

Approximate Bayesian Computation

Outline

1. What is Approximate Bayesian Computation?
2. When do we use ABC instead of other methods would we use it?
3. How do we use it?
 - a) Choices in the ABC-rejection algorithm
 - b) Short introduction to more advanced ABC

1. What is Approximate Bayesian Computation?

Bayesian inference is based on the idea of updating belief with new evidence

- **Belief:** Prior distribution. Parameters are random variables instead of fixed quantities (they have their own distribution)
- **Evidence:** Likelihood function tells you the probability of the data given the parameters

Bayesian inference

θ : Mathematical model parameter, D : data

$$P(\theta|D) = \frac{P(D|\theta)P(\theta)}{P(D)}$$

Bayesian inference

θ : Mathematical model parameter, D : Data

$$P(\theta|D) \propto P(D|\theta)P(\theta)$$

Bayesian inference

θ : Mathematical model parameter, D : Data

$$P(\theta|D) \propto P(D|\theta)P(\theta)$$



**Probability of data
given θ (likelihood)**

EVIDENCE

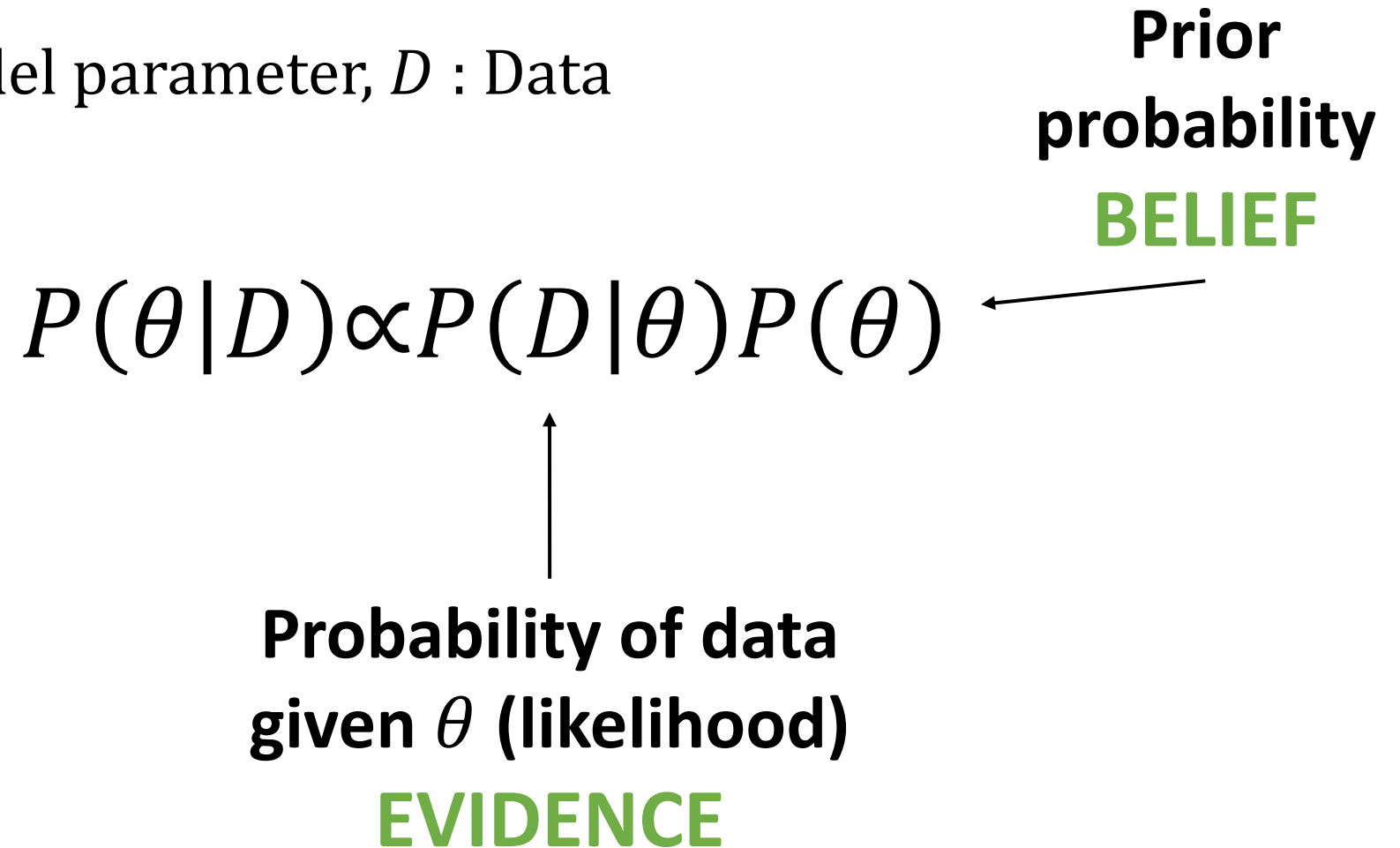
