

# Inference for State Space Models



# Objective



Explore the link between climate and  
Dengue in Thailand

# 3 steps

Intro to epidemic modeling and simulation with SSM

Inference: parameter estimation and model selection

Dengue and climate in Thailand

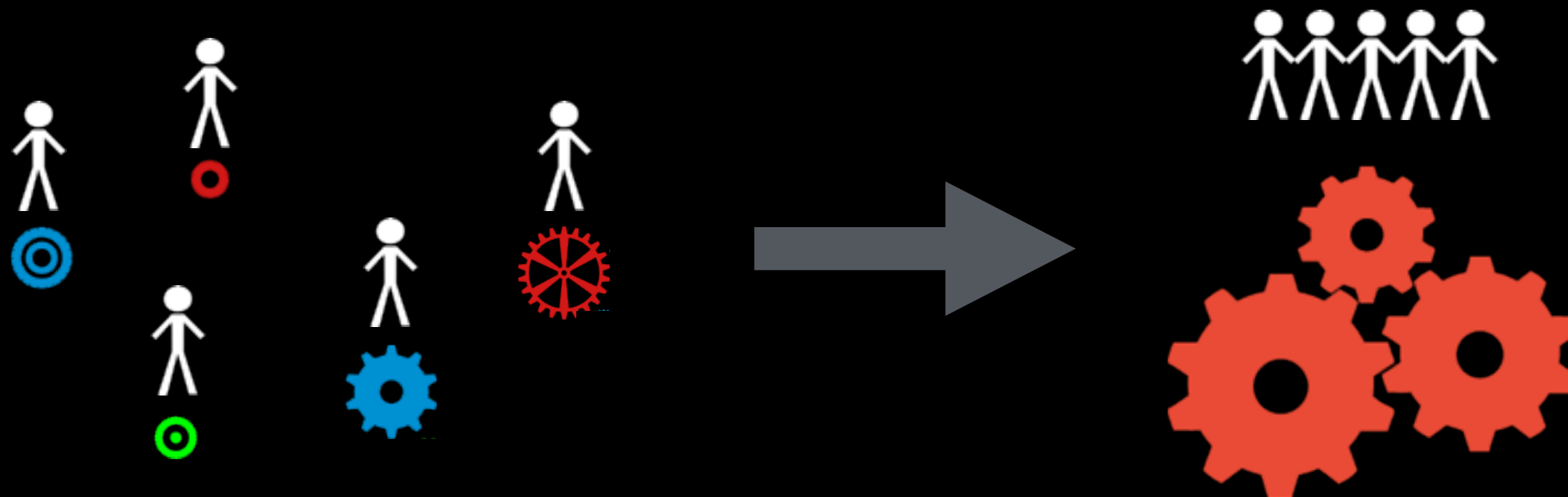
# Intro to epidemic modeling and simulation with SSM







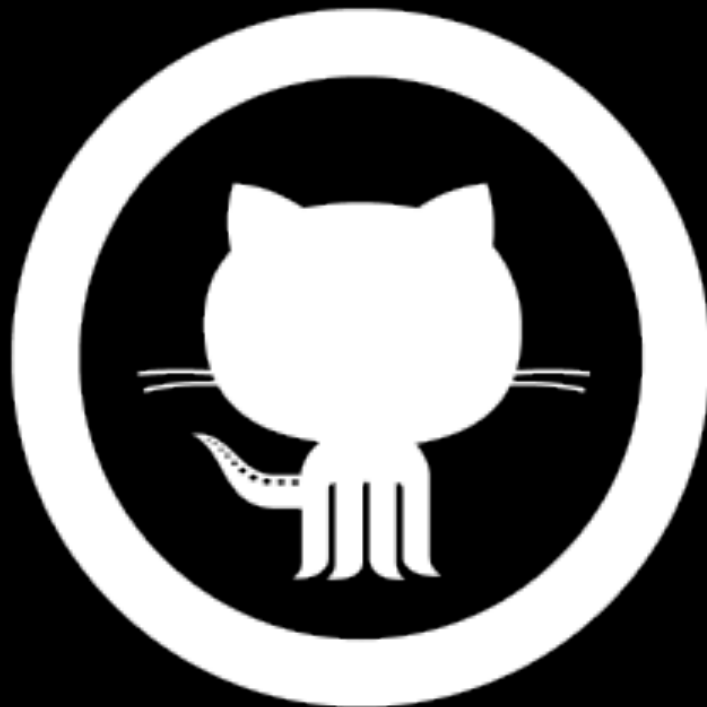
Modelling complex & dynamic quantities:  
reorganising to meet up with technical challenges.



