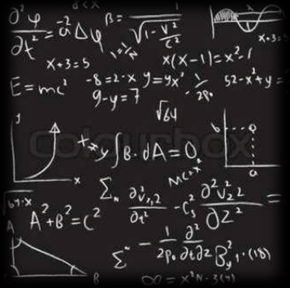


Models and Data

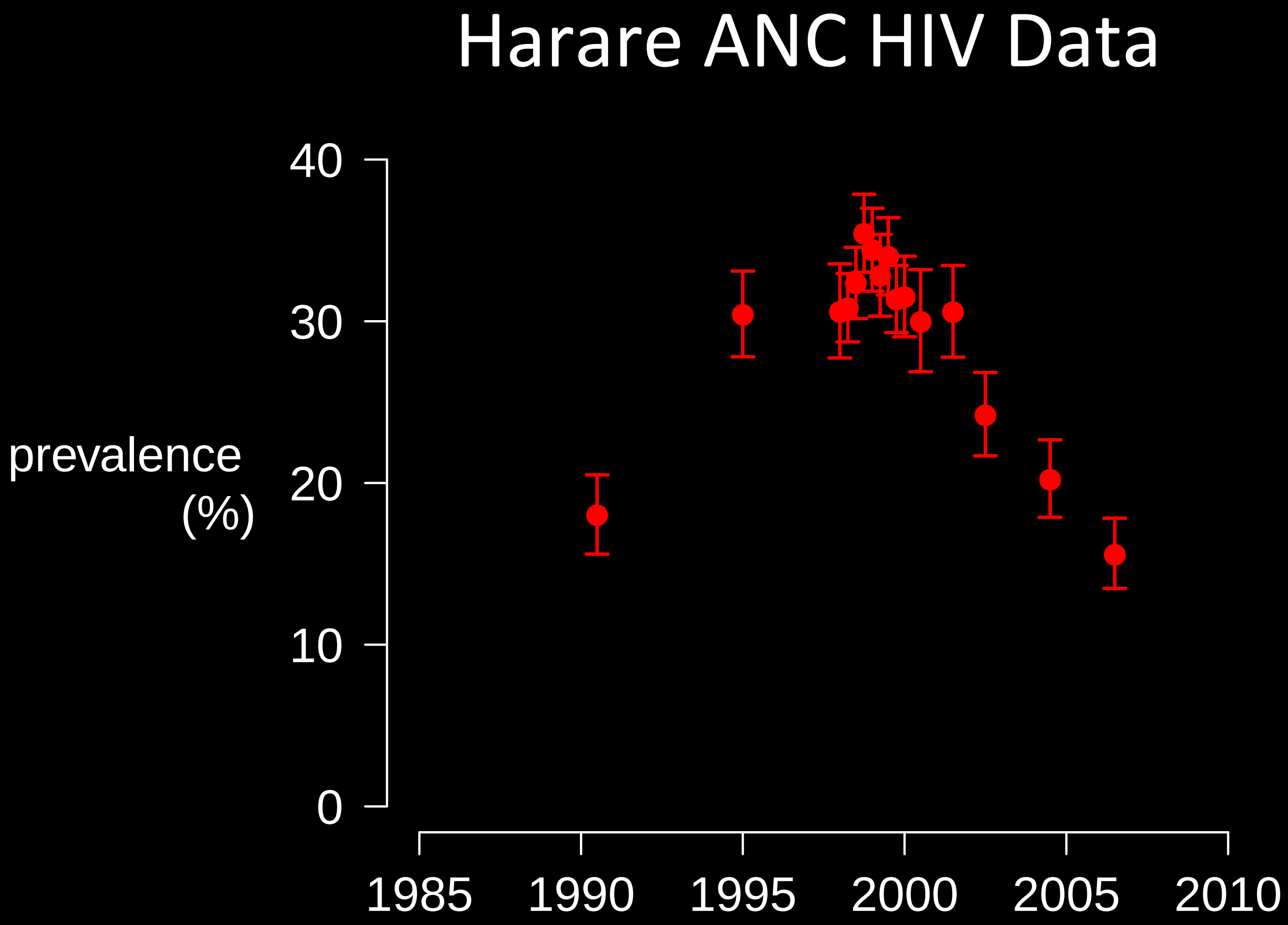
Introduction to Model Fitting

DAIDD 2015

Steve Bellan, PhD, MPH

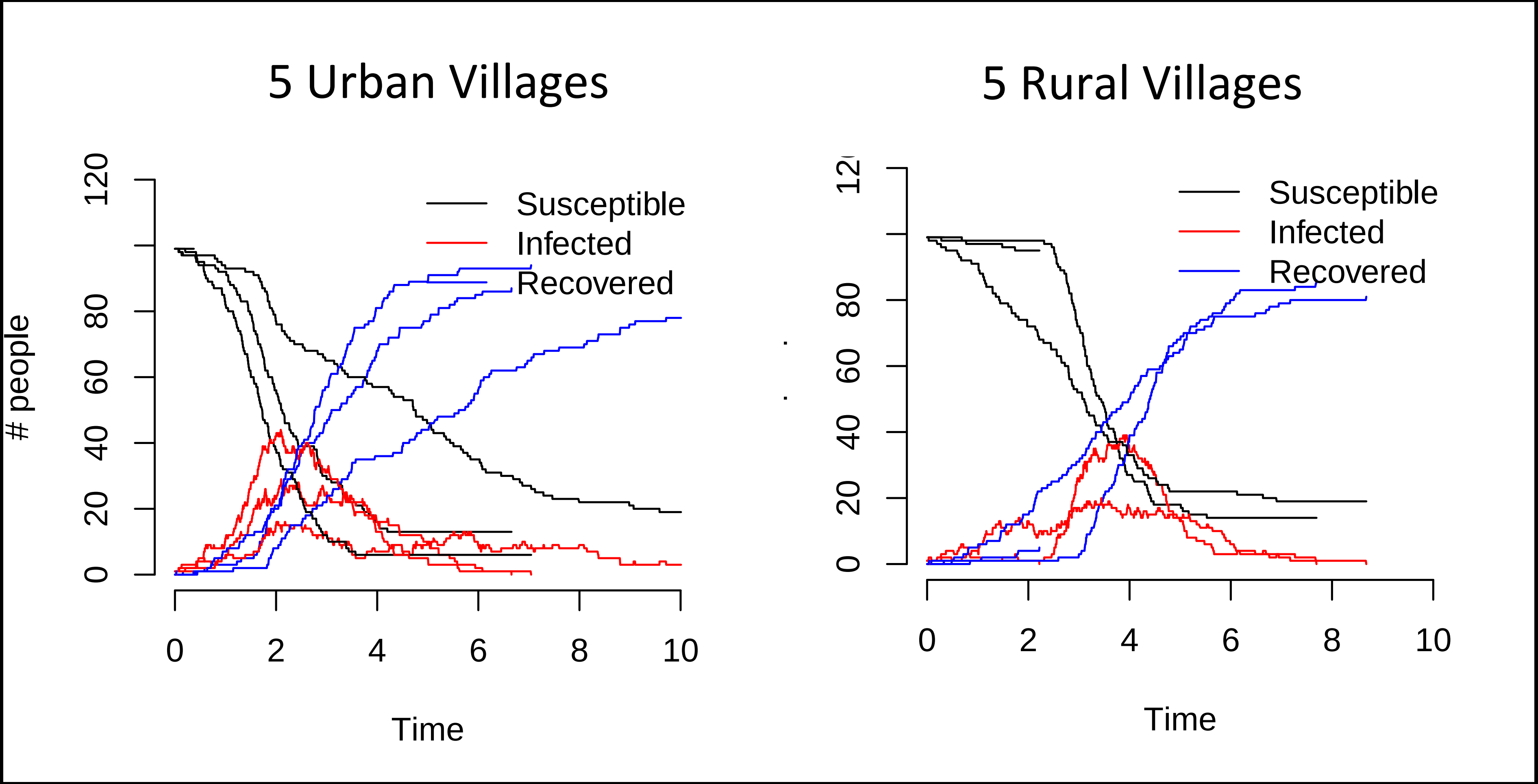
University of Texas at Austin

What happened?



Are these different?

Measles Outbreaks

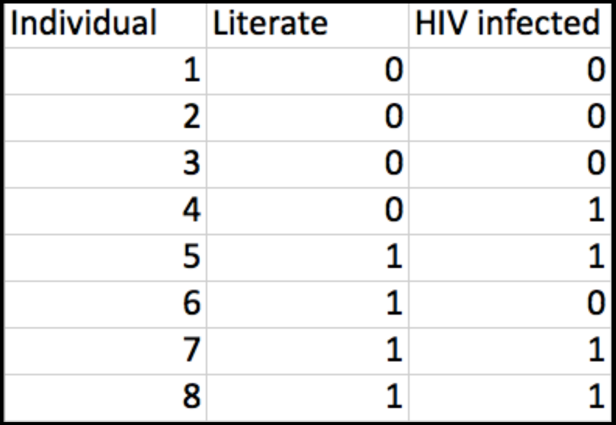


5 Urban Villages

5 Rural Villages

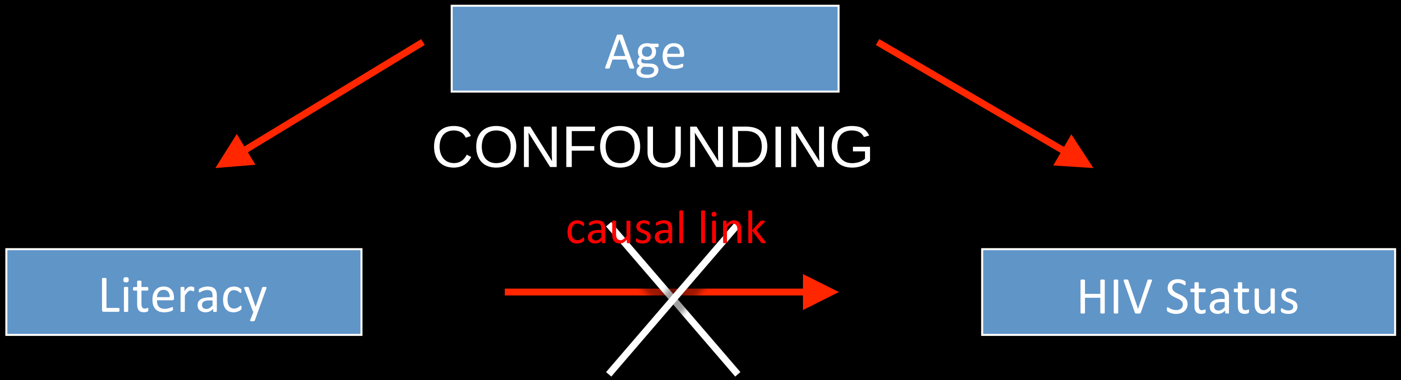
Classical Epidemiology

- Does literacy cause HIV?



Individual	Literate	HIV infected
1	0	0
2	0	0
3	0	0
4	0	1
5	1	1
6	1	0
7	1	1
8	1	1

- Find correlations that imply causality by accounting for
  1. random error: do we have enough data?
  2. bias: are design & analysis valid?



Age

CONFOUNDING

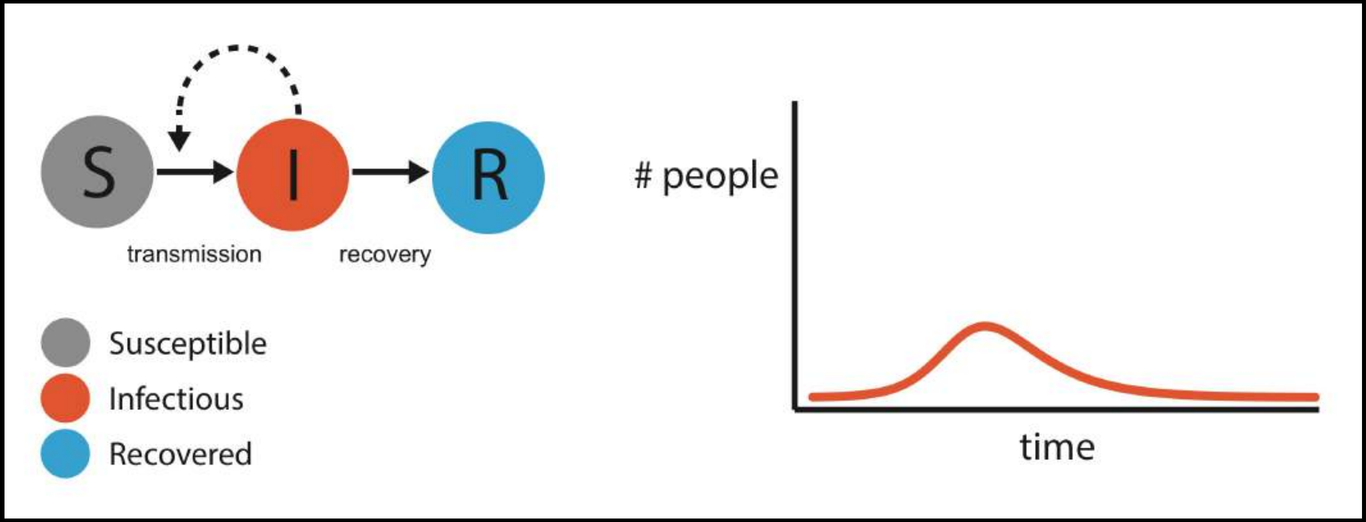
Literacy

causal link

HIV Status

Mechanistic Epidemiology

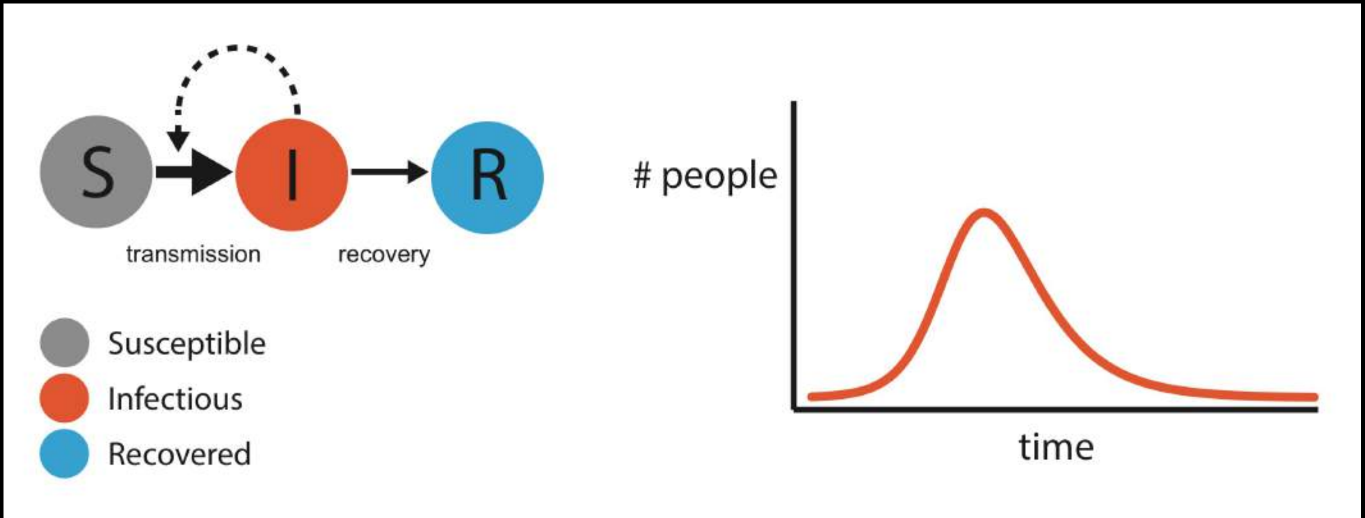
- Scale up from individual processes to population patterns
- "What if" scenarios not amenable to experimentation



Mechanistic Epidemiology

- Scale up from individual processes to population patterns
- "What if" scenarios not amenable to experimentation

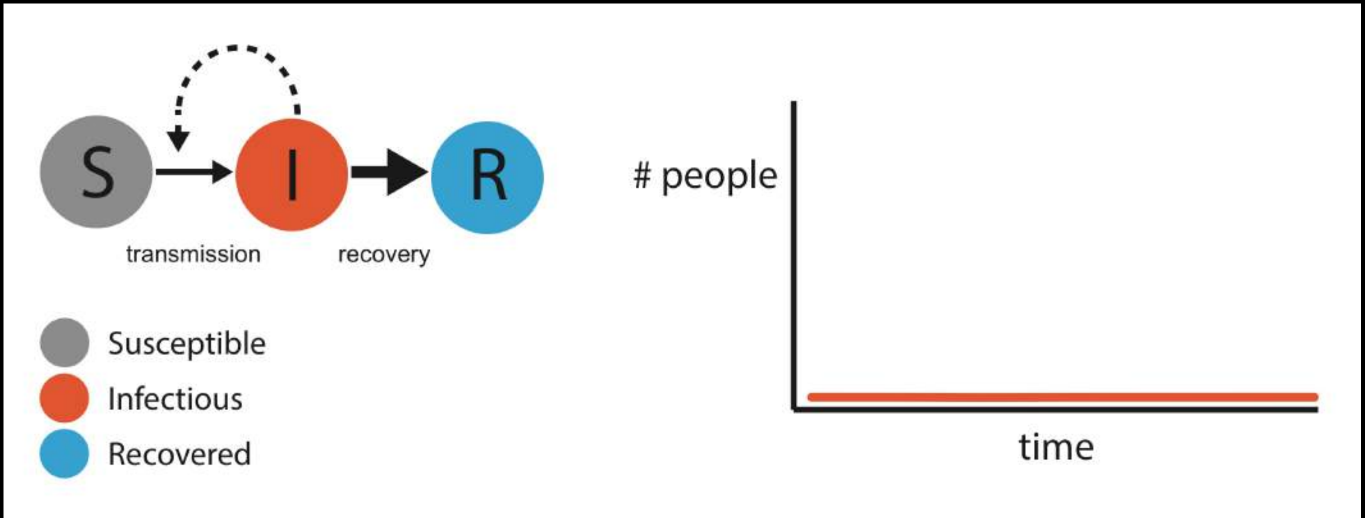
What if each person exposed 50% more people?



Mechanistic Epidemiology

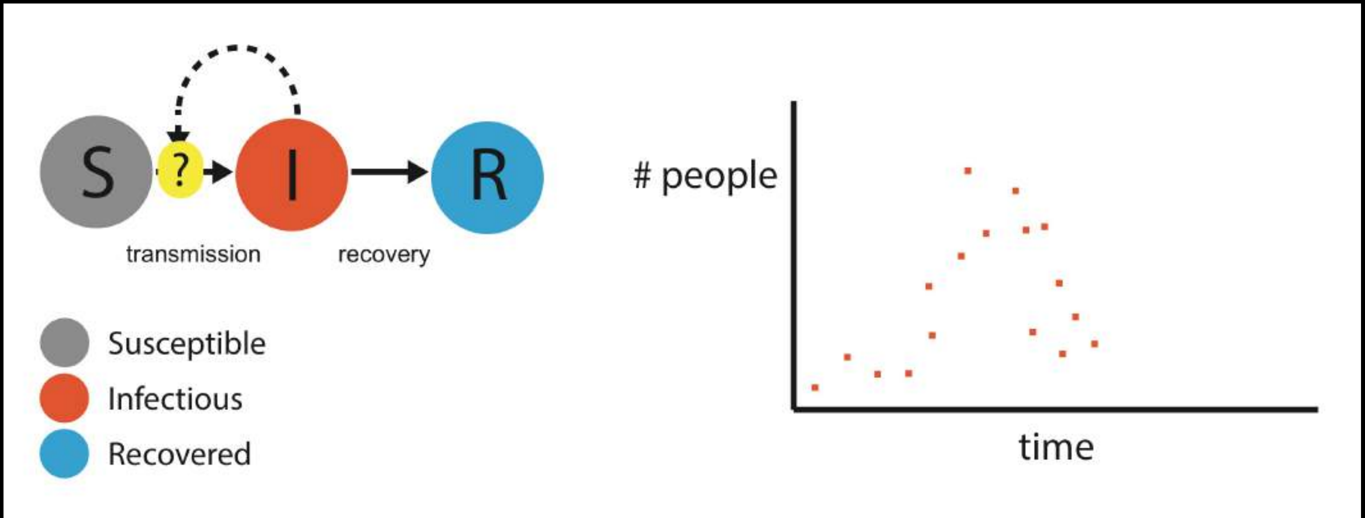
- Scale up from individual processes to population patterns
- "What if" scenarios not amenable to experimentation

What if we treated people and doubled the rate of recovery?



Mechanistic Epidemiology

- Scale up from individual processes to population patterns
- "What if" scenarios not amenable to experimentation
- Estimating parameters by fitting available data



Mechanistic Epidemiology

- Scale up from individual processes to population patterns
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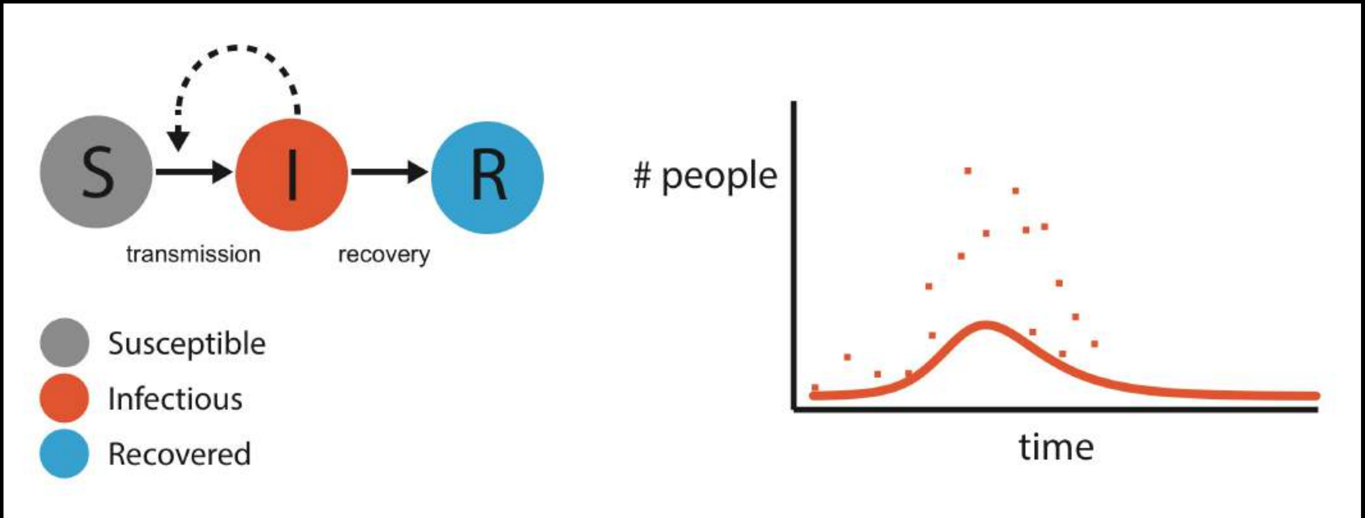
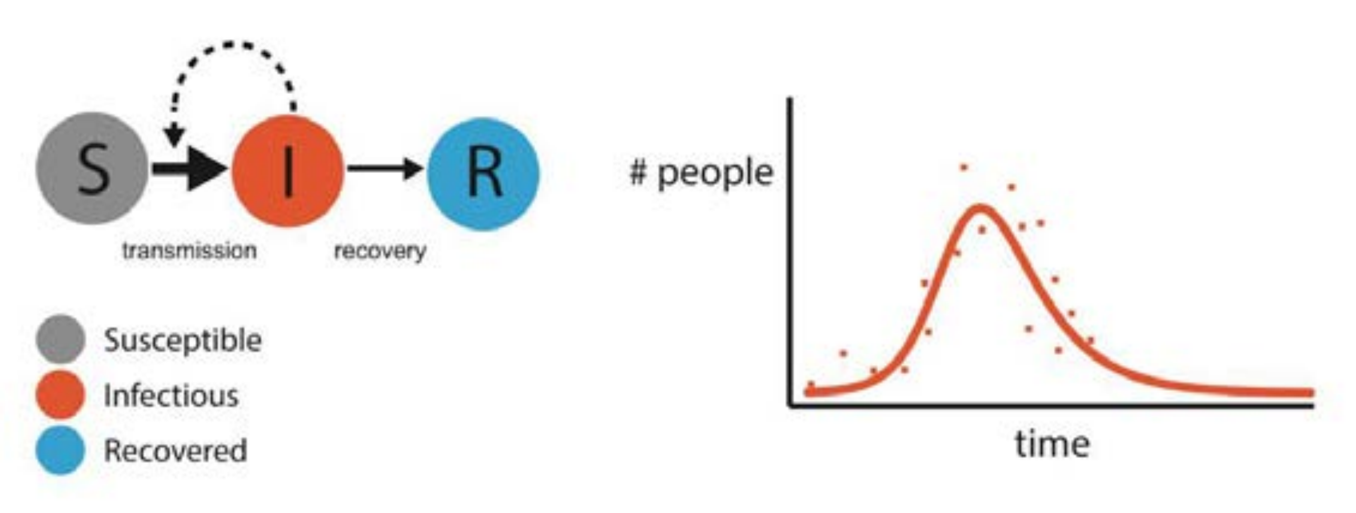


Mechanistic Epidemiology

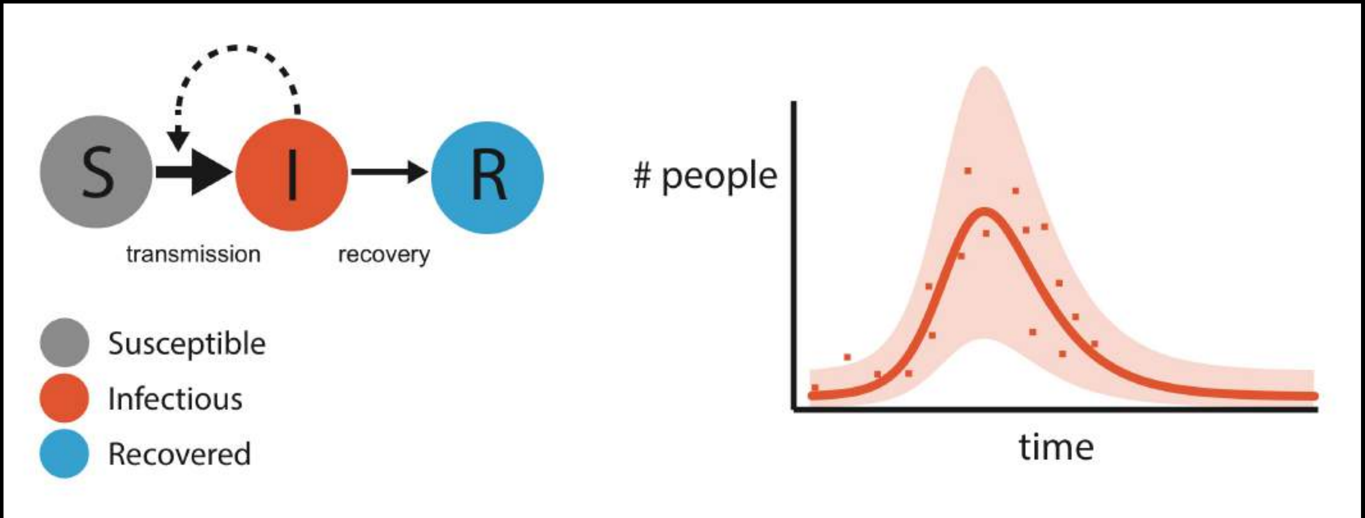
- Scale up from individual processes to population patterns
- "What if" scenarios not amenable to experimentation
- Estimating parameters by fitting available data



