#### Fitting dynamic models to data

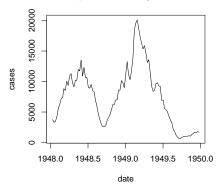
Jonathan Dushoff, McMaster University http://lalashan.mcmaster.ca/DushoffLab

2016 Summer Course on Mathematical Modeling and Analysis of Infectious Diseases

National Taiwan University

#### Measles data

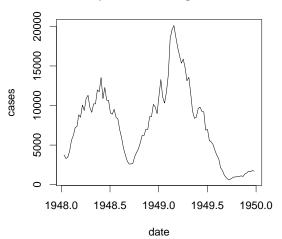
#### Measles reports from England and Wales



- Reconstruct the number of susceptibles
- Divide the data into generations
- ightharpoonup Fit  $\mathcal{R}_0$
- Predict

### Why did I get the wrong answer?

#### Measles reports from England and Wales



## Why did I get the wrong answer?

- Model structure may be wrong
- Population structure may be wrong
- Stochasticity in disease observation and recording
- Stochasticity in transmission
- Multi-parameter estimation
  - Generation intervals

### Outline

### Conceptual framework

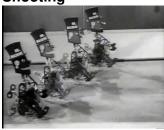
- How do we assume our data relate to our model world?
  - No error: We could attempt to model everything we see, in exact detail
  - Observation error: we could assume that the world is perfectly deterministic, but our observations are imperfect
  - Process error: we could assume that we observe perfectly, but that the world is stochastic
  - Both kinds of error: the world is stochastic, and our observations are imperfect

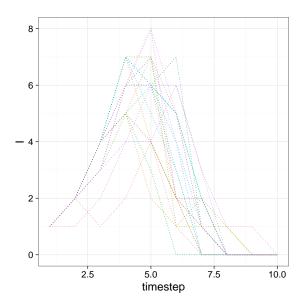
#### No error

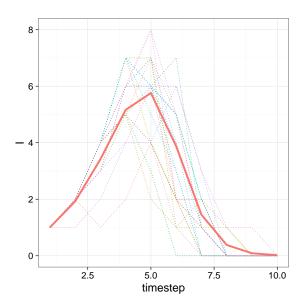
- Impossible
- ▶ Even if possible, not clear what we would learn

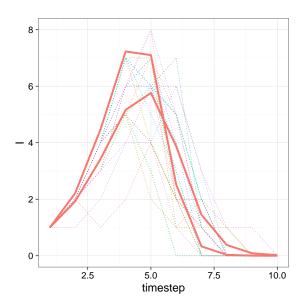
## Observation error only

- Point your model at the target
- Give it starting conditions and parameters
- Let it go
- Compare final results to observations

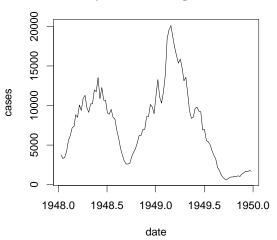








#### Measles reports from England and Wales



## Process error only

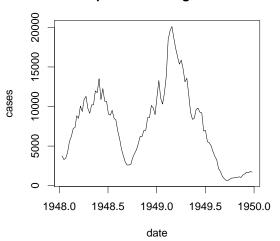
- Look at each step separately.
- See how the model is doing for that step.
- Reset based on observed data before taking the next step

#### Stepping

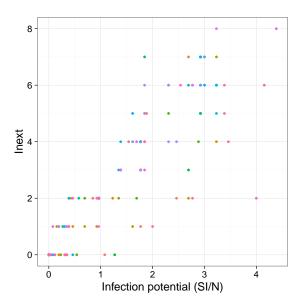


## Stepping

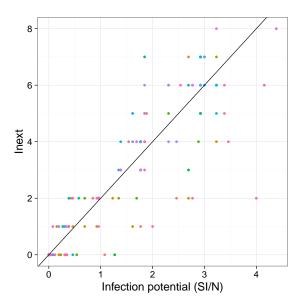
#### Measles reports from England and Wales



# Stepping



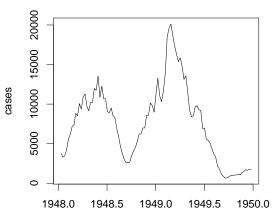
# Stepping



## Observation and process error

- Latent variable models
  - We need to keep track of, and integrate over, things that we don't observe

#### Measles reports from England and Wales

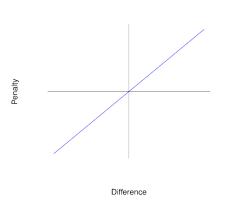


### Outline

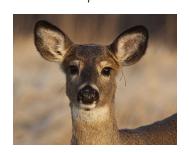
#### How to fit?

