

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

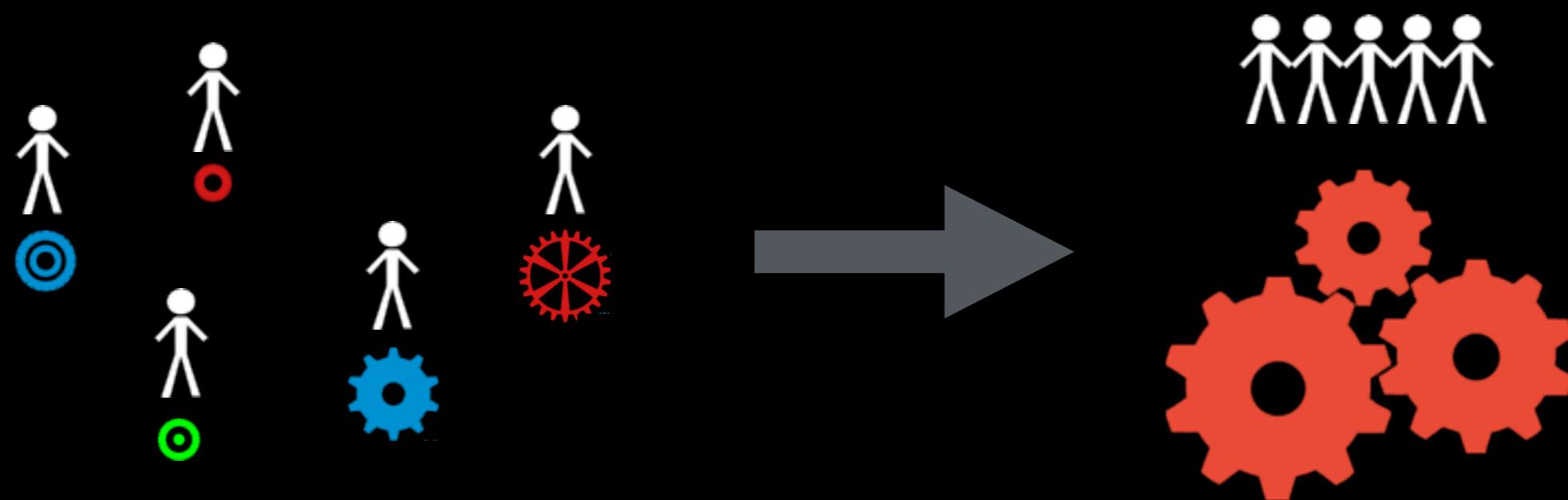
Dengue and climate in Thailand

Intro to epidemic modeling and simulation with SSM



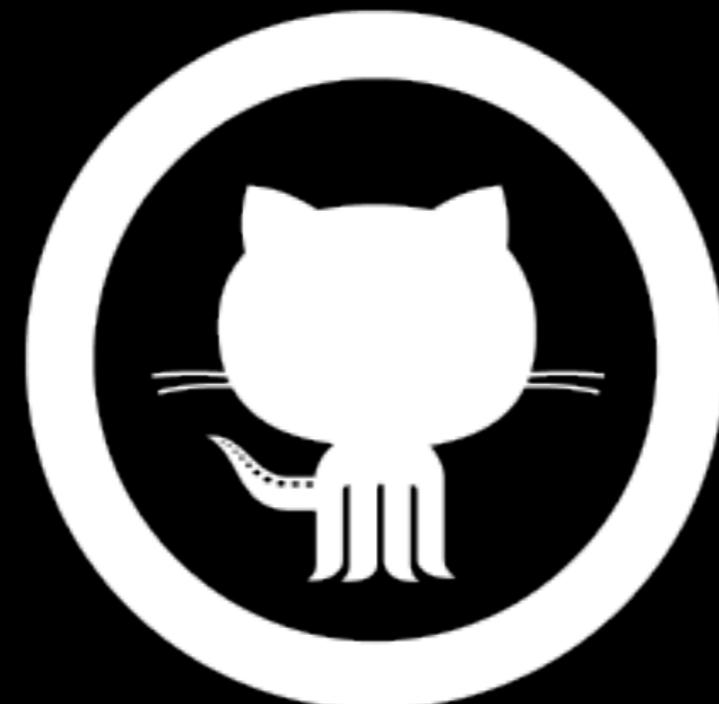


Modelling complex & dynamic quantities:
reorganising to meet up with technical challenges.



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

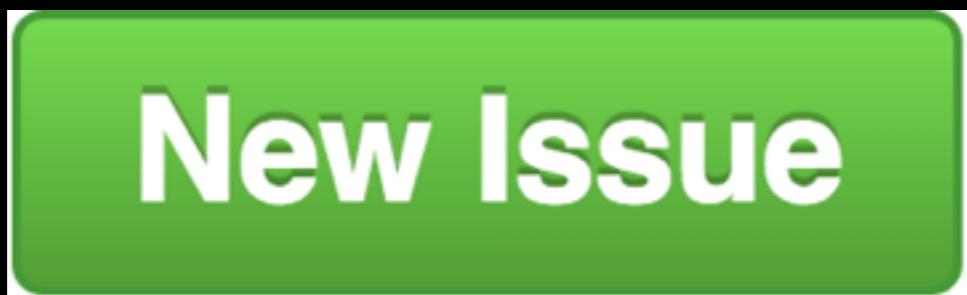
Open Source
community + you



[Sign up for GitHub](#)

<https://github.com/>

WHY?



Question?
Raise issues

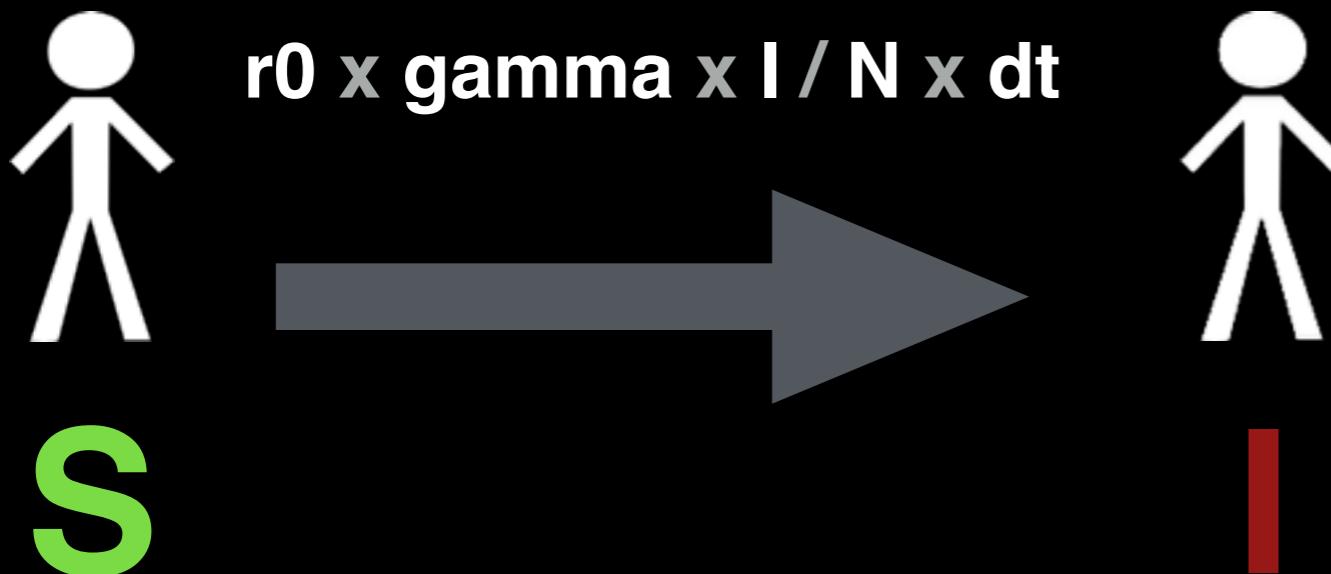
Support!