Bayesian inference

θ : Mathematical model parameter, D : Data

$$P(\theta|D) \propto P(D|\theta)P(\theta)$$

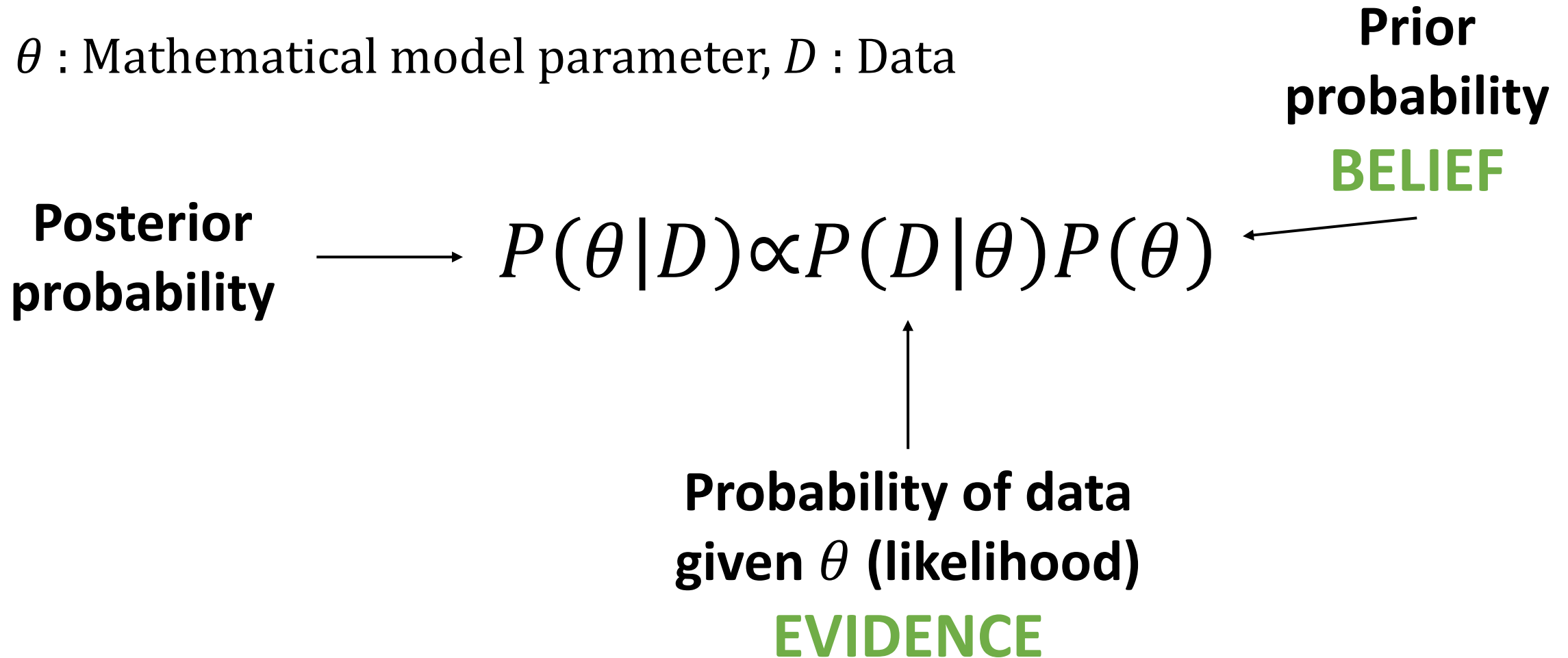
Prior probability
BELIEF

Probability of data given θ (likelihood)
EVIDENCE



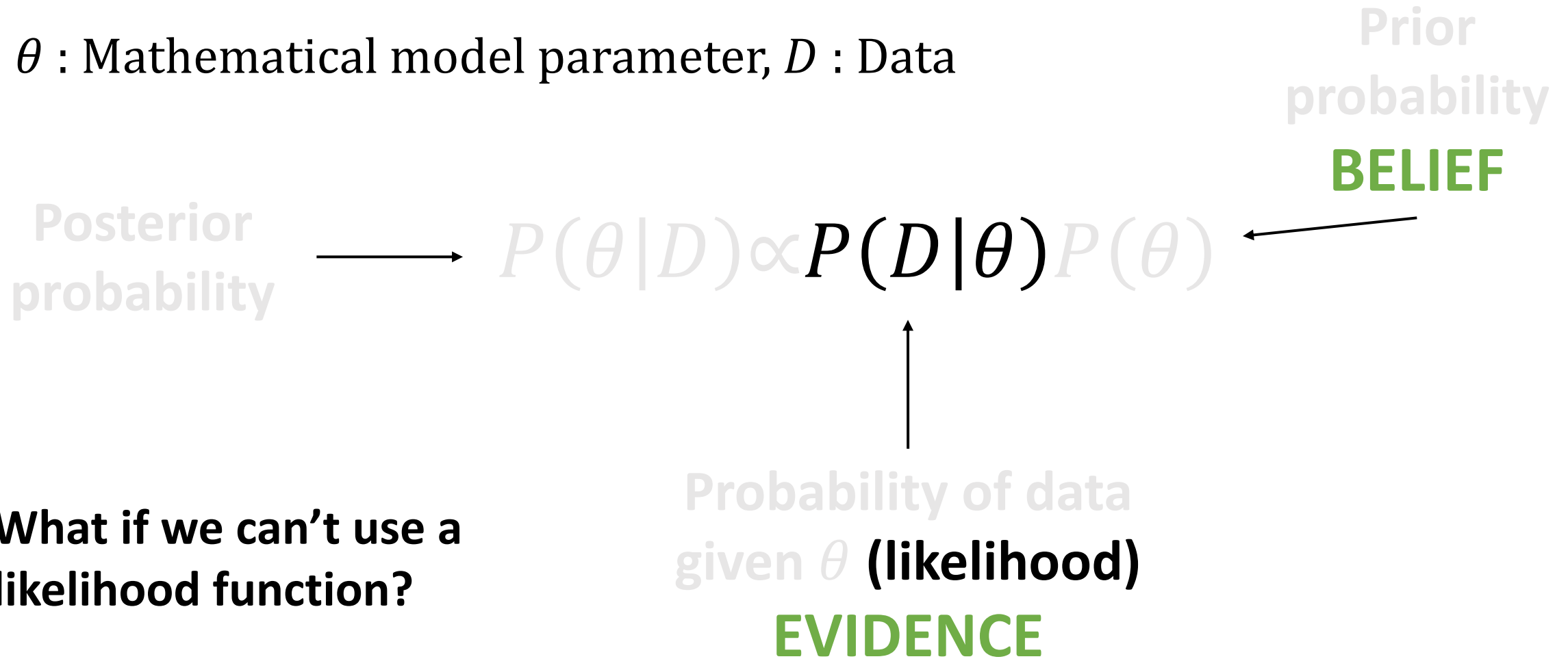
Bayesian inference

θ : Mathematical model parameter, D : Data

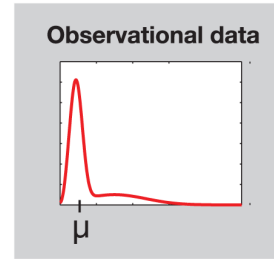


Bayesian inference

θ : Mathematical model parameter, D : Data

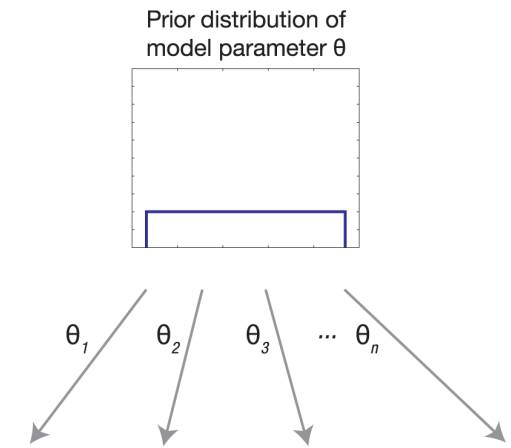
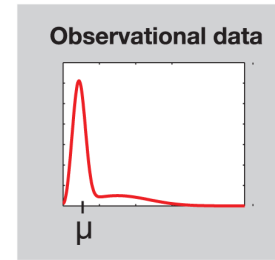