- Solving an equation
- By eye (fiddling with parameters)
- Minimizing a distance function
- Likelihood

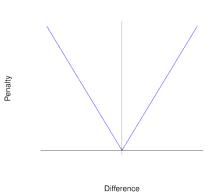
#### Distance functions



$$D=\sum_i y_i-\hat{y}_i$$



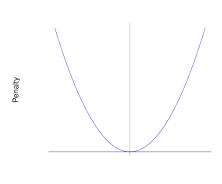
#### Distance functions



$$D=\sum_{i}|y_{i}-\hat{y}_{i}|$$



#### Distance functions



Difference

$$D = \sum_{i} (y_i - \hat{y}_i)^2$$



### Outline

#### Likelihoods

Assume that the difference between the estimate  $\hat{y}_i$  and the data point  $y_i$  is normally distributed. What is the log likelihood?

$$L = \prod_{i} \frac{1}{\sigma \sqrt{2\pi}} \exp\left(\frac{-(\hat{y}_i - y_i)^2}{2\sigma^2}\right)$$

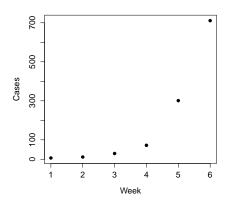
$$\ell = \sum_{i} -\log(\sigma\sqrt{2\pi}) - \sum_{i} \frac{(\hat{y}_{i} - y_{i})^{2}}{2\sigma^{2}}$$

- We minimize the likelihood by minimizing the sum of squares
  - and then solving for  $\sigma$

#### Least squares → likelihood

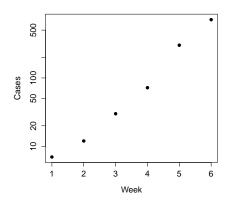
- Attaching your least squares fit to a likelihood means:
  - You can use it for statistical inference (LRT)
  - You can challenge the assumptions

## Mexican flu example



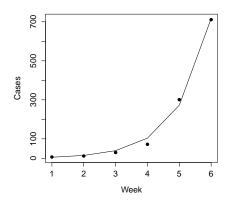
- ► How fast is it growing? *r*
- ► How hard will it be to control? R<sub>0</sub>

## A different perspective



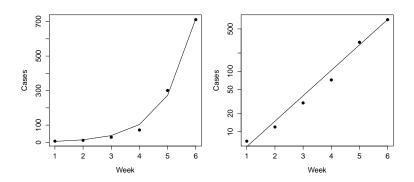
- We could make the normal assumption on either scale
- How much does it matter?

#### Normal assumption

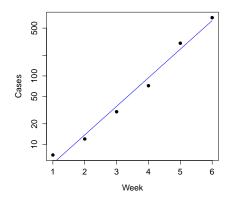


- Least squares on the linear scale
- **1**0:50 :: 980:1020
- Gives relatively too much weight to large observations

# Normal assumption

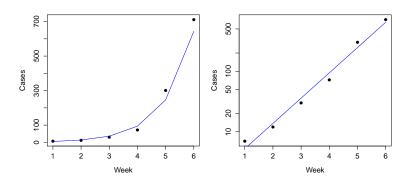


## Lognormal assumption



- Least squares on the log scale
- **3:5::300:500**
- Gives relatively too much weight to small observations

# Lognormal assumption



#### A more realistic error distribution

- My case counts are individuals
- What distributions can I use to reflect that?
- \* Poisson or binomial
  - ▶ \* WRONG!
  - ▶ \* *Sorry*:
    - \* OK, technically it's right, but you shouldn't do it.

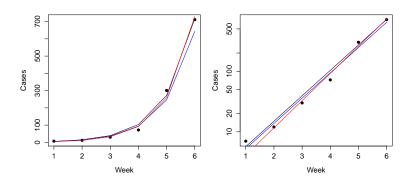
# Reality is complicated

- Poisson and binomial reflect only individual-level variation
  - No temporal variation
  - No clustered sampling
  - **.** . . .