Keep informed

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

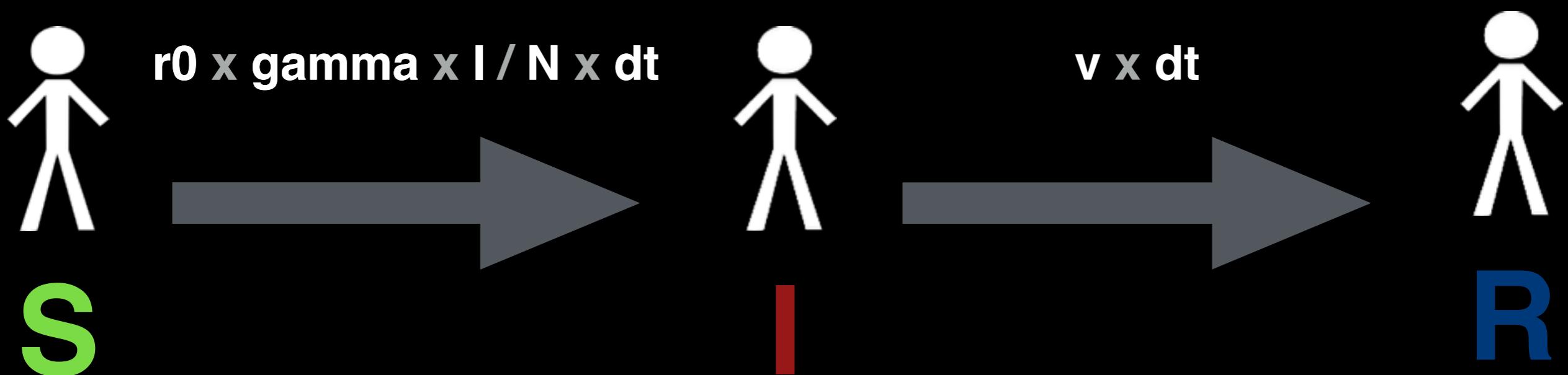
In your terminal: > ssm -V

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



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

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

$$dI_t = v \times dt$$

SIR First steps

change directory



```
> cd SIR-city
```

```
> ls
```



list content



Saint-Fuscien
Amiens
Paris

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

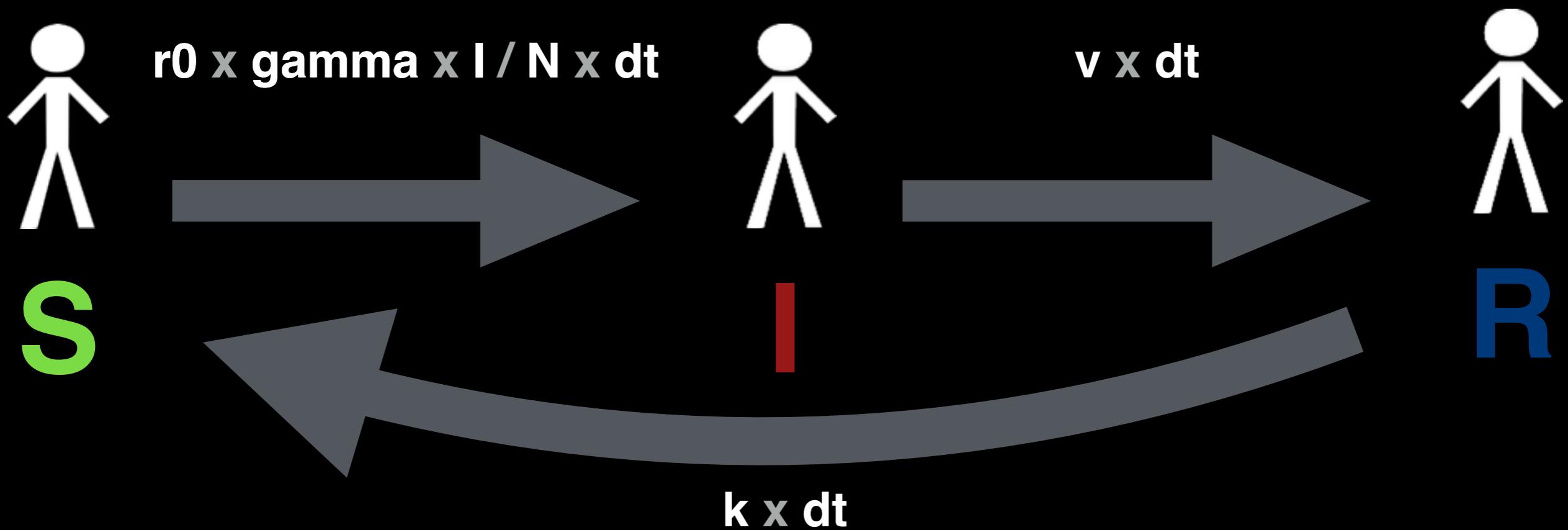
SIR Explore

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"}

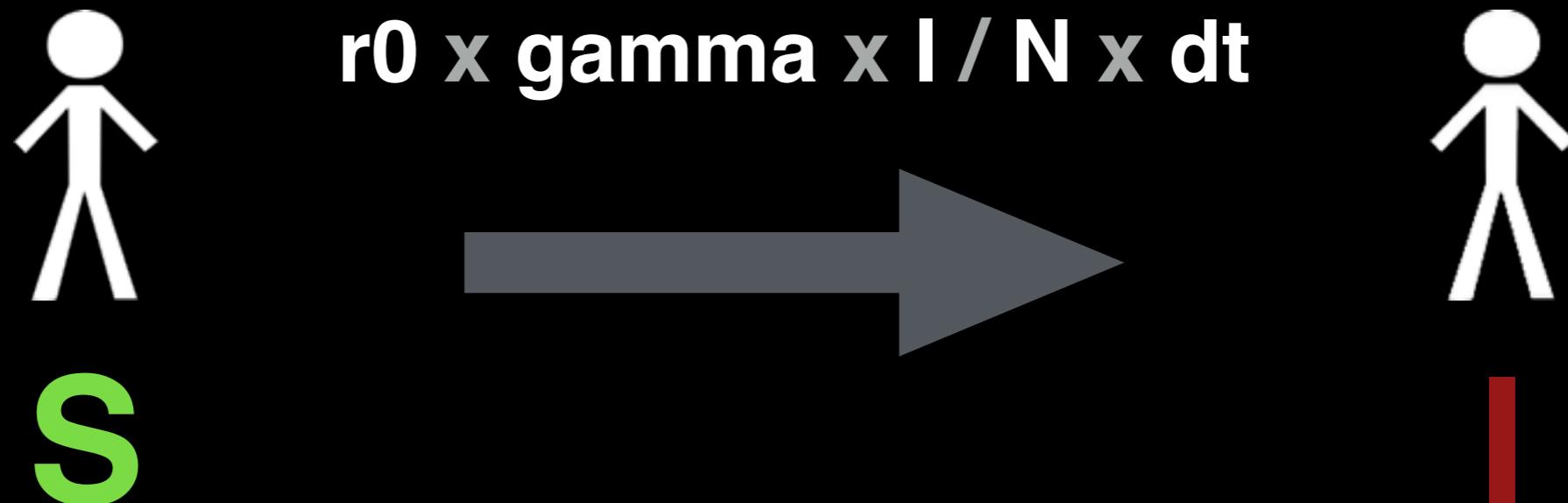
inputs + ...
{ "name": "k", "description": "rate of immunity loss",
"data": { "resource": "pr_k"}, "transformation": "1/pr_k",
"to_resource": "1/k" },

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



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

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



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

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

Number of particles
Run id
More particles



SIR Let's try with noise

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

Number of particles



Run id



Even more particles

SIR Let's try with noise

Number of particles



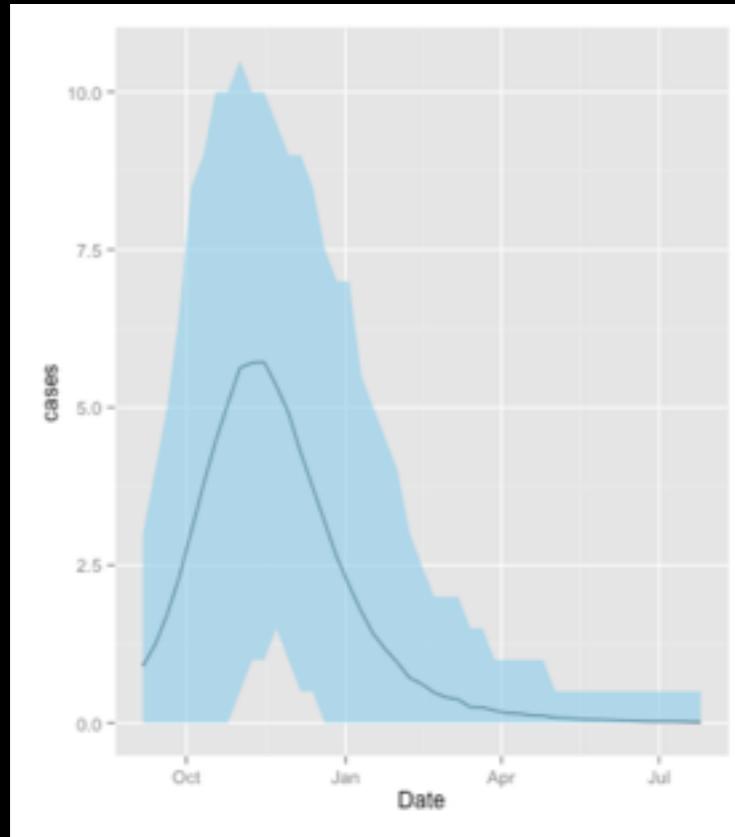
```
> cat ./package.json | ./simul psr --hat -J 1000  
> cat ./package.json | ./simul sde --hat -I 1 -J 1000
```