ABC rejection algorithm



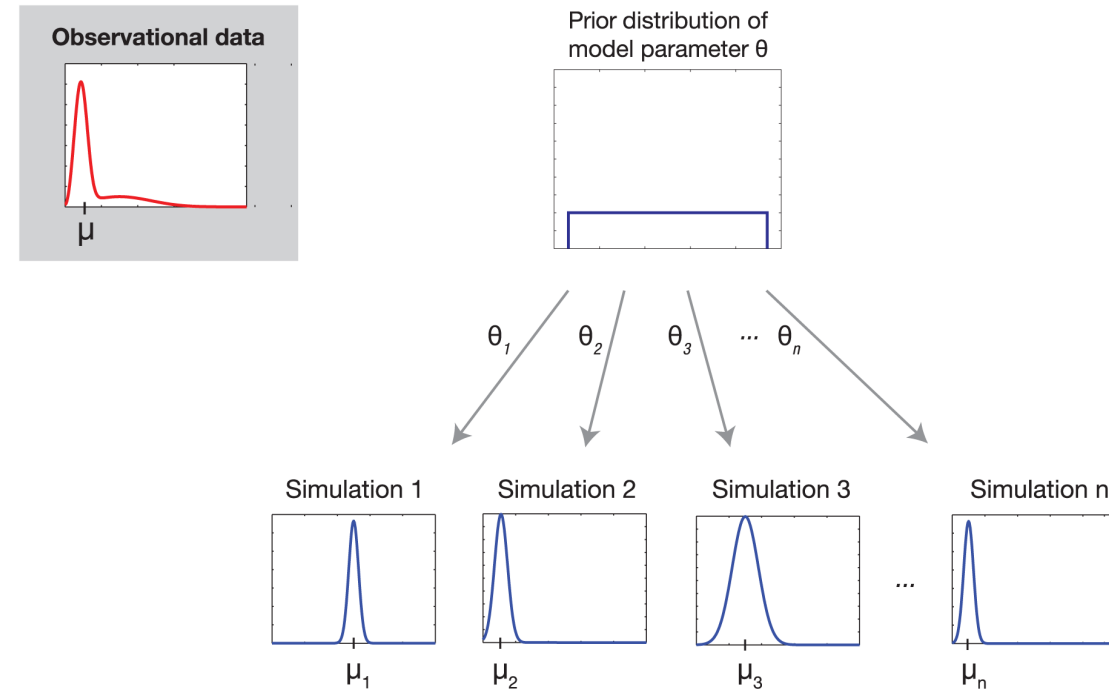
ABC rejection algorithm

1. Sample θ^* from the prior distribution $P(\theta)$



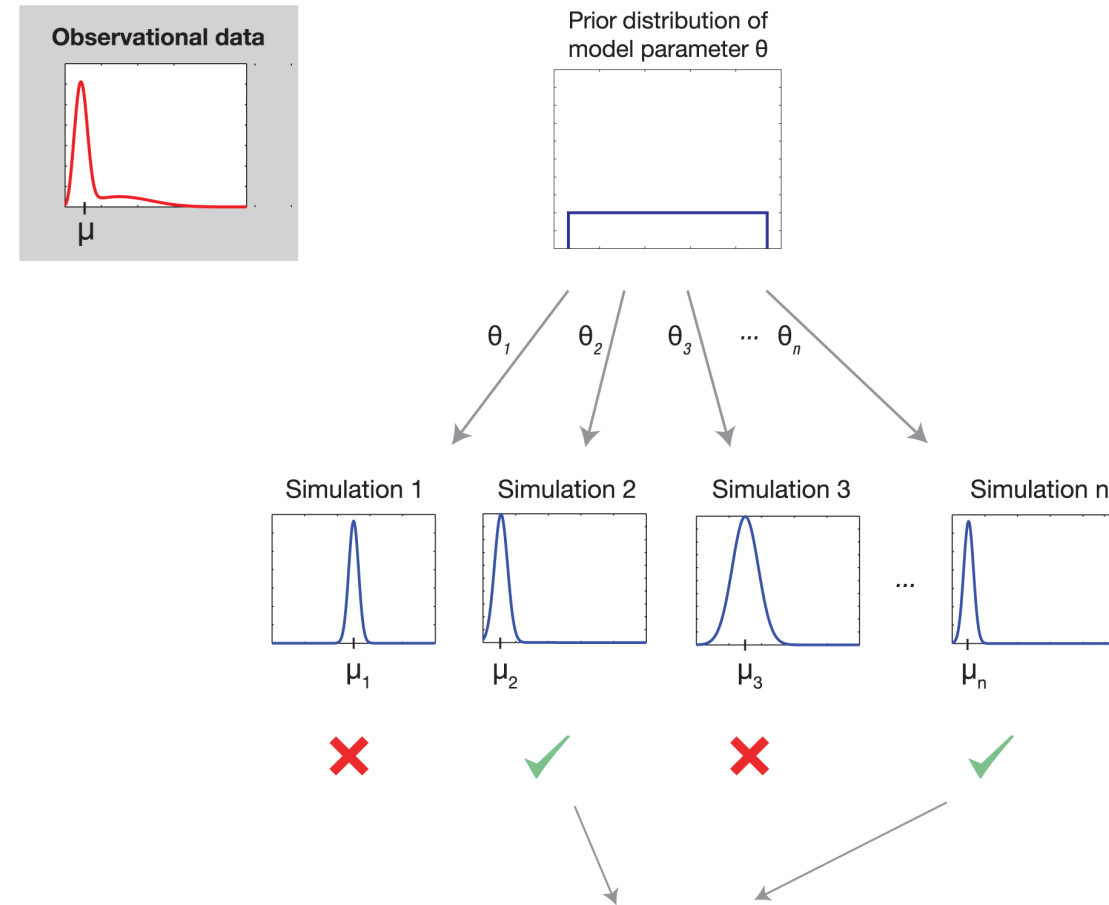
ABC rejection algorithm

1. Sample θ^* from the prior distribution $P(\theta)$
2. Simulate a dataset D^* from your model using θ^*



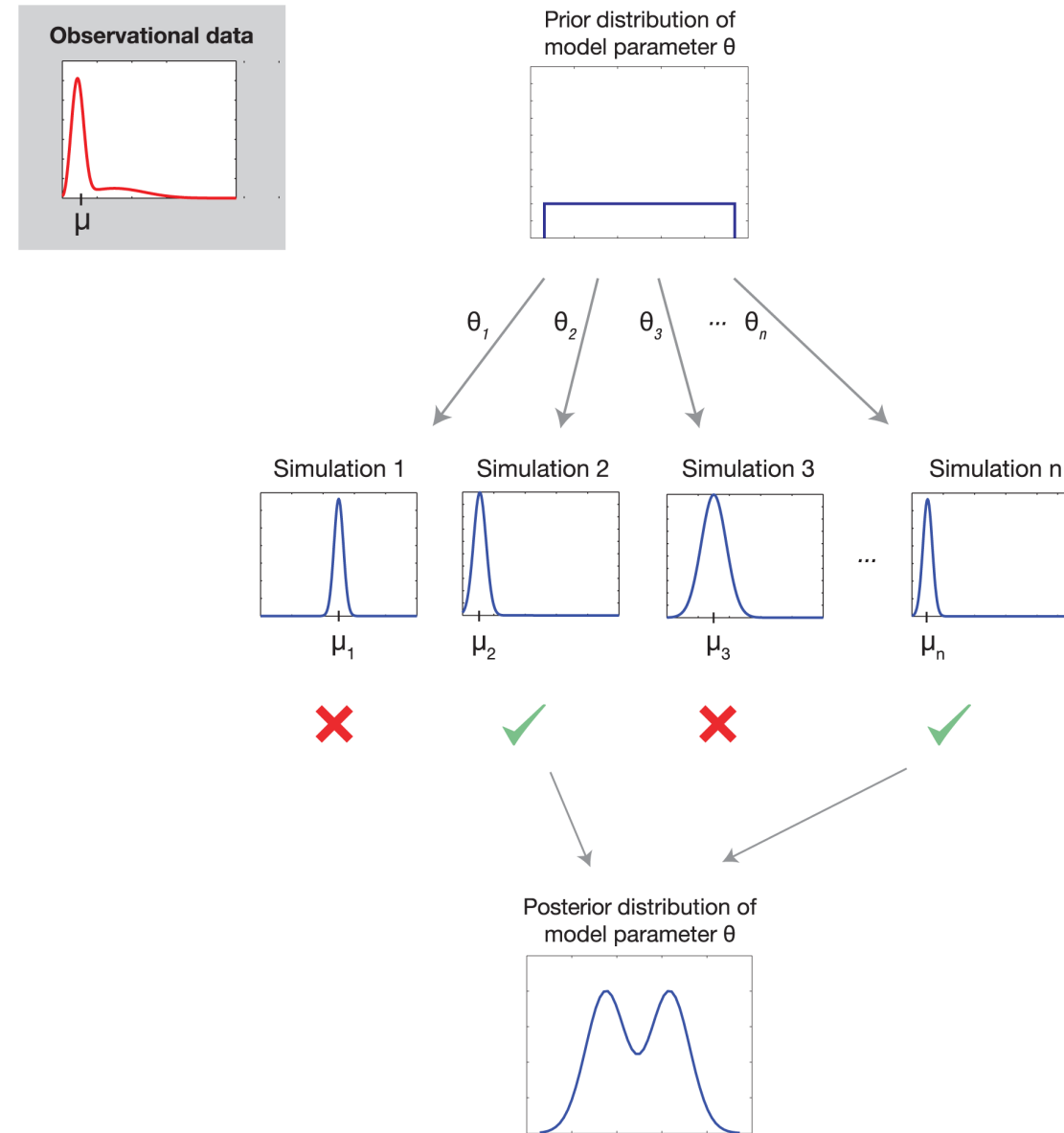
ABC rejection algorithm

1. Sample θ^* from the prior distribution $P(\theta)$
2. Simulate a dataset D^* from your model using θ^*
3. If $d(D, D^*) \leq \epsilon$ accept θ^* , otherwise reject



ABC rejection algorithm

1. Sample θ^* from the prior distribution $P(\theta)$
2. Simulate a dataset D^* from your model using θ^*
3. If $d(D, D^*) \leq \epsilon$ accept θ^* , otherwise reject
4. Repeat until you have accepted N accepted samples



ABC rejection algorithm

1. Sample θ^* from $P(\theta)$
2. Simulate a dataset D^* from your model using θ^*
3. **Calculate the summary statistic for the observed data $\mu = S(D)$ and simulated data $\mu = S(D^*)$**
4. **If $d(S(D), S(D^*)) \leq \epsilon$ accept θ^* , otherwise reject**
5. Repeat until you have accepted N accepted samples