Mechanistic Epidemiology

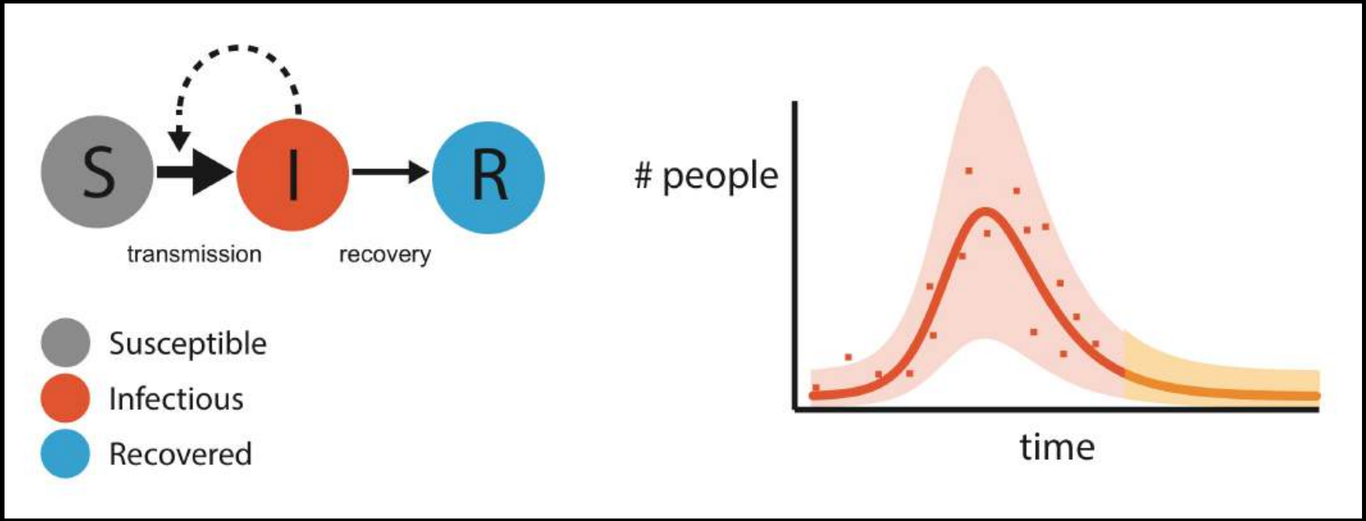
- Scale up from individual processes to population patterns
- "What if" scenarios not amenable to experimentation
- Estimating parameters by fitting available data

Estimate transmission rate or other model parameters
(with confidence intervals)



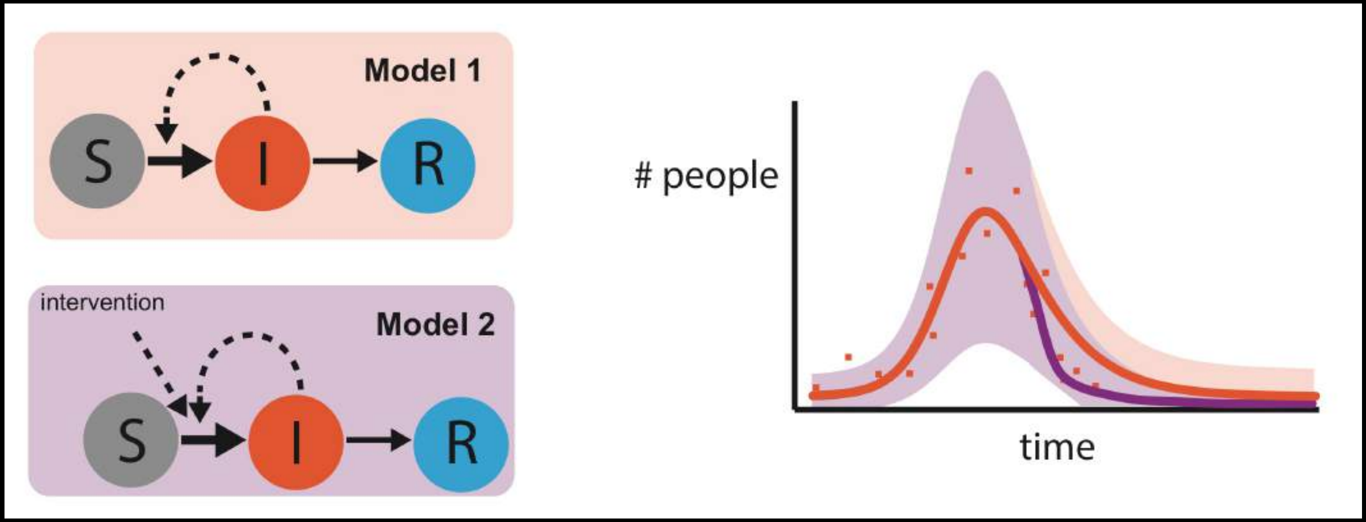
Mechanistic Epidemiology

- Scale up from individual processes to population patterns
- "What if" scenarios not amenable to experimentation
- Estimating parameters by fitting available data
- Prediction



Mechanistic Epidemiology

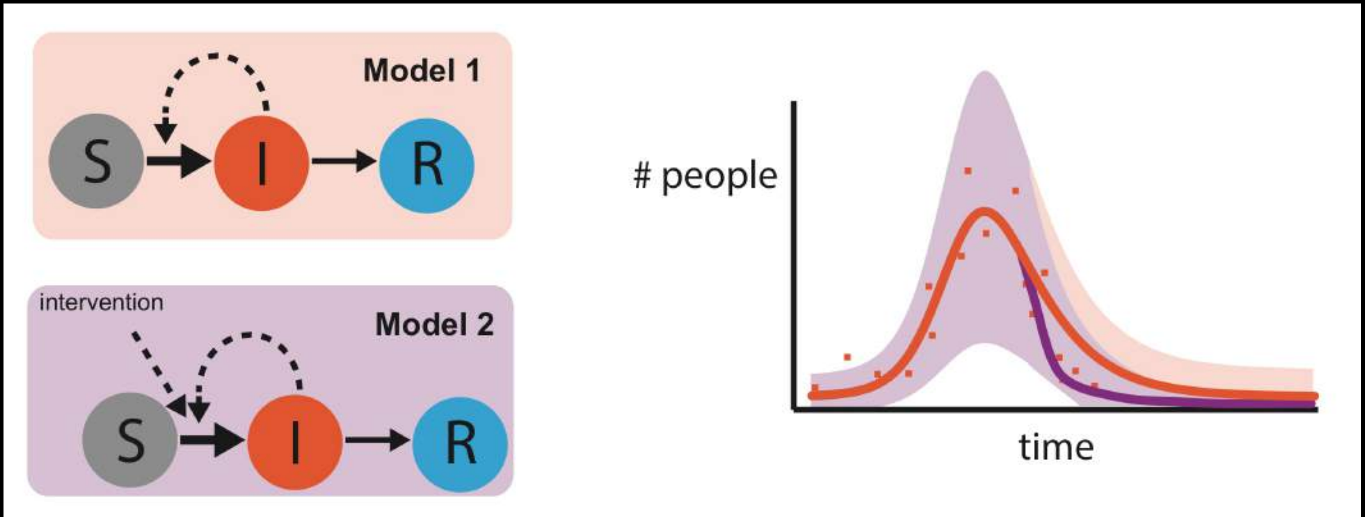
- Scale up from individual processes to population patterns
- "What if" scenarios not amenable to experimentation
- Estimating parameters by fitting available data
- Prediction
- Model selection (choosing between alternative hypotheses)



Mechanistic Epidemiology

- Scale up from individual processes to population patterns
- "What if" scenarios not amenable to experimentation
- Estimating parameters by fitting available data
- Prediction
- Model selection

data focus emerged in last 10 years



Why fit models to data?

- Estimate quantities/parameters of interest

- Inference: Test hypotheses

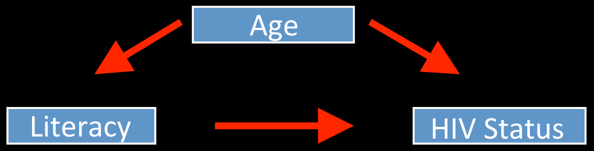
- Model assessment:

  Assess plausibility or model comparison

- End goal: explain observed patterns or predict

Statistical Models

- A familiar starting point



- Analogous to fitting dynamical models

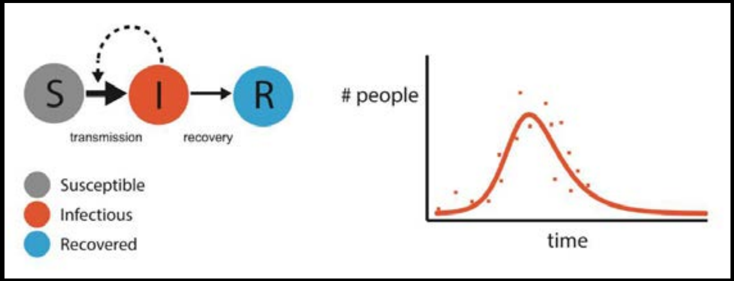
- Abstraction of real relationships

- Explaining variation in data through correlational relationships (hopefully causal)

Dynamic Models and Time Series Data

- Dynamic models evolve through time

- and simulate time series



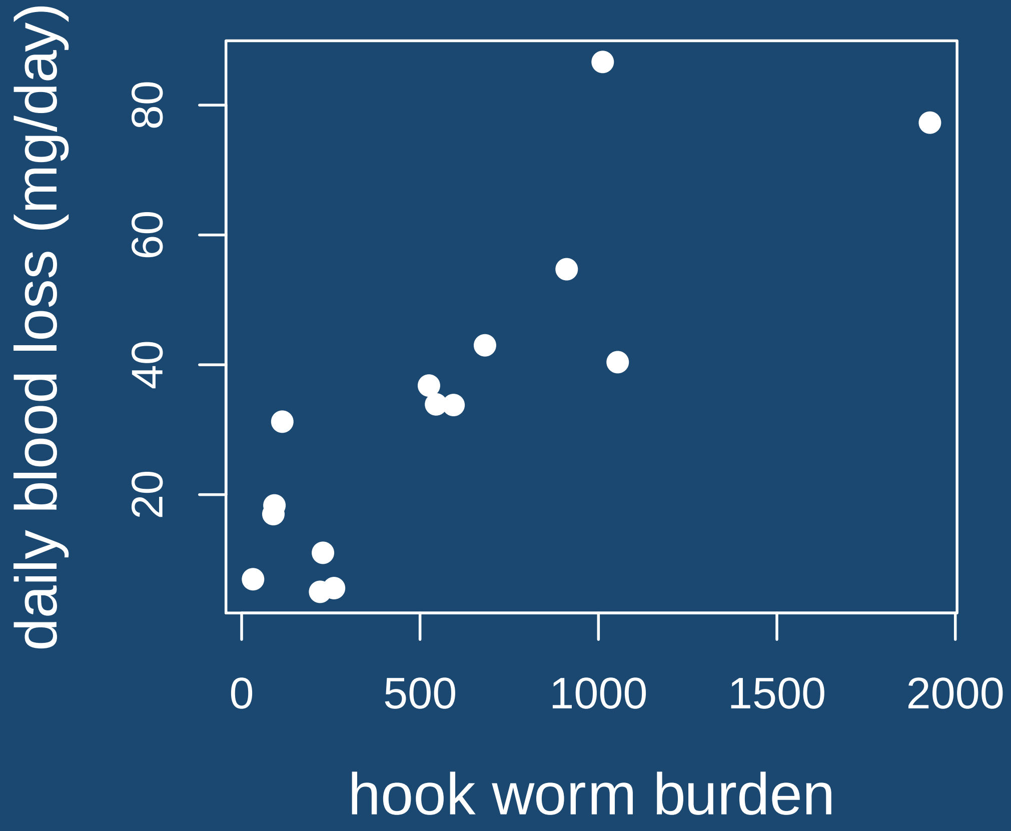
- Informally compare observed time series & simulated time series

- Fitting models to data formally compares them

Linear Regression

How does hook worm burden affect blood loss?

Is there any relationship?



Data in Epicalc R Library taken from Areekul et al. (1970).

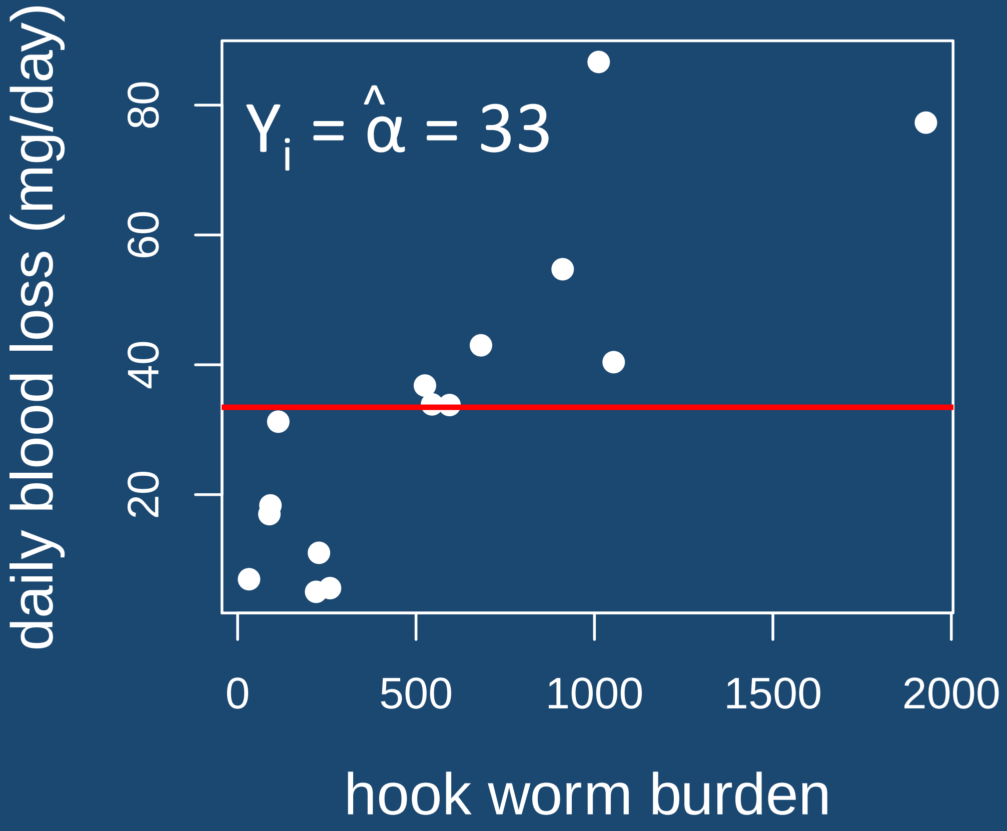
Linear Regression

Null hypothesis: No relationship

$Y = \alpha$

Is this a good fit?

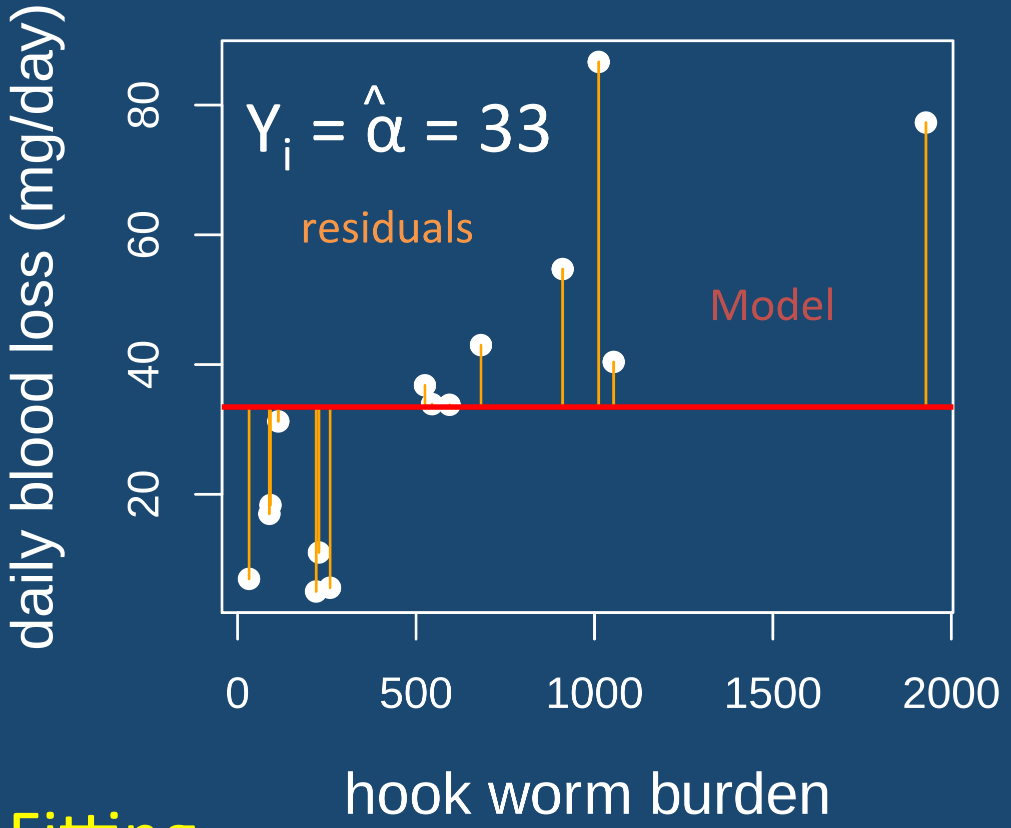
How can we get a better fit, or the best fit?



Linear Regression

Null hypothesis: No relationship

$$Y_i = \alpha + \varepsilon_i$$



Is this a good fit?

How can we get a better fit, or the best fit?

One option is Least Squares Fitting

Choose a line $Y = \hat{\alpha} + \hat{\beta}X$ to minimize $\Sigma(\text{residuals})^2$

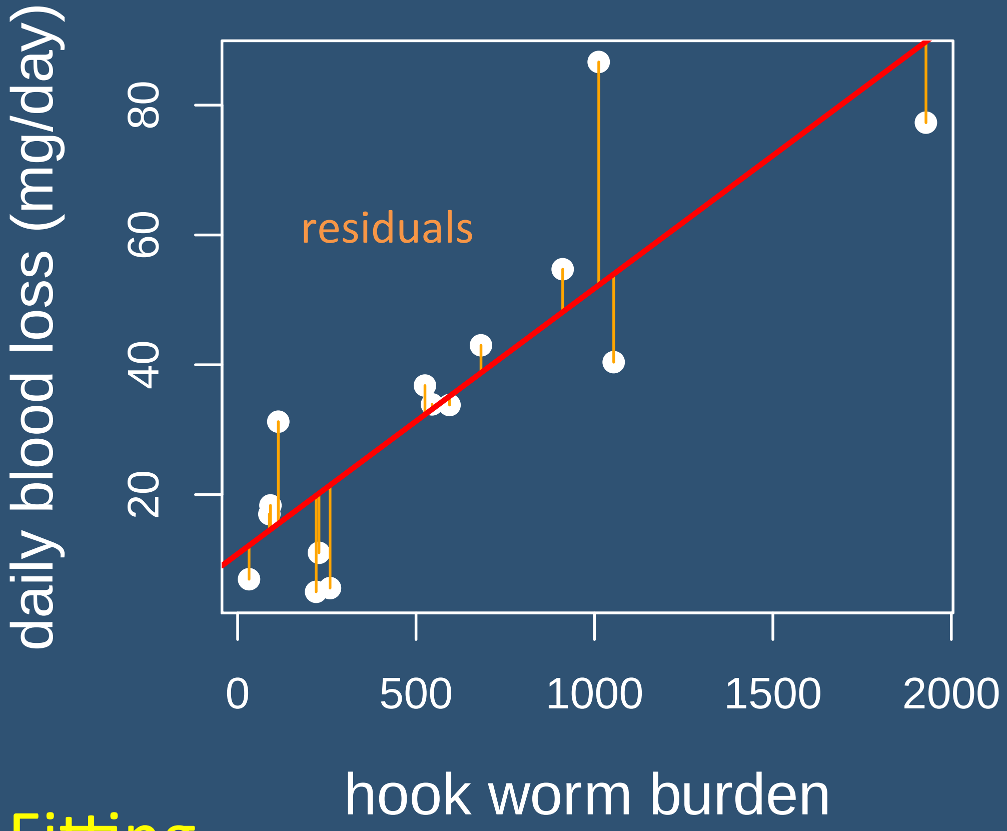
Linear Regression

Null hypothesis: No relationship

$$Y_i = \alpha + \beta X_i + \varepsilon_i$$

Is this a good fit?

How can we get a better fit, or the best fit?

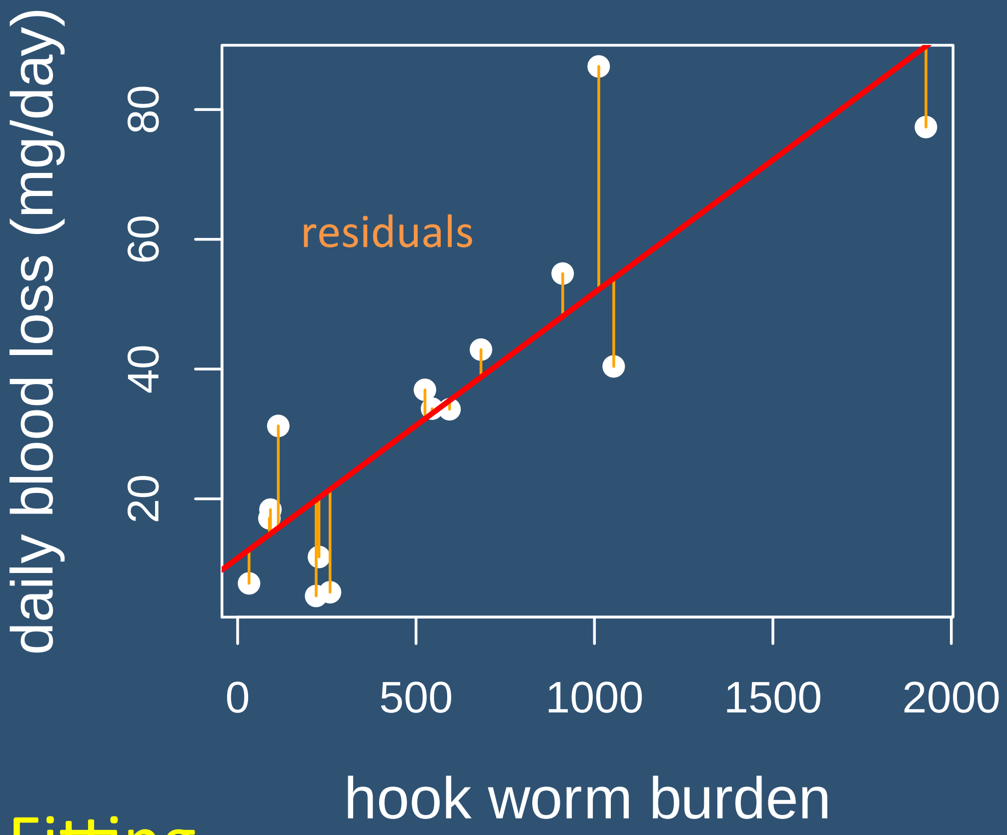


One option is Least Squares Fitting

Choose a line $Y = \hat{\alpha} + \hat{\beta}X$ to minimize $\Sigma(\text{residuals})^2$

Linear Regression

$$\overbrace{Y_i}^{\text{expected daily blood loss}} = \underbrace{\alpha}_{\text{intercept}} + \underbrace{\beta}_{\text{effect of hook worm burden}}\overbrace{X_i}^{\text{hook worm burden}} + \underbrace{\varepsilon_i}_{\text{error}}$$



One option is Least Squares Fitting

Choose a line $Y = \hat{\alpha} + \hat{\beta}X$ to minimize $\Sigma(\varepsilon_i)^2$

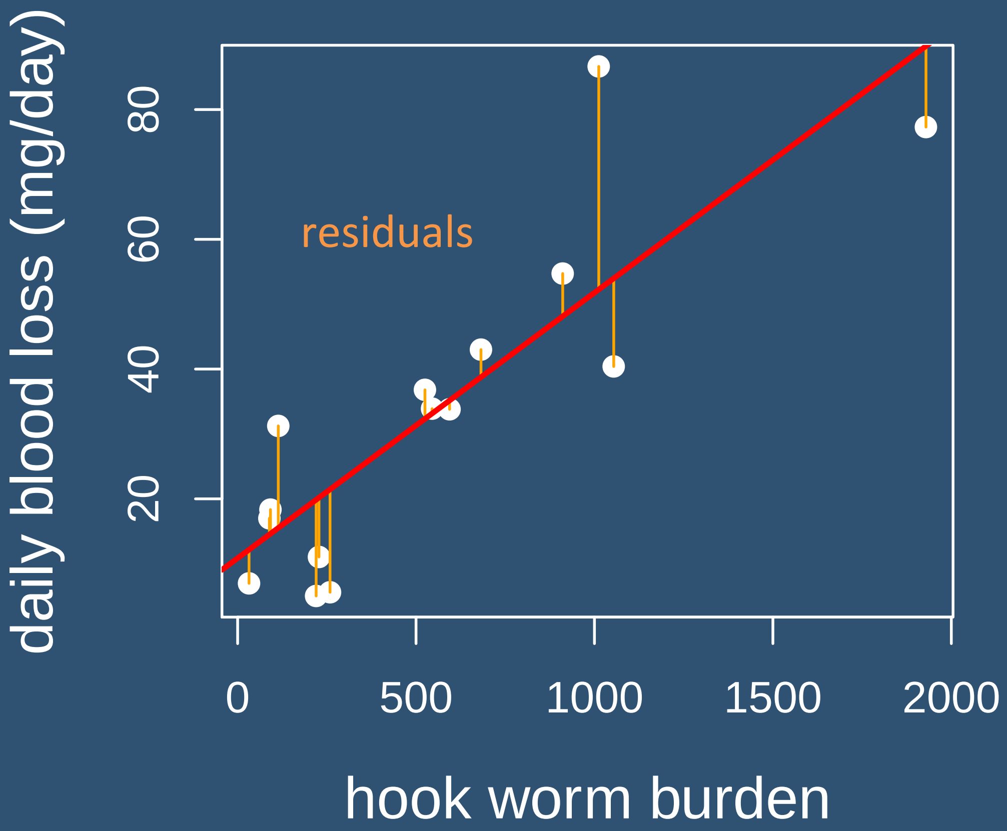
Linear Regression

Another option is

Maximum Likelihood

$$Y_i = \alpha + \beta X_i + \varepsilon_i$$

$$\varepsilon_i \sim N(0, \sigma^2)$$



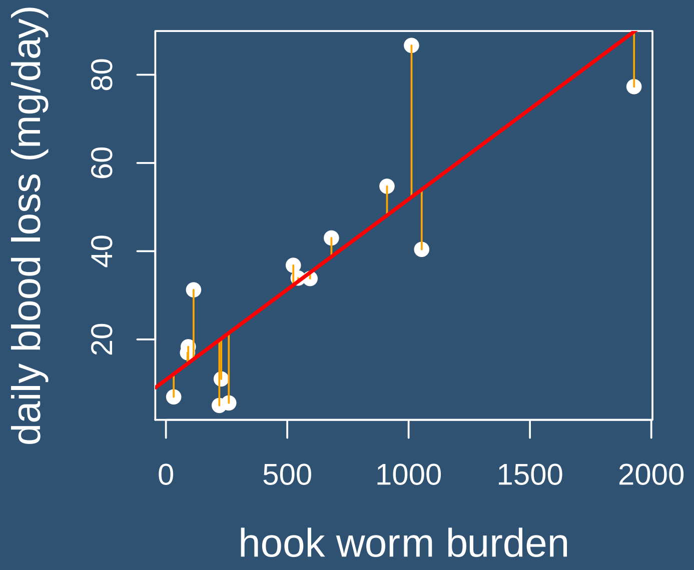
Choose $\hat{\alpha}$, $\hat{\beta}$, $\hat{\sigma}$ to maximize the likelihood

