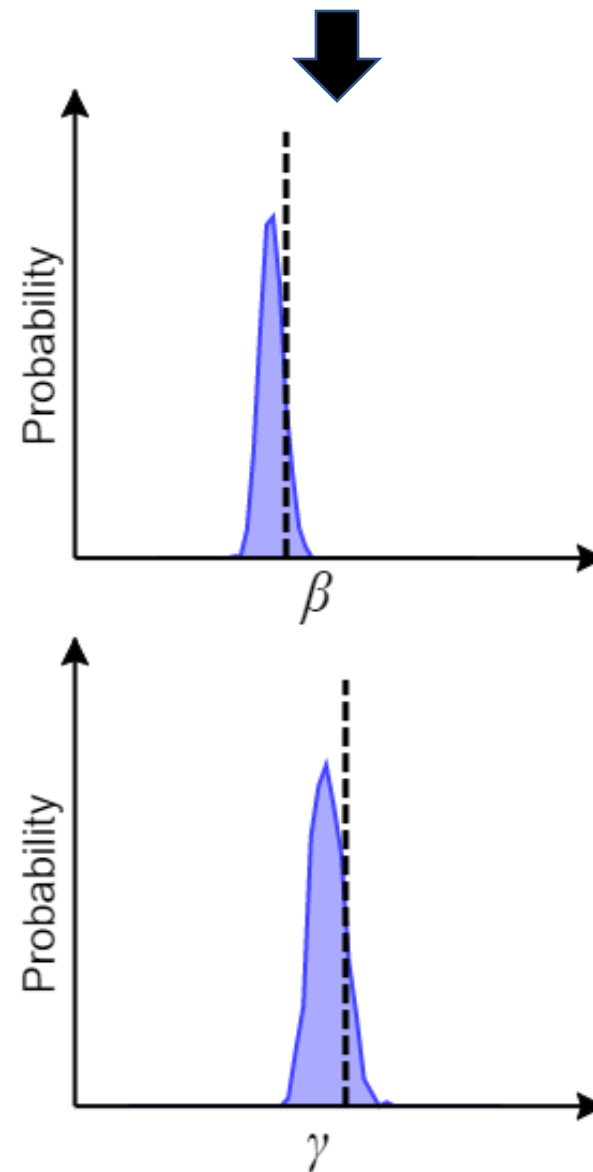


ABC rejection sampling

EXAMPLE: $EF_{\text{cutoff}} = 10^3$



Posterior estimate $\pi(\theta/y)$



ABC rejection sampling



- Very simple to implement
- Only need to be able to simulate from the model



- Becomes computationally very slow for small EF_{cutoff}
 - For complex system not possible to get good posterior estimate
- WHY?
 - Because most samples from prior $\pi(\theta)$ have a low posterior probability $\pi(\theta|y)$
 - This is the motivation behind ABC-SMC...

ABC Sequential Monte Carlo (ABC-SMC)

- Run over several generations G
- For each generation g a different EF_{cutoff}^g is used, such that

$$EF_{\text{cutoff}}^1 > EF_{\text{cutoff}}^2 > \dots > EF_{\text{cutoff}}^G$$

Generation 1

- 1) Sample θ from prior $\pi(\theta)$.
- 2) Simulate ξ .
- 3) Calculate EF .
- 4) If $EF < EF_{\text{cutoff}}^1$ accept.
Repeat.



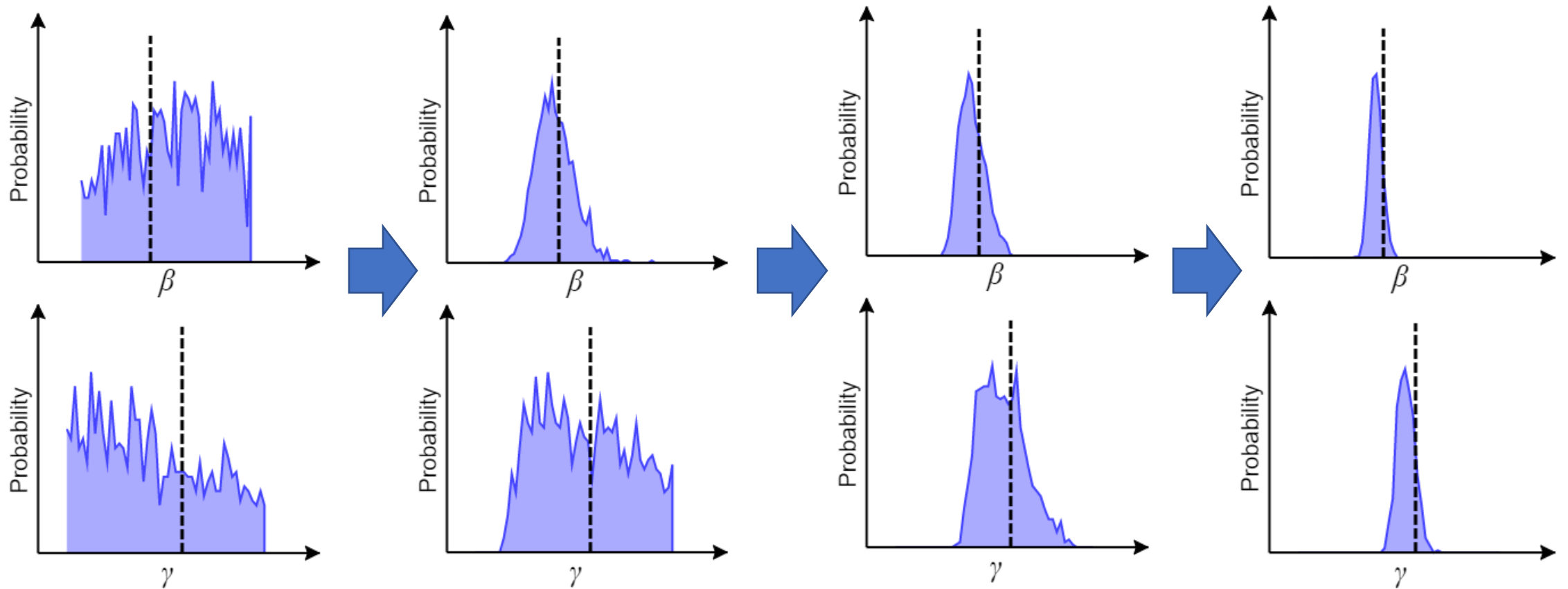
Generation g

- 1) Sample θ using previous generation outputs as an importance sampler (with associated weight).
- 2) Simulate ξ .
- 3) Calculate EF .
- 4) If $EF < EF_{\text{cutoff}}^g$ accept.
Repeat.



$g = g + 1$

ABC Sequential Monte Carlo (ABC-SMC)



Generation 1

EF_{cutoff} $EF_{\text{cutoff}}^1 = 10^6$

Acceptance: 38%

Generation 2

$EF_{\text{cutoff}}^2 = 10^5$

33%

Generation 3

$EF_{\text{cutoff}}^3 = 10^4$

20%

Generation 4

$EF_{\text{cutoff}}^4 = 10^3$

10%

ABC Sequential Monte Carlo (ABC-SMC)



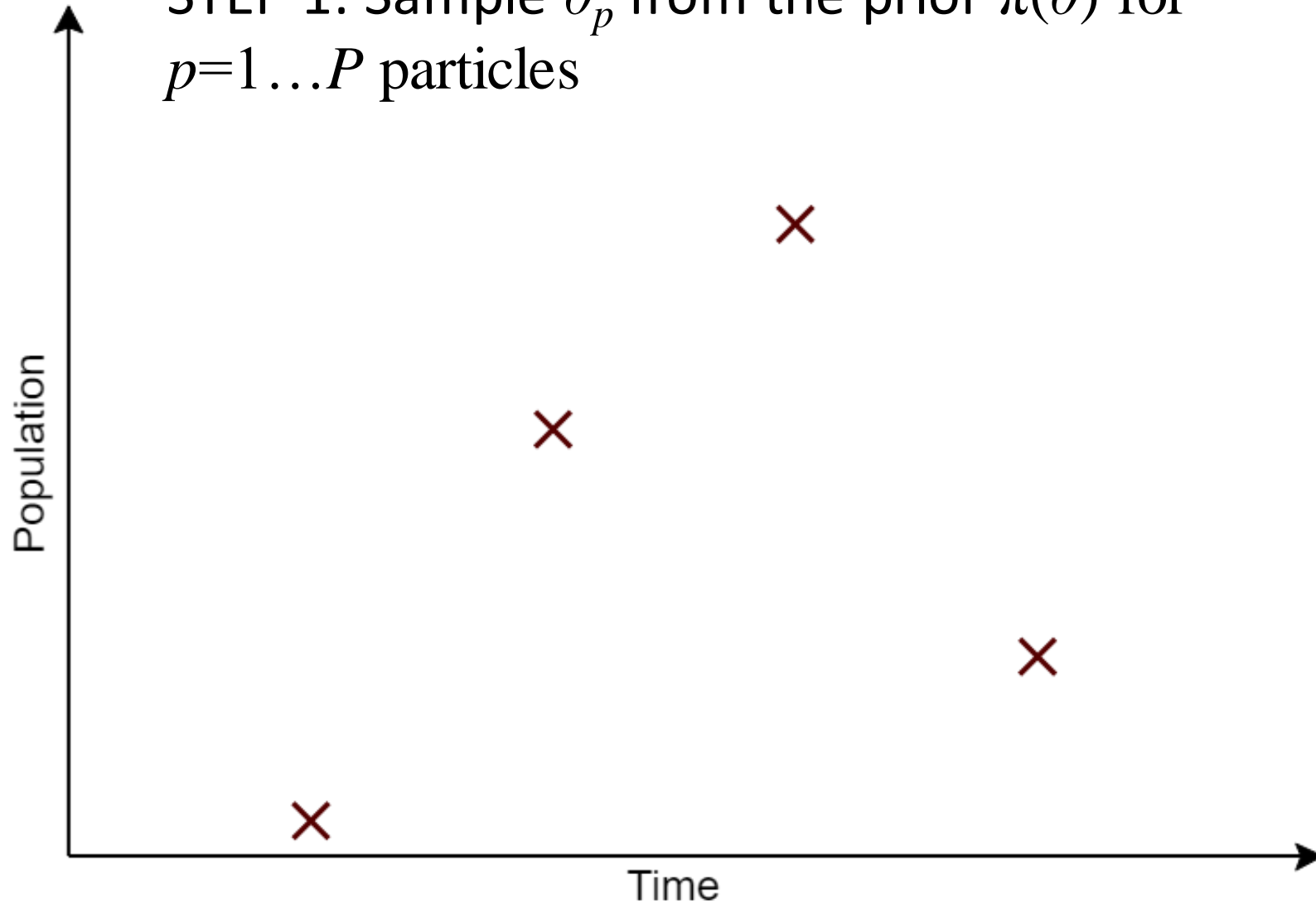
- Relatively simple to implement
 - Requires careful optimisation of EF_{cutoff}^g
- Only need to be able to simulate from the system
- Usually much faster than ABC rejection sampling



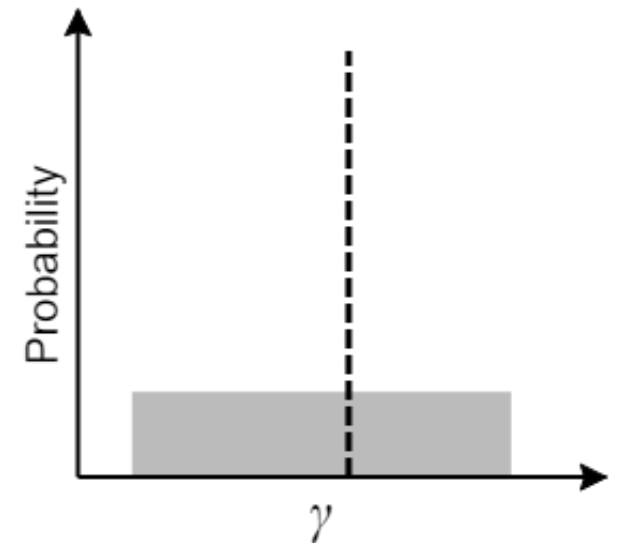
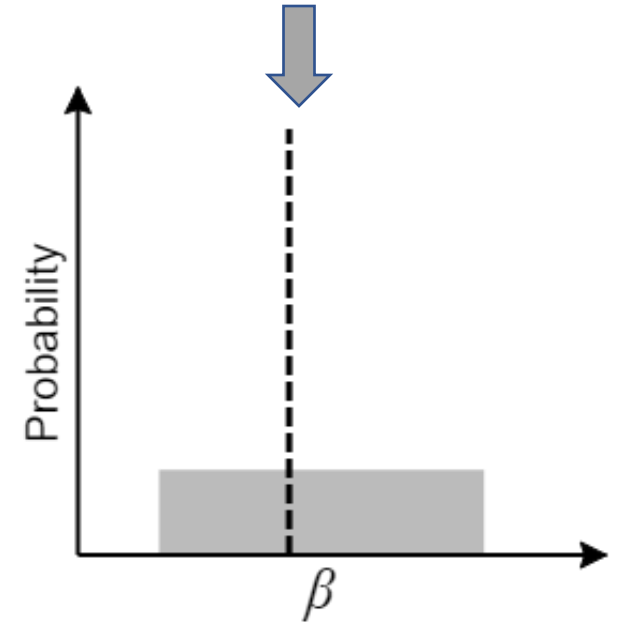
- Can become computationally slow for small EF_{cutoff}
- WHY?
 - 1) Large number of parameters
 - Importance weights results in small effective sample size
 - 2) Significant stochasticity
 - Even correct parameters leads to a poor probability for simulating the data

ABC-MBP

STEP 1: Sample θ_p from the prior $\pi(\theta)$ for $p=1 \dots P$ particles

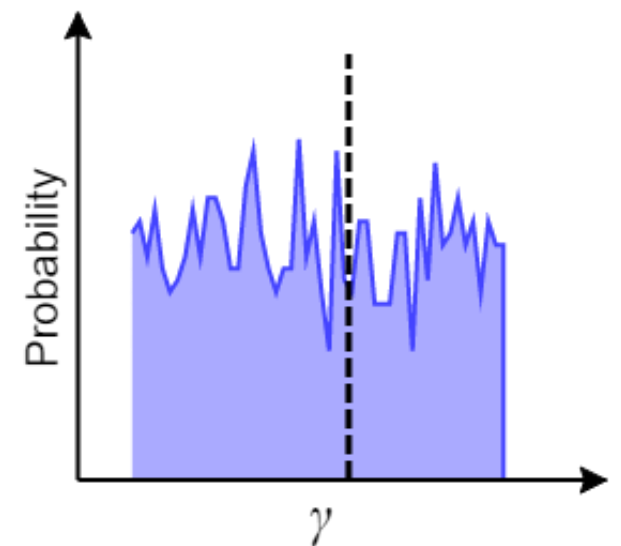
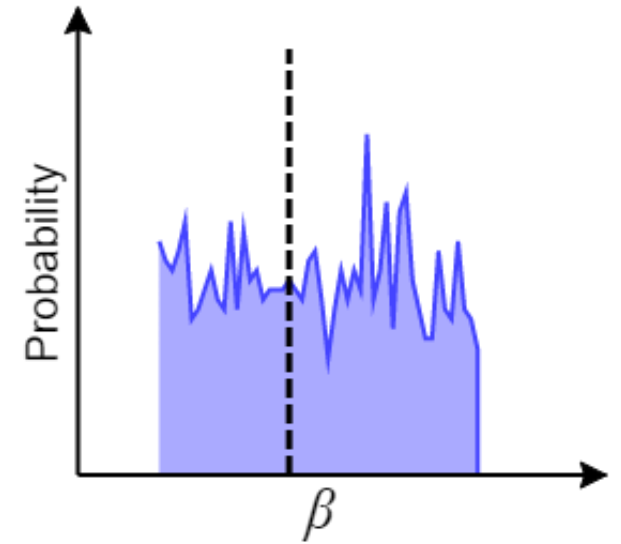
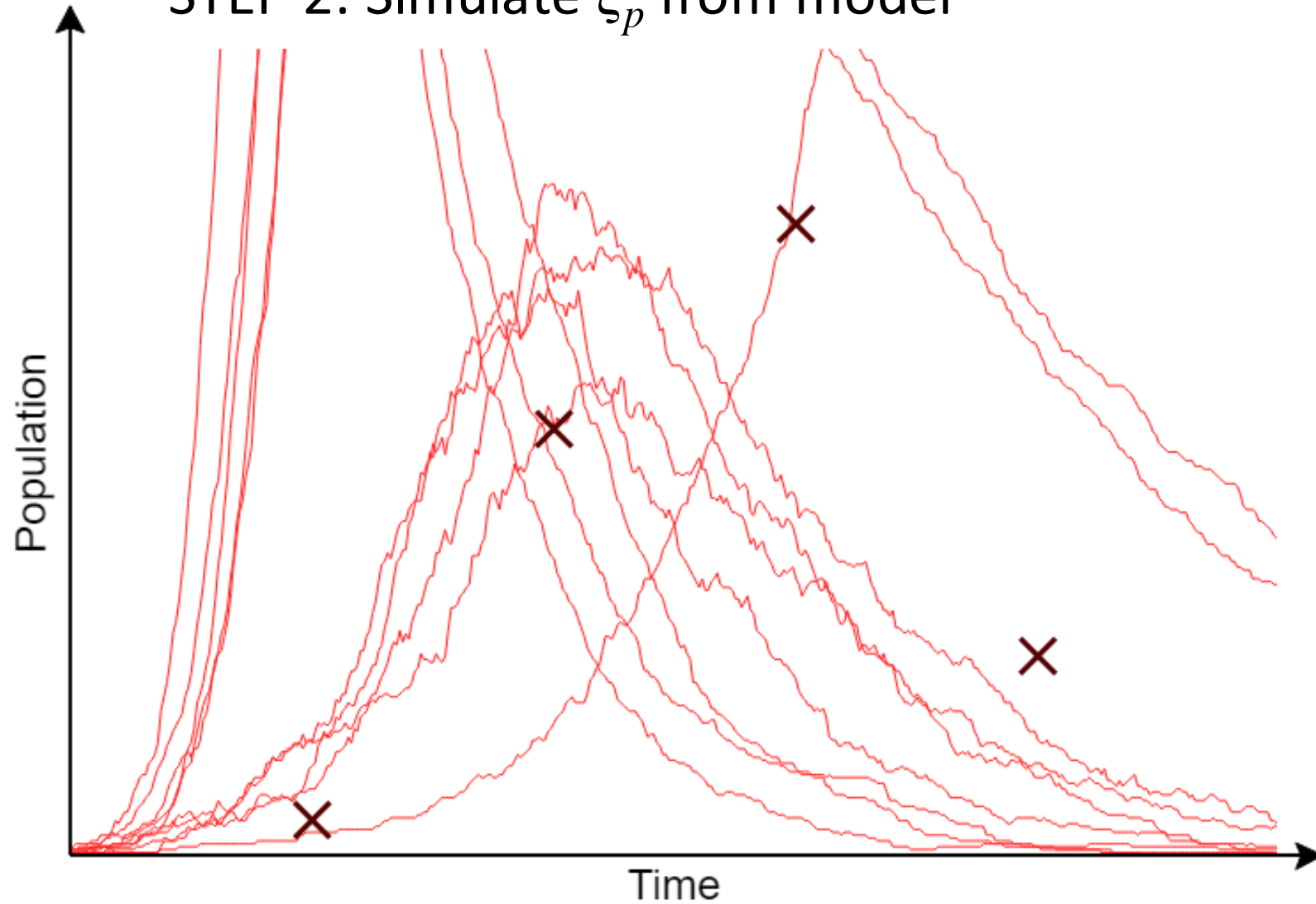


