Lab 6 Summary

MLE fitting of a dynamic model to prevalence data

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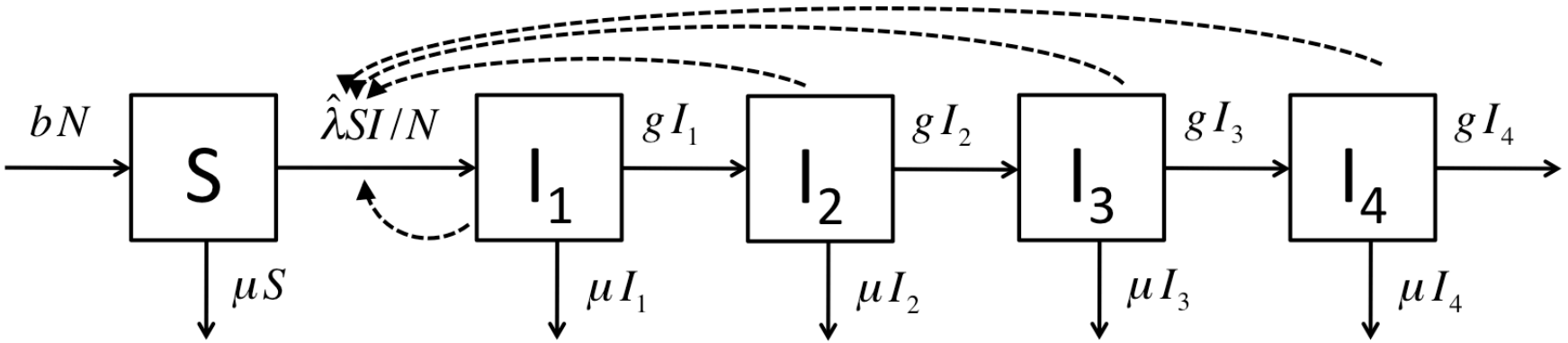
Goals

- Understand how to simulate cross-sectional prevalence data around a simulated epidemic trajectory
- Calculate the likelihood of prevalence data through time, given a fully specified epidemic model
- Understand that the likelihood is a function of the hypothesized model parameters (and structure) and that “fitting” the dynamic model involves maximizing this likelihood
- Understand why we transform parameters for fitting
- Think about how the choice of optimization algorithms affects the outcome of the optimization
- Create 95% confidence intervals and contours for a multivariate model fit

Summary: Background



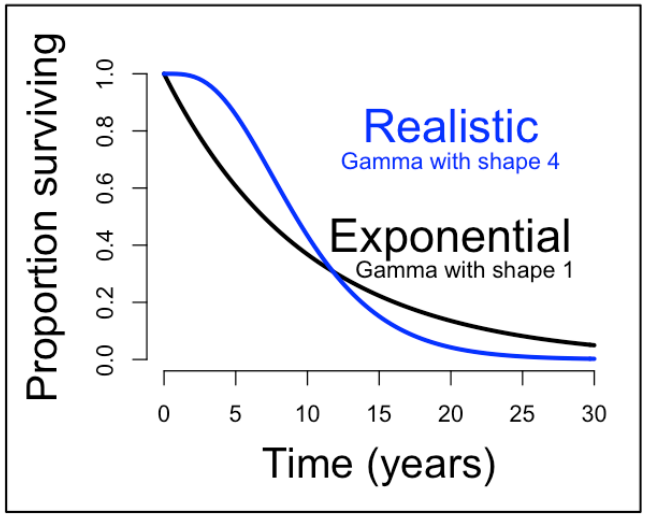
$$N = S + I; \quad I = I_1 + I_2 + I_3 + I_4$$

