Approaches to dynamic fitting

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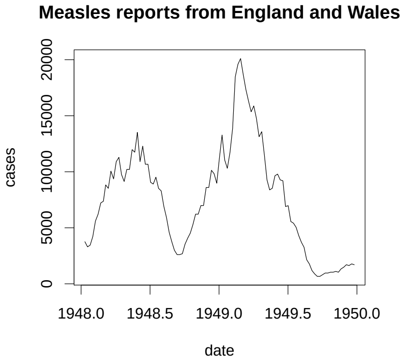
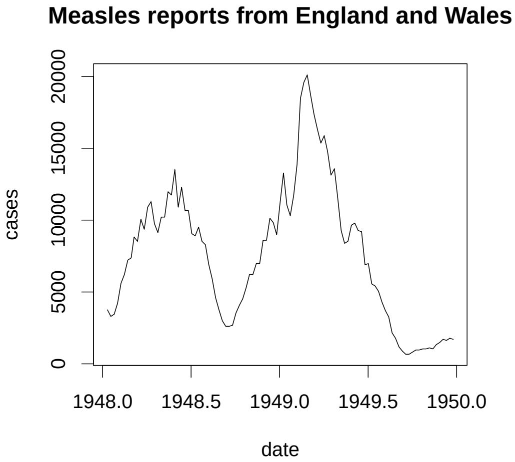
Measles data

- 

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

Why did I get the wrong answer?



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

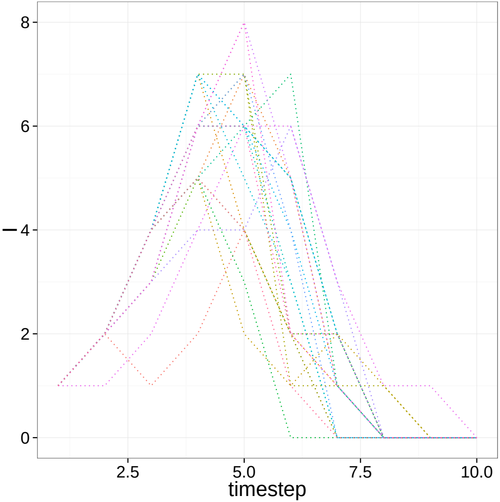
- Impossible
- Even if possible, not clear what we would learn

Observation error only

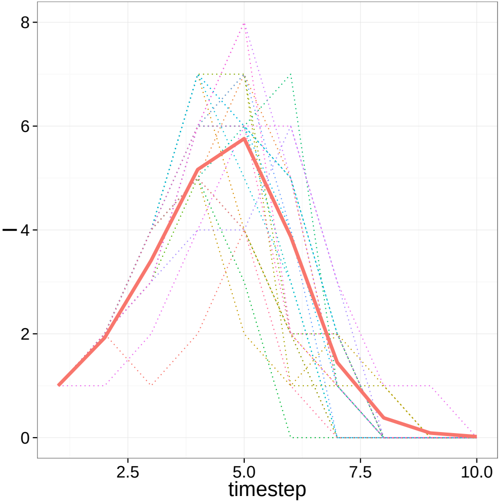
- Point your model at the target
- Give it starting conditions and parameters
- Let it go
- Compare final results to observations

