

Stochastic models for simulation and inference

Molecular Epidemiology of Infectious Diseases
Lecture 10

March 28th, 2022

The road ahead

Last week: Modeling epidemic dynamics with SIR models

This week: Stochastic models for simulation and inference

Next week: putting everything together with phylodynamic modeling

**Why include
stochasticity in our
models?**

Why include stochasticity?

- To account for true randomness in a process (e.g. rolling dice)
- To account for uncertainty/heterogeneity in a process
- To capture realistic amounts of variability in observed data

Accounting for true randomness

Some processes might be truly random or stochastic (e.g. electrons in quantum theory), but this is scientifically and philosophically debatable.

Rather, it is often convenient to model a physical process as random.

Example: we model the outcome of rolling dice as a random variable because the physics required to model this deterministically is very complicated and would require us to know a lot of information.

“I, in any case, am convinced He [God] **does not play dice** with the **universe**.”

Einstein (1926)

Accounting for uncertainty

We often model processes at much smaller and larger scales than we are interested in using *phenomenological models*.

Example: The transmission rate of a foliar pathogen from one plant to another could be modeled mechanistically if we knew a lot about the number of spores on each leaf, spore viability, relative humidity, wind speeds, ect.

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In this sense, stochasticity is a hedge against our own ignorance.

Capturing variability in data

Empirical data often include much more heterogeneity and variability than our simple deterministic models would suggest.

Including stochasticity in our models allows us to account for this variability when performing statistical inference.

Simulating data often requires us to add randomness in order to generate an ensemble of different possible outcomes.

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**How do we include
stochasticity in our
models?**

Different types of stochasticity

Observational noise: error in our observations that don't actually affect the process under study (e.g. misreporting of infections).

Example: Normally distributed noise or errors in linear regression:

$$y = \beta x + \epsilon$$

Different types of stochasticity

Observational noise: error in our observations that don't actually affect the process under study (e.g. misreporting of infections).

Process noise: randomness in a process that changes the dynamic behavior of the system under study.

Environmental noise: internal or external perturbations (e.g. climatic factors like relative humidity affecting transmission rates).

Demographic stochasticity: randomness in the timing and outcome of individual events at the individual level (e.g. the time at which a given individual is born and dies).

Modeling environmental noise

Environmental stochasticity is normally modeled as random noise due to external factors entering our model:

For dynamical systems like SIR models, we can add noise to the rates of change using stochastic differential equations:

$$\frac{dI}{dt} = \beta SI - \gamma I + \xi \beta SI$$

ξ is a “noise” increment, generally a random Normal variate.

Modeling demographic stochasticity

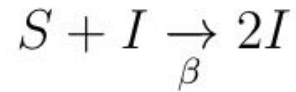
Demographic stochasticity requires us to consider randomness in the timing and outcome of individual events.

Individuals are treated as discrete (whole) units, so that the number of individuals is always an integer.

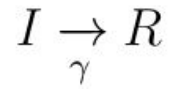
We can think about individual events as resulting from reactions involving one or more individuals.

Modeling demographic stochasticity

For a stochastic SIR model, we have transmission events resulting from the interaction of susceptible and infected hosts:



Recovery events convert infecteds into recovered hosts:



Event driven simulation

If we want to simulate with demographic stochasticity for a population with many individuals and competing events/reactions, we can use the following general approach:

1. Simulate or draw the time of the next event.
2. Choose type of event that occurs at that time
3. Update the time and the population states to reflect any changes in the number of individuals of each type.

Step 1: Finding the next event time

To draw the time of the next event we:

- a) First compute the rate of each reaction or event type:

$$\lambda_T = \beta SI \qquad \lambda_R = \gamma I$$

- b) Sum the individual rates to find the total rate:

$$\lambda_{Total} = \lambda_T + \lambda_R$$

- c) Draw the time to the next event from an exponential distribution:

$$\text{Time to next event} = \Delta_t \sim \text{Exponential}(\lambda_{Total})$$

Step 2: Choose the event type

In order to choose what type of event occurs we:

- a) Find the relative probability of each event type:

$$P(\text{Transmission}) = \frac{\lambda_T}{\lambda_T + \lambda_R}$$

$$P(\text{Recovery}) = \frac{\lambda_R}{\lambda_T + \lambda_R}$$

- b) Choose the event type according to the relative probability of each event (i.e. a single draw from a multinomial distribution).