$$\hat{\lambda} = \lambda e^{-aP}$$

$$g = 4\delta$$

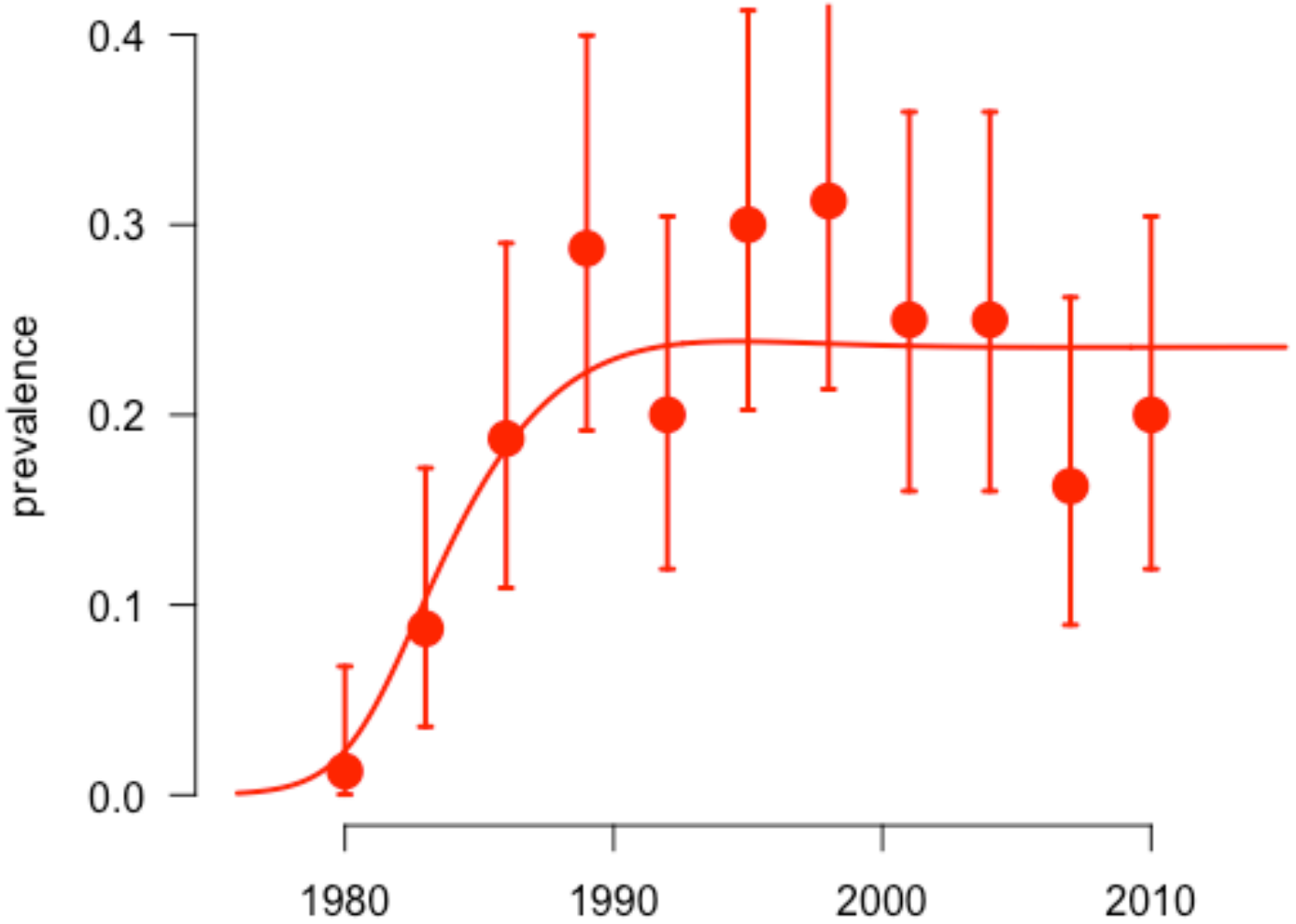
$b =$ *per capita* birth rate

$\mu =$ *per capita* background mortality rate



Realistic survival times

Summary: Simulated Data



Summary: Parameter Transformation

Why?

