

Statistics for Linguists with R – a SIGIL course

Unit 2: Corpus Frequency Data & Statistical Inference

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<http://SIGIL.R-Forge.R-Project.org/>

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Frequency estimates & comparison

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- evidence from frequency comparisons / estimates

A simple toy problem

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- ◆ We have doubts and want to verify this claim

From research question to statistical analysis

**corpus
data**

**linguistic
question**

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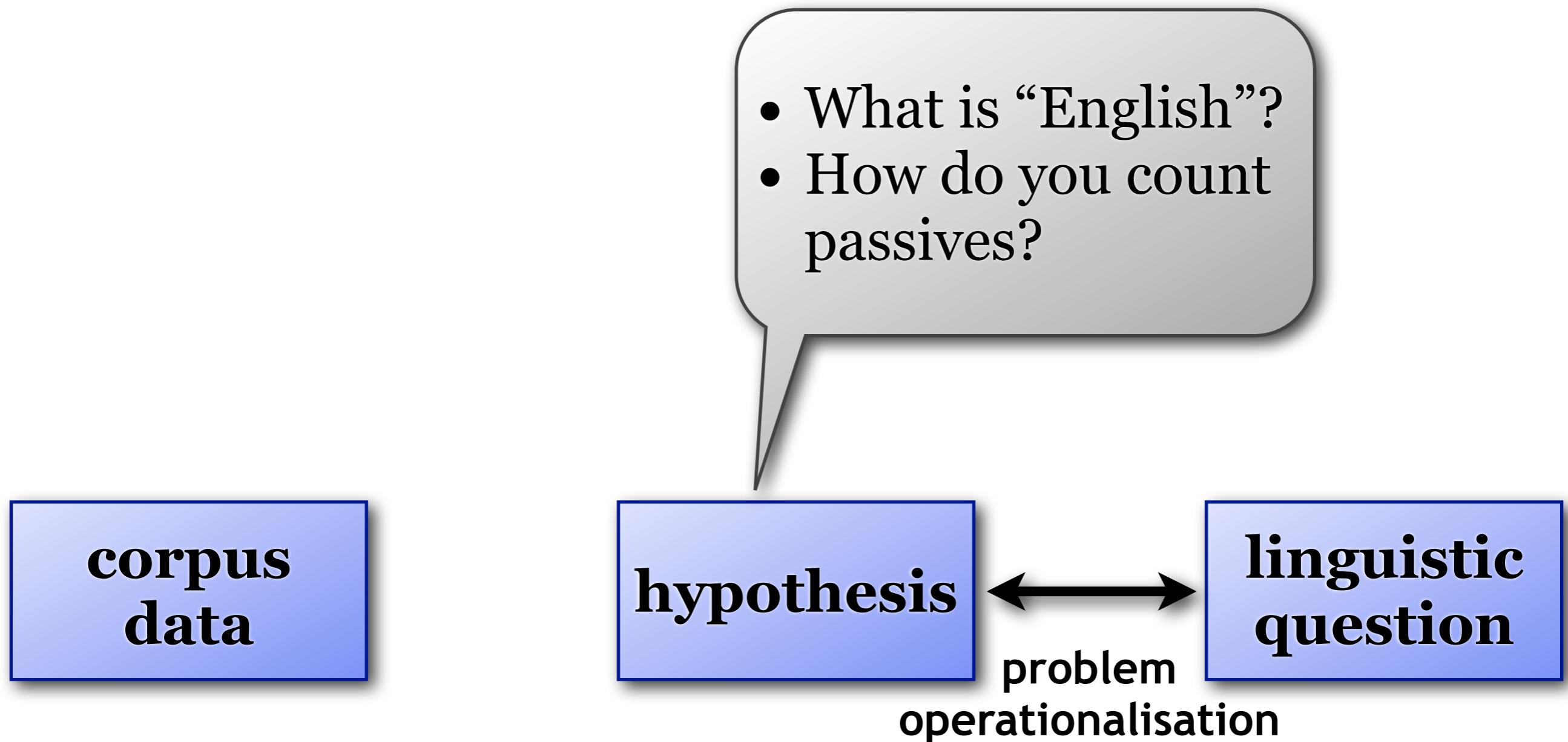
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From research question to statistical analysis



From research question to statistical analysis



**corpus
data**

hypothesis

**linguistic
question**

problem
operationalisation

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- ◆ Here: professional writing by native speakers of AmE (⇒ target audience of style guide)

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- ◆ Types vs. tokens

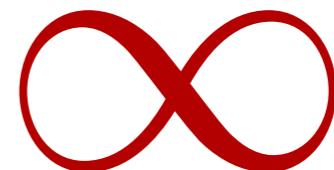
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- ◆ **Absolute frequency** is not meaningful here



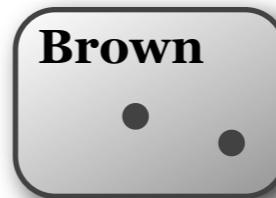
Against “absolute” frequency

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- ◆ Are there **20,000** passives?
 - Brown (1M words)

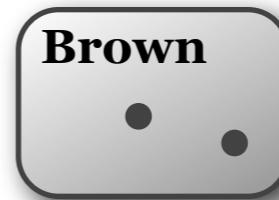
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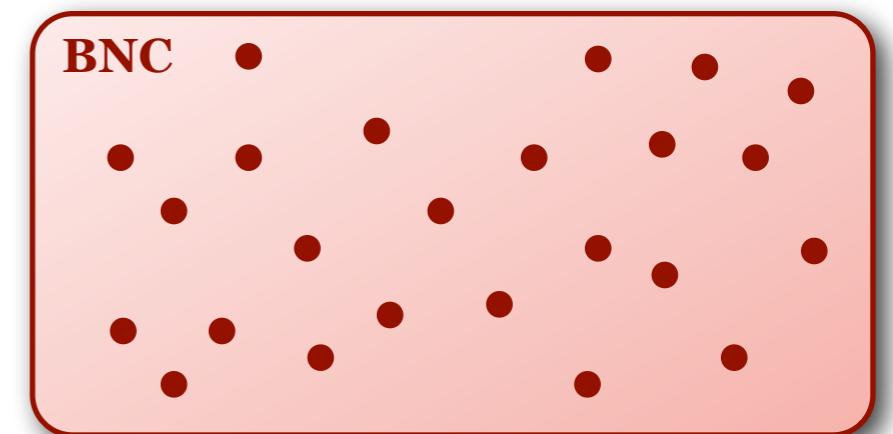
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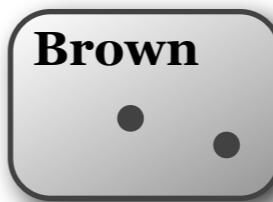
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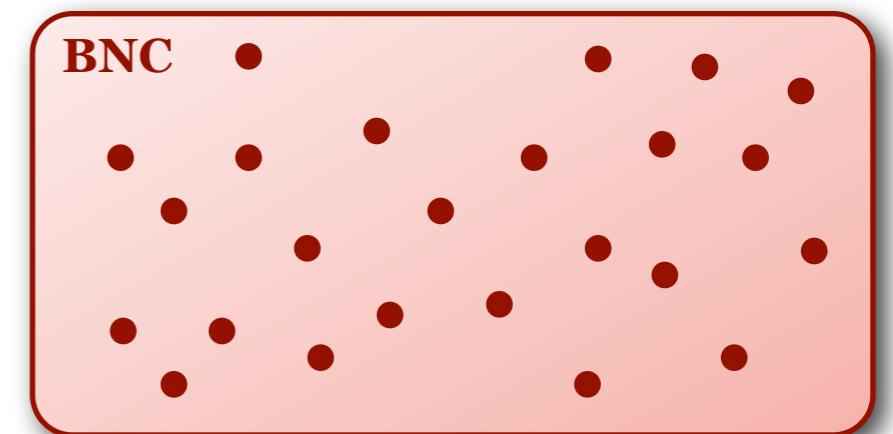
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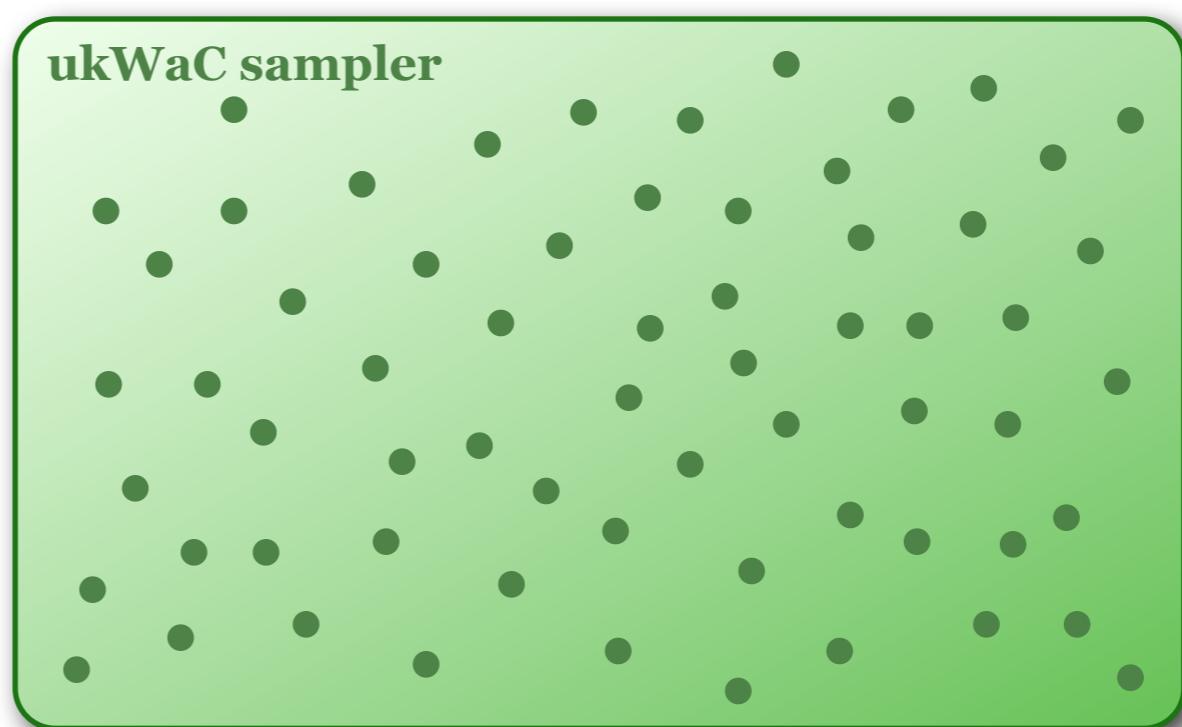
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- ◆ Or **5.1 million**?

- ukWaC sampler
(450M words)



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- ◆ What is a sensible unit of measurement?

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 - every VP can be in active or passive voice
 - frequency of passives only has a meaningful interpretation by comparison with frequency of potential passives

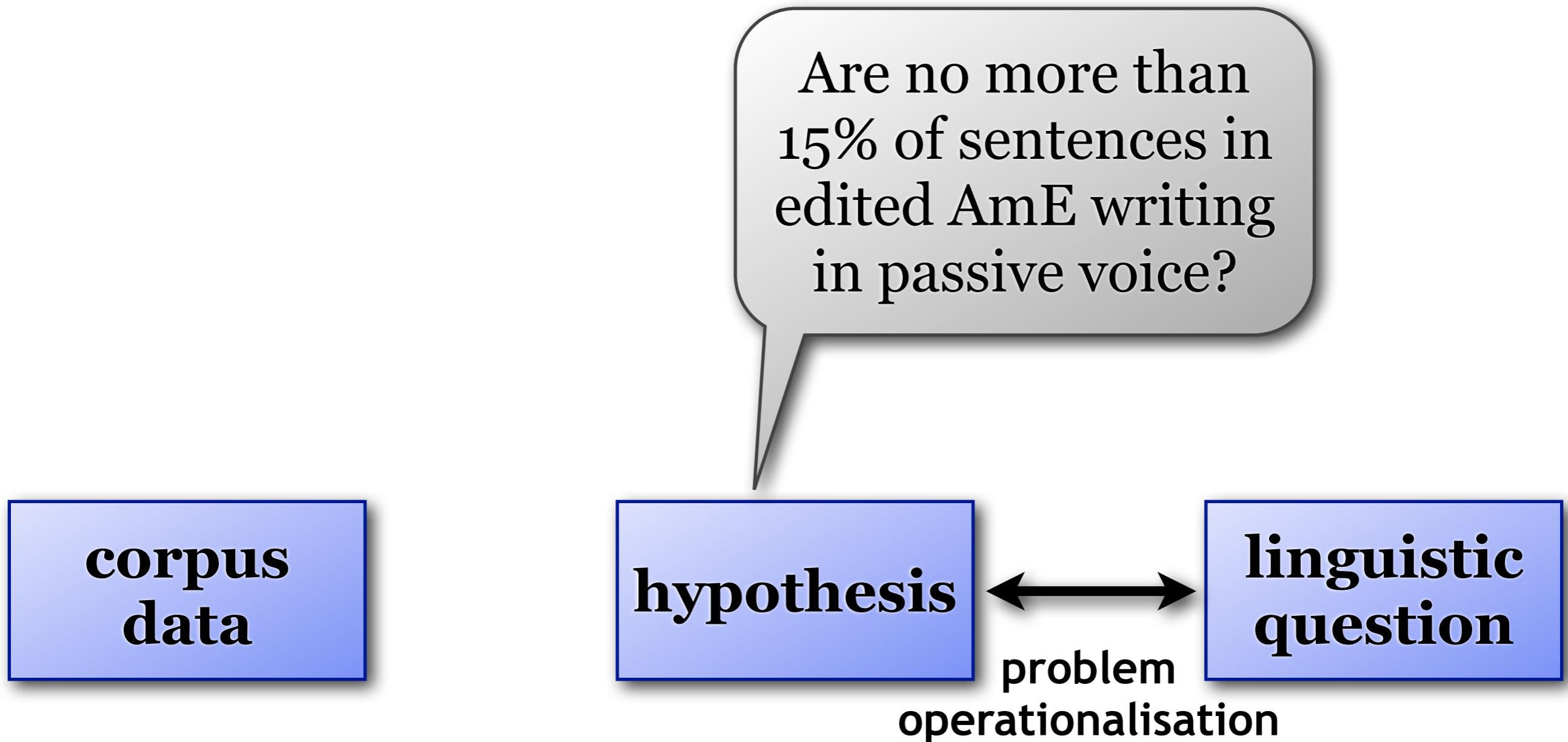
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- ◆ **Relative frequency = proportion π**

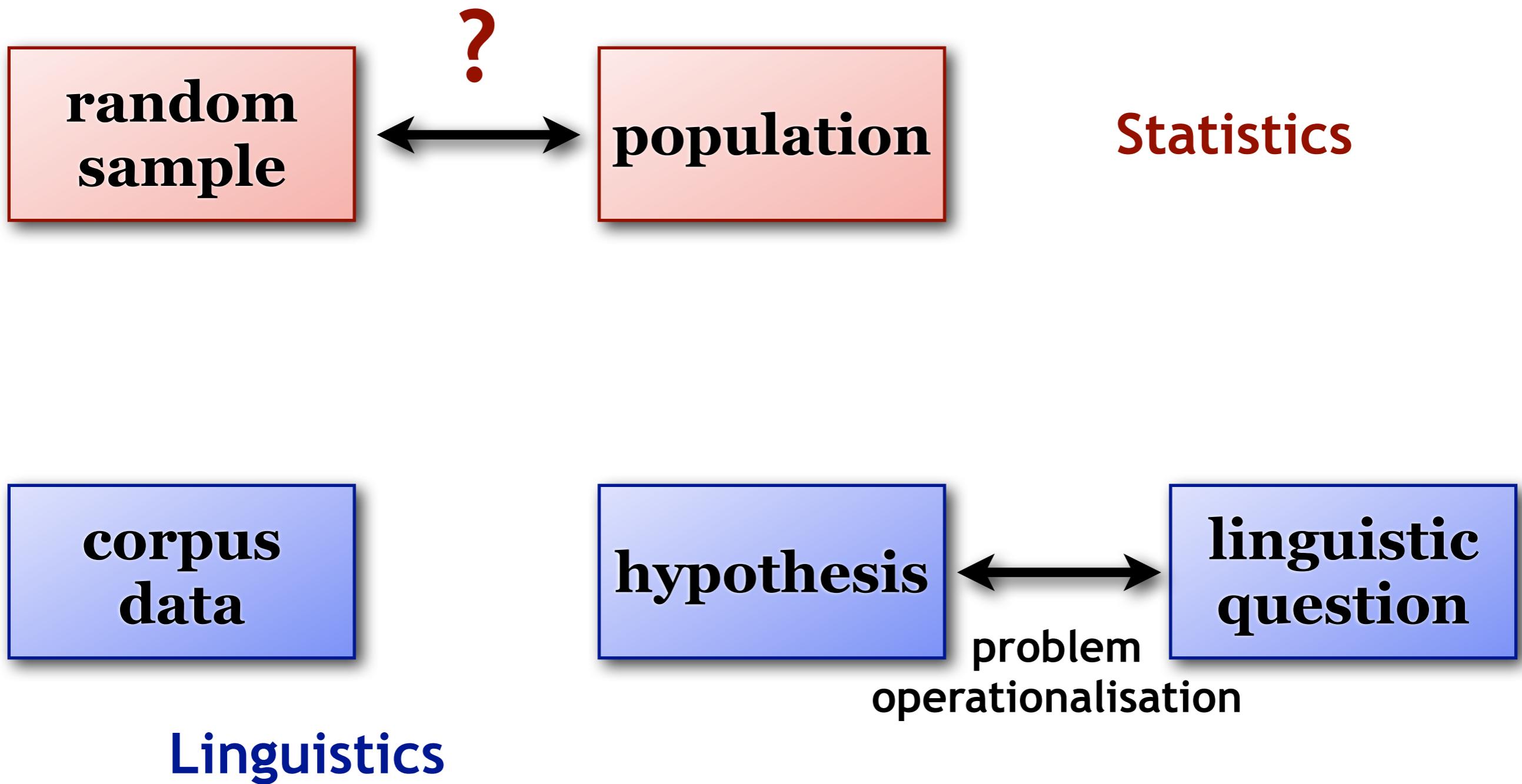
From research question to statistical analysis