Shooting

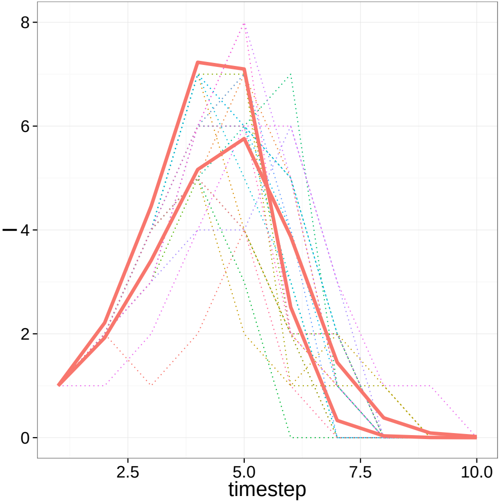
Shooting



Shooting



Shooting

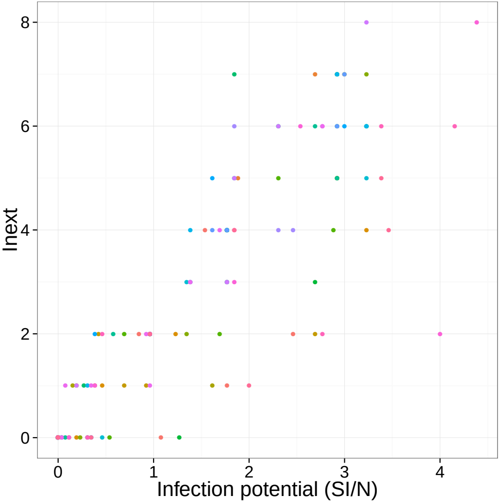


Process error only

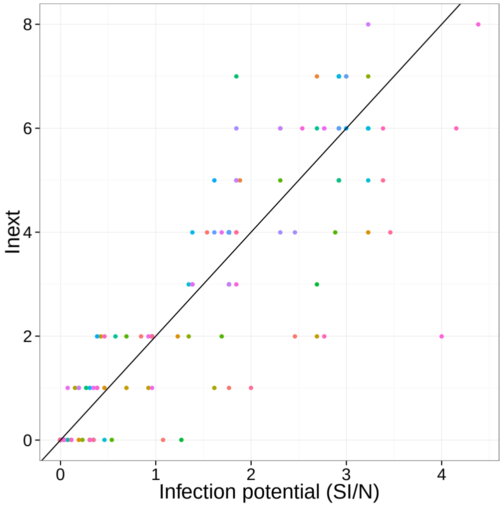
- Look at each step separately.
- See how the model is doing for that step.
- Reset based on observed data before taking the next step

Stepping

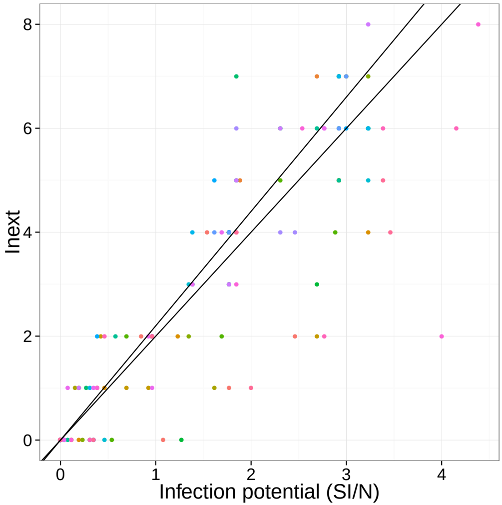
Stepping



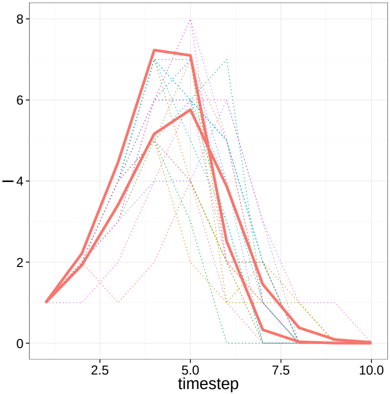
Stepping

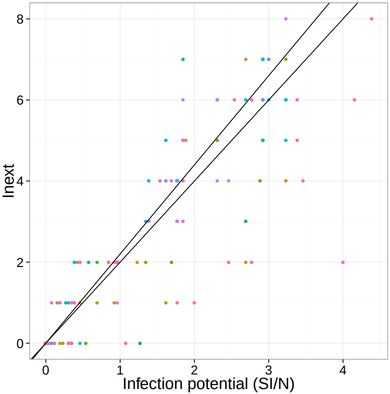


Stepping



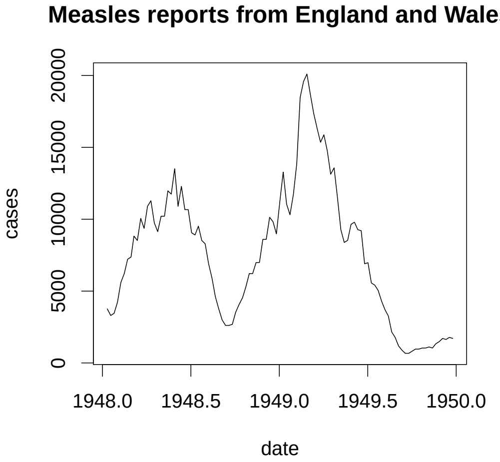
Comparing approaches





Observation and process error

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



Outline

How to fit?