Sample from prior (grey)



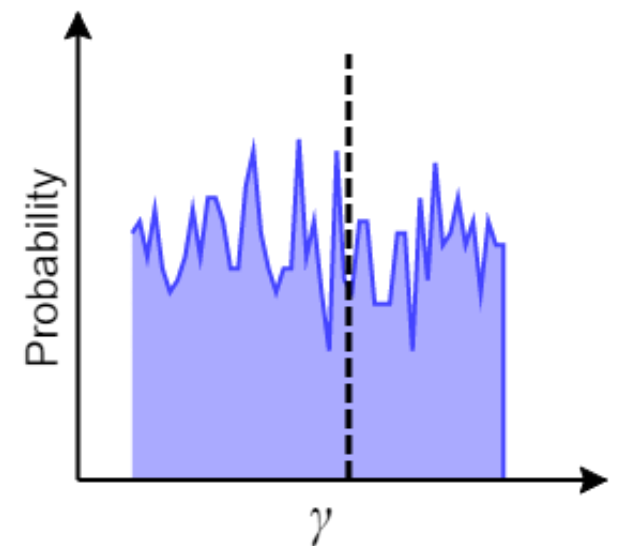
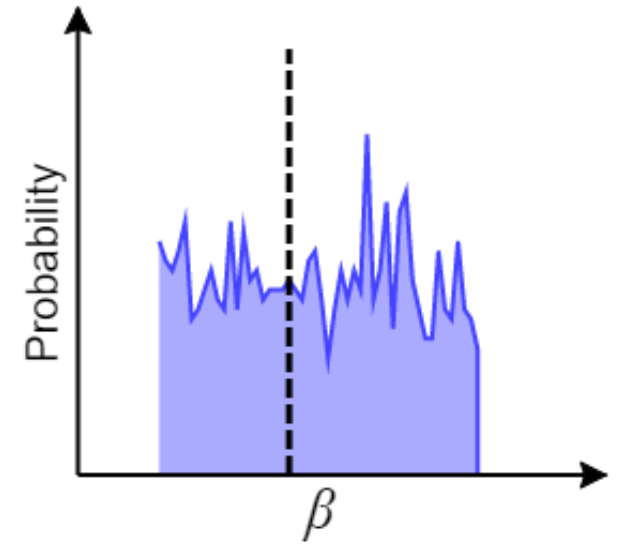
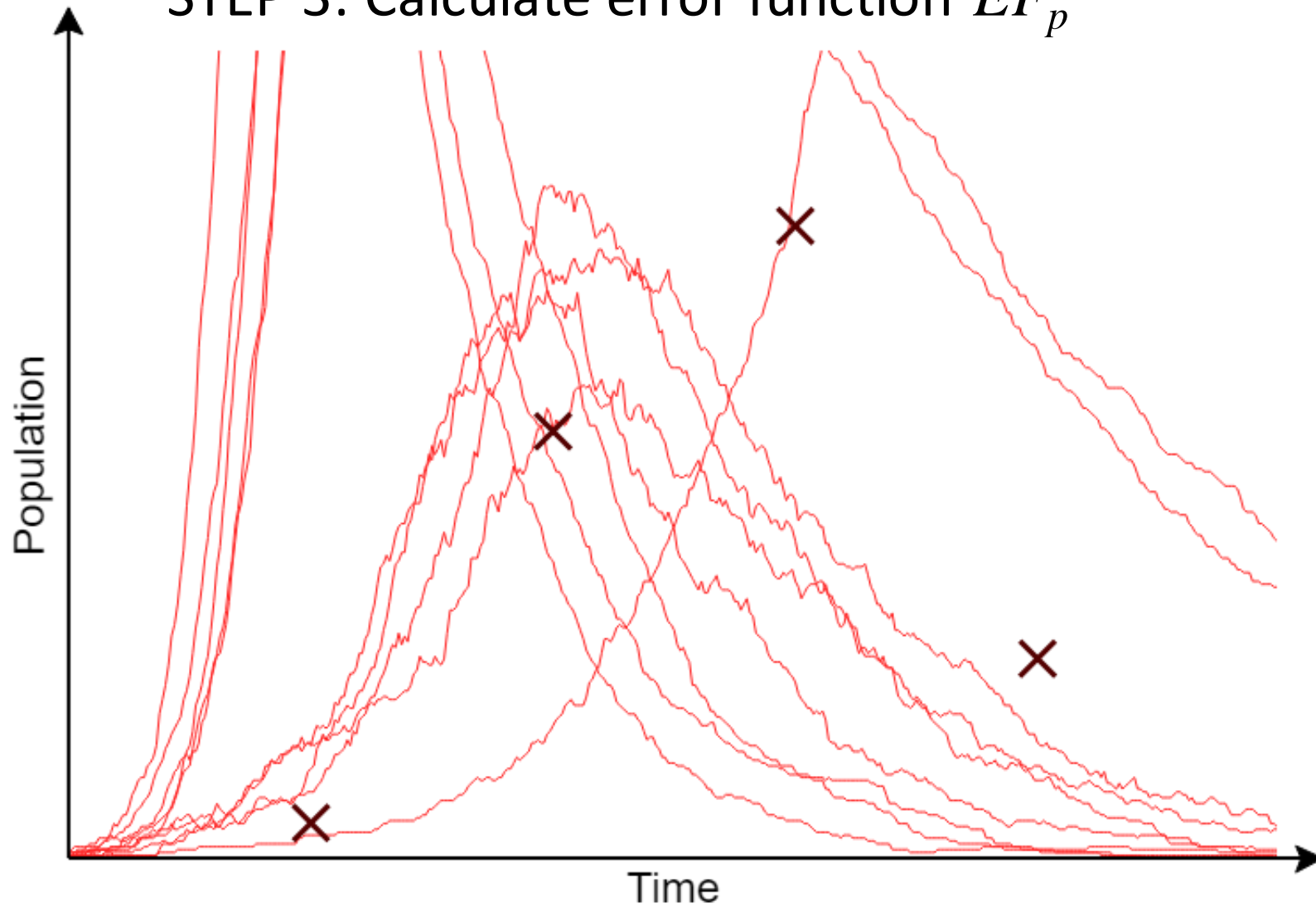
ABC-MBP

STEP 2: Simulate ξ_p from model



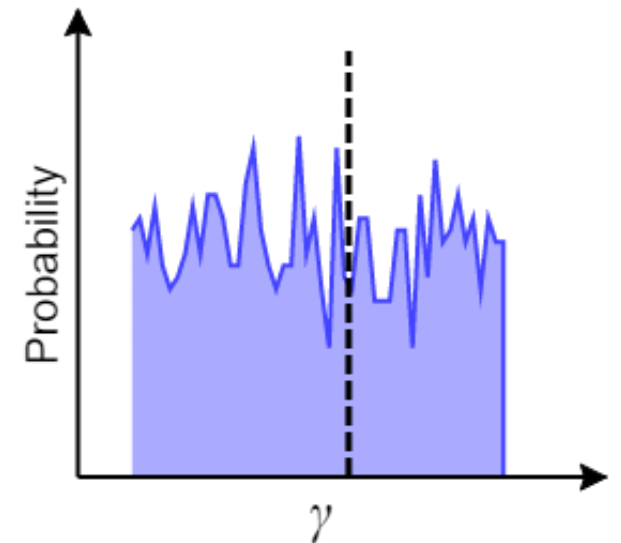
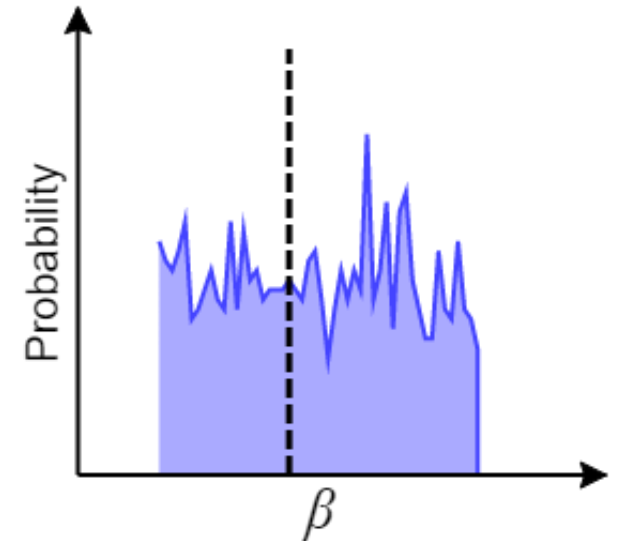
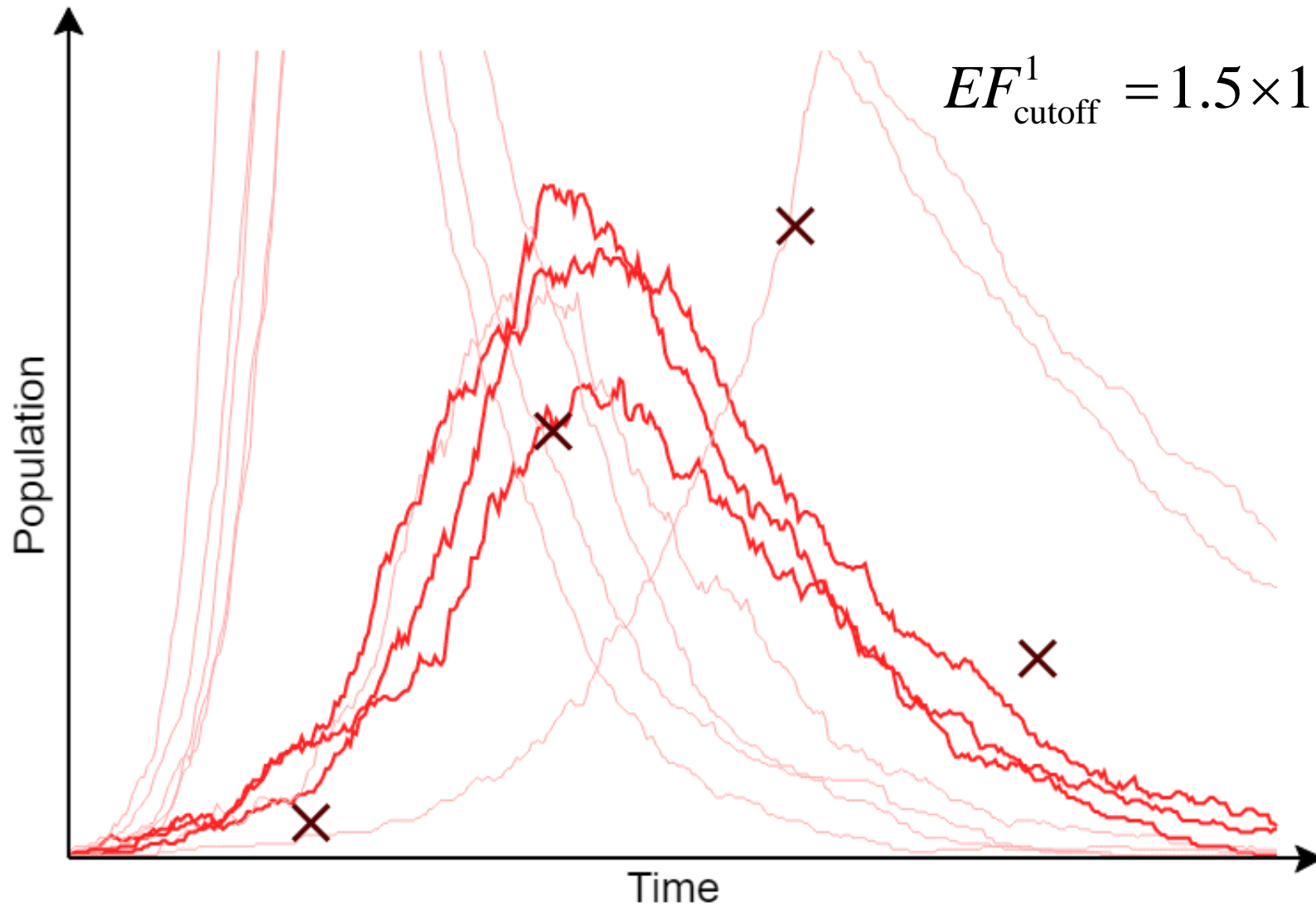
ABC-MBP

STEP 3: Calculate error function EF_p



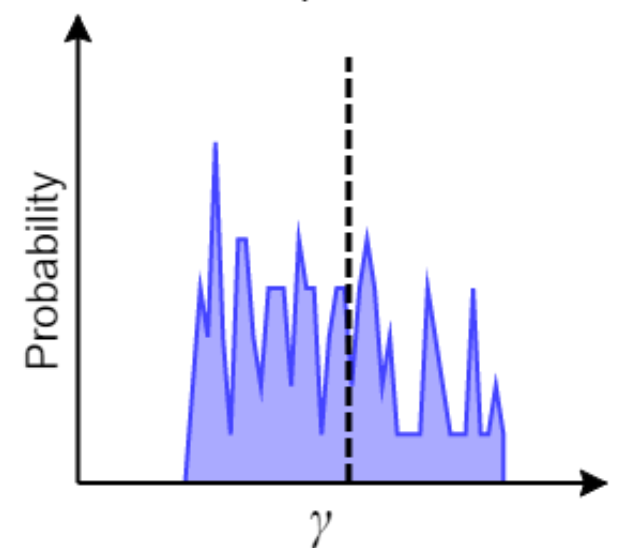
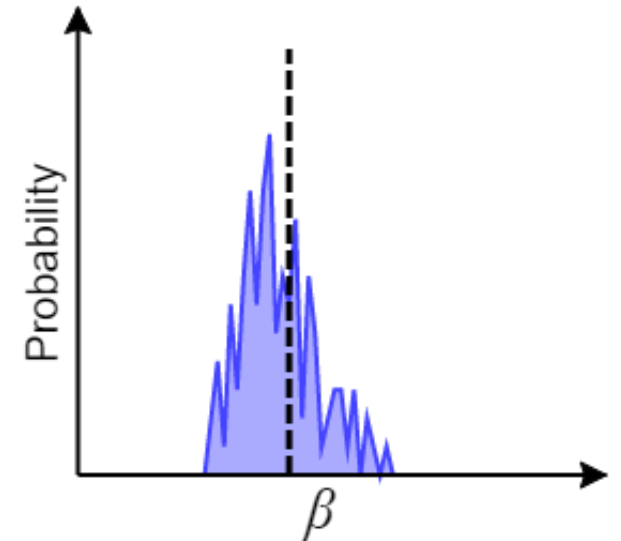
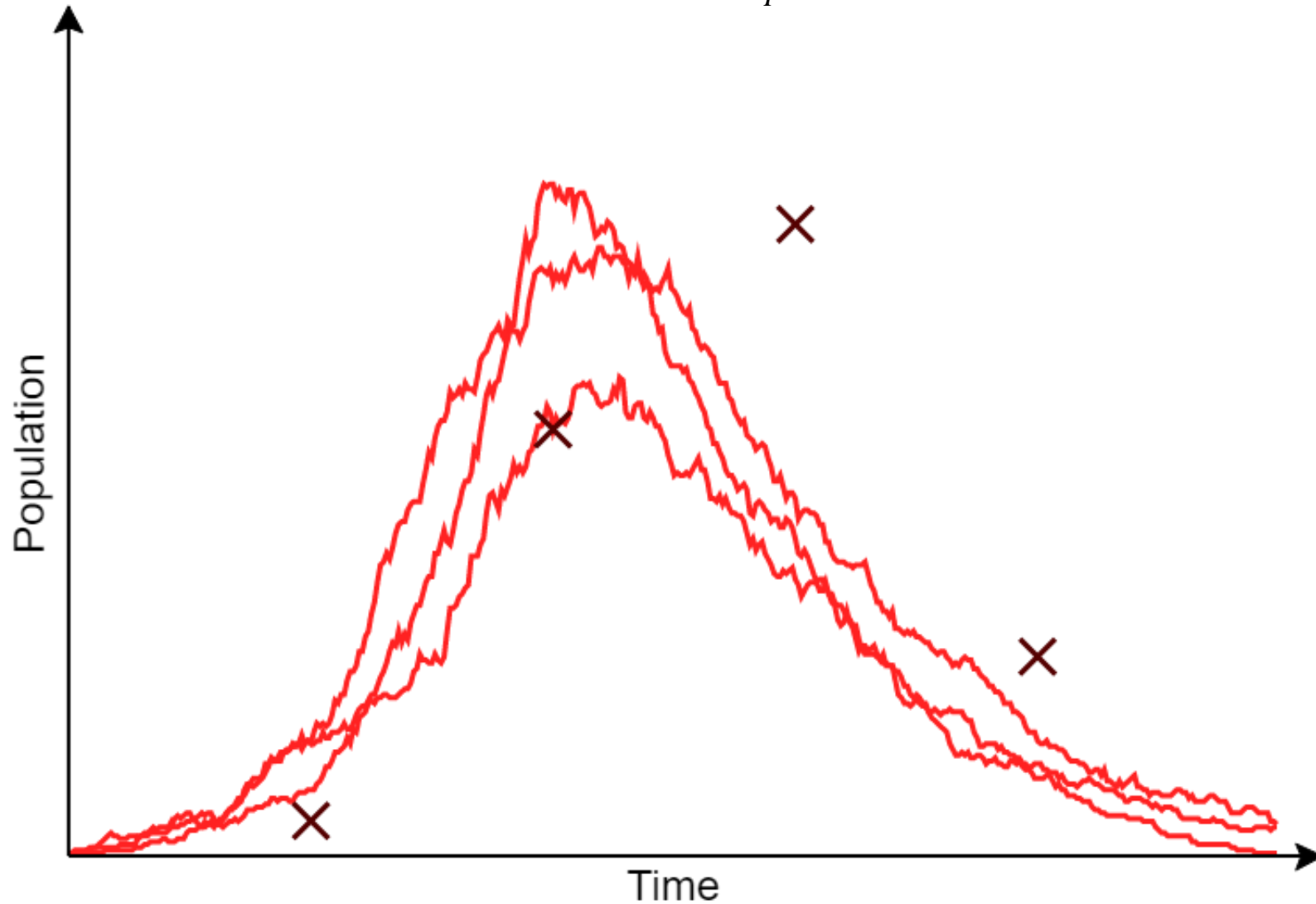
ABC-MBP