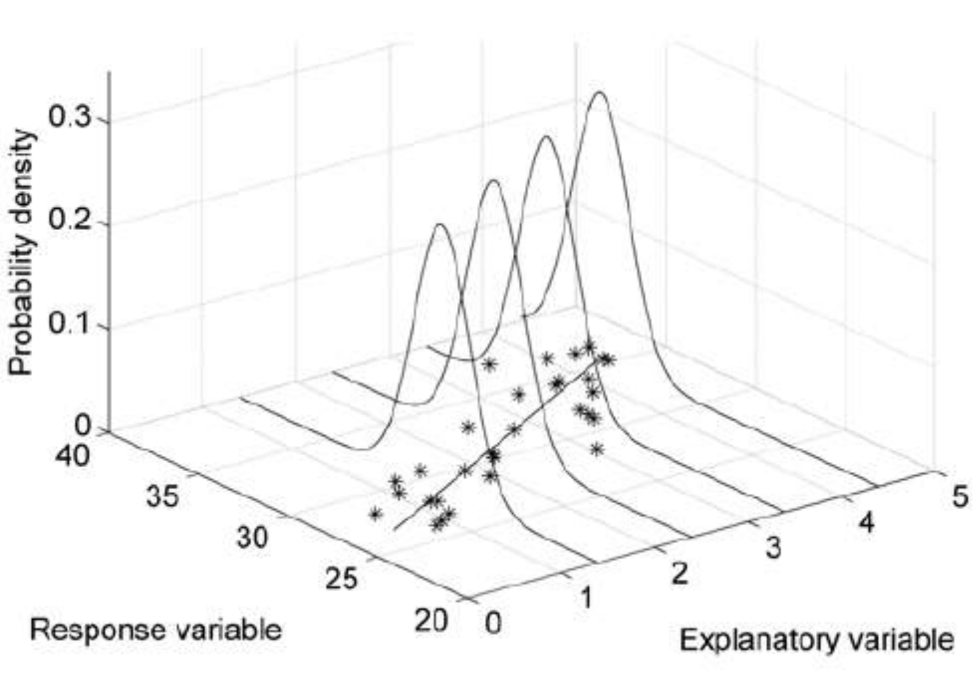
i.e. probability of observed data given a model

Linear Regression

Maximum Likelihood

$$Y_i \sim N(\alpha + \beta X_i,\ \sigma^2)$$





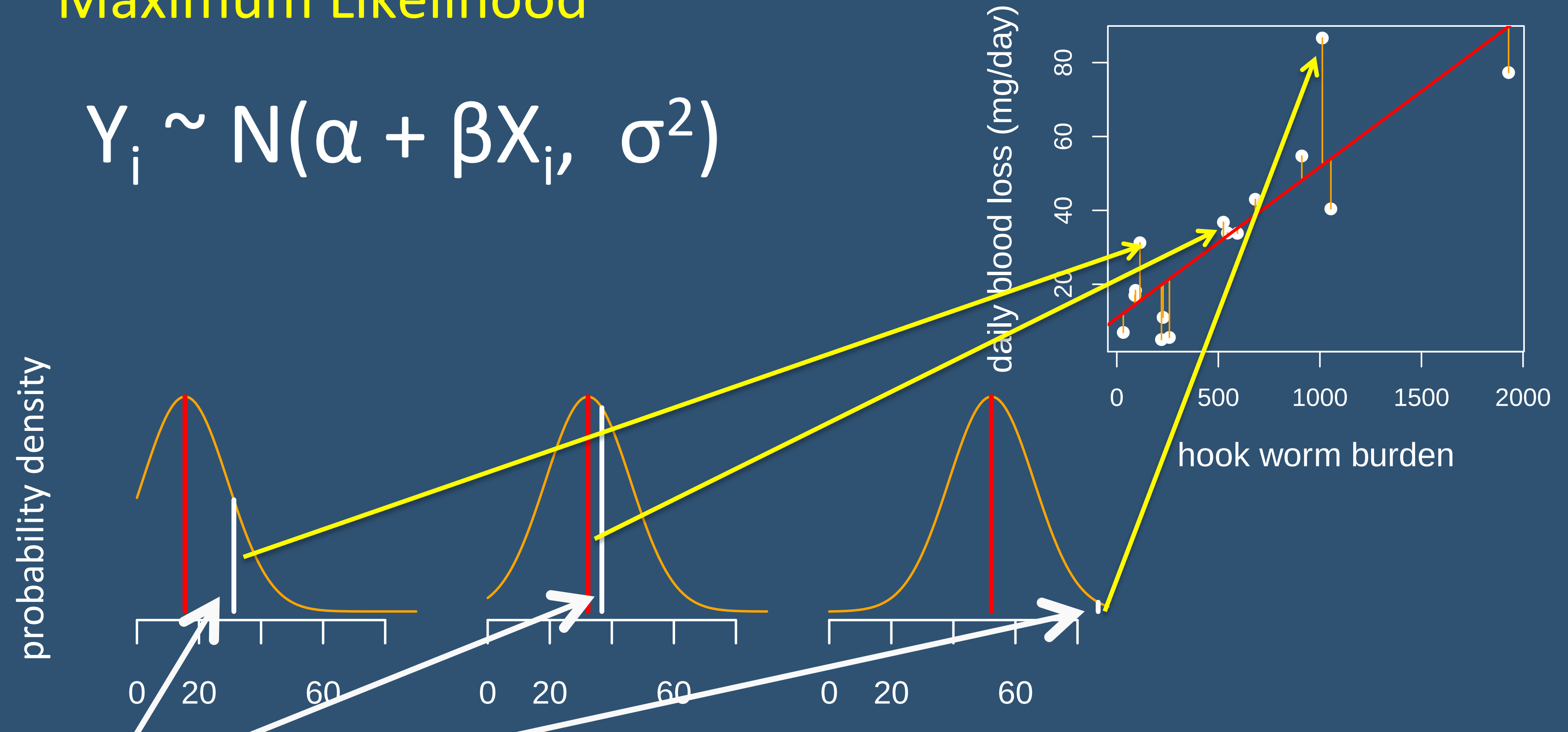
Choose $\hat{\alpha}$, $\hat{\beta}$, $\hat{\sigma}$ to maximize the likelihood

i.e. probability of observed data given a model

Linear Regression

Maximum Likelihood

$$Y_i \sim N(\alpha + \beta X_i,\ \sigma^2)$$

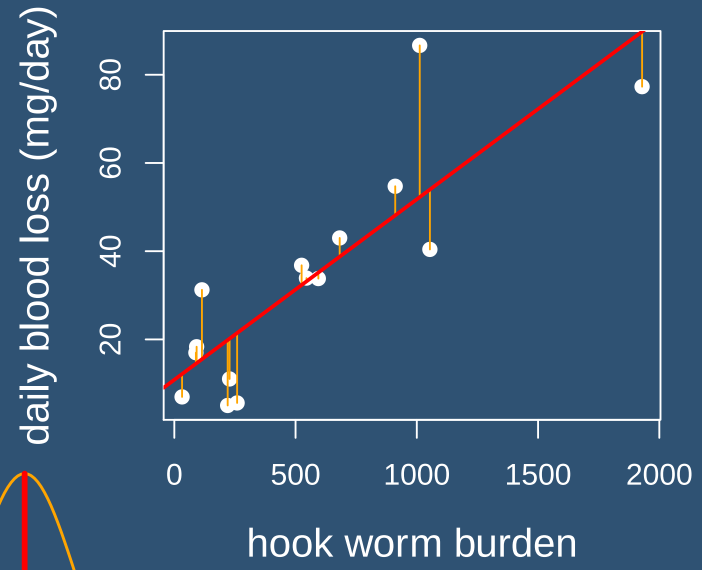


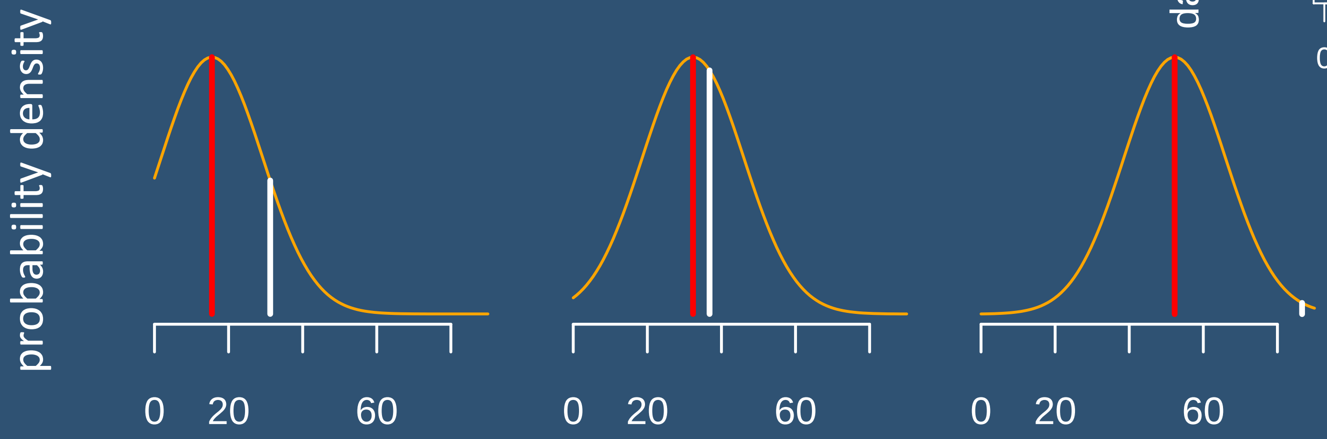
$$P(Y_i \mid \hat{\alpha}, \hat{\beta}, \hat{\sigma}) = \frac{1}{\hat{\sigma}\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{Y_i - (\hat{\alpha} + \hat{\beta} X_i)}{\hat{\sigma}}\right)^2}$$

Linear Regression

Maximum Likelihood

$$Y_i \sim N(\alpha + \beta X_i,\ \sigma^2)$$

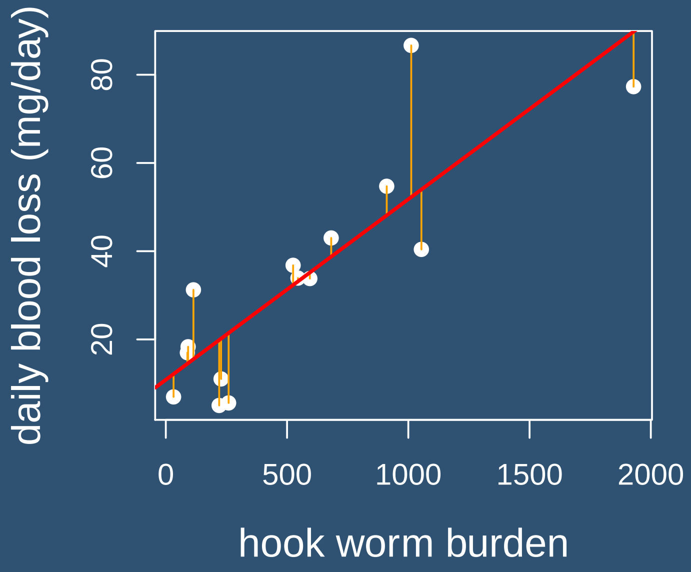




$$P(Y_1,\ldots,Y_n \mid \hat{\alpha},\hat{\beta},\hat{\sigma}) = \prod_{i=1}^{n} P(Y_i \mid \hat{\alpha},\hat{\beta},\hat{\sigma})$$

Linear Regression

Maximum Likelihood



function of data

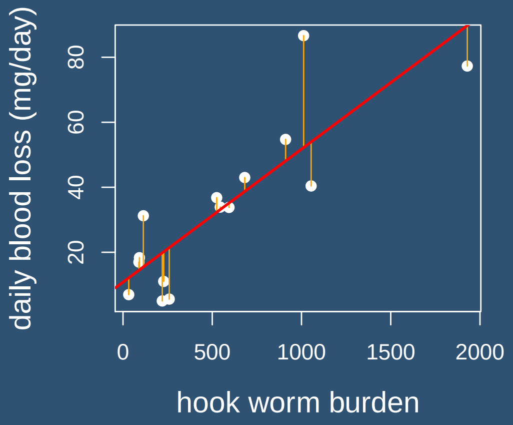
$$\text{PDF:}\quad \underset{}{\overset{\downarrow}{P}}(\overbrace{Y_1,\ldots,Y_n} \mid \hat{\alpha},\hat{\beta},\hat{\sigma}) = \prod_{i=1}^{n} P(Y_i \mid \hat{\alpha},\hat{\beta},\hat{\sigma})$$

$$\text{LIKELIHOOD:}\quad \underset{\uparrow}{L}(\underbrace{\hat{\alpha},\hat{\beta},\hat{\sigma}} \mid Y_1,....,Y_n) = \prod_{i=1}^{n} P(Y_i \mid \hat{\alpha},\hat{\beta},\hat{\sigma})$$

function of parameters

Linear Regression

Parameter Estimation & Inference



Null hypothesis: $\beta = 0$

$\hat{\beta} = 0.04$

P(estimating a β this extreme |null)

P = 6.99e-05 < 0.05,

so we reject the null hypothesis.

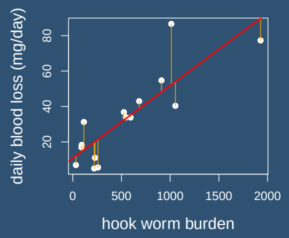
Confidence intervals

Collection of
non-rejectable null hypotheses

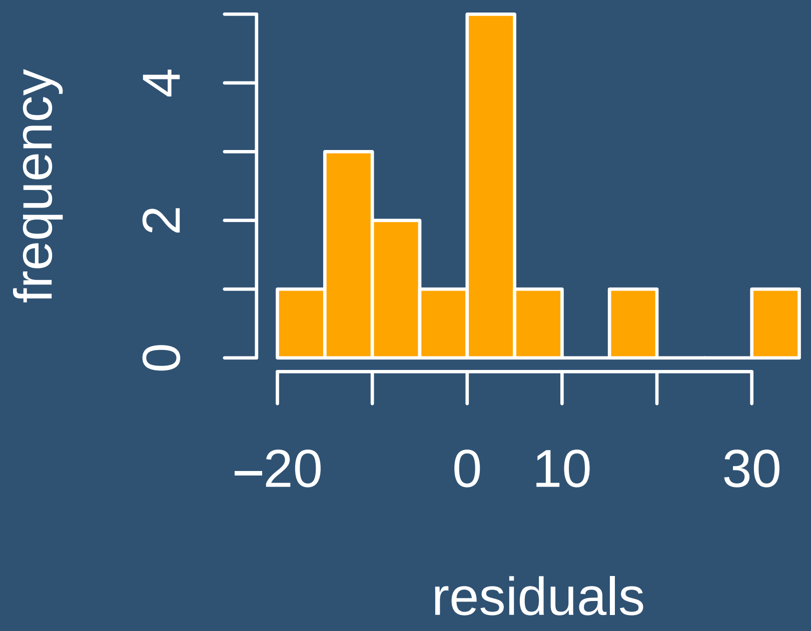
$\hat{\beta} = 0.04\ (0.025, 0.056)$

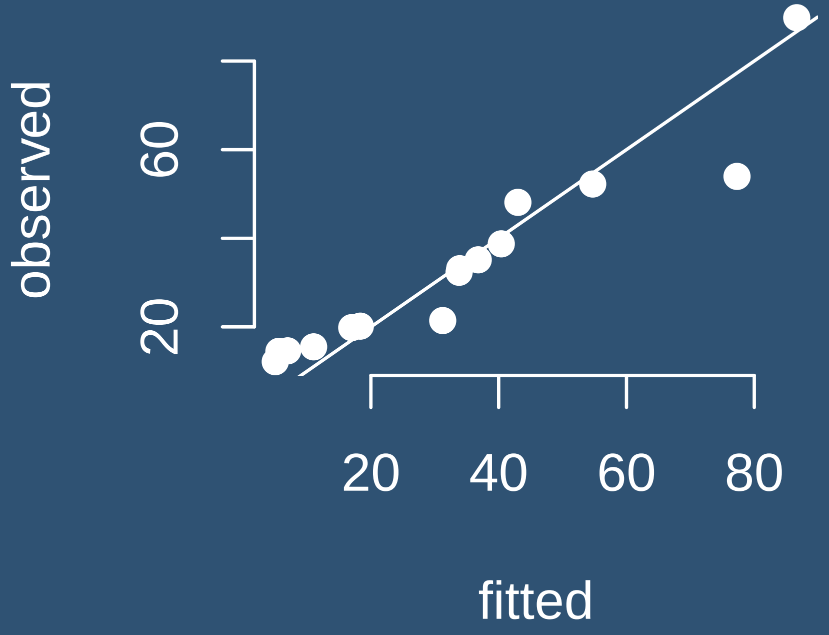
Is it a good model:

Checking Assumptions

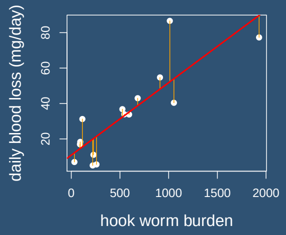


Normality





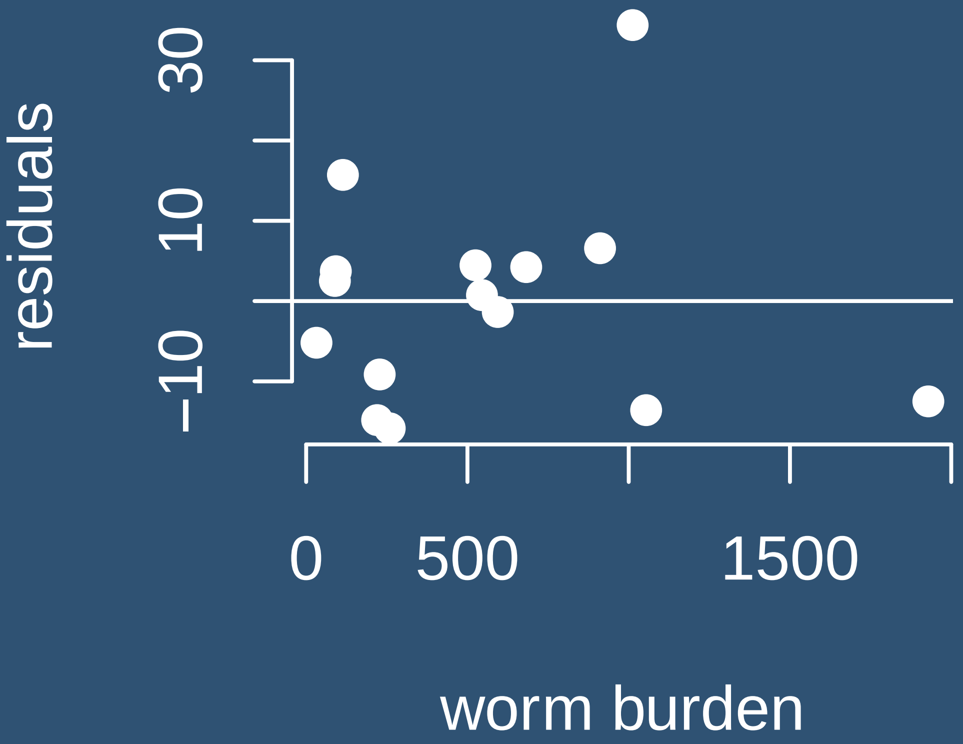
Is it a good model:
Checking Assumptions



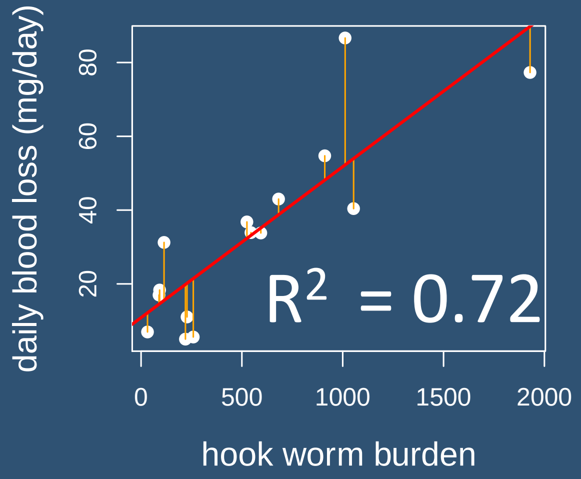
Linearity

Independence

Constant Variance



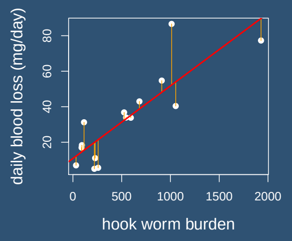
Is it a good model:
Goodness of Fit



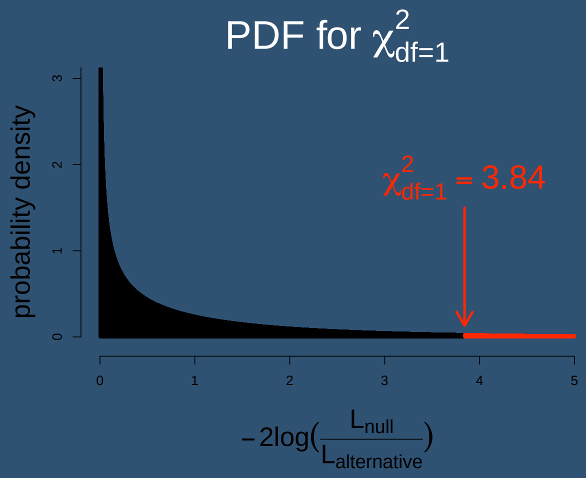
R^2 = (correlation coefficient)^2

How much of the variation in Y is explained by the model?

Is it a good model:
Goodness of Fit



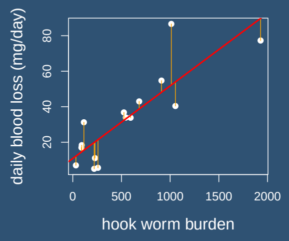
Chi Squared
Goodness of Fit Test



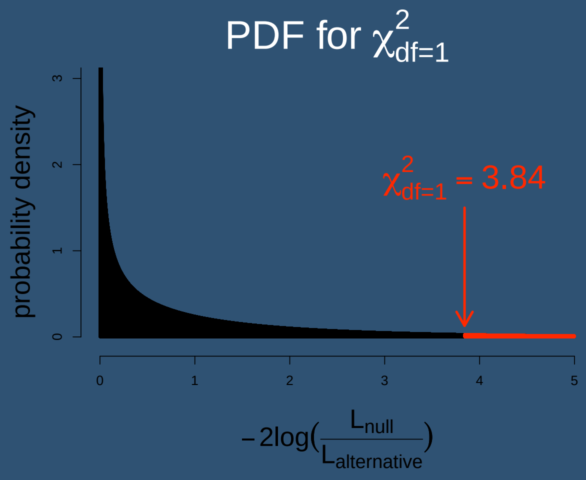
$$\chi^2 = \frac{1}{n-1}\sum_{i=1}^{n}\frac{(Observed_i - Expected_i)^2}{\sigma^2}$$

- Does the observed data differ significantly from our model?
- If not, then we cannot reject our model as a bad model.
- But we cannot accept our model (the null hypothesis) !

Is it a good model:
Goodness of Fit



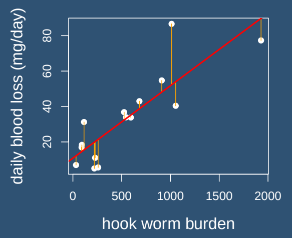
Likelihood Ratio Test (G test, Analysis of Deviance, ANOVA)



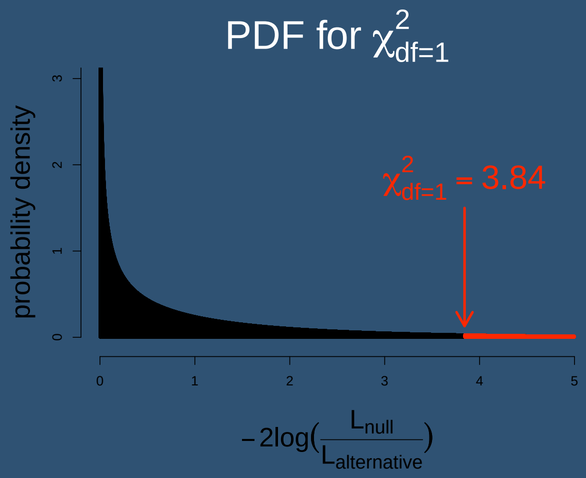
Under the null hypothesis:

$$2\log\frac{L_{MLE}}{L_{Null}} \sim \chi^2_{\text{df = difference in \# of parameters}}$$

Is it a good model:
Model Selection



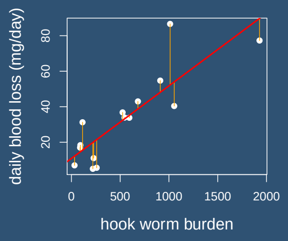
Likelihood Ratio Test (G test, Analysis of Deviance, ANOVA)



Under the null hypothesis:

$$2\log\frac{L_{\text{more parameters}}}{L_{\text{less parameters}}} \sim \chi^2_{\text{df = difference in \# of parameters}}$$

Is it a good model:
Model Selection



Akaike's Information Criterion (AIC)

$$\text{AIC} = -2\log(L) + 2\underbrace{(\#\text{ of parameters})}_{\text{penalty for adding parameters}}$$

Rank proposed models by AIC: lowest is best.

All models within 2 of lowest should be considered.

Overfitting

- You can always fit N data points with N parameters.

- How many is too many?

- Bias/Variance Tradeoff

- AIC, Cross-validation

Collinearity

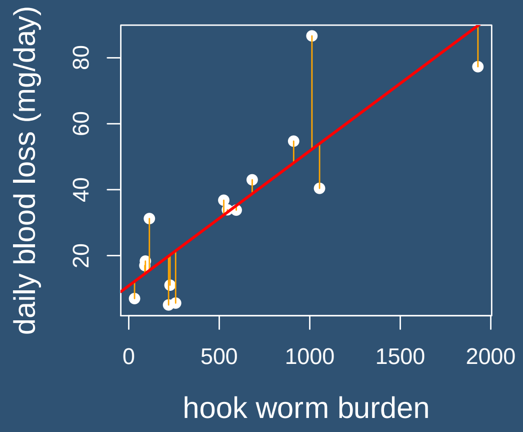
- Independent variables that vary with each other

Non-Identifiability

- Multiple parameter sets fit about equally well

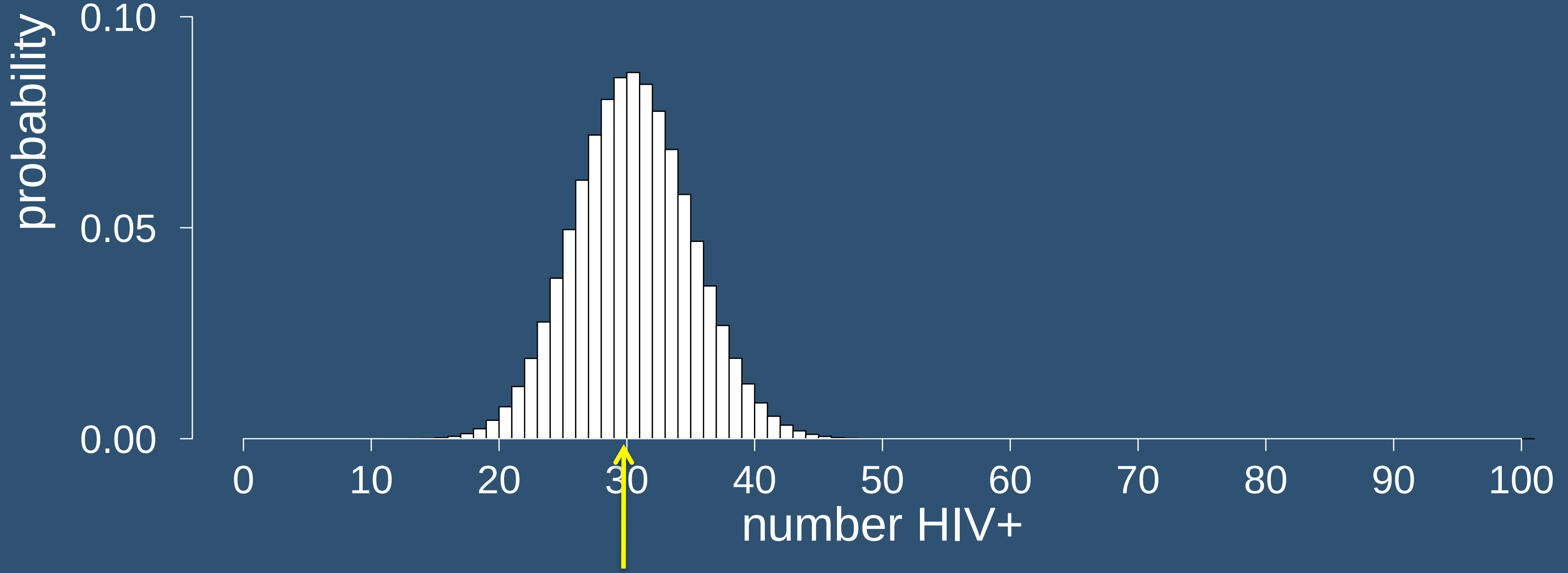
What did we just do?