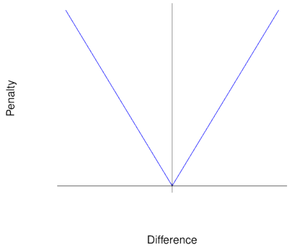
- Solving an equation
- By eye (fiddling with parameters)
- *Minimizing a distance function*
- Likelihood

Distance functions

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

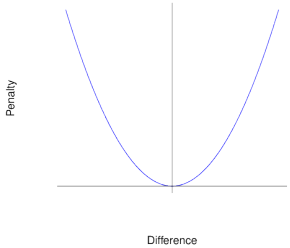
Distance functions

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



Distance functions

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



Outline

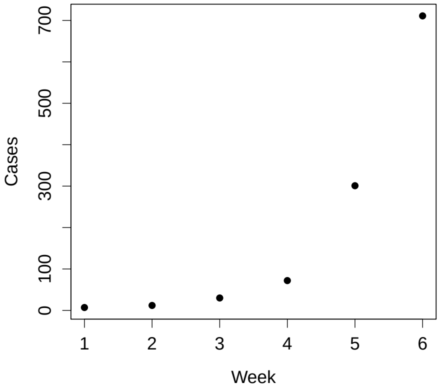
Likelihoods

- 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 σ

Least squares $\rightarrow$ likelihood

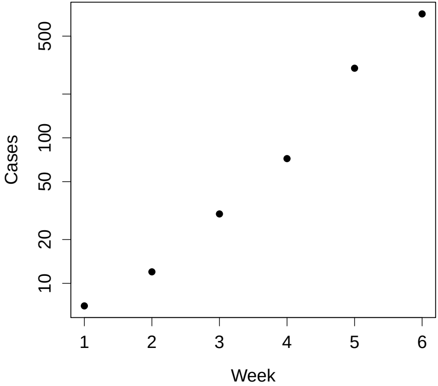
- Attaching your least squares fit to a likelihood means:
  - You can *use it* for statistical inference (LRT)
  - You can *challenge* the assumptions

Mexican flu example



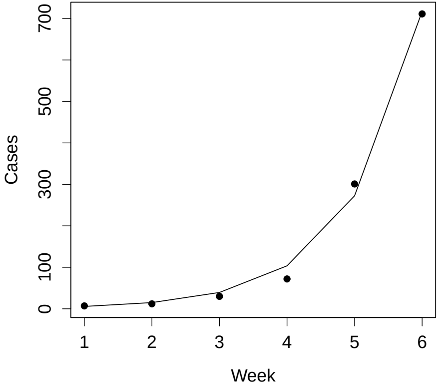
- How fast is it growing? r
- How hard will it be to control? $\mathcal{R}_0$

A different perspective

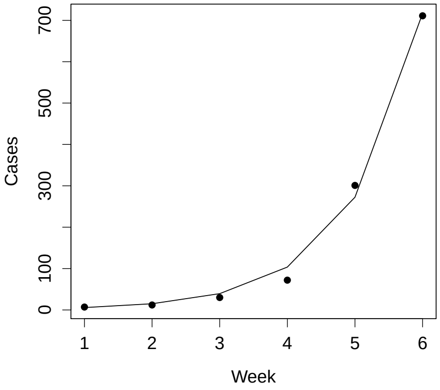


- We could make the normal assumption on either scale
- How much does it matter?

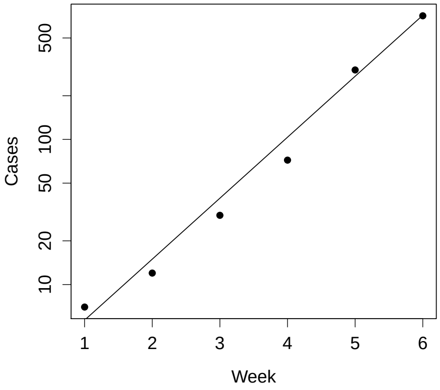
Normal assumption



- Least squares on the linear scale
- 10:50 :: 980:1020
- Gives relatively too much weight to large observations