Most optimization algorithms assume the inputs are defined on a scale from $-\infty$ to ∞

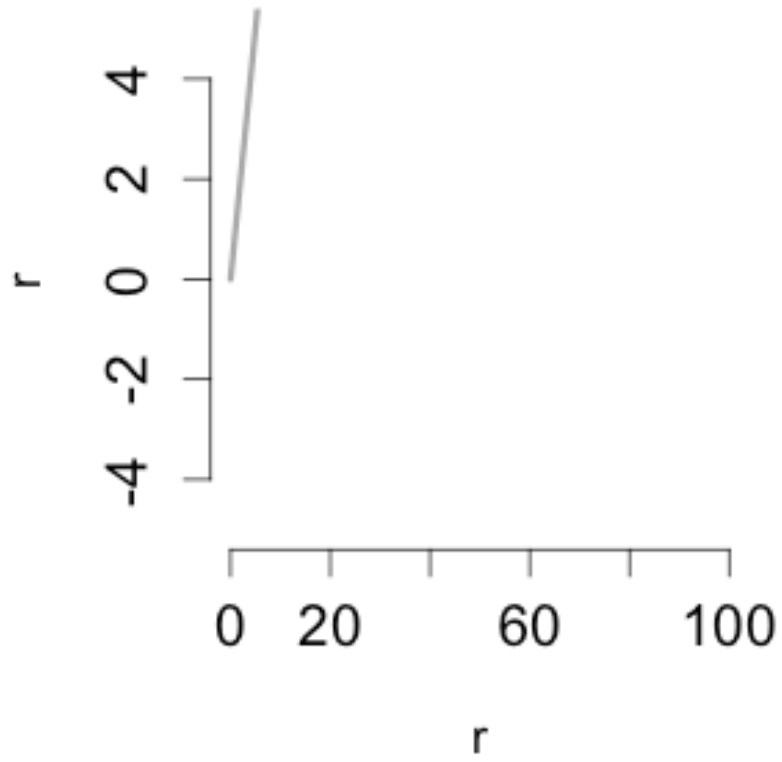
More efficiently explore parameter space

How?