STEP 4: Set EF_{cutoff}^1 such that half particles have $EF_p < EF_{\text{cutoff}}^1$



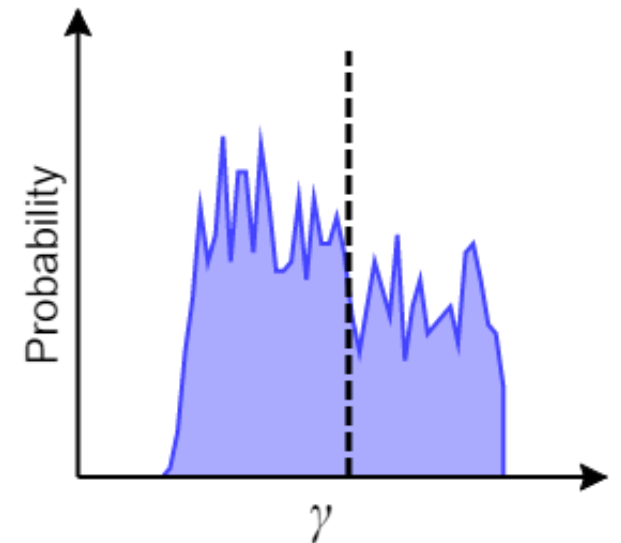
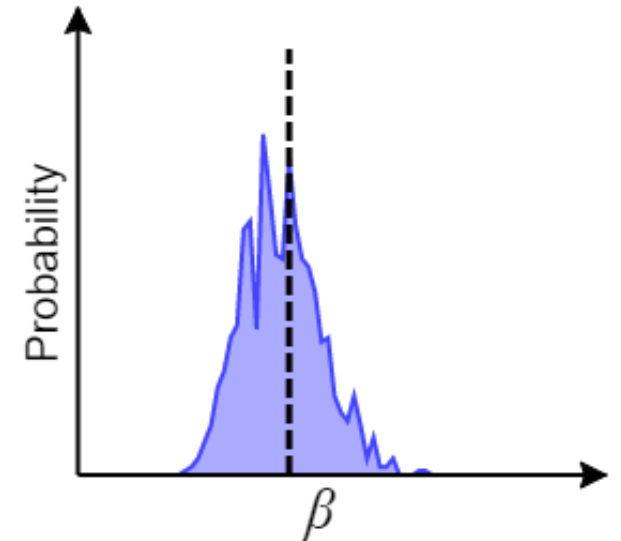
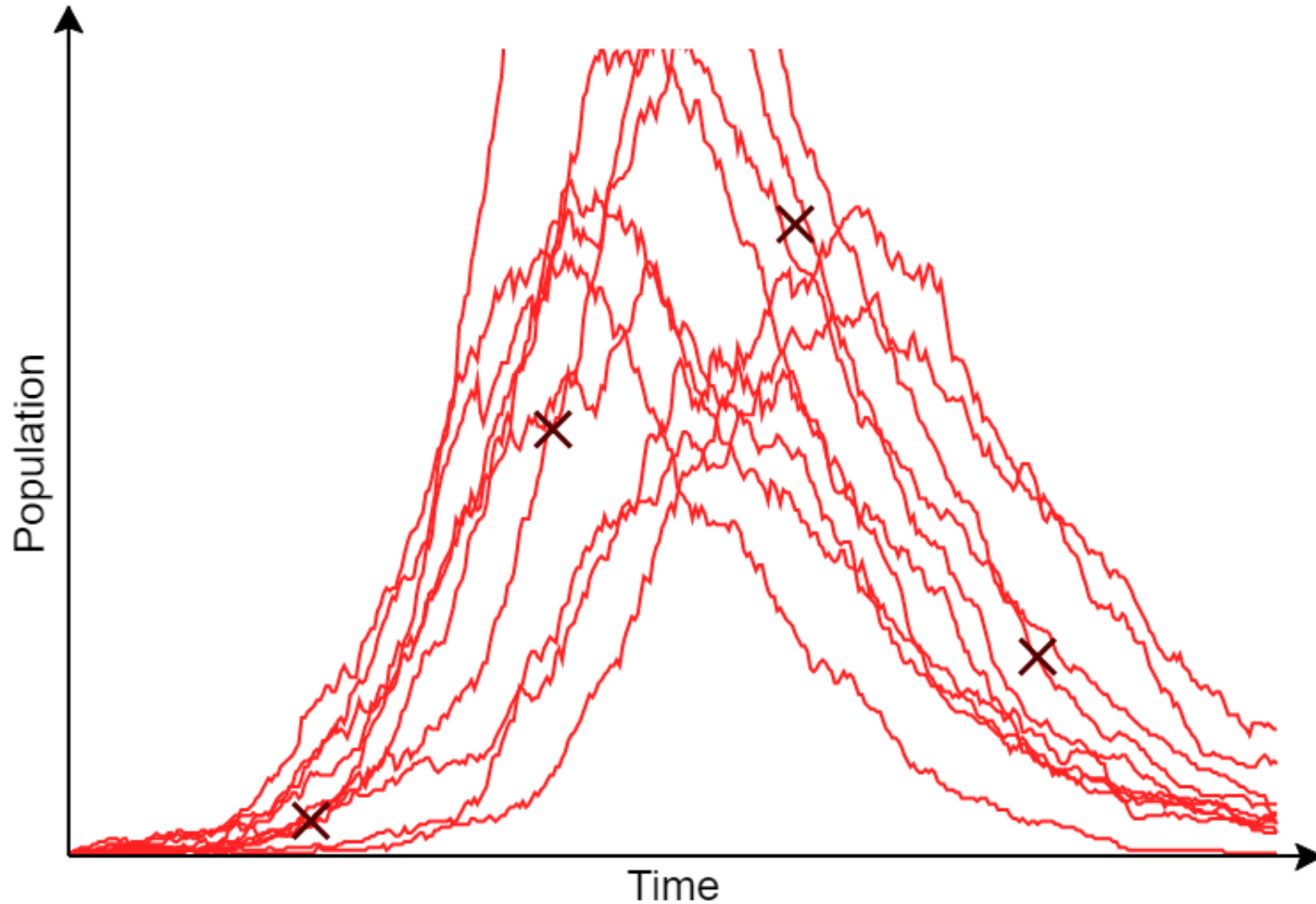
ABC-MBP

STEP 5: Particles with $EF_p < EF_{\text{cutoff}}^1$ are duplicated and others culled



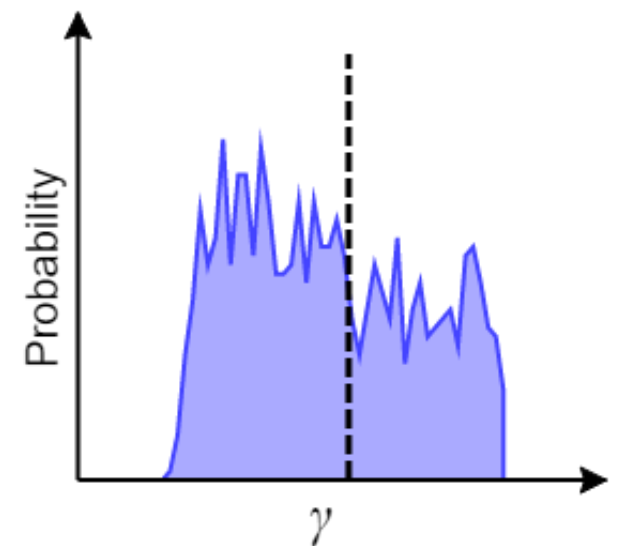
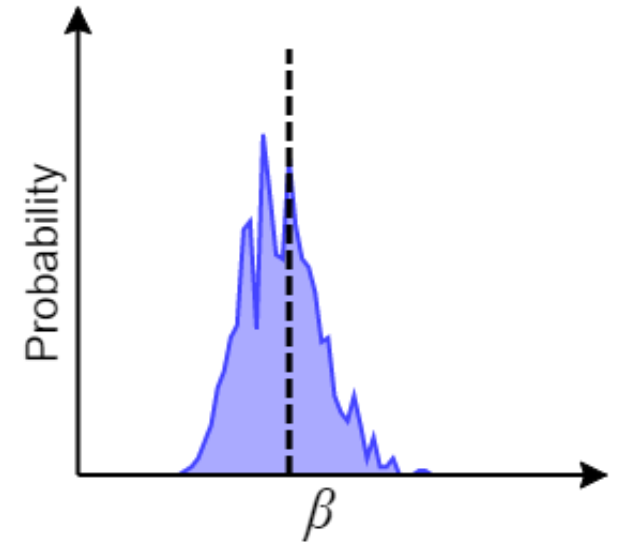
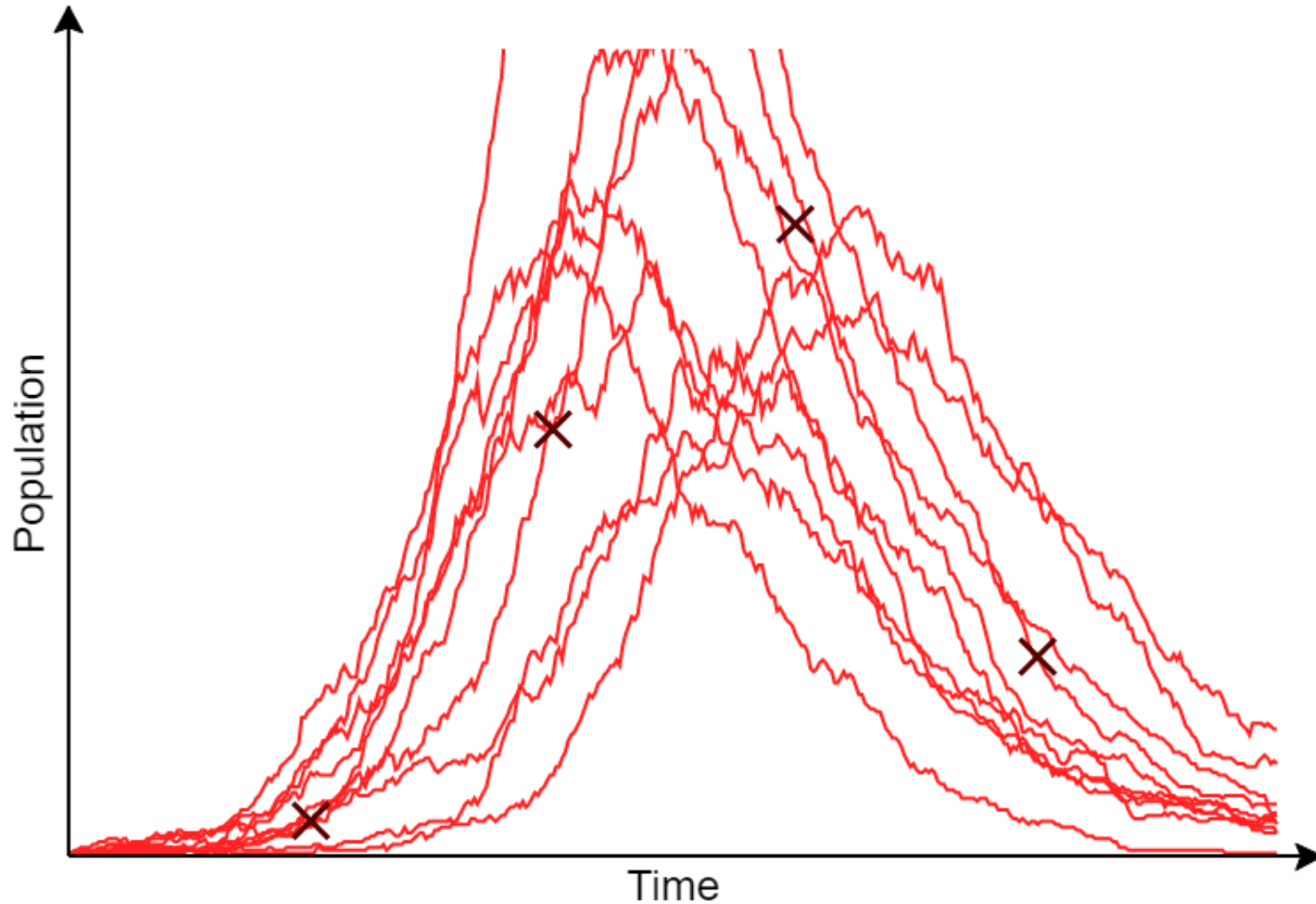
ABC-MBP

STEP 6: MBPs are applied to allow particles to explore posterior space



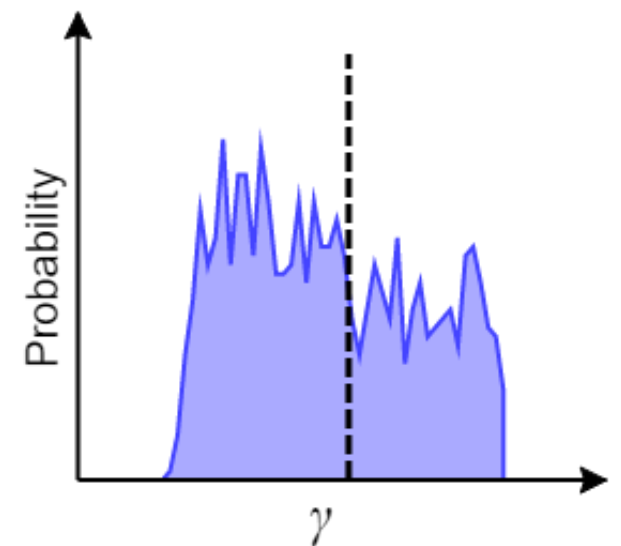
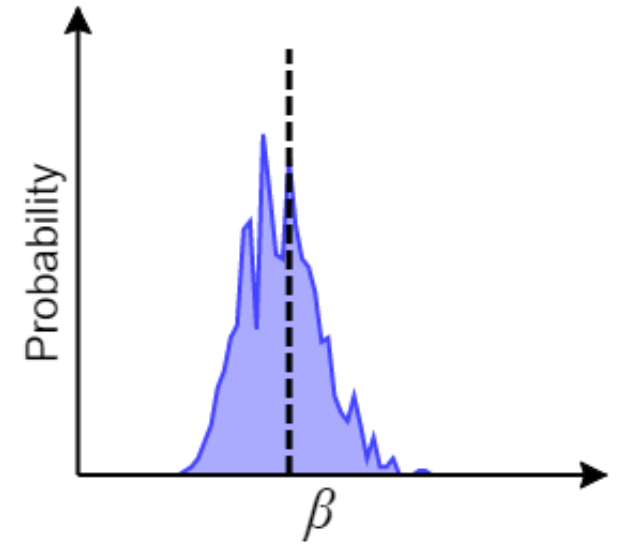
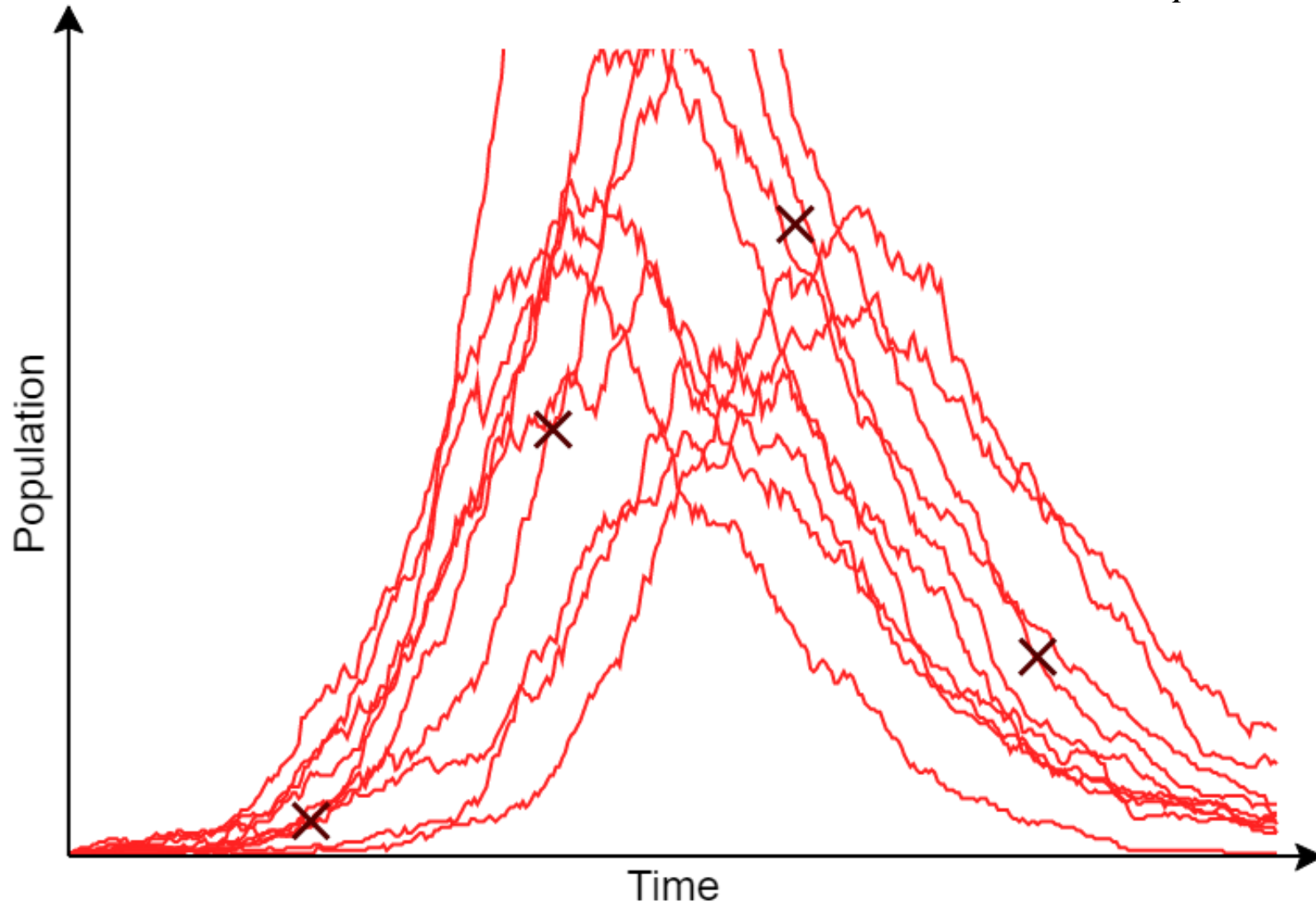
ABC-MBP

This completes the first generation. Repeat over more generations...