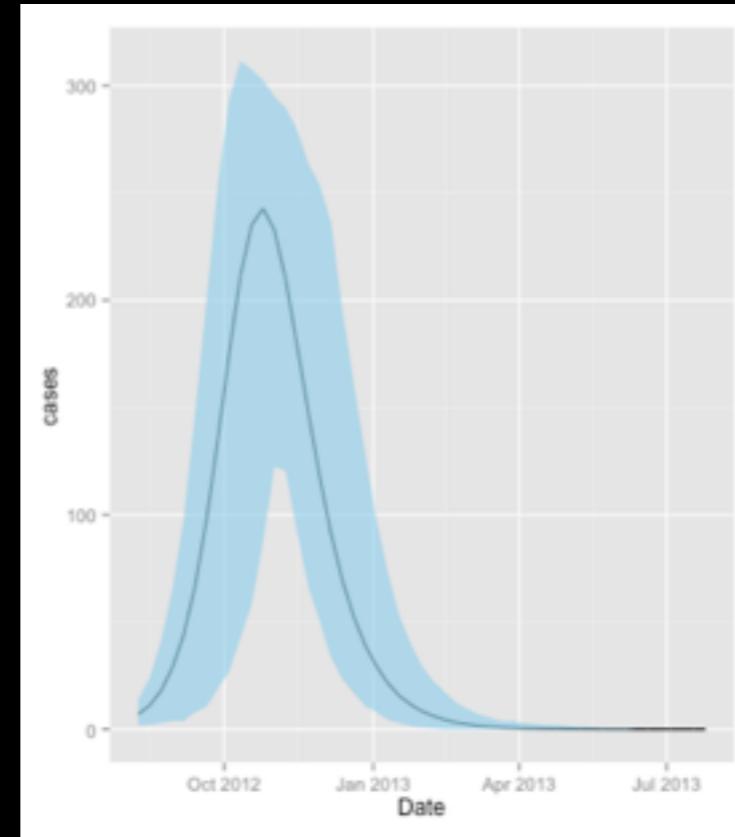
Run id

Generate trajectory confidence intervals

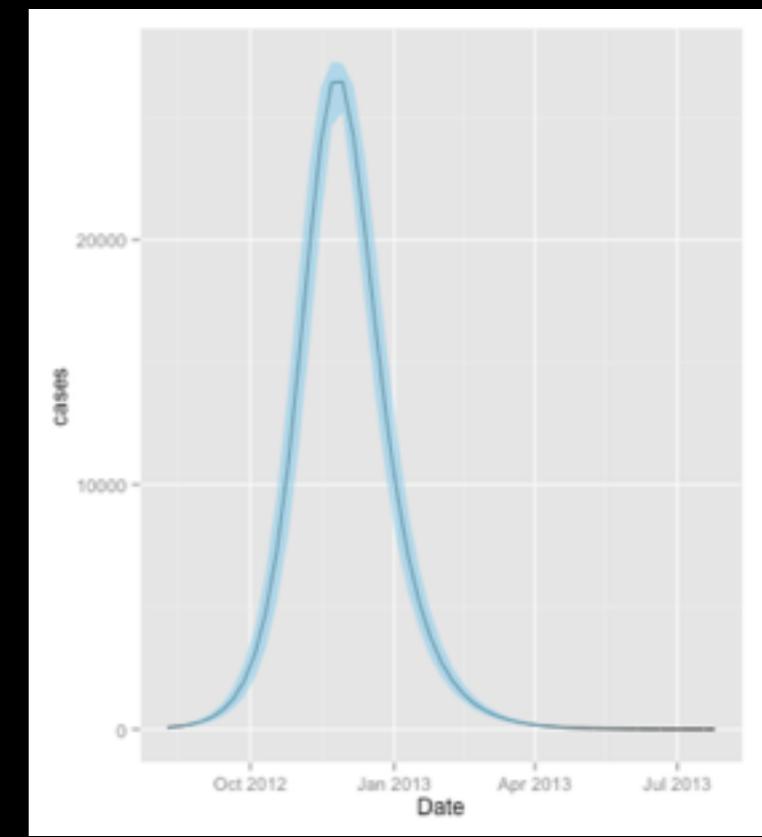
→ use `ssm.plot.hat`



Saint-Fuscien
1'000 inhabs.



Amiens
100'000 inhabs.

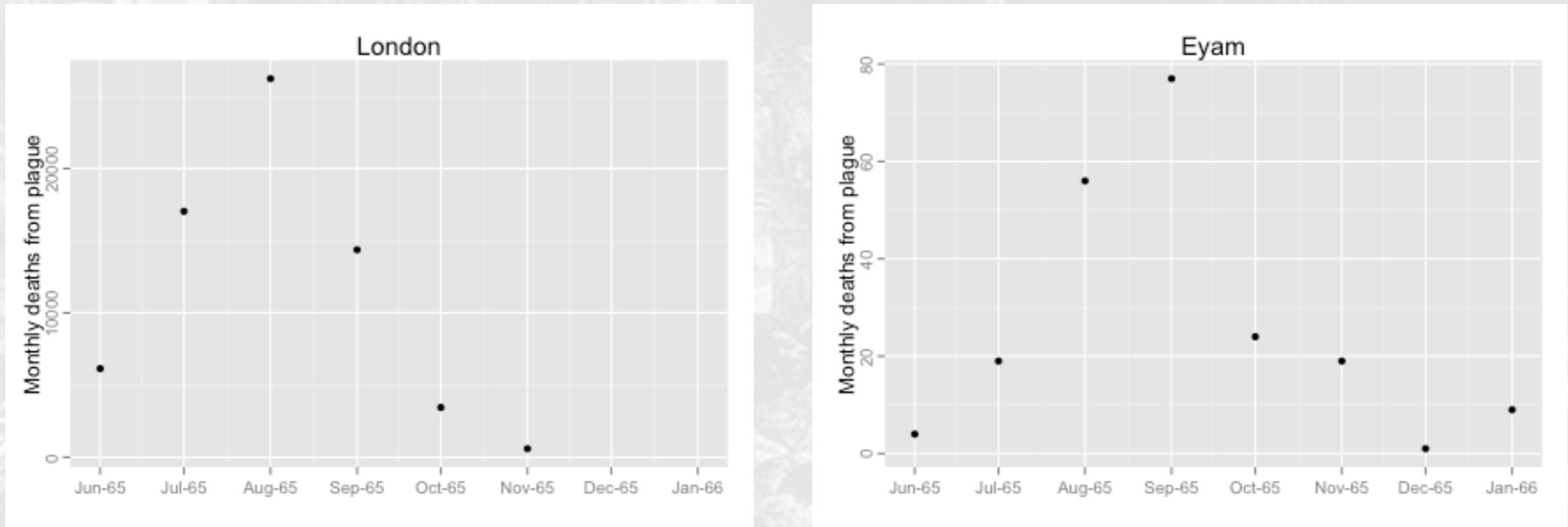


Paris
10M inhabs.

Inference: parameter estimation and model selection



A first real example

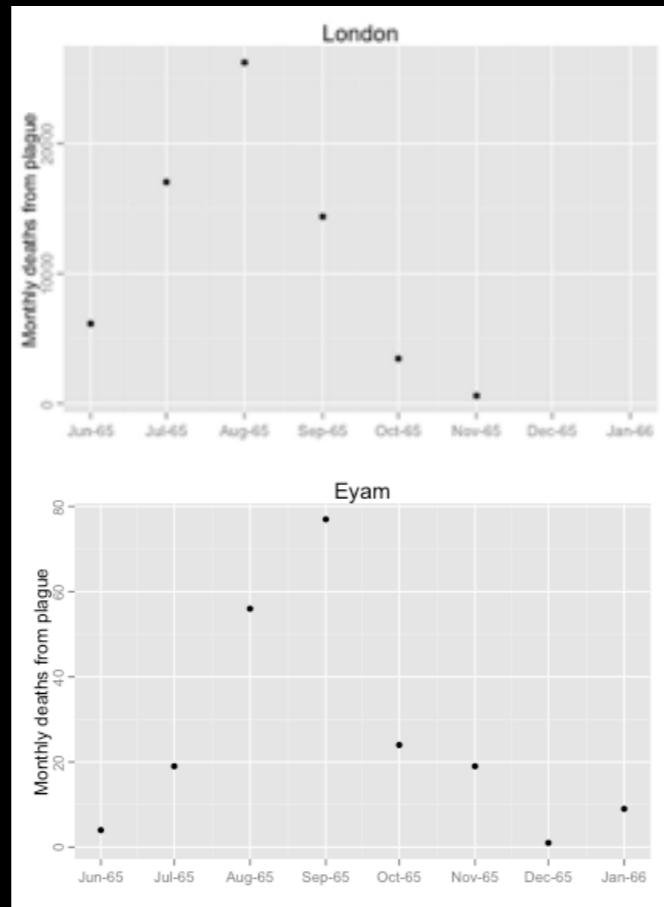


What was life expectancy with plague?
Were infection patterns similar in
London and Eyam?

life_exp? r0_London? r0_Eyam?