- Asked a question about a relationship
- Made some observations (data)
- Formulated the relationship into a model
- Fitted the model to data
- Assessed model fit/quality (model selection)
- Inference/parameter estimation
- Improved our understanding of the world



In a population of 1,000,000 people with a true prevalence of 30%, the probability distribution of number of positive individuals if 100 are sampled:

$$f(x) = \binom{100}{x} (0.3)^{x} (0.7)^{100-x}$$



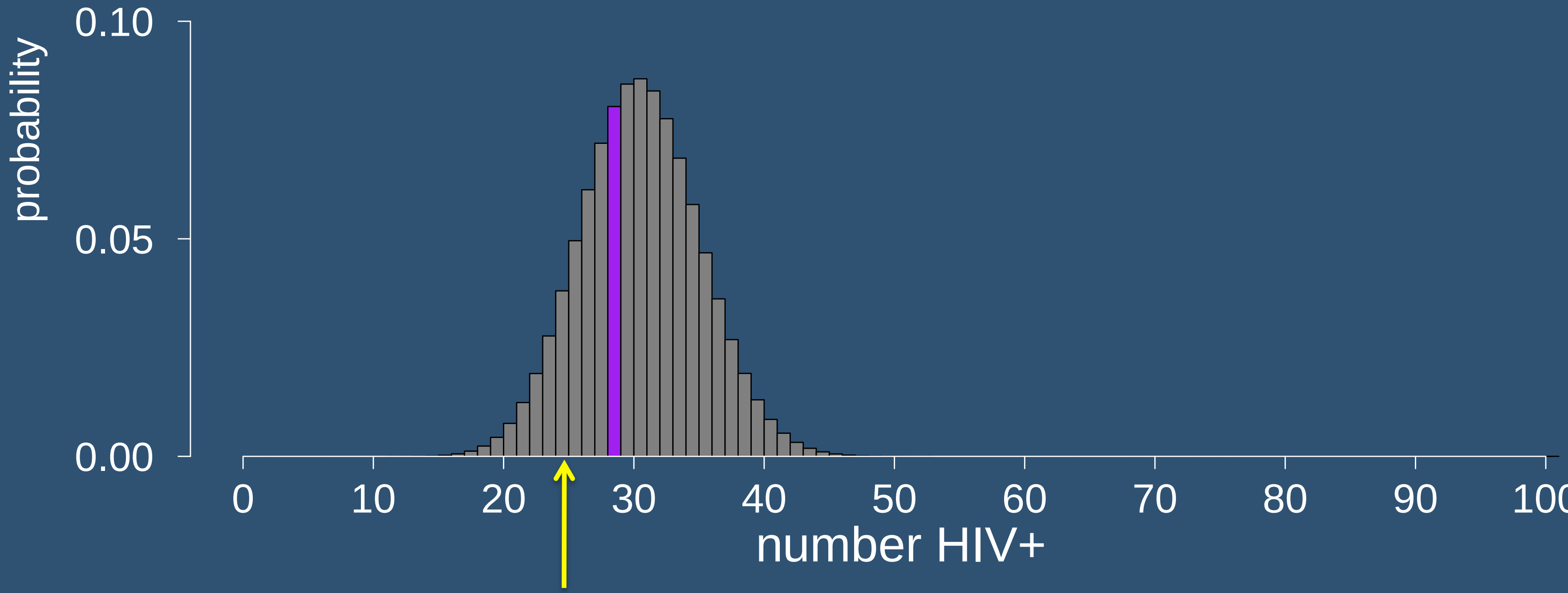
We sample 100 people once and 28 are positive:

```
> rbinom(n = 1, size = 100, prob = .3)
[1] 28
```

Introduction to Likelihood

hypothetical prevalence: 30 %

dbinom(28, 100, 0.3) = 0.0804

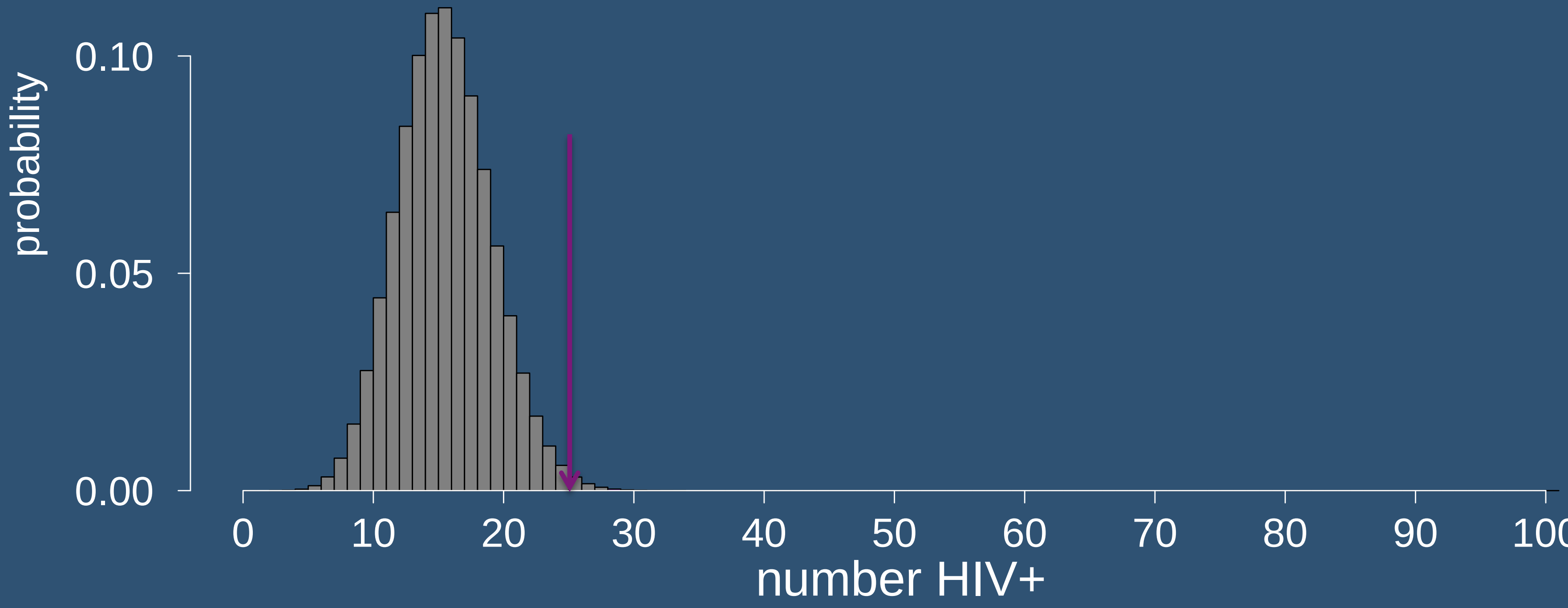


We sample 100 people once and 28 are positive:

```
> rbinom(n = 1, size = 100, prob = .3)
[1] 28
```

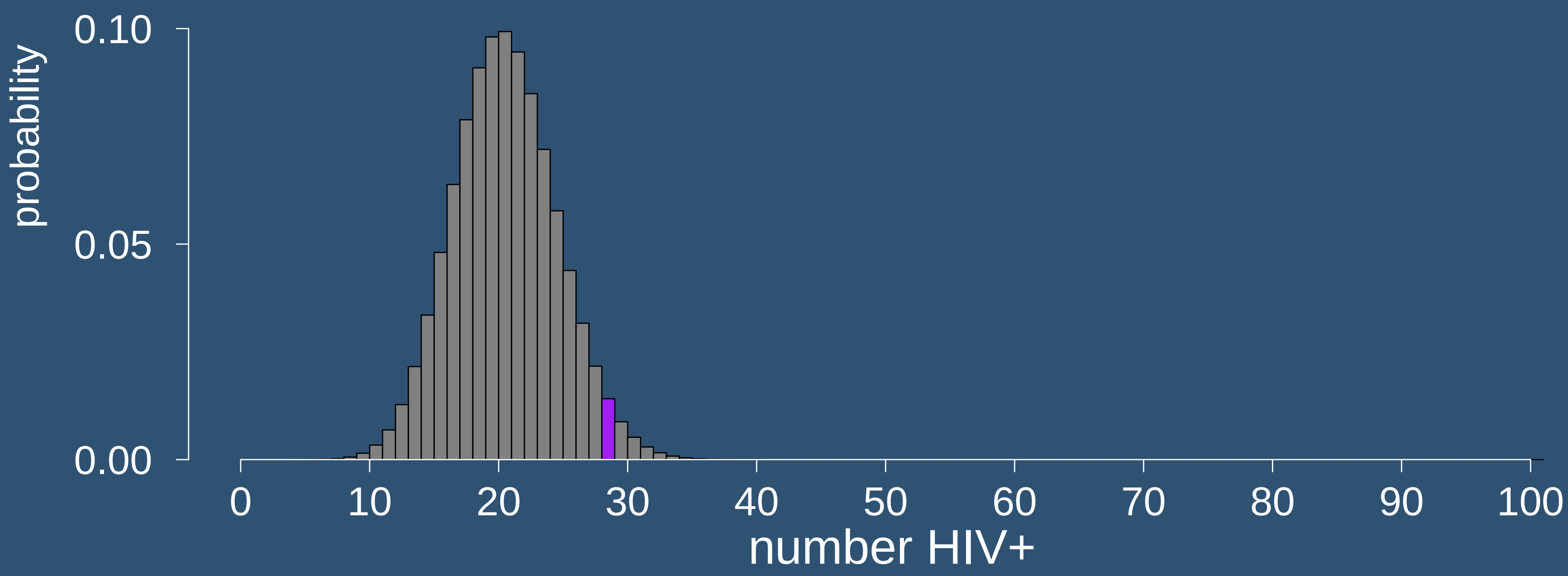
hypothetical prevalence: 15 %

dbinom(28, 100, 0.15) = 0.000353



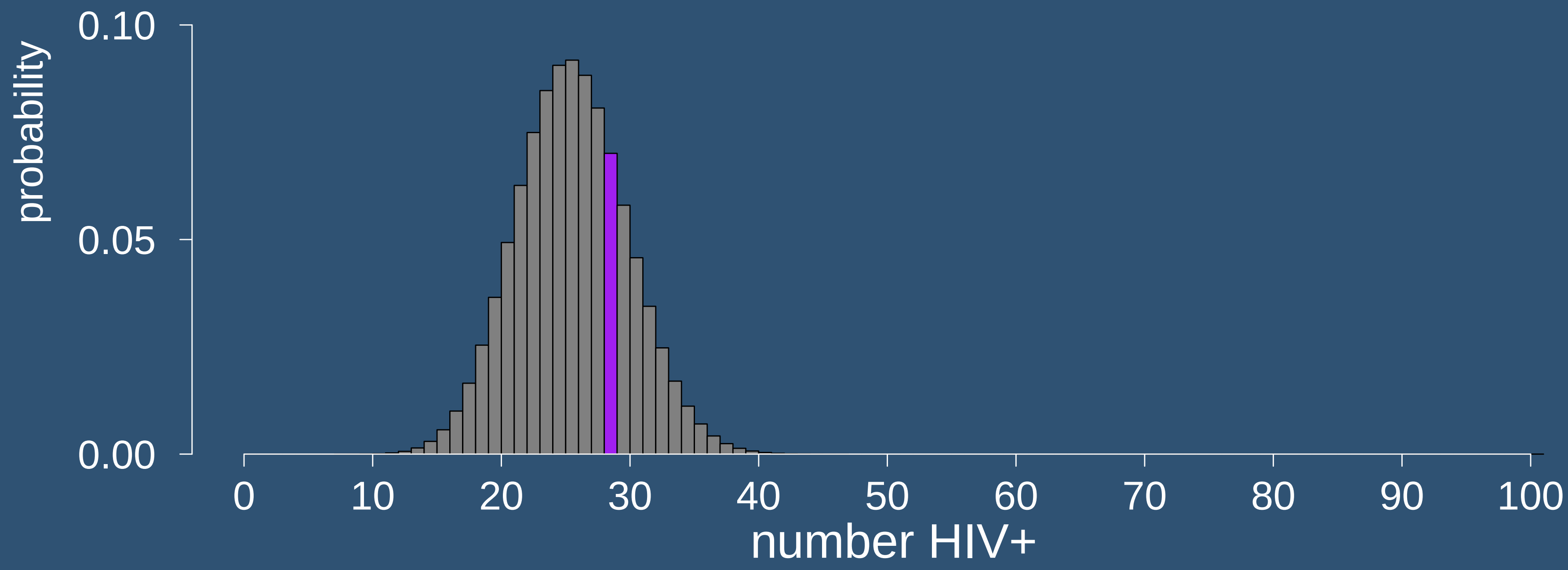
hypothetical prevalence: 20 %

dbinom(28, 100, 0.2) = 0.0141



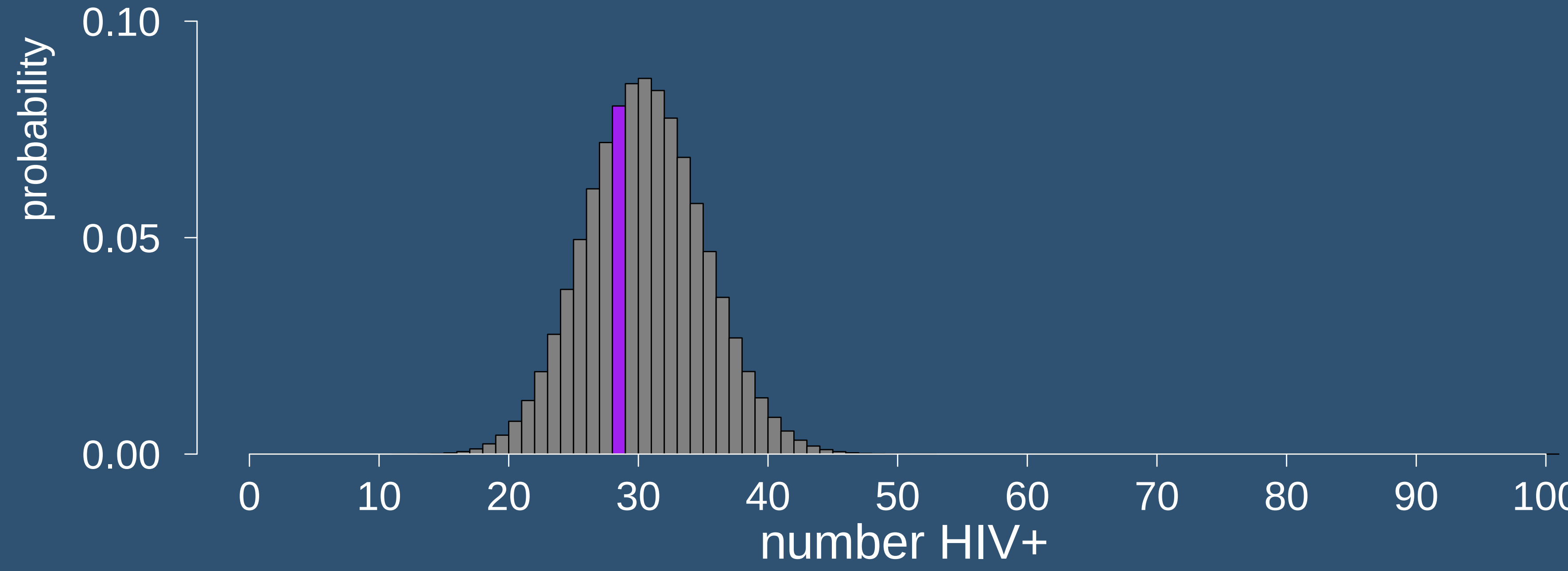
hypothetical   prevalence: 25 %

dbinom(28, 100, 0.25) = 0.0701



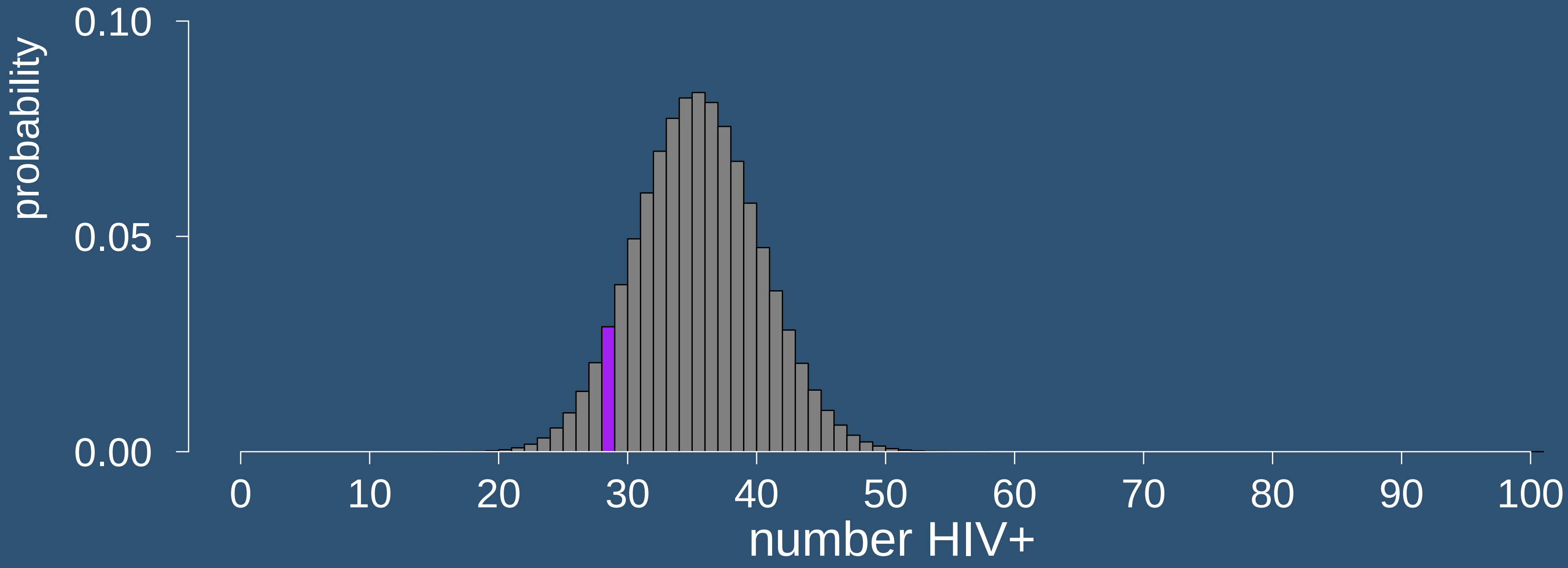
hypothetical prevalence: 30 %

dbinom(28, 100, 0.3) = 0.0804



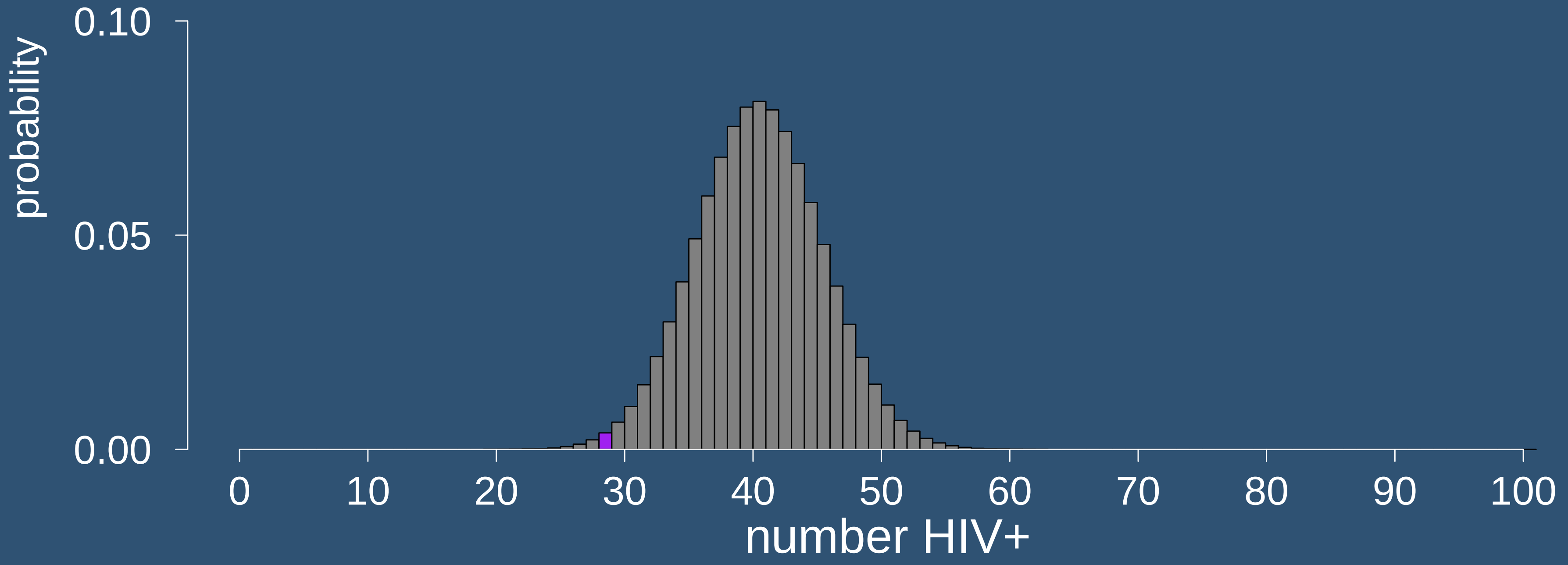
hypothetical   prevalence: 35 %

dbinom(28, 100, 0.35) = 0.029

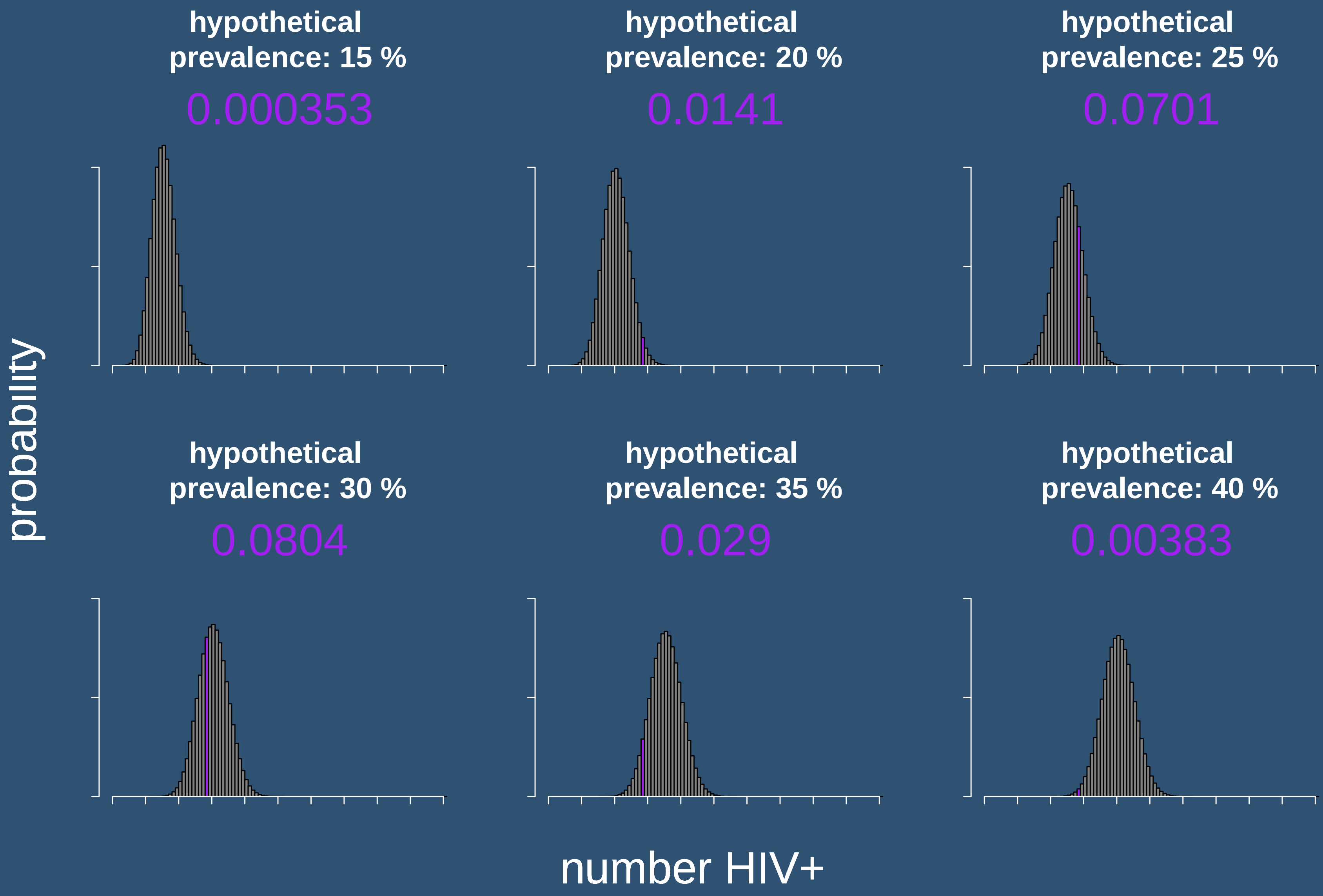


hypothetical   prevalence: 40 %

dbinom(28, 100, 0.4) = 0.00383



Which prevalence gives the greatest probability of observing exactly 28/100?