ABC-MBP

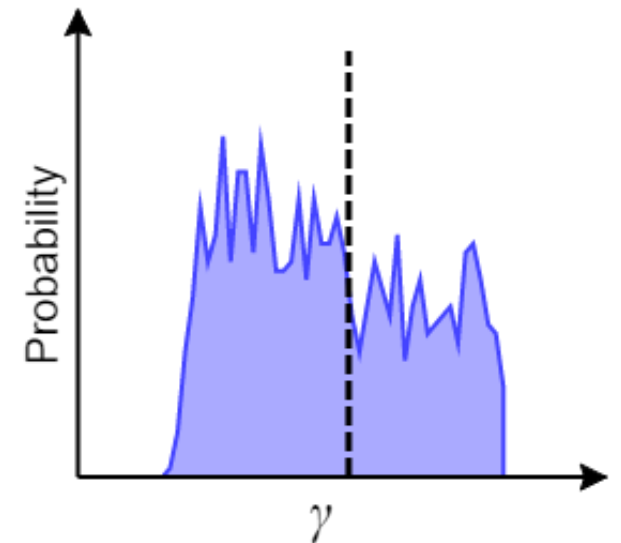
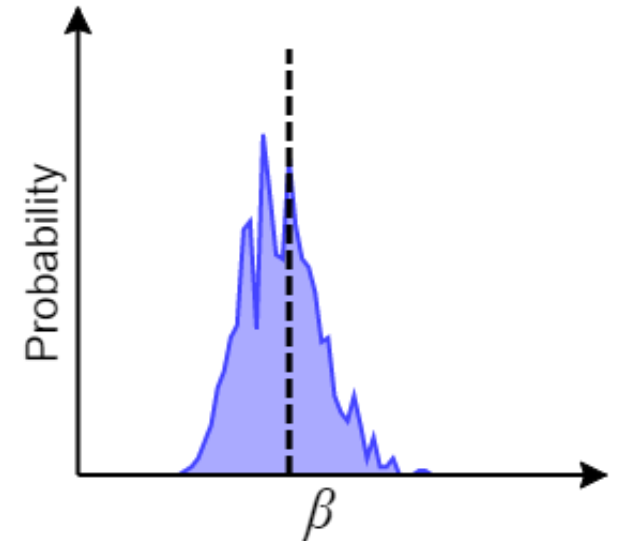
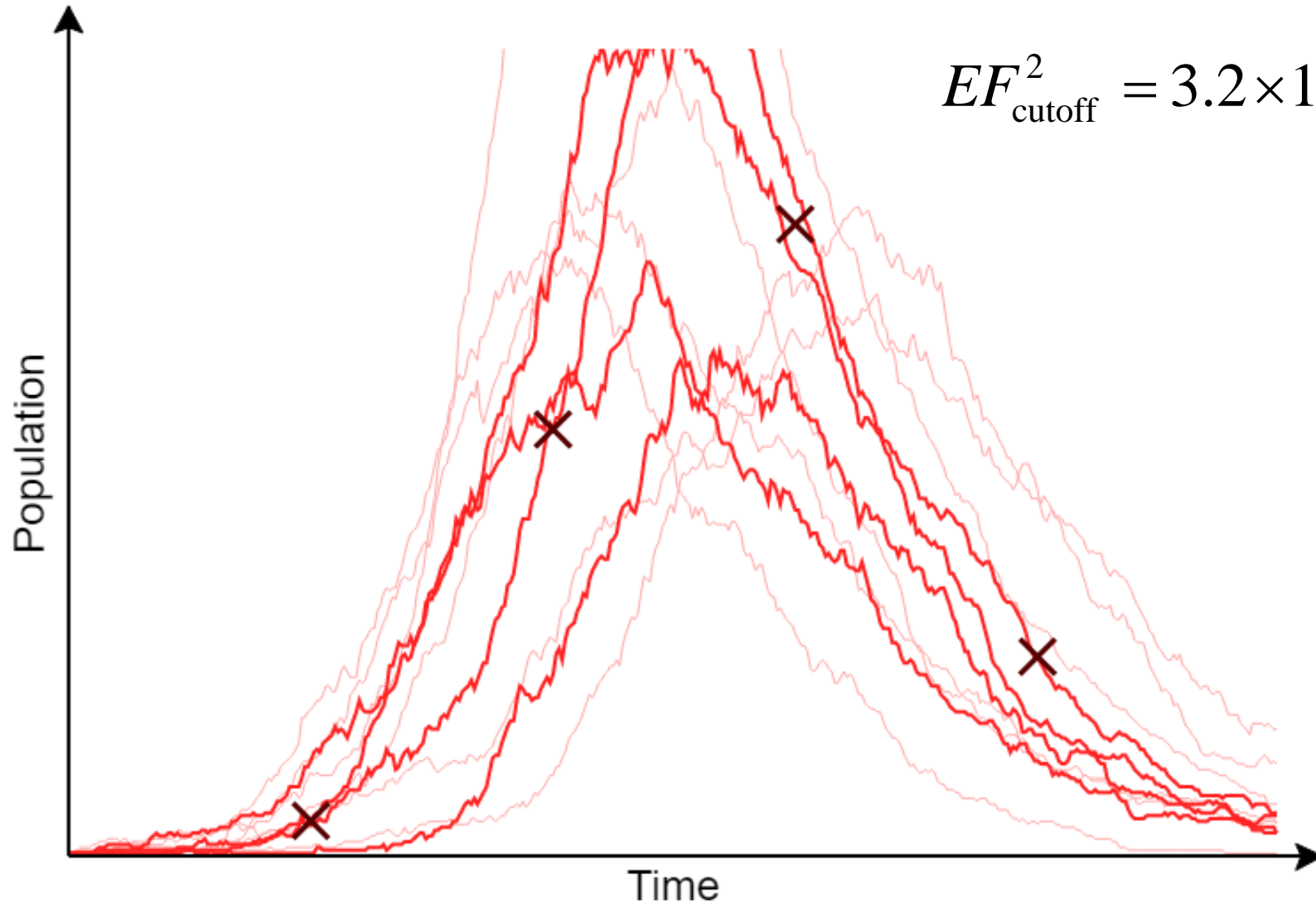
Generation 2: Calculate error function EF_p



ABC-MBP

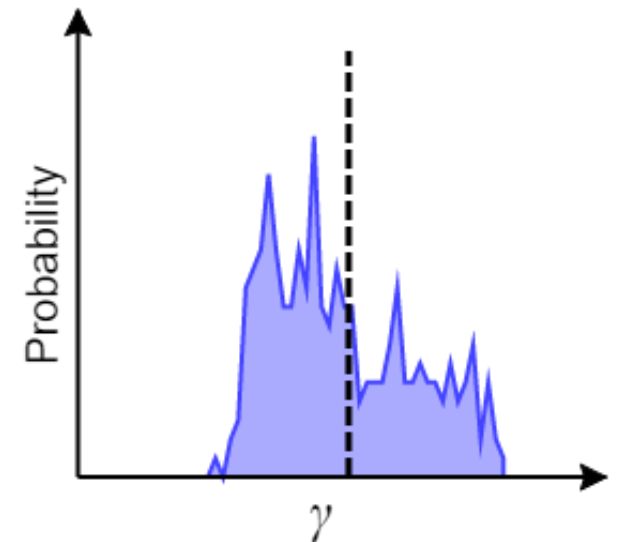
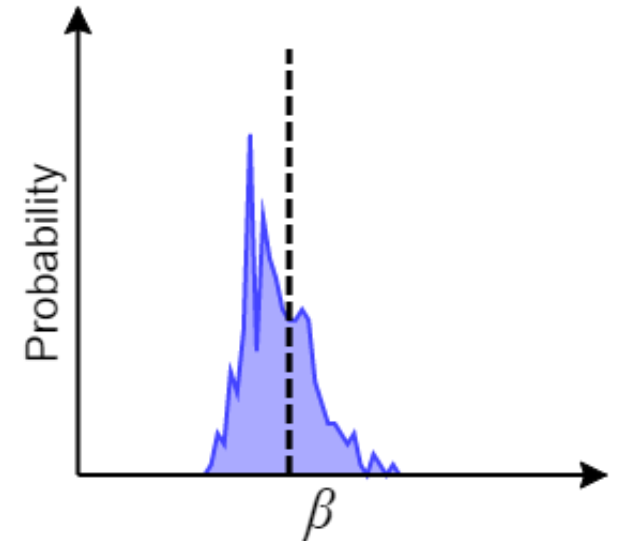
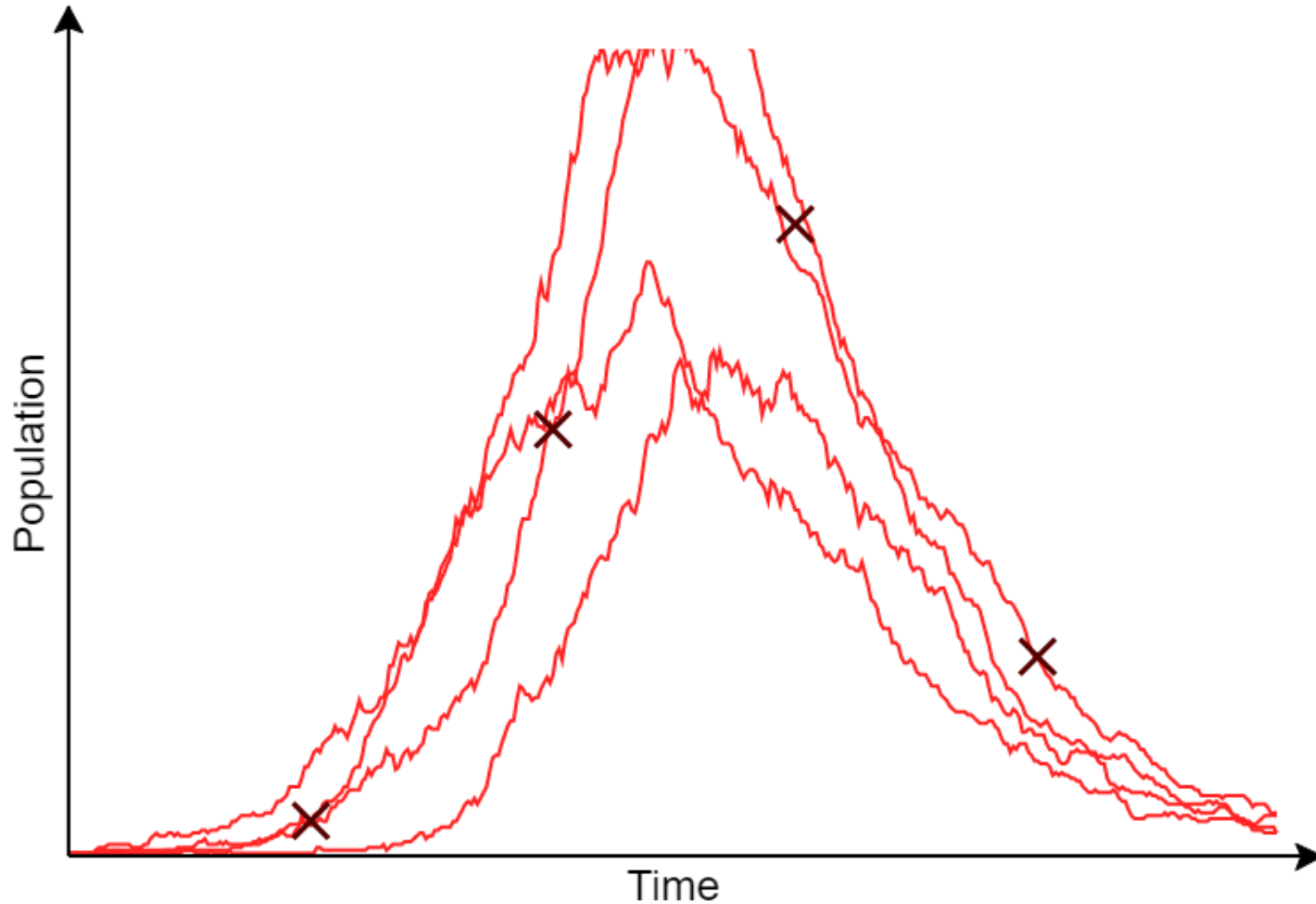
Generation 2: Set EF_{cutoff}^2 such that half particles have $EF_p < EF_{\text{cutoff}}^2$

$$EF_{\text{cutoff}}^2 = 3.2 \times 10^4$$



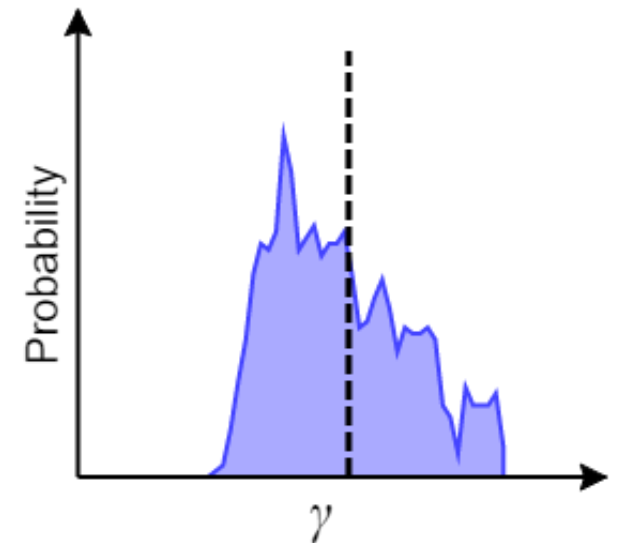
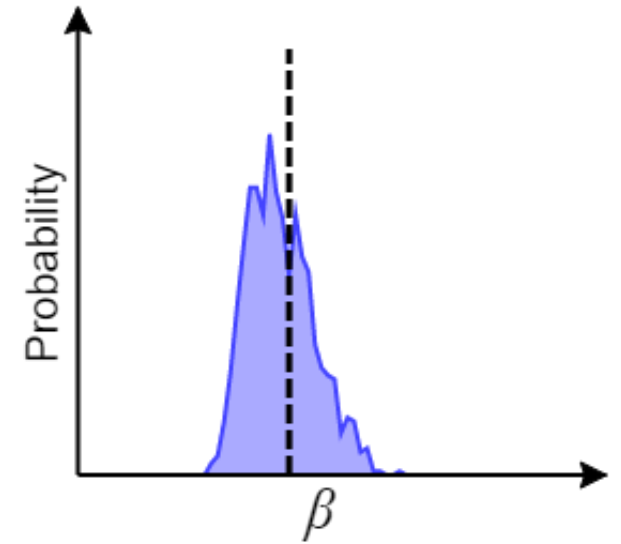
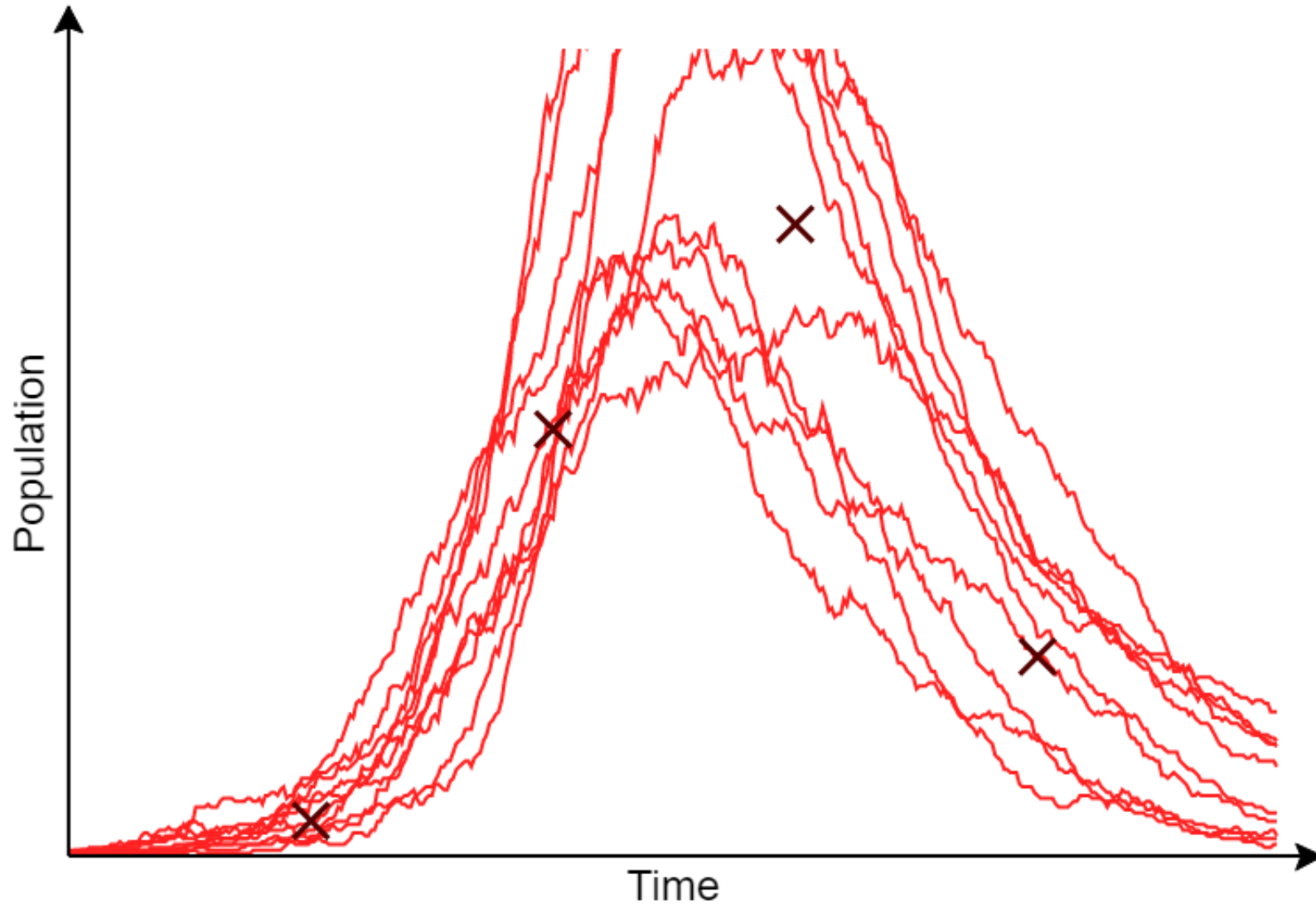
ABC-MBP

Generation 2: Particles with $EF_p < EF_{\text{cutoff}}^2$ are duplicated, others culled.