Step 3: Update time and states

Update the system by moving ahead to the next event time and updating the appropriate population states.

For example, if the next event is a transmission event we set:

$$t \rightarrow t + \Delta t$$

$$S \rightarrow S - 1$$

$$I \rightarrow I + 1$$

Event driven simulation

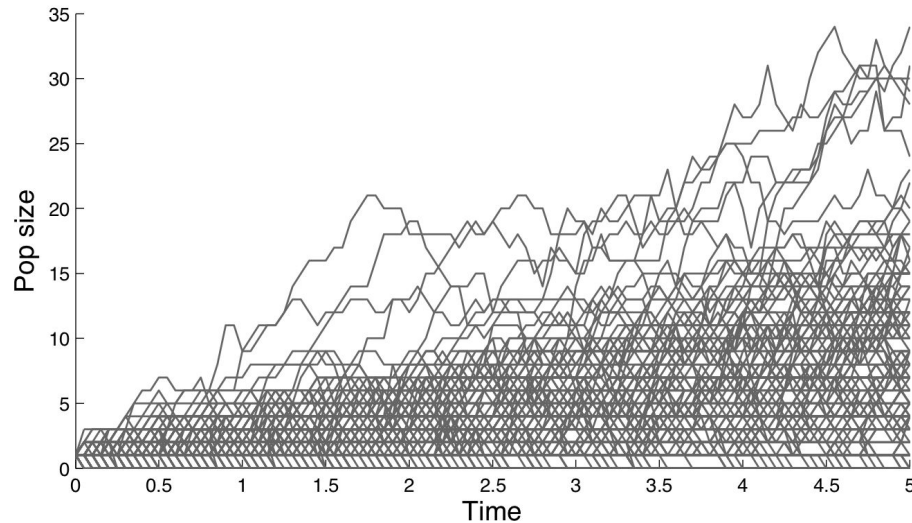
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This process is repeatedly iterated until some *end condition* is met.

Stochastic epidemic dynamics

Stochasticity is especially important when populations are small and individual events have a large effect on the overall dynamics.



The general SSA

The general stochastic simulation algorithm (SSA) can be used to simulate any continuous time, discrete state Markov process. It is sometimes referred to as the Gillespie algorithm (Gillespie, 1977).

- 1.) Label all events E_1, E_2, \dots, E_N
- 2.) Compute the rate λ_i of each event type i
- 3.) Compute the total rate λ_{Total} by summing the individual rates.
- 4.) Draw the next event time from an exponential distribution with rate λ_{Total}
- 5.) Choose event type E according to the relative event probabilities
- 6.) Update time and states

**The stochastic
simulation algorithm
can be used to
simulate just about
everything!**

Applications of the SSA

We can apply the SSA to simulate:

- Epidemic dynamics with stochasticity
- Phylogenetic and transmission trees
- Molecular evolution for sequence data

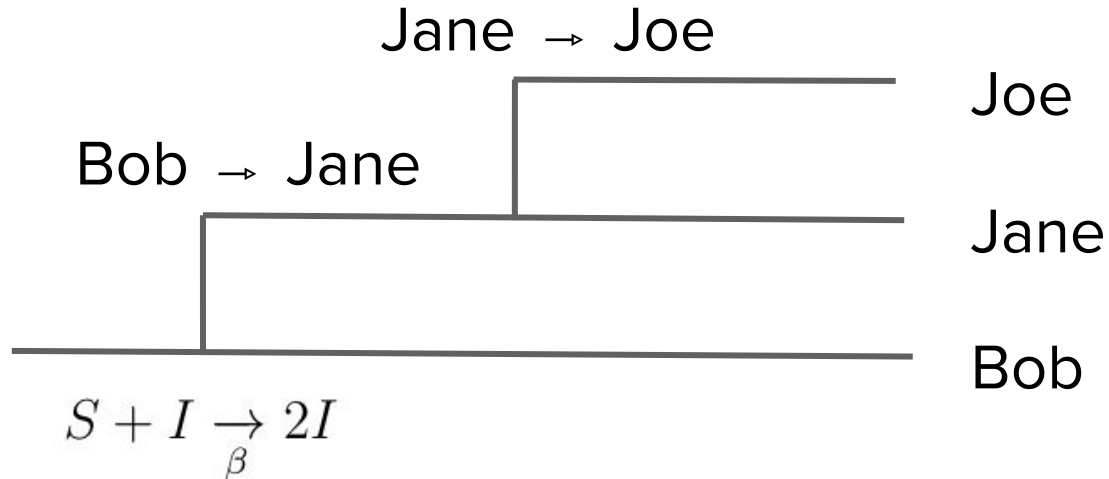
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We can apply the SSA to simulate:

- Epidemic dynamics with stochasticity
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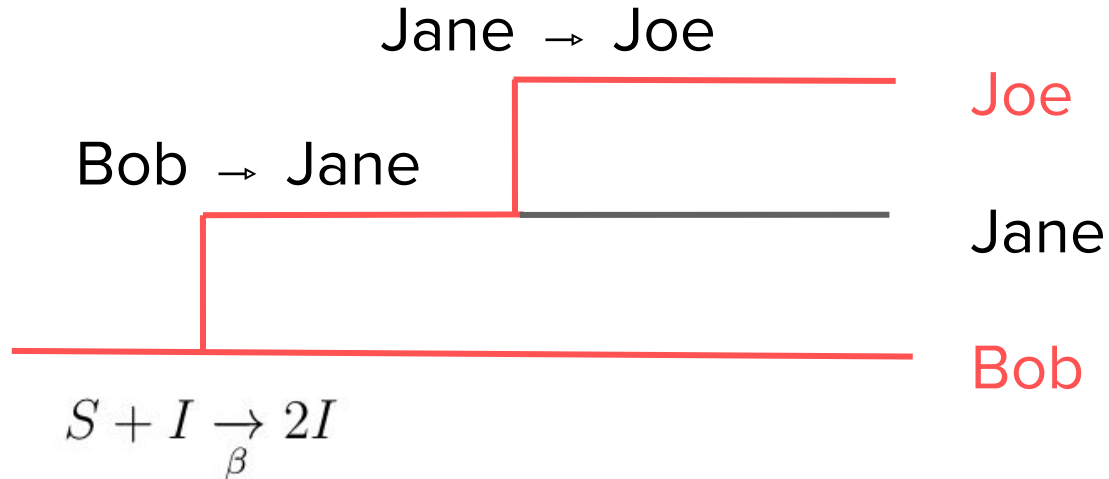
Simulating transmission trees

We can simulate the transmission tree while simulating epidemic dynamics under the SSA by recording the ancestry of the population in terms of parent child relationships:



Simulating transmission trees

We can then trace the ancestry of sampled individuals backwards through time to obtain the transmission tree:



Simulating trees and epidemics

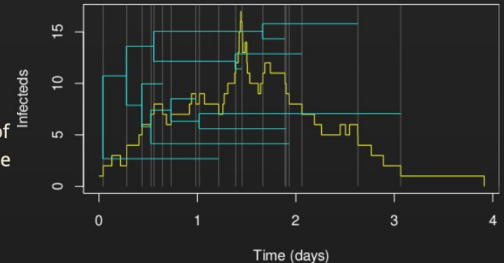
MASTER is a BEAST 2 package that allows for efficient stochastic simulation of population dynamics and trees.

MASTER

Moments and Stochastic Trees from Event Reactions

Project maintained by [Tim Vaughan](#)

MASTER is a software package aimed at providing a general means of creating simulators for stochastic models of structured and unstructured population dynamics. It also supports the simulation of inheritance trees and networks under these same models.



Installation

MASTER is a **BEAST 2** package and can therefore be installed easily from within BEAUti. Simply download and install the latest version of BEAST 2 from the [web site](#), open BEAUti, then choose "File->Manage Packages" and select MASTER from the package list that appears. MASTER simulations can then be run by simply running BEAST and selecting the MASTER-specific XML input file.

Simulating trees and epidemics

MASTER is a BEAST 2 package that allows for efficient stochastic simulation of population dynamics and trees.