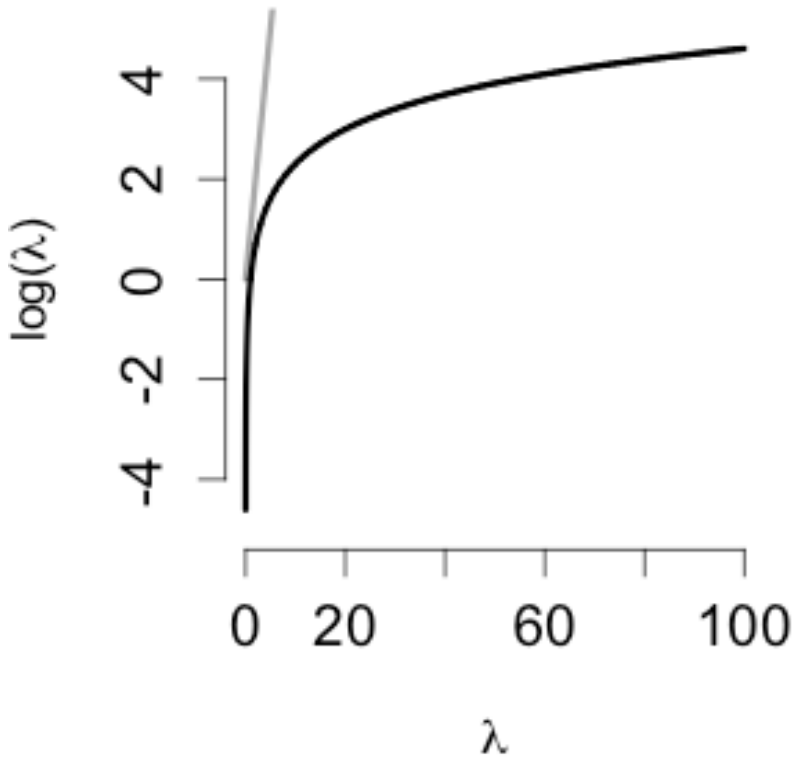
ICI3D

Parameters with strictly positive values

$y =$ r $ln(r)$



Linear

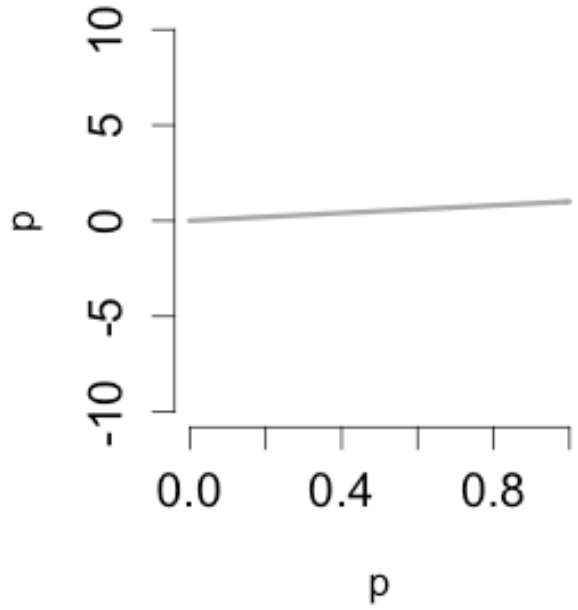


Log scale

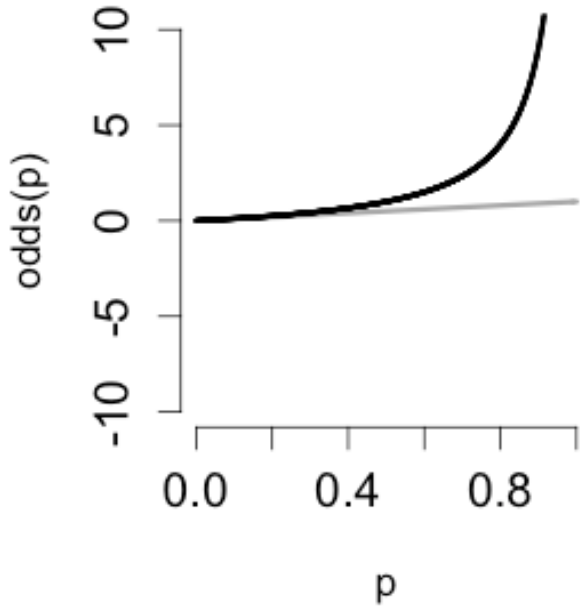
ICI3D

Parameters bounded between 0 and 1

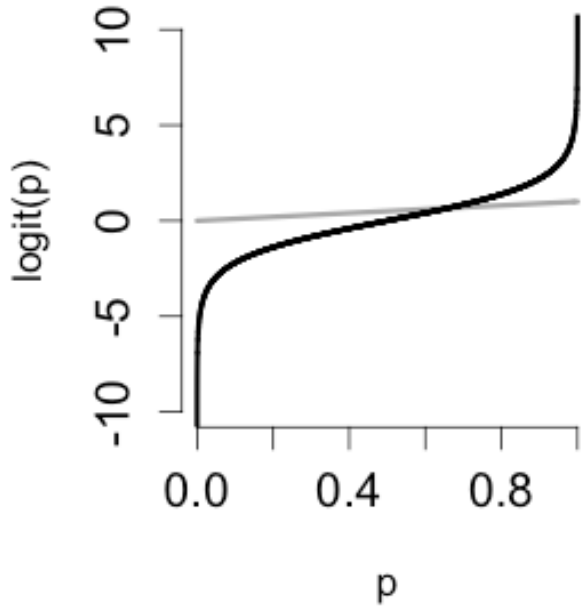
$$y = p \qquad \frac{p}{1-p} \qquad ln\left(\frac{p}{1-p}\right)$$