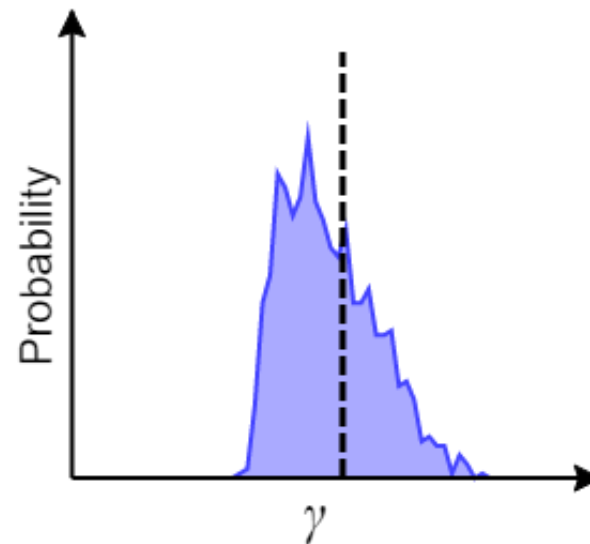
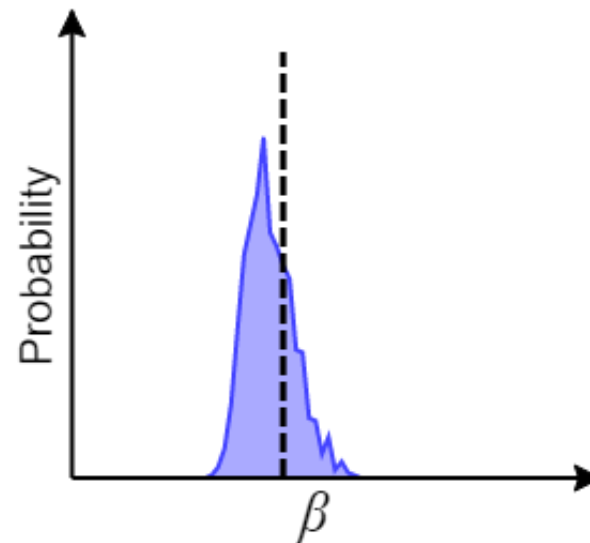
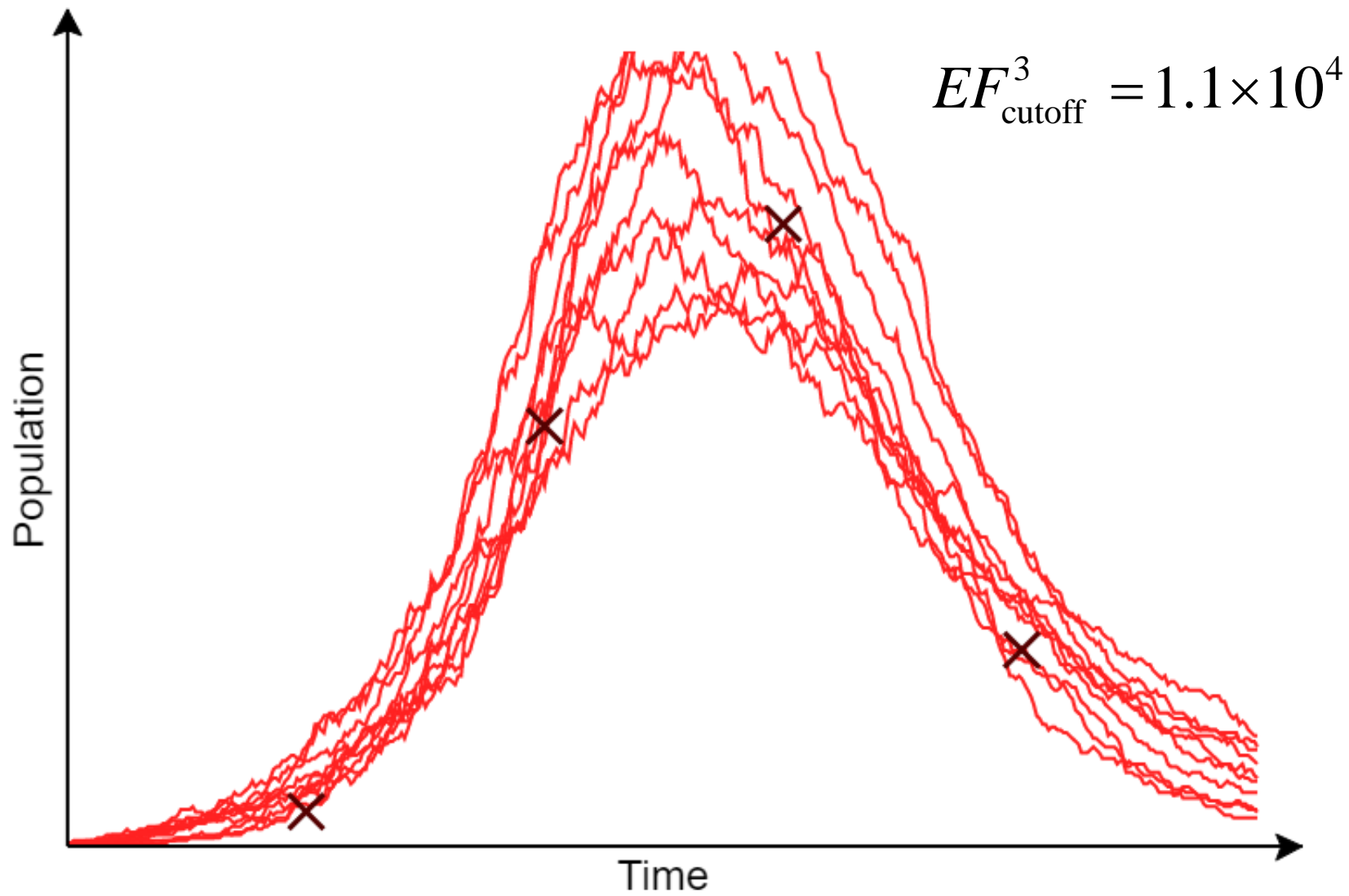
ABC-MBP

Generation 2: MBPs applied to allow particles to explore posterior space



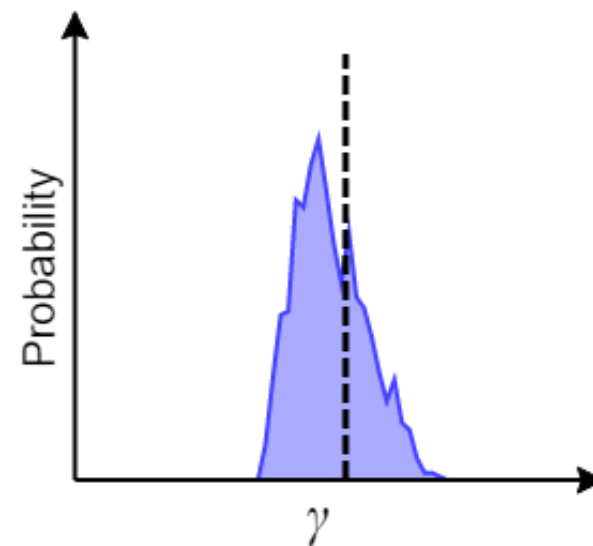
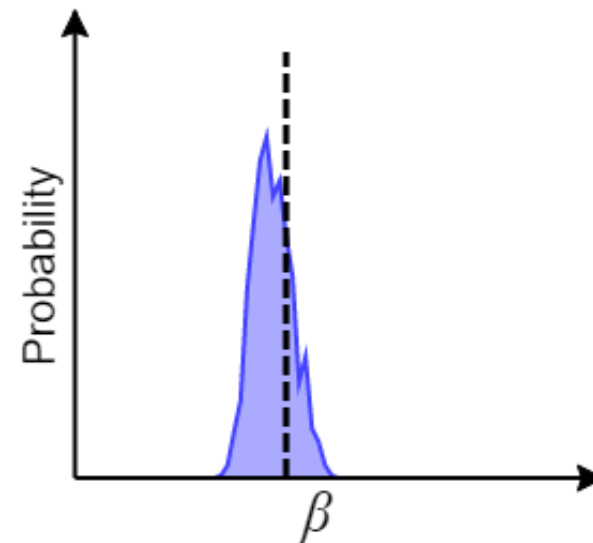
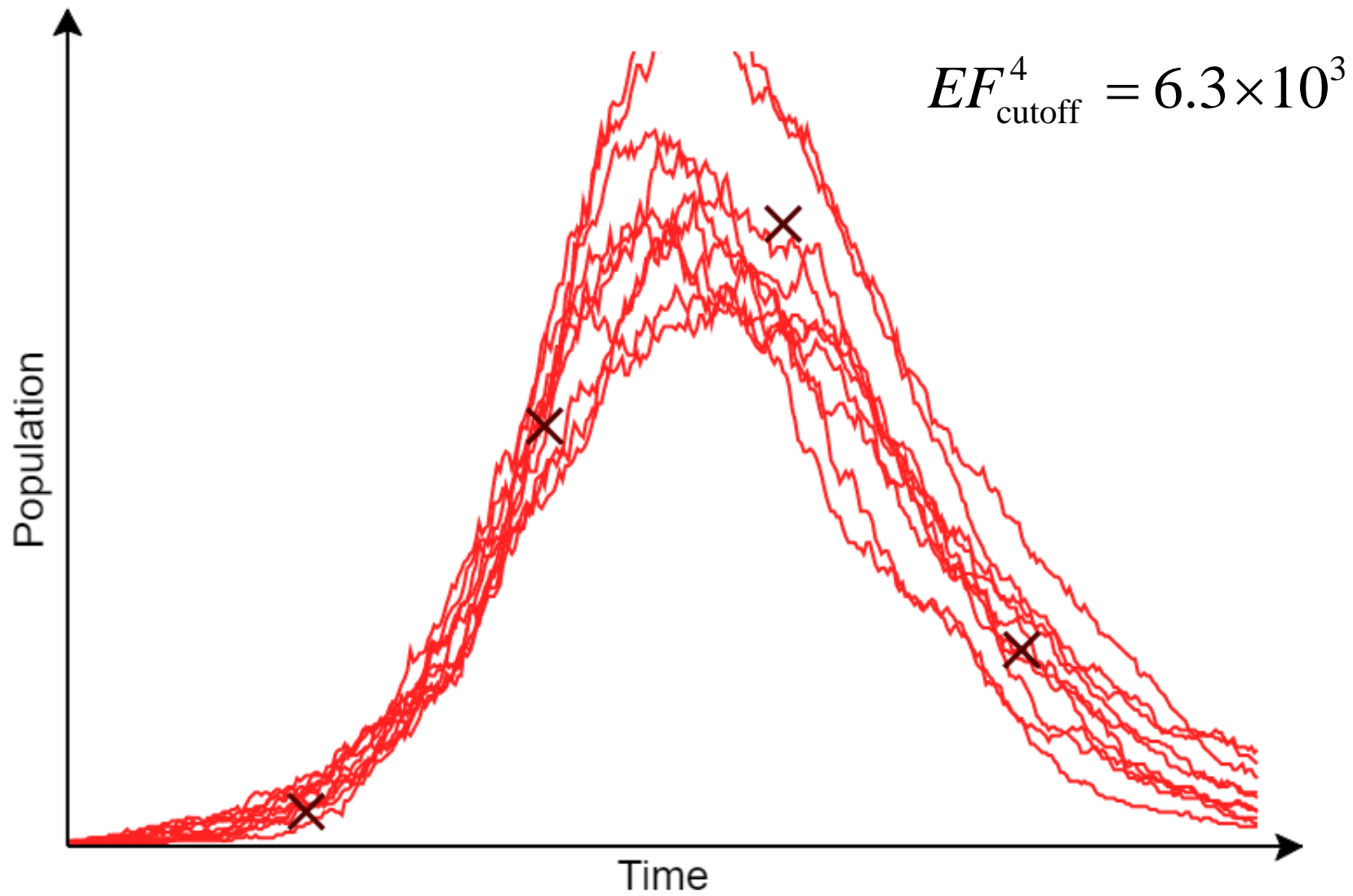
ABC-MBP

Generation 3:



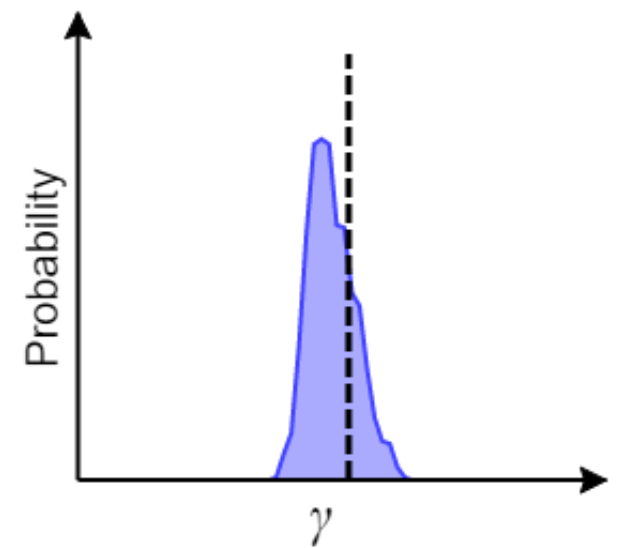
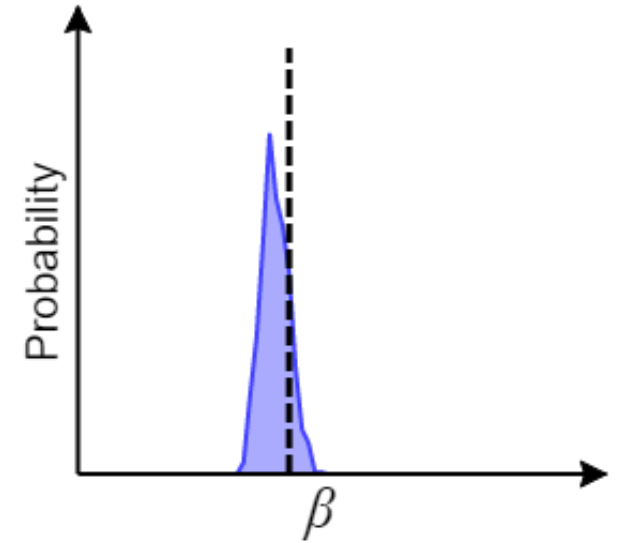
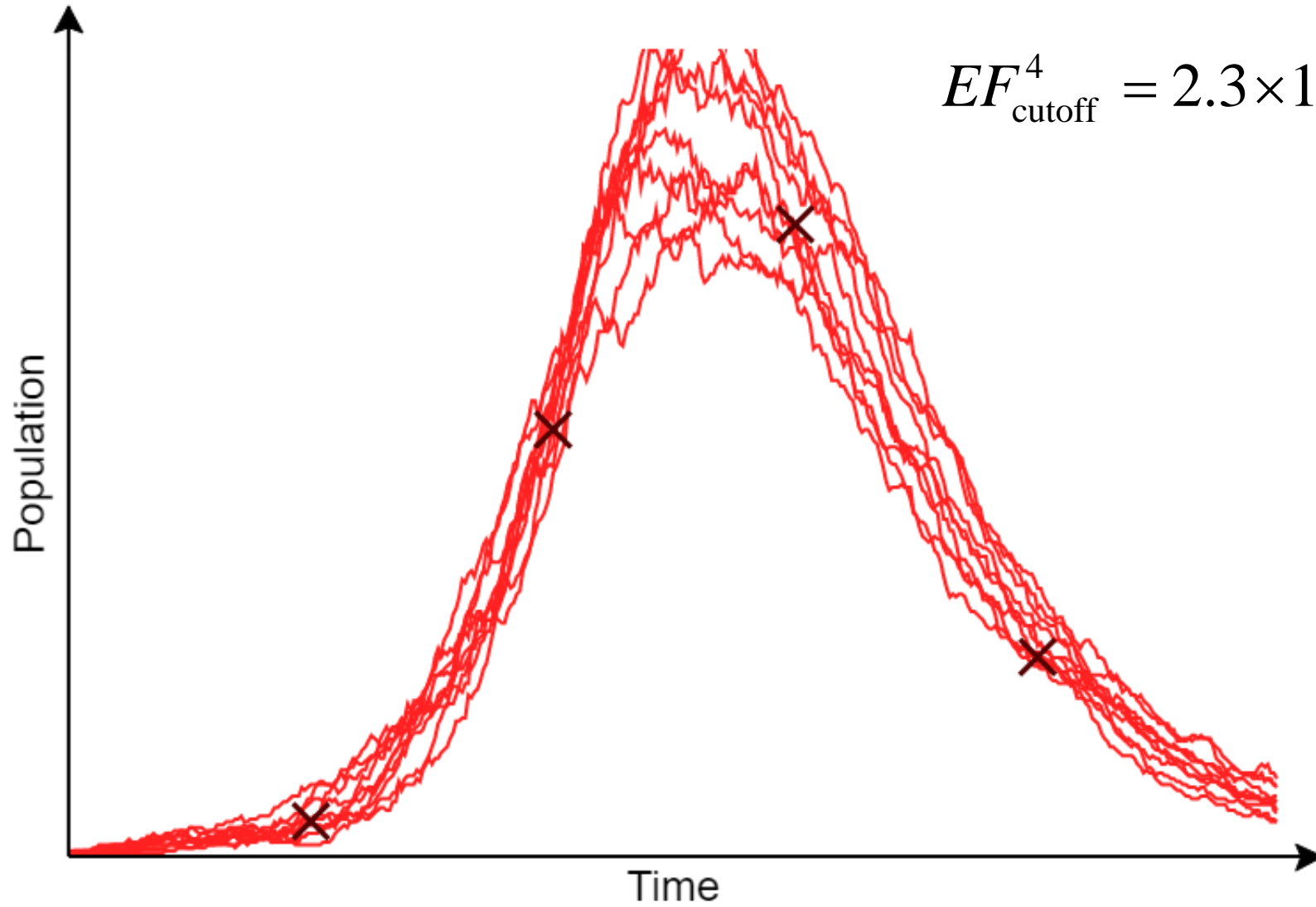
ABC-MBP