<https://github.com/standard-analytics/ssm>

**Open Source  
community**

**+ you**



Sign up for GitHub

<https://github.com/>

# WHY?

**New Issue**

**Question?  
Raise issues**



**Star**

**4**

**Support!**



**Watch ▼**

**8**

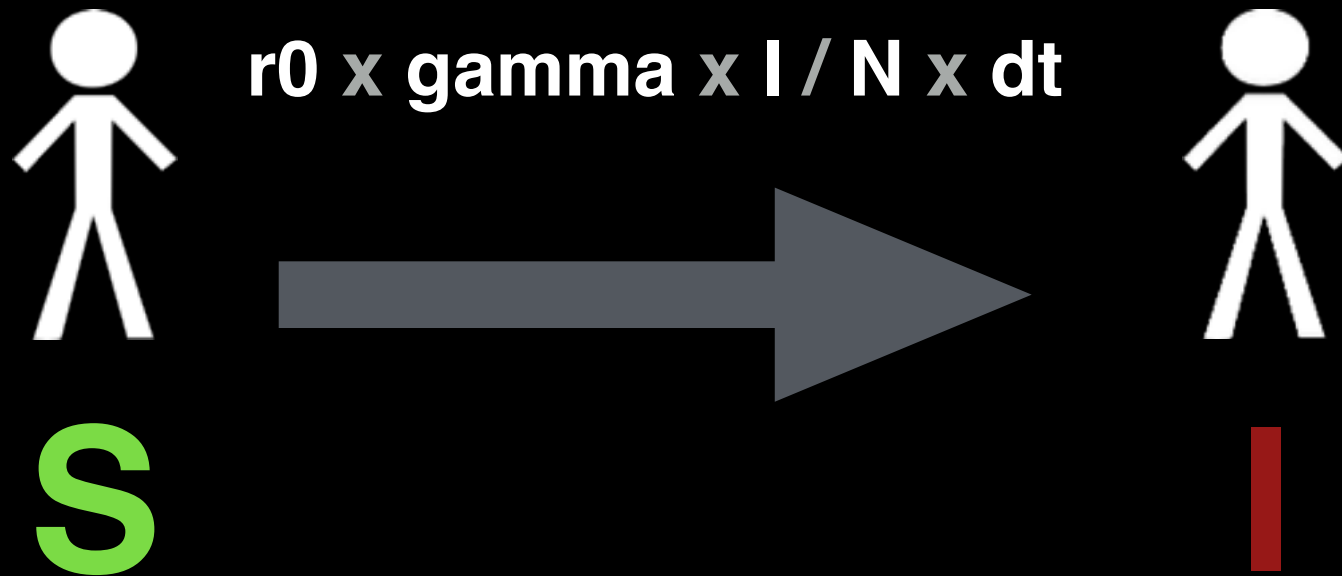
**Keep informed**

**Is SSM properly installed  
on your machines?**

**In your terminal: `> ssm -V`**

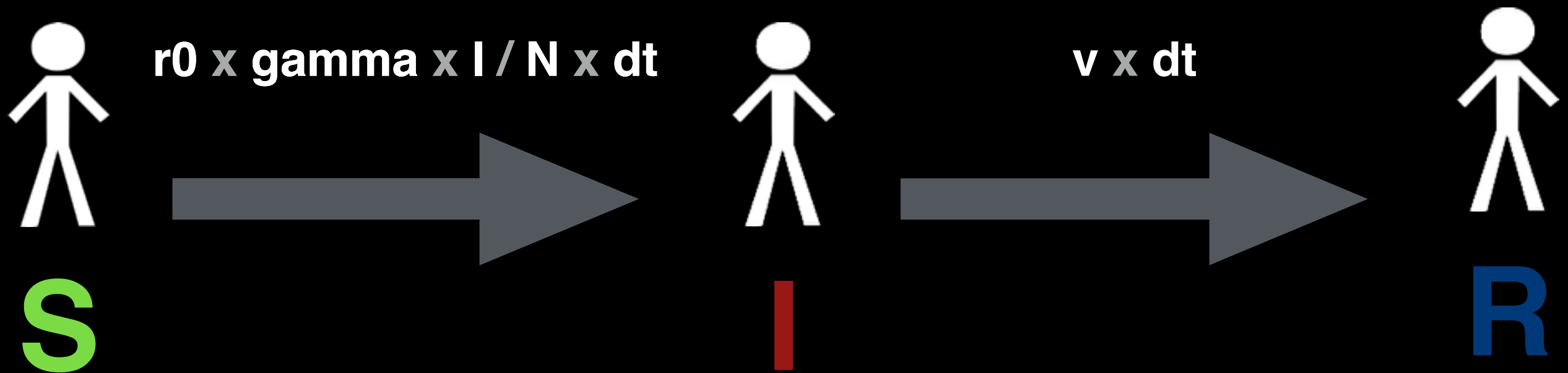


# SI Intro



$$dS_t = -r_0 \times \text{gamma} \times I / N \times S \times dt$$
$$dI_t = r_0 \times \text{gamma} \times I / N \times S \times dt$$

# SIR Intro



$$dS_t = -r_0 \times \text{gamma} \times I / N \times S \times dt$$

$$dI_t = r_0 \times \text{gamma} \times I / N \times S \times dt - v \times dt$$

$$dR_t = v \times dt$$

# SIR First steps

change directory



```
> cd SIR-city
```

```
> ls
```



Saint-Fuscien

Amiens

Paris

list content

package.json???

JSON: JavaScript Object Notation

# JSON

double-quotes only!



Lists: [ `“a”`, 3, ... ]

Objects: { `“a”`: `“A”`, `“b”`: 3, ... }

Flexible, readable format.

Popular open standard.

# SIR

Let's get to it

Closer look at the “model” object.



# SIR Simulation

```
> ssm install package.json  
> cd bin  
> ./simul --help  
> cat ../package.json | ./simul --traj
```

→ X\_0.csv

# SIR Plot X\_0.csv

Open TD.R in R

!!! Set TD-STRU to be Working Directory

Plot X\_0.csv with ssm.plot.X

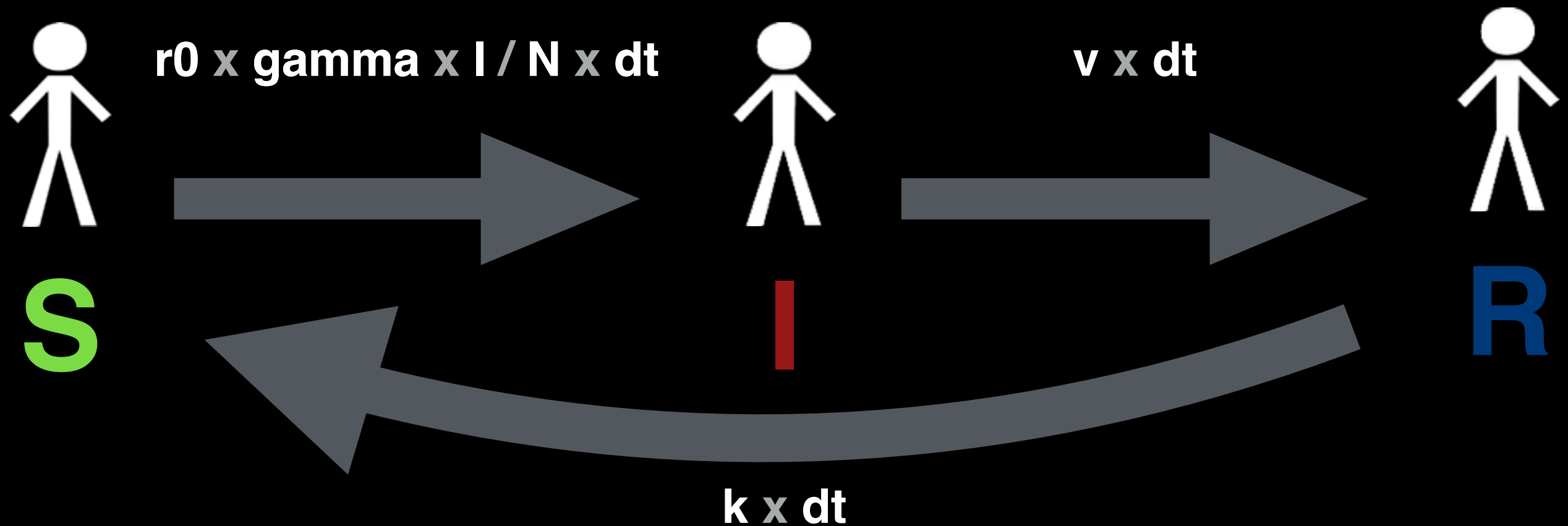
# SIR Explore

Explore different values of  $R_0$  and  $d$

Under which minimal conditions does an epidemic burst?

According to the SIR model, what will be the number of susceptibles on December 13th, 2012?

# SIRS Make your own model



$$dS_t = -r_0 \times \text{gamma} \times I / N \times S \times dt + k \times dt$$

$$dI_t = r_0 \times \text{gamma} \times I / N \times S \times dt - v \times dt$$

$$dR_t = v \times dt - k \times dt$$

# SIRS

Make your own model

What should qualitatively be the impact of immunity loss on the number of susceptibles on December 13th, 2012?



# SIRS Make your own model

Duplicate and rename SIR.