hypothetical prevalence: 15 %

0.000353

hypothetical prevalence: 20 %

0.0141

hypothetical prevalence: 25 %

0.0701

hypothetical prevalence: 30 %

0.0804

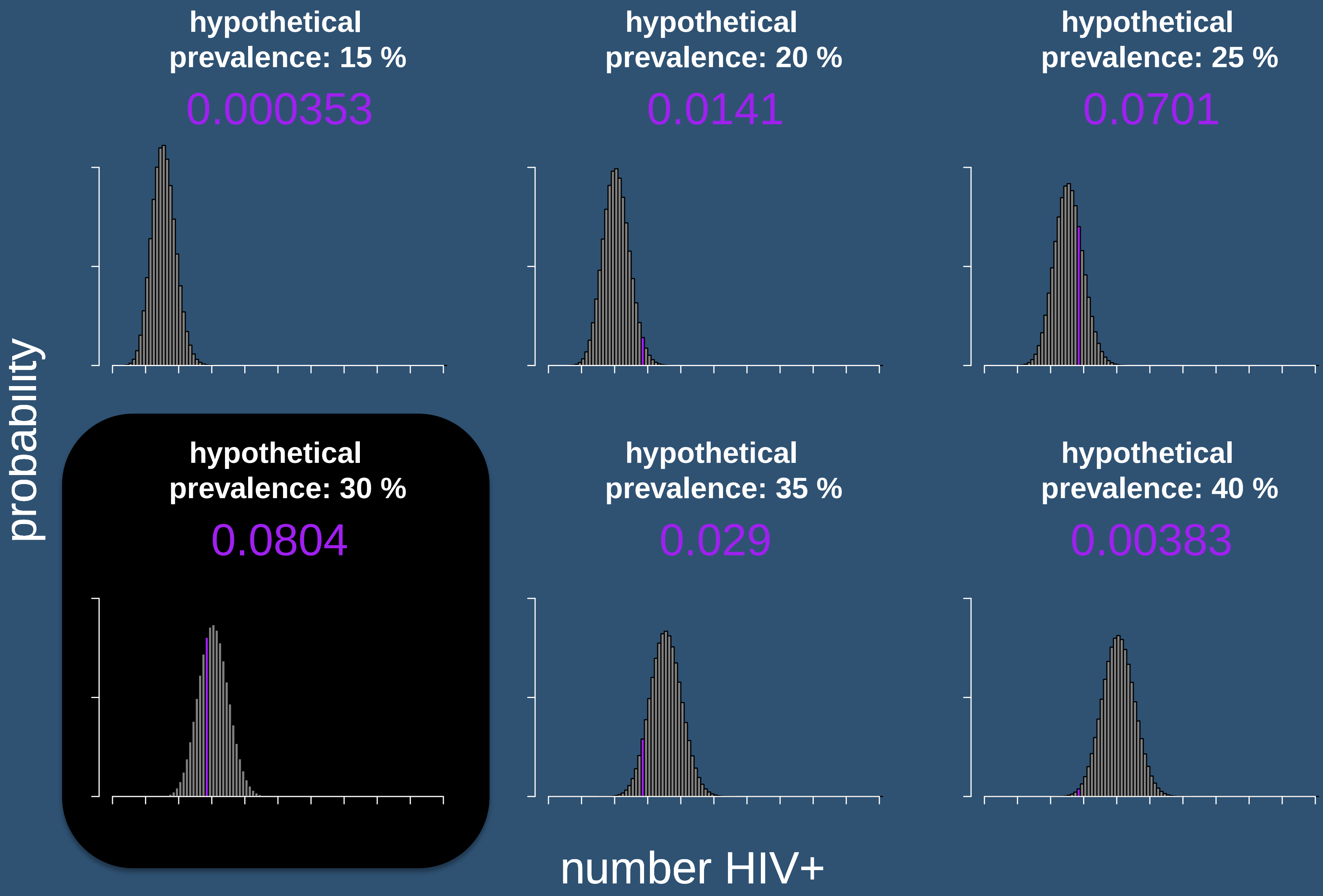
hypothetical prevalence: 35 %

0.029

hypothetical prevalence: 40 %

0.00383

Which of these prevalence values is most likely given our data?



hypothetical prevalence: 15 %

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0.0701

hypothetical prevalence: 30 %

0.0804

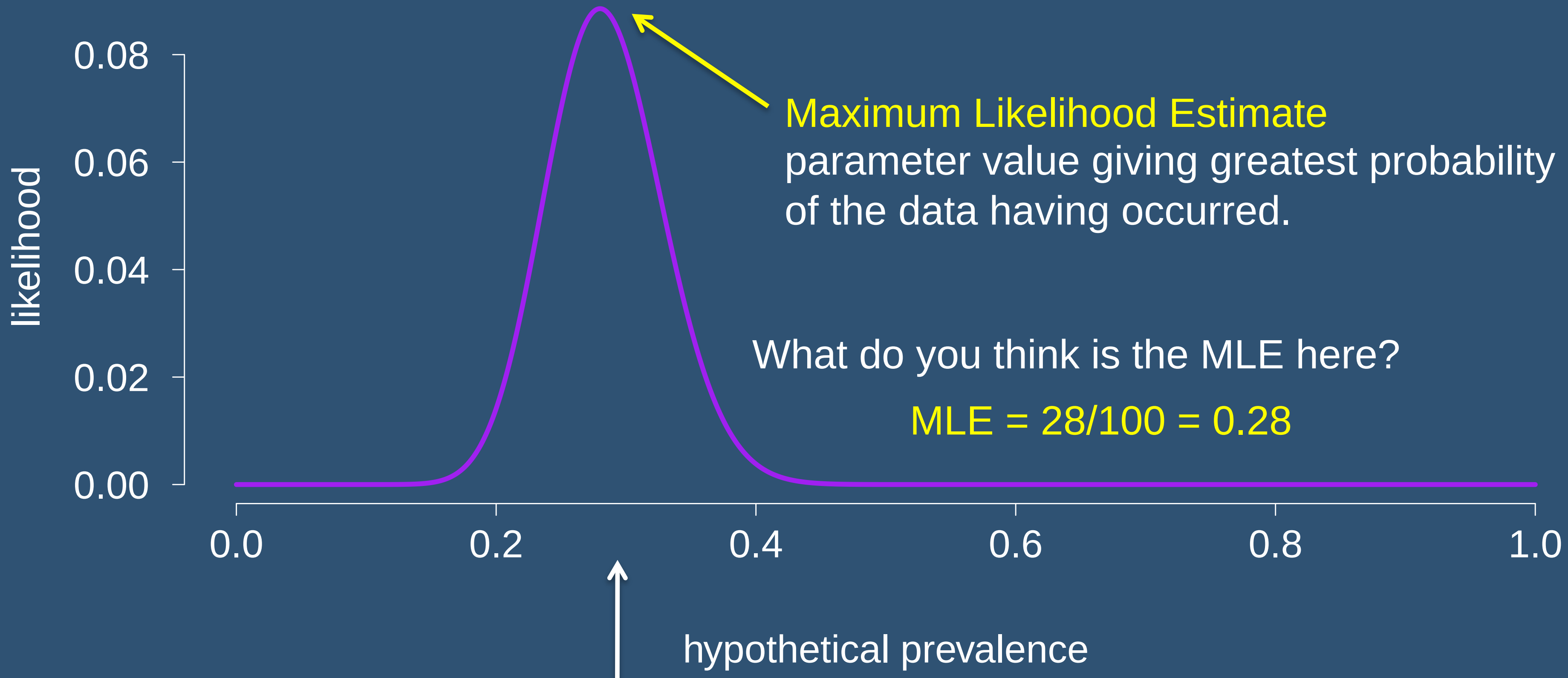
hypothetical prevalence: 35 %

0.029

hypothetical prevalence: 40 %

0.00383

p(our data given prevalence) = LIKELIHOOD



Maximum Likelihood Estimate
parameter value giving greatest probability of the data having occurred.

What do you think is the MLE here?

MLE = 28/100 = 0.28

true unknown value = 0.30

different null hypotheses

Defining Likelihood

- L(parameter | data) = p(data | parameter)
- Not a probability distribution.
- Probabilities taken from many different distributions.

function of x

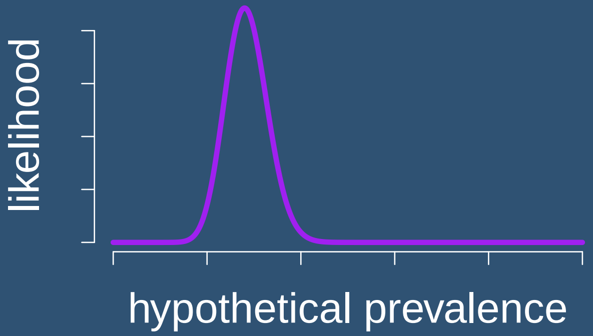
PDF: $f(x|p) = \binom{n}{x}(p)^{x}(1-p)^{n-x}$

LIKELIHOOD: $L(p|x) = \binom{n}{x}(p)^{x}(1-p)^{n-x}$

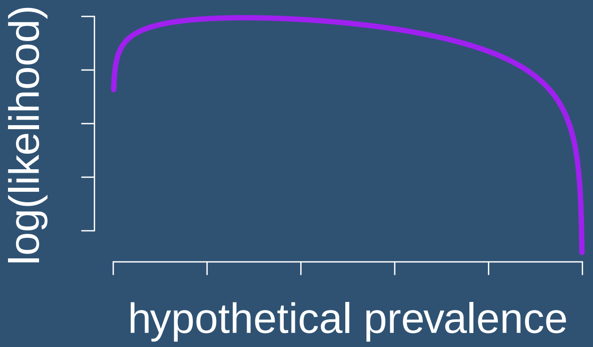
function of p

Deriving the Maximum Likelihood Estimate

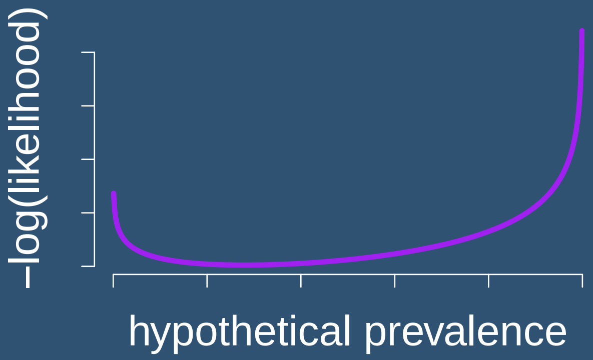
$$\overbrace{L(p)}^{\text{maximize}} = \binom{n}{x}(p)^{x}(1-p)^{n-x}$$



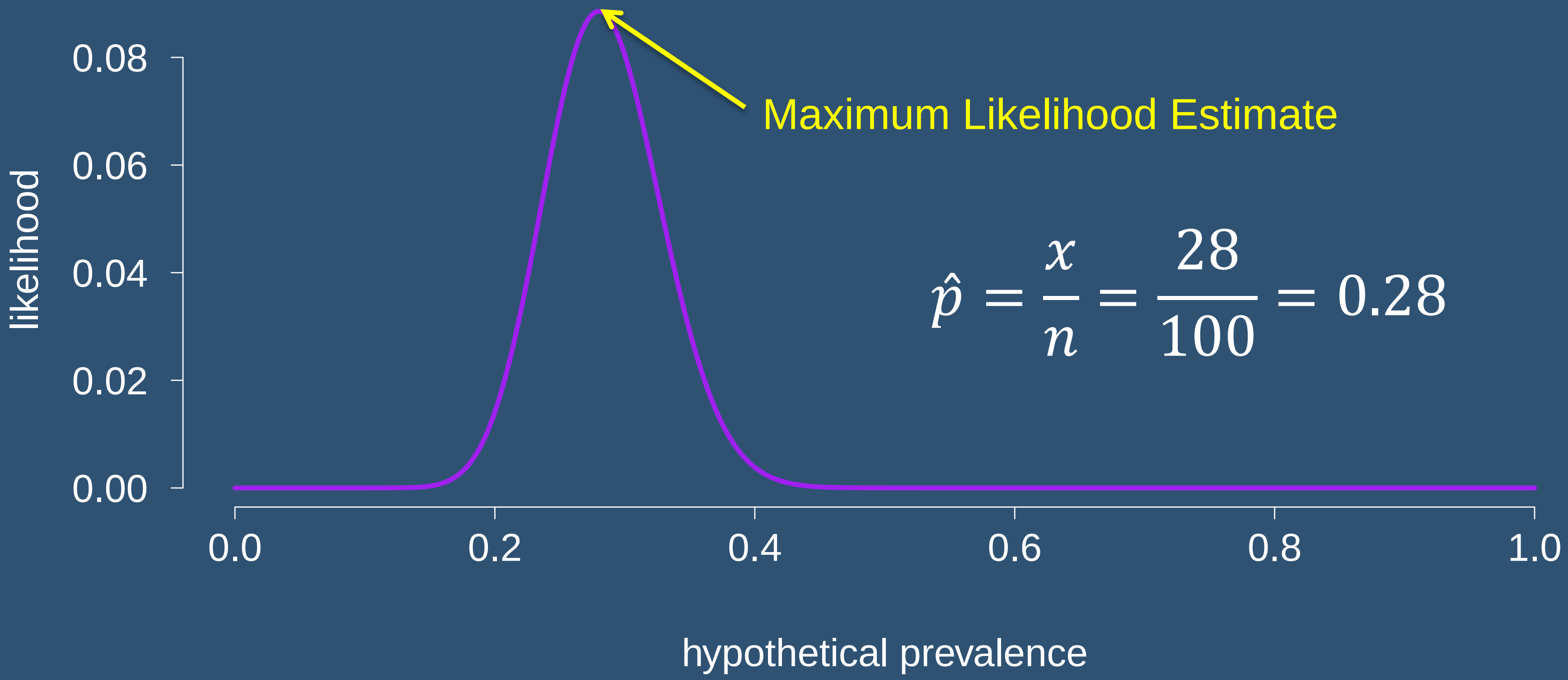
$$\overbrace{\log\big(L(p)\big)}^{\text{maximize}} = \log\left[\binom{n}{x}(p)^{x}(1-p)^{n-x}\right]$$



$$\overbrace{l(p)}^{\text{minimize}} = -\log\left[\binom{n}{x}(p)^{x}(1-p)^{n-x}\right]$$

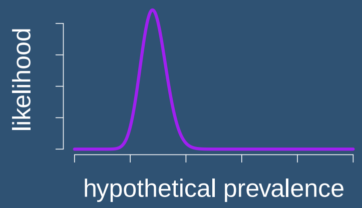


Likelihood

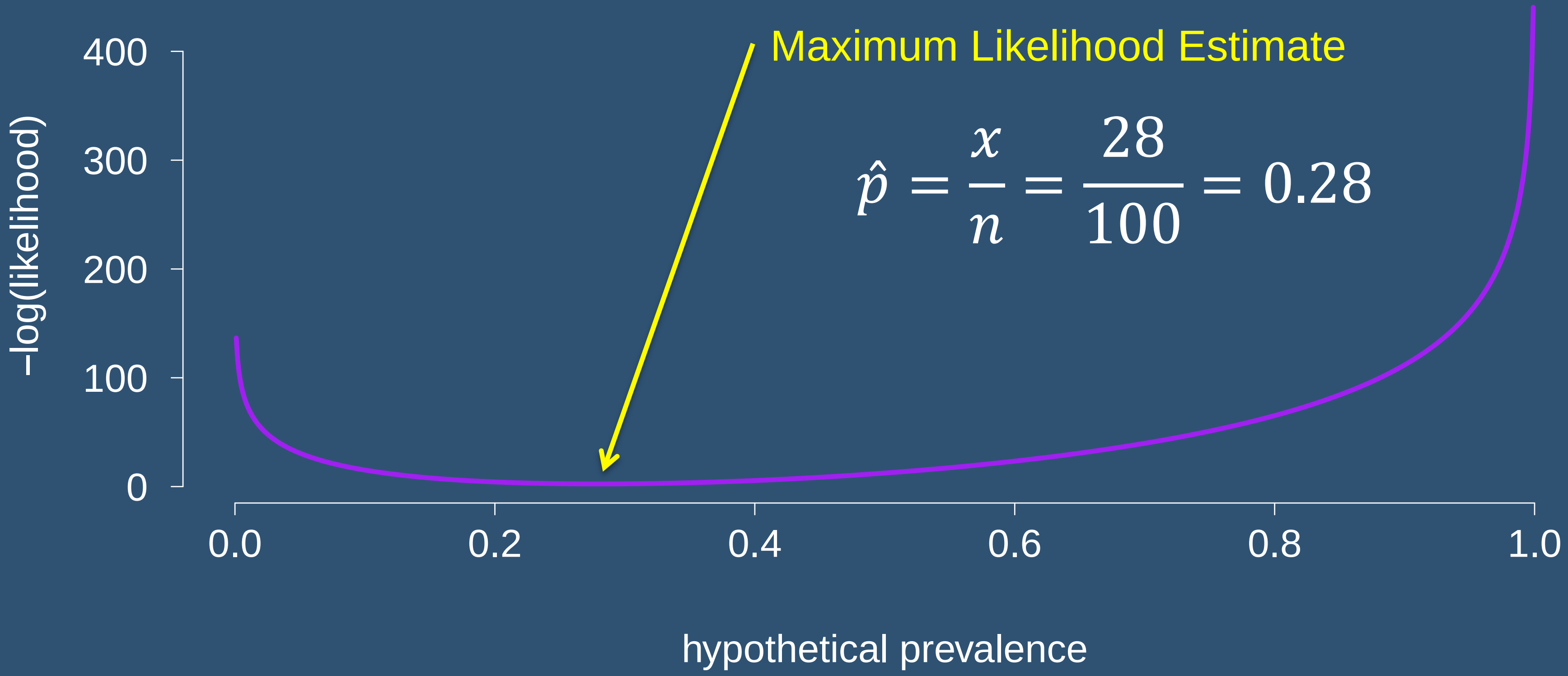


Maximum Likelihood Estimate

$$\hat{p} = \frac{x}{n} = \frac{28}{100} = 0.28$$



we usually minimize the –log(likelihood)



$$\hat{p} = \frac{x}{n} = \frac{28}{100} = 0.28$$

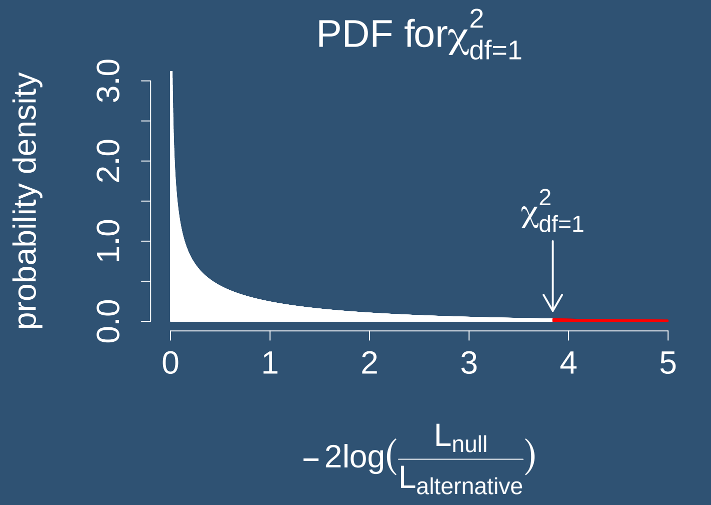
Building Confidence Intervals

Likelihood Ratio Test

If the null hypothesis were true then

$$2\log\left(\frac{L(\text{alternative hypothesis})}{L(\text{null hypothesis})}\right)\sim\chi^2_{df=1}$$

Why does this work?



- Adding irrelevant parameters *always* improves the fit.

- How much should fit improve due to chance alone by adding an irrelevant parameter?

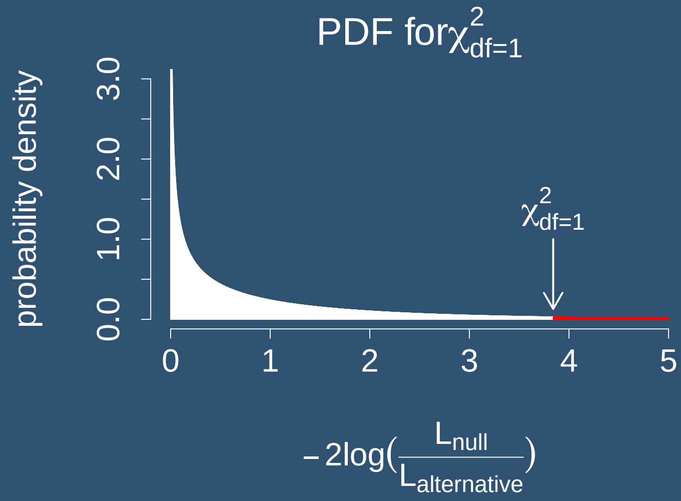
- Fit improvement, as measured above, is approximately χ^2_{df} distributed with df = to the difference in parameters used to fit.

Building Confidence Intervals

Likelihood Ratio Test

If the null hypothesis were true then

$$2\log\left(\frac{L(\text{alternative hypothesis})}{L(\text{null hypothesis})}\right) \sim \chi^2_{df=1}$$



$$2\log(L_{\text{MLE}}) - 2\log(L_{\text{null}}) \sim \chi^2_{df=1}$$

$$-2l_{MLE} + 2l_{null} \sim \chi^2_{df=1}$$

So if our α = .05, then we reject any null hypothesis for which

$$-2l_{MLE} + 2l_{null} > \ \chi^2_{df=1,\alpha=.05} = 3.84$$

```
> qchisq(p = .95, df = 1)
[1] 3.841459
```

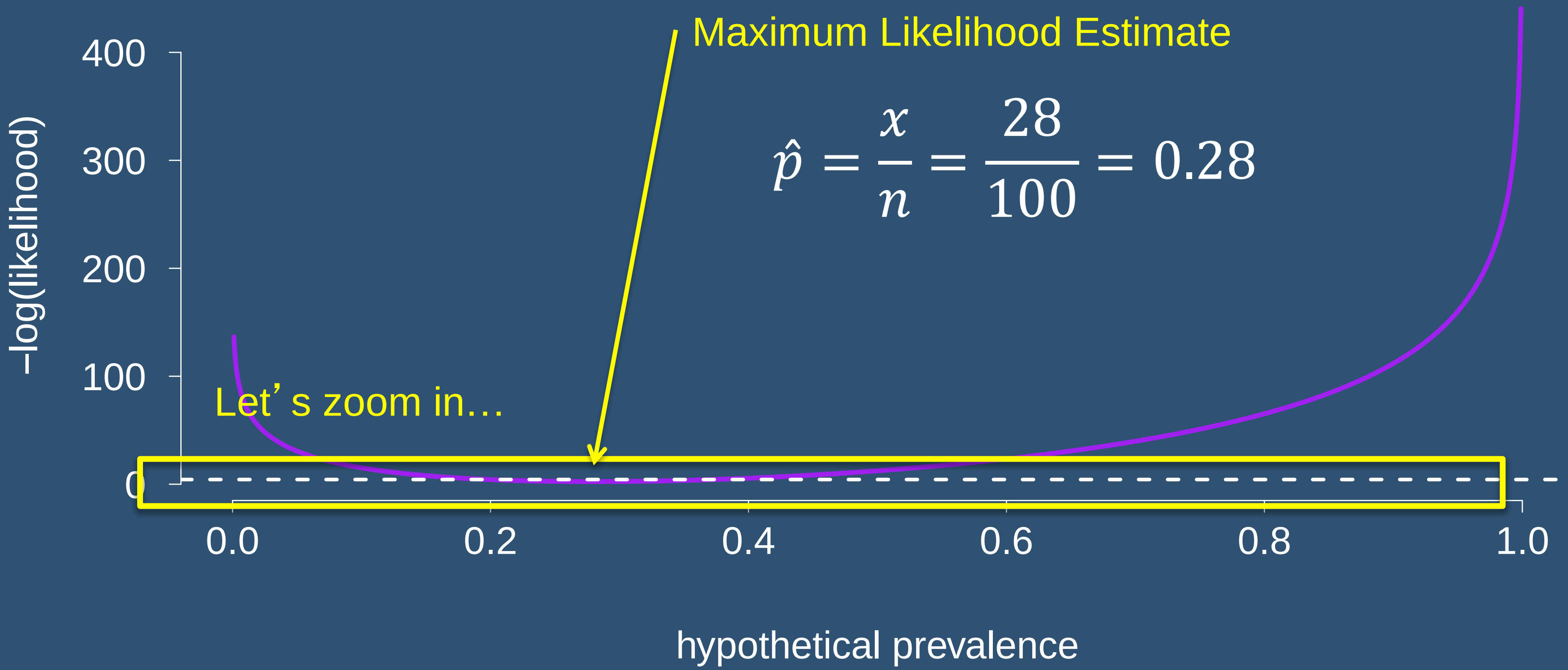
$$l_{null} - l_{MLE} > 1.92$$

If log(L_{MLE}) – log(L_{null})> 1.92,

we reject that null hypothesis.

Building Confidence Intervals
Likelihood Ratio Test

we usually minimize the –log(likelihood)