Generation 4:



ABC-MBP

Generation 5:



Model based proposals (MBPs)

Covariance estimate
obtained from all particles



Tunable constant



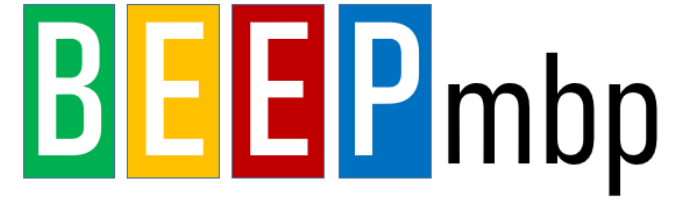
• STEP 1: Propose a new parameter set $\theta'_p \sim \text{MVN}(\theta_p, s^g \Sigma^g)$,

• STEP 2: *Modify* ξ_p to generate ξ'_p

• STEP 3: Calculate EF'_p

• STEP 4: If $EF'_p \geq EF_{cut}$ reject,
otherwise accept with probability: $\max \left\{ \frac{\pi(\theta'_p)}{\pi(\theta_p)}, 1 \right\}$

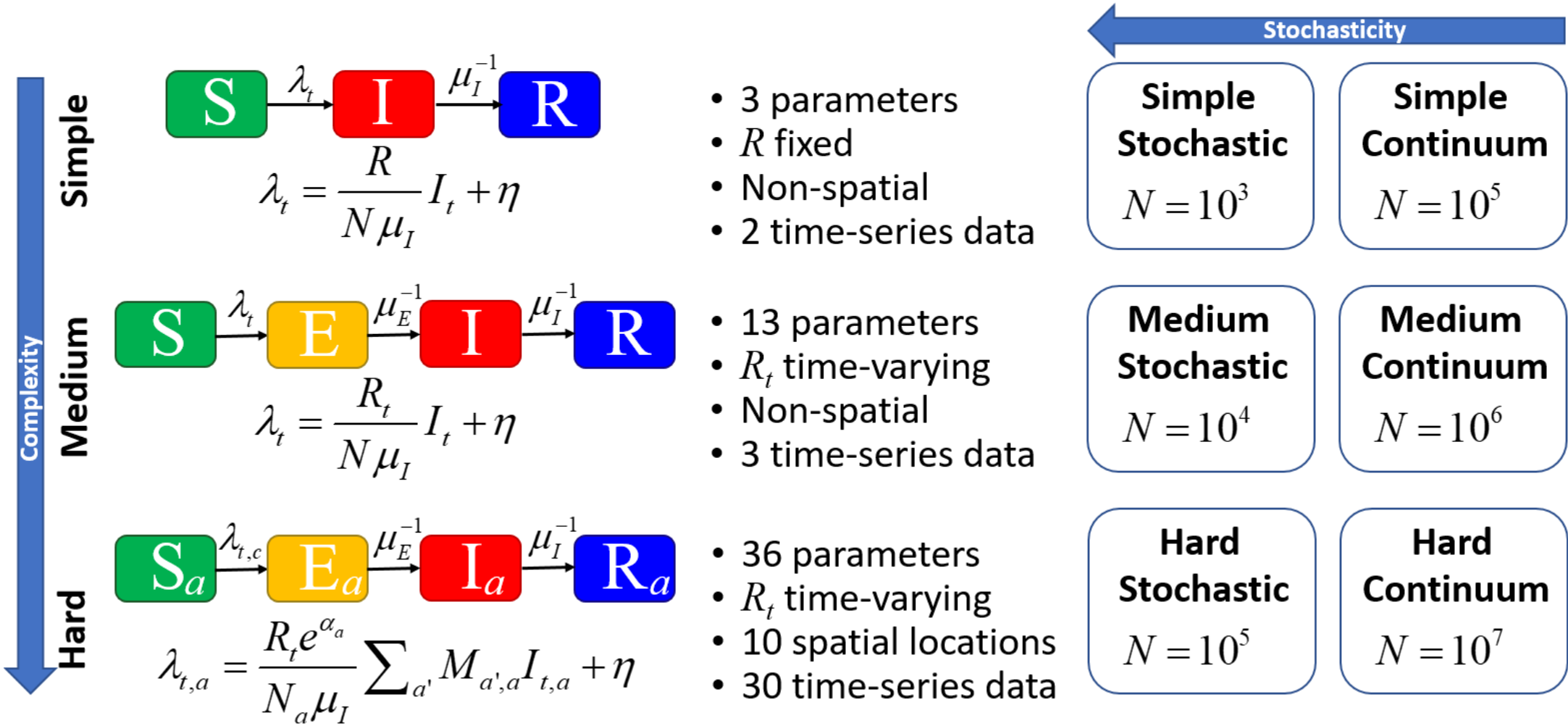
BEEPmbp



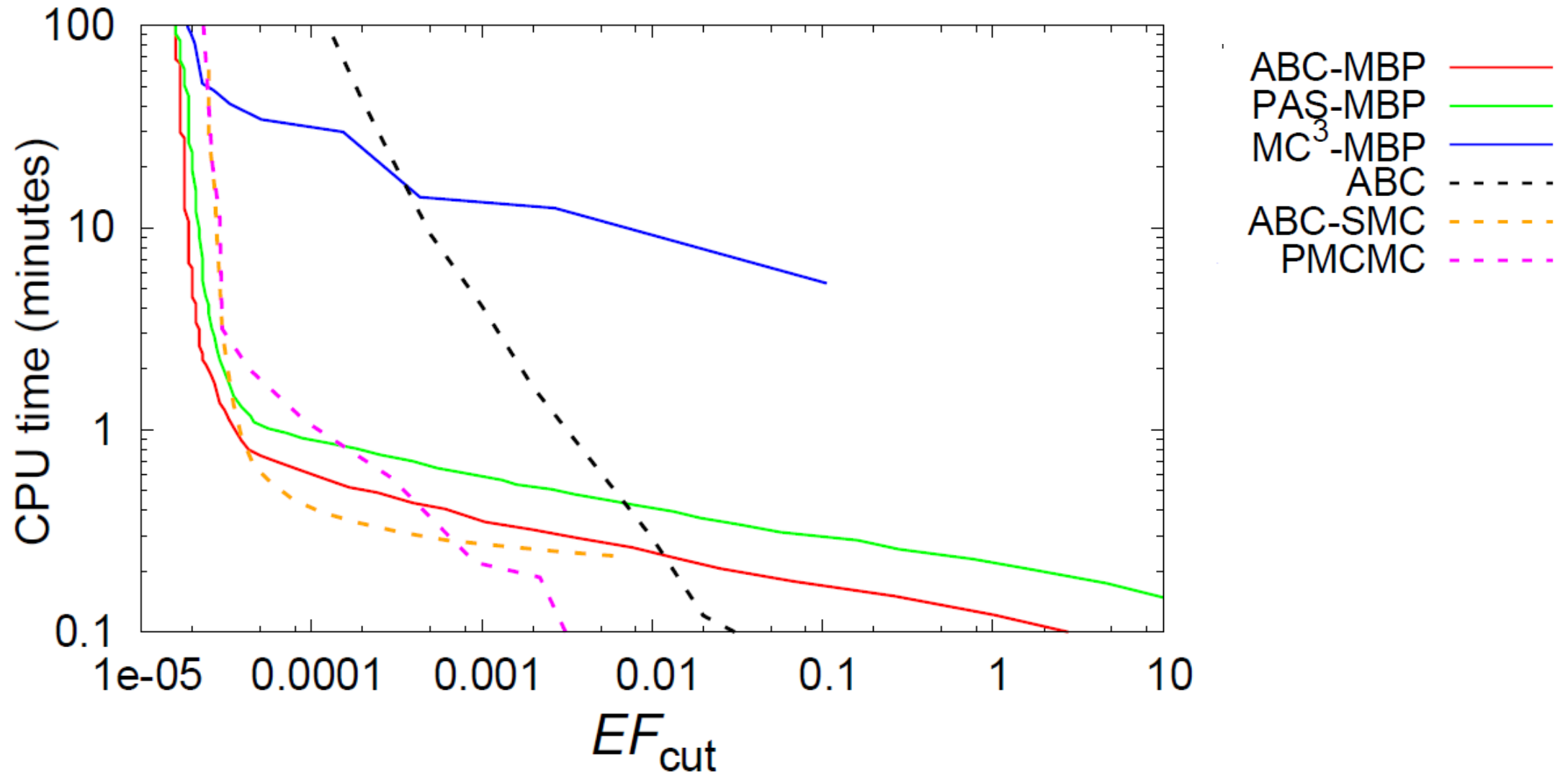
- “Bayesian Estimation of Epidemic Parameters using Model-Based Proposals”
 - Open source software tool for fitting epidemiological models
 - Parallel implementation suitable for HPC
- Supports potential spatial and demographic stratification
- Different data types:
 - Time-series transition data (*e.g.* daily cases)
 - Time-series population data (*e.g.* numbers in hospital)
 - Marginal distributions (*e.g.* age distribution of deaths)