ABC rejection algorithm

1. Sample θ^* from $P(\theta)$
2. Simulate a dataset D^* from your model using θ^*
3. **Calculate the summary statistic for the observed data $\mu = S(D)$ and simulated data $\mu = S(D^*)$**
4. **If $d(S(D), S(D^*)) \leq \epsilon$ accept θ^* , otherwise reject**
5. Repeat until you have accepted N accepted samples



Summary statistic for model trajectory

The diagram illustrates the ABC rejection algorithm. It consists of five numbered steps. Step 3 is highlighted with a blue callout box. Step 4 is also highlighted with a blue callout box. The callout for step 3 points to the text 'Calculate the summary statistic for the observed data $\mu = S(D)$ and simulated data $\mu = S(D^*)$ '. The callout for step 4 points to the text 'If $d(S(D), S(D^*)) \leq \epsilon$ accept θ^* , otherwise reject'.

Distance measure between summary statistic and data

1. What is Approximate Bayesian Computation?

A method to approximate the posterior distribution $P(\theta|D)$ without a likelihood function

$$P(\theta|D) \approx P(\theta|d(S(D), S(D^*))) \leq \epsilon$$

2. When do we use ABC instead of other methods?

2. When do we use ABC instead of other methods?

- Data quality is poor, which means we have to aggregate it
- The likelihood function might be costly to evaluate (it takes a long time)
 - Large data sets
 - Complicated likelihood function

2. When do we use ABC instead of other methods?

- Data quality is poor, which means we have to aggregate it
- The likelihood function might be costly to evaluate (it takes a long time)
 - Large data sets
 - Complicated likelihood function
- Intuitive method of model fitting
 - Parameter \rightarrow model trajectory \rightarrow accept or reject

3. How do we use ABC?

a. Choices in the ABC- rejection algorithm

Choice of summary statistic(s) $\mathbf{S}(\mathbf{D})$

- This is how we choose whether to accept or reject parameter values
- Sufficient summary statistic will give the same result as the likelihood
- "no other statistic that can be calculated from the same sample provides any additional information as to the value of the parameter"

Choice of summary statistic(s) $\mathbf{S}(\mathbf{D})$

- This is how we choose whether to accept or reject parameter values
- Sufficient summary statistic will give the same result as the likelihood
- "no other statistic that can be calculated from the same sample provides any additional information as to the value of the parameter"
- If we haven't written down a likelihood then we can't know if our summary statistics are sufficient...

Choice of summary statistic(s) $\mathbf{S}(\mathbf{D})$

- This is how we choose whether to accept or reject parameter values
- Sufficient summary statistic will give the same result as the likelihood
- "no other statistic that can be calculated from the same sample provides any additional information as to the value of the parameter"
- In practice
 - Look at published model fitting studies using ABC methods for ideas for sufficient statistics
 - **Check with simulated data!**

Number of particles (N)

- The more the better, but computation time must be taken into account

Tolerance value ϵ

- Determines whether you accept or reject parameter(s) based on how closely the model prediction matches you data
 - Too small and the algorithm will take a long time to run
 - Too big and the final distribution of particles will be too wide

Tolerance value ϵ

- Determines whether you accept or reject parameter(s) based on how closely the model prediction matches you data
 - Too small and the algorithm will take a long time to run
 - Too big and the final distribution of particles will be too wide
- The magnitude of the tolerance value ϵ will depend on your distance measure

For example, if the summary of the data $S(D)$ is the cumulative number of cases, we could have:

- $S(D) = 100\,000$ (from the data)
- $S(D^*) = 99\,900$ (model prediction)
- If the distance measure $d()$ is the sum of squared difference the,
$$d(S(D), S(D^*)) = (100\,000 - 99\,900)^2 = (100)^2 = 10\,000$$

The prediction was 100 people short of the data, distance measure is 10 000. Hence here a reasonable choice of tolerance might be $\epsilon = 10\,000$.