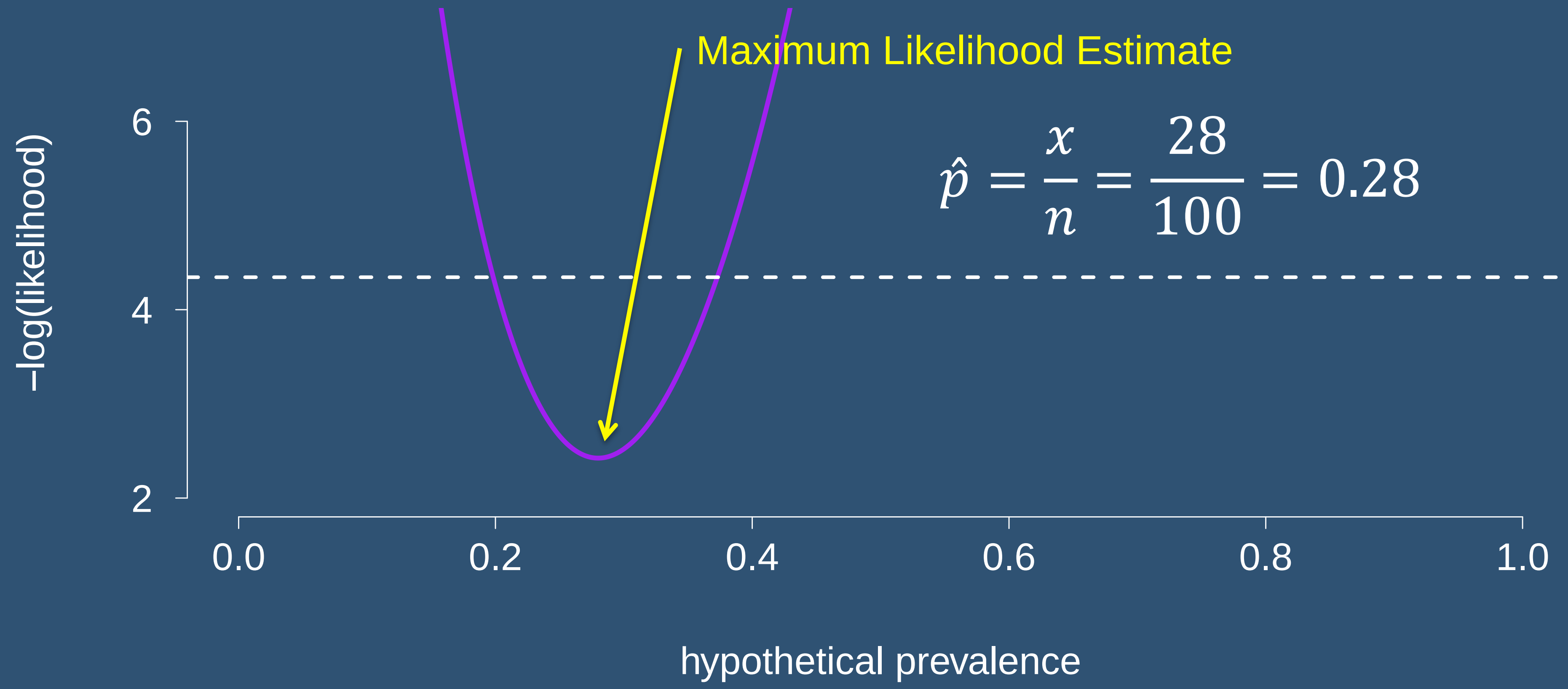
Maximum Likelihood Estimate

$$\hat{p} = \frac{x}{n} = \frac{28}{100} = 0.28$$

Let’s zoom in…

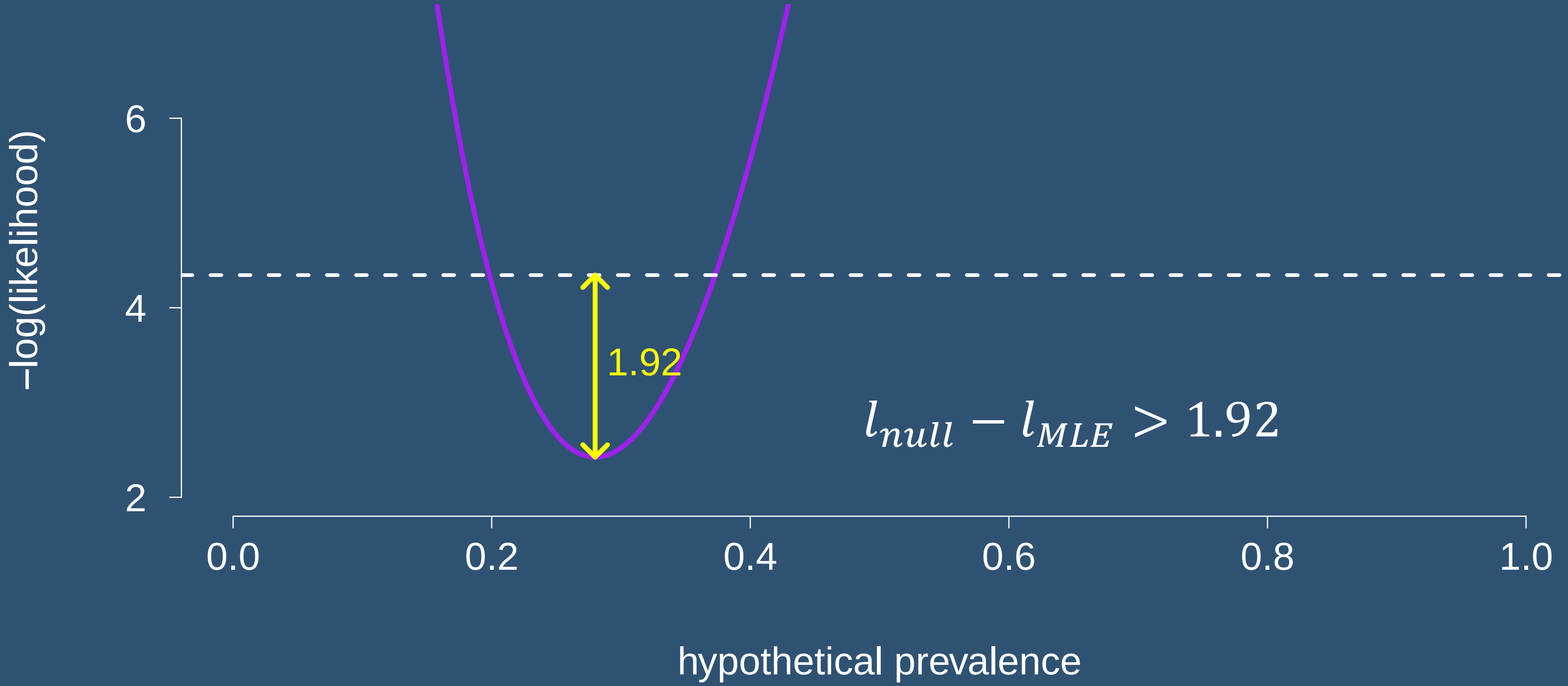
Building Confidence Intervals

Likelihood Ratio Test



$$\hat{p} = \frac{x}{n} = \frac{28}{100} = 0.28$$

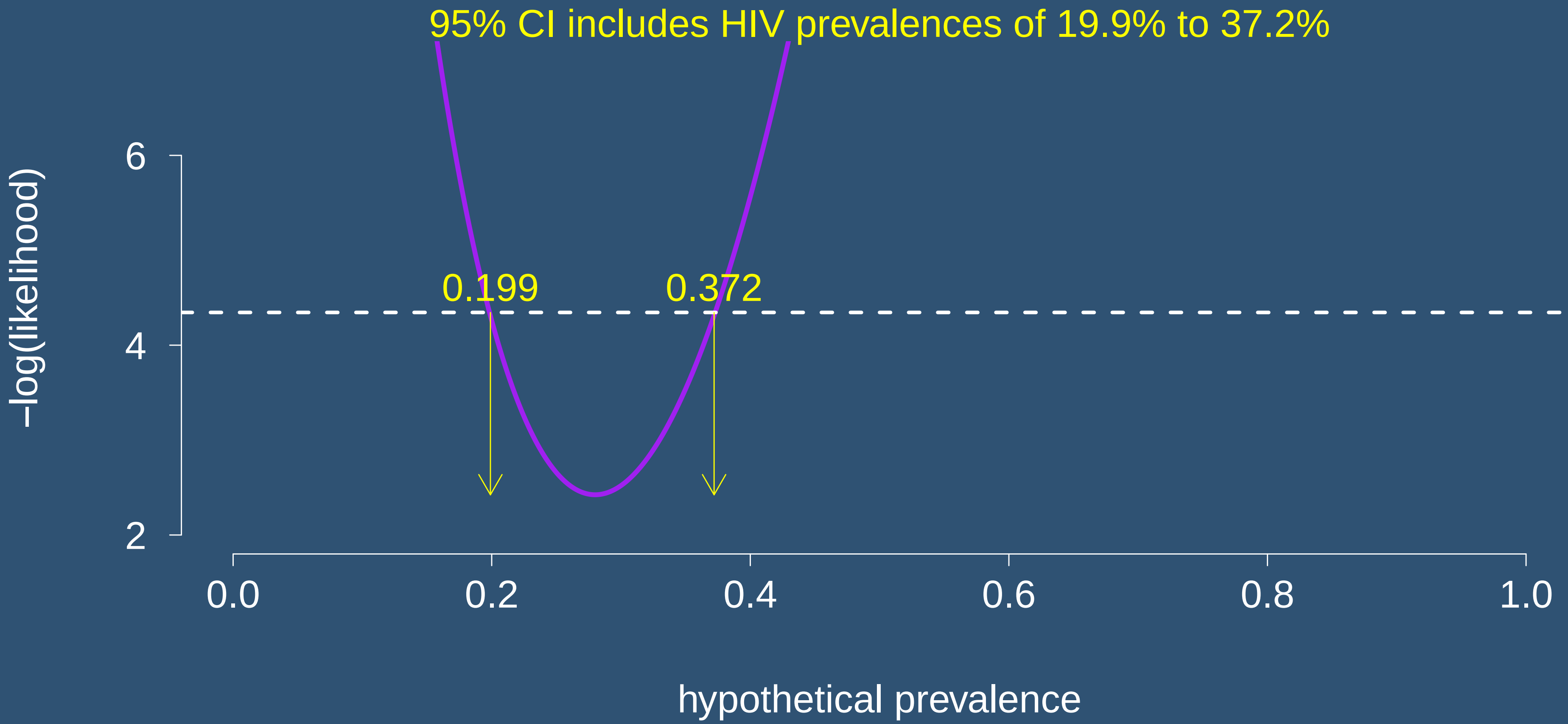
Building Confidence Intervals
Likelihood Ratio Test



$$l_{null} - l_{MLE} > 1.92$$

Building Confidence Intervals

Likelihood Ratio Test



Statistical Models & Dynamic Models

Statistical Models

- Account for bias and random error to find correlations that may imply causality.
- Often the first step to assessing relationships.
- Assume independence of individuals (at some scale).

Dynamic Models

- Systems Approach: Explicitly model multiple mechanisms to understand their interactions.
- Links observed relationships at different scales.
- Explicitly focuses on dependence of individuals

By developing dynamic models in a probabilistic framework we can account for dependence, random error, and bias while linking patterns at multiple scales.

Fitting Dynamic Models to Data

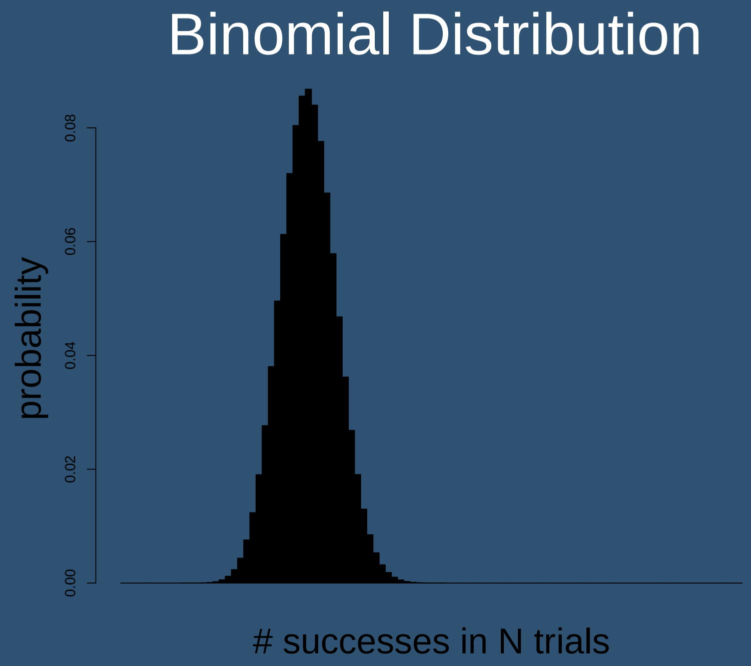
Adapt our dynamic models in a probabilistic framework so we can ask:

What is the probability that a model would have generated the observed data?

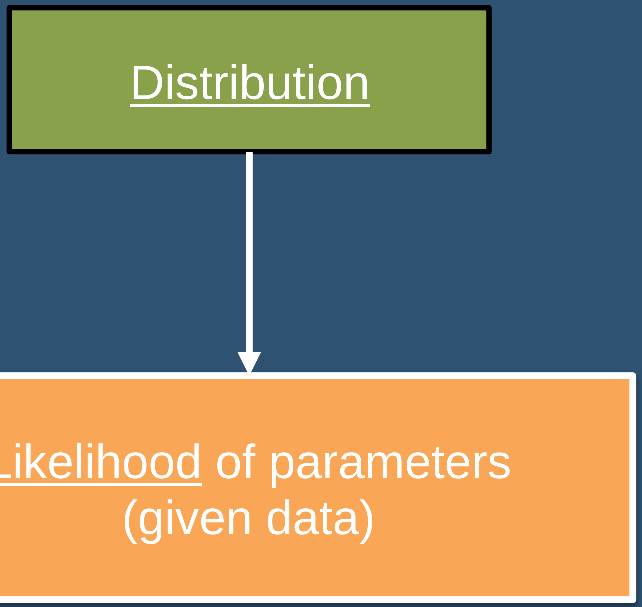
↓

What is the likelihood of a model given the data?

Likelihood of parameters
(given data)

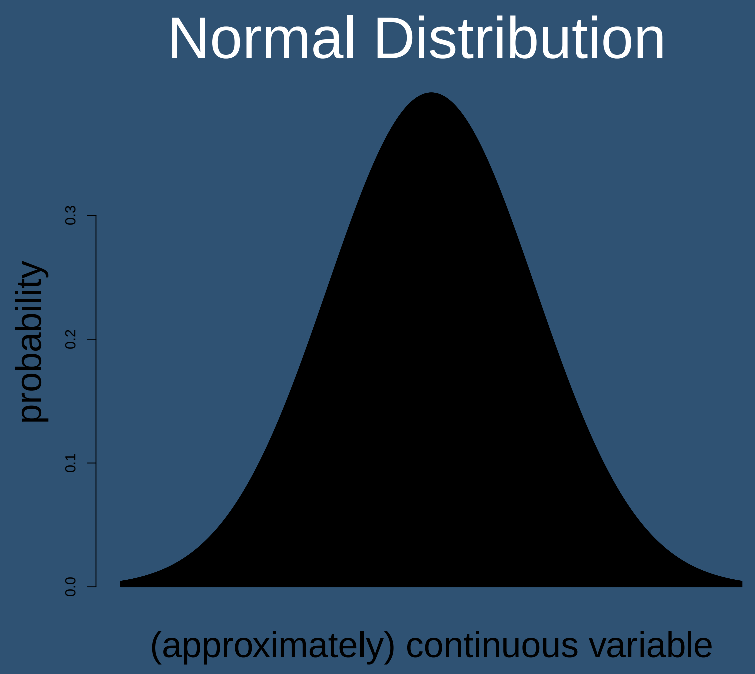


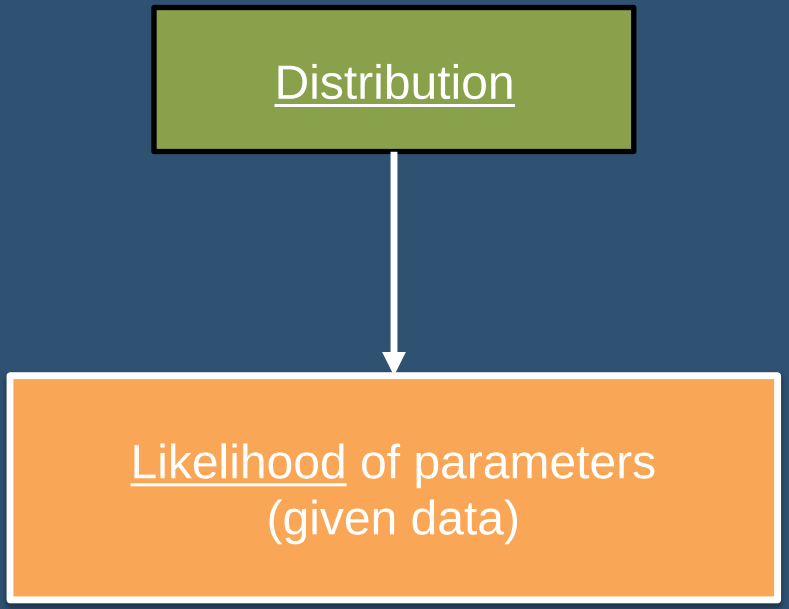
Binomial Distribution



Distribution

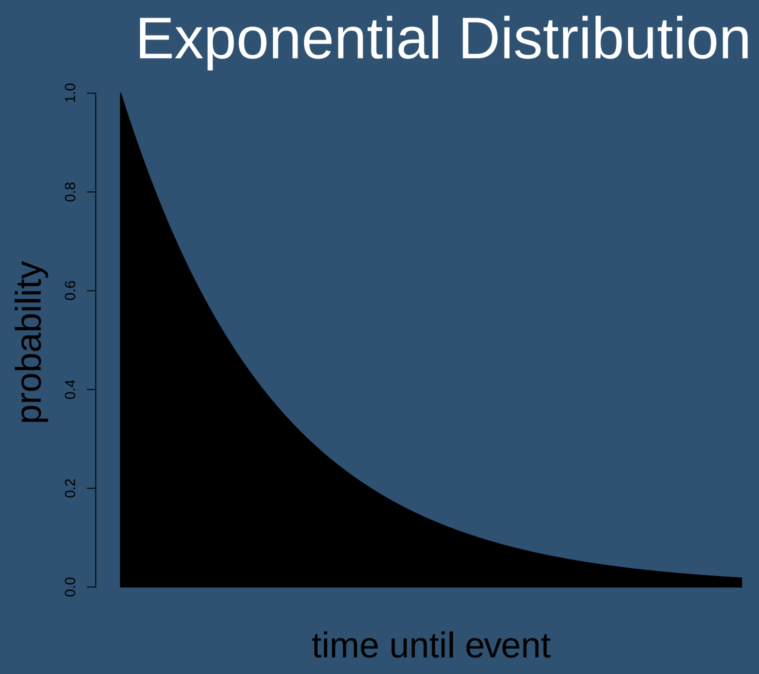
Likelihood of parameters
(given data)

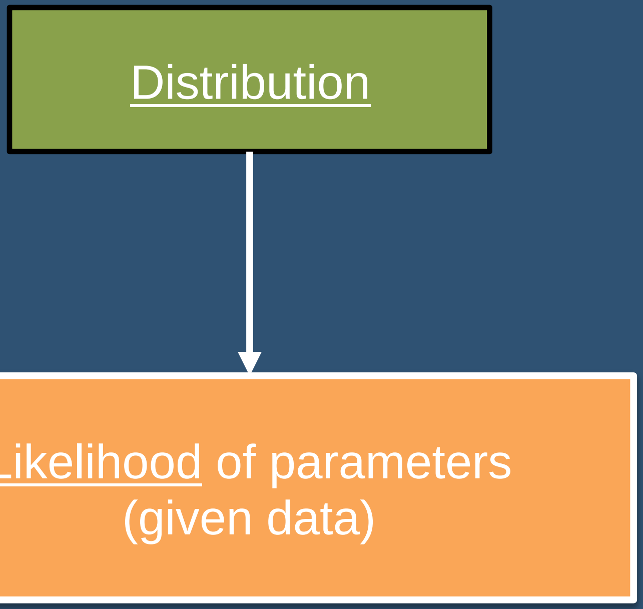




Distribution

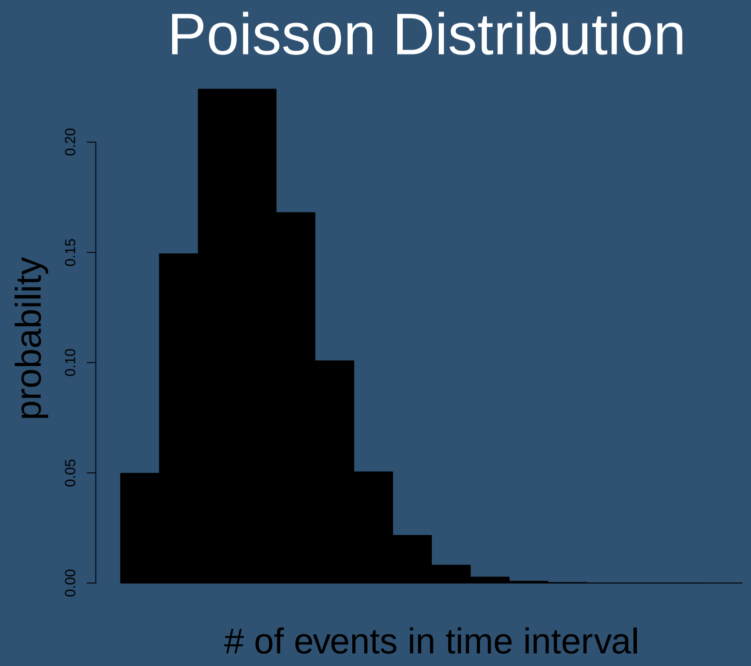
Likelihood of parameters
(given data)

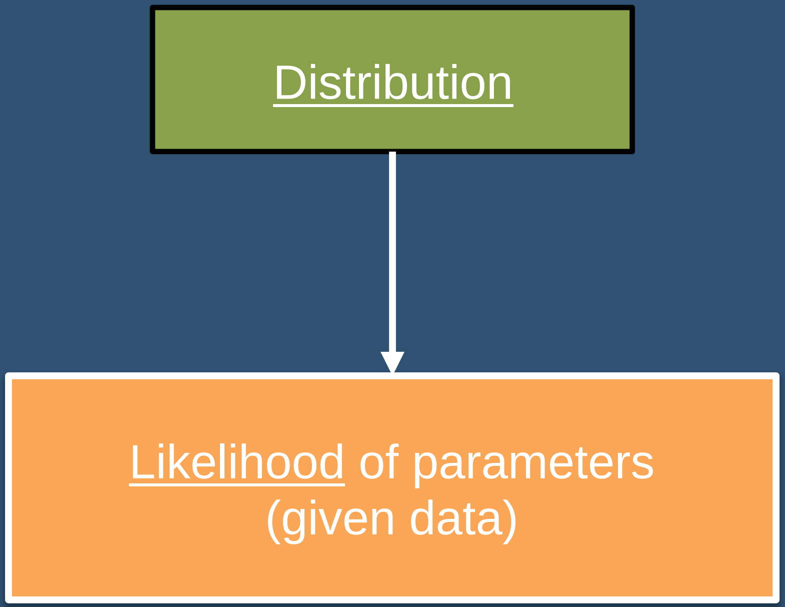




Distribution

Likelihood of parameters
(given data)

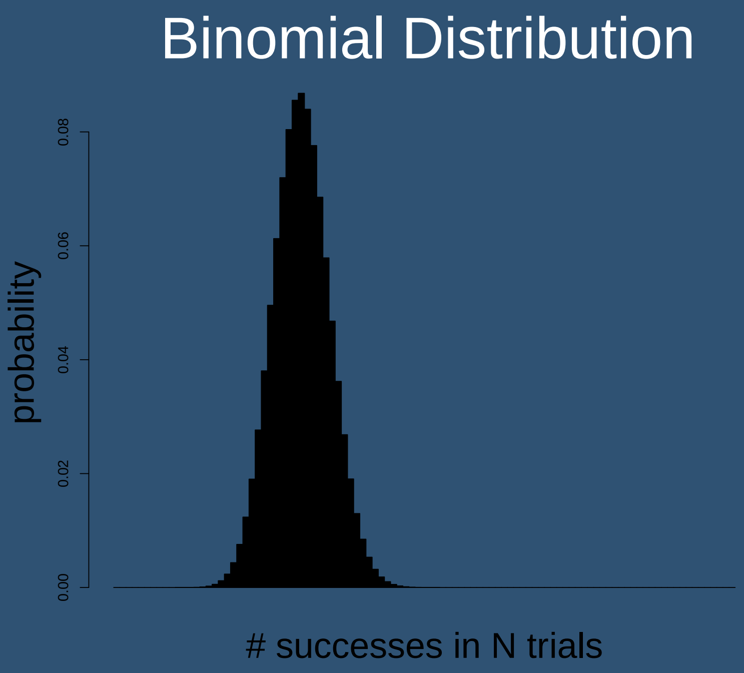


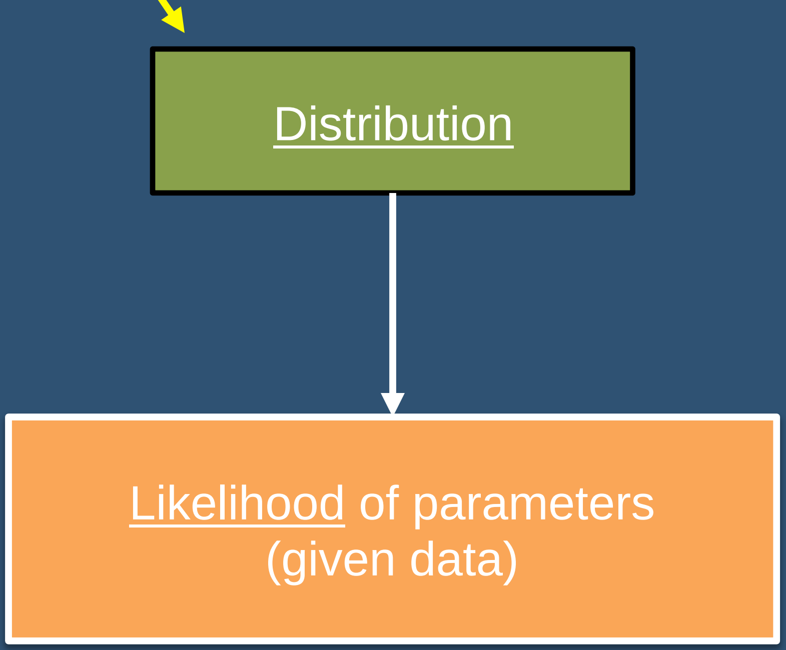


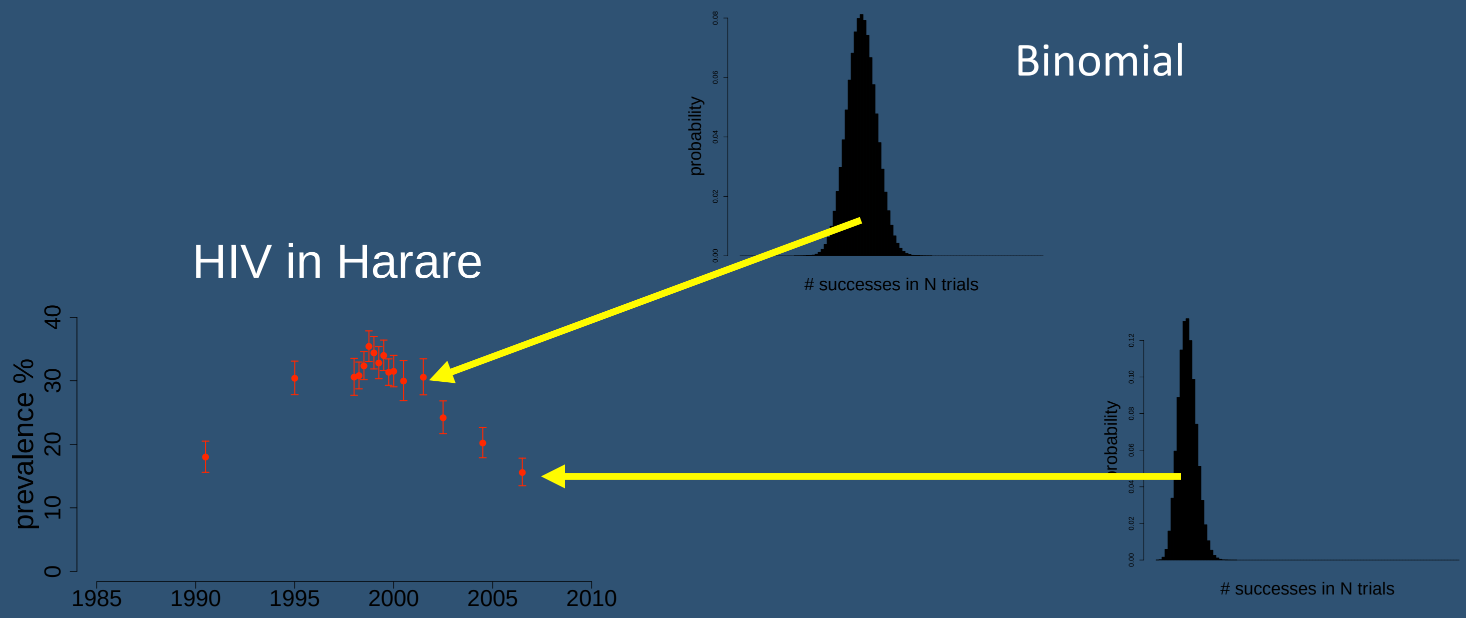
Distribution

Likelihood of parameters (given data)