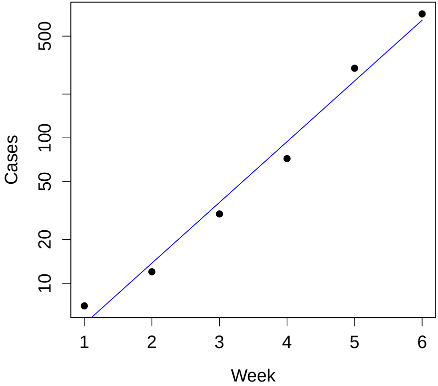


Cases
0
100
300
500
700
1
2
3
4
5
6
Week

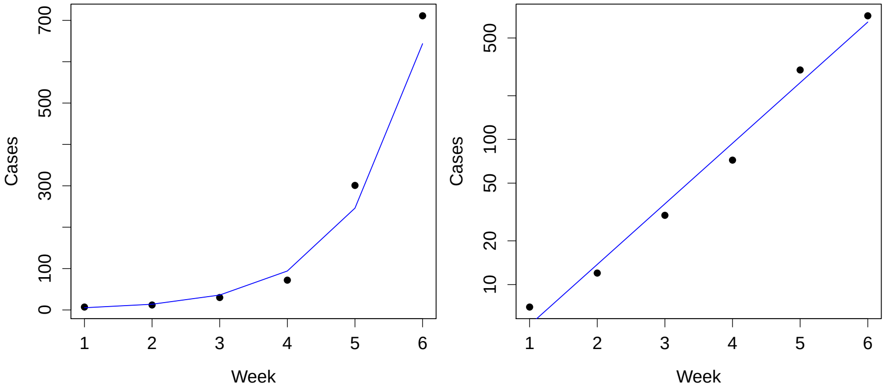


Cases
10
20
50
100
500
1
2
3
4
5
6
Week

Lognormal assumption



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


Cases
700
500
300
100
0
1
2
3
4
5
6
Week
Cases
500
100
50
20
10
1
2
3
4
5
6
Week

A more realistic error distribution

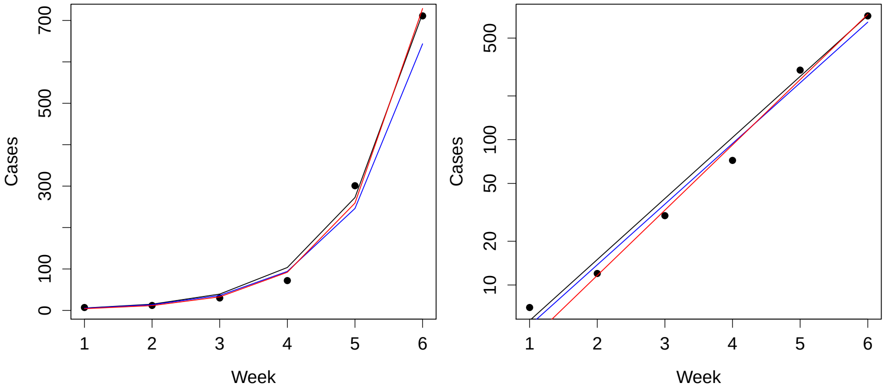
- My case counts are *individuals*
- What distributions can I use to reflect that?
- WRONG!
- *Sorry:*
  - OK, technically it's right, but you shouldn't do it.

Reality is complicated

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

Distribution diagram

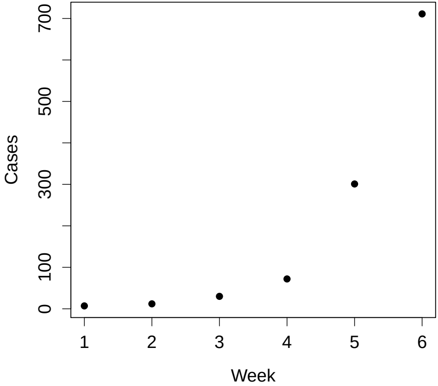
Negative binomial fits



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?

Identifiability



- What if we tried to estimate $\mathcal{R}_0$ from data like these?