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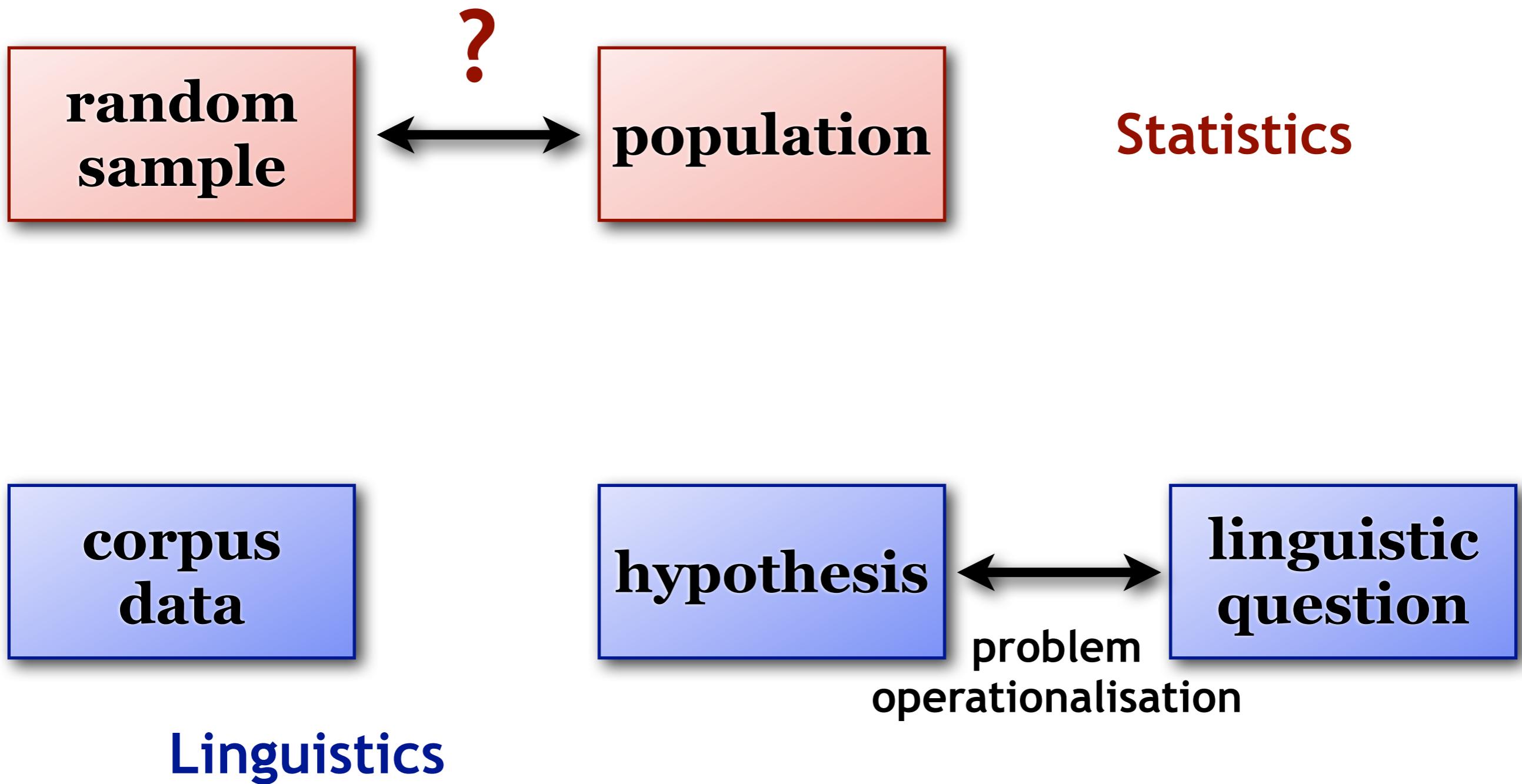
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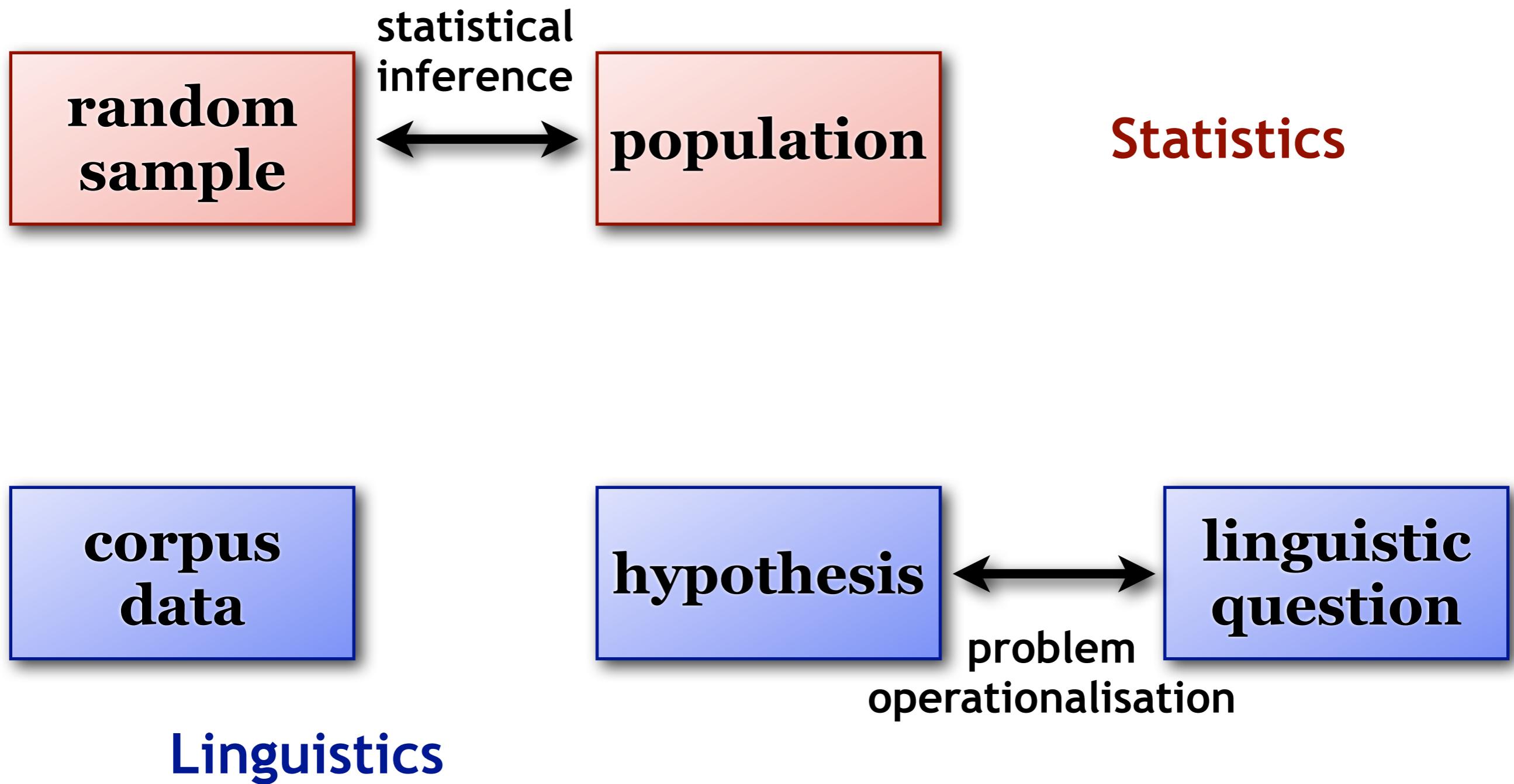
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- ◆ Many statistical methods are readily available

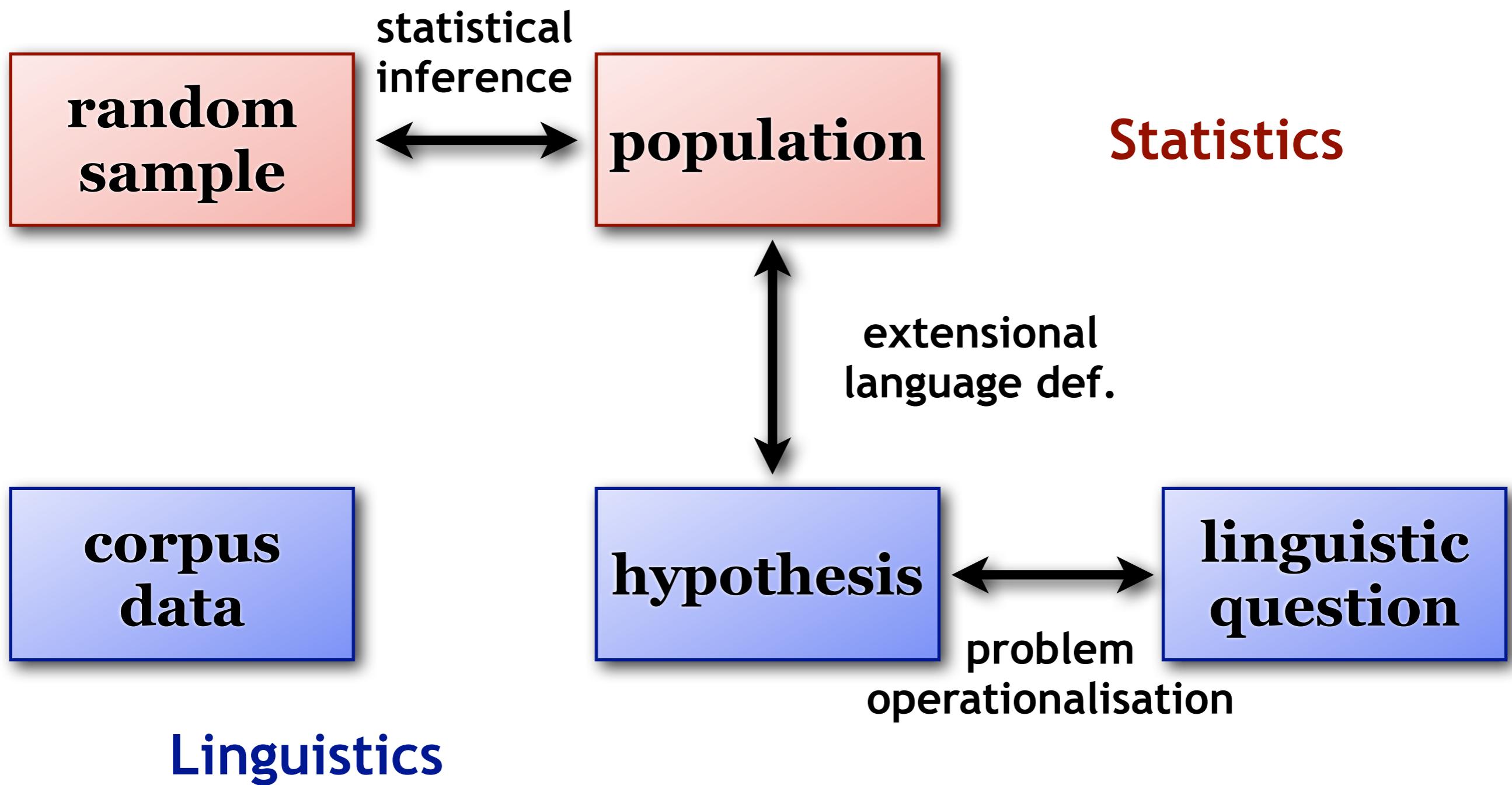
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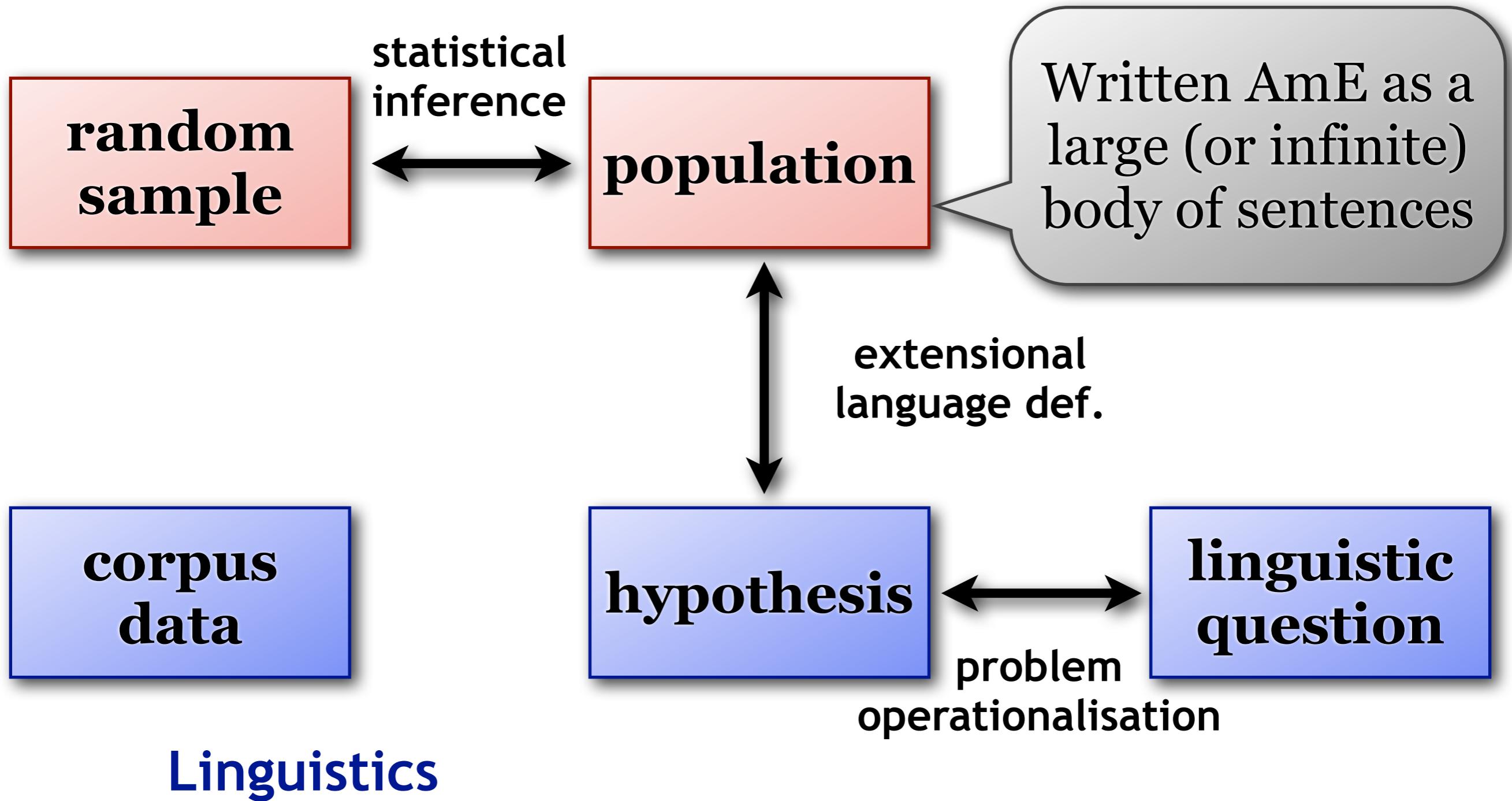
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The library metaphor

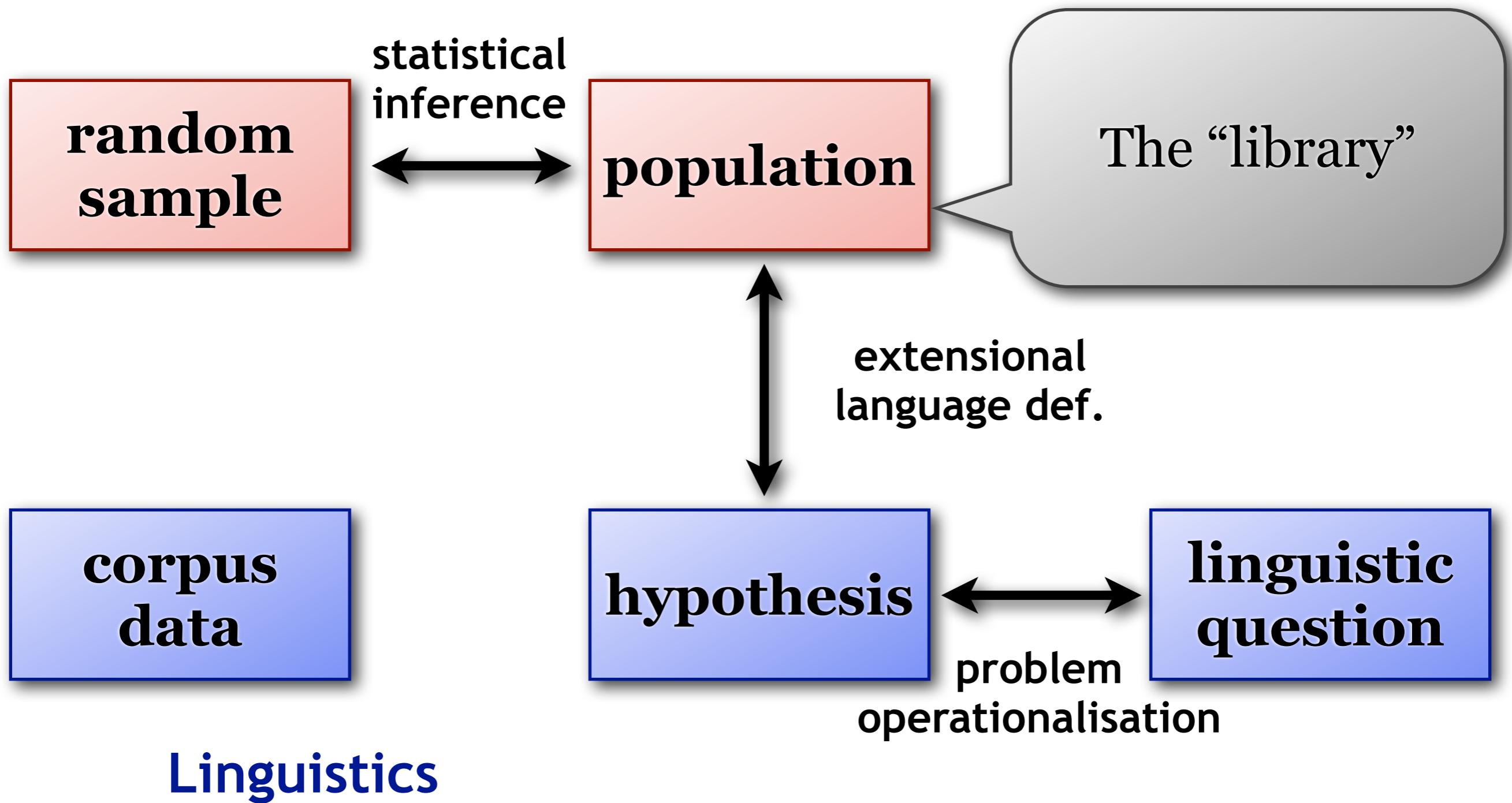
The library metaphor

- ◆ Extensional definition of a language:
“All utterances made by speakers of the language under appropriate conditions, plus all utterances they *could* have made”