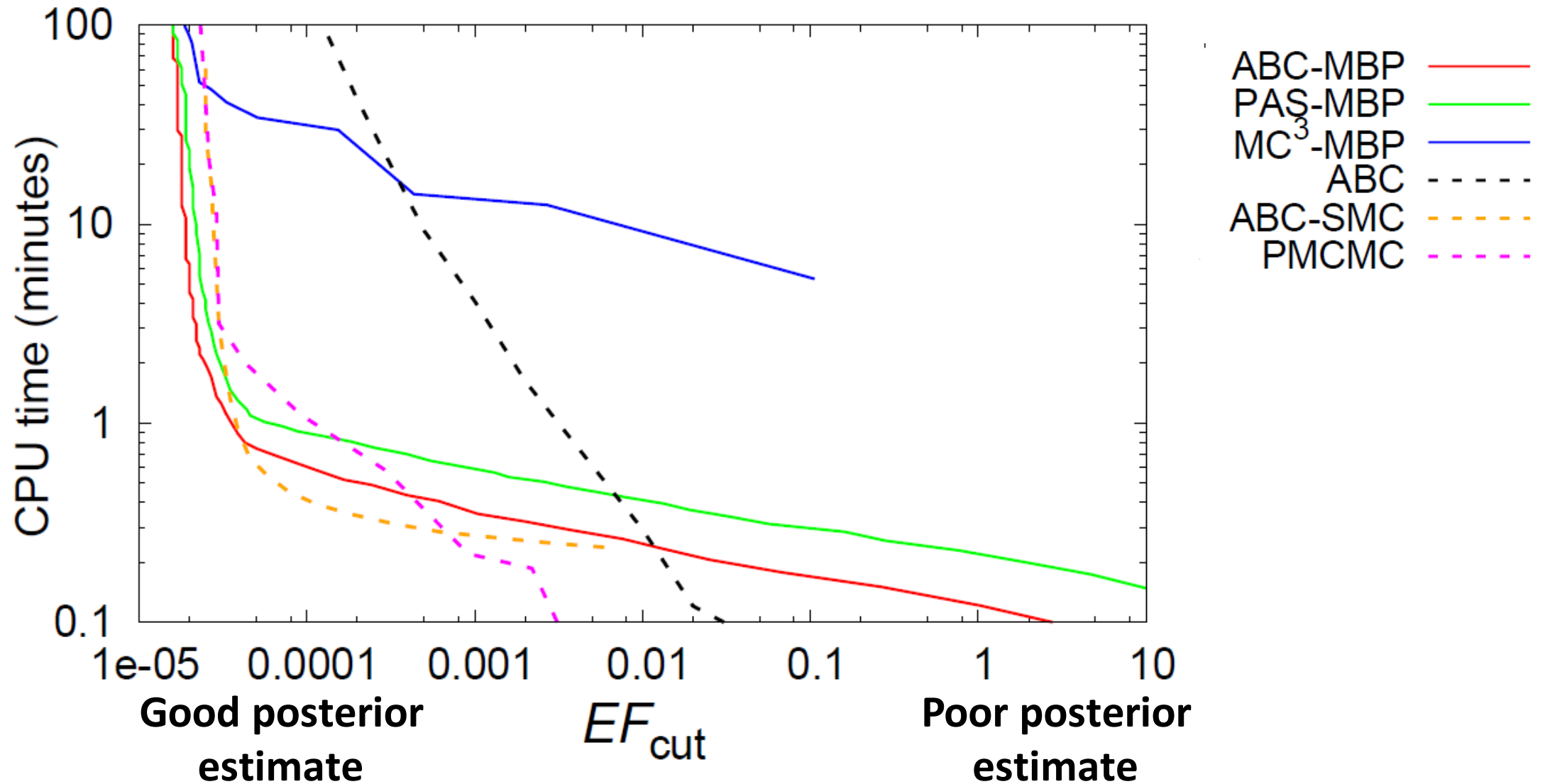
Benchmark models for speed comparison



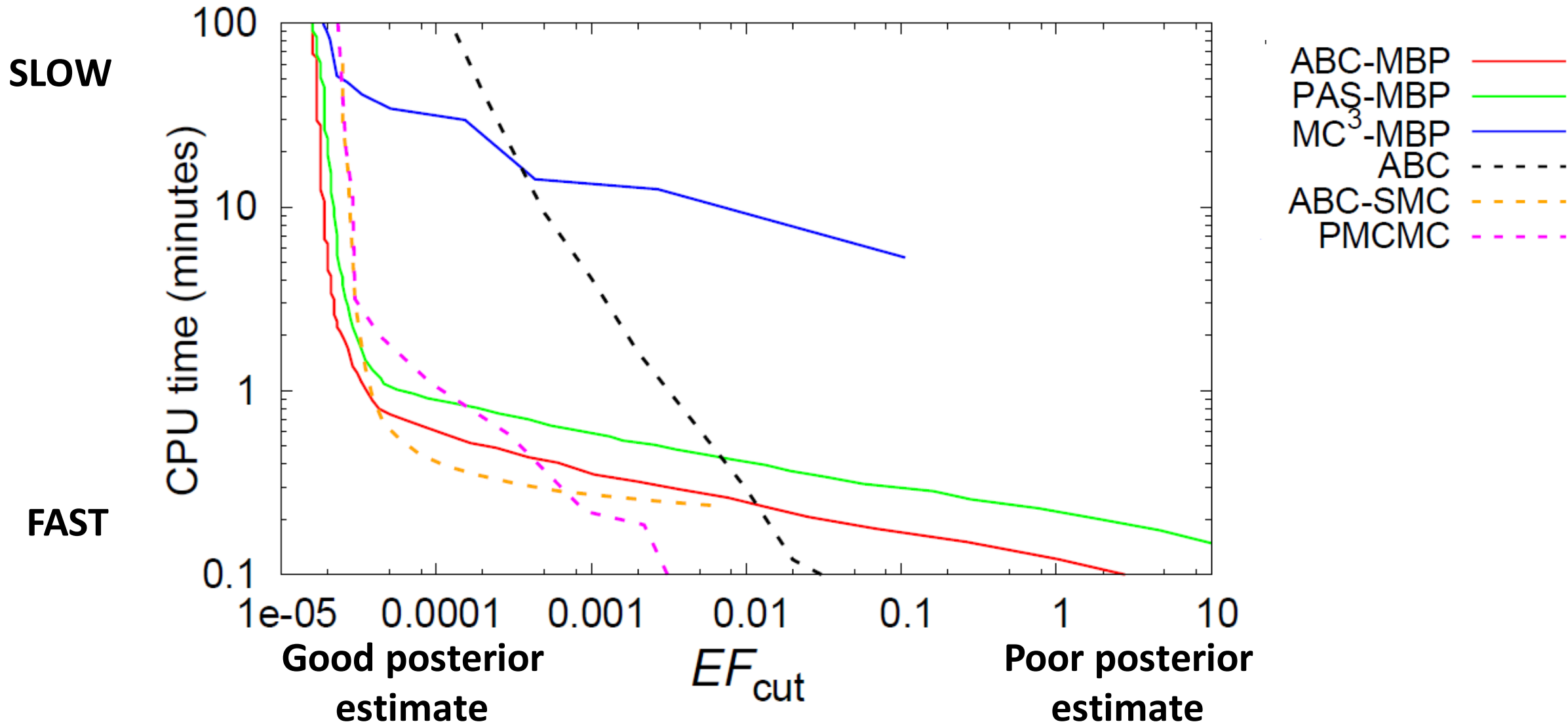
Simple Model: SIR



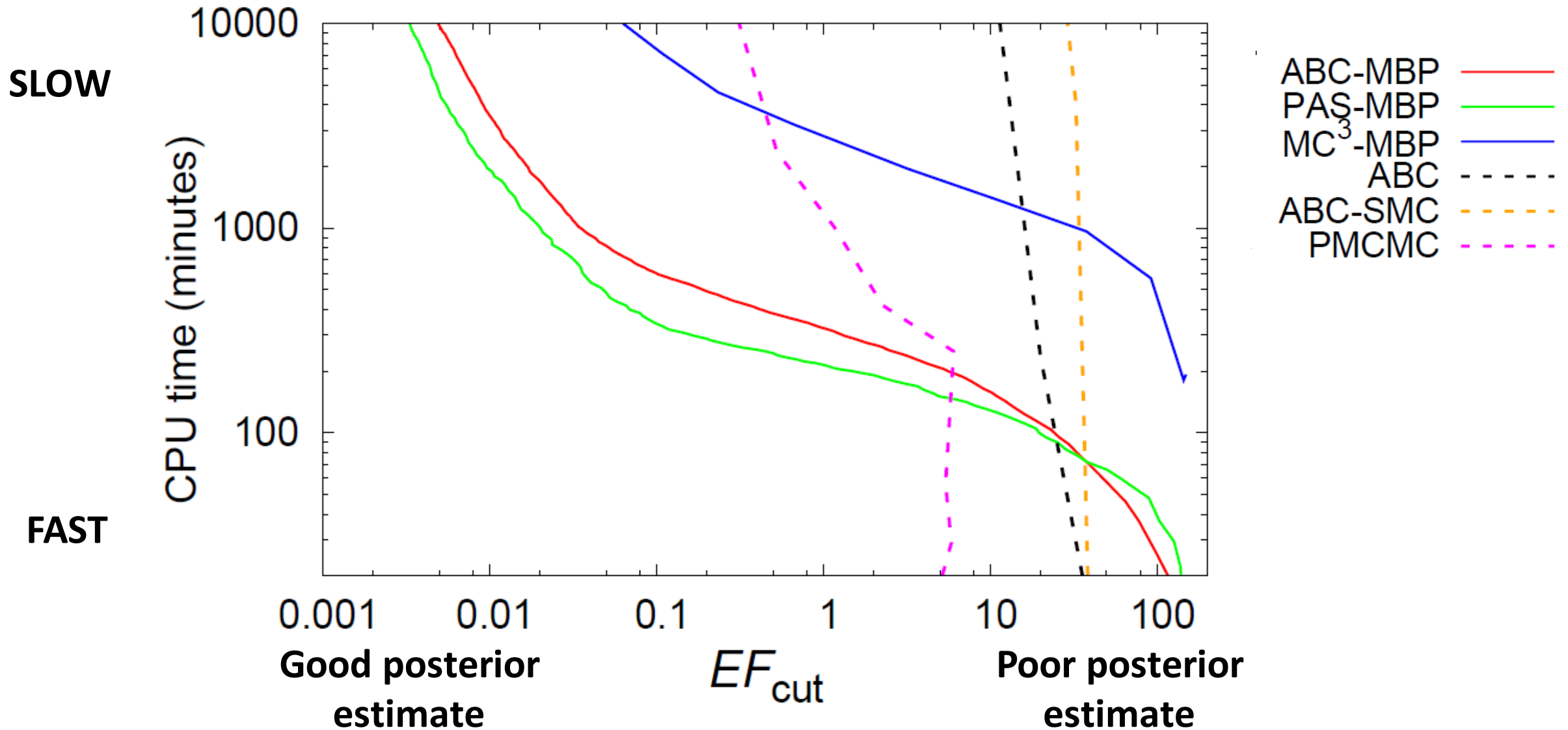
Simple Model: SIR



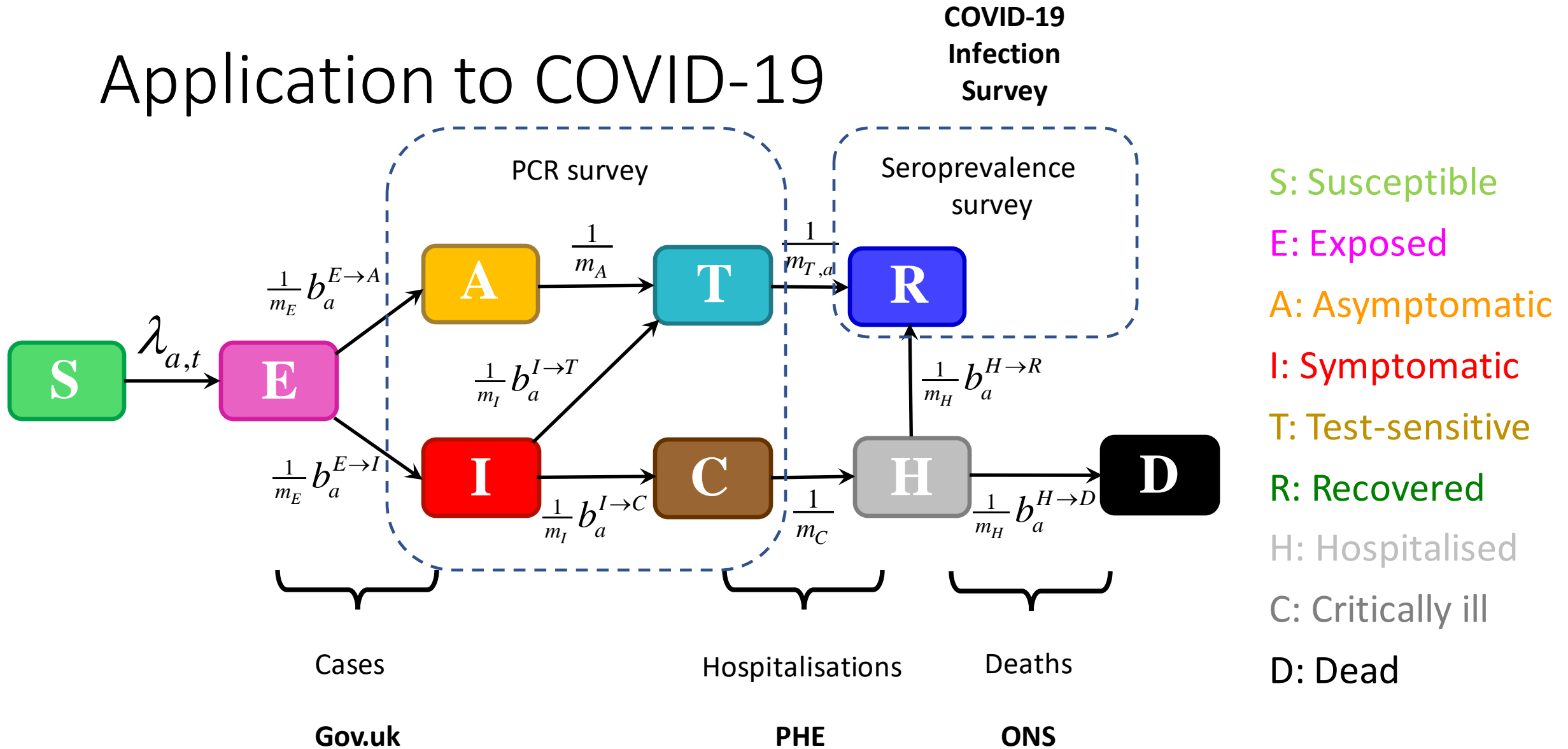
Simple Model: SIR



Complex Model: Spatial SEIR with time variation

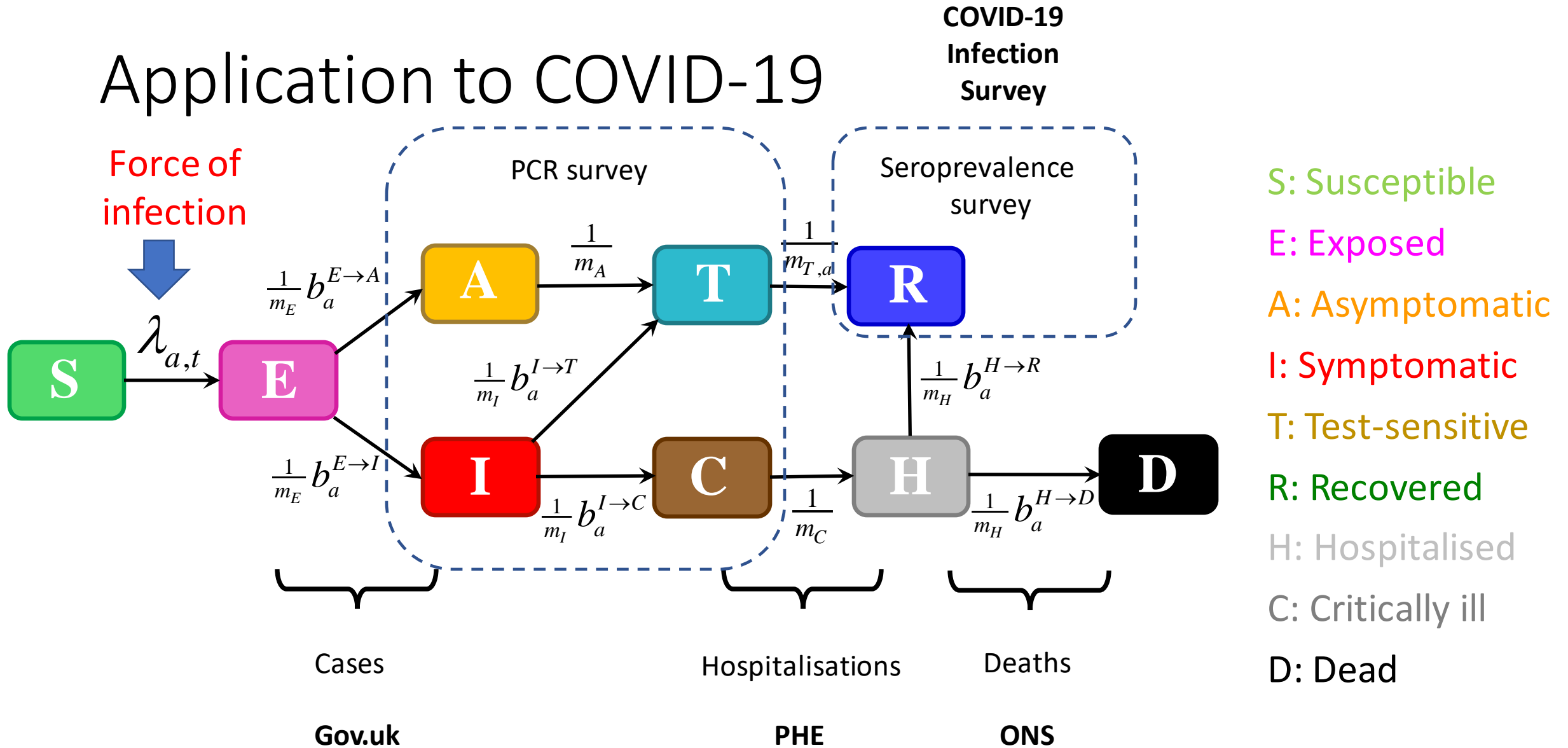


Application to COVID-19



18 age categories $a = \{0-4, 5-9, \dots, 75-79, 80+, \text{Care homes}\}$

Application to COVID-19



18 age categories $a = \{0-4, 5-9, \dots, 75-79, 80+, \text{Care homes}\}$

Force of infection

$$\lambda_{a,t} = \beta \left[\frac{1}{P_a} \sum_{a',c} C_{t,a,a'} \varphi_c N_{c,a',t} \right] + \frac{1}{f} \eta_t$$

Transmission rate

Infectivity of state c

individuals in state c in age group a' at time t

Force of infection in age group a at time t

Age contact matrix

External source of infection

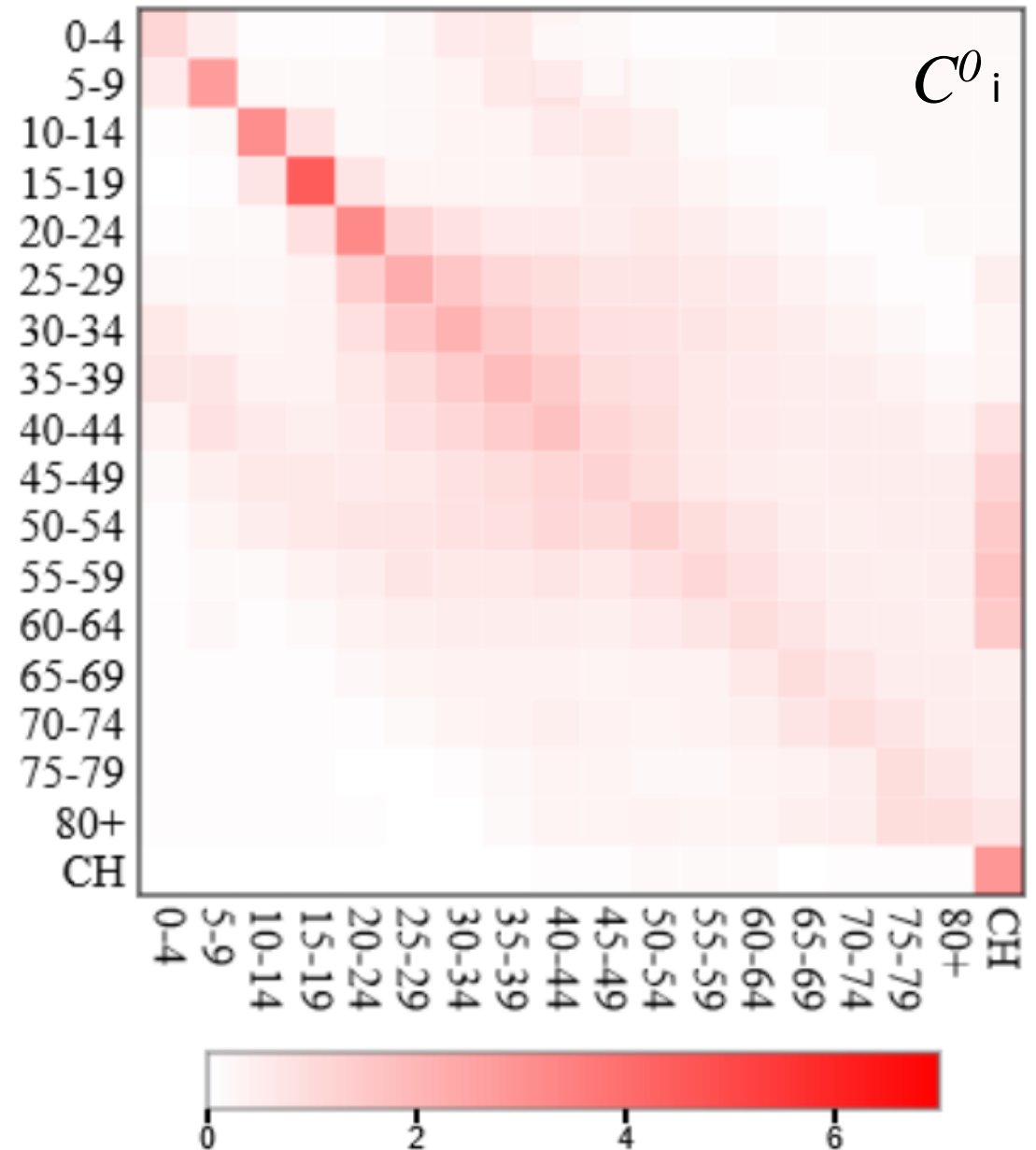
The diagram illustrates the force of infection equation. A blue arrow points from the text 'Force of infection in age group a at time t ' to the variable $\lambda_{a,t}$. Another blue arrow points from 'Transmission rate' to the variable β . A third blue arrow points from 'Age contact matrix' to the term $C_{t,a,a'}$. A fourth blue arrow points from 'Infectivity of state c ' to the variable φ_c . A fifth blue arrow points from '# individuals in state c in age group a' at time t ' to the term $N_{c,a',t}$. A sixth blue arrow points from 'External source of infection' to the term η_t .

Age contact matrix C

- A baseline contact matrix C^0 is taken from the BBC Pandemic! study

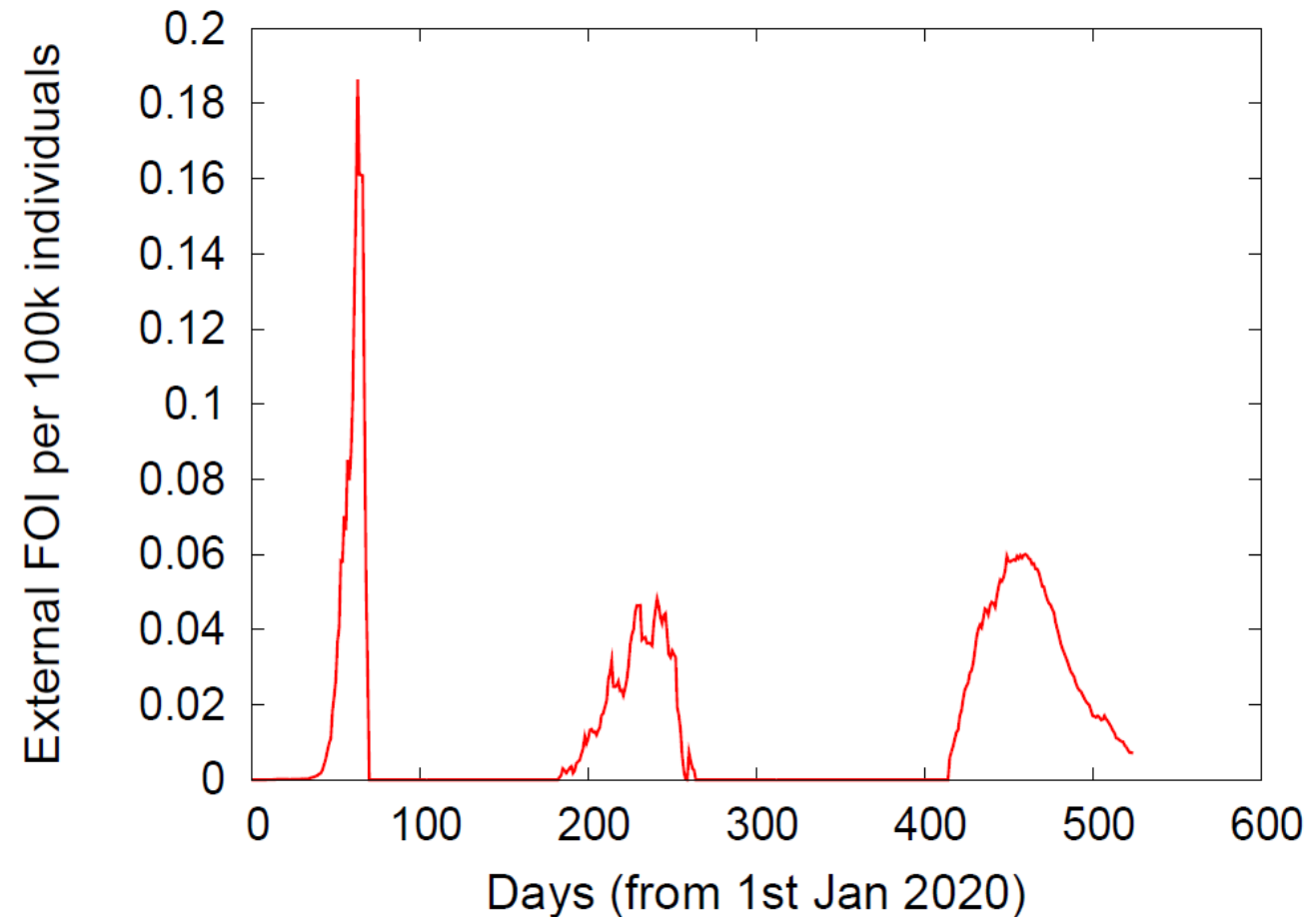
$$C_{t,a,a'} = f_t v_a C^0_{a,a'} v_{a'}.$$