$p(y|\theta)$ Likelihood

$p($



)
life_exp
r0_London
r0_Eyam

Bayes Formula

Posterior



Likelihood

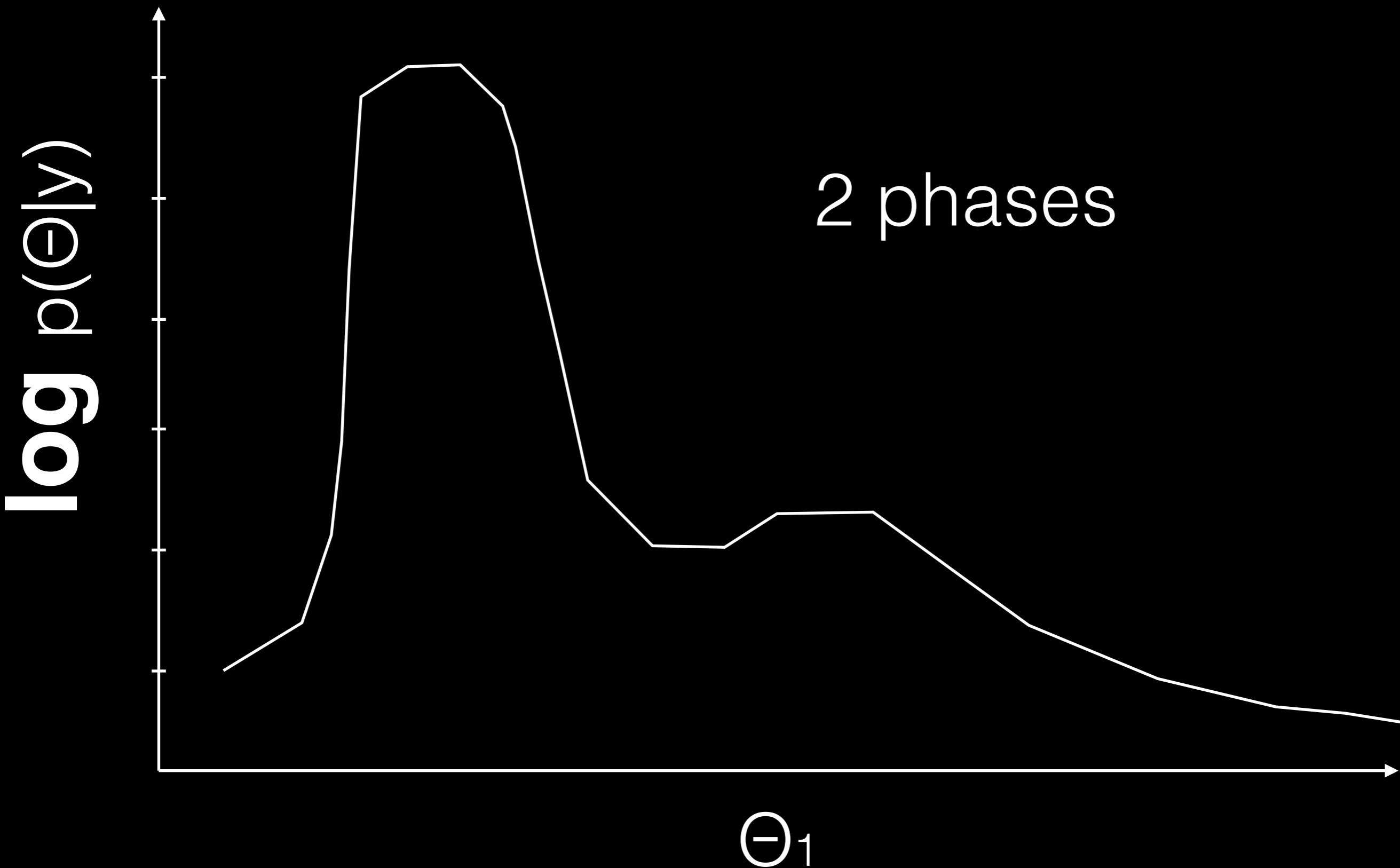


Prior

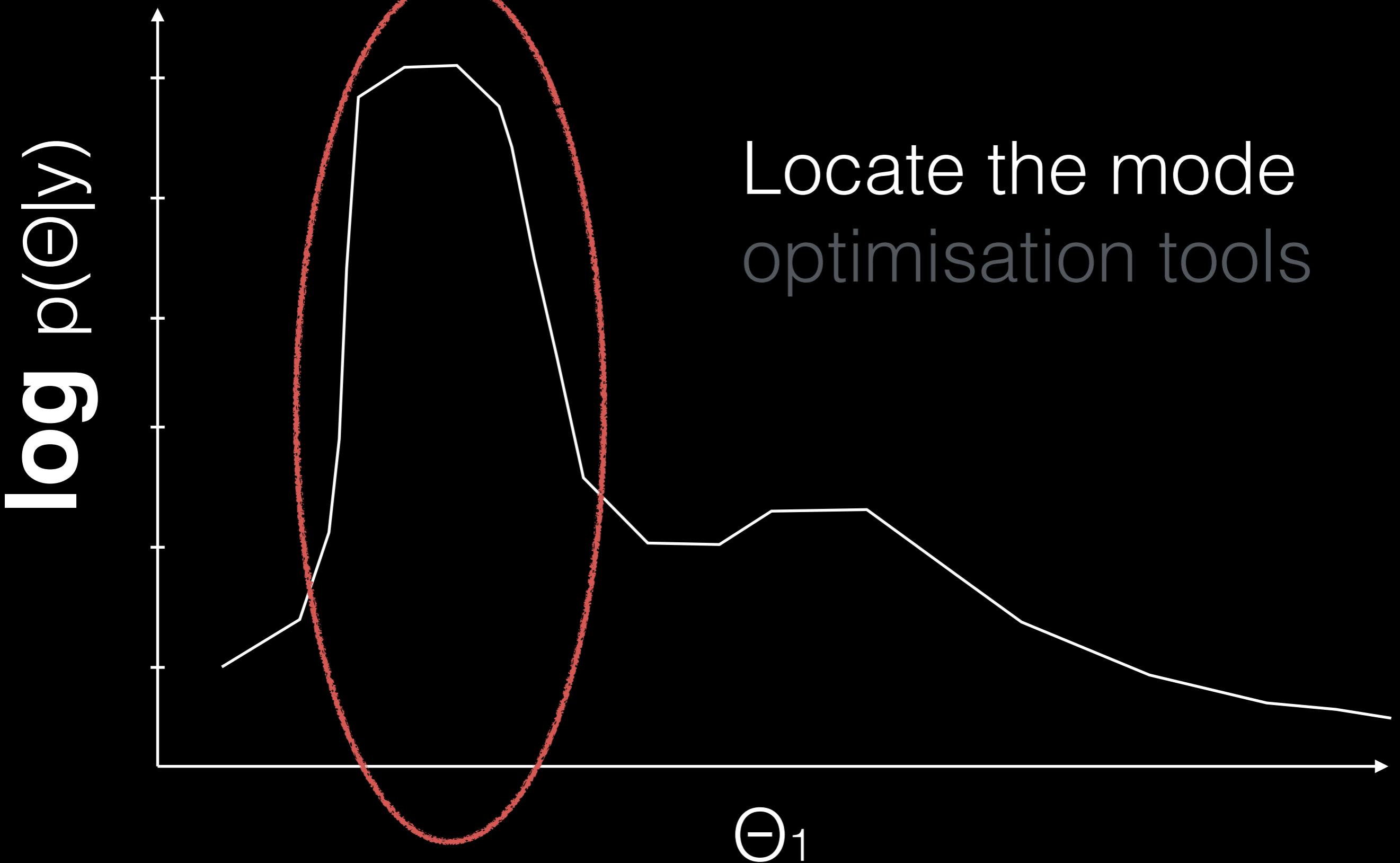


$$p(\Theta|y) \propto p(y|\Theta)p(\Theta)$$

Inference Exploring $p(\Theta|y)$



Inference Exploring $p(\Theta|y)$



Inference Exploring $p(\Theta|y)$

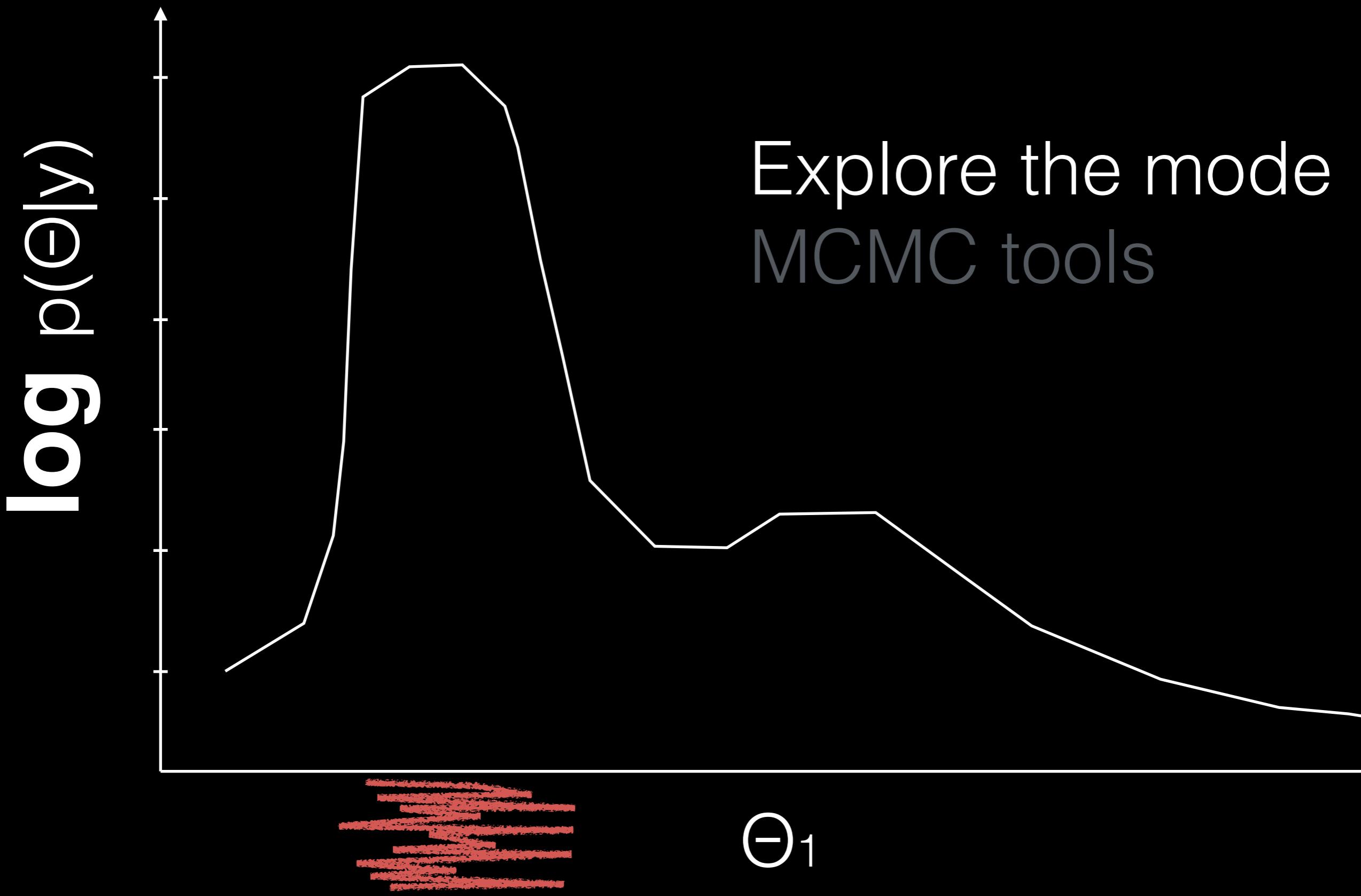


Illustration Manual inference

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