Modify it to obtain an SIRS model.

reactions **+** `...,  
{"from": "R", "to": "S", "rate": "k", "description": "recovery"}`

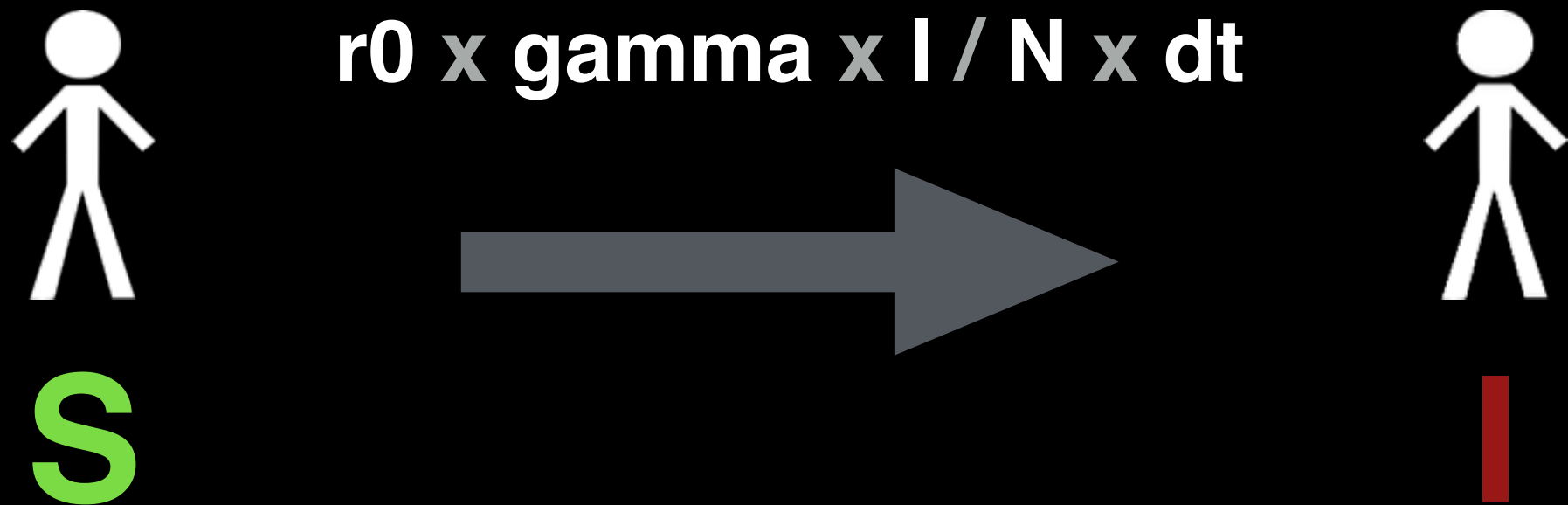
inputs **+** `...,  
{"name": "k", "description": "rate of immunity loss",  
"data": {"resource": "pr_k", "transformation": "1/pr_k",  
"to_resource": "1/k" },`

resources **+** `{ "name": "pr_k", "description": "duration of immunity",  
"data": { "distribution": "fixed", "value": 250.0 } },`

# The role and influence of demographic stochasticity

# Noise Poisson process formalism

For every individual:



infection is a random process

# Noise Poisson process formalism

For  $S_t$  individuals:

$$p(n \text{ infections}) \approx \binom{S_t}{n} r_0 \times \text{gamma} \times I / N \times dt$$

→ tractable stochastic model

# Noise SDE formalism

Going further, following Ethier & Kurtz 1986:

drift

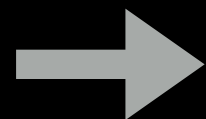


volatility



$$dS_t = -r_0 \times \text{gamma} \times I / N \times S_t \times dt - \text{sqrt}(r_0 \times \text{gamma} \times I / N \times S_t) dB_t$$

$$dI_t = r_0 \times \text{gamma} \times I / N \times S_t \times dt + \text{sqrt}(r_0 \times \text{gamma} \times I / N \times S_t) dB_t$$



*Diffusion approximation*

For more details, see: Dargatz (2007). *A diffusion approximation for an epidemic model.*



# To remember

psr    best tractable approximation

sde    continuous approximation  
classical mathematical object  
theory only for large populations

# SIR Let's try with noise

```
> cat ../package.json | ./simul psr --traj  
> cat ../package.json | ./simul sde --traj -I 1
```



Run id

Plot and compare X\_0.csv and X\_1.csv

# SIR Let's try with noise

Number of particles



```
> cat ../package.json | ./simul psr --traj -J 3
```

```
> cat ../package.json | ./simul sde --traj -I 1 -J 3
```



Run id

More particles

# SIR Let's try with noise

Number of particles



```
> cat ../package.json | ./simul psr --traj -J 1000
```

```
> cat ../package.json | ./simul sde --traj -I 1 -J 1000
```



Run id

Even more particles

# SIR Let's try with noise

Number of particles



```
> cat ../package.json | ./simul psr --hat -J 1000
```

```
> cat ../package.json | ./simul sde --hat -I 1 -J 1000
```