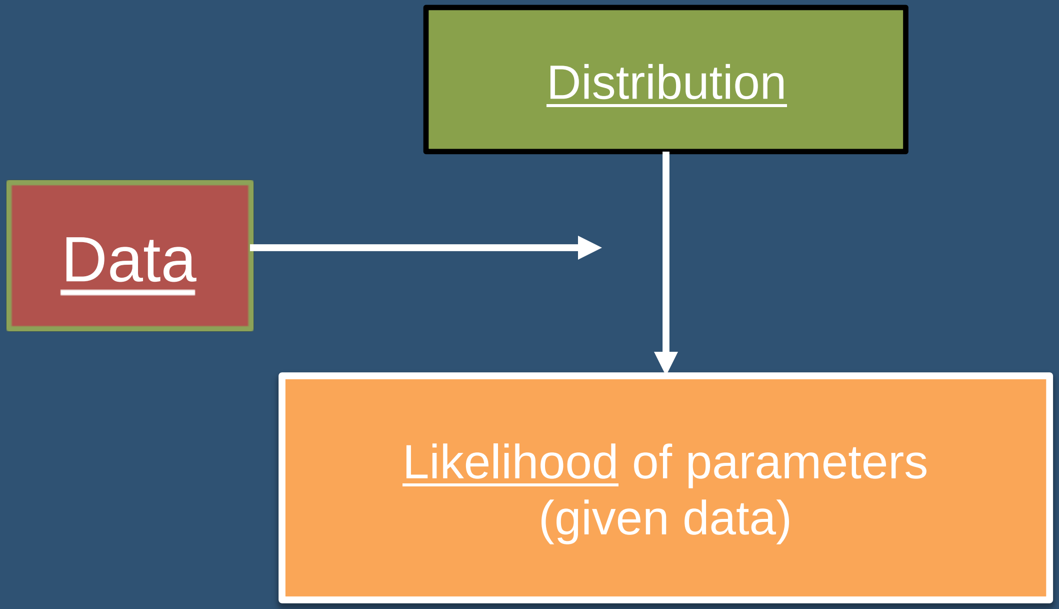
Stochastic Component of Model





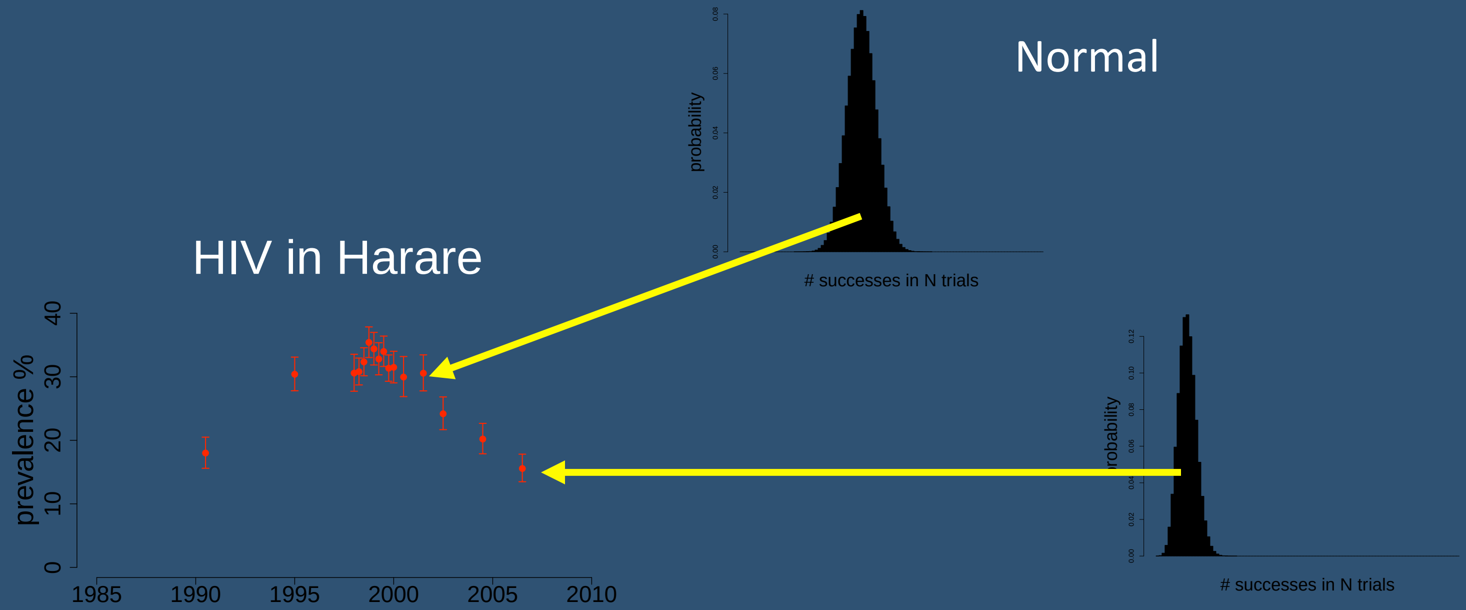

HIV in Harare

Binomial


Distribution

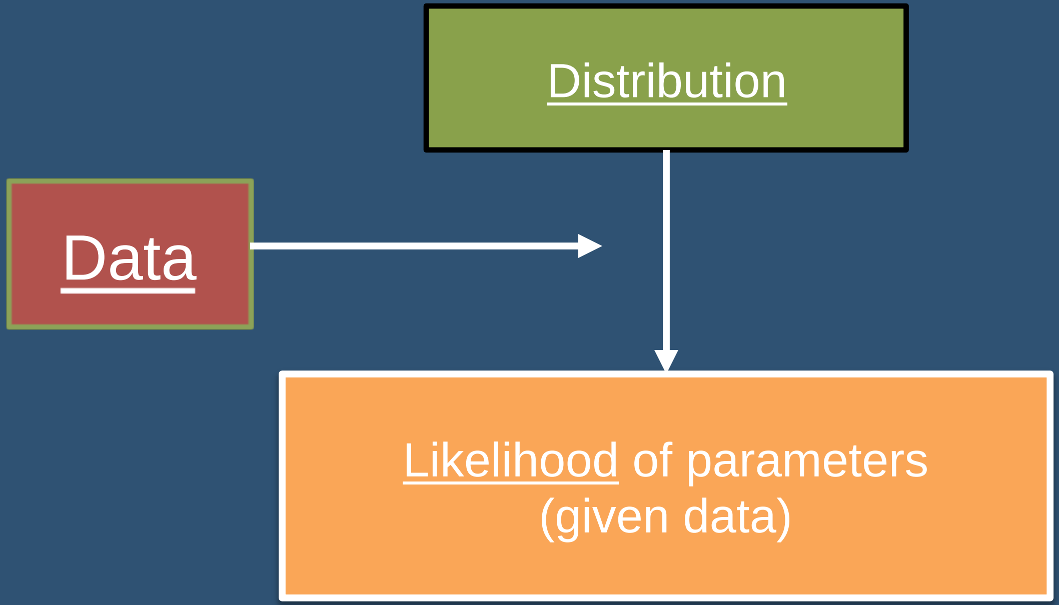
Data

Likelihood of parameters (given data)



HIV in Harare

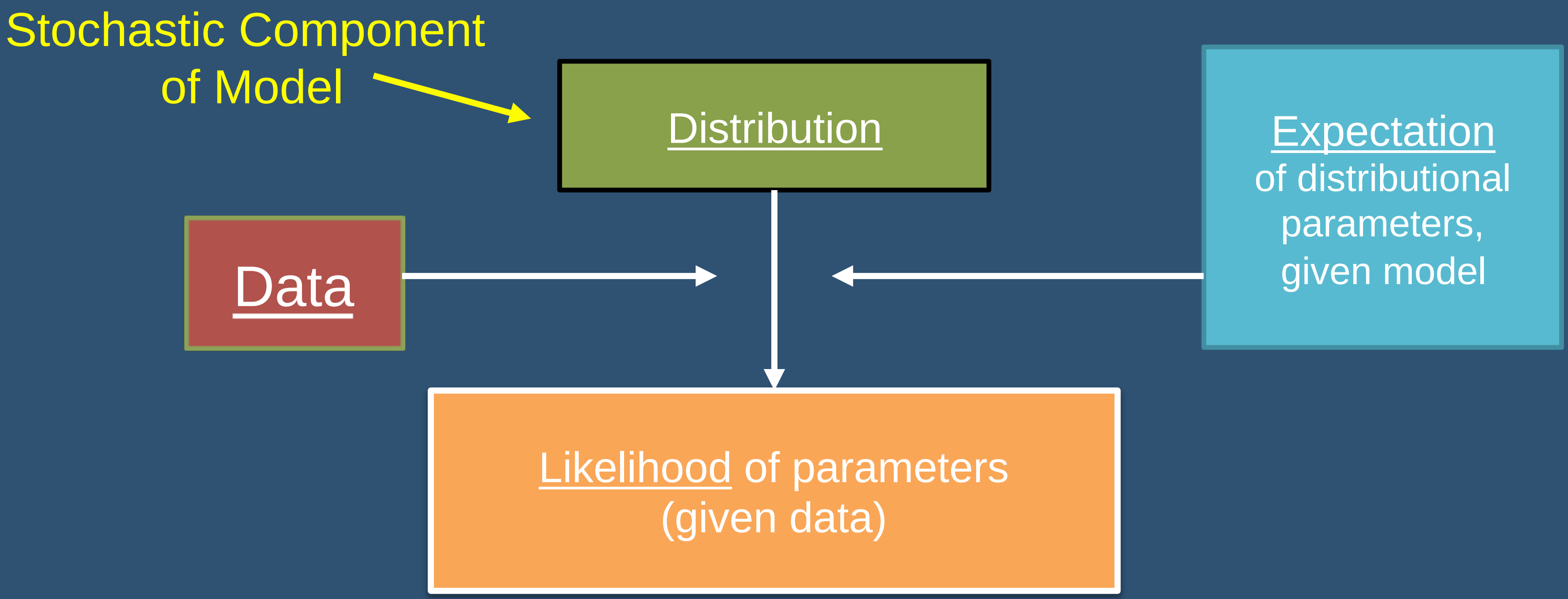
Normal



Distribution

Data

Likelihood of parameters
(given data)



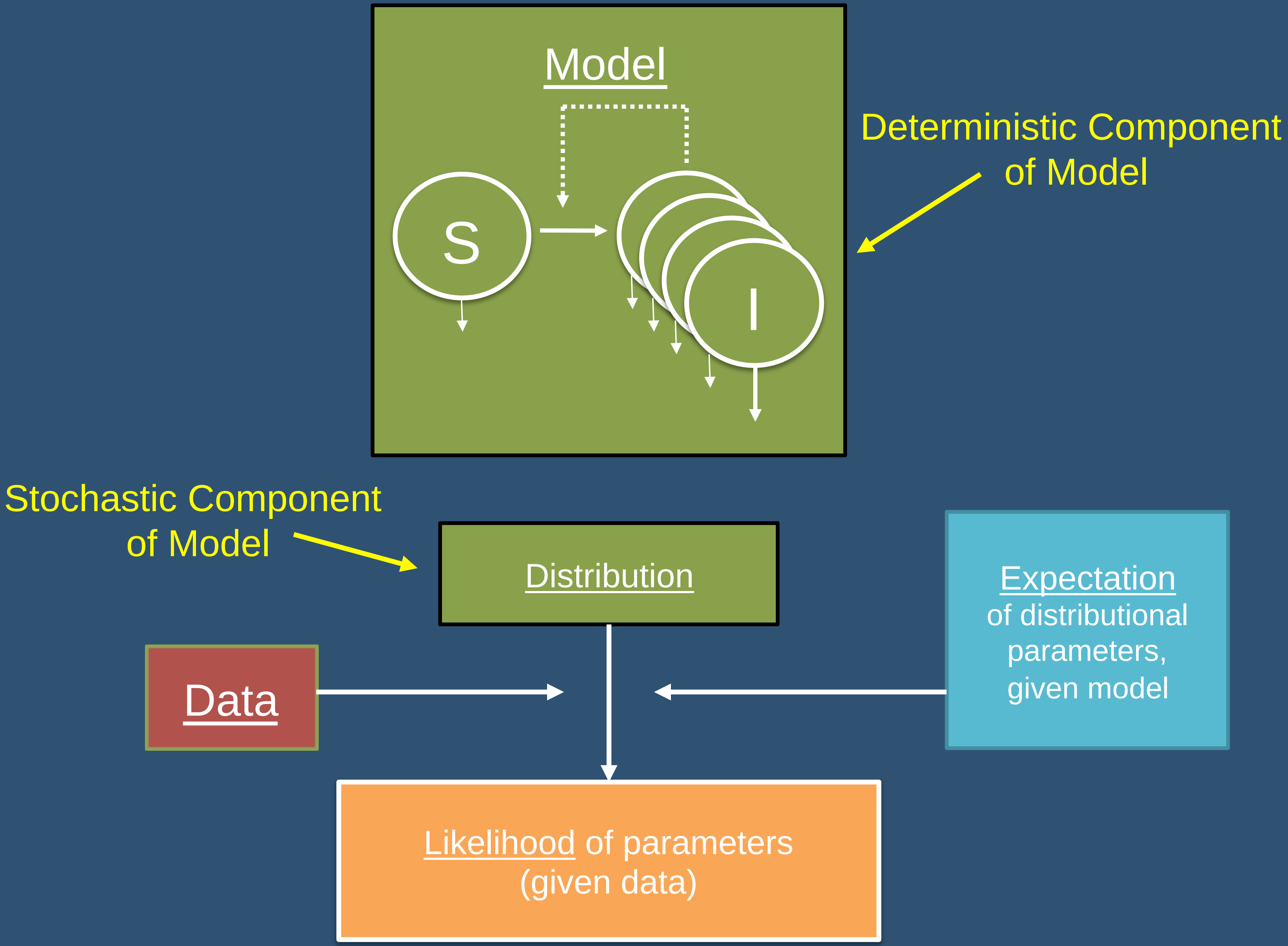
Stochastic Component of Model

Distribution

Data

Expectation of distributional parameters, given model

Likelihood of parameters (given data)



Model

Deterministic Component of Model

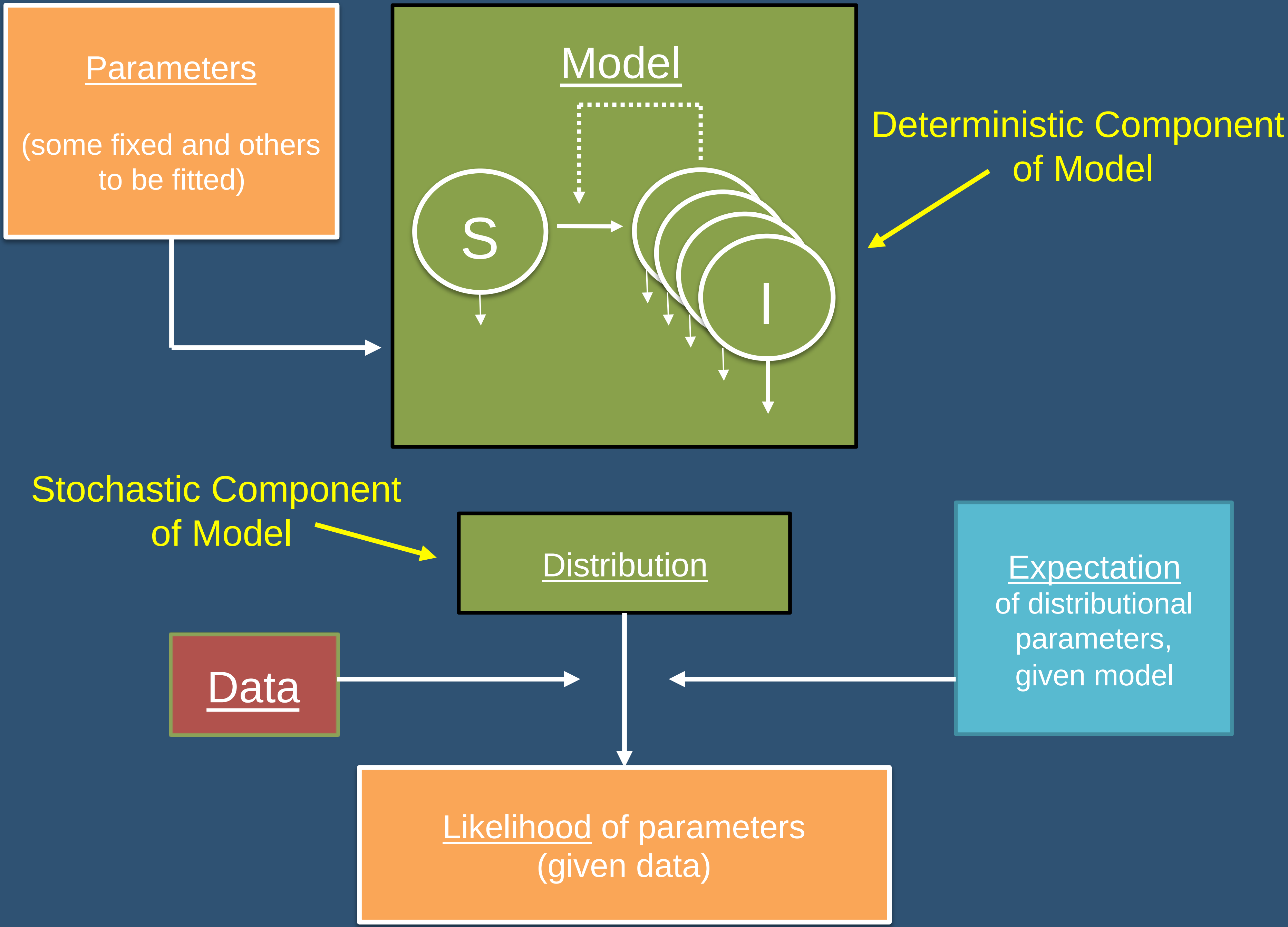
Stochastic Component of Model

Distribution

Data

Expectation of distributional parameters, given model

Likelihood of parameters (given data)



Parameters

(some fixed and others to be fitted)

Model

Deterministic Component of Model

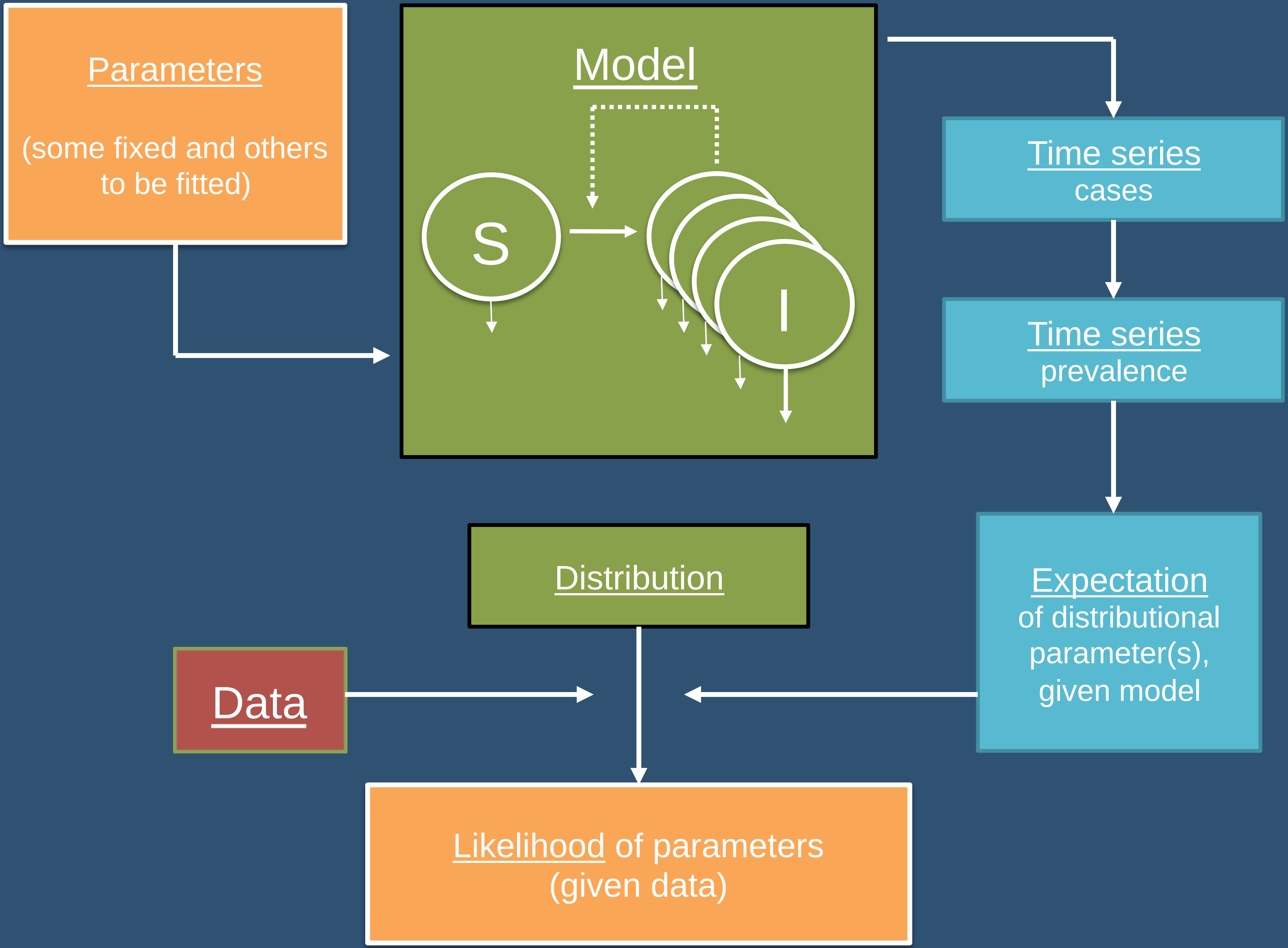
Stochastic Component of Model

Distribution

Data

Expectation of distributional parameters, given model

Likelihood of parameters (given data)



Parameters

(some fixed and others to be fitted)

Model

Time series
cases

Time series
prevalence

Expectation
of distributional parameter(s), given model

Distribution

Data

Likelihood of parameters (given data)

Collinearity

- Independent variables that vary with each other

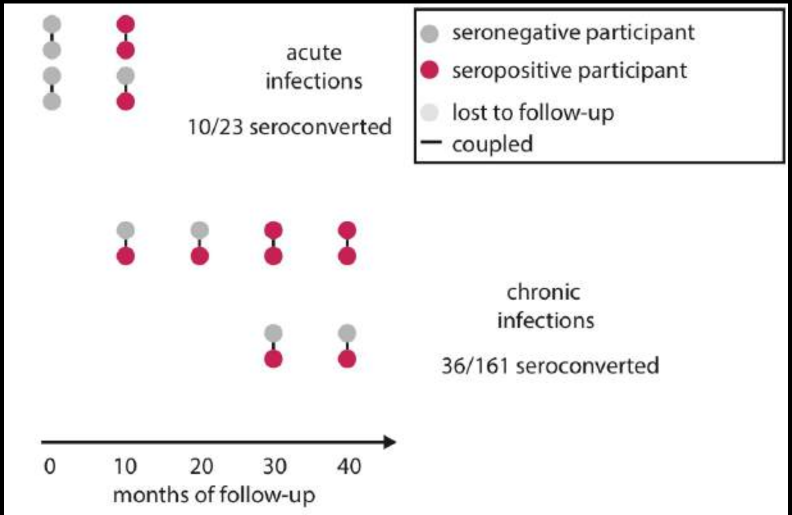
Non-Identifiability

- Multiple parameter sets fit about equally well
- Can be informative in dynamic models

Rakai *Retrospective Couples* Cohort

7x as infectious for first 5 month

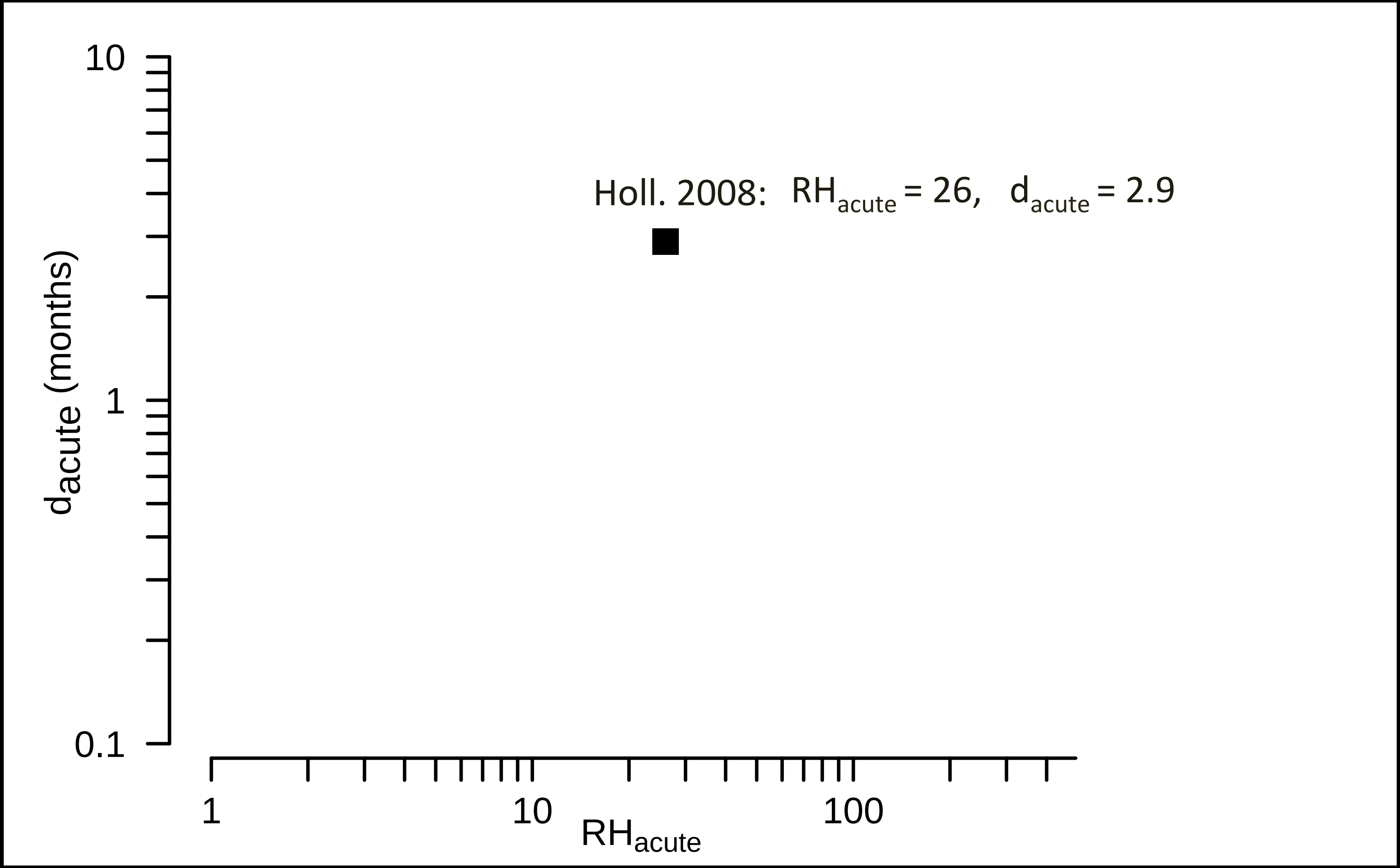
$$EHM_{acute} = 30$$



Comparing Results

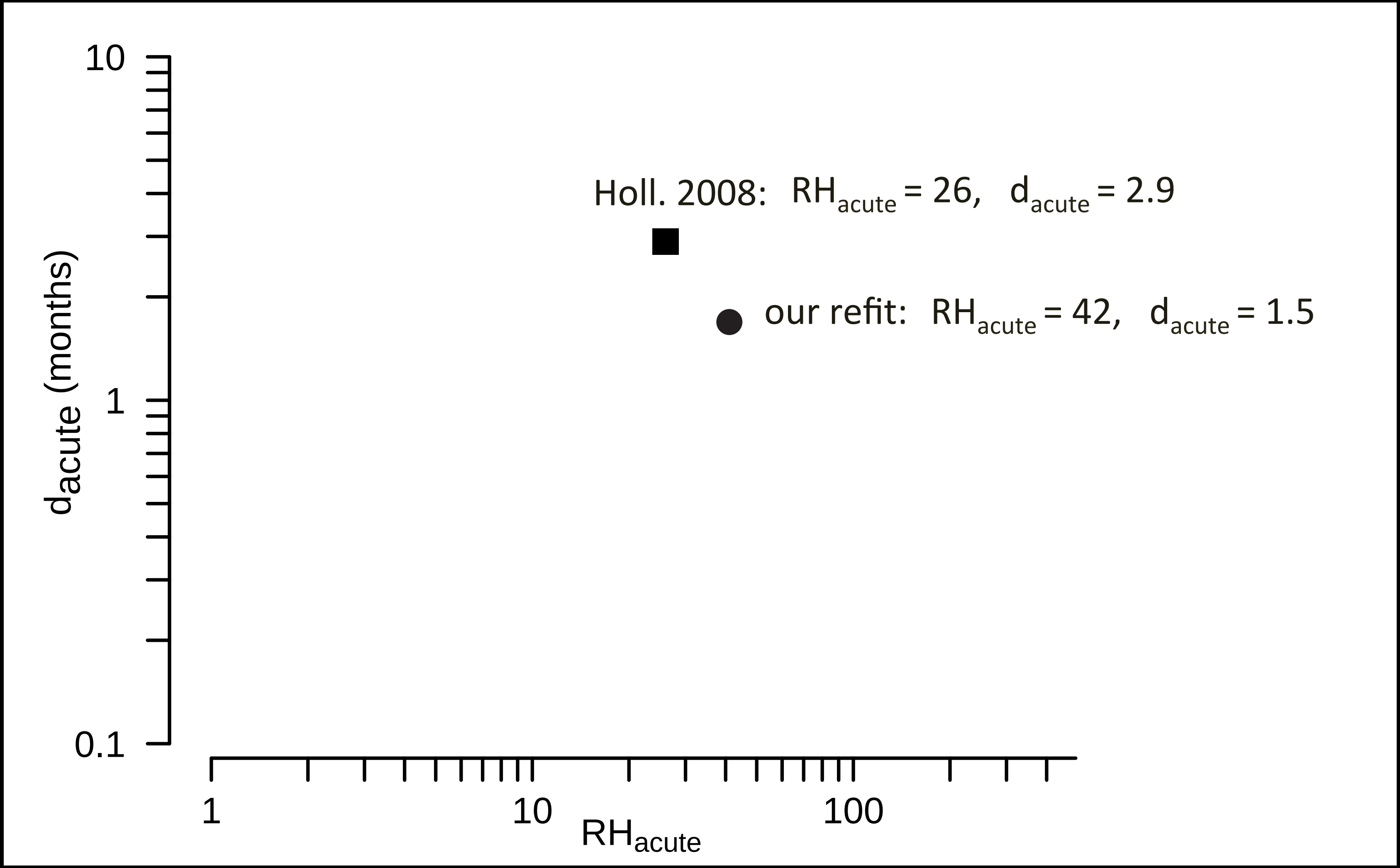
Study	RH_{acute}	d_{acute} (months)
Wawer et al. (2005)	7.25 (3.05 – 17.3)	5
Hollingsworth et al. (2008)	26	2.9 (1.23-6)