# Distribution diagram

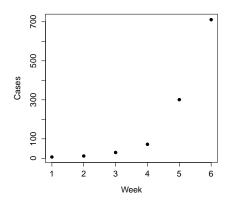
# Negative binomial fits



### Comparison

- Realistic error distribution provides (apparently) better fits
- Confidence intervals
  - Normal: r = 0.96-0.97/wk
  - Lognormal: r = 0.64-1.29/wk
  - Negative binomial: r = 0.90−1.14/wk
- How would you test these methods?
  - \* Validation: use simulated data to see if your method is reliable

# Identifiability



- What if we tried to estimate R₀ from data like these?
  - ▶ \* Disease could be fast with low  $\mathcal{R}_0$  or slow with high  $\mathcal{R}_0$ .

#### Outline

# Modern approaches

- Why are people using model worlds with no observation error?
  - or no process error?
- Sometimes they are good enough (model validation)
- Combining both is hard

## **Filtering**

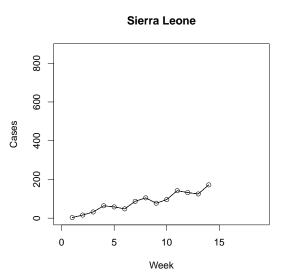
- Filtering is a little like shooting
  - Simulate from beginning to end, but use stochastic simulations
- You need a lot of simulations, and often ways of selecting and refining them
- A popular, state-of-the-art method is implemented in the R package pomp

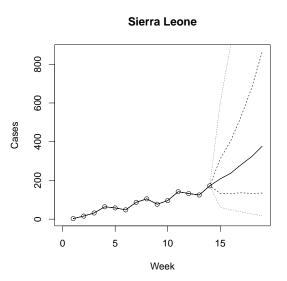
#### Latent variable methods

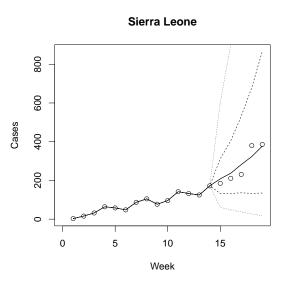
- Latent variable methods are a little like stepping
  - ▶ But we step to and from unknown values (our latent variables), so we need a way of exploring many possibilities
- Popular, state-of-the-art methods are available in the R packages rjags and rstan

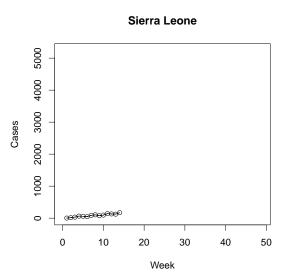
# Multi-parameter inference

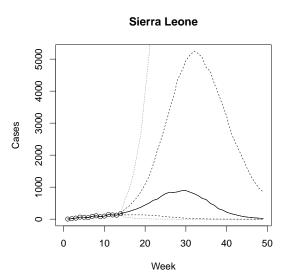
- Modern methods are already hard, and when you consider various sources of uncertainty, you're really on the bleeding edge
- Many high-profile models for Ebola, for example failed to consider process error.
- The biggest paper talking about process error neglected uncertainty in generation intervals
- Once you do multi-parameter inference, you may find that confidence intervals are very large – this may reflect the reality of knowledge, but may not make you look good

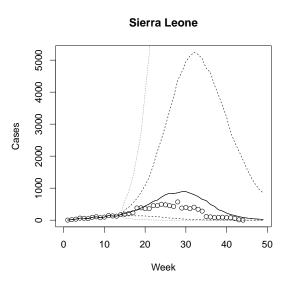












#### Outline

#### Likelihood

- Maximum likelihood and likelihood are not the same thing
- Bayesian approaches and frequentist approaches (including maximum likelihood) both depend on calculating (or approximating) likelihood

#### Frequentist inference

- ➤ To do frequentist inference on these complicated likelihoods, we need to:
  - estimate likelihoods
  - find the maximum likelihood
  - use the likelihood ratio test to find confidence intervals
- This is hard

#### Bayesian inference

- To do Bayesian inference on these complicated likelihoods, we need to:
  - construct prior distributions
  - estimate likelihoods
  - estimate the posterior
- Usually a little less hard
  - But still requires more assumptions

#### Conclusion

- We need dynamics to understand links between processes and outcomes
  - How do things work?
- We need statistics to understand uncertainty
  - What can we learn from data
- Combining these two is difficult, but progress is being made.