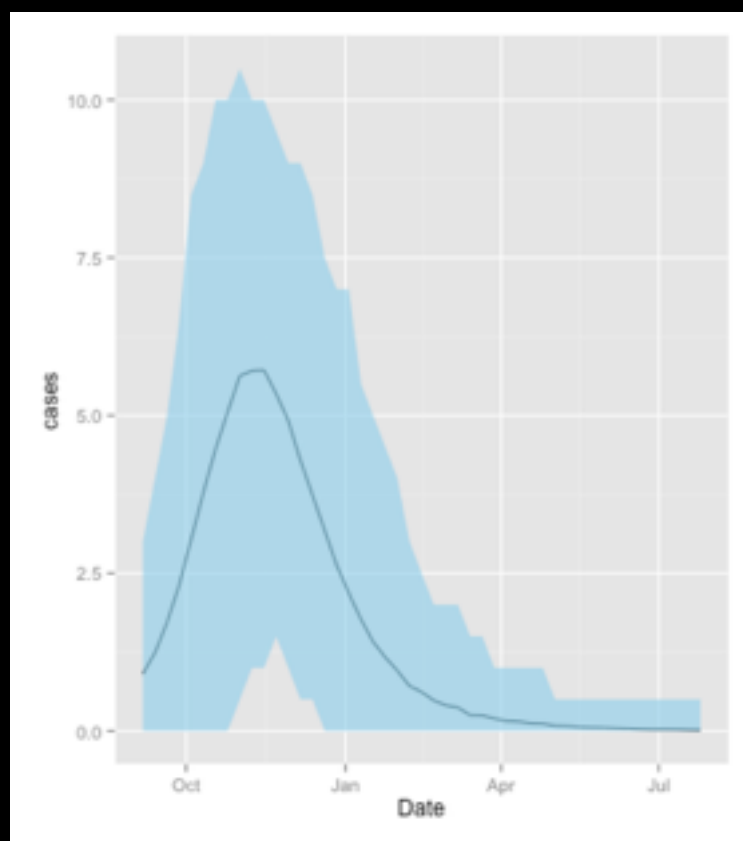


Run id

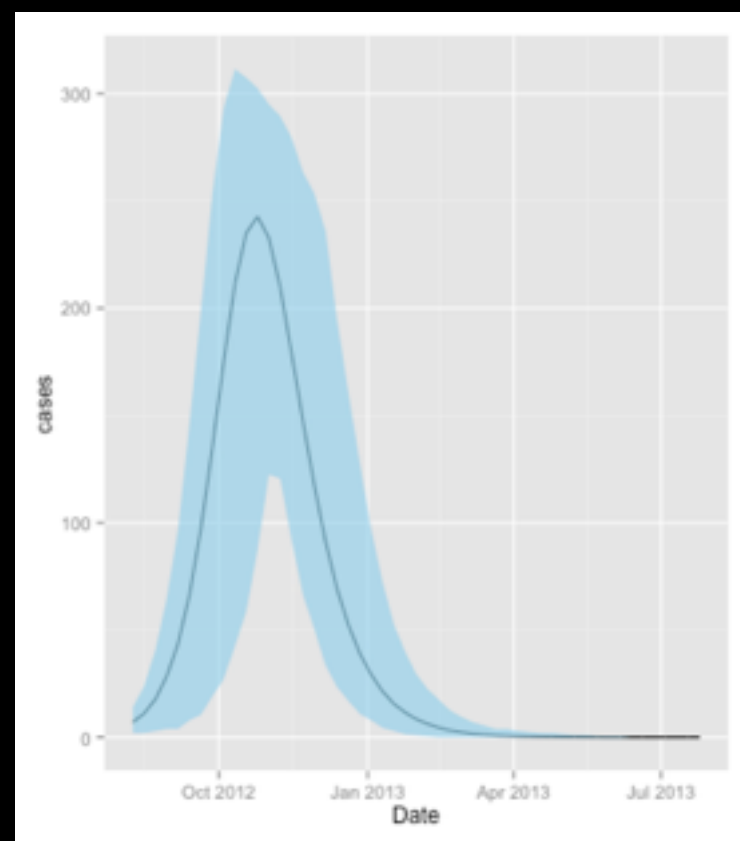
Generate trajectory confidence intervals