3. How do we use ABC?

b. Short introduction to more advanced ABC

Improvements to ABC rejection algorithm: ABC-Sequential Monte Carlo (ABC-SMC)

- Instead of one tolerance ϵ , there is a vector of tolerances $\epsilon_1, \dots, \epsilon_T$
1. We perform ABC rejection with a very large tolerance ϵ_1 and store our N accepted parameter values as population 1.

Improvements to ABC rejection algorithm: ABC-Sequential Monte Carlo (ABC-SMC)

- Instead of one tolerance ϵ , there is a vector of tolerances $\epsilon_1, \dots, \epsilon_T$
1. We perform ABC rejection with a very large tolerance ϵ_1 and store our N accepted parameter values as population 1.
 2. Then we propose parameters by re-sampling parameters from population 1 and perturb the parameters by a small amount. Accept/reject according ϵ_2 .
 3. Add **weight** to each parameter value according to the prior distribution, how likely you were to obtain that value from perturbation and the previous weights.

Improvements to ABC rejection algorithm: ABC-Sequential Monte Carlo (ABC-SMC)

- Instead of one tolerance ϵ , there is a vector of tolerances $\epsilon_1, \dots, \epsilon_T$
- 1. We perform ABC rejection with a very large tolerance ϵ_1 and store our N accepted parameter values as population 1.
- 2. Then we propose parameters by re-sampling parameters from population 1 and perturb the parameters by a small amount. Accept/reject according ϵ_2 .
- 3. Add **weight** to each parameter value according to the prior distribution, how likely you were to obtain that value from perturbation and the previous weights.
 - Repeat steps 2-3 T times, sampling from the previous population. Each time decrease the tolerance value.

Practical

In summary: ABC

- Can be used when data quality is poor, likelihood is complex or unknown and is an intuitive model fitting technique
- ***But*** you have to specify a suitable summary statistic(s)
- ABC can be slow, there are many extensions: ABC-SMC, ABC-PMC etc.

Reading

General introductions

- McKinley, Trevelyan J.; Vernon, Ian; Andrianakis, Ioannis; McCreesh, Nicky; Oakley, Jeremy E.; Nsubuga, Rebecca N.; Goldstein, Michael; White, Richard G. Approximate Bayesian Computation and Simulation-Based Inference for Complex Stochastic Epidemic Models. *Statist. Sci.* 33 (2018), no. 1, 4--18. doi:10.1214/17-STS618.
<https://projecteuclid.org/euclid.ss/1517562021>
- Sunnåker M, Busetto AG, Numminen E, Corander J, Foll M, et al. (2013) Approximate Bayesian Computation. *PLOS Computational Biology* 9(1): e1002803. <https://doi.org/10.1371/journal.pcbi.1002803>
- Hartig, F. , Calabrese, J. M., Reineking, B. , Wiegand, T. and Huth, A. (2011), Statistical inference for stochastic simulation models – theory and application. *Ecology Letters*, 14: 816-827. doi:[10.1111/j.1461-0248.2011.01640.x](https://doi.org/10.1111/j.1461-0248.2011.01640.x)
- **Toni T, Welch D, Strelkowa N, Ipsen A, Stumpf MPH. (2009). Approximate Bayesian computation scheme for parameter inference and model selection in dynamical systems. *J. R. Soc. Interface* 6 187-202; DOI: 10.1098/rsif.2008.0172.**

Reading

Examples of ABC

- Conlan, A.J., McKinley, T.J., Karolemeas, K., Pollock, E.B., Goodchild, A.V., Mitchell, A.P., Birch, C.P., Clifton-Hadley, R.S. and Wood, J.L., (2012). Estimating the hidden burden of bovine tuberculosis in Great Britain. *PLoS Computational Biology*, 8(10), p.e1002730.
- McKinley, T., Cook, A. R. and Deardon, R. (2009). Inference in epidemic models without likelihoods. *Int. J. Biostat.* 5.
- Beaumont MA, Zhang W, and Balding DJ. (2002) Approximate Bayesian Computation in Population Genetics. *GENETICS*. 162 (4) 2025-2035.