Linear

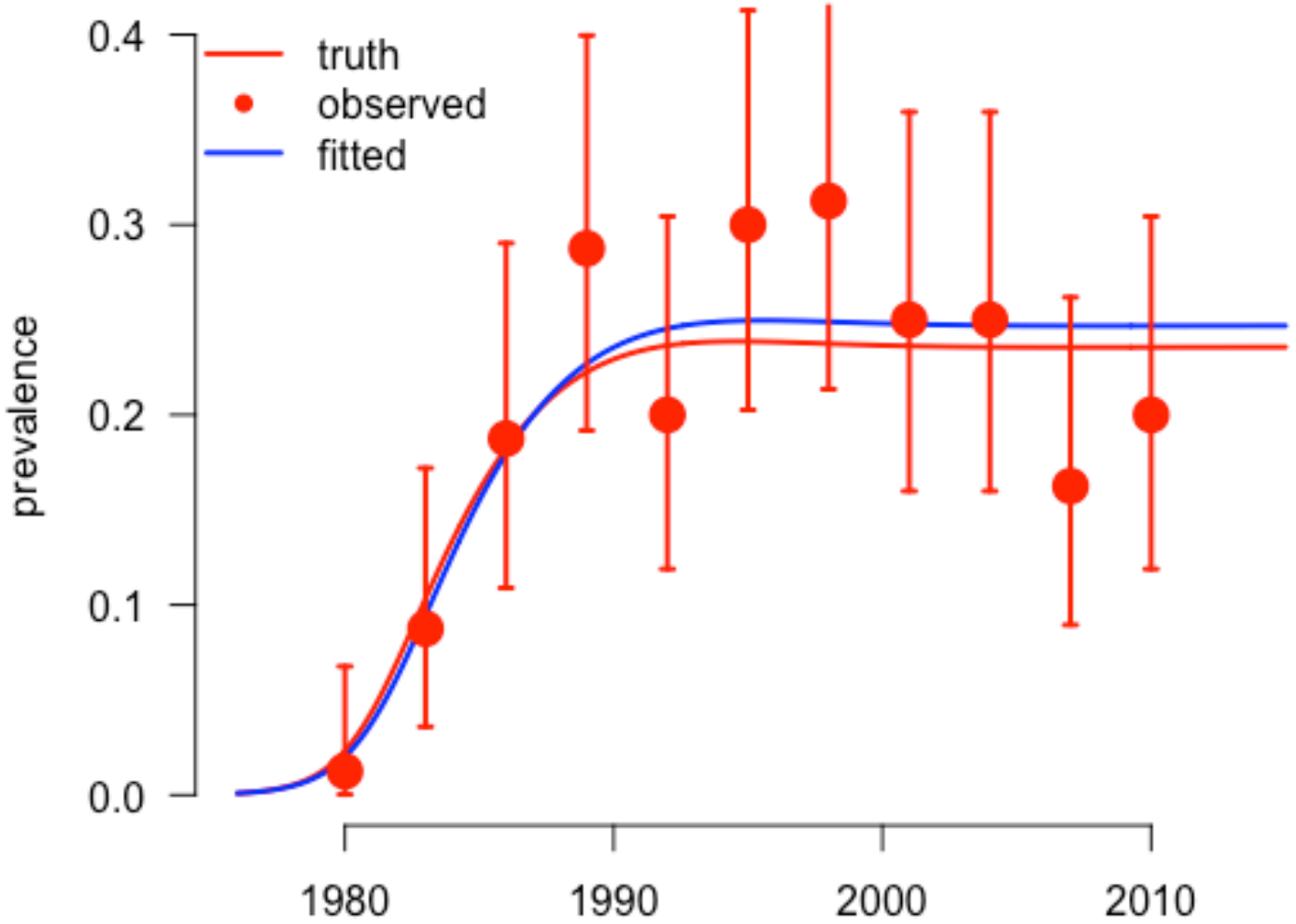


Odds

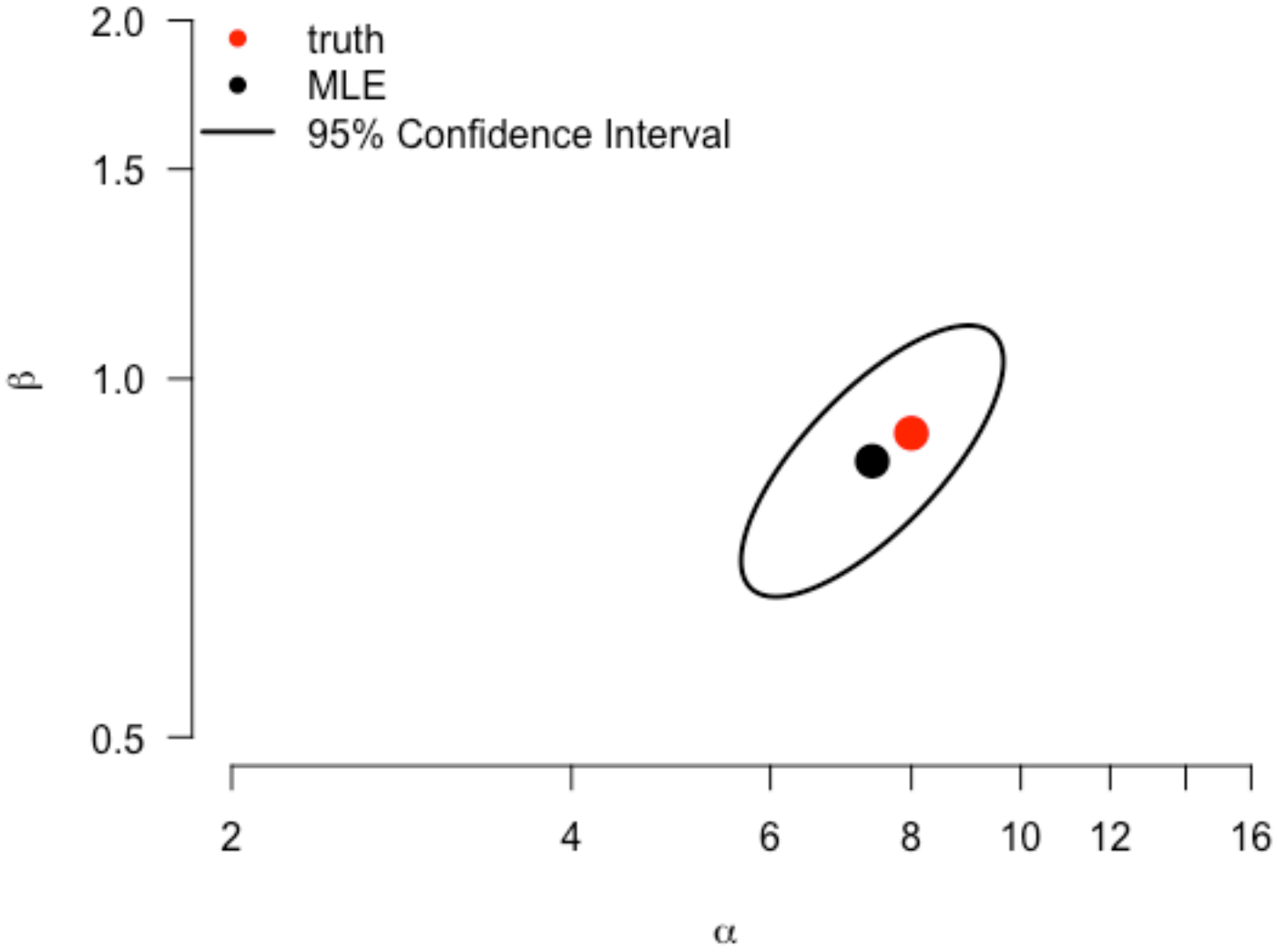


Log odds

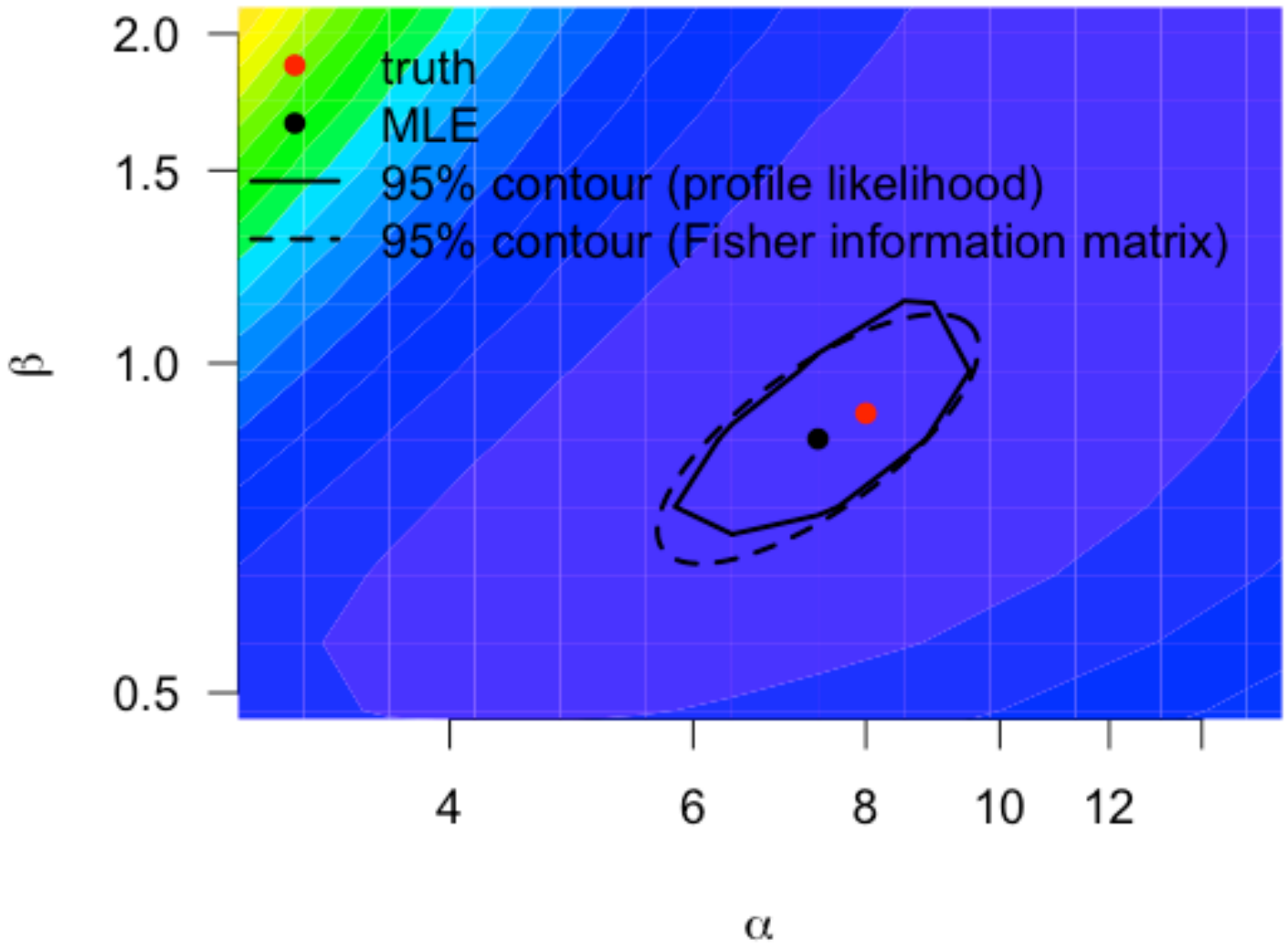
Summary: Fitting simulated Data



Summary: Confidence intervals



Summary: Confidence intervals



Summary: Take-away points

- Always fit fake data (eg, simulated by your model) **before** attempting to fit real data
  - Validate the fitting approach / identify any errors (eg, in your code)
- Transform parameters to scales that span the real numbers
- Think about what your optimization algorithms are doing and choose an approach that will be both efficient and accurate

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Attribution: **Juliet R.C. Pulliam & Steve E. Bellan**, Clinic on the Meaningful Modeling of Epidemiological Data

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