Introduction to Likelihood

Meaningful Modeling of Epidemiologic Data, 2016
AIMS, Muizenberg, South Africa

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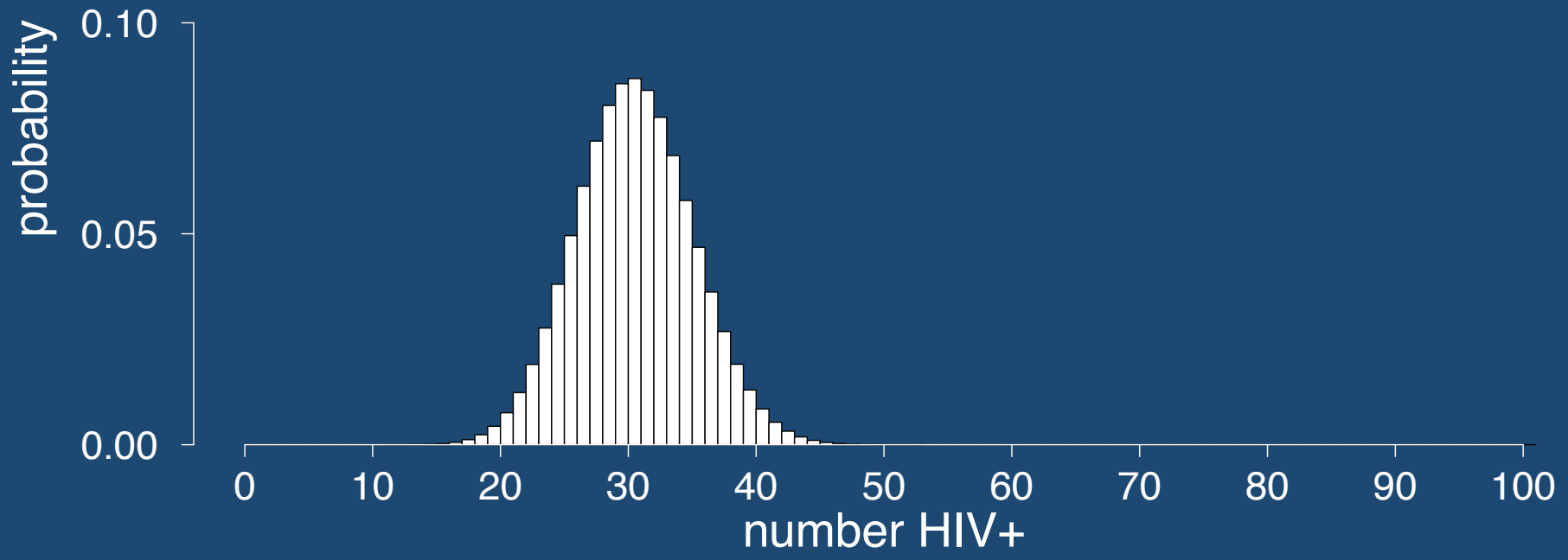
University of Texas at Austin

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:

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




```
barplot(dbinom(x = 0:100, size = 100, prob = .3), names.arg = 0:size)
```

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:

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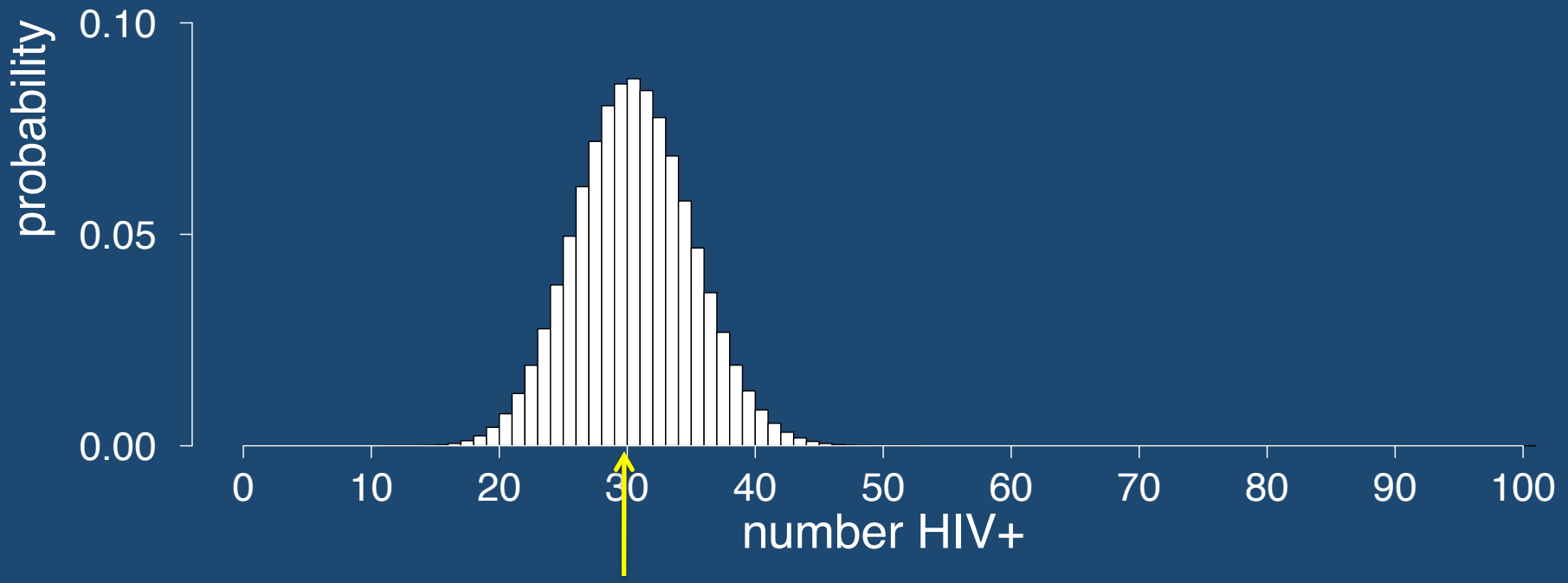
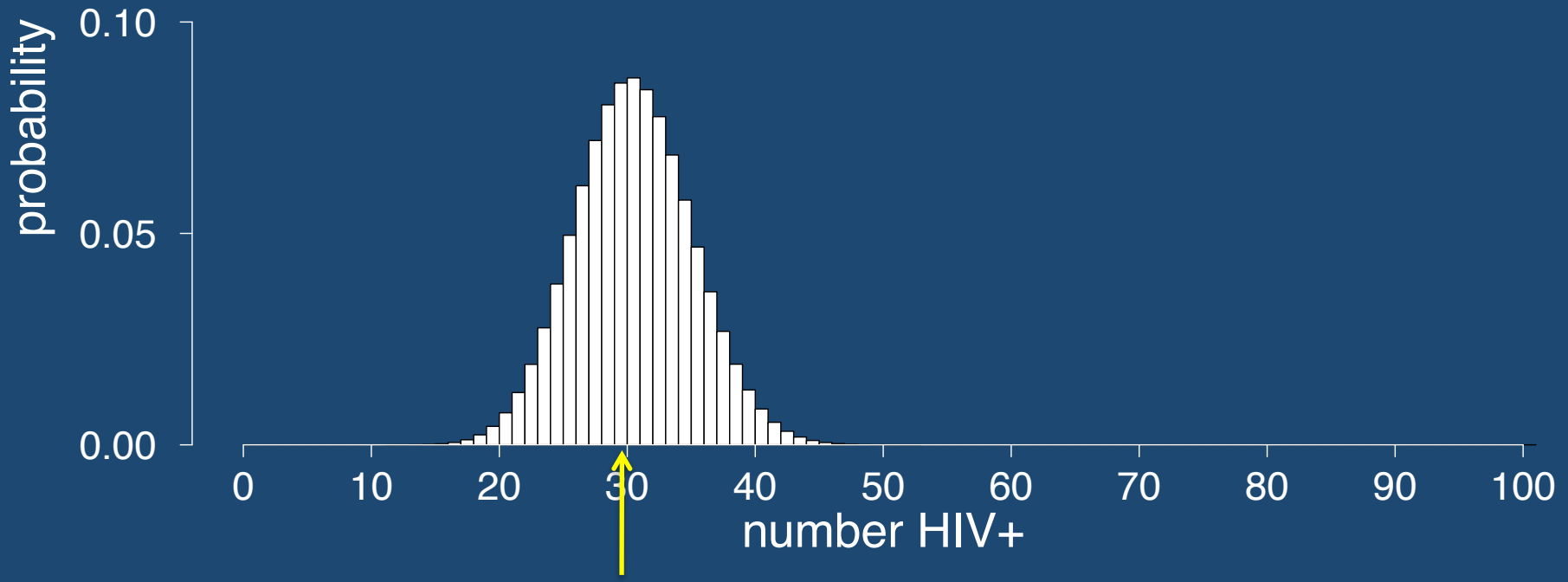


We sample 100 people once and 28 are positive:

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

We don't know the true prevalence!

But we can calculate the probability of 28 or a more extreme value occurring for a given prevalence.



We sample 100 people once and 28 are positive:

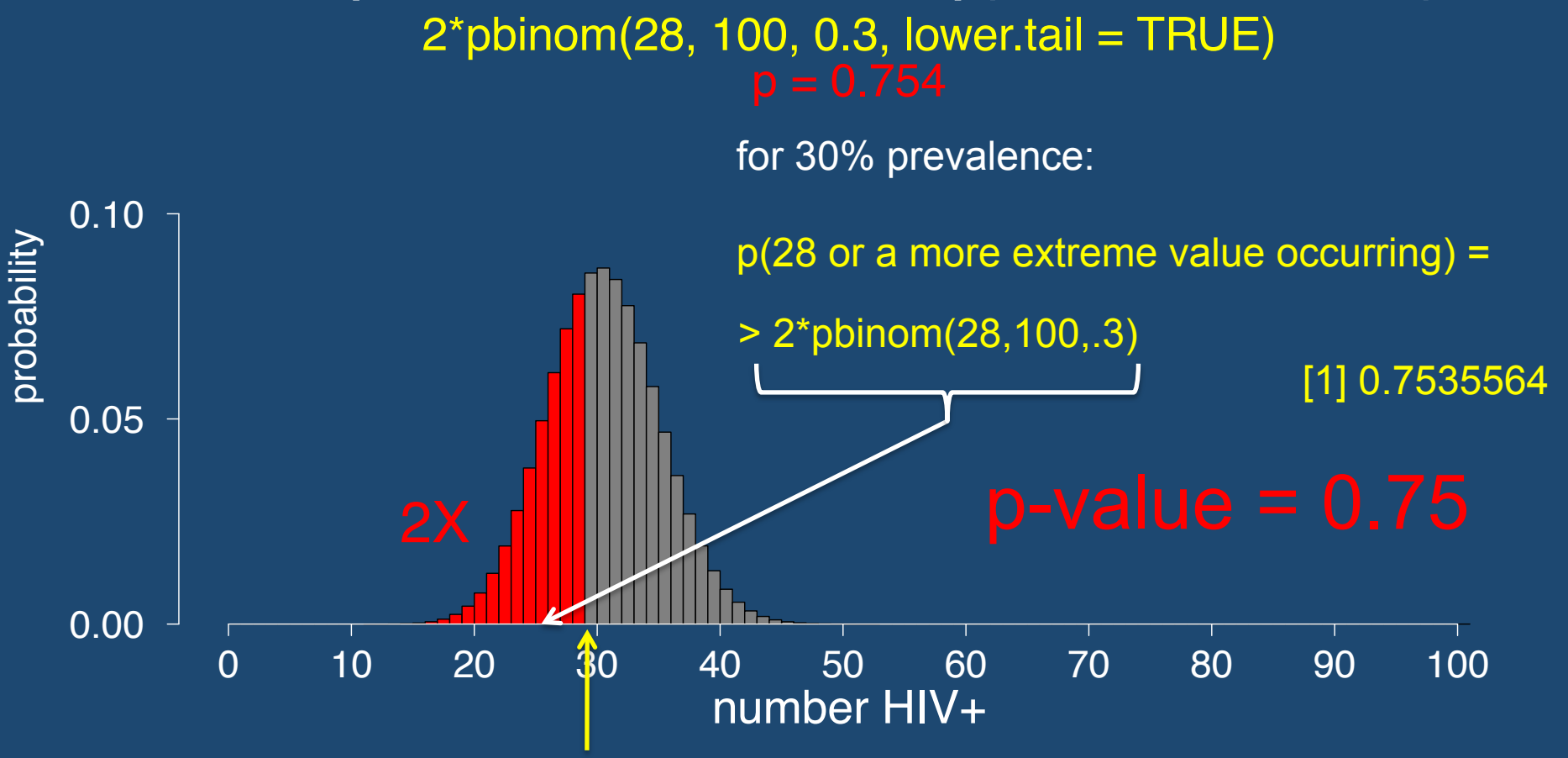
```
> rbinom(n = 1, size = 100, prob = .3)
[1] 28
```