Events are specified as “reactions” in an input XML file.

```
<run spec='Trajectory'
      simulationTime='50'>

  <model spec='Model' id='model'>
    <population spec='Population' id='S' populationName='S'/>
    <population spec='Population' id='E' populationName='E'/>
    <population spec='Population' id='I' populationName='I'/>
    <population spec='Population' id='R' populationName='R'/>

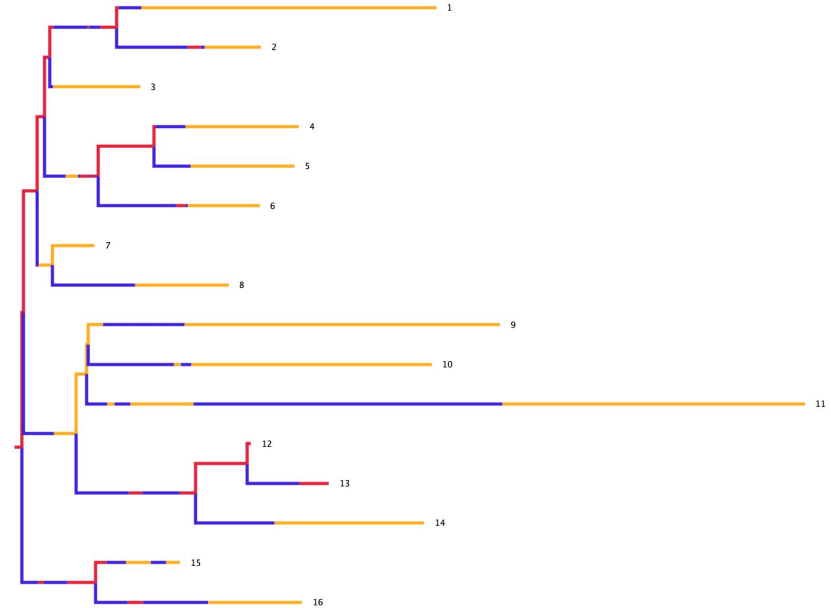
    <reaction spec='Reaction' reactionName="Infection" rate="0.05">
      S + I -> I + E
    </reaction>
    <reaction spec='Reaction' reactionName="Incubation" rate="0.4">
      E -> I
    </reaction>
    <reaction spec='Reaction' reactionName="Recovery" rate="0.2">
      I -> R
    </reaction>
  </model>
</run>
```

Simulating trees and epidemics

MASTER is a BEAST 2 package that allows for efficient stochastic simulation of population dynamics and trees.

Events are specified as “reactions” in an input XML file.

Epidemic dynamics and trees are saved as output.



Packages for simulating trees

Popular choices include:

- MASTER <https://tgvaughan.github.io/MASTER/>
 - Forward-time stochastic simulations of epidemics and trees
 - Very flexible model specification (e.g. easy to add different types of hosts))
- msprime <https://tskit.dev/msprime>
 - Backwards-time coalescent simulator
 - Allows for different (deterministic) demographic histories
 - Great for simulating ARGs and sequences with recombination

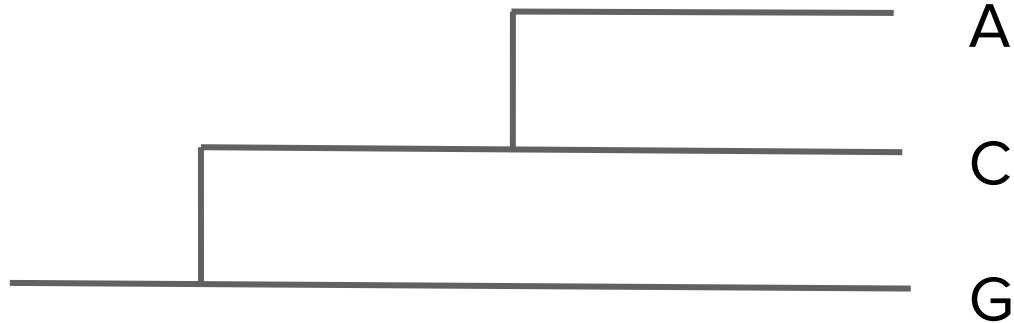
Applications of the SSA

We can apply the SSA to simulate:

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Simulating sequences on trees

We can use the SSA to simulate molecular evolution along each lineage in a phylogeny to obtain simulated sequence data at the tips:

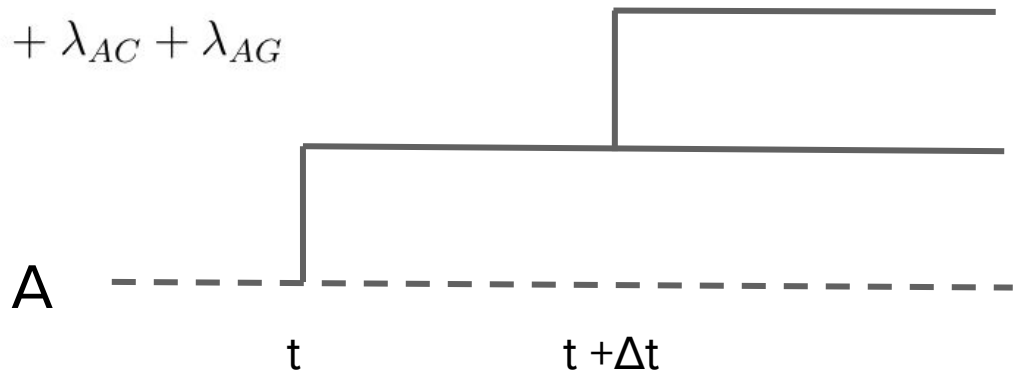


Simulating sequences on trees

Step 1: Compute the rate at which all substitution events occur to find the total mutation rate and then draw time to first mutation:

Time to next event = $\Delta_t \sim \text{Exponential}(\lambda_{Total})$

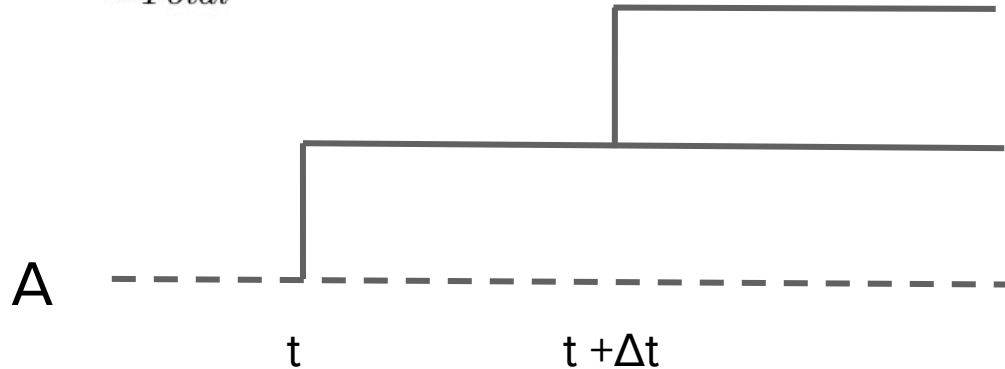
$$\lambda_{Total} = \lambda_{AT} + \lambda_{AC} + \lambda_{AG}$$



Simulating sequences on trees

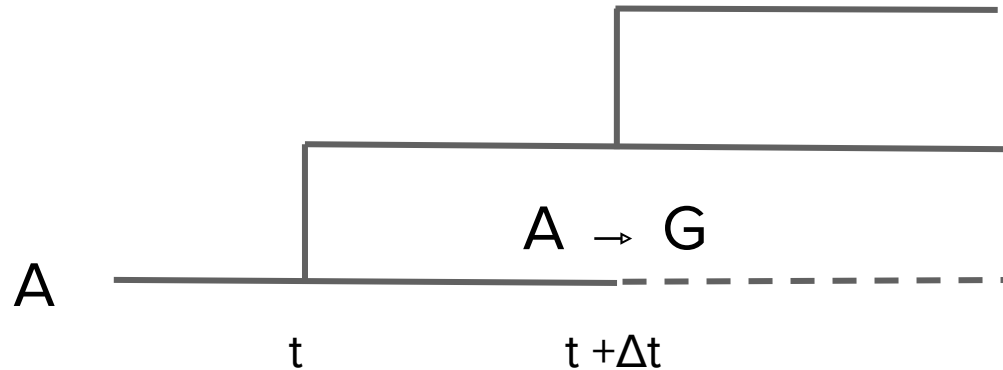
Step 2: Choose the type of substitution event the occurs at the next event time:

$$P(A \rightarrow G) = \frac{\lambda_{AG}}{\lambda_{Total}}$$



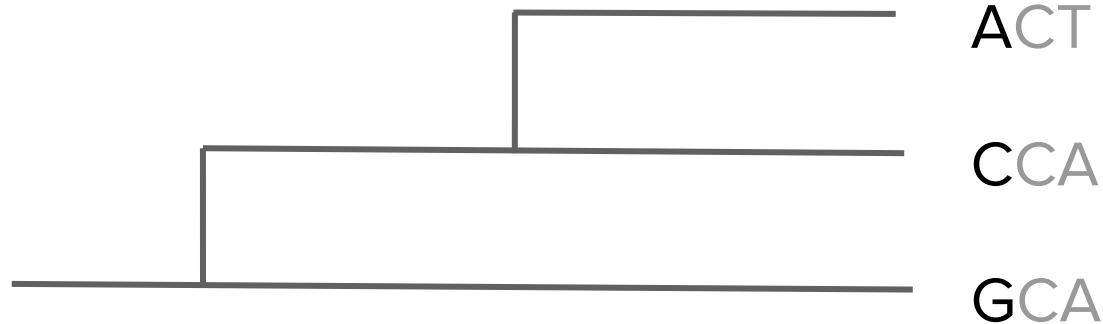
Simulating sequences on trees

Step 3: Update the time and the state of the lineage to reflect the mutation event:



Simulating sequences on trees

We can repeat this process for all lineages and all sites in order to generate mock sequence data at the tips:



Packages for simulating sequence data

Popular choices include:

- Seq-Gen <https://github.com/rambaut/Seq-Gen>
- Seq-Gen implementation in BEAST2

<https://www.beast2.org/2014/04/28/simulation-studies-with-beast-2.html>

- Pyvolve (Spielman & Wilke, 2015) in Python

**Why perform
simulation studies?**

Why do simulation studies?

Program errors: Scientific software often contains bugs since it is generally not written or extensively tested by professional software engineers

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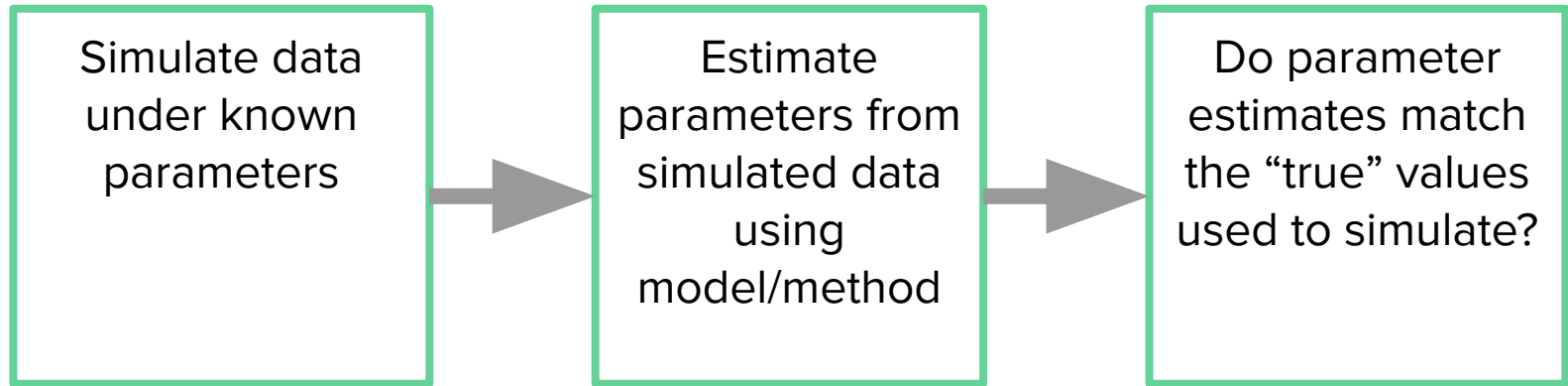
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Statistical validity: Inferential methods often make many assumptions that may not be appropriate for your study system or data.

Simulation as sanity check

Can we get back out what we put in?



**Performing simple
simulation studies
identifies preventable
errors and makes
science as a whole
much more
reproducible.**