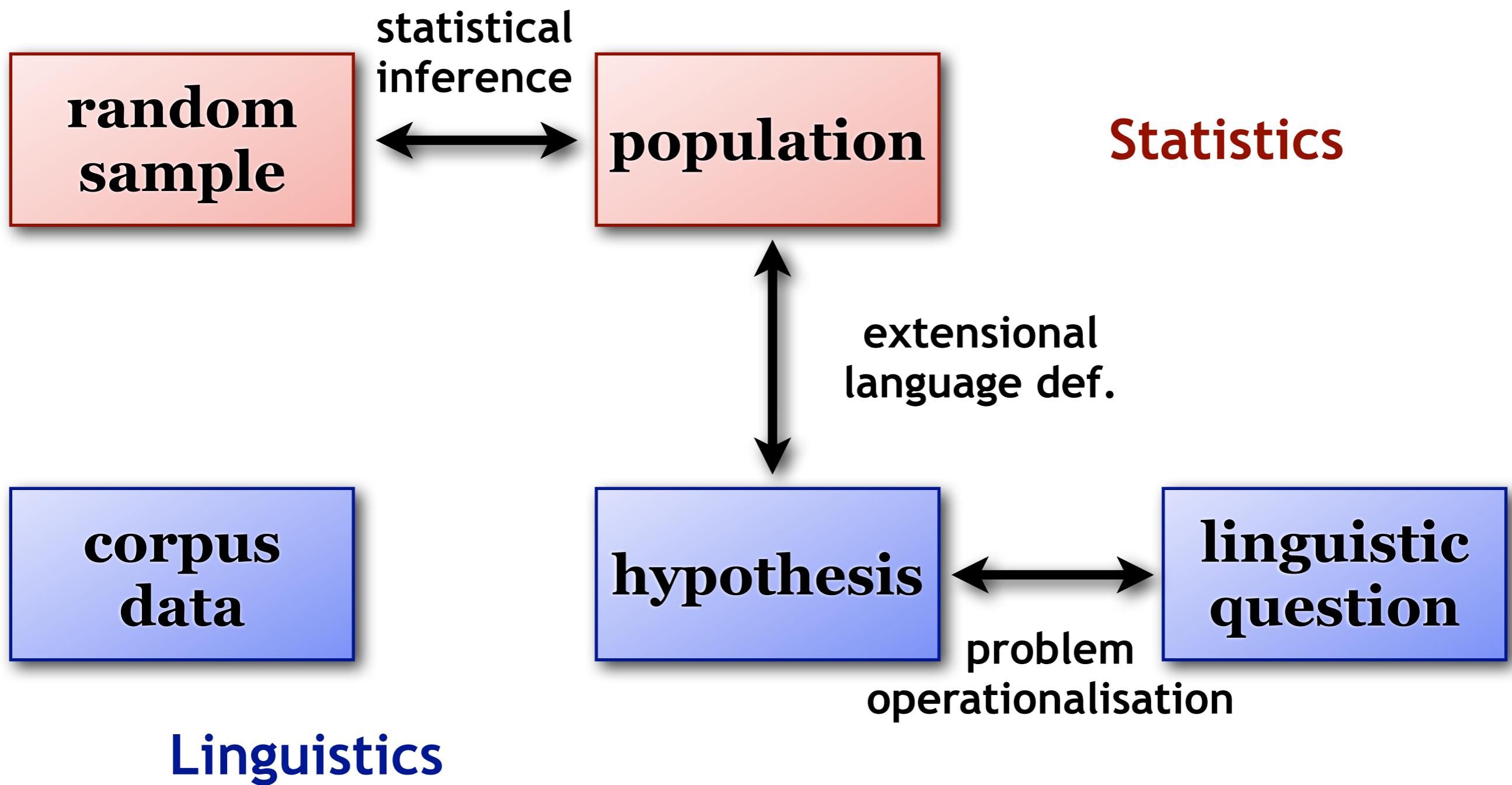
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- ◆ Extensional definition of a language:
“All utterances made by speakers of the language under appropriate conditions, plus all utterances they *could* have made”
 - ◆ Imagine a huge library with all the books written in a language, as well as all the hypothetical books that have never been written
- **library metaphor** (Evert 2006)

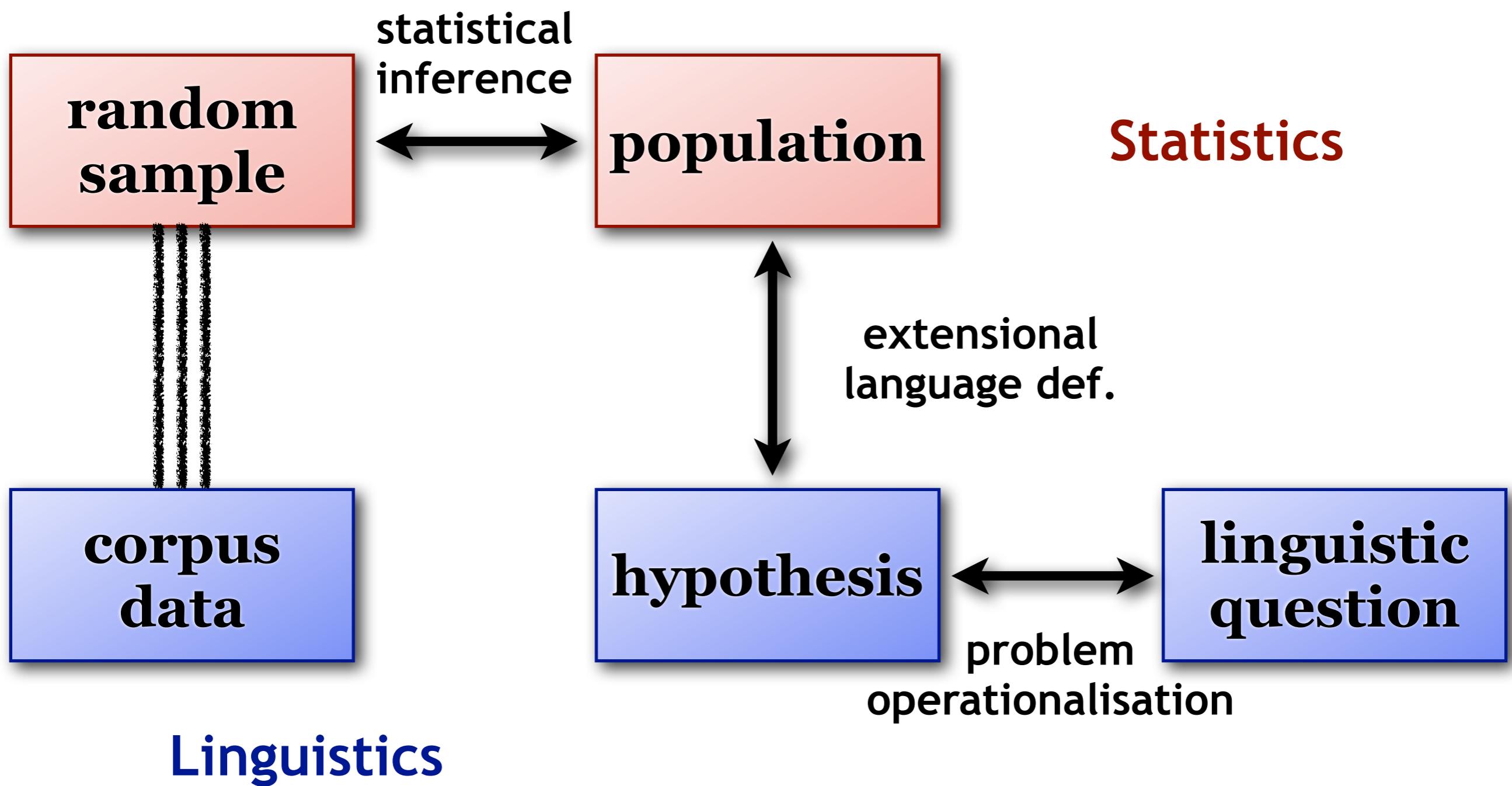
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A random sample of a language

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- ◆ Objects = whatever **unit of measurement** the proportions of interest are based on
 - we need to take a random sample of such units

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 - repeat ***n*** times for **sample size *n***

Types, tokens and proportions

- ◆ Proportions and relative sample frequencies are defined formally in terms of types & tokens
- ◆ Relative frequency of type v in sample $\{t_1, \dots, t_n\}$
= proportion of tokens t_i that belong to this type

$$p = \frac{f(v)}{n}$$

frequency of type
sample size

- ◆ Compare relative sample frequency p against (hypothesised) population proportion π

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- ◆ Example: verb subcategorisation
 - relevant types = **itr.**, **tr.**, **ditr.**, **PP-comp.**, **X-comp**, ...
 - verb token = occurrence of selected verb in text

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 - $p > \pi$ → reject claim of style guide?
- ◆ Take another sample, just to be sure
 - observe 13 passives → $p = 13\% = .13$
 - $p < \pi$ → claim of style guide confirmed?

Sampling variation

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Sampling variation

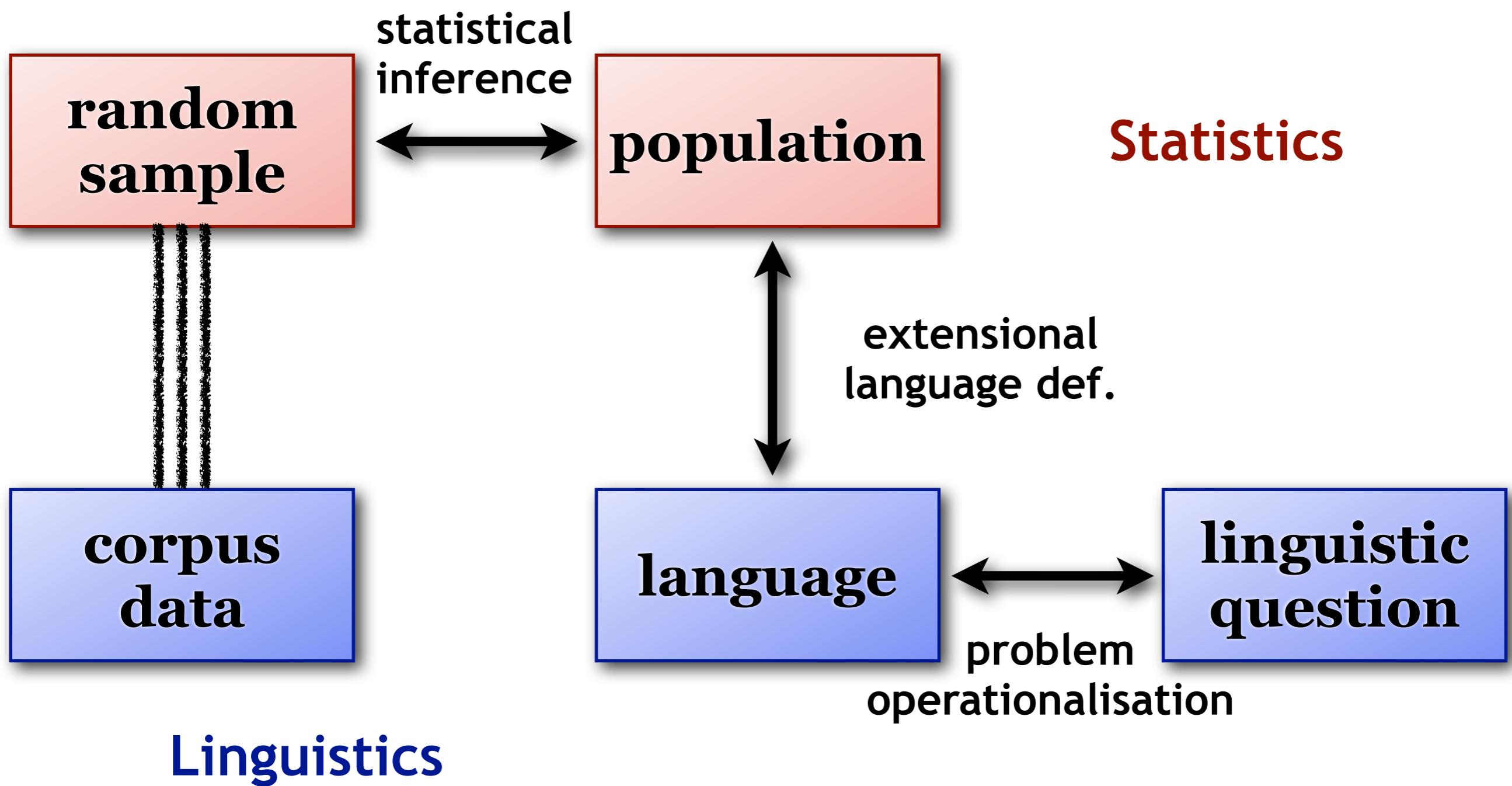
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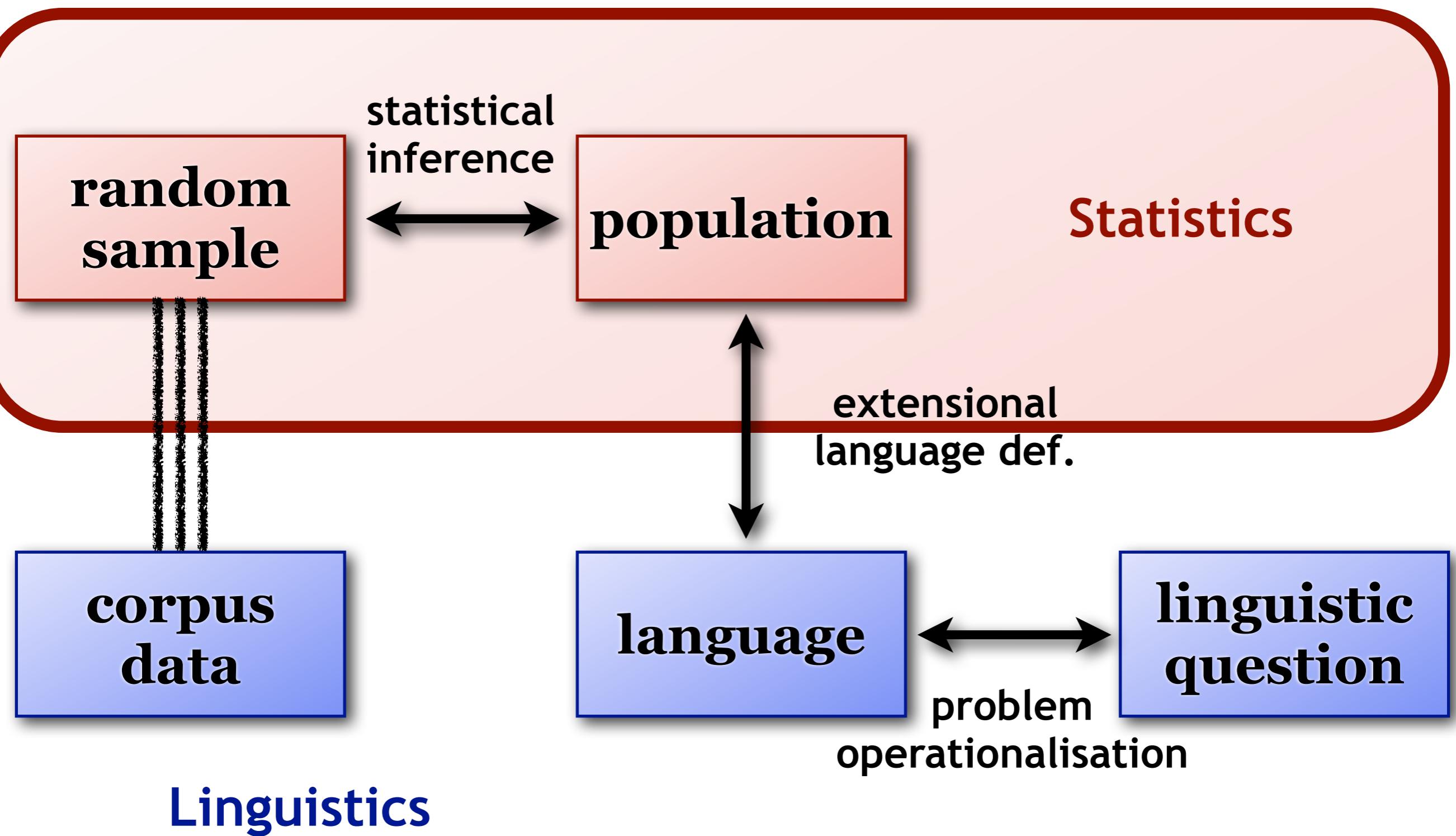
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- ◆ The main purpose of statistical methods is to estimate & correct for sampling variation
 - that's all there is to inferential statistics, really



Reminder: The role of statistics



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Linguistics

The null hypothesis

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- ◆ Need to control risk of a type I error

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 - each one draws a random sample of size $n = 100$
 - how many of the samples have the expected $k = 15$ passives, how many have $k = 19$, etc.?
 - if we are willing to reject H_0 for $k = 19$ passives in a sample, all corpus linguists with such a sample will publish a false result
 - risk of type I error = percentage of such cases