→ use ssm.plot.hat

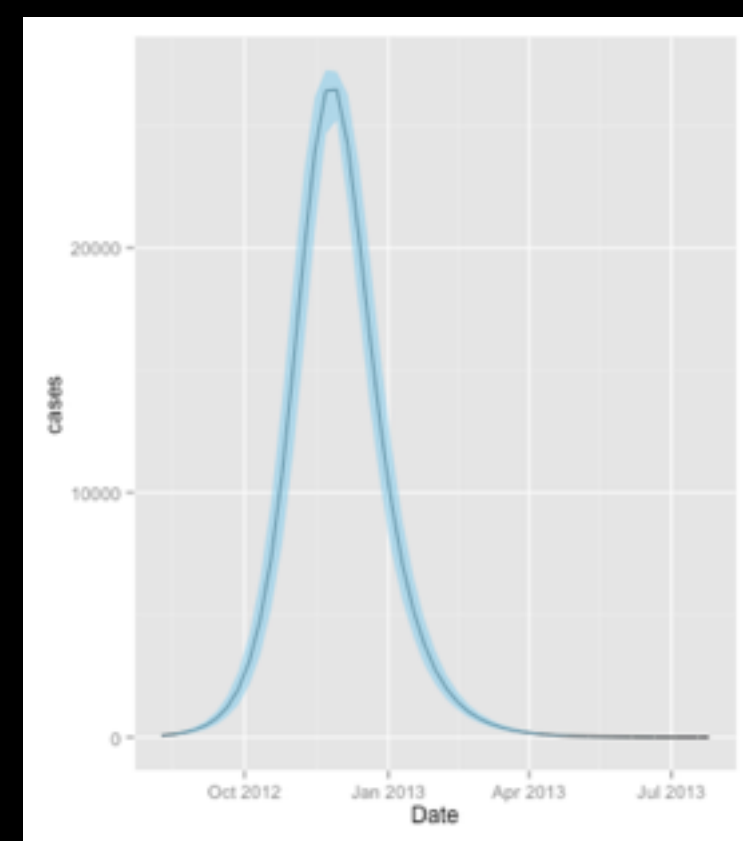




**Saint-Fuscien**  
1'000 inhabs.



**Amiens**  
100'000 inhabs.

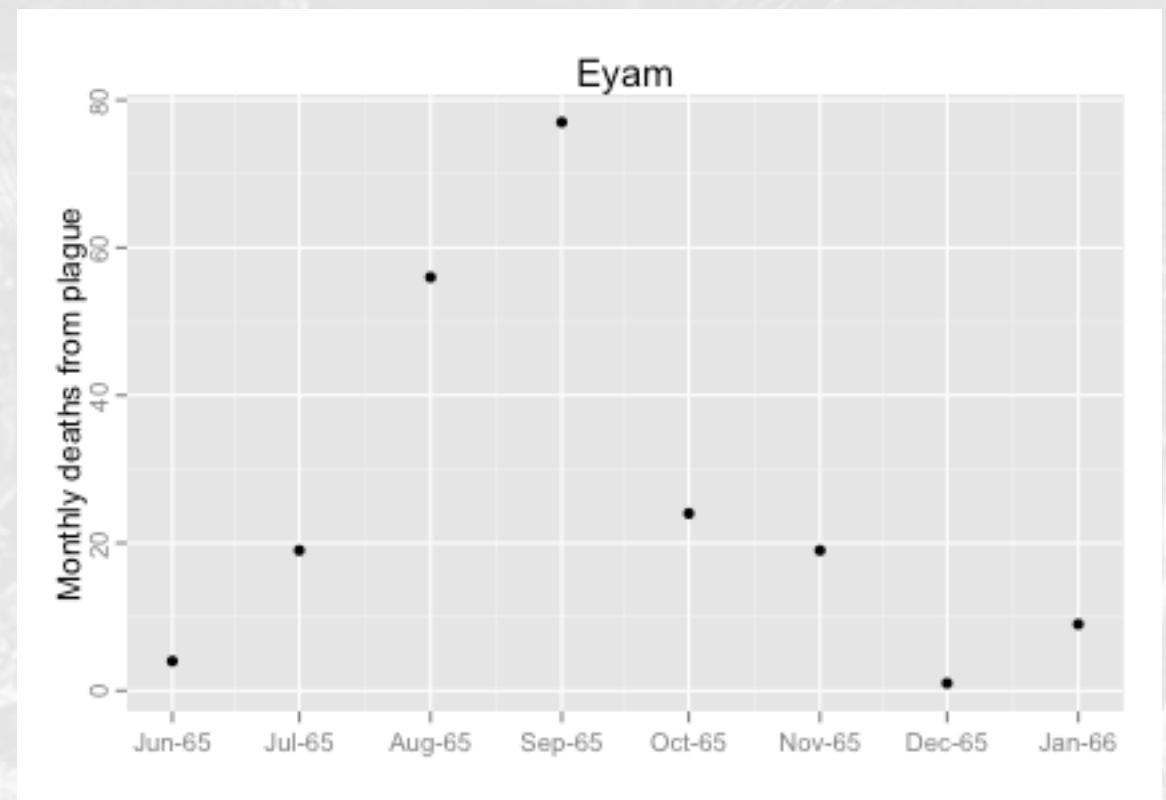
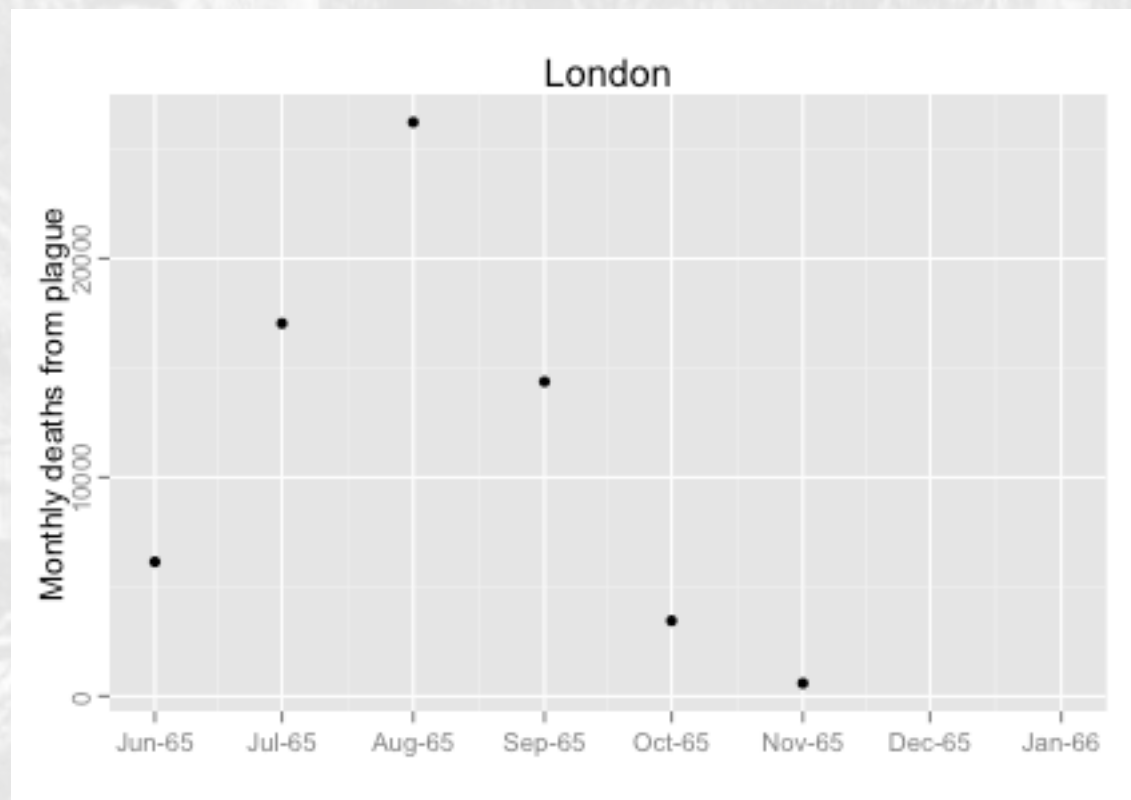


**Paris**  
10M inhabs.

# Inference: parameter estimation and model selection



# A first real example

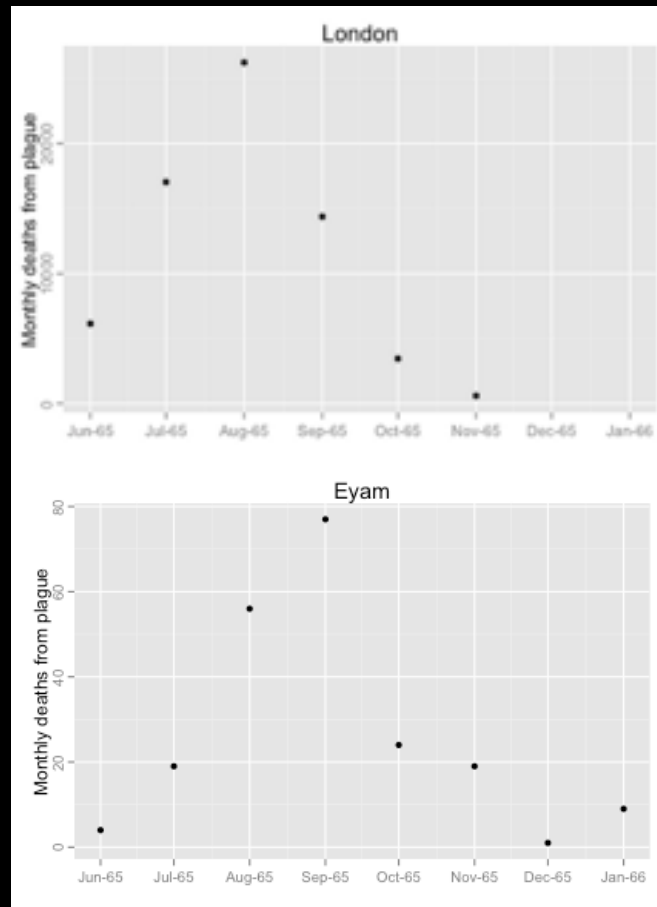


What was life expectancy with plague?  
Were infection patterns similar in  
London and Eyam?

life\_exp? r0\_London? r0\_Eyam?

$p(y|\Theta)$  Likelihood

$p($



$\left[ \begin{array}{l} \text{life\_exp} \\ \text{r0\_London} \\ \text{r0\_Eyam} \end{array} \right]$