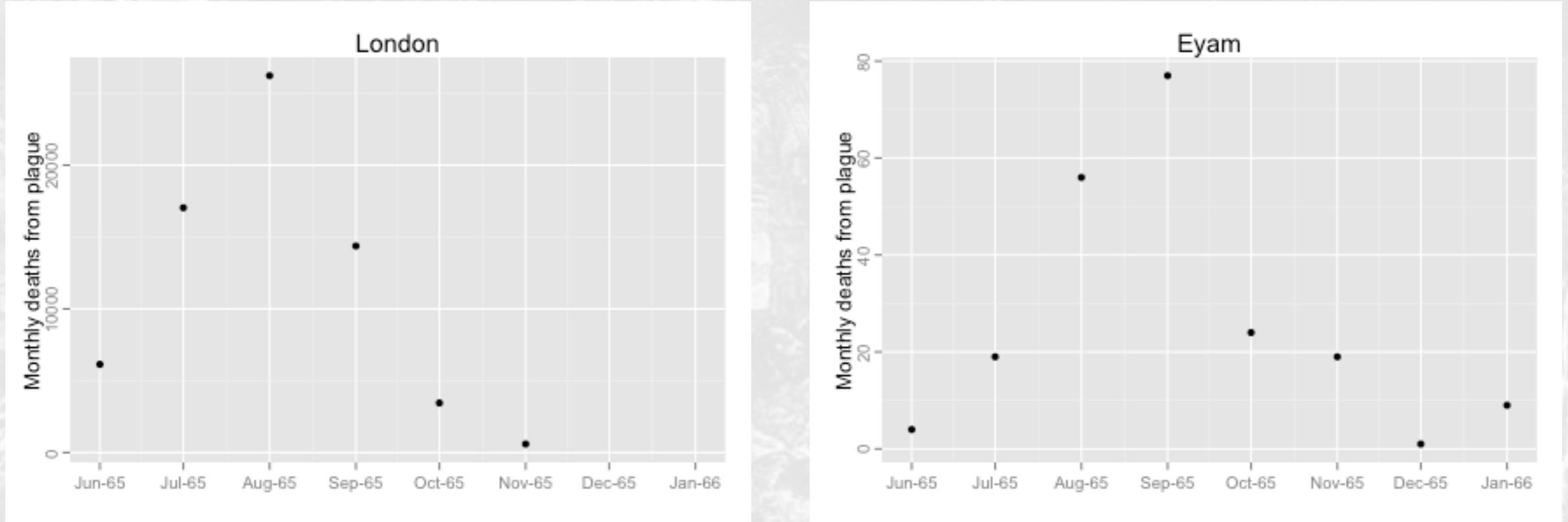
In the parent directory:

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

```
> ssm run
```

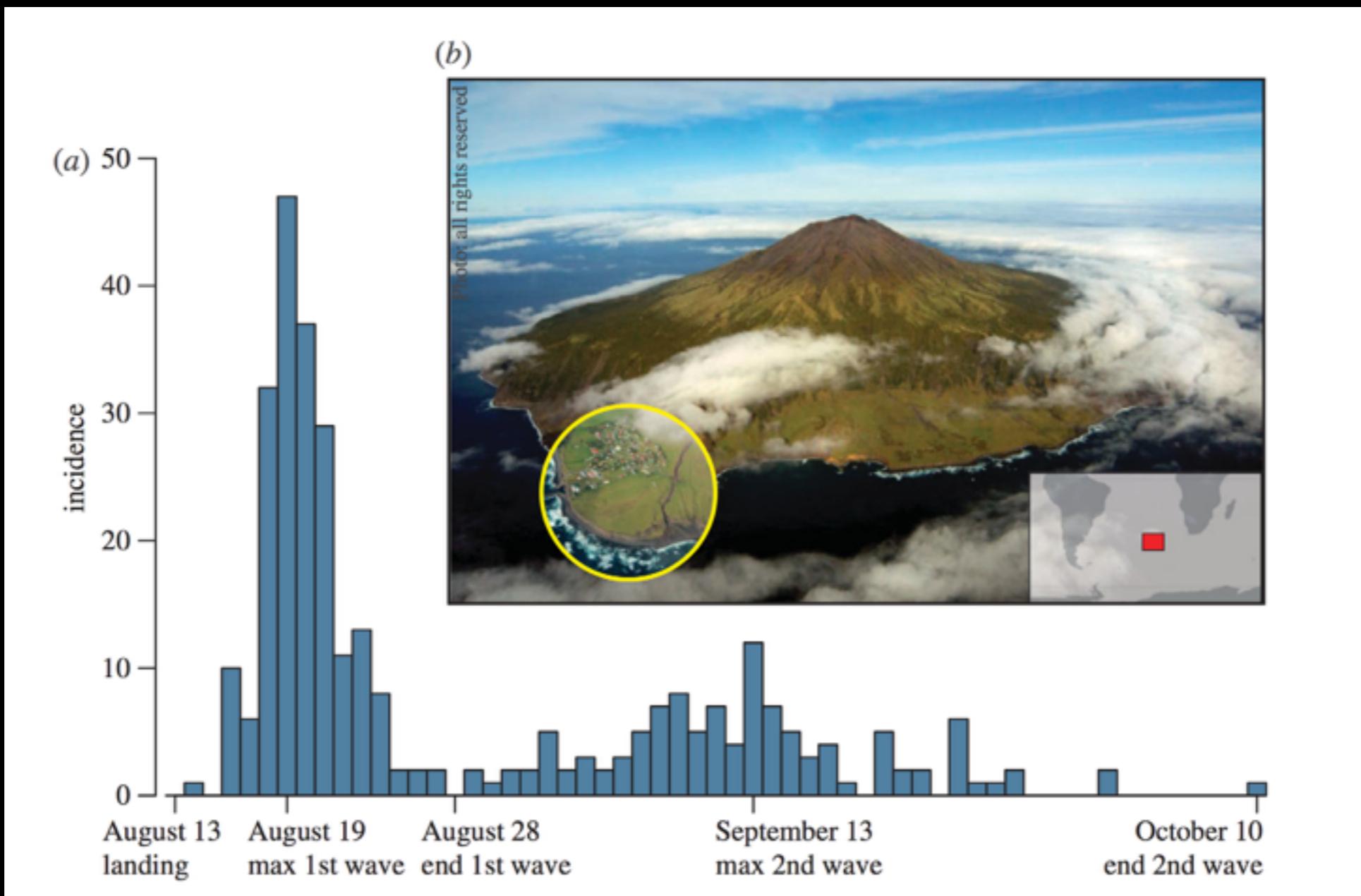
use `ssm.plot.trace`, and `ssm.plot.post`

A first real example



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

A second real example

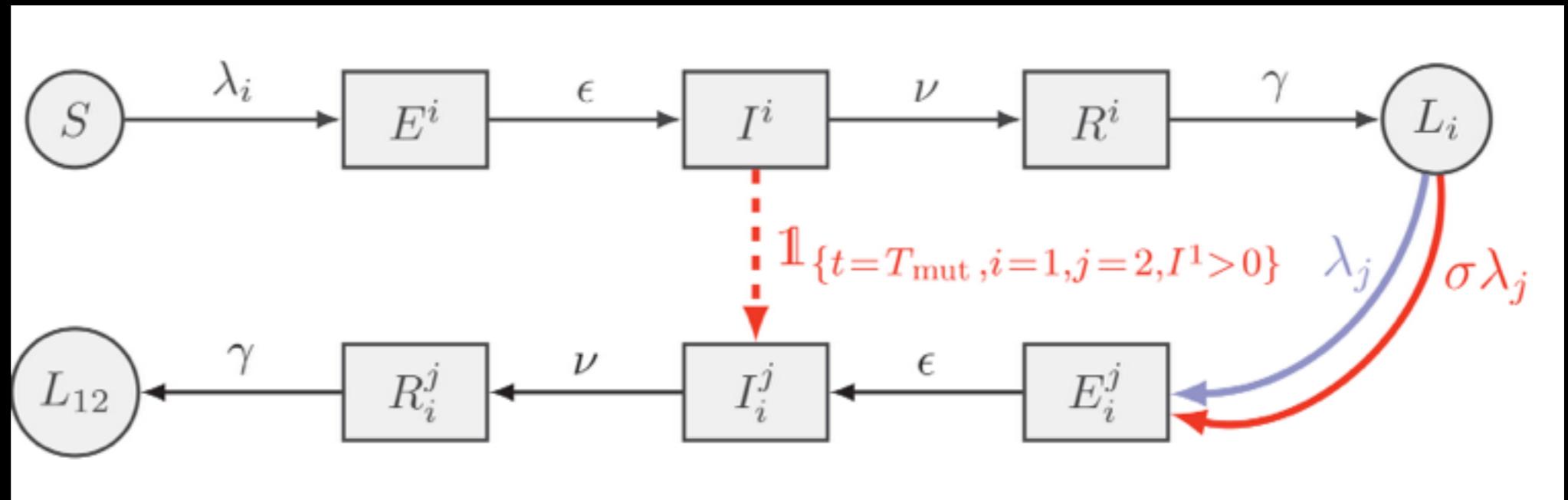


Explaining rapid reinfections in multiple-wave influenza outbreaks: Tristan da Cunha 1971 epidemic as a case study