Cumulative Probability & P Values

If true prevalence were 30%, then p(28 or more extreme) is

2*pbinom(28, 100, 0.3, lower.tail = TRUE)

p = 0.754

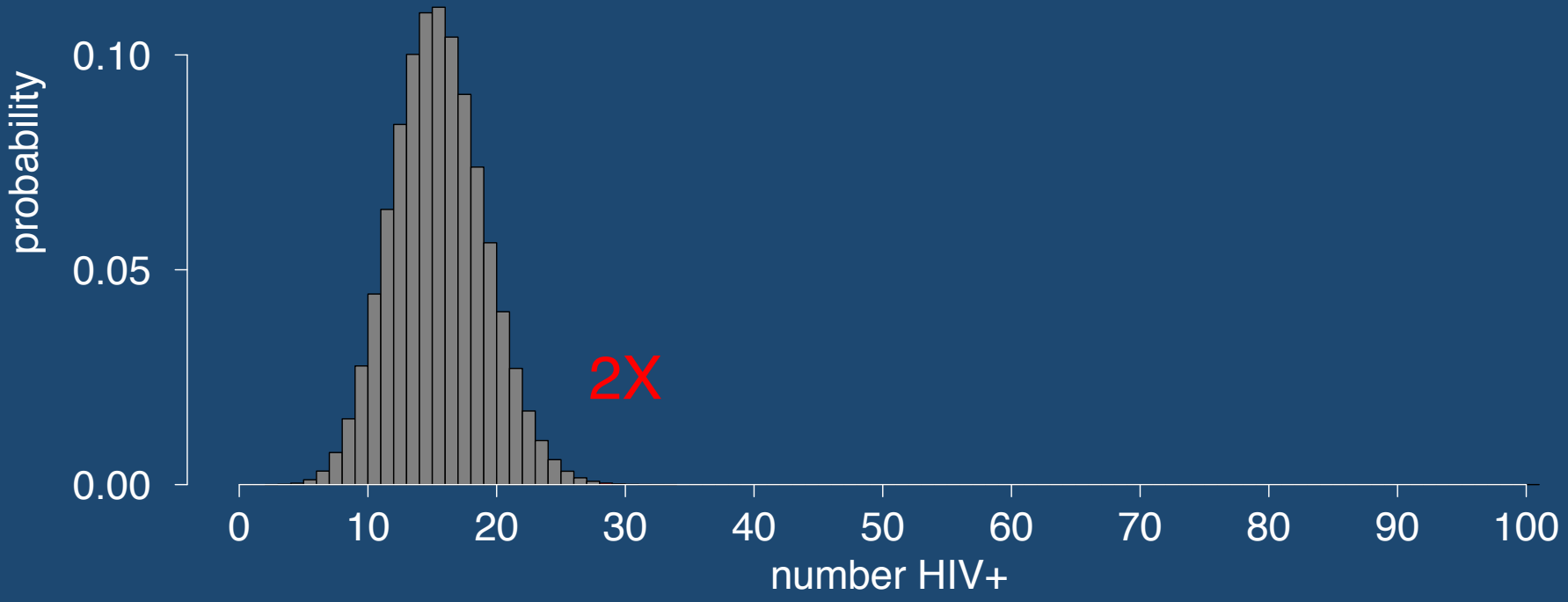


We sample 100 people once and 28 are positive.

If true prevalence were 15%, then p(28 or more extreme) is

2*pbinom(28–1, 100, 0.15, lower.tail = FALSE)

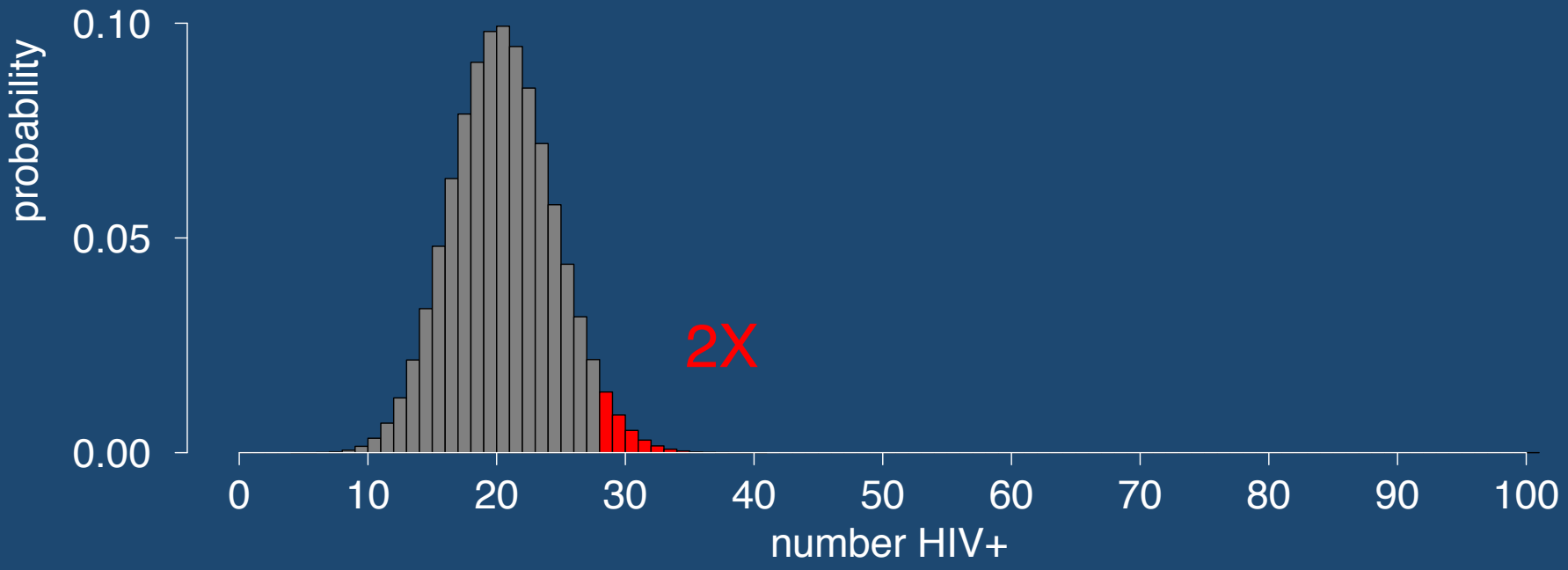
p = 0.00123



If true prevalence were 20%, then p(28 or more extreme) is

2*pbinom(28–1, 100, 0.2, lower.tail = FALSE)

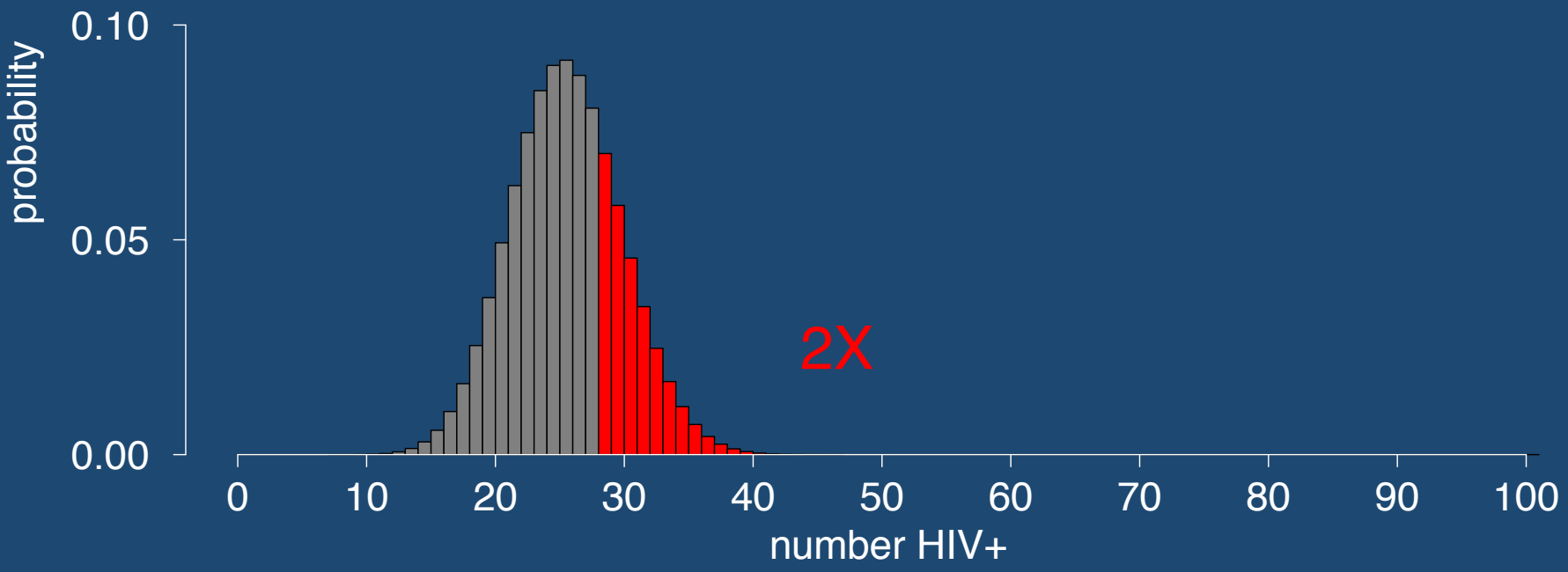
p = 0.0683



If true prevalence were 25%, then p(28 or more extreme) is

2*pbinom(28–1, 100, 0.25, lower.tail = FALSE)

p = 0.555



If true prevalence were 30%, then p(28 or more extreme) is

2*pbinom(28, 100, 0.3, lower.tail = TRUE)

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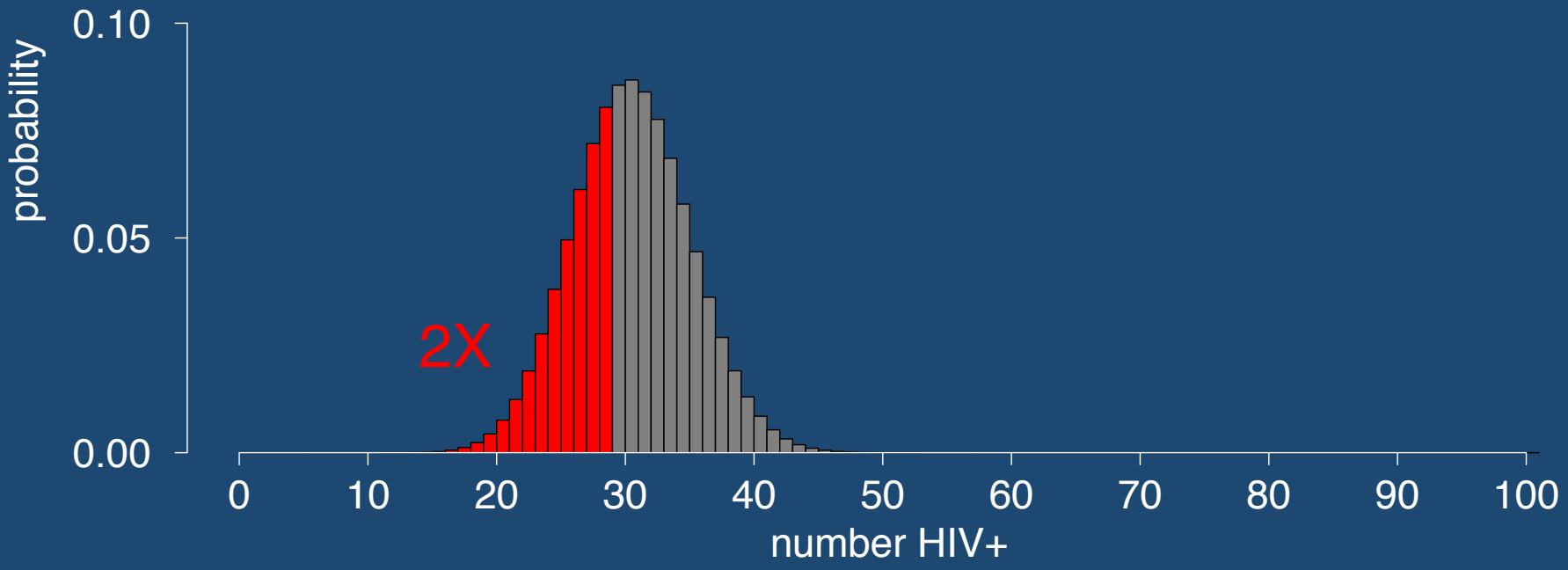
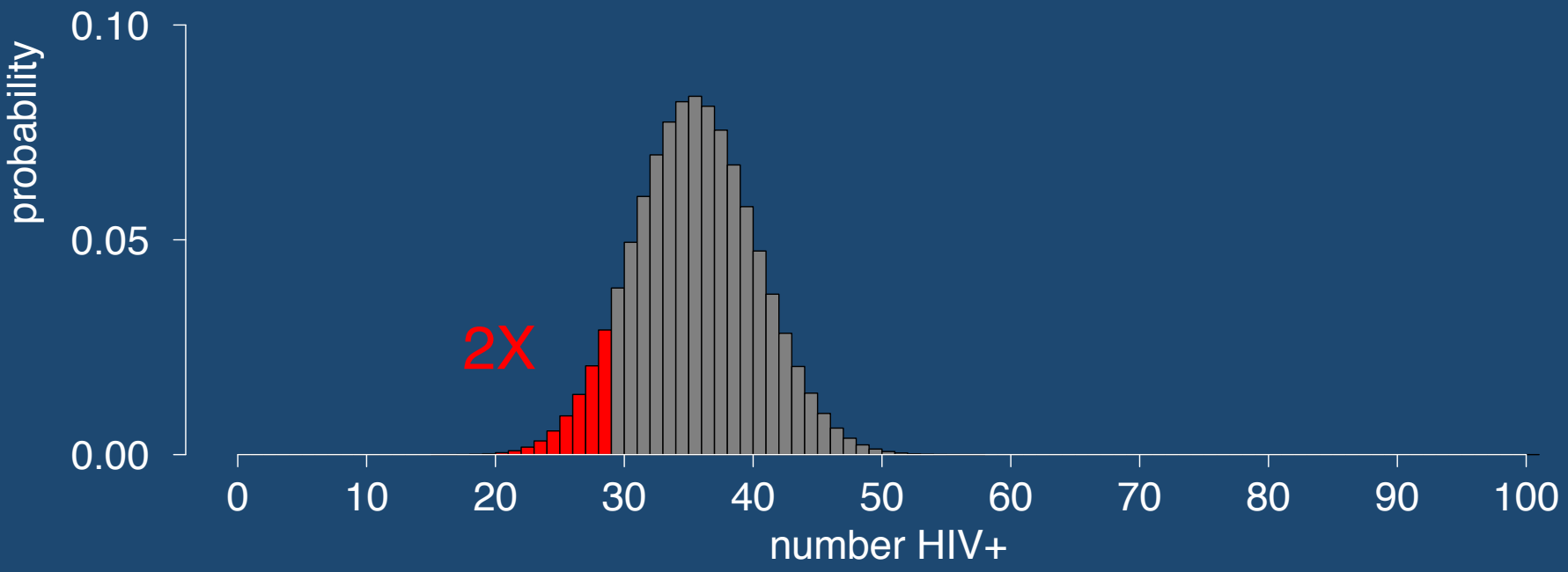