# Bayes Formula

Posterior



Likelihood



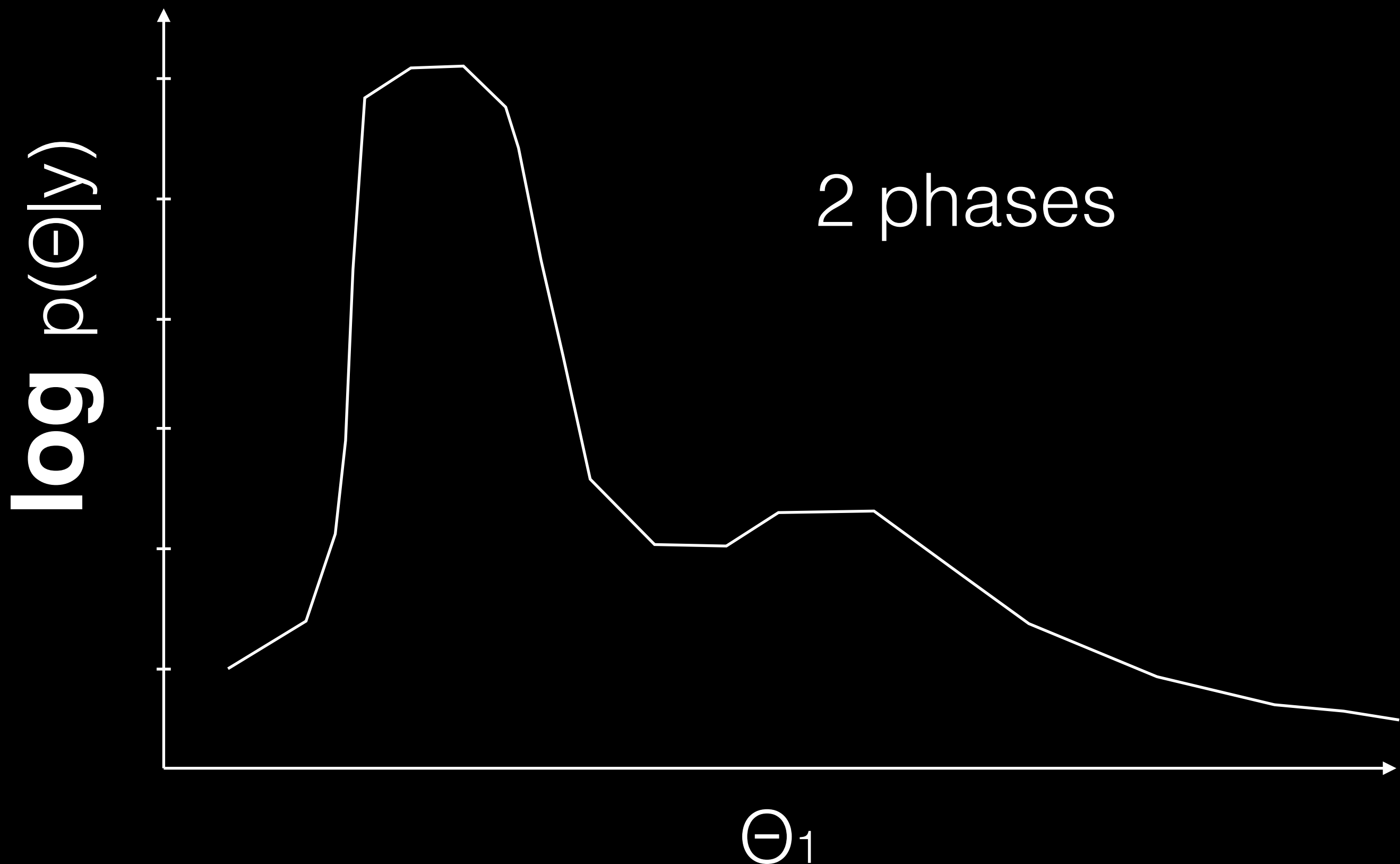
Prior



$$p(\Theta|y) \propto p(y|\Theta)p(\Theta)$$

# Inference

Exploring  $p(\Theta|y)$



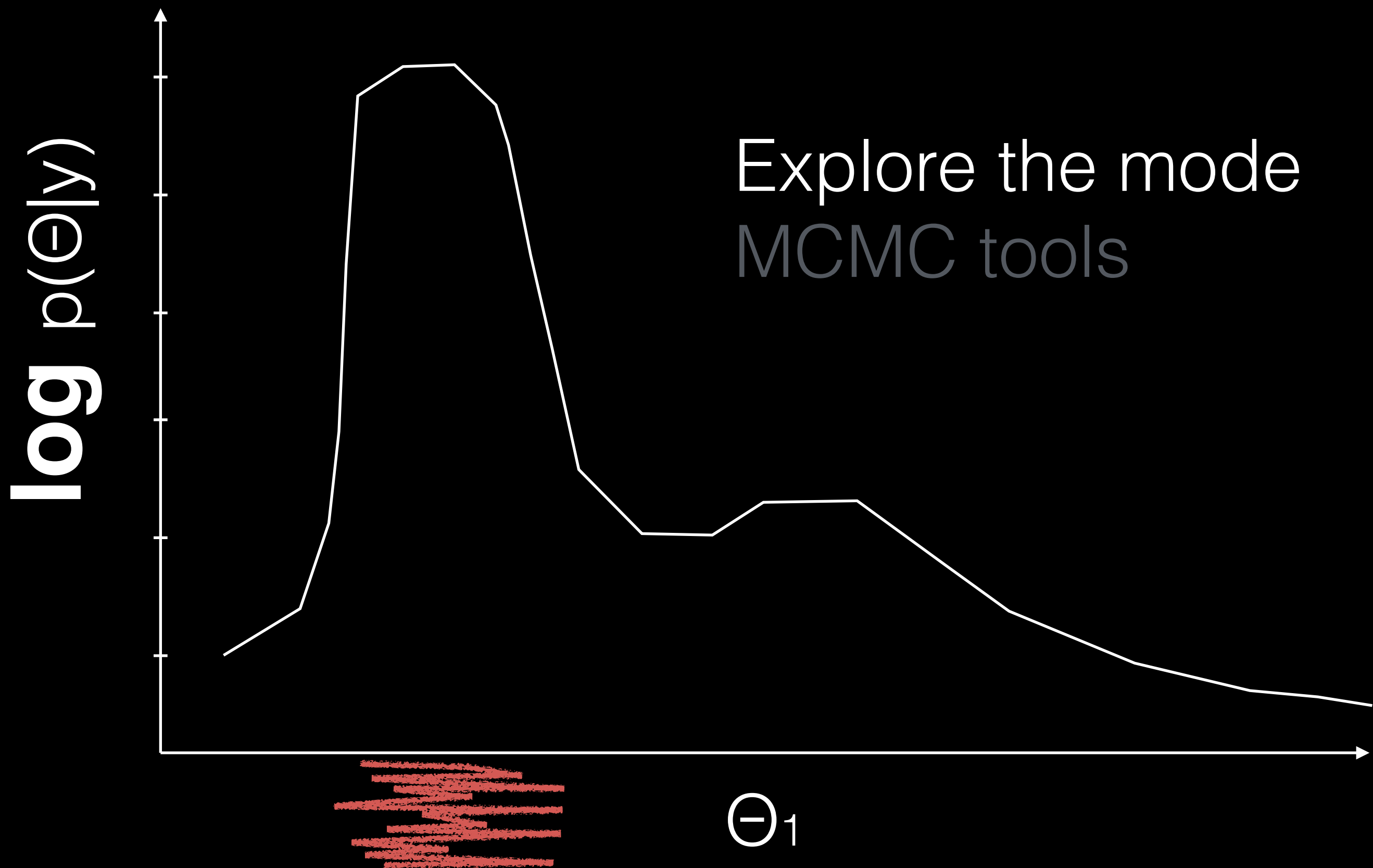
# Inference

Exploring  $p(\Theta|y)$



# Inference

Exploring  $p(\Theta|y)$





# Illustration Manual inference

Install the model, and in the bin directory:

```
> cat ../package.json | ./simplex -M 1000 --trace > mle.json
```

```
> cat mle.json | ./pmcmc -M 1000 --trace > mle.json
```