- This is altered by
 - A time varying factor which accounts for government interventions and changing social behaviour
 - Age modifying factor



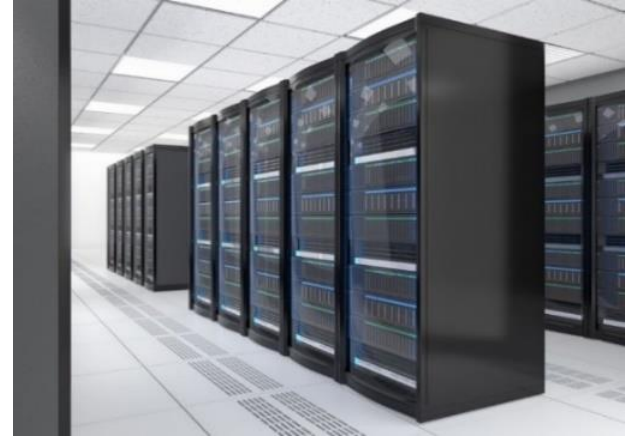
External force of infection η

- COVID-19 enters the UK via individuals moving to and from other countries
- Estimate external force of infection by using:
 - Global flight data from CAA
 - Global Covid-19 data from Johns Hopkins University



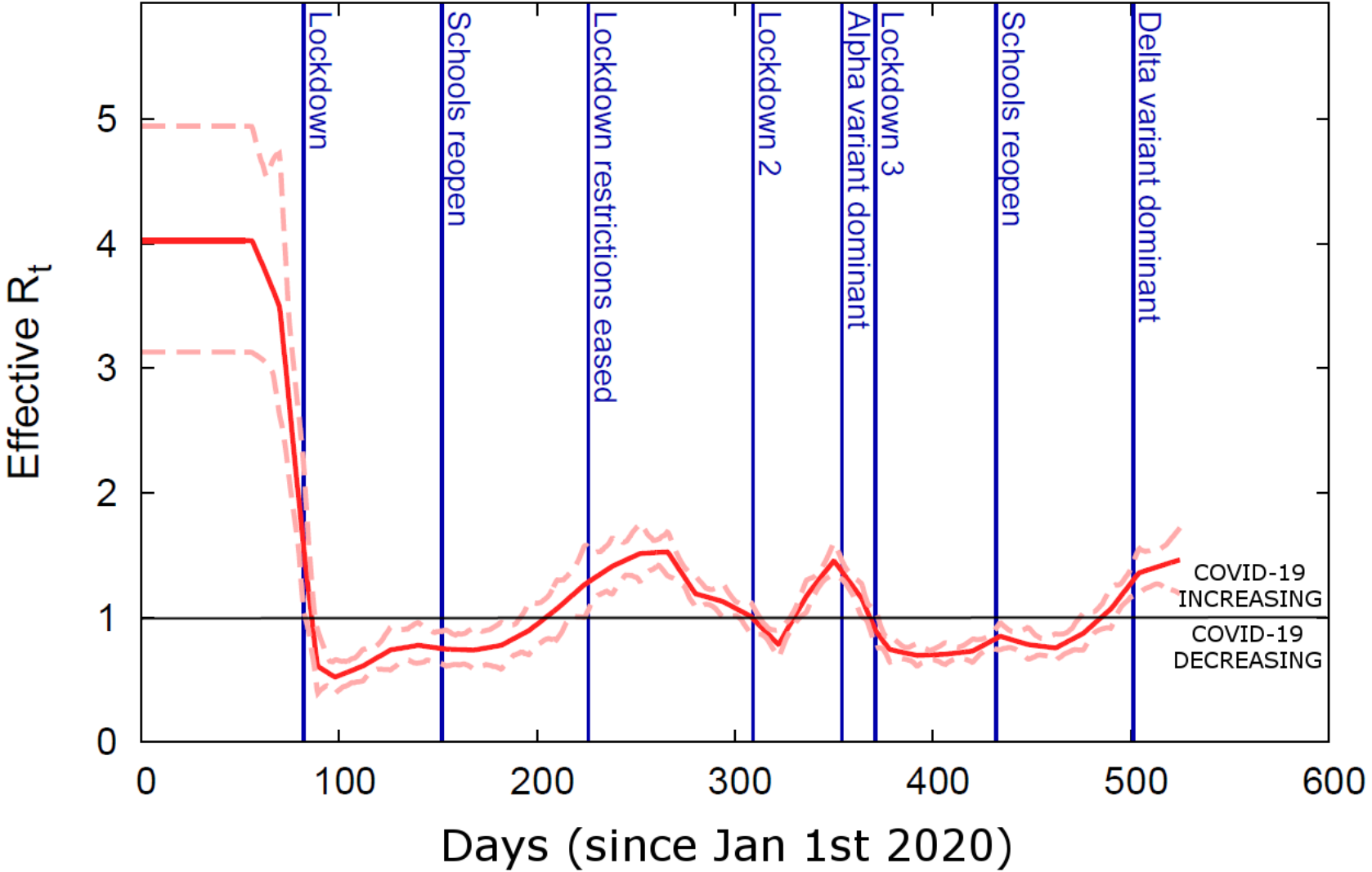
Inference

- Model contains ~150 parameters
- Data contains ~9000 observations in total
 - Spread across many time series
- Inference performed using ABC-MBP
 - DiRAC HPC
 - ~5 hours when running on 256 cores



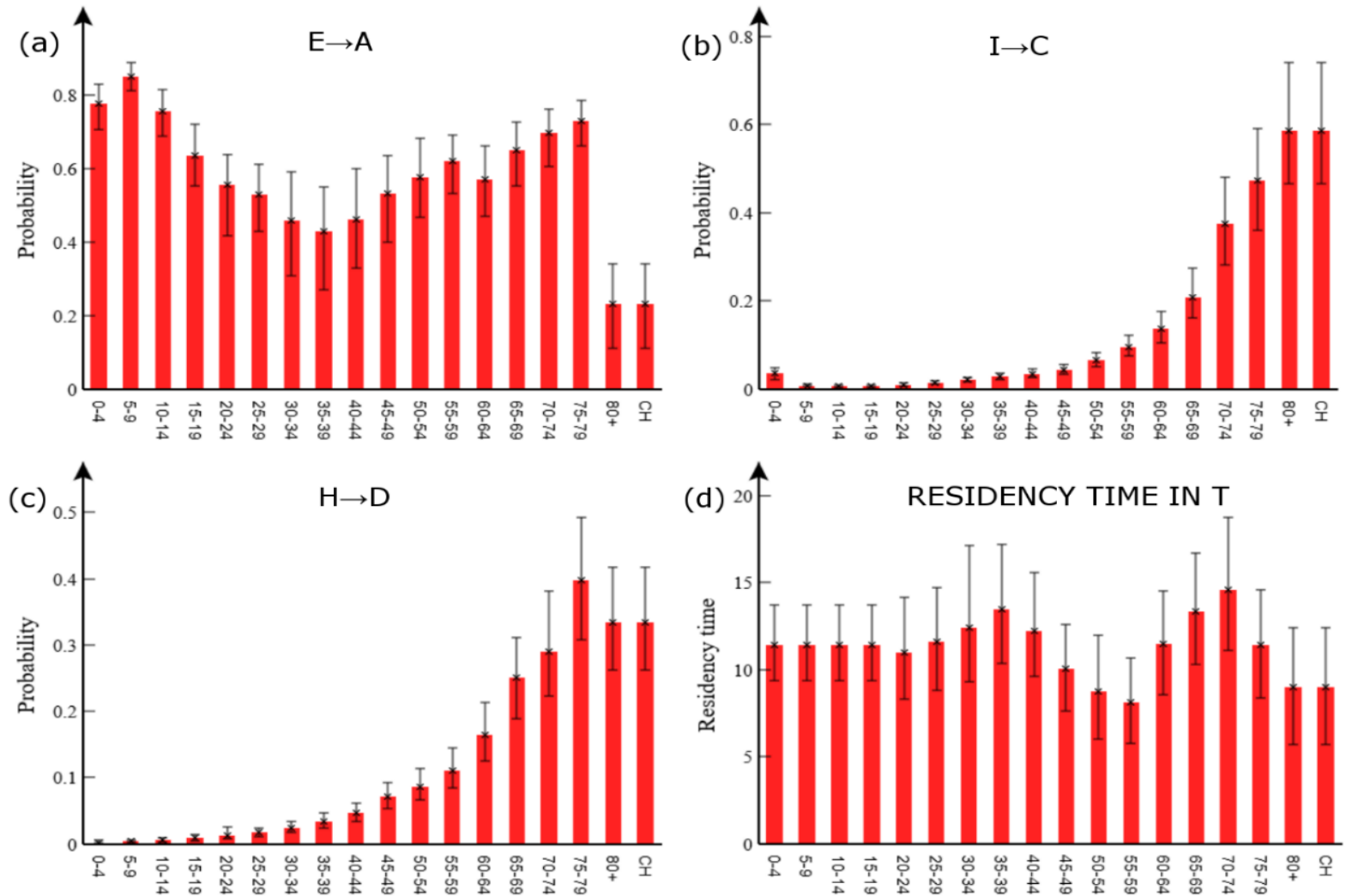
DiRAC

Results: Reproduction number



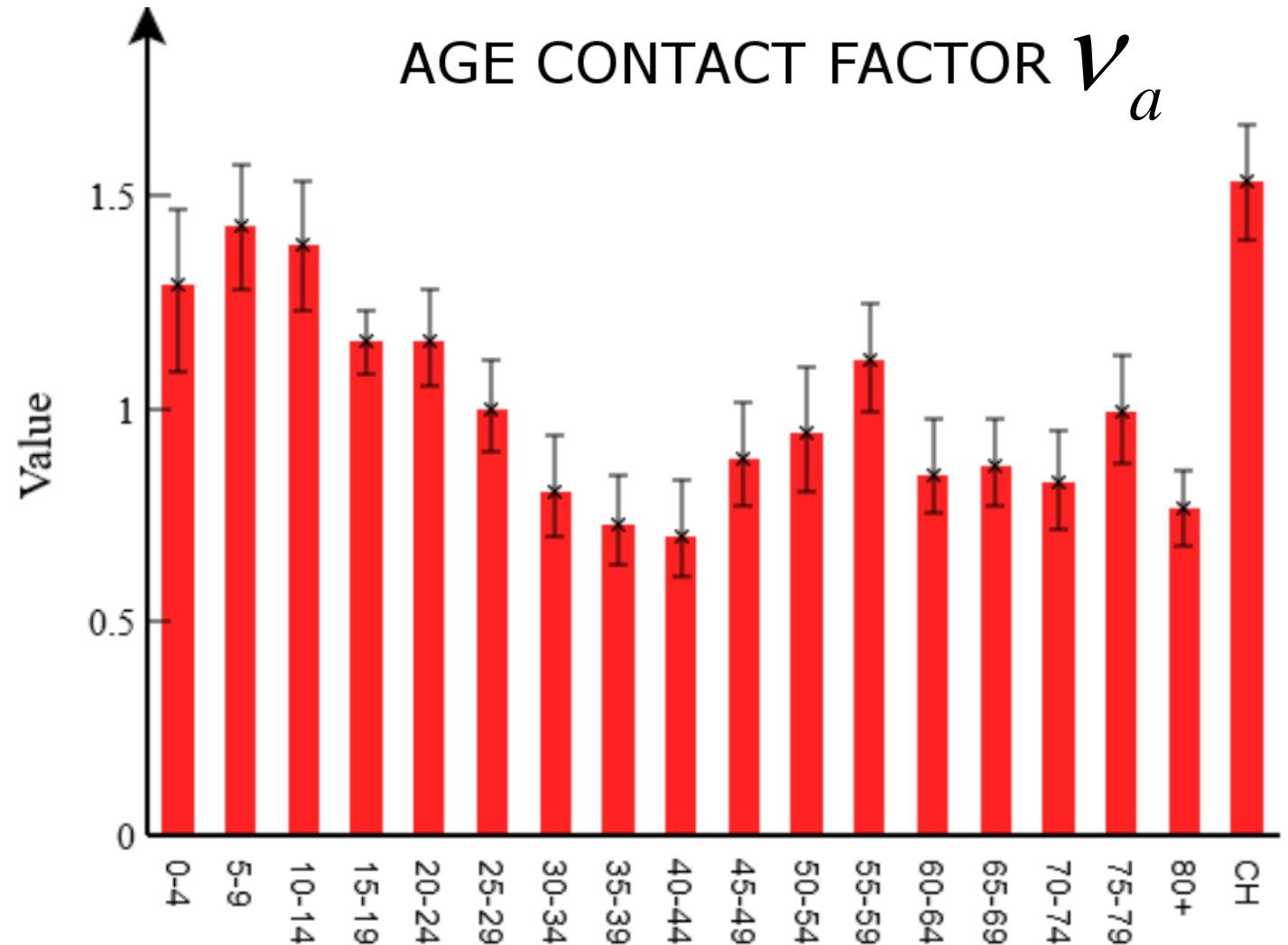
Compartmental parameter estimates

- Obtain a fully parameterised age-structured model
- Improved predictions and simulation studies



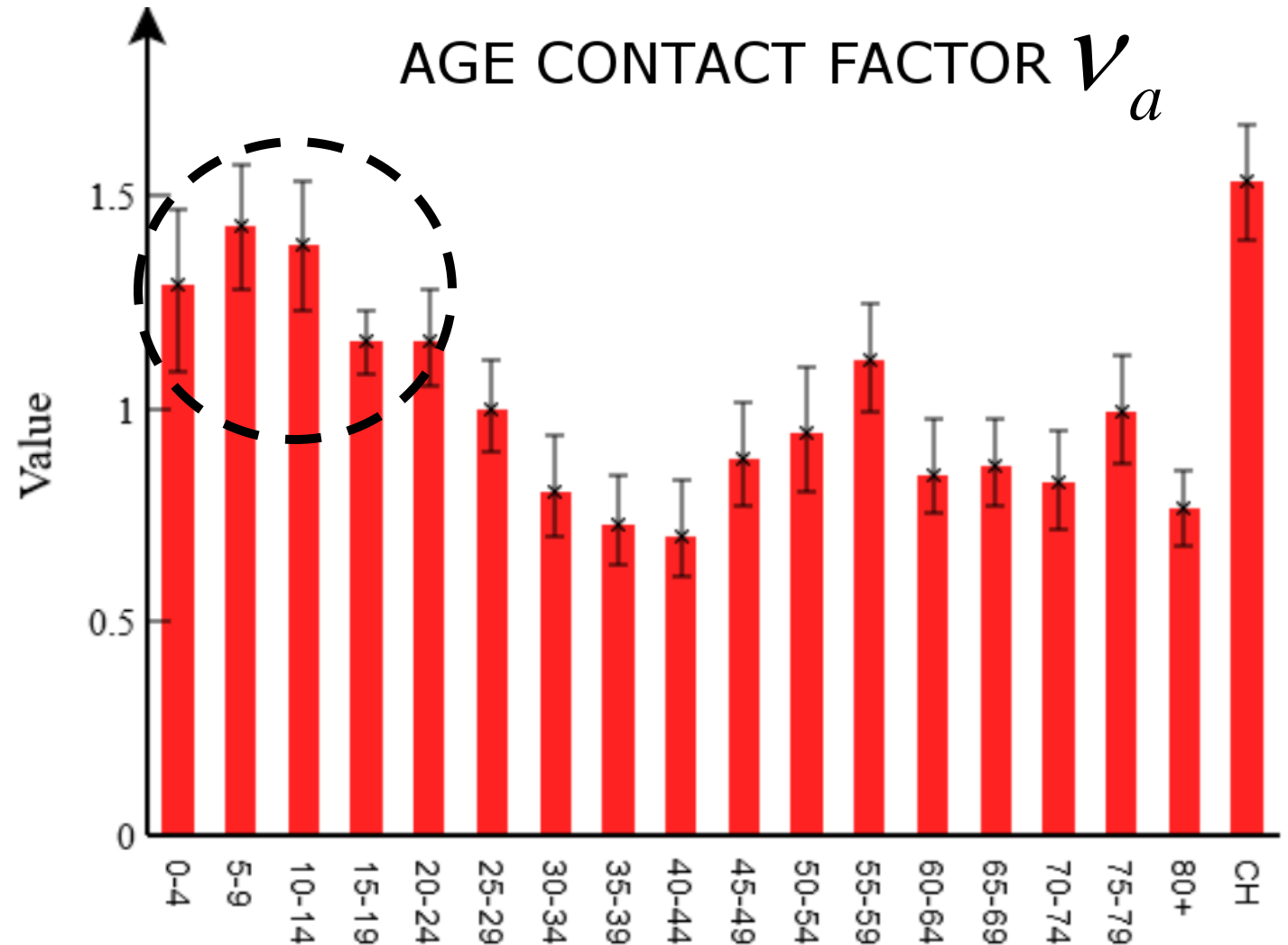
Age contact matrix C

- This shows the relative modification in the contact matrix compared to the expectation obtained from the BBC Pandemic study



Age contact matrix C

- This shows the relative modification in the contact matrix compared to the expectation obtained from the BBC Pandemic study
- We find higher relative rates of effective contacts in younger individuals compared to older individuals



SUMMARY



Summary

- Developed a new inference methodology ABC-MBP
 - Orders of magnitude faster than other existing approaches
 - Generic and not specific to Covid-19 or epidemiology
- Created software tool BEEPmbp
 - Incorporate many inference algorithms
 - Flexible to different model specification and data types
- Application to an age-structure model of Covid-19

Future

- Covid-19 provides a huge data source
 - Many opportunities for new ways to analyse
- Current work...
 - Spatial models nationally and internationally
 - Trying to assess the impact of government interventions and travel restrictions
- What can we apply to the next animal disease outbreak?
- What should we do differently next time?



Acknowledgments



Supervisors:

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Martin Burke (BioSS)

Helen Brown (The Roslin Institute)

RSEs:

Ian Hinder (Manchester)

Robin Williams (Bristol)

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gov.scot