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 - randomly picking sentences from our metaphorical library is like drawing balls from an infinite urn
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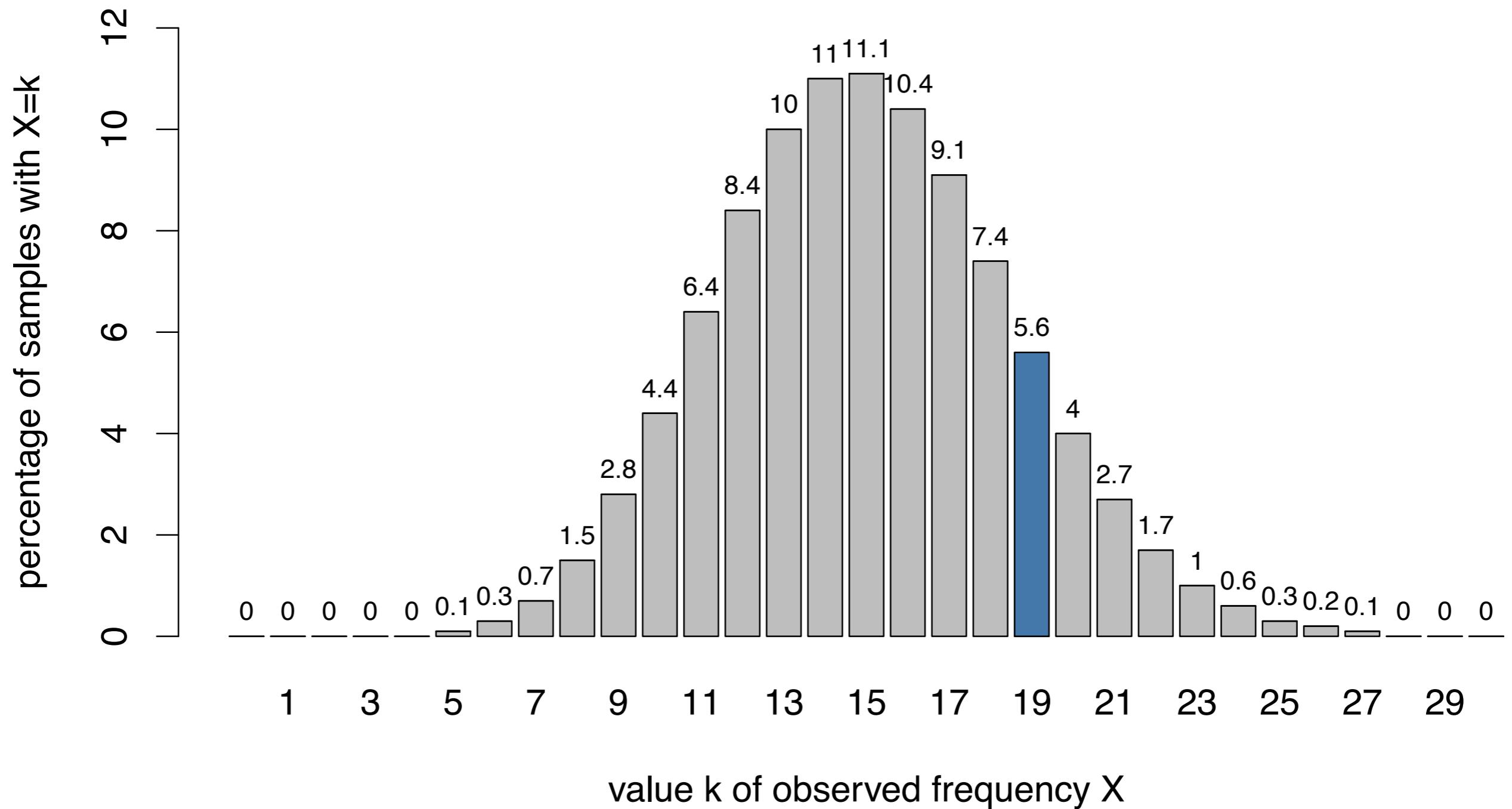
percentage of samples = **probability**

<http://xkcd.com/1374/>

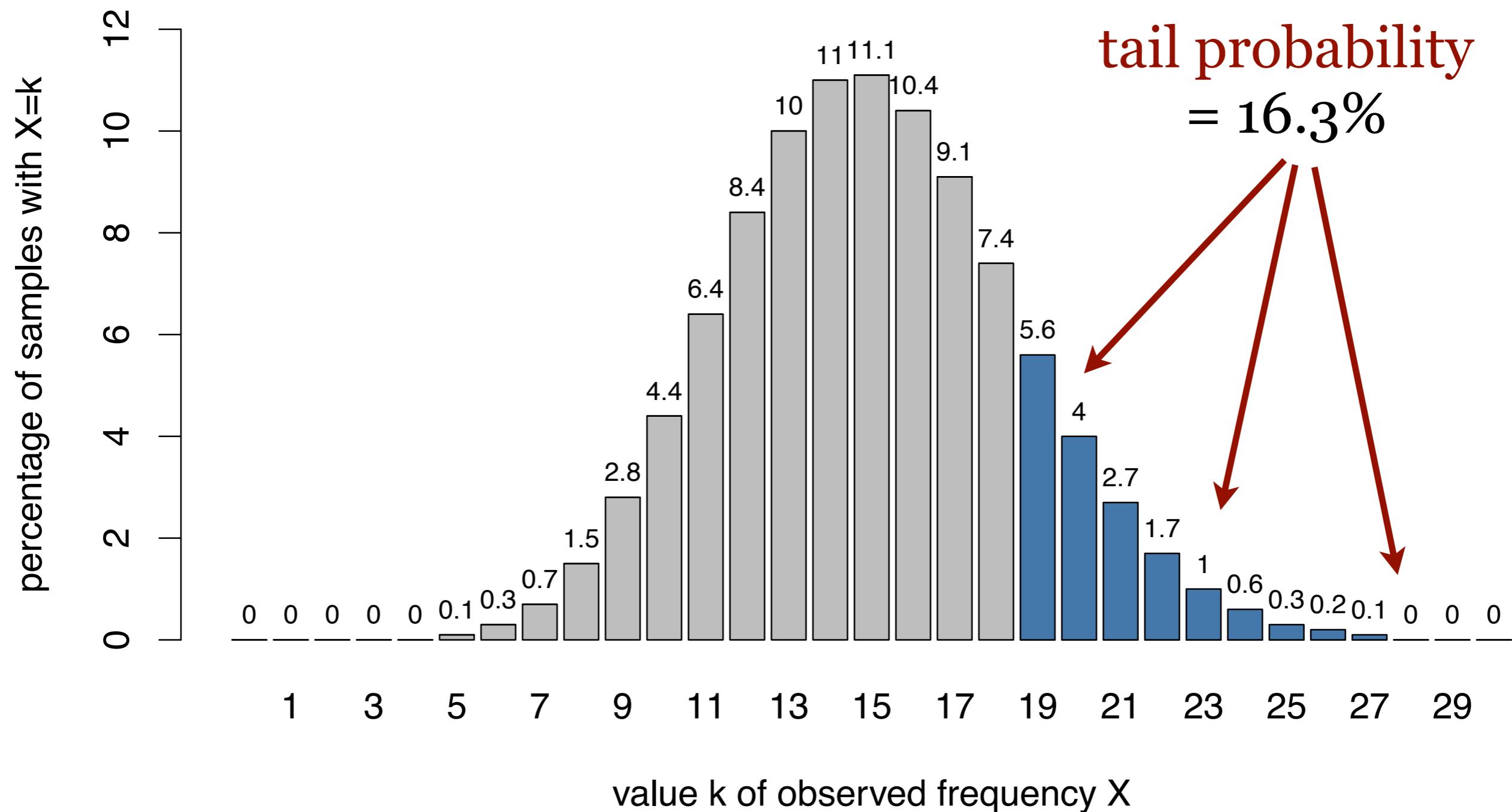


Comic relief

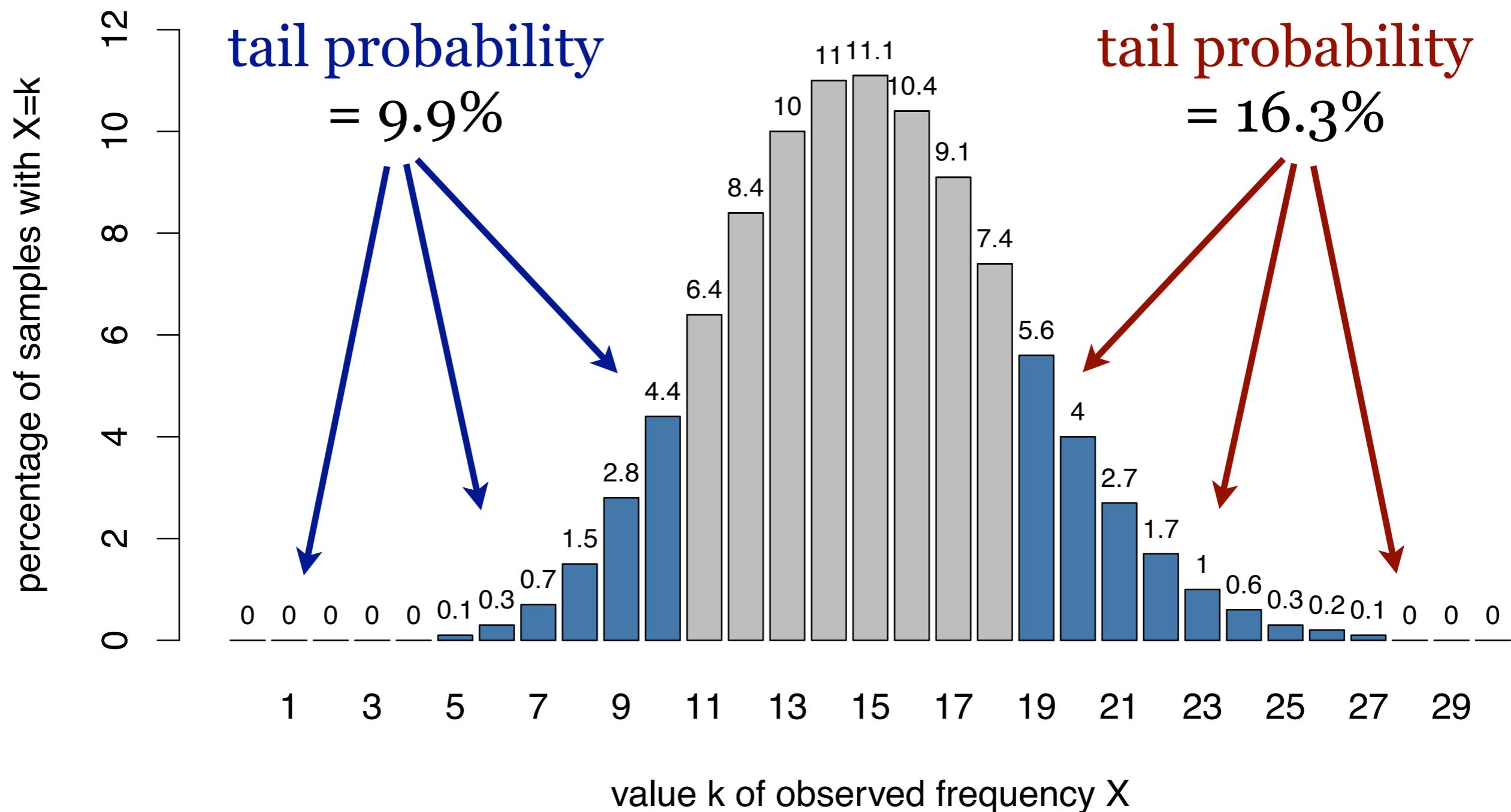
Binomial sampling distribution



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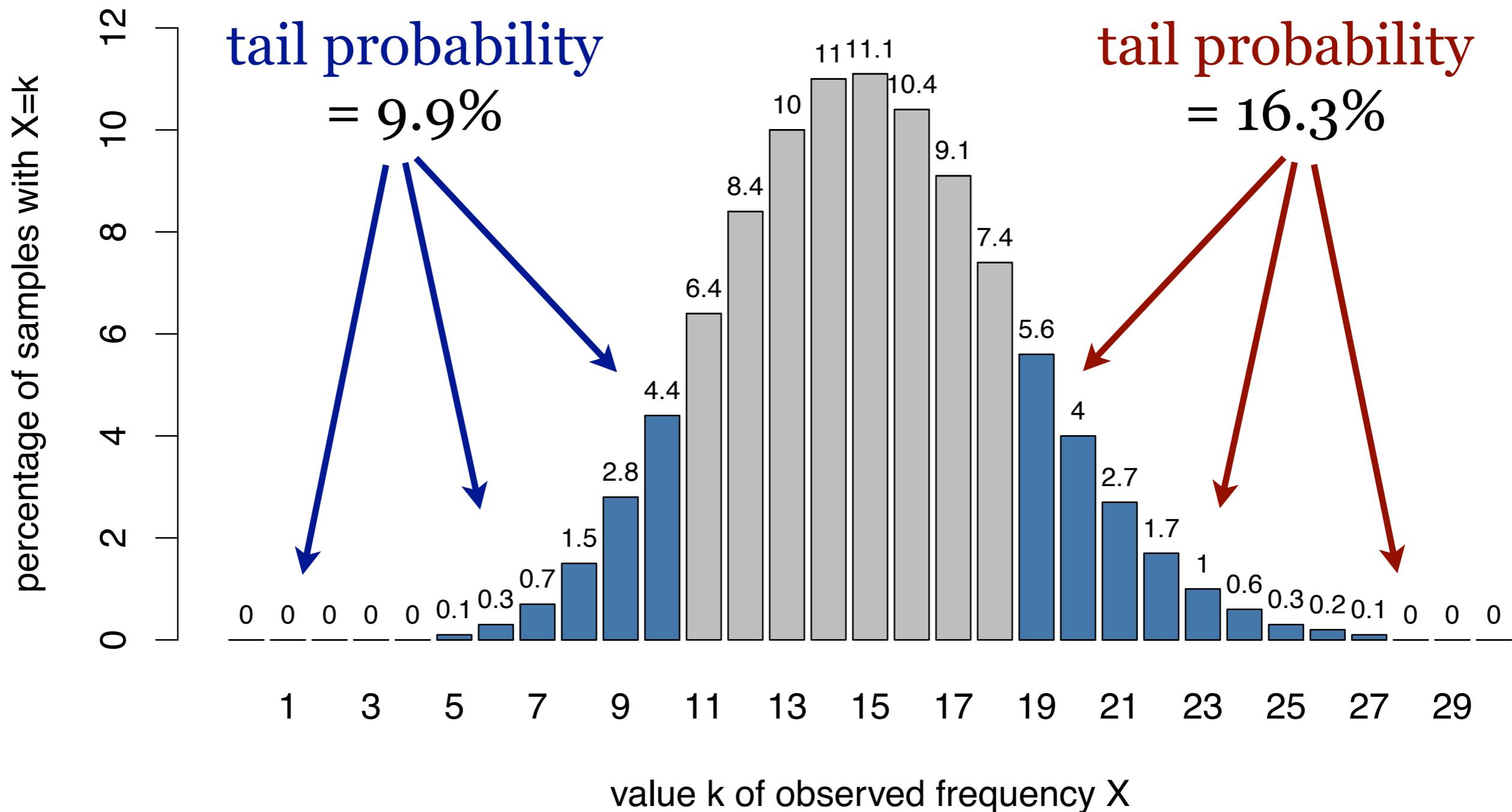


Binomial sampling distribution



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→ risk of false rejection = **p-value** = 26.2%



Statistical hypothesis testing

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◆ Statistical **hypothesis tests**

- define a **rejection criterion** for refuting H_0
- control the risk of false rejection (**type I error**) to a “socially acceptable level” (**significance level α**)
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 - **p-value** = risk of type I error given observation, interpreted as amount of evidence against H_0
- ◆ Two-sided vs. one-sided tests
 - in general, two-sided tests are recommended (safer)
 - one-sided test is plausible in our example

Hypothesis tests in practice

SIGIL: Corpus Frequency Test Wizard

[back to main page](#)

This site provides some online utilities for the project **Statistical Inference: A Gentle Introduction for Linguists (SIGIL)** by [Marco Baroni](#) and [Stefan Evert](#). The main SIGIL homepage can be found at purl.org/stefan.evert/SIGIL.

One sample: frequency estimate (confidence interval)

[back to top](#)

Frequency count	Sample size
19	100
<input type="checkbox"/> extrapolate to <input type="text"/> items	
<input type="button" value="Calculate"/>	

Clear fields 95% confidence interval
in automatic format
with 4 significant digits

Two samples: frequency comparison

[back to top](#)

Frequency count	Sample size
Sample 1	19
	100
Sample 2	25
	200

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Frequency count	Sample size
19	100
<input type="checkbox"/> extrapolate to <input type="text"/> items	
<input type="button" value="Calculate"/>	

95% confidence interval
in automatic format

Two samples: frequency comparison

Frequency count	Sample size	
Sample 1	19	100
Sample 2	25	200

- <http://sigil.collocations.de/wizard.html>
- <http://vassarstats.net/>
- SPSS, SAS, Excel, ...
- We want to do it in , of course

[back to top](#)

Binomial hypothesis test in R

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- ◆ Relevant R function: `binom.test()`

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- ◆ Relevant R function: `binom.test()`
- ◆ We need to specify
 - **observed data:** 19 passives out of 100 sentences
 - **null hypothesis:** $H_0: \pi = 15\%$

Binomial hypothesis test in R

- ◆ Relevant R function: `binom.test()`
- ◆ We need to specify
 - **observed data:** 19 passives out of 100 sentences
 - **null hypothesis:** $H_0: \pi = 15\%$
- ◆ Using the `binom.test()` function:

```
> binom.test(19, 100, p=.15) # two-sided  
> binom.test(19, 100, p=.15, # one-sided  
           alternative="greater")
```

Binomial hypothesis test in R

```
> binom.test(19, 100, p=.15)
```

Exact binomial test

data: 19 and 100

number of successes = 19, number of trials = 100, p-value = 0.2623

alternative hypothesis: true probability of success is not equal to 0.15

95 percent confidence interval:
0.1184432 0.2806980

sample estimates:
probability of success
0.19

Rejection criterion & significance level

Rejection criterion & significance level

```
> binom.test(19, 100, p=.15)$p.value  
[1] 0.2622728
```

$p > .05$ n.s.