use `ssm.plot.trace`, and `ssm.plot.post`

# Illustration

## Automated pipeline

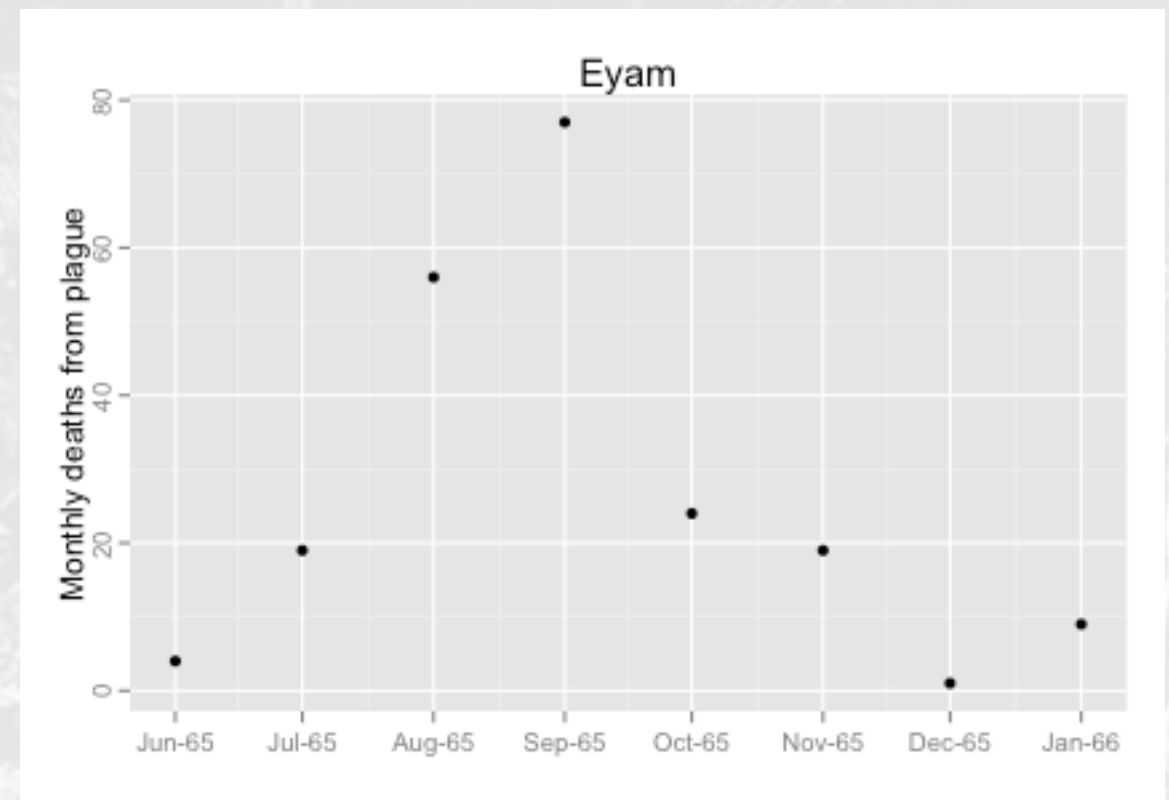
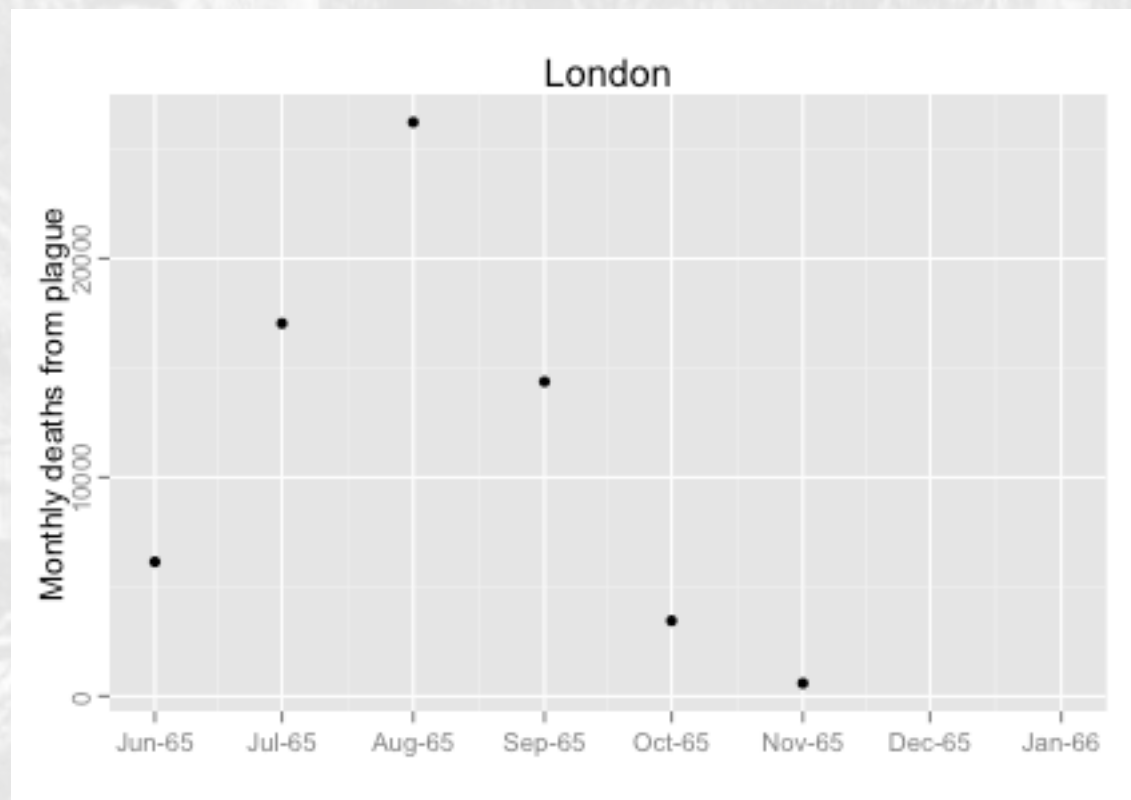
In the parent directory:

```
> ssm bootstrap package.json
```

```
> ssm run
```