If true prevalence were 35%, then p(28 or more extreme) is

2*pbinom(28, 100, 0.35, lower.tail = TRUE)

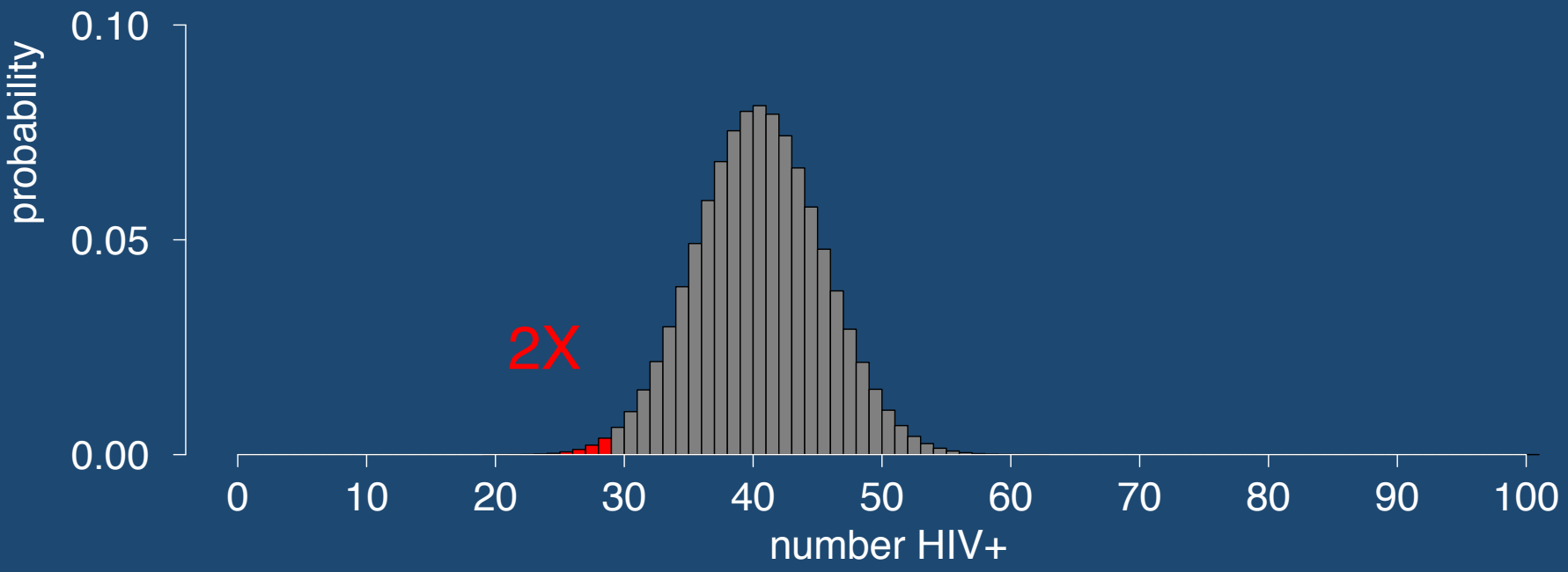
p = 0.17



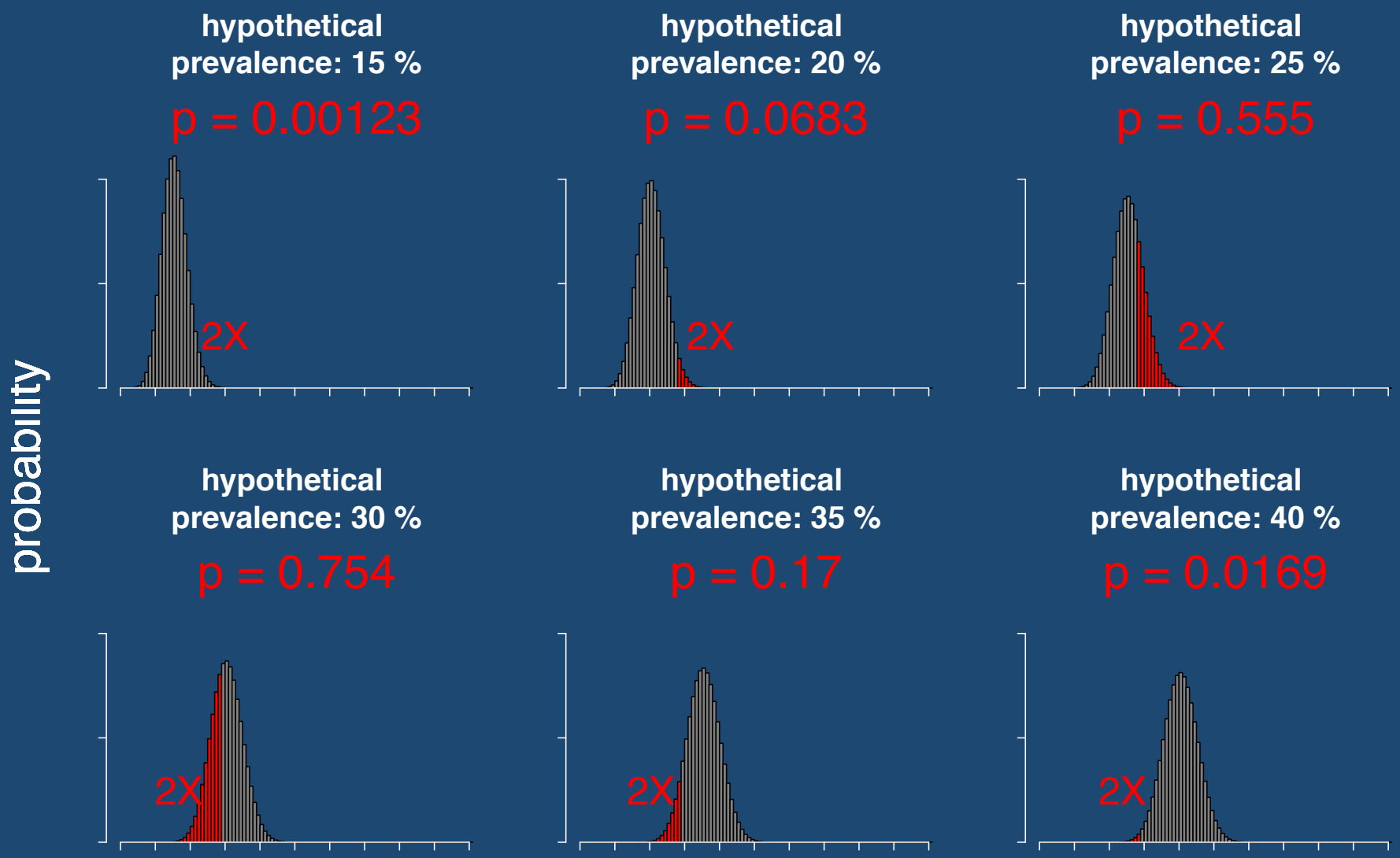
If true prevalence were 40%, then p(28 or more extreme) is

2*pbinom(28, 100, 0.4, lower.tail = TRUE)

p = 0.0169



Summary


hypothetical prevalence: 15 %
p = 0.00123
2X
hypothetical prevalence: 20 %
p = 0.0683
2X
hypothetical prevalence: 25 %
p = 0.555
2X
hypothetical prevalence: 30 %
p = 0.754
2X
hypothetical prevalence: 35 %
p = 0.17
2X
hypothetical prevalence: 40 %
p = 0.0169
2X
probability
number HIV+

Which hypotheses do we reject?