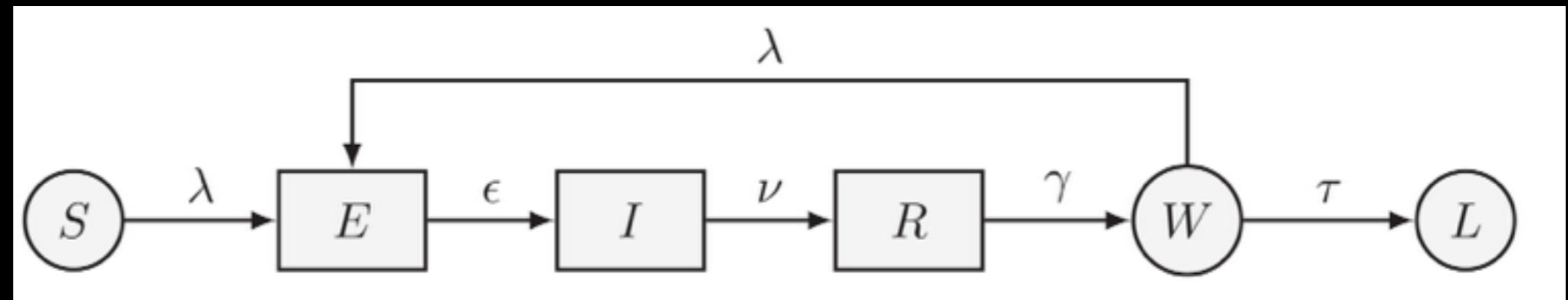
Two theories

Mut

Strain
mutation



Win
Reinfection
window



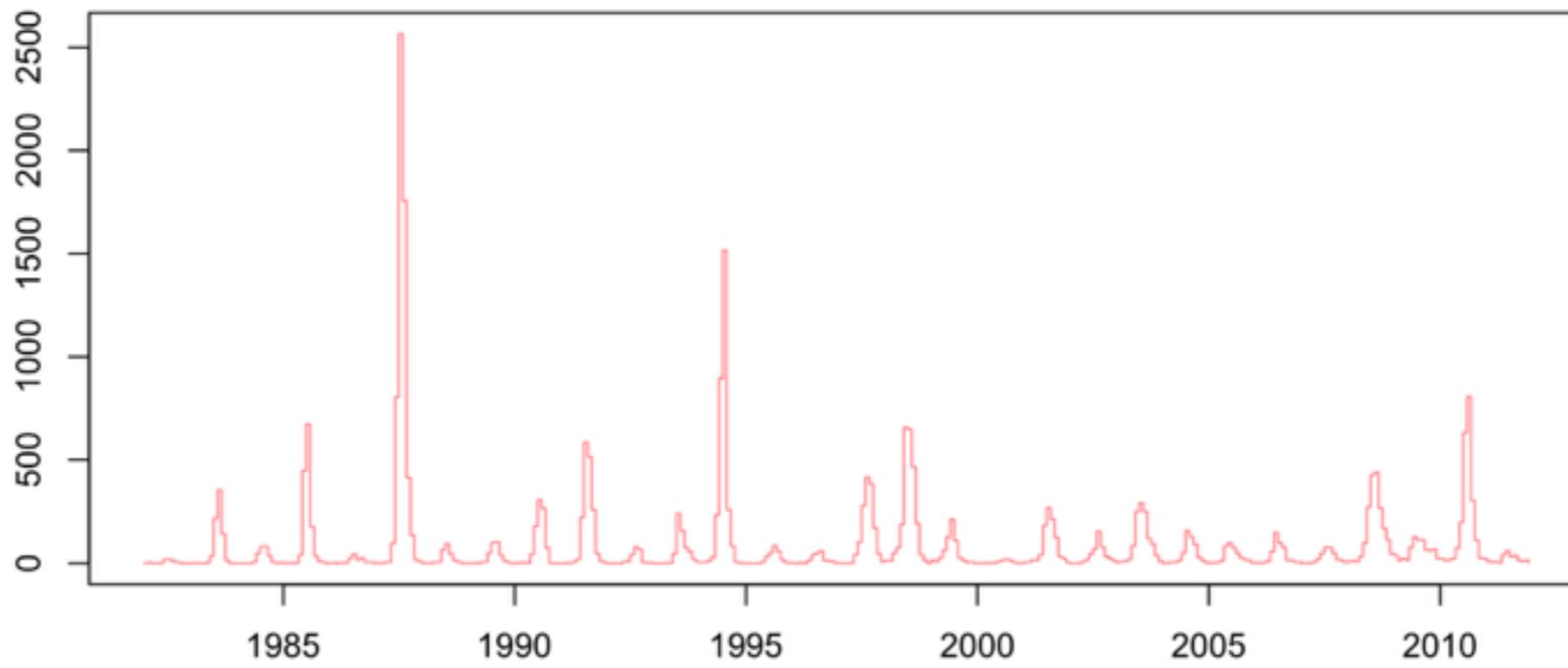
Fit both models. Conclude.

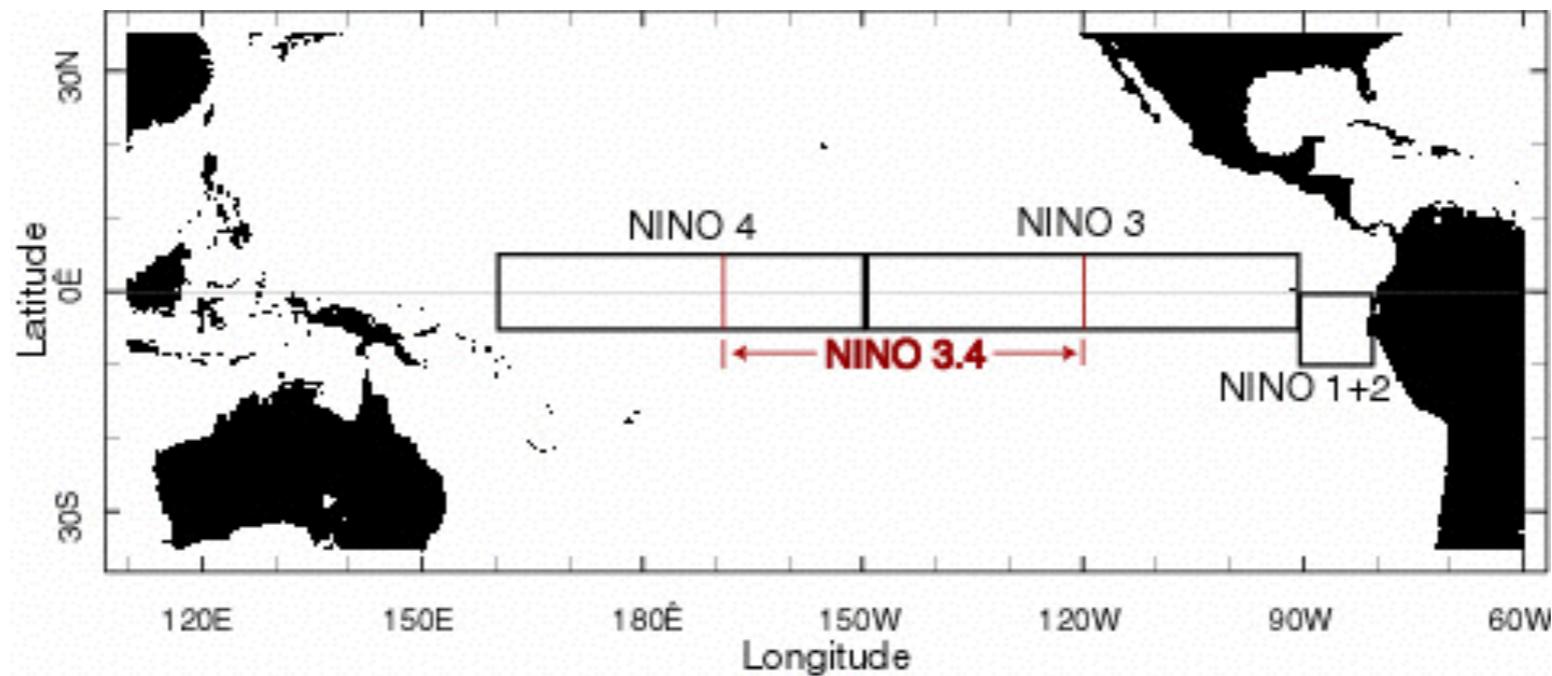
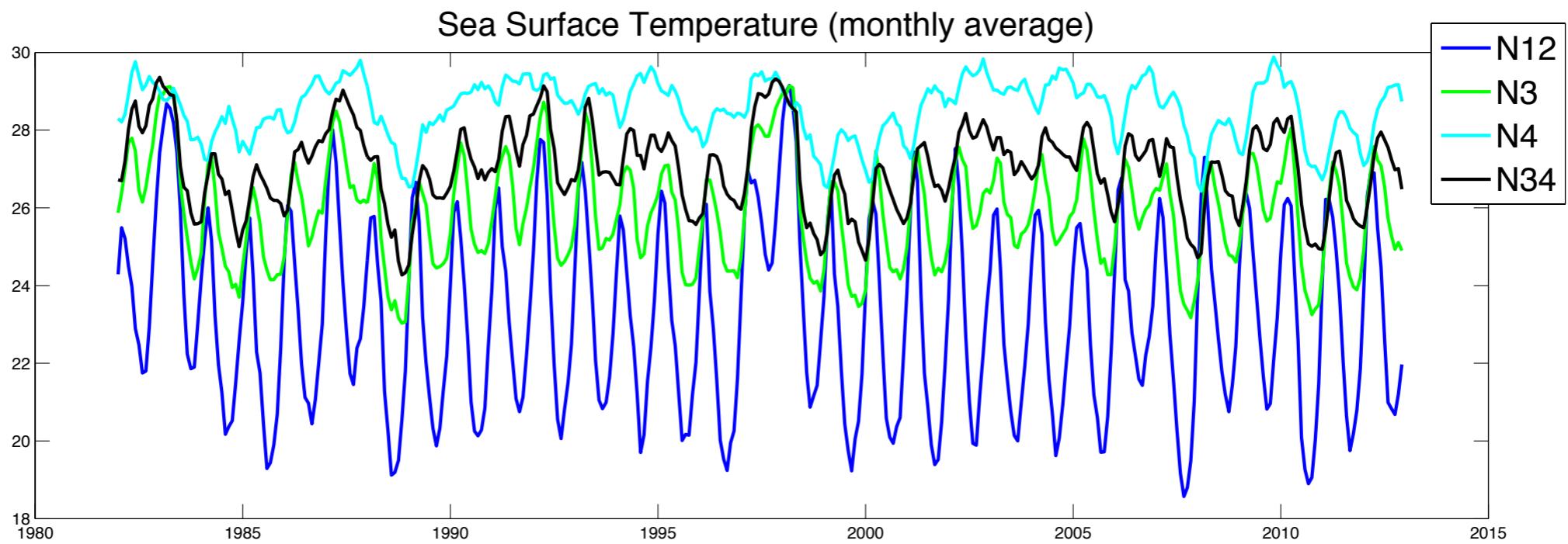
Objective