Rejection criterion & significance level

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> binom.test(23, 100, p=.15)$p.value  
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```

$p < .05 = \alpha$ *

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[1] 0.03430725
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$p < .05 = \alpha$ *

```
> binom.test(25, 100, p=.15)$p.value  
[1] 0.007633061
```

$p < .01 = \alpha$ **

Rejection criterion & significance level

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> binom.test(19, 100, p=.15)$p.value  
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$p < .05 = \alpha$ *

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> binom.test(25, 100, p=.15)$p.value  
[1] 0.007633061
```

$p < .01 = \alpha$ **

```
> binom.test(29, 100, p=.15)$p.value  
[1] 0.0003529264
```

$p < .001 = \alpha$ ***

Type II errors

Type II errors

- ◆ Rejection criterion controls risk of type I error
 - only for situation in which H_0 is true

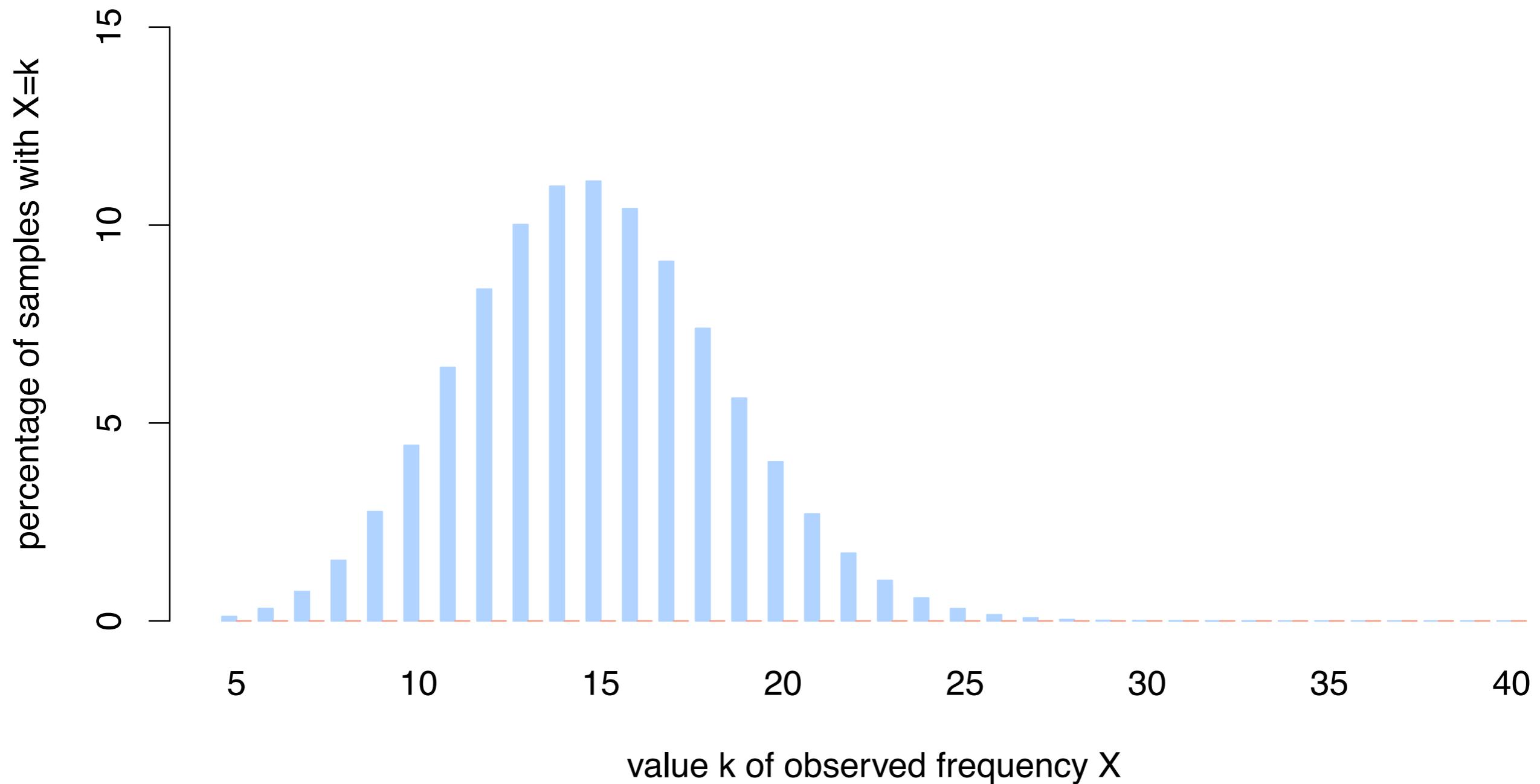
Type II errors

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 - for situation in which H_0 is not true
→ rejection correct, non-rejection is an error

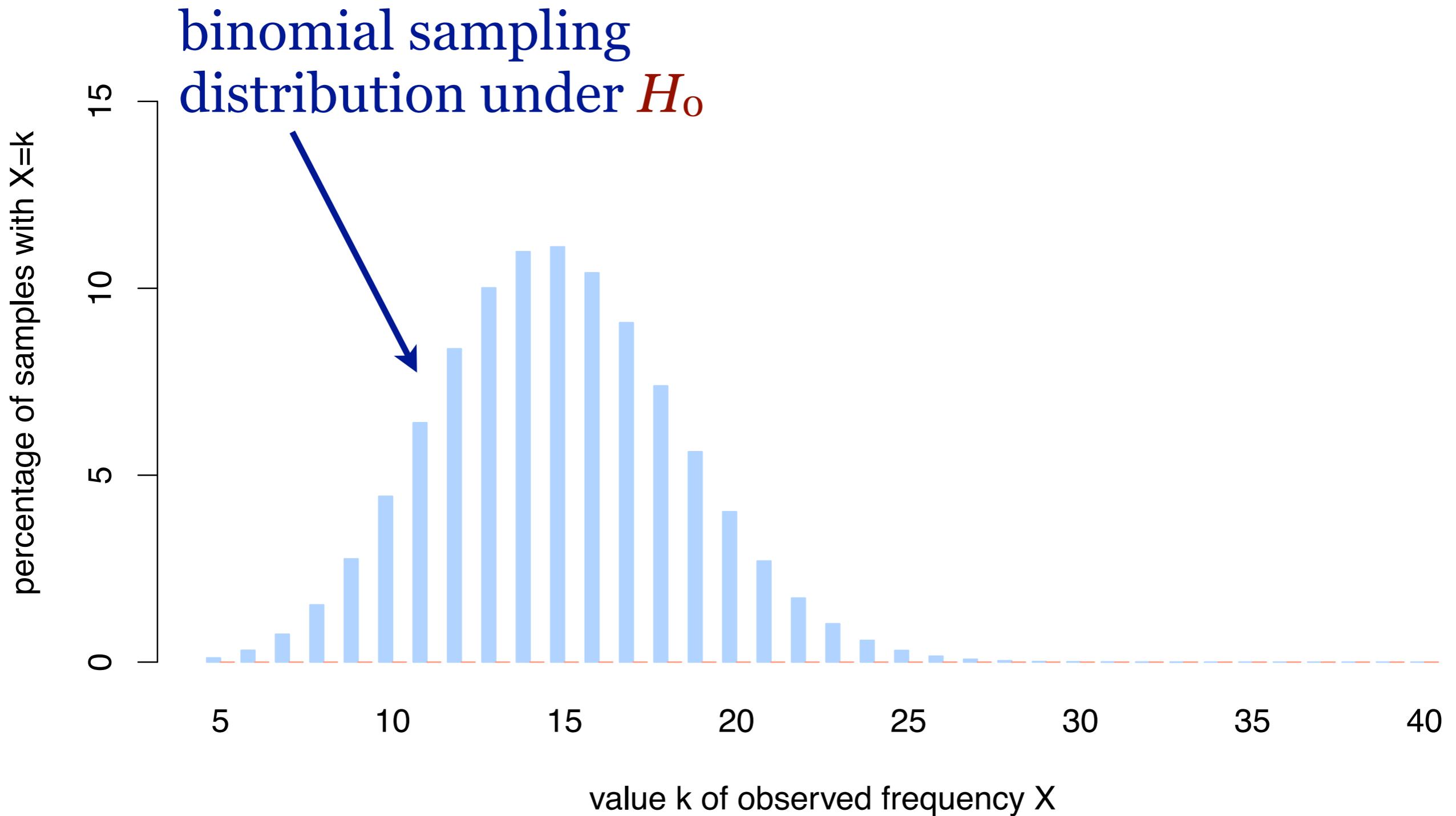
Type II errors

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 - only for situation in which H_0 is true
- ◆ Type II error = failure to reject incorrect H_0
 - for situation in which H_0 is not true
→ rejection correct, non-rejection is an error