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

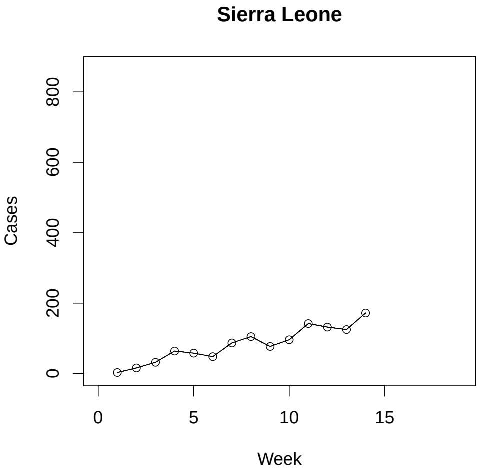
Latent variable methods

- 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

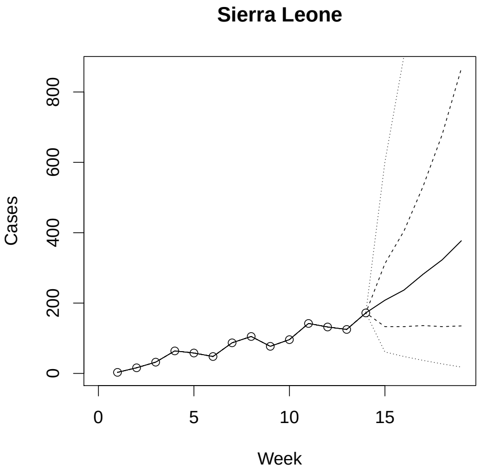
Multi-parameter inference

- 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

Assessing and reporting uncertainty



Assessing and reporting uncertainty



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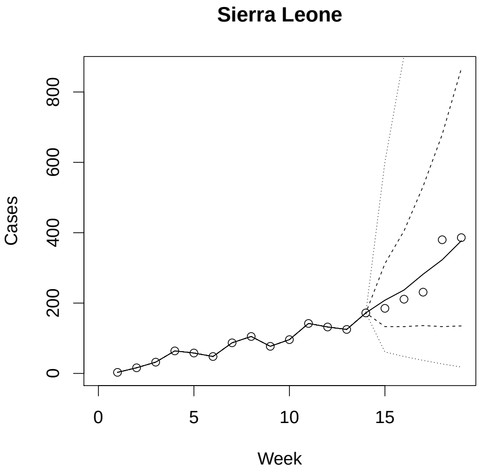

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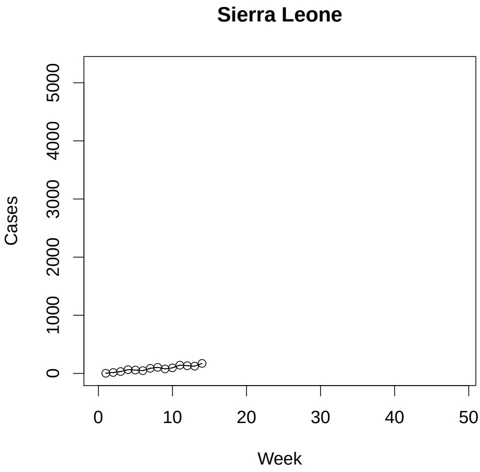

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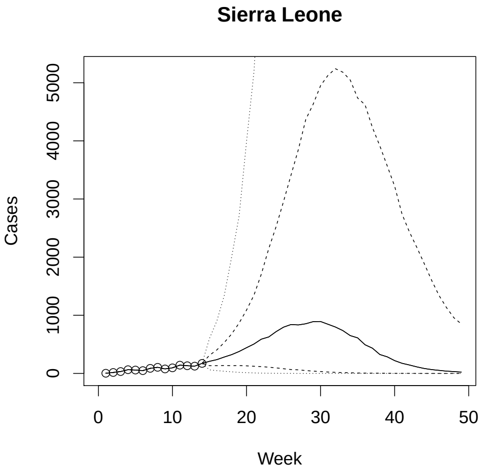
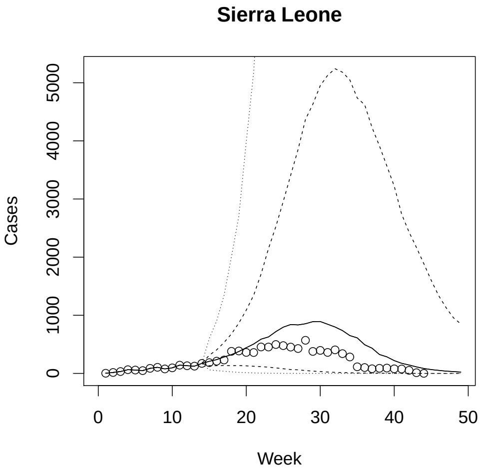


Assessing and reporting uncertainty



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
- Also hard, but sometimes easier than the frequentist approach