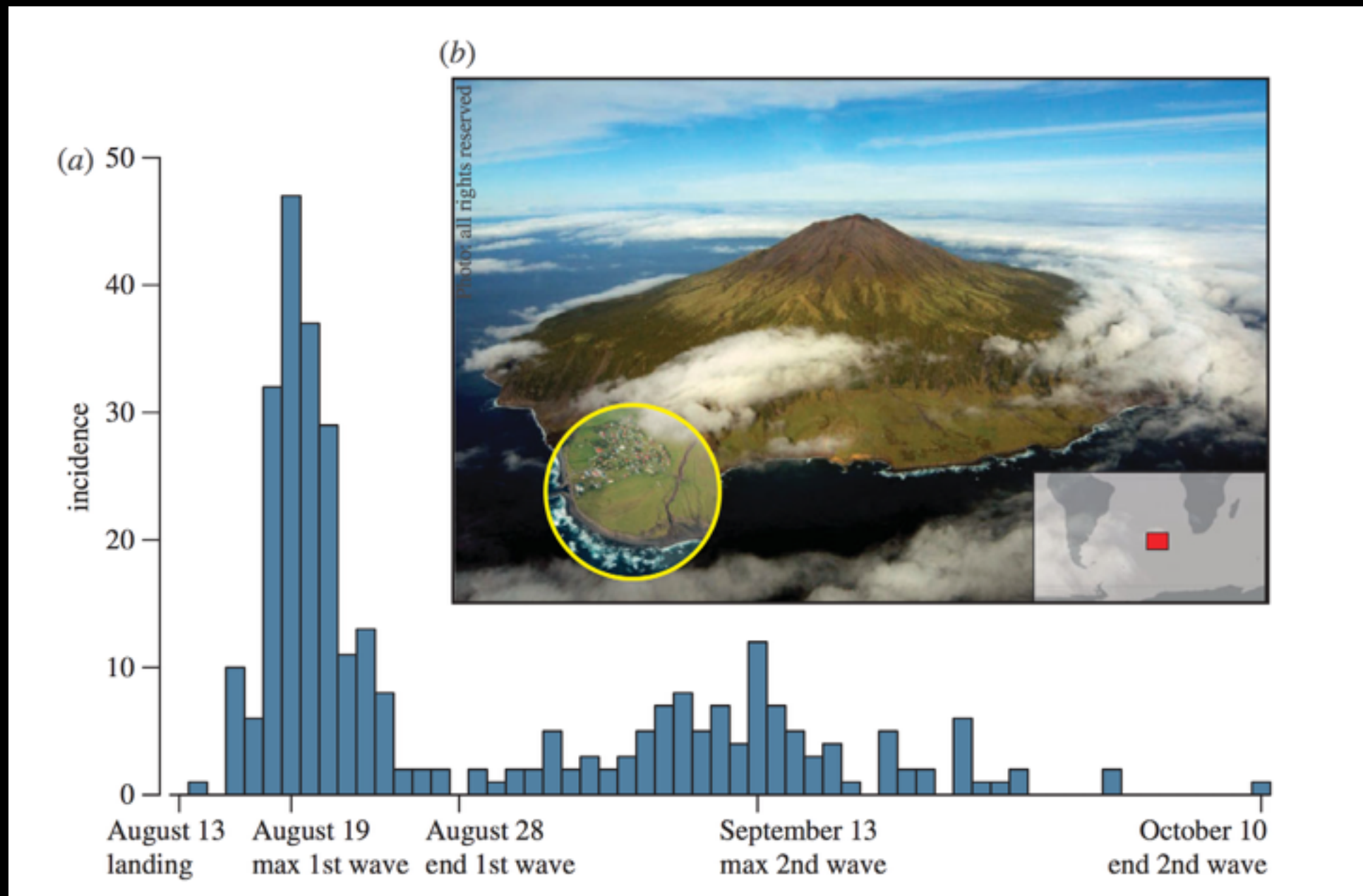
use `ssm.plot.trace`, and `ssm.plot.post`

# A first real example



What was life expectancy with plague?  
Were infection patterns similar in  
London and Eyam?

# A second real example

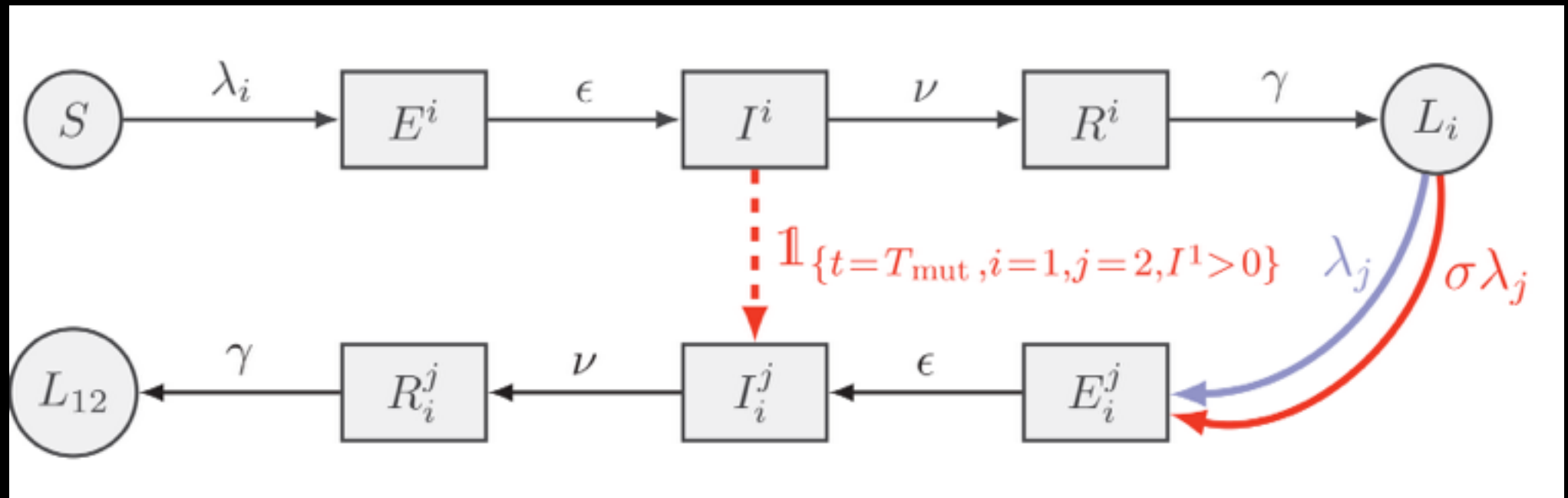


Explaining rapid reinfections in multiple- wave influenza outbreaks: Tristan da Cunha 1971 epidemic as a case study

# Two theories

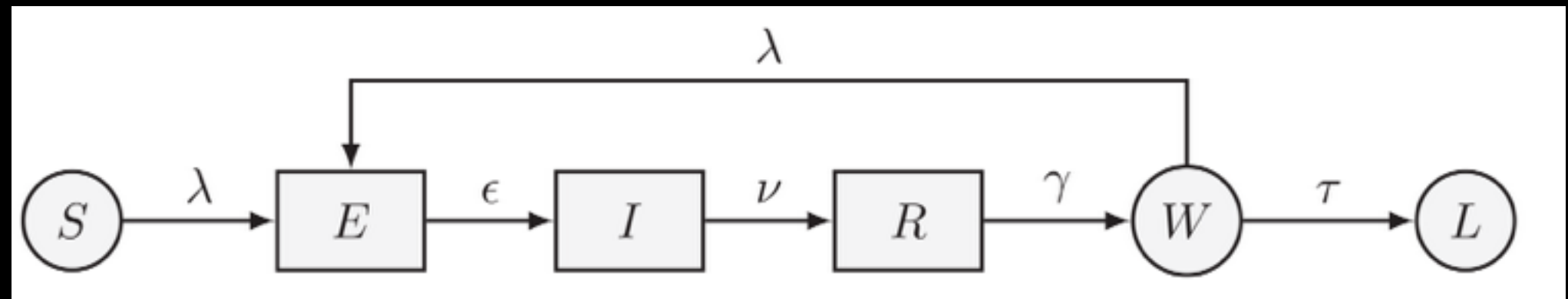
Mut

Strain  
mutation



Win

Reinfection  
window



Fit both models. Conclude.