- ◆ What is the risk of a type II error?
 - depends on true population proportion π
 - intuitively, risk of type II error will be low if the difference $\delta = \pi - \pi_0$ (the **effect size**) is large enough

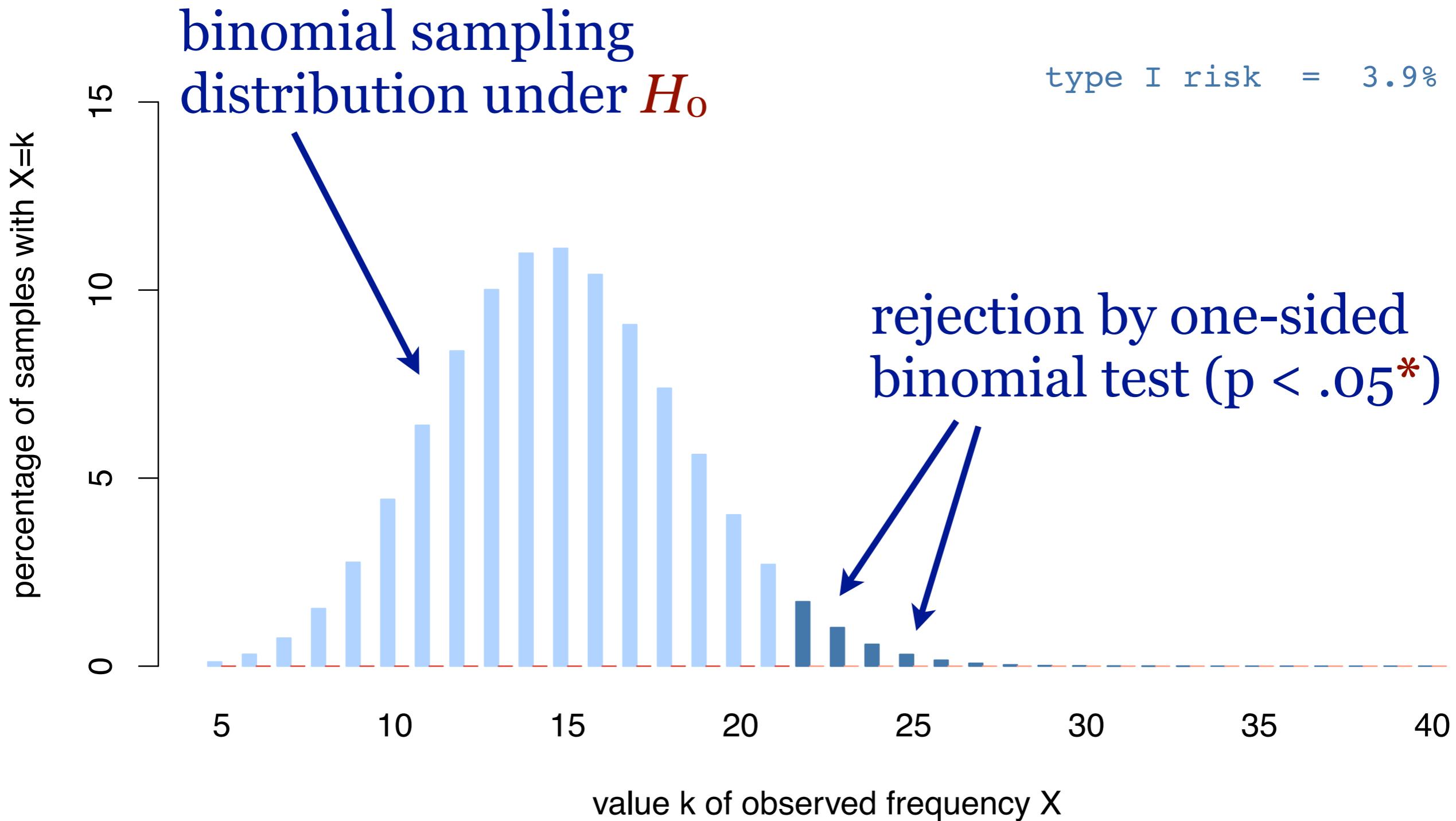
Type II errors



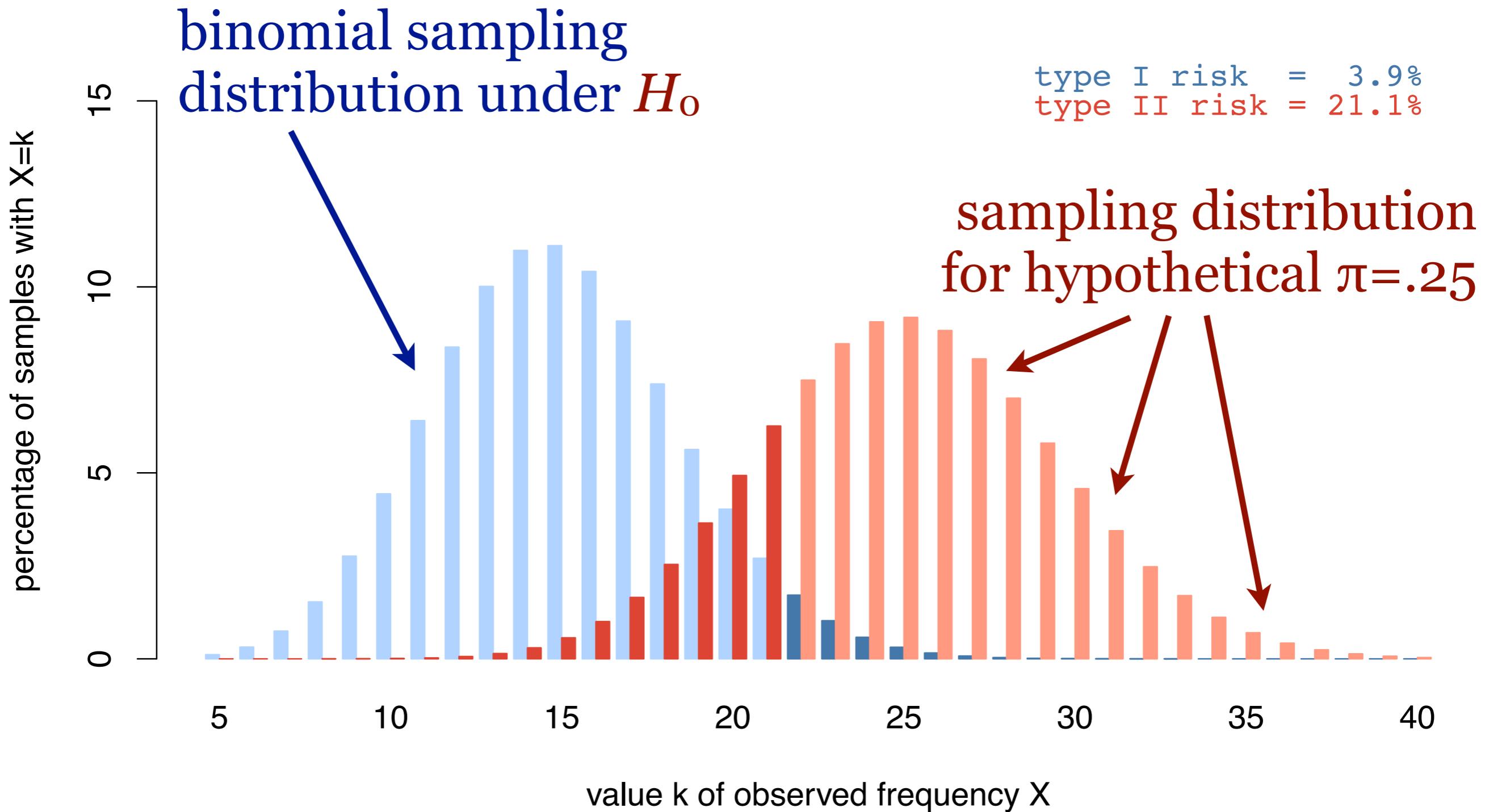
Type II errors



Type II errors



Type II errors

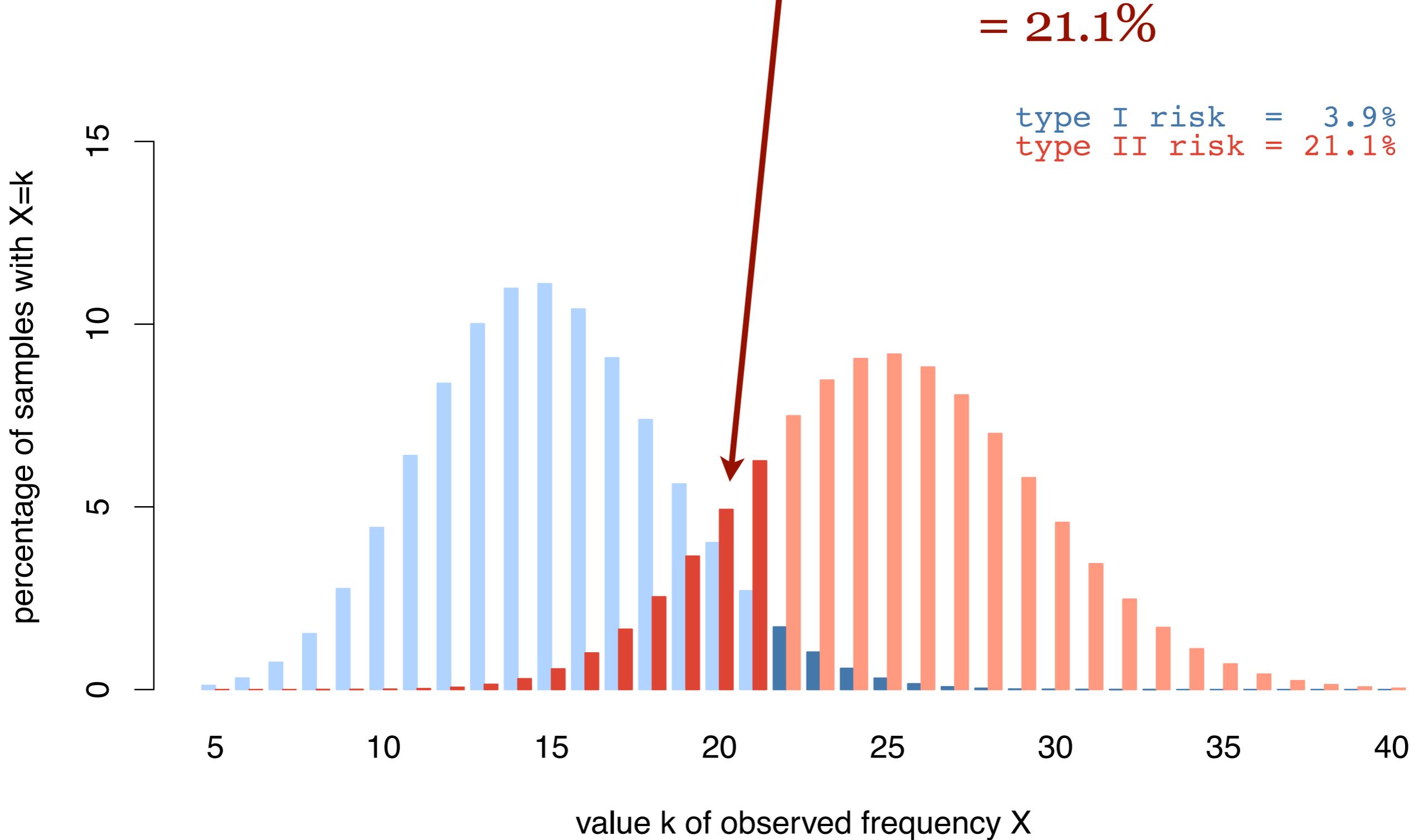


Type II errors

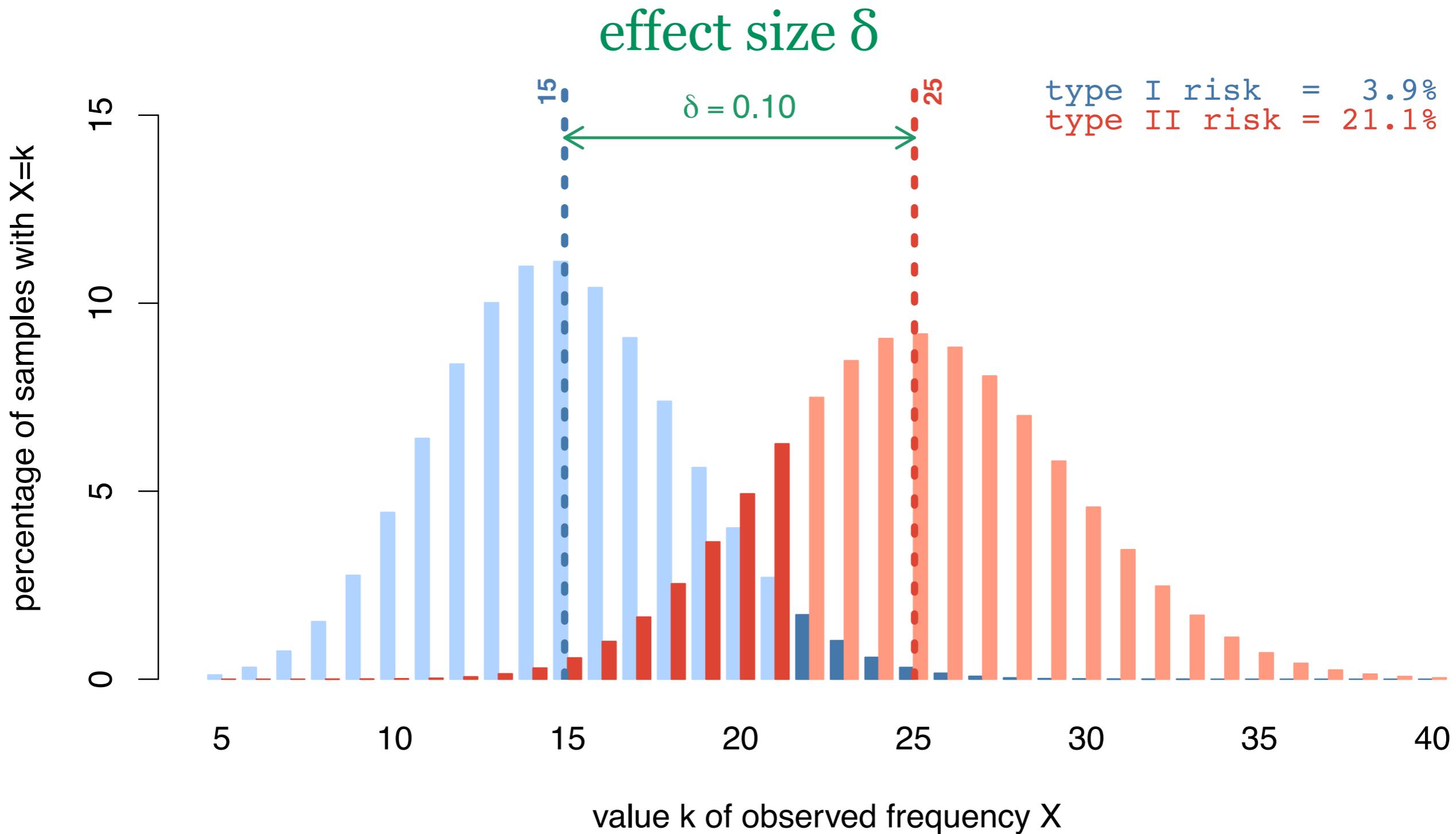
type II risk for $k \leq 21$

= 21.1%

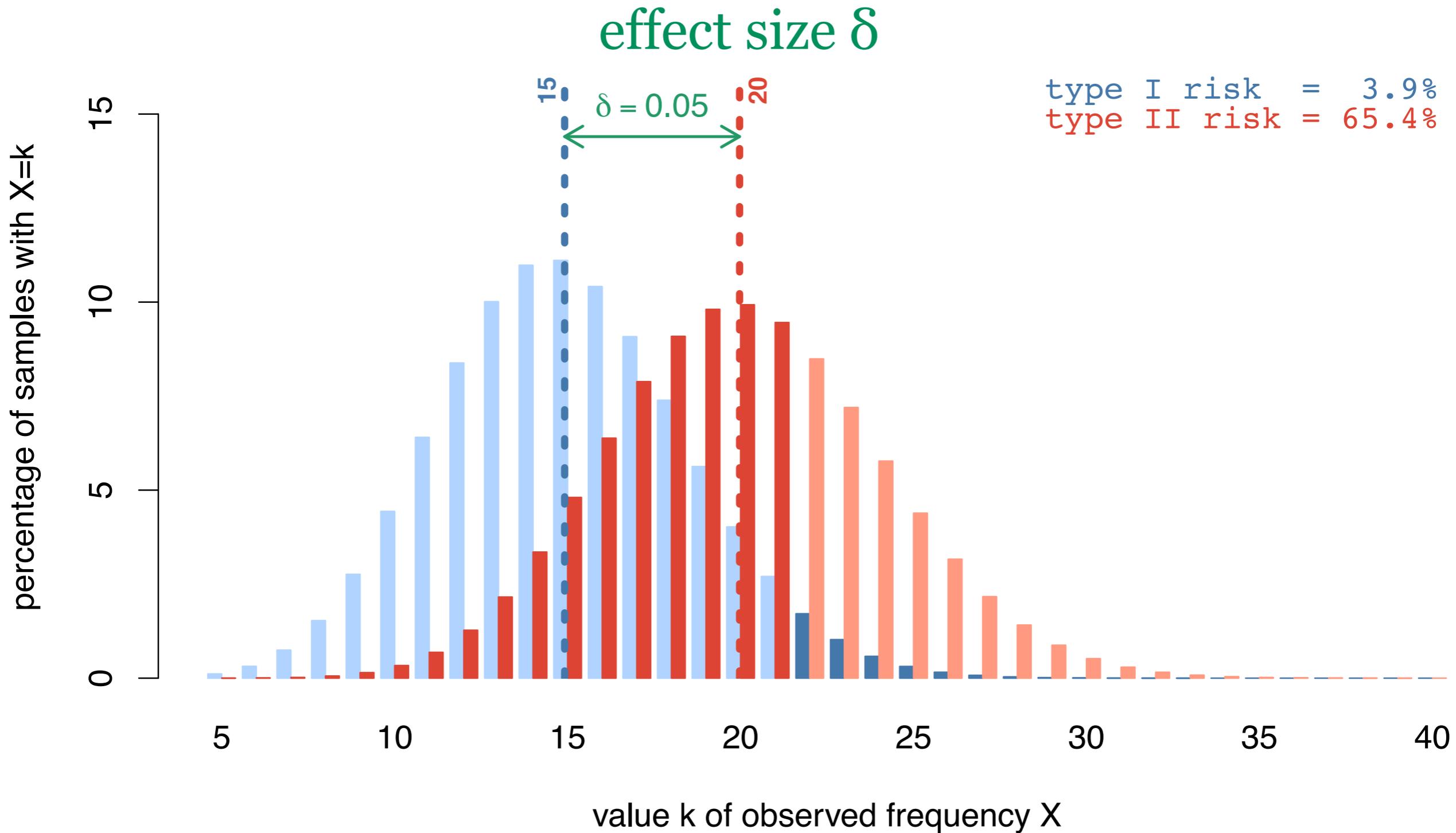
type I risk = 3.9%
type II risk = 21.1%



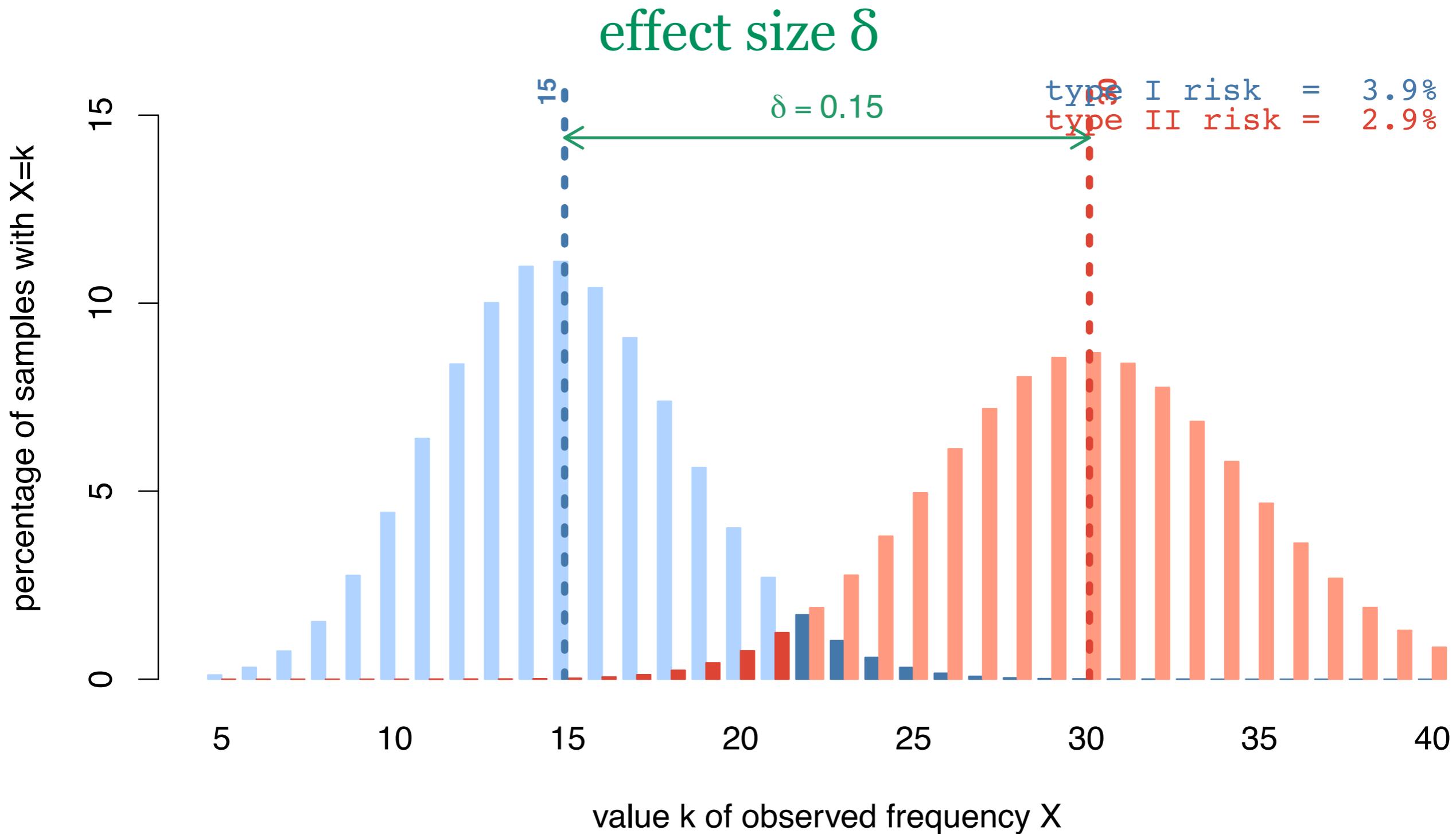
Type II errors & effect size



Type II errors & effect size

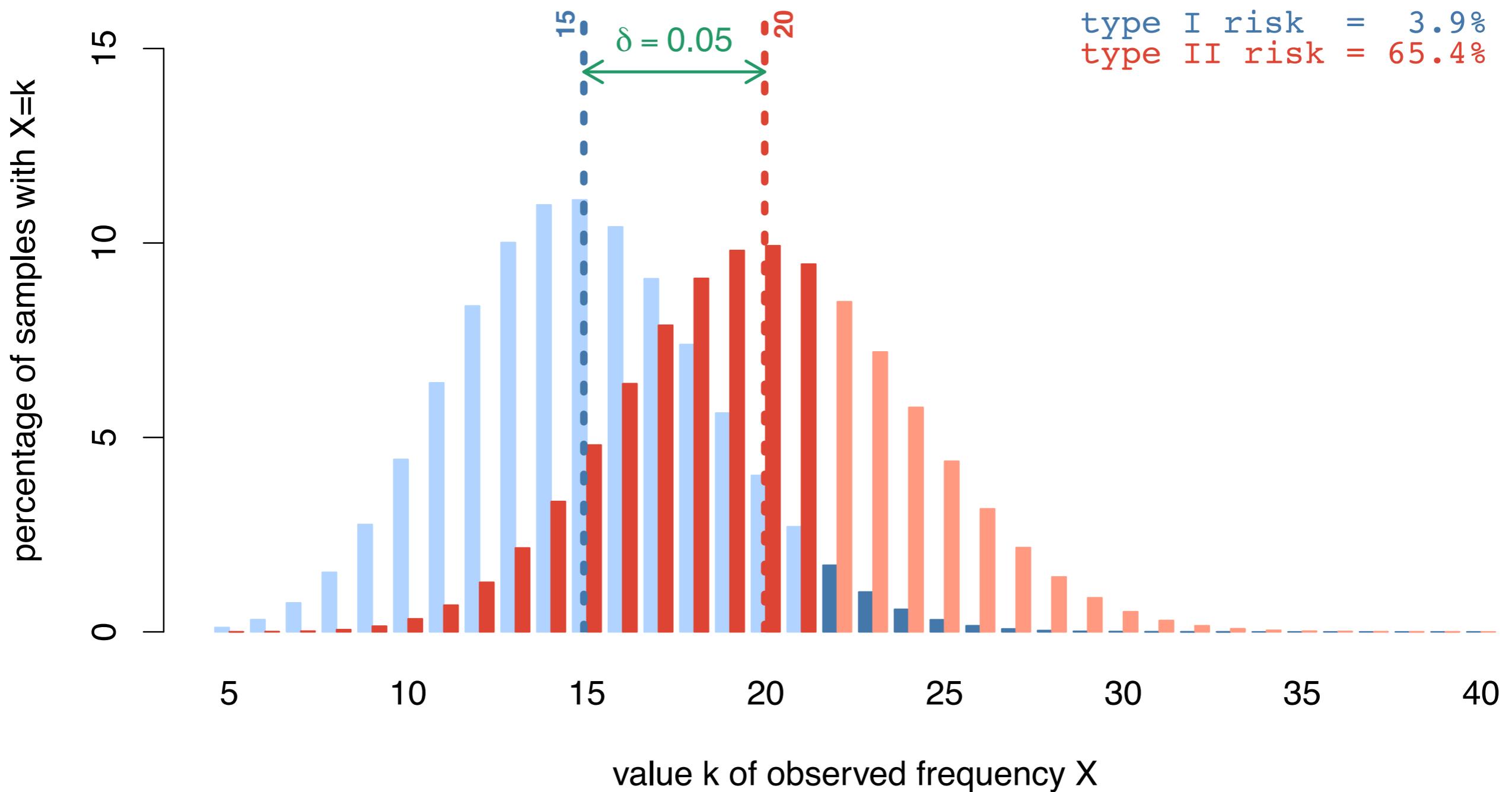


Type II errors & effect size



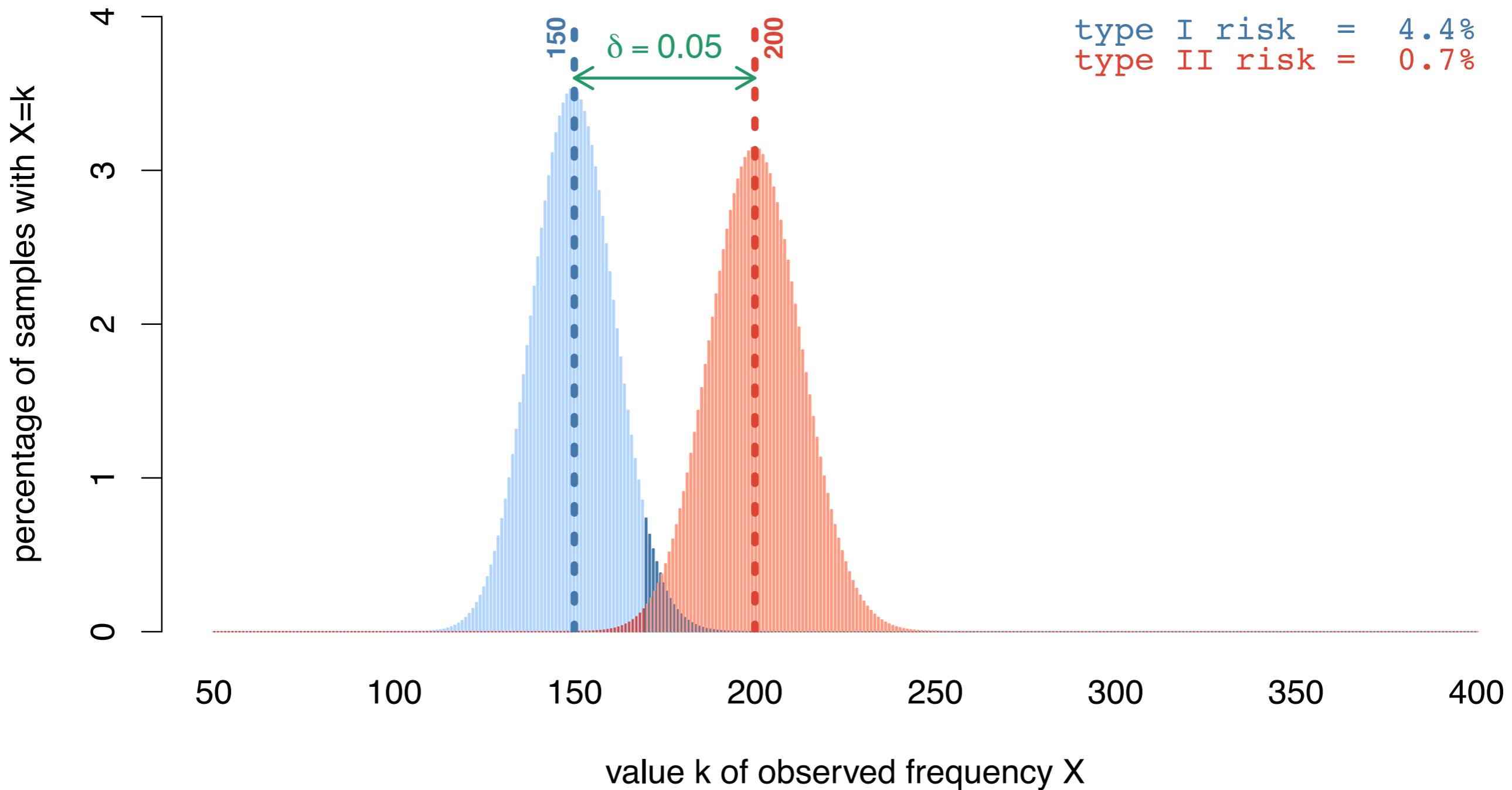
Type II errors & sample size

$n = 100$



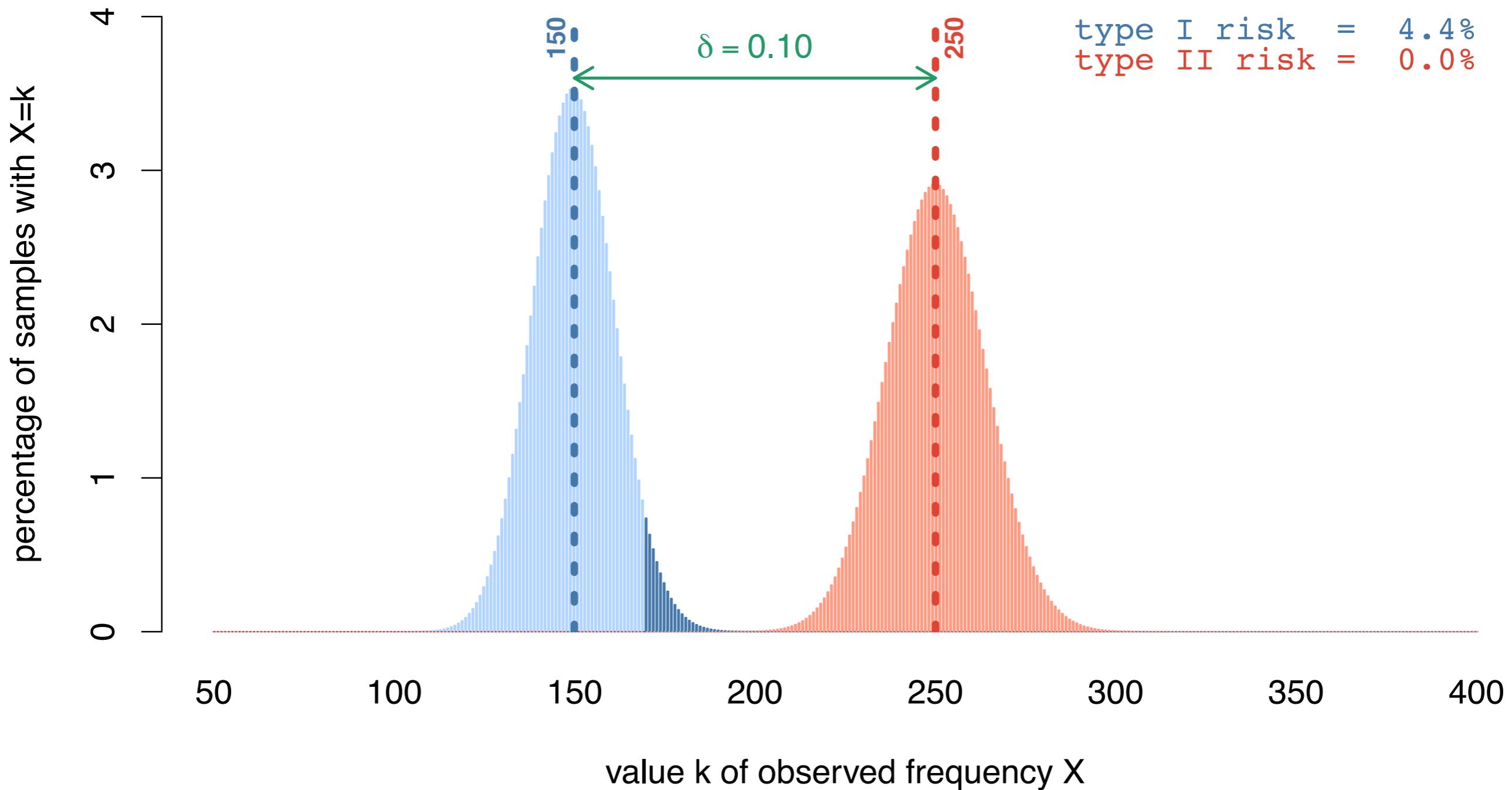
Type II errors & sample size

$n = 1000$



Type II errors & sample size

$n = 1000$



Power

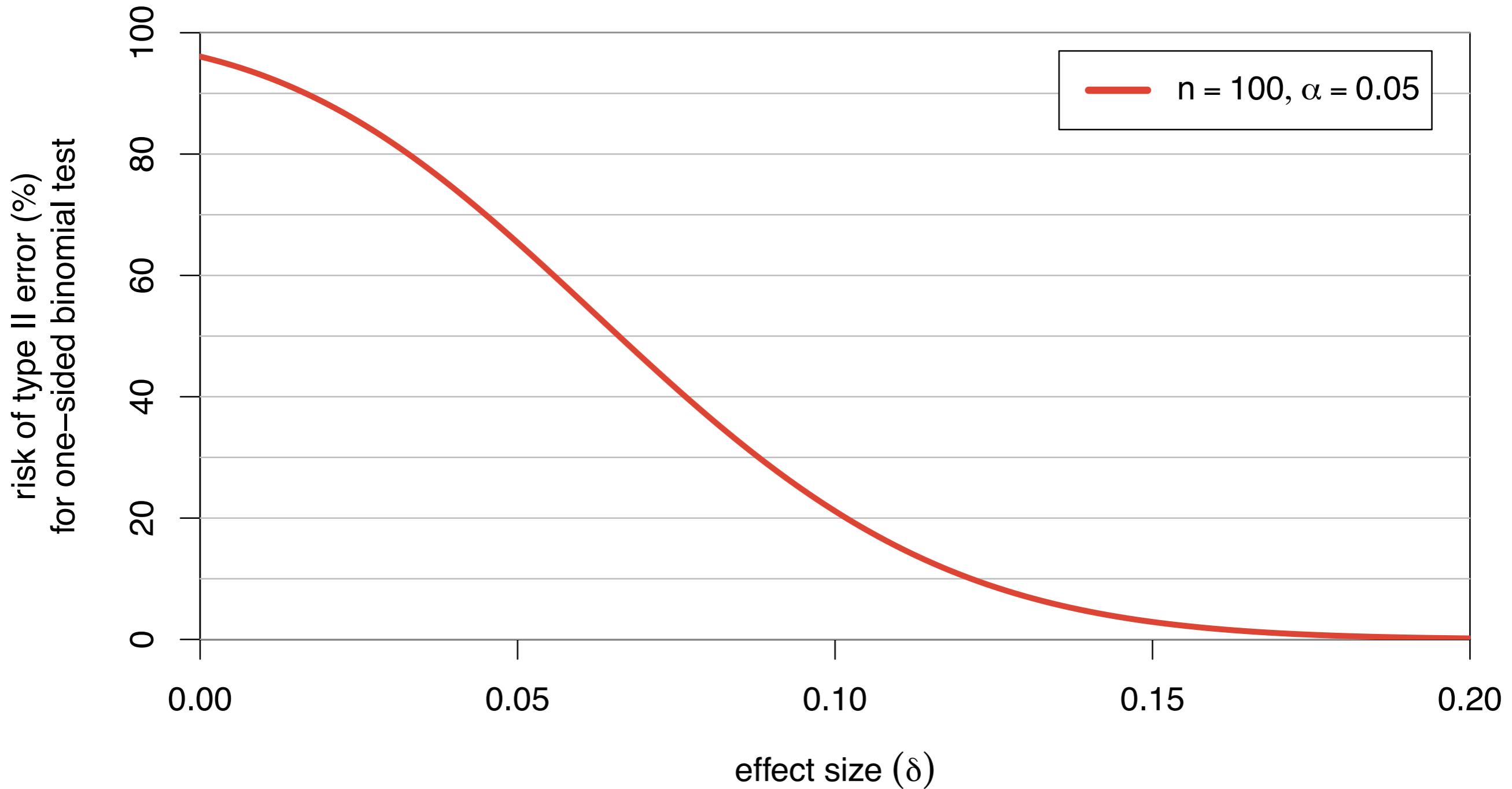
Power

- ◆ Type II error = failure to reject incorrect H_0
 - the larger the difference between H_0 and the true population proportion, the more likely it is that H_0 can be rejected based on a given sample
 - a **powerful** test has a low **type II error**
 - power analysis explores the relationship between effect size and risk of type II error

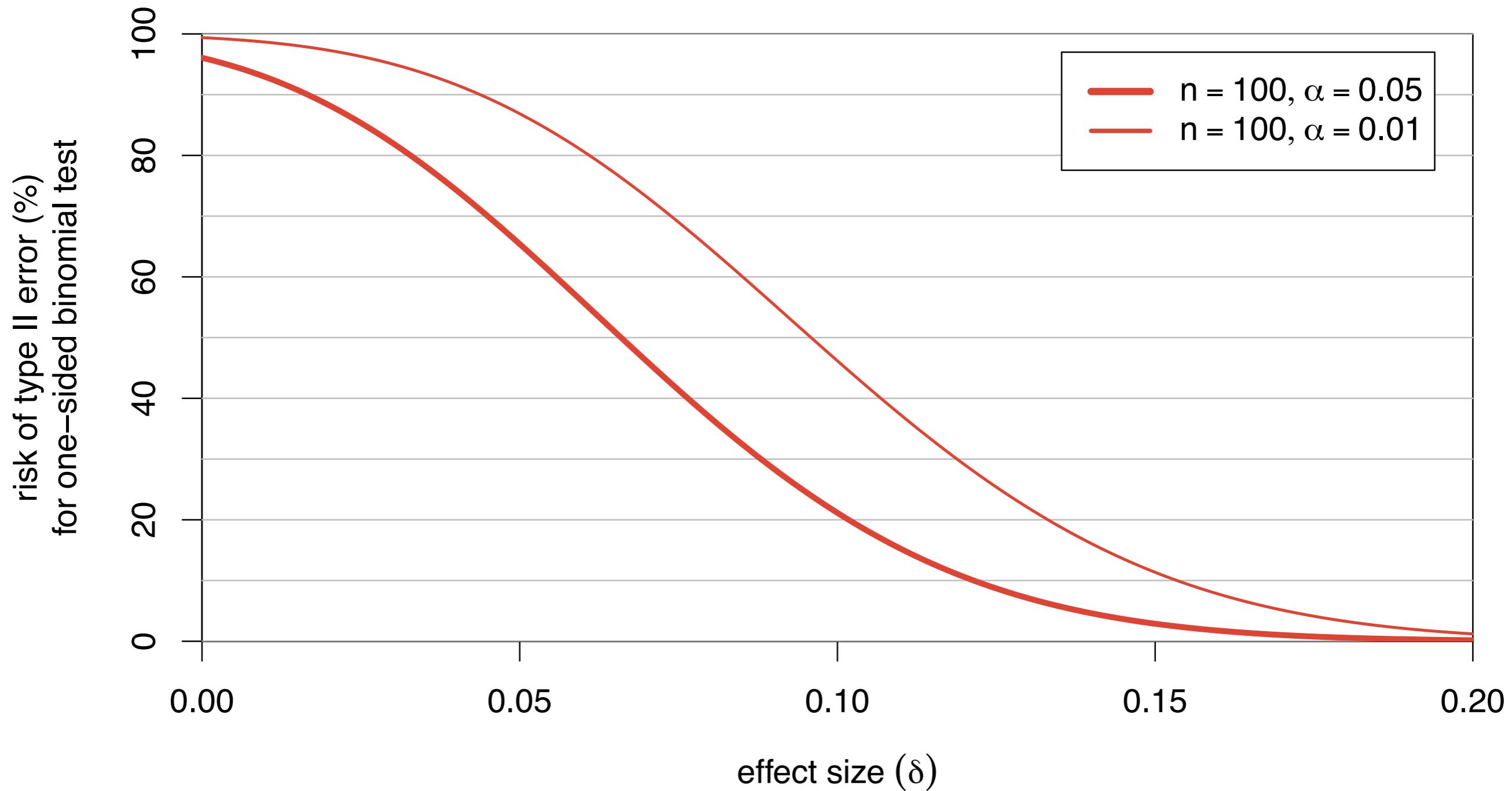
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 - power analysis explores the relationship between effect size and risk of type II error
- ◆ Key insight: larger sample = more power
 - relative sampling variation becomes smaller
 - power also depends on significance level

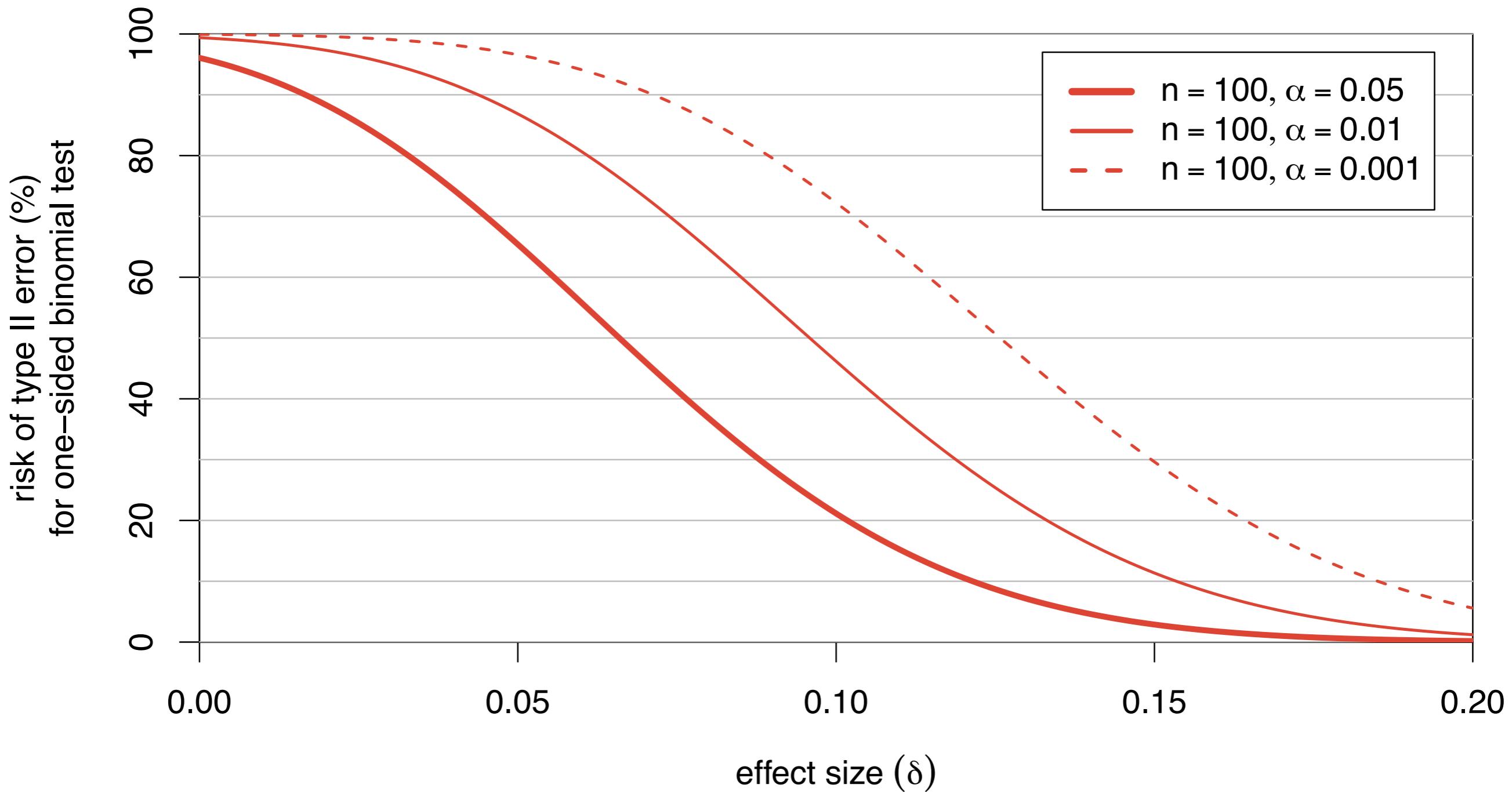
Power analysis for binomial test



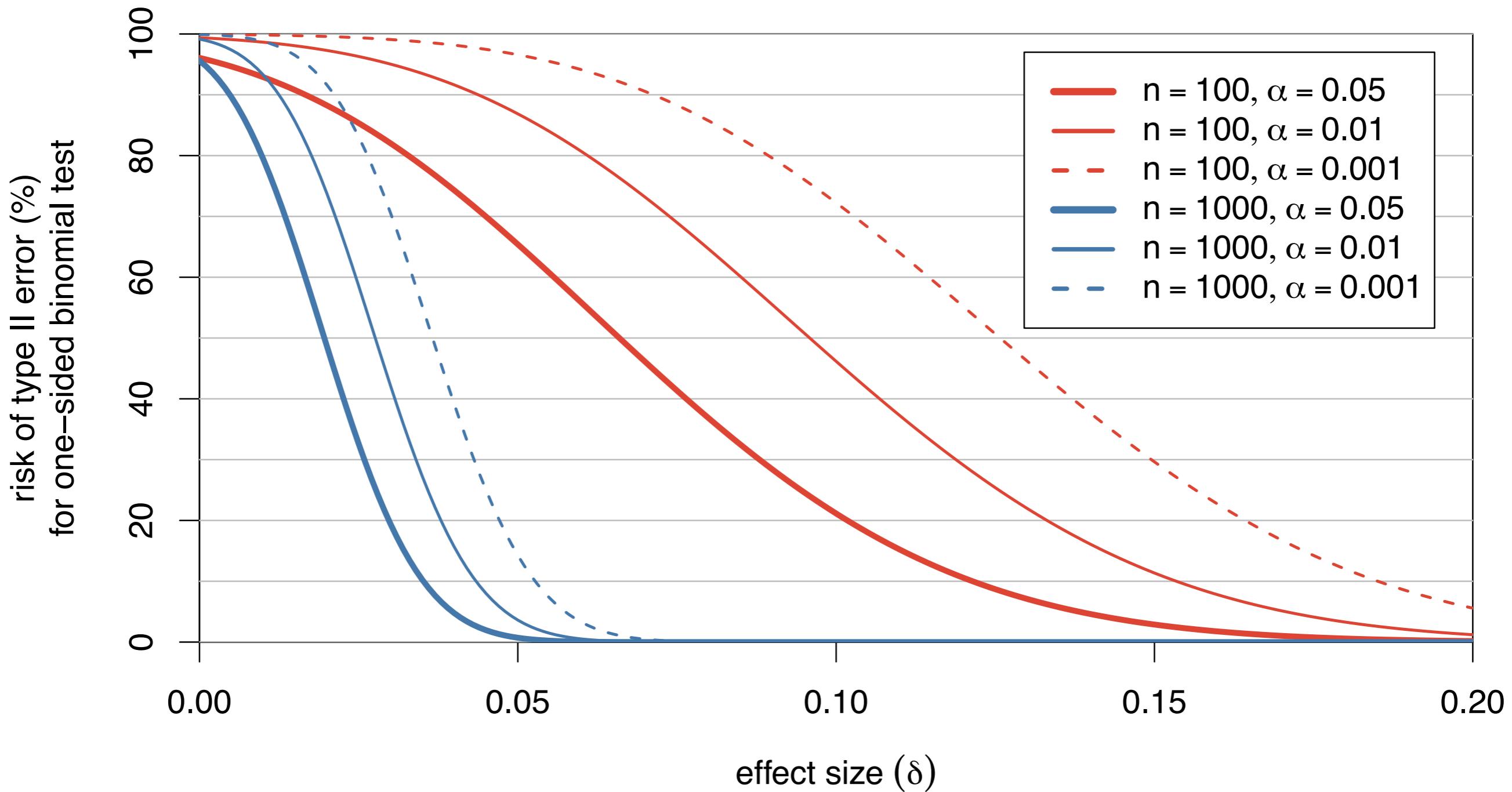
Power analysis for binomial test



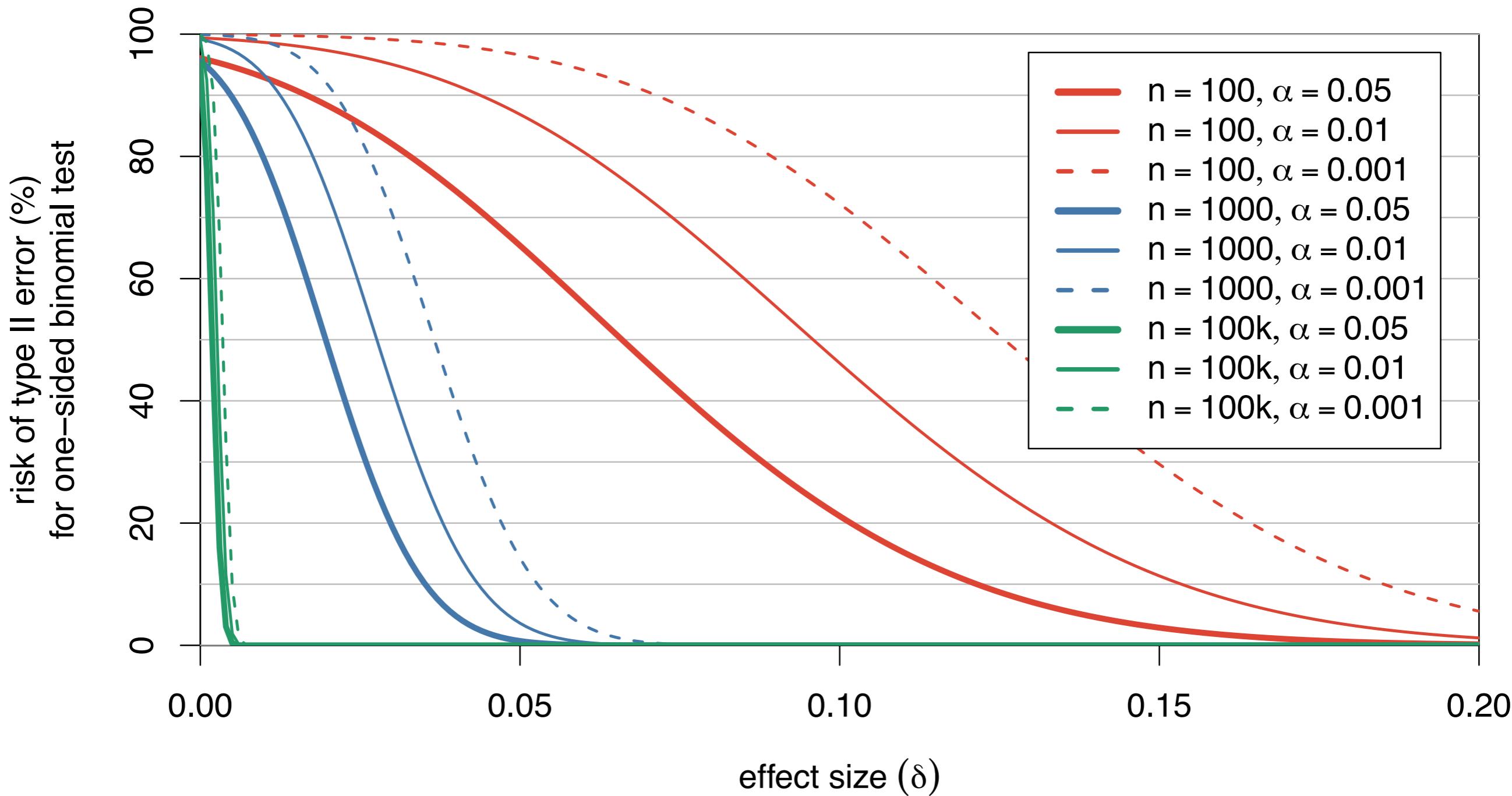
Power analysis for binomial test



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- ◆ Key factors determining the power of a test
 - **sample size** → more evidence = greater power
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- ◆ Influence of hypothesis test procedure
 - one-sided test more powerful than two-sided test
 - parametric tests more powerful than non-parametric
 - statisticians look for “uniformly most powerful” test
- ◆ Tests can become too powerful!
 - reject H_0 for 15.1% passives with $n = 1,000,000$

Parametric vs. non-parametric

- ◆ People often talk about parametric and non-parametric tests without precise definition
- ◆ Parametric tests make stronger assumptions
 - not just normality assuming (= Gaussian distribution)
 - binomial test: strong random sampling assumption
→ might be considered a parametric test in this sense!
- ◆ Parametric tests are usually more powerful
 - strong assumptions allow less conservative estimate of sampling variation → less evidence needed against H_0

Trade-offs in statistics

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- ◆ Inferential statistics is a trade-off between type I errors and type II errors
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 - i.e. between **significance** and **power**
- ◆ Significance level
 - determines trade-off point
 - low significance level $\alpha \rightarrow$ low power
- ◆ Conservative tests
 - put more weight on avoiding type I errors \rightarrow weaker
 - most non-parametric methods are conservative

Confidence interval

Confidence interval

- ◆ We now know how to test a null hypothesis H_0 , rejecting it only if there is sufficient evidence
- ◆ But what if we do not have an obvious null hypothesis to start with?
 - this is typically the case in (computational) linguistics

Confidence interval

- ◆ We now know how to test a null hypothesis H_0 , rejecting it only if there is sufficient evidence
- ◆ But what if we do not have an obvious null hypothesis to start with?
 - this is typically the case in (computational) linguistics
- ◆ We can estimate the true population proportion from the sample data (relative frequency)
 - sampling variation → range of plausible values
 - such a **confidence interval** can be constructed by inverting hypothesis tests (e.g. binomial test)

Confidence interval

observed data:

$$k = 190 \ / \ n = 1000$$

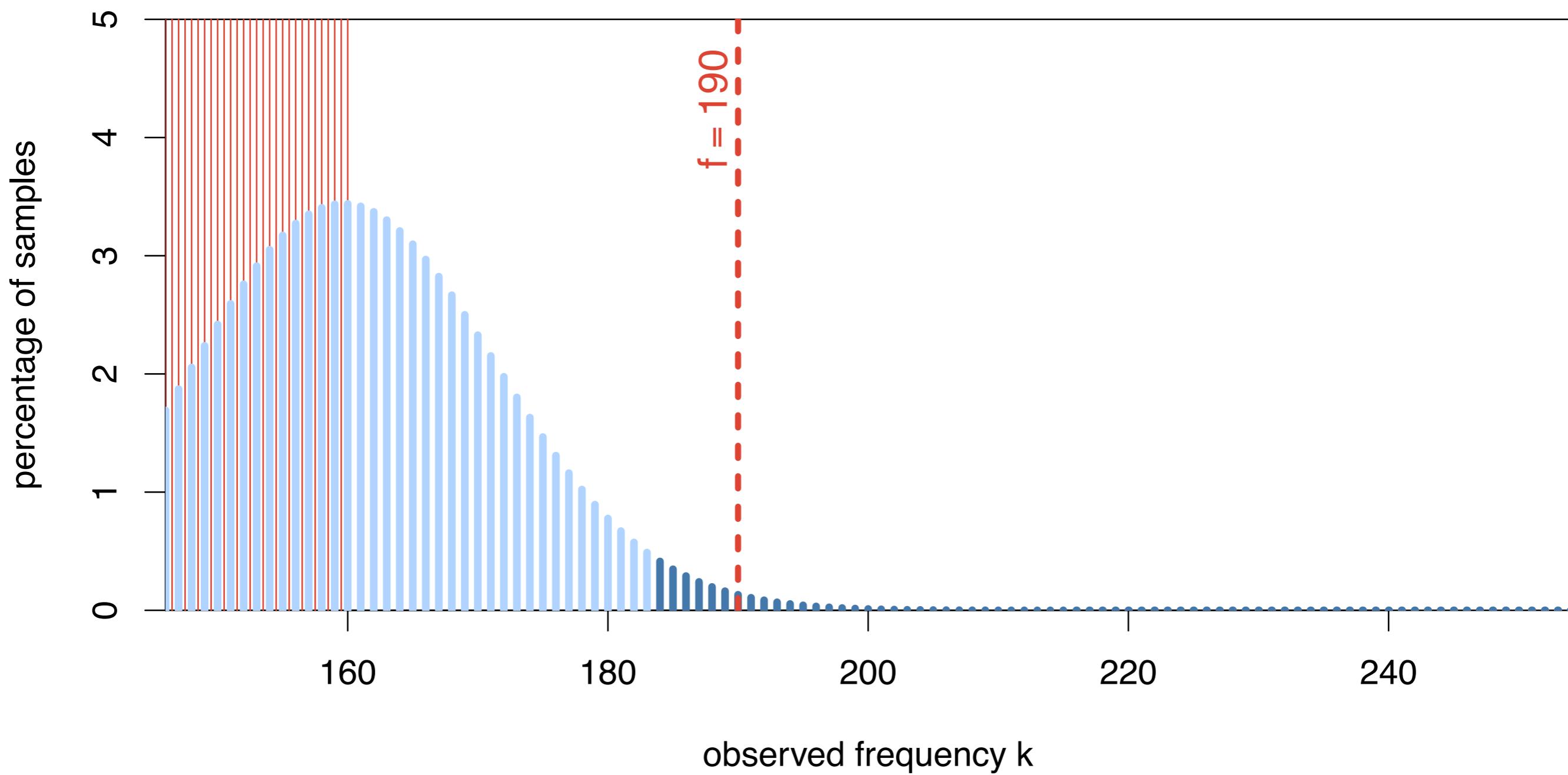
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0 : \mu = 16\% \rightarrow \text{rejected}$



Confidence interval

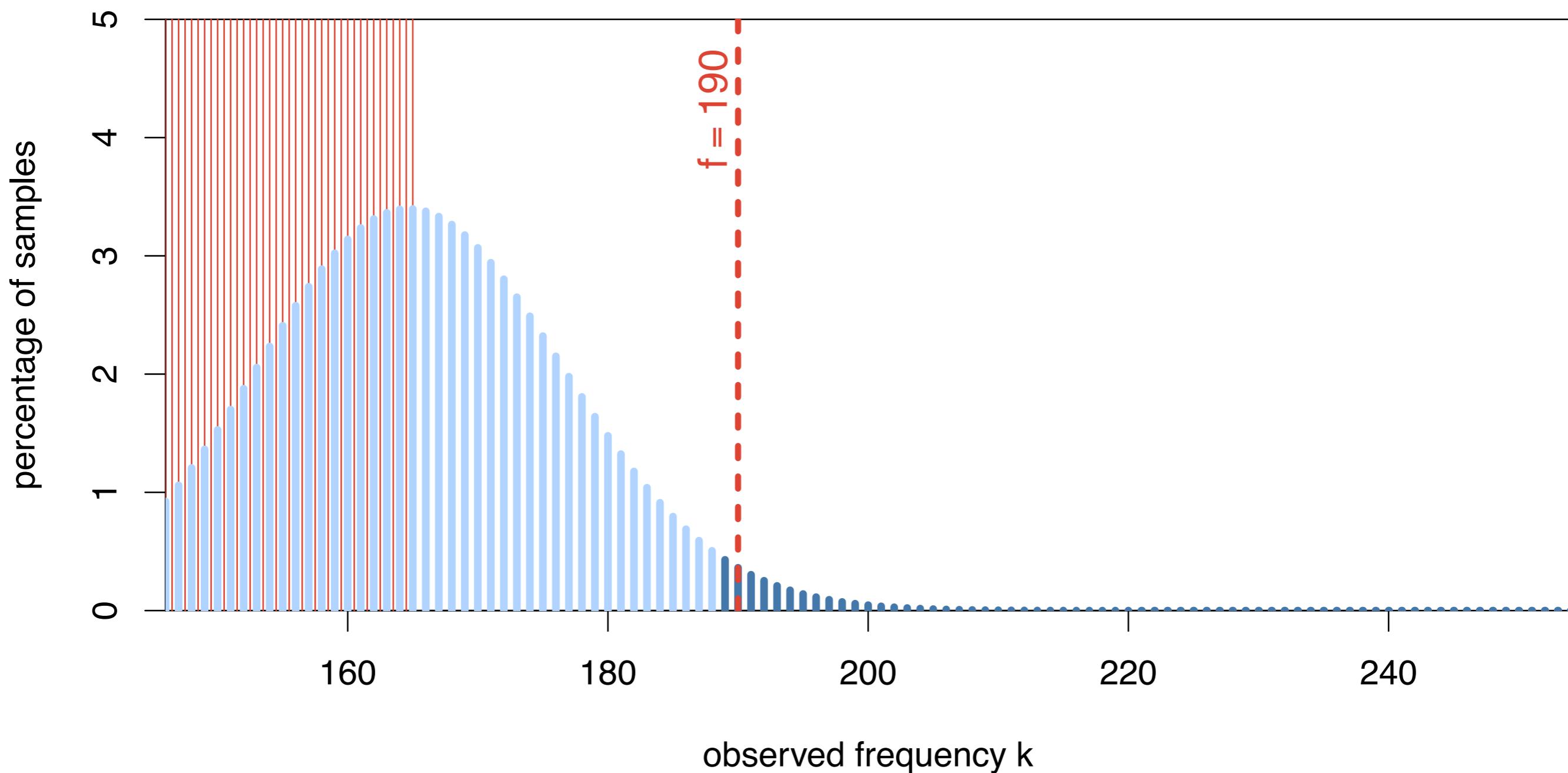
observed data:

$$k = 190 / n = 1000$$

95% confidence

$$p < .05 = \alpha$$

$H_0: \mu = 16.5\% \