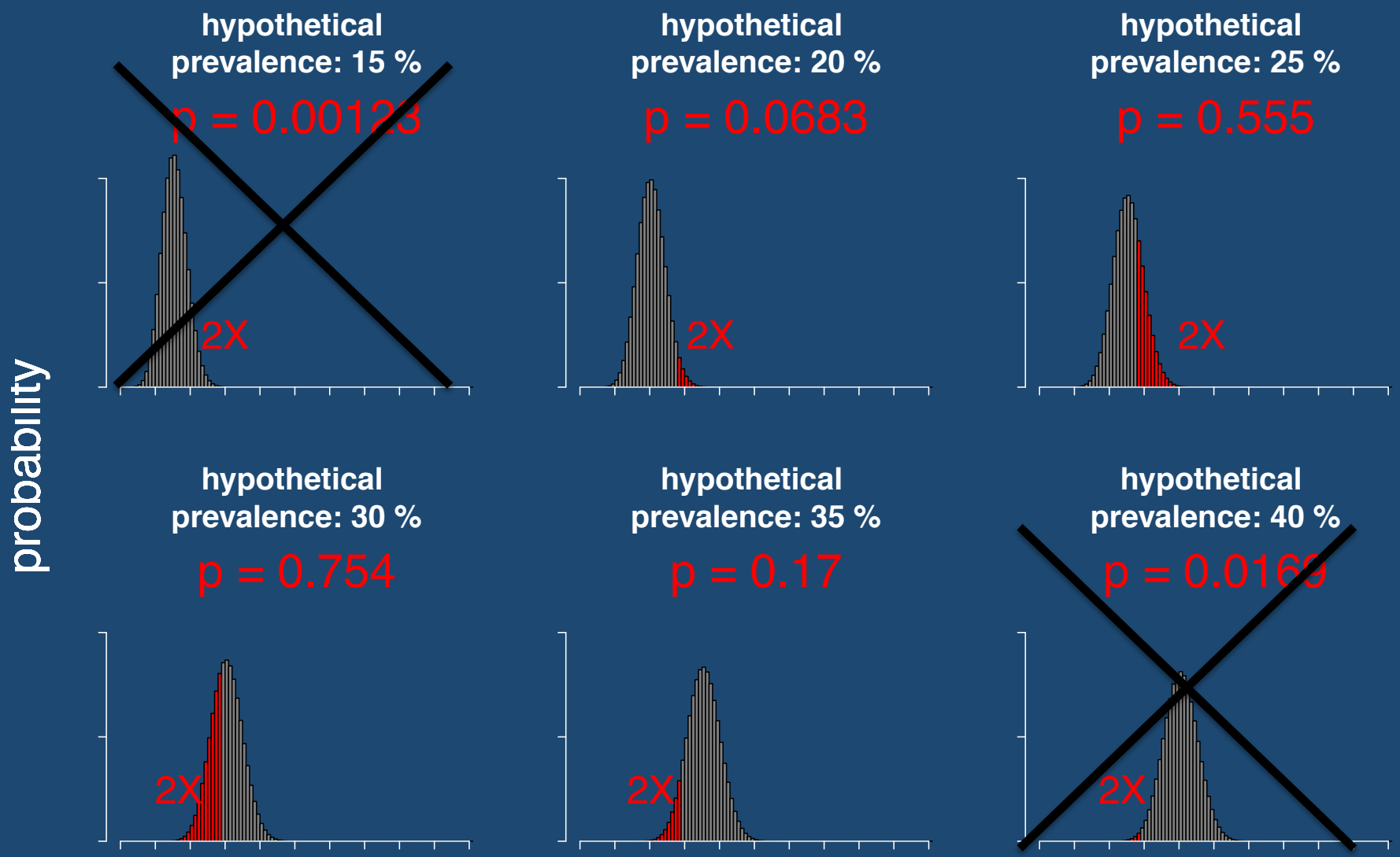
IF GIVEN THE HYPOTHESIS

p value < cutoff

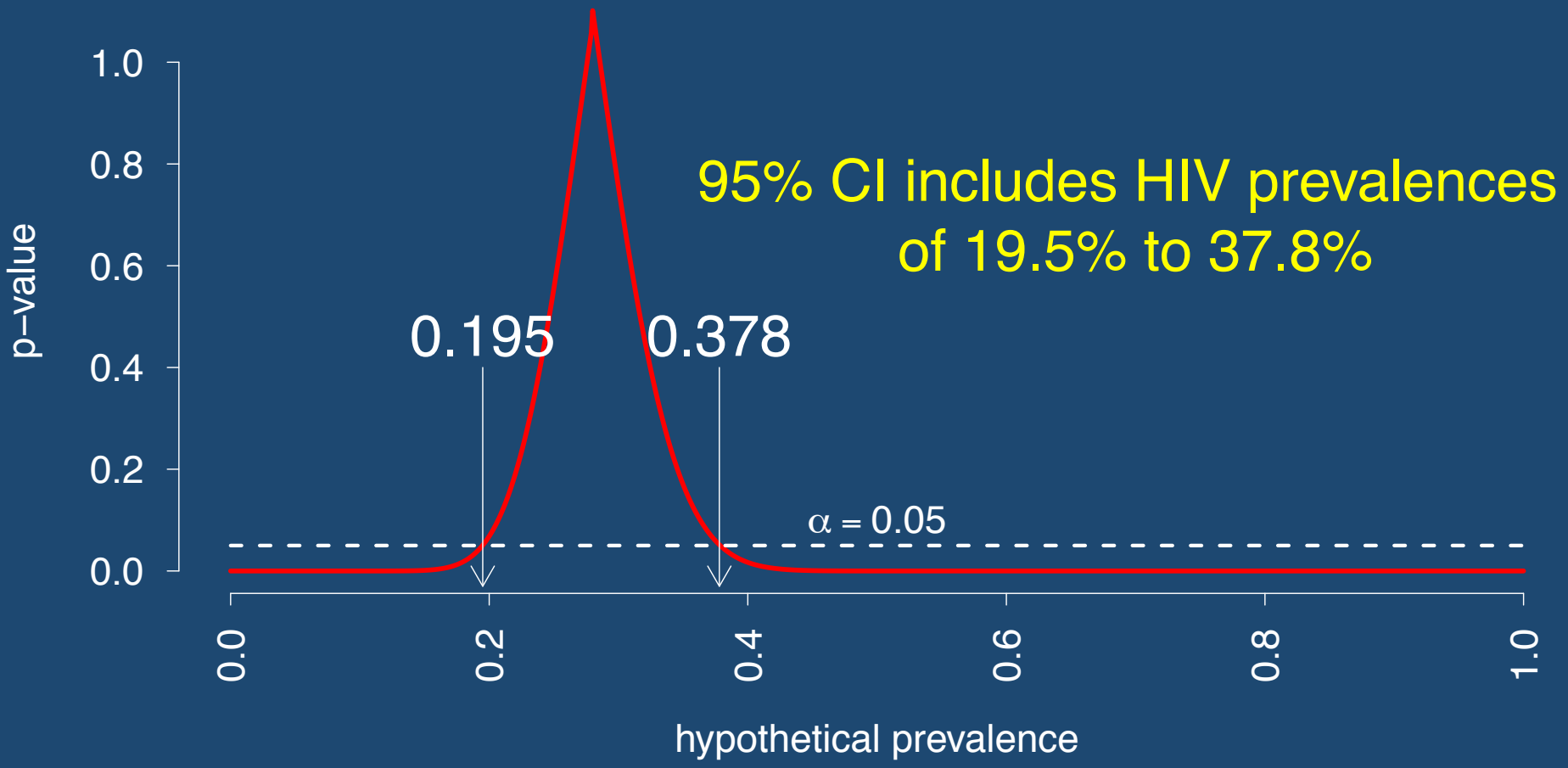
THEN REJECT HYPOTHESIS

Cutoff usually chosen as $\alpha = 0.05$

Which hypotheses do we reject?



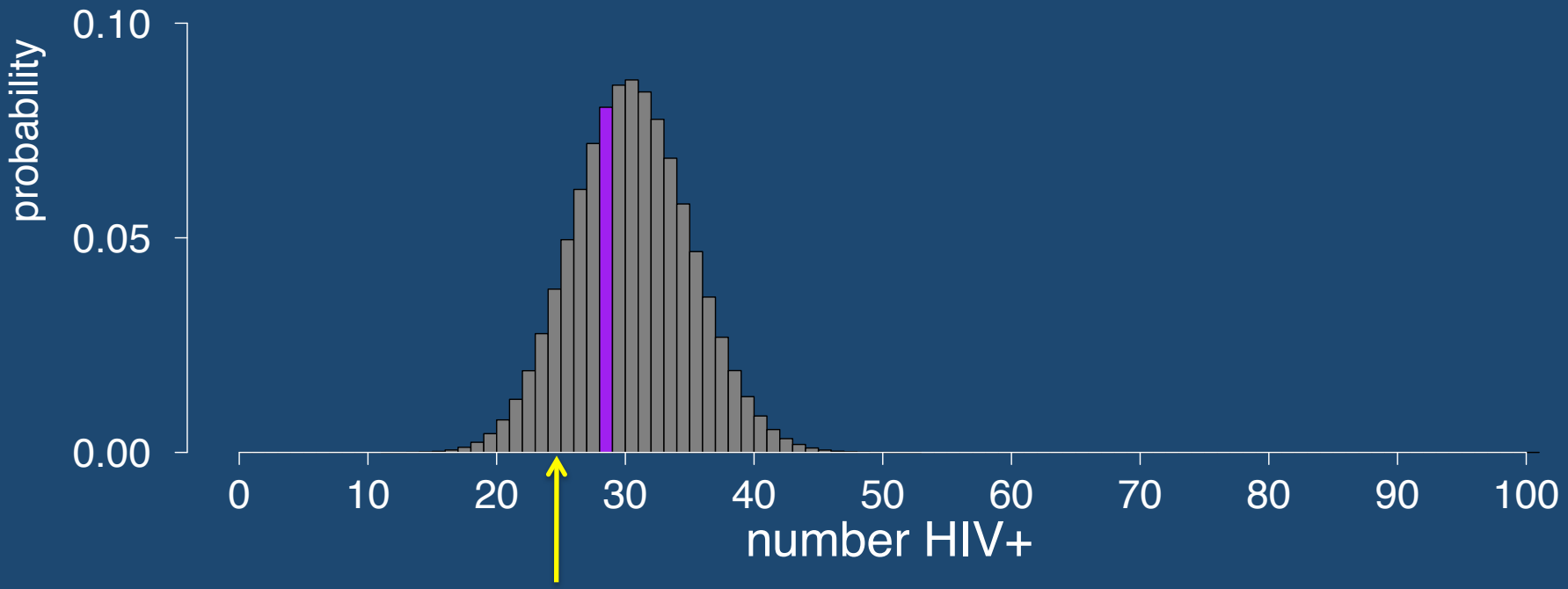
Which hypotheses do we NOT reject:
CONFIDENCE INTERVAL



Let's take another approach

hypothetical prevalence: 30 %

dbinom(28, 100, 0.3) = 0.0804



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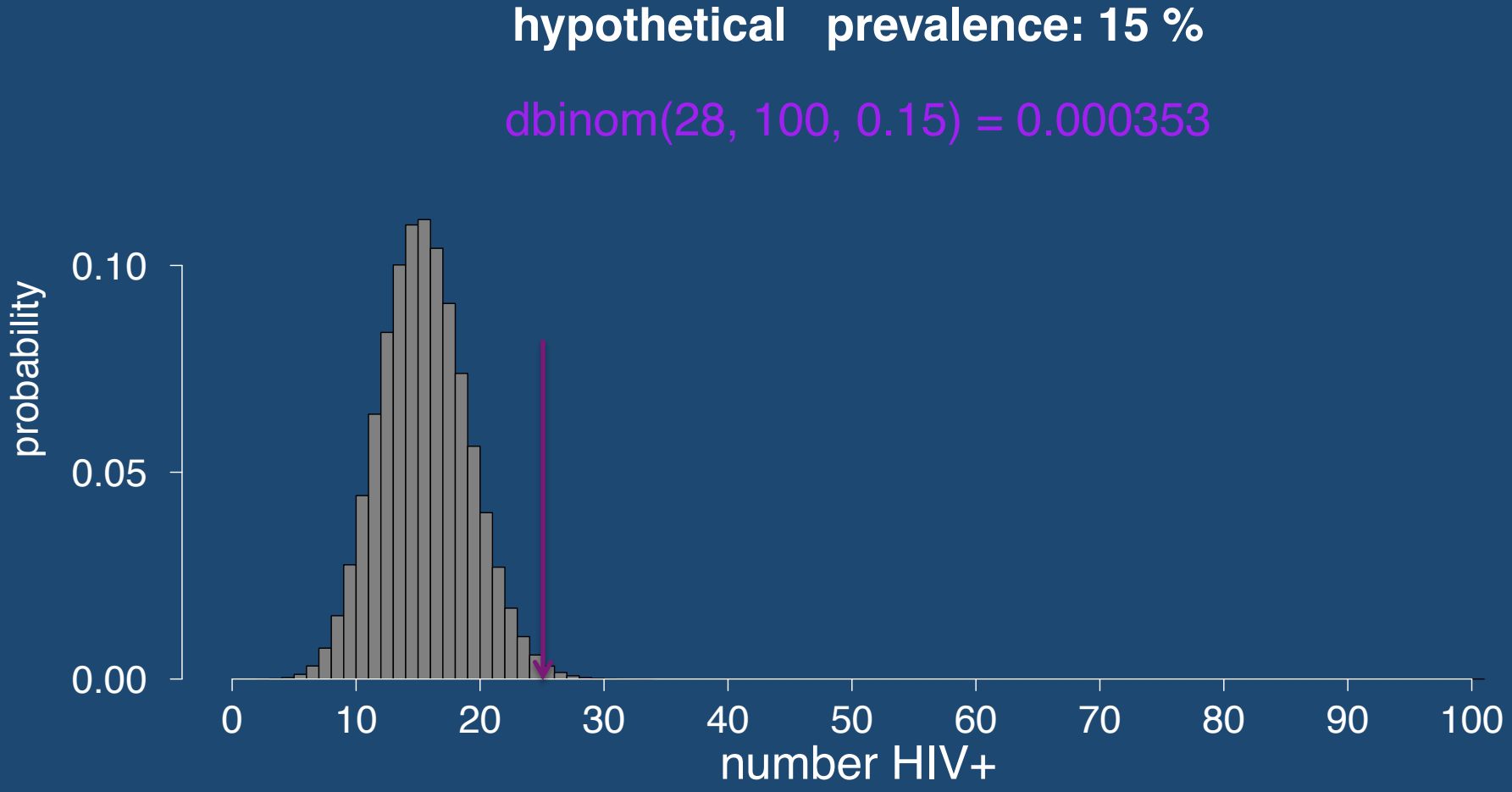
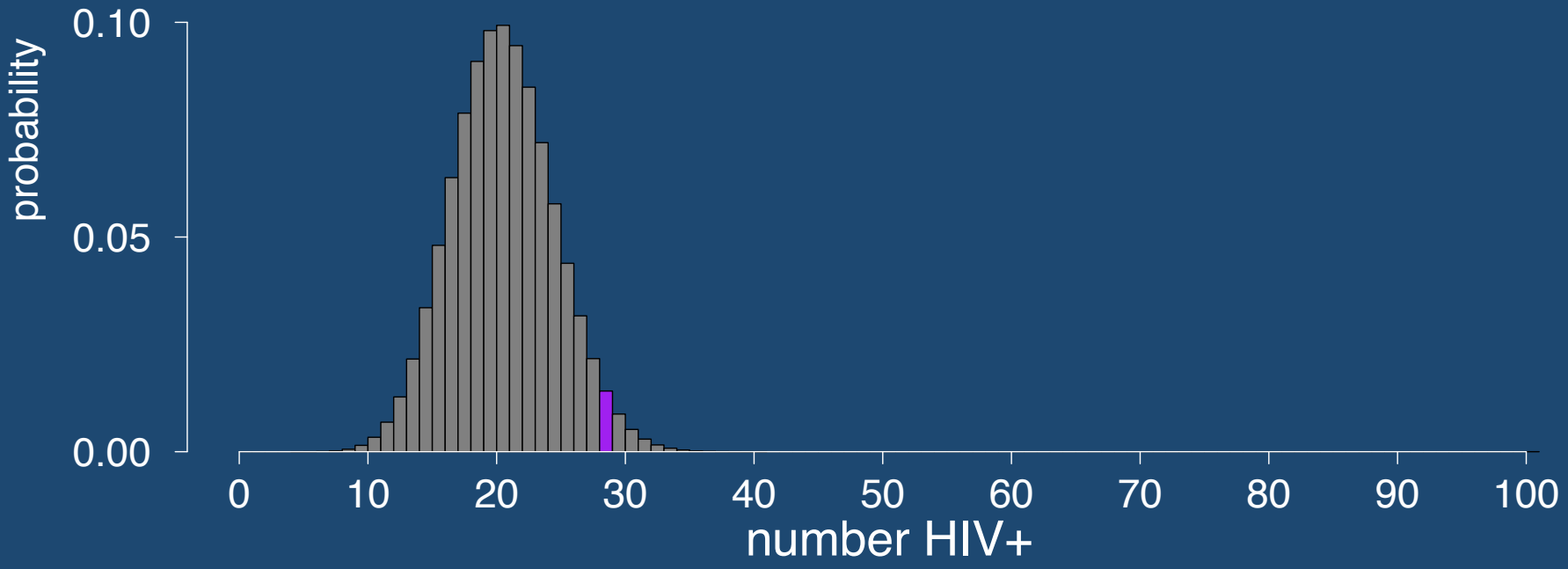

hypothetical prevalence: 15 %
dbinom(28, 100, 0.15) = 0.000353
probability
0.10
0.05
0.00
0
10
20
30
40
50
60
70
80
90
100
number HIV+

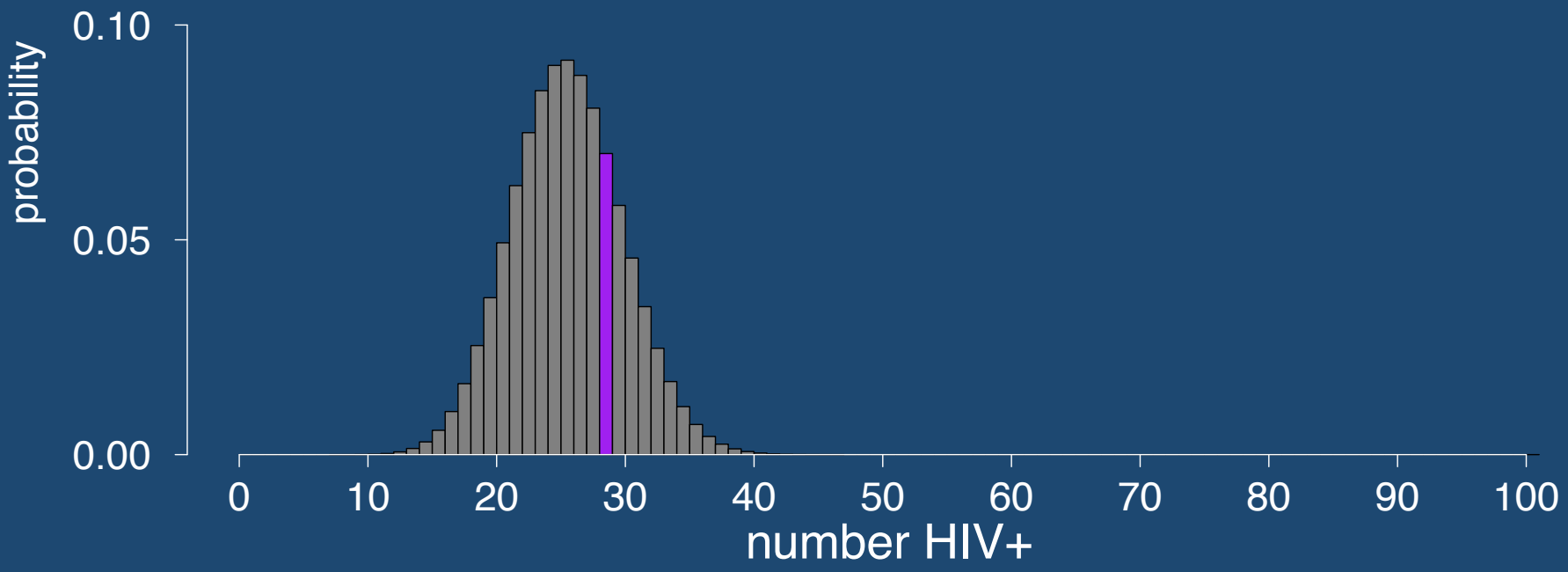
hypothetical prevalence: 20 %

dbinom(28, 100, 0.2) = 0.0141



hypothetical prevalence: 25 %

dbinom(28, 100, 0.25) = 0.0701



hypothetical prevalence: 30 %

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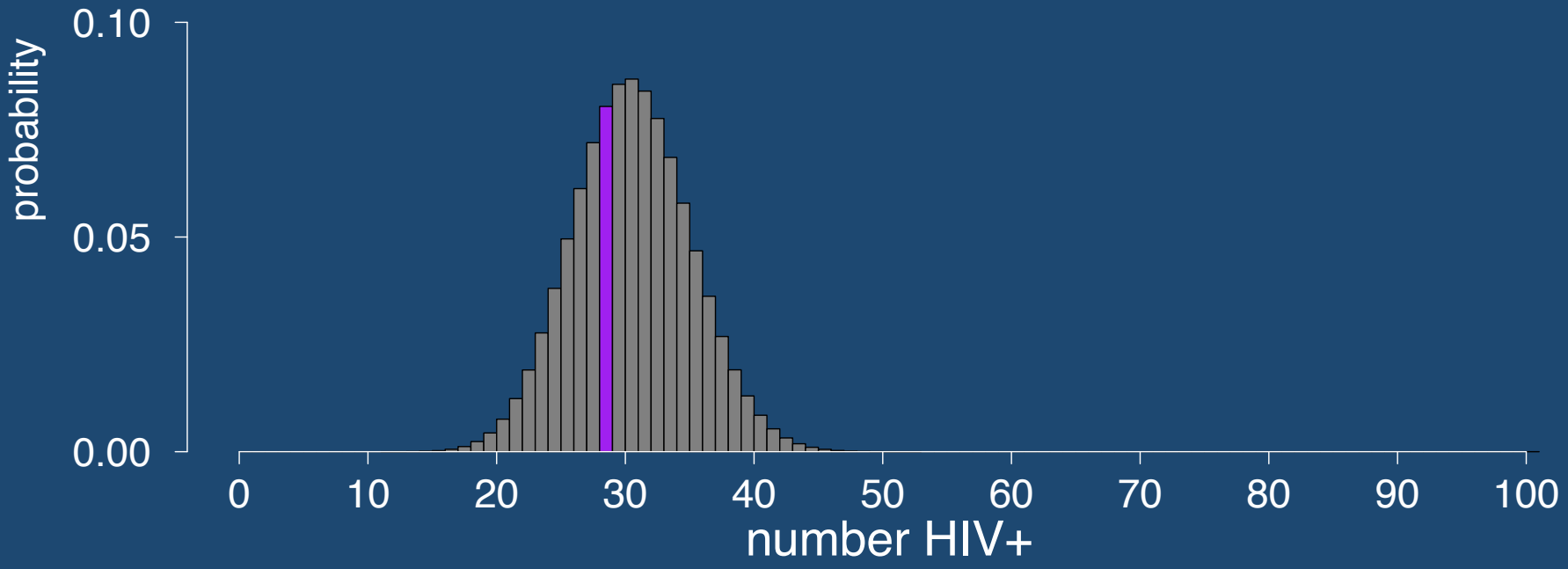
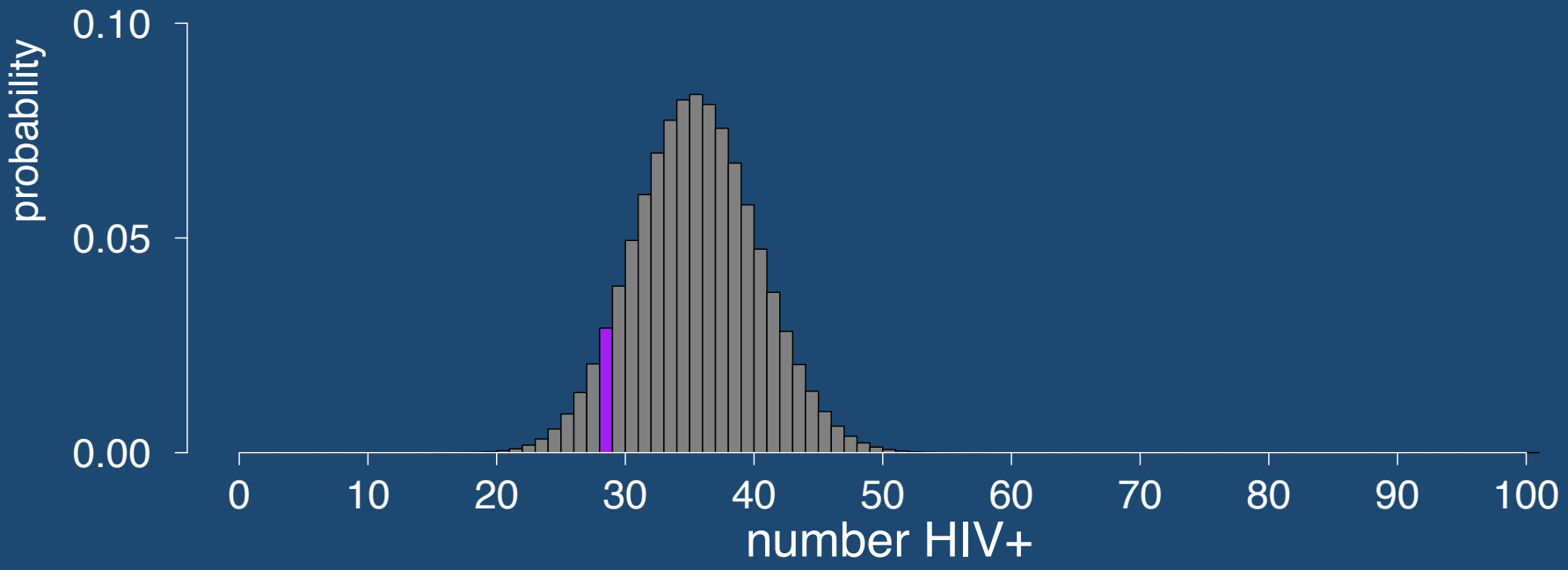


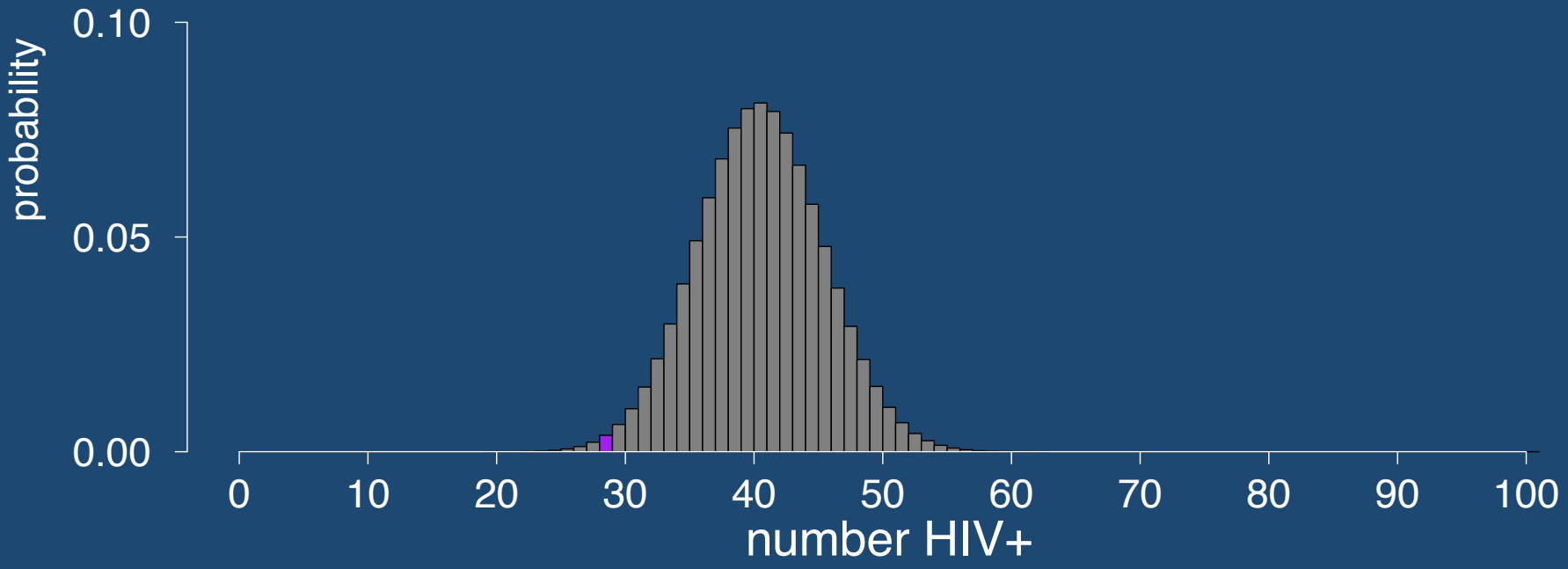
hypothetical prevalence: 35 %

dbinom(28, 100, 0.35) = 0.029

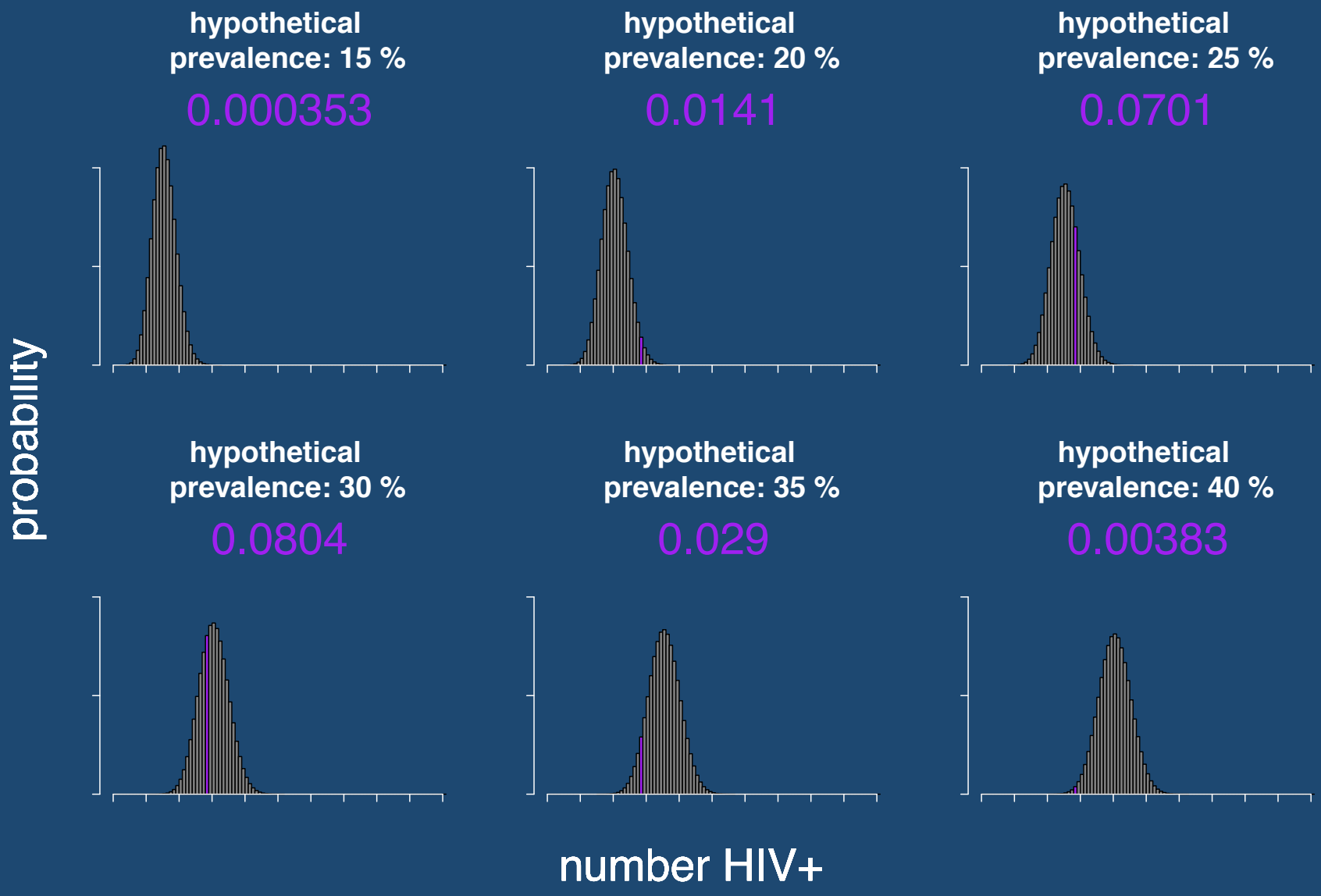


hypothetical prevalence: 40 %

dbinom(28, 100, 0.4) = 0.00383



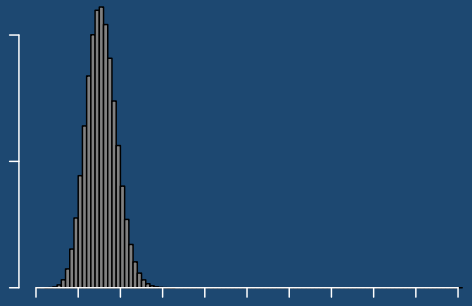
Which prevalence gives the greatest probability of observing exactly 28/100?



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

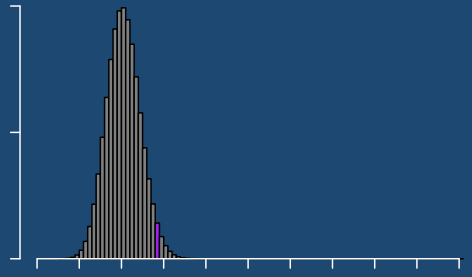
hypothetical prevalence: 15 %

0.000353



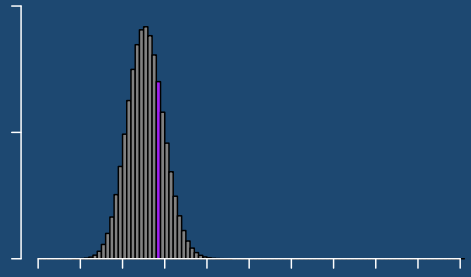
hypothetical prevalence: 20 %

0.0141



hypothetical prevalence: 25 %

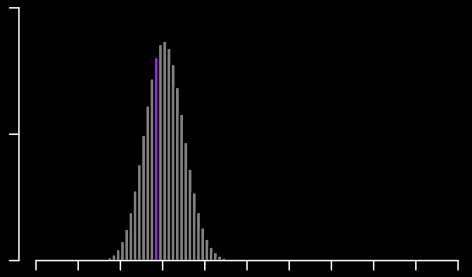
0.0701



probability

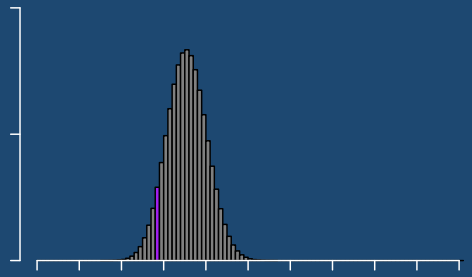
hypothetical prevalence: 30 %

0.0804



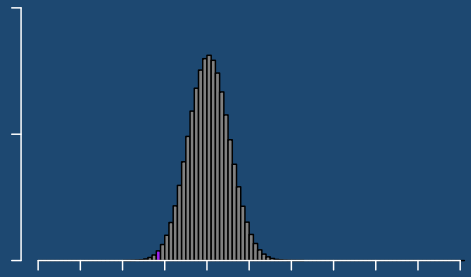
hypothetical prevalence: 35 %

0.029



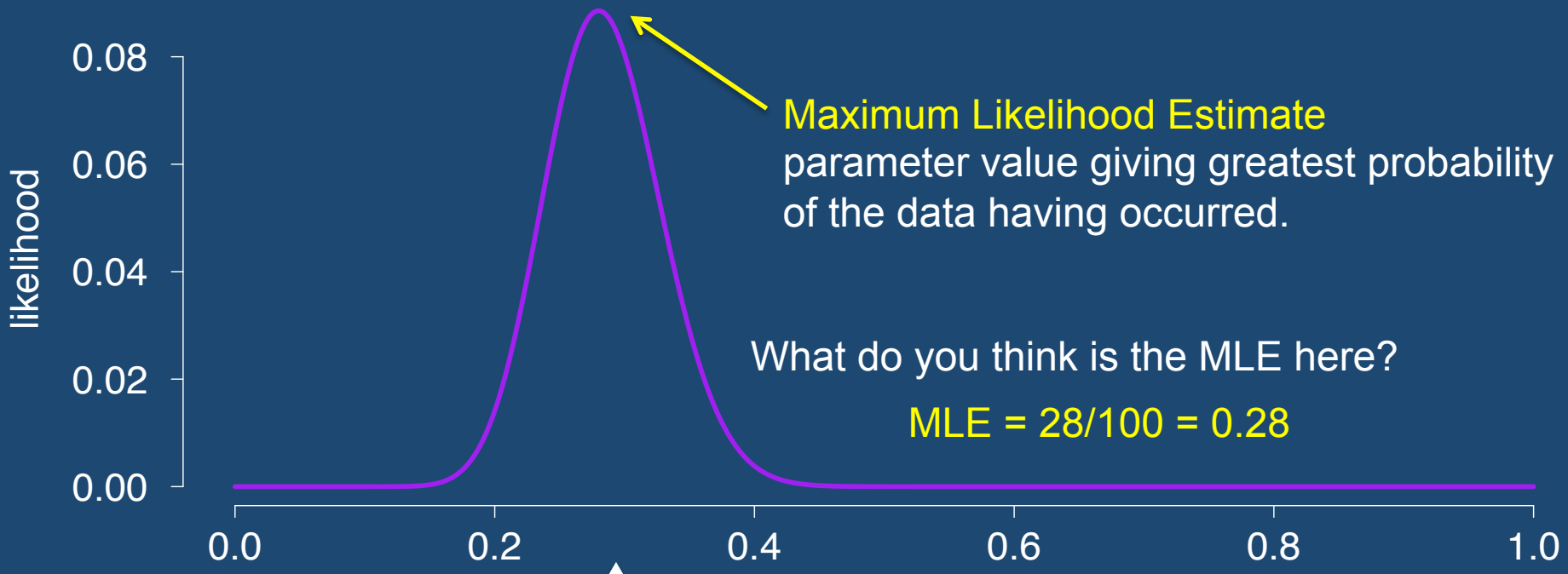
hypothetical prevalence: 40 %

0.00383



number HIV+

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

hypothetical prevalence

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

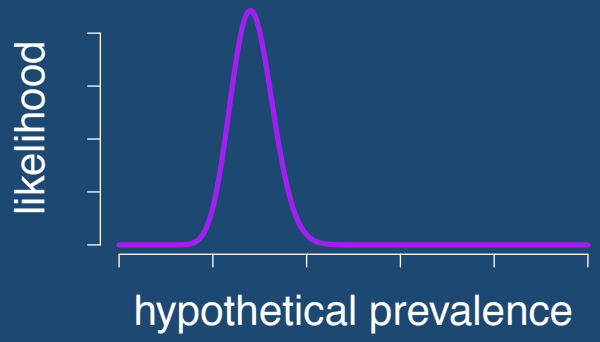
LIKELIHOOD: $L(p|x) = \binom{n}{x}(p)^x(1-p)^{n-x}$

function of p

Deriving the Maximum Likelihood Estimate

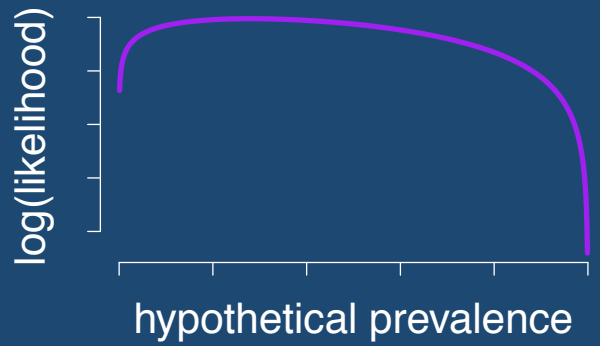
maximize

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



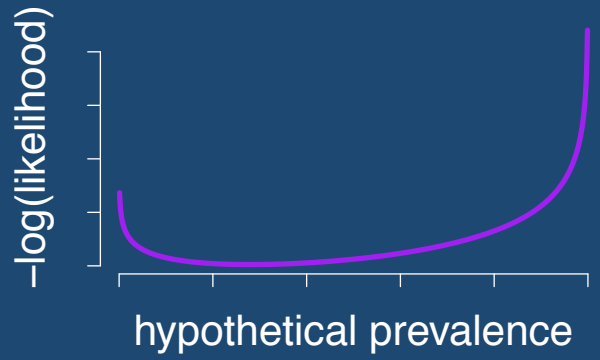
maximize

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



minimize

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



Deriving the Maximum Likelihood Estimate

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

$$l(p) = -\log\binom{n}{x} - \log(p^x) - \log((1-p)^{n-x})$$

$$l(p) = -\log\binom{n}{x} - x\log(p) - (n-x)\log(1-p)$$

Deriving the Maximum Likelihood Estimate

$$l(p) = -\log\binom{n}{x} - x\log(p) - (n-x)\log(1-p)$$

$$\frac{dl(p)}{p} = 0 - \frac{x}{p} - \frac{-(n-x)}{(1-p)}$$

$$0 = -\frac{x}{\hat{p}} + \frac{(n-x)}{(1-\hat{p})}$$

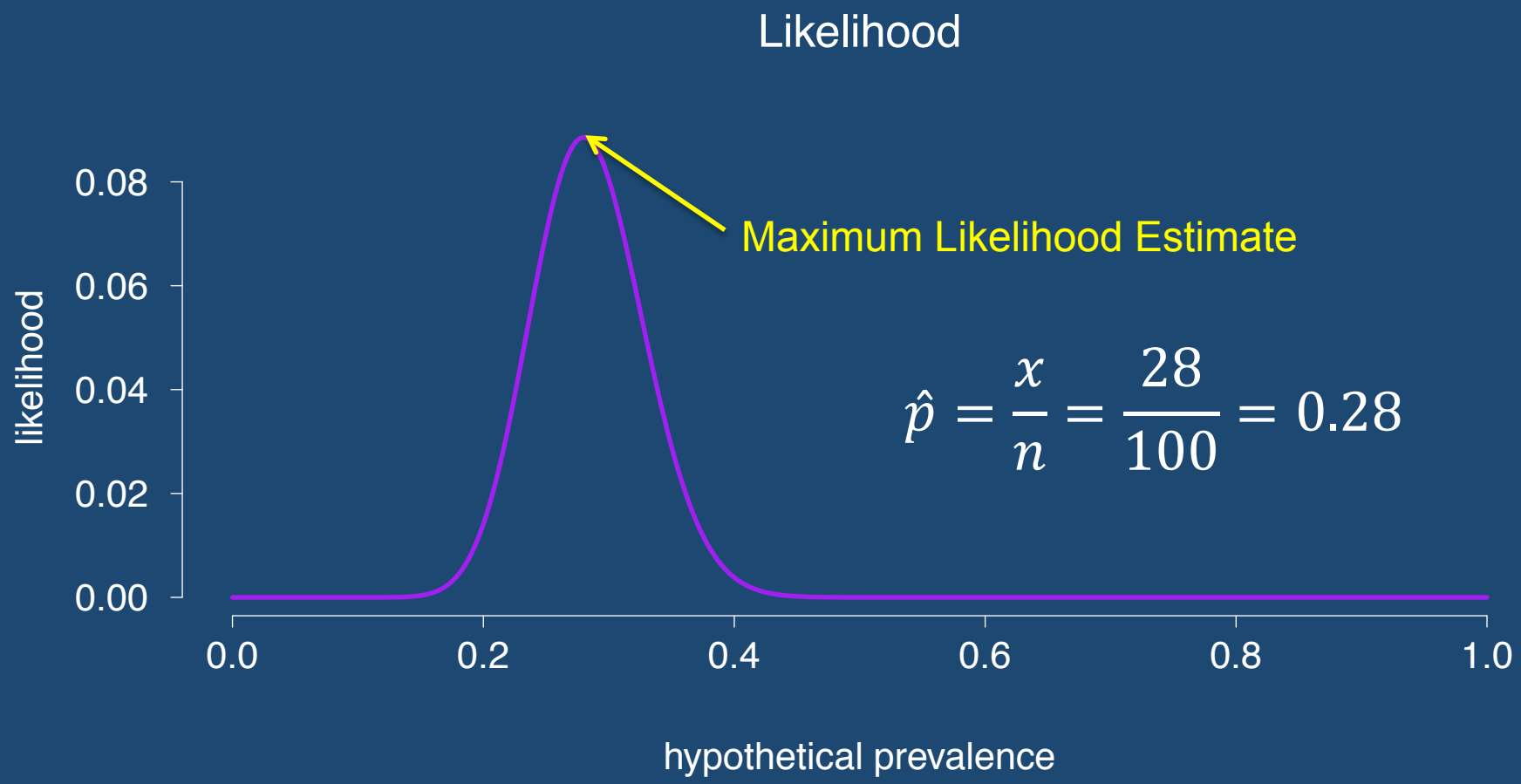
$$0 = \frac{-(1-\hat{p})x + \hat{p}(n-x)}{(1-\hat{p})}$$

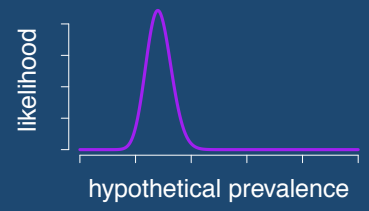
$$0 = -x + \hat{p}x + \hat{p}n - \hat{p}x$$

$$0 = -x + \hat{p}n$$

$$\hat{p} = \frac{x}{n}$$

The proportion of positives!


Likelihood
Maximum Likelihood Estimate
$\hat{p} = \frac{x}{n} = \frac{28}{100} = 0.28$
likelihood
0.08
0.06
0.04
0.02
0.00
0.0
0.2
0.4
0.6
0.8
1.0
hypothetical prevalence



we usually minimize the –log(likelihood)

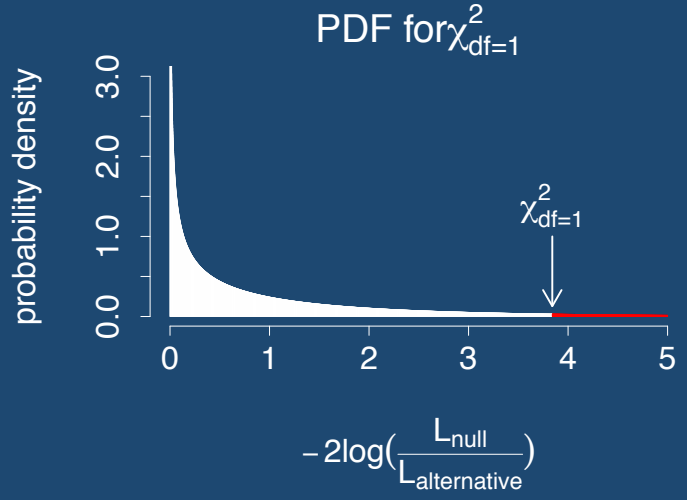
Maximum Likelihood Estimate

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

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

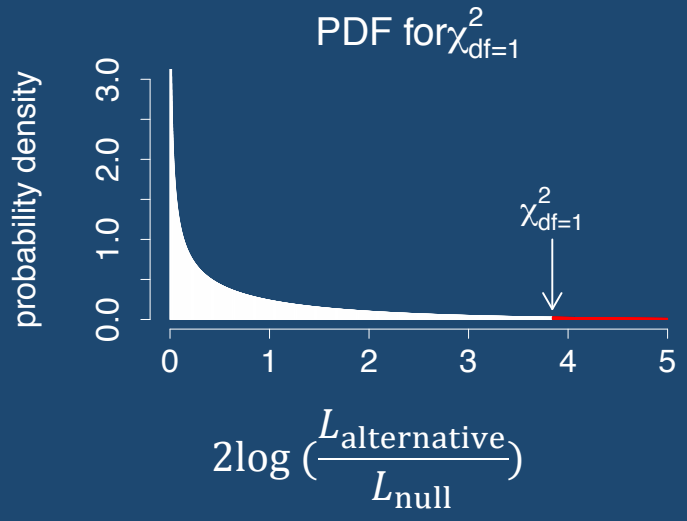
Likelihood Ratio Test

If the null hypothesis were true then

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

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

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



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
```

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

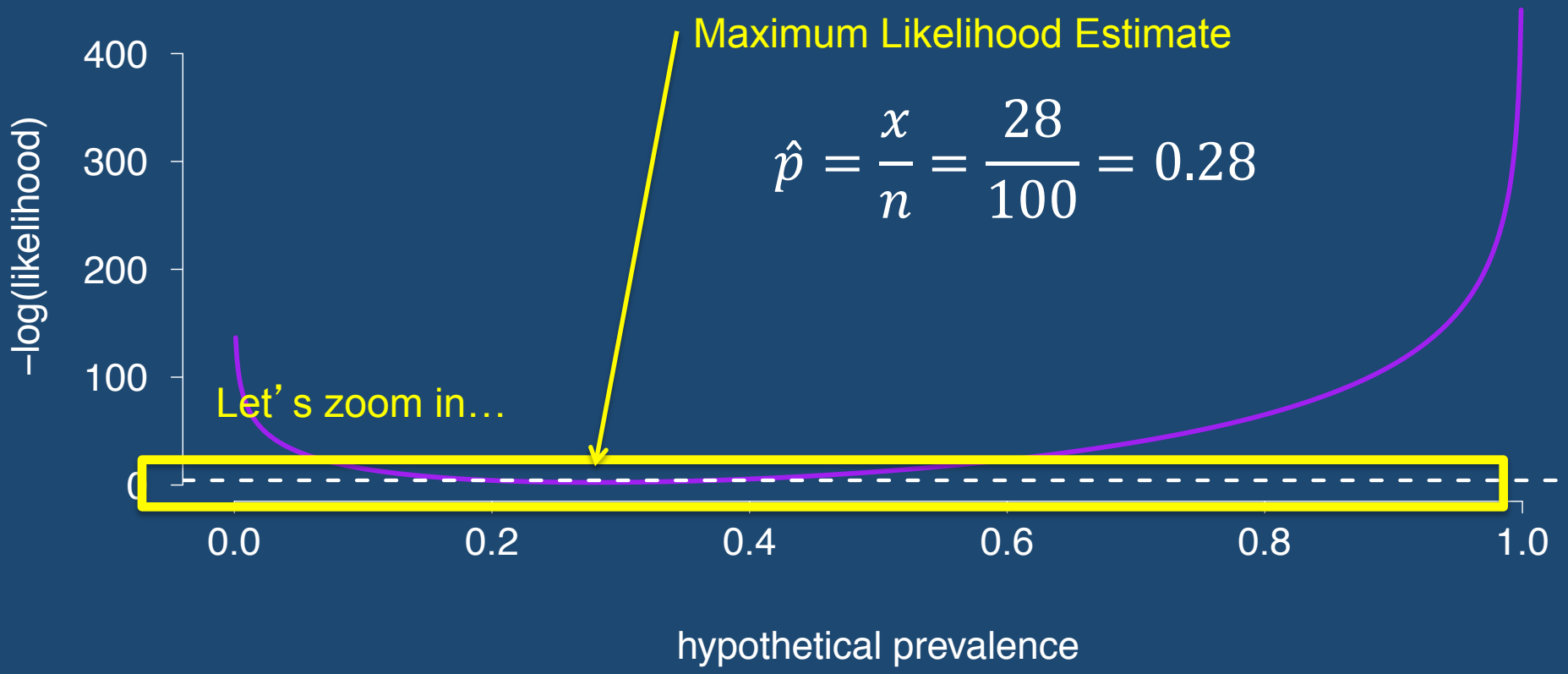
If $\log(L_{MLE}) - \log(L_{null}) > 1.92$,

we reject that null hypothesis.

Building Confidence Intervals

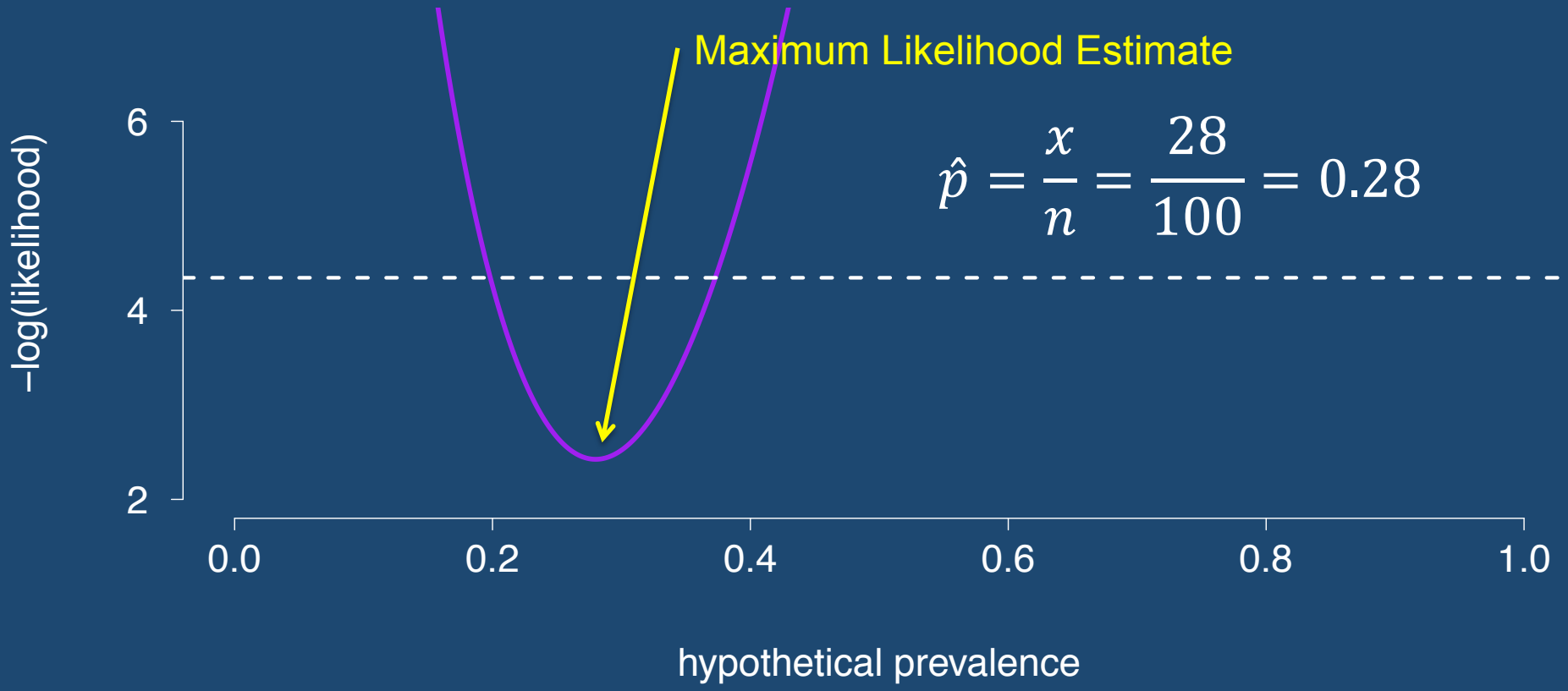
Likelihood Ratio Test

we usually minimize the –log(likelihood)



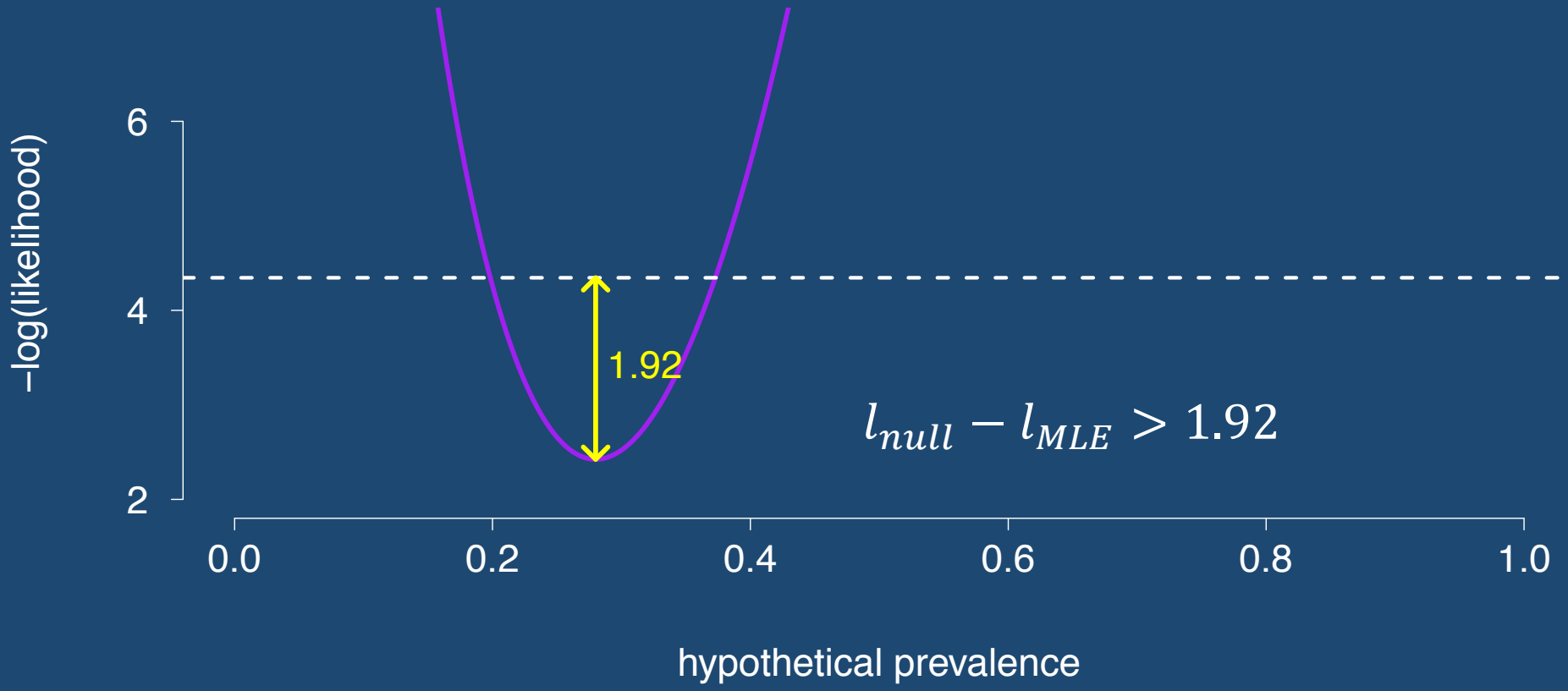
Building Confidence Intervals

Likelihood Ratio Test



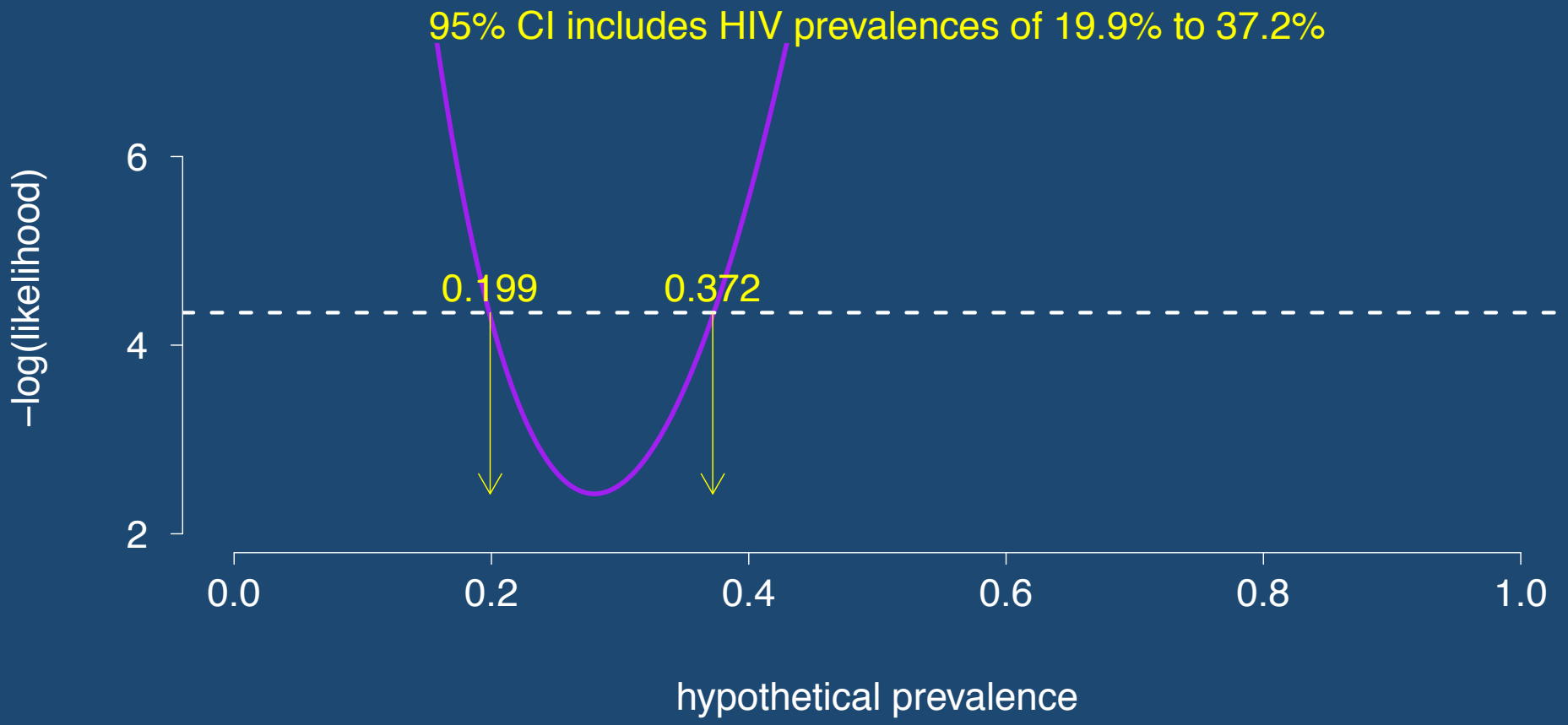
Building Confidence Intervals

Likelihood Ratio Test

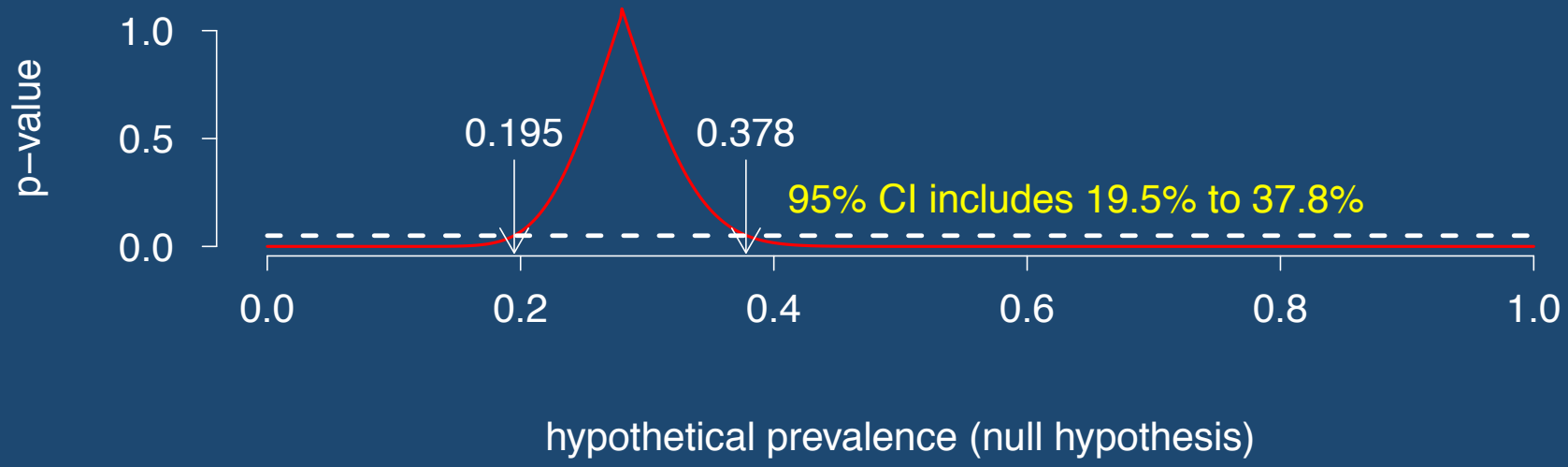


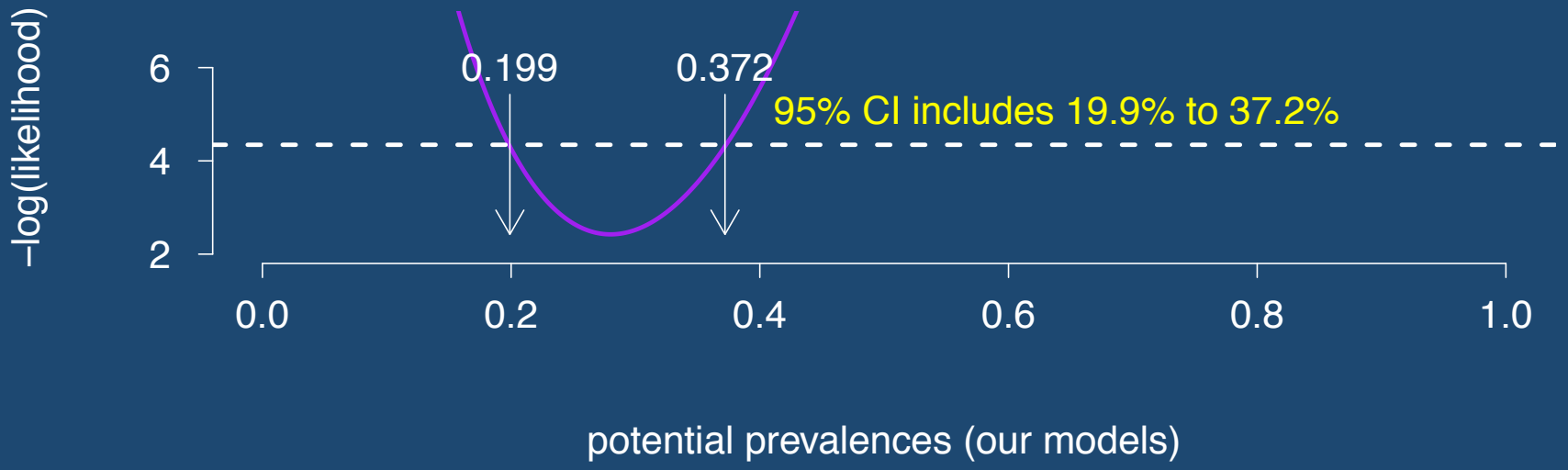
Building Confidence Intervals

Likelihood Ratio Test



Comparing Confidence Intervals





Advantages of Likelihood

- Practical method for
  estimating parameters
  estimating variance of our estimates

- Easily adaptable to different probability distributions & dynamic models

Likelihood Profile Confidence Intervals

- Profiles one parameter,
  with all others flexibly fit.

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AIMS African Institute for Mathematical Sciences

SACEMA DST/NRF Centre of Excellence in Epidemiological Modelling and Analysis

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