Collinearity in Fitted Parameters



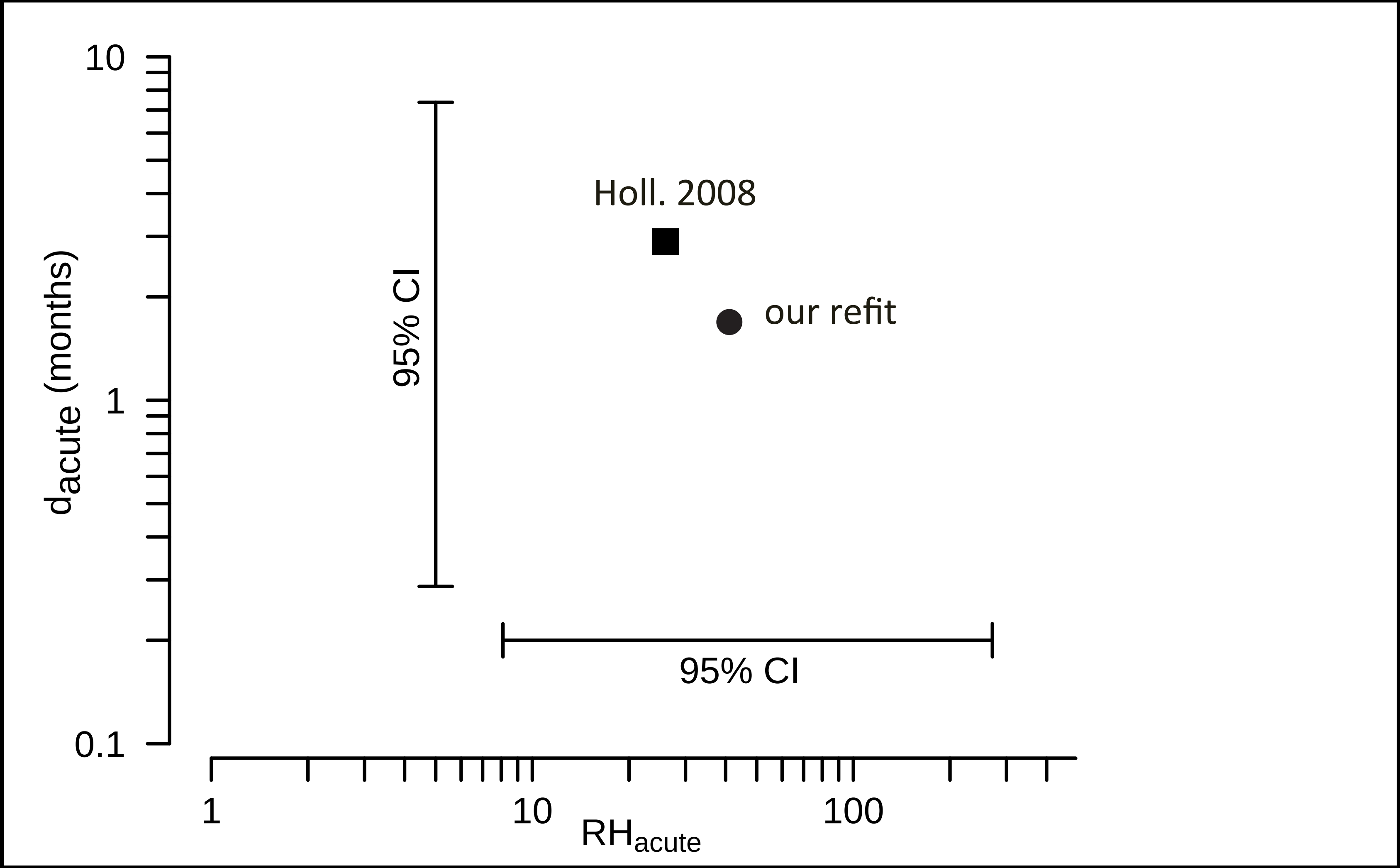
Revisit original data & method.

Collinearity in Fitted Parameters



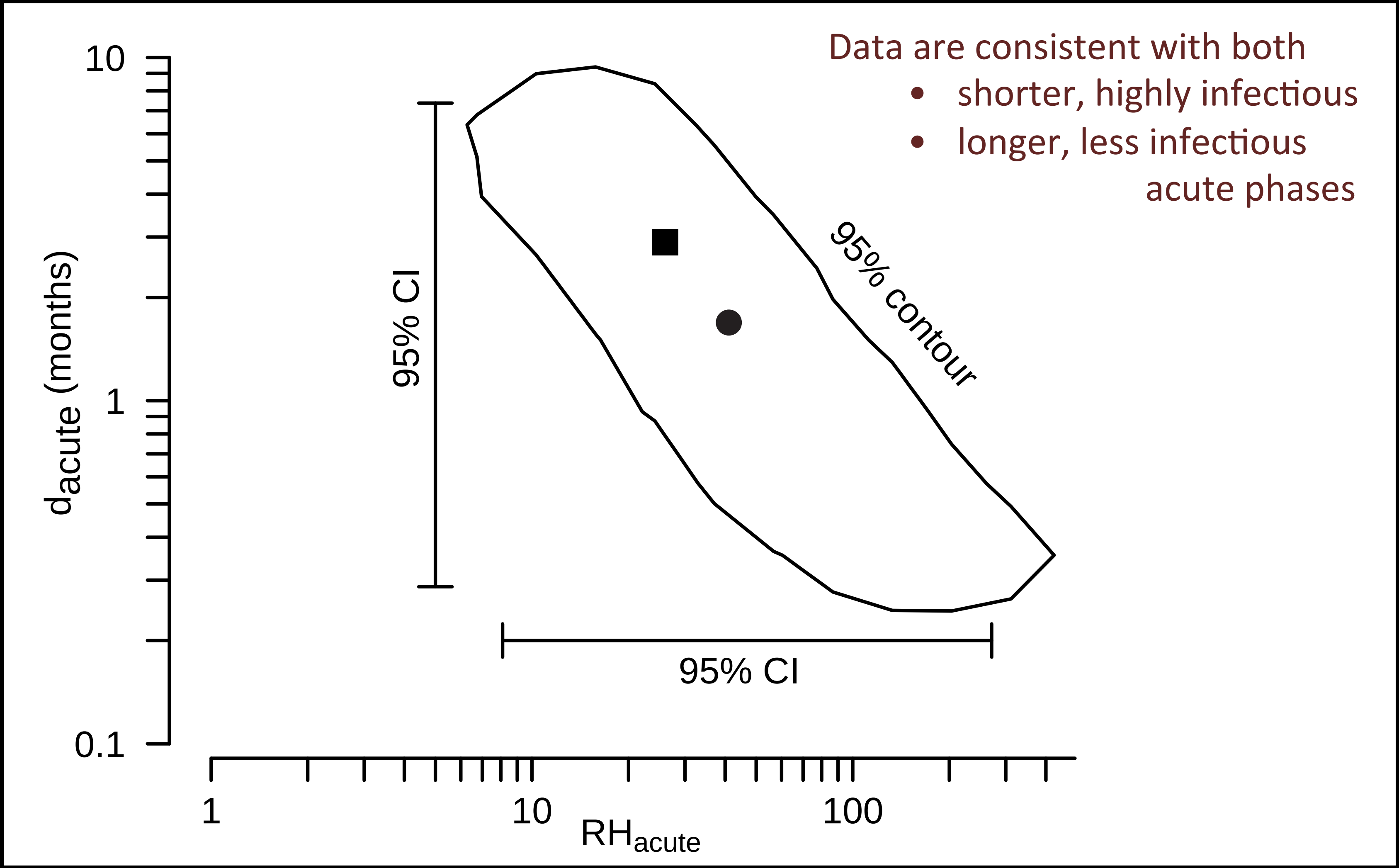
Refit the same model using Bayesian MCMC

Collinearity in Fitted Parameters



Refit the same model using Bayesian MCMC

Collinearity in Fitted Parameters

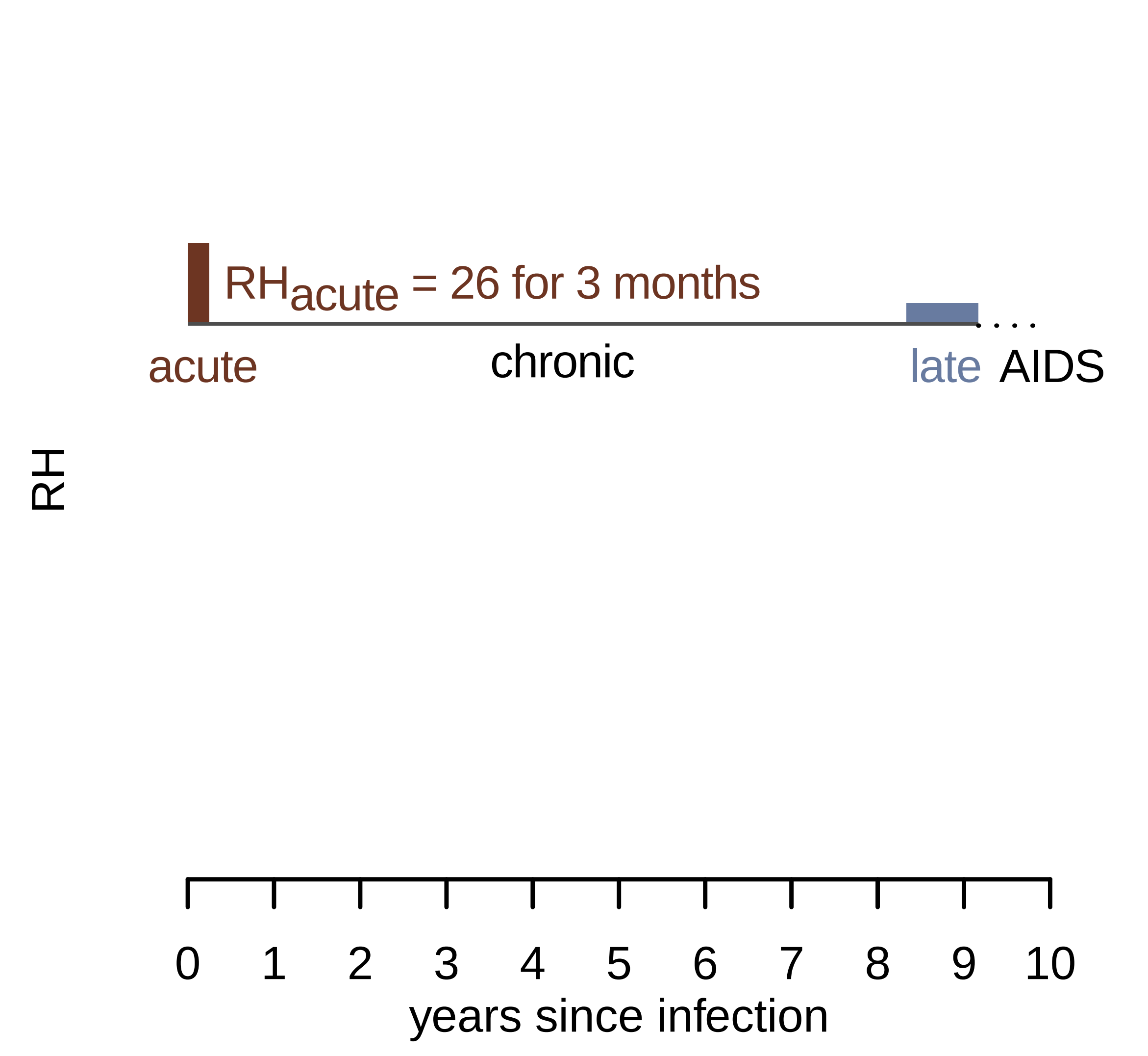


Data are consistent with both

- shorter, highly infectious
- longer, less infectious acute phases

Refit the same model using Bayesian MCMC

Collinearity in Fitted Parameters



What is actually Identifiable?

Excess Hazard-Months due to acute phase

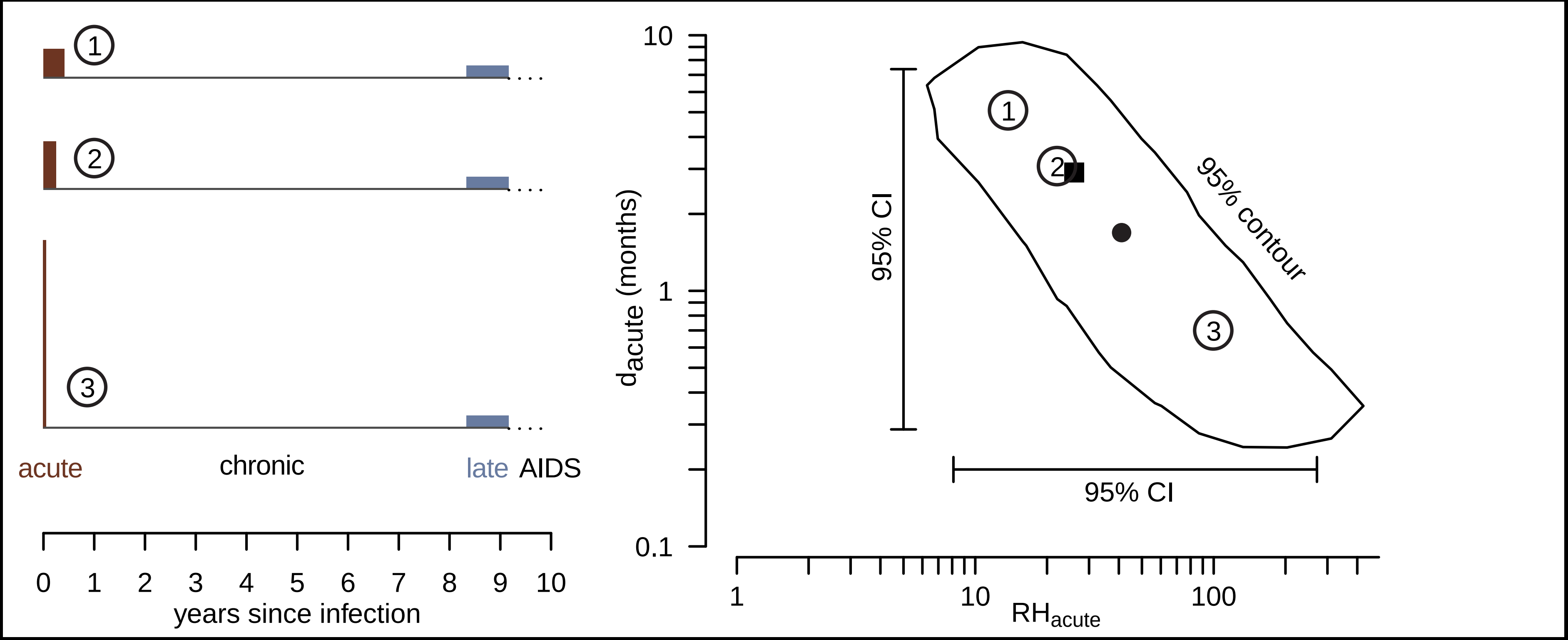
$EHM_{acute} = (RH_{acute}\text{-}1)d_{acute}$

$EHM_{acute} = 25*3 = 75$

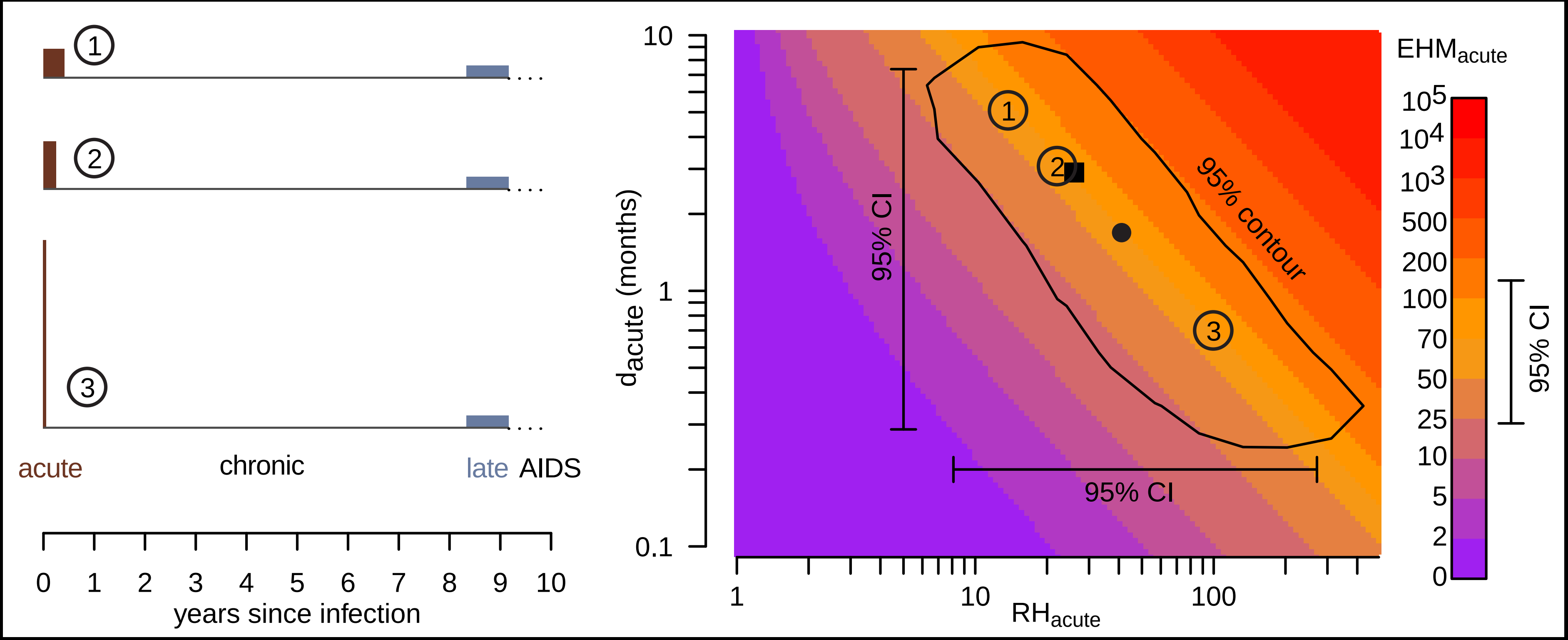
$EHM_{acute} = 15*5 = 75$

$EHM_{acute} = 100*3/4 = 75$

Excess Hazard Months (EHM_{acute})



Excess Hazard Months (EHM_{acute})



RH_{acute} and d_{acute} are not identifiable from 10-month interval cohorts

We should focus on EHM_{acute}

Formally vs Informally Fitting

- Recently, fitting models to data expected
- Unnecessary for demonstration of qualitative dynamics
- Necessary for

    parameter estimation

    inference

    formal model comparison

Learning More: Methods for Fitting

- Least Squares

- Frequentist Maximum Likelihood Fitting

- Bayesian Posterior Estimation (usually MCMC)

Simulating to test methods

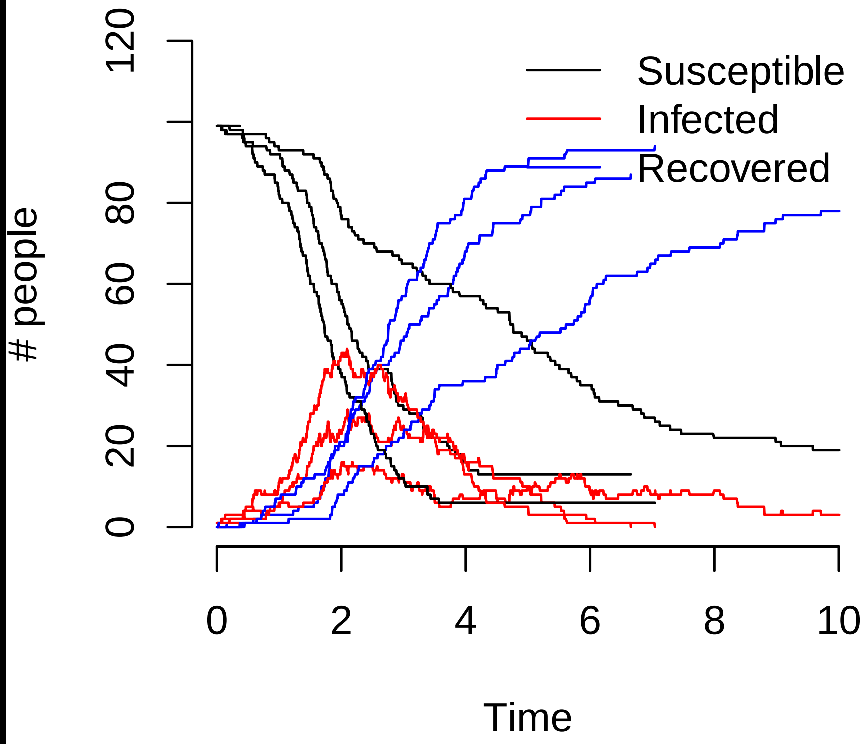
- Create model

- Simulate data

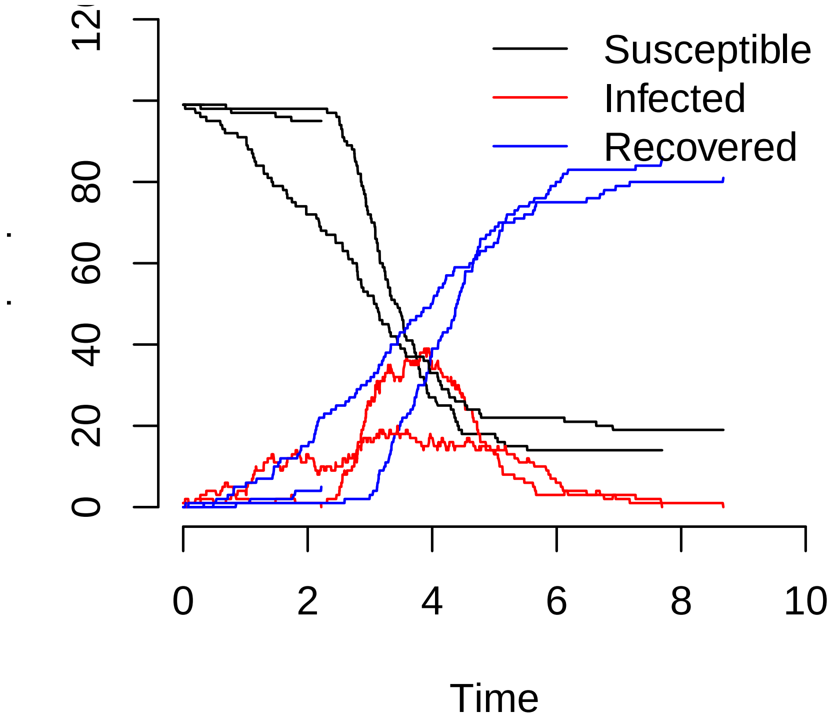
- Can you estimate the inputted parameters for the simulation by fitting?

Simulating to test methods

5 Urban Villages



5 Rural Villages



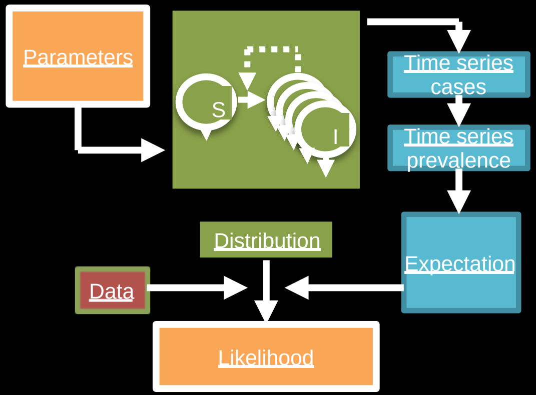
Summary

- Why we fit

  parameter estimation

  inference

  formal model comparison



- How we fit

  Create a probabilistic framework that links our model to data—ie, write a likelihood

- What to consider when fitting

  Assumptions

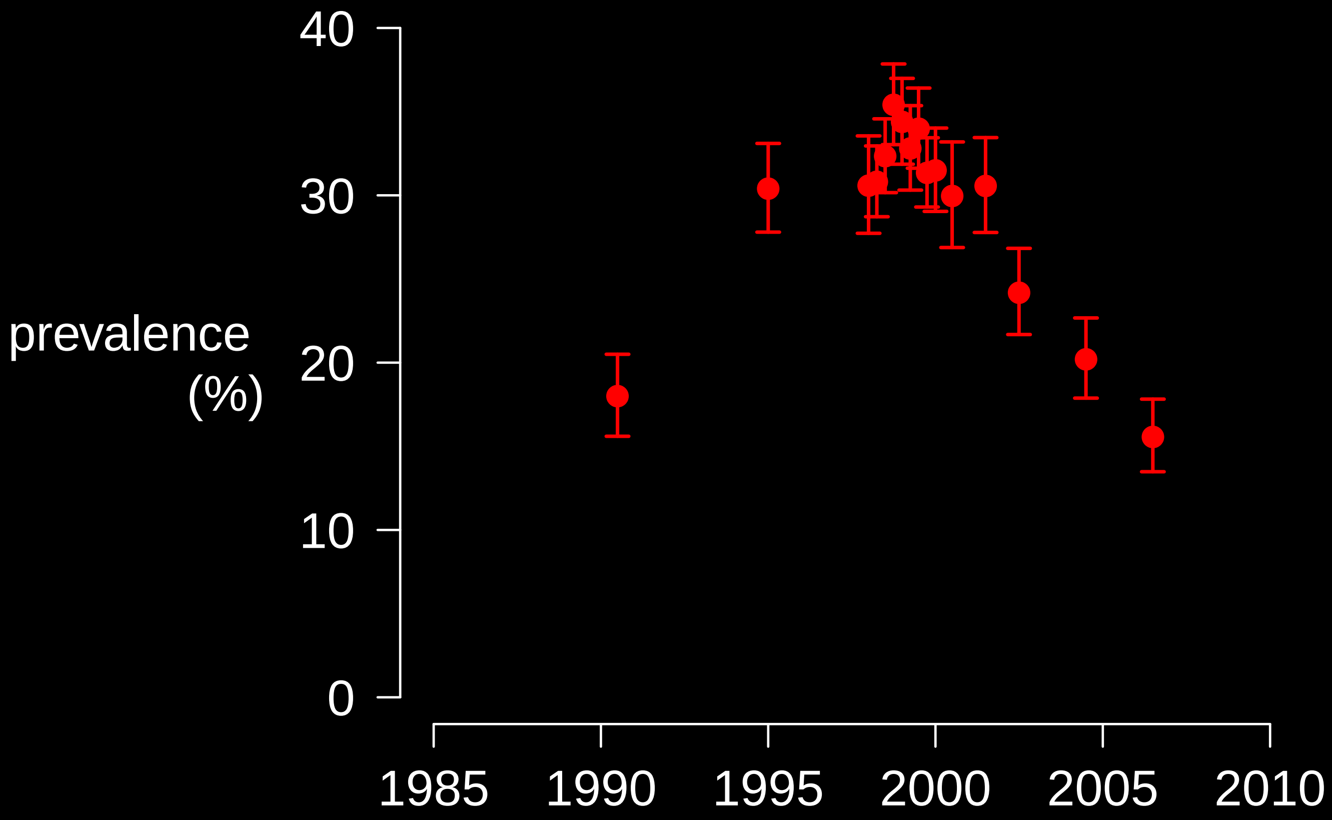
  Overfitting

  Goodness of fit

  Identifiability

What happened?

Harare ANC HIV Data


prevalence
(%)