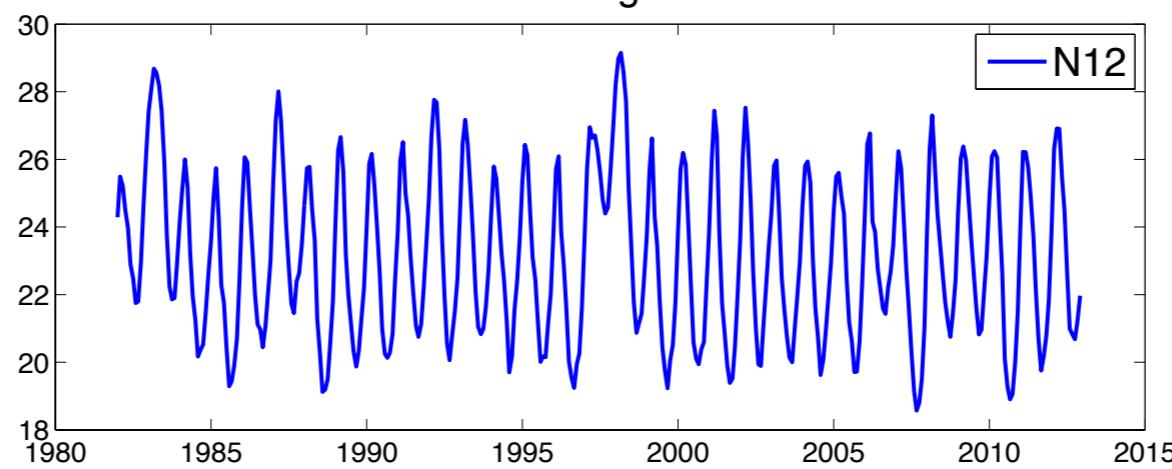
Explore the link between climate and
Dengue in Thailand

Monthly recorded cases
Chiang Mai district

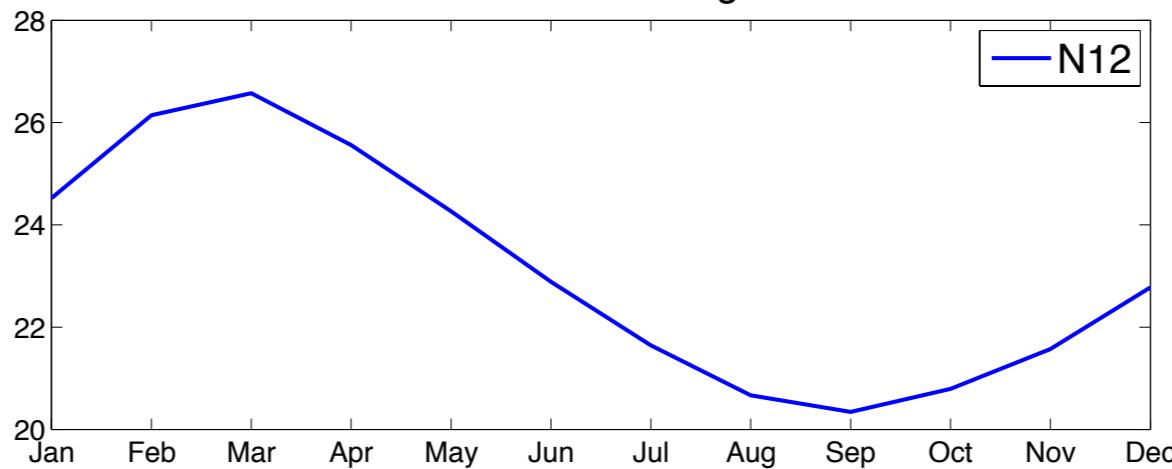




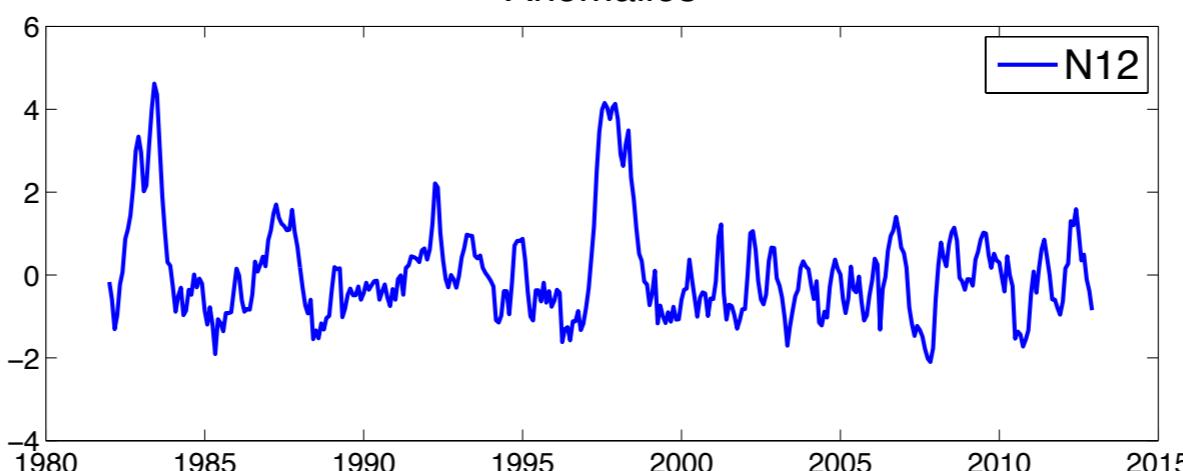
Full Signal



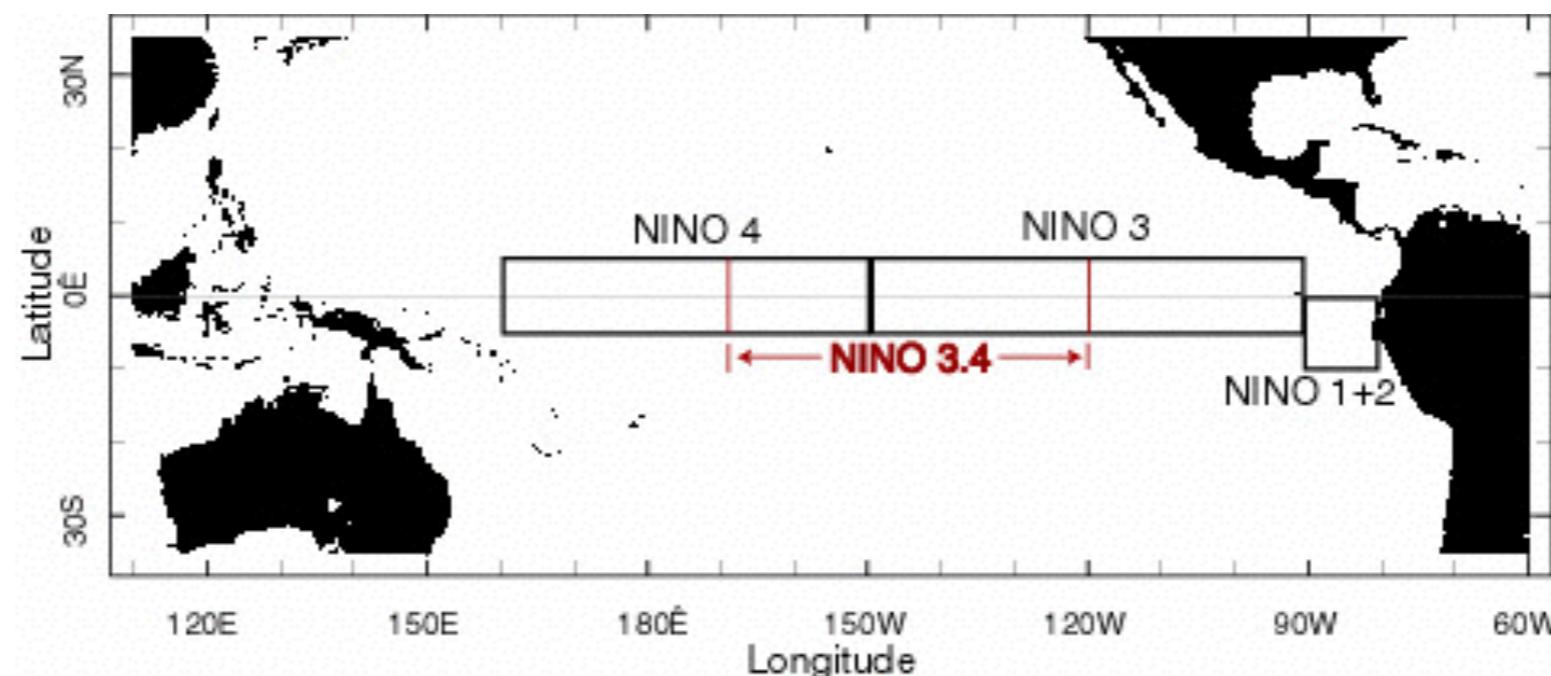
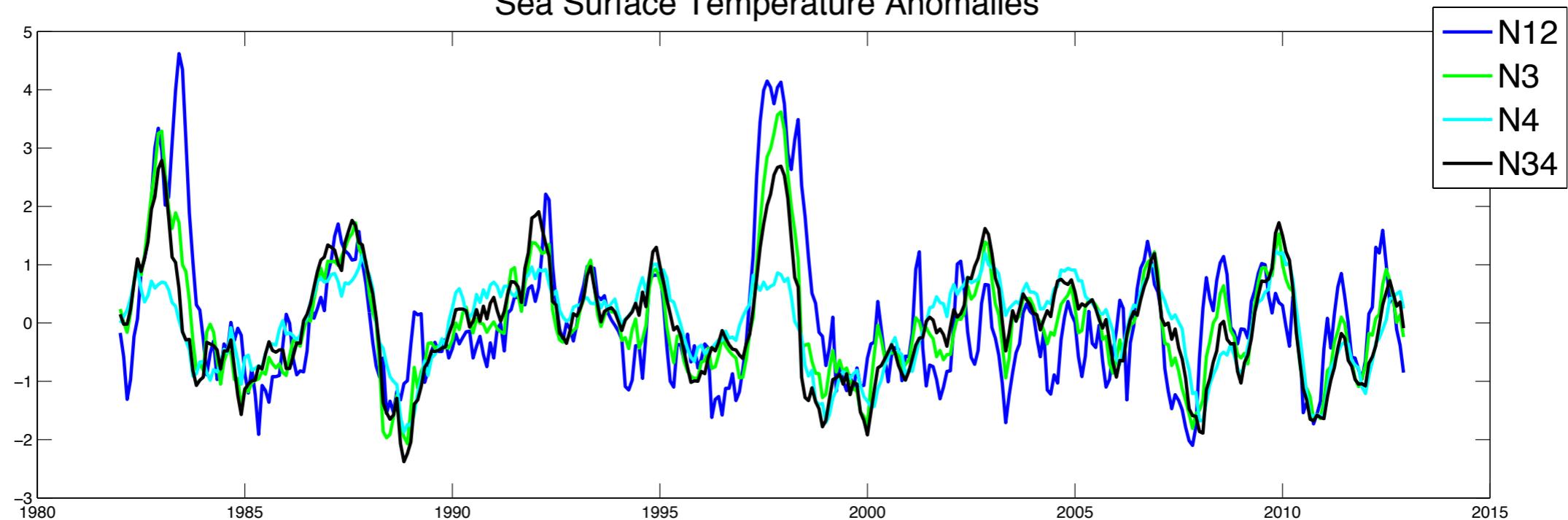
Mean Periodic Signal



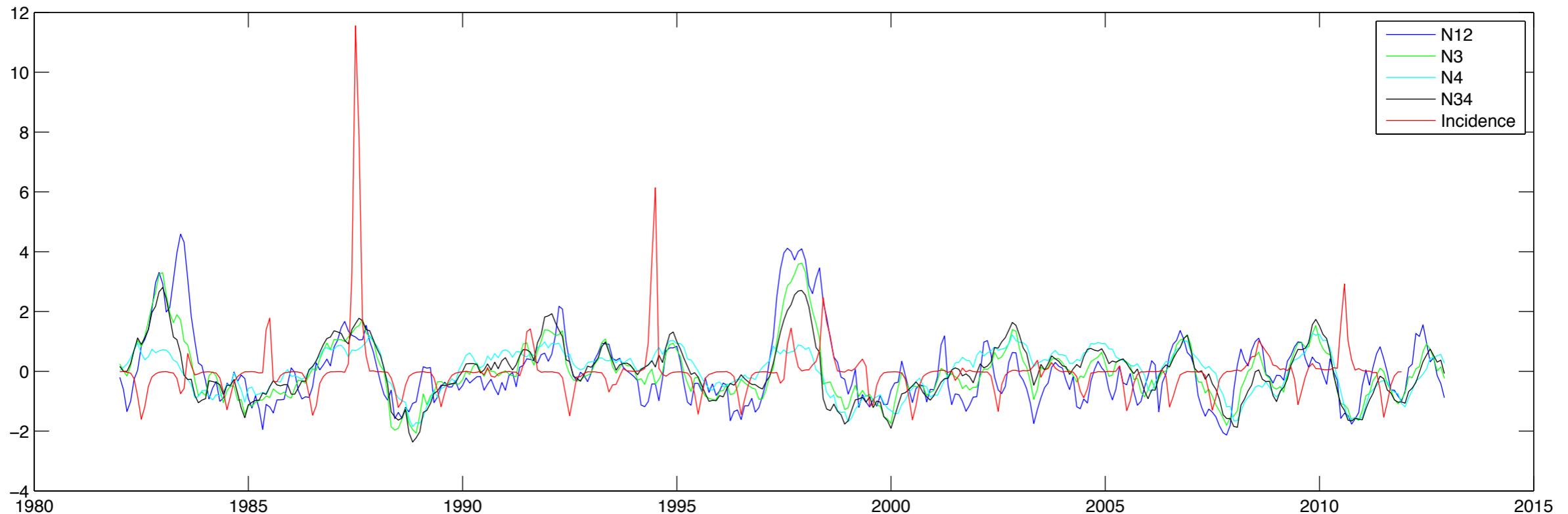
Anomalies



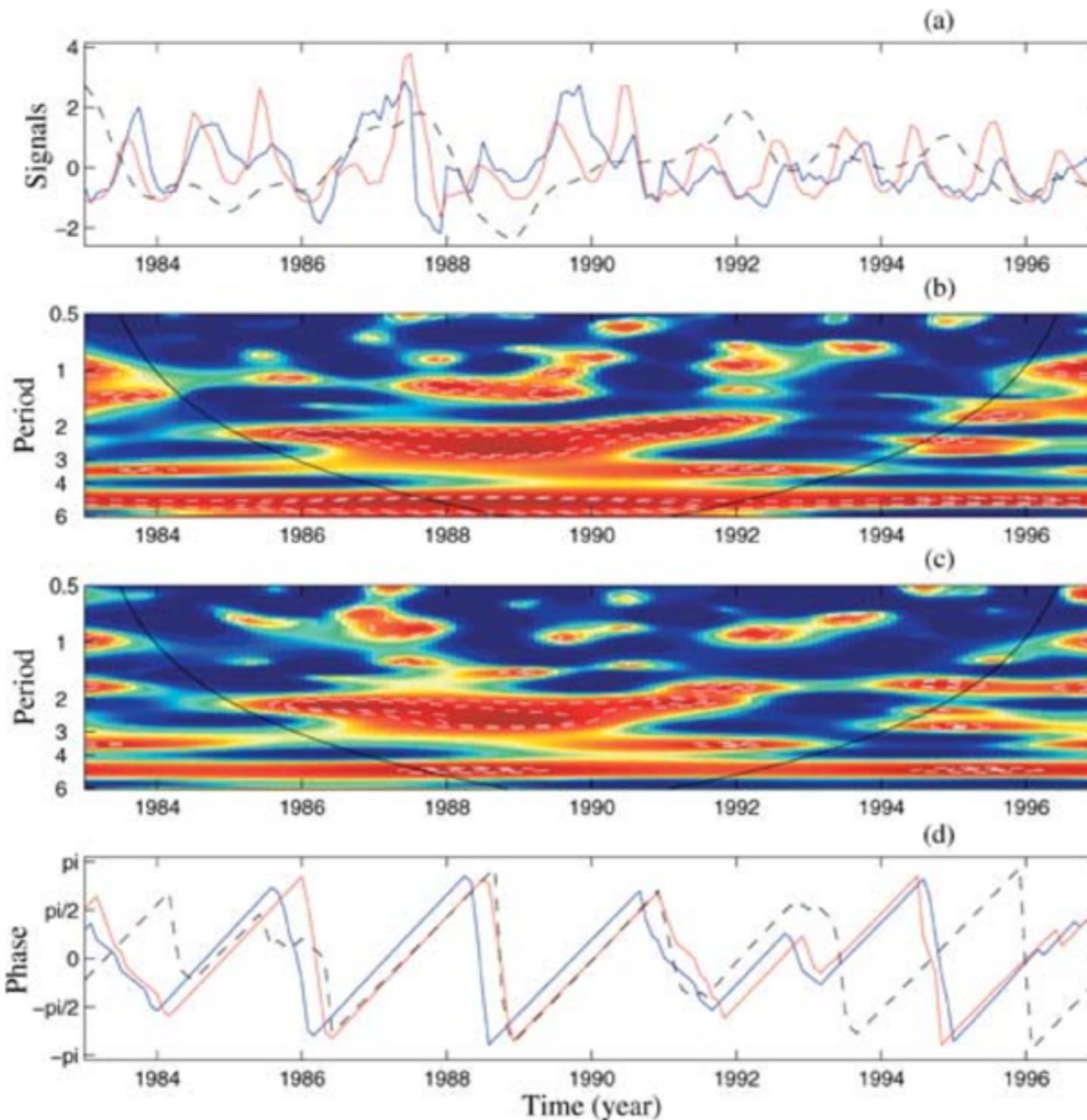
Sea Surface Temperature Anomalies



At first sight



	Lag (months)	Correlation	p-value
N12	-6	0,17	0,001
N3	-6	0,17	0,001
N4	-6	0,16	0,002
N34	-6	0,19	0,0002



“(...) significant association between El Niño, climate variables, and DHF incidence for Bangkok and for the rest of Thailand.’

“Dengue in Bangkok seems to precede the oscillations of the Nino 3 index.”

“These findings do not exclude an important role for other factors, such as intrinsic disease dynamics, in explaining patterns of dengue incidence in Thailand.”

Cazelles, B., Chavez, M., McMichael, A. J., & Hales, S. (2005). Nonstationary influence of El Niño on the synchronous dengue epidemics in Thailand. *PLoS medicine*, 2(4), e106.

Is a model with specific
climatic forcing better than a
classic sinusoidal forcing?

You
have:

- Severe cases data
- Tempmax/min , rain
and humidity
- Population size

-Understand/check the model following the ref.

-Understand what happens with the MLE. Could you improve the fit?

-Plot and make first explorations of raw data in R.

```
Clim = read.csv('2strains-Dengue-Thailand/data/  
dataClim_Chaiyaphum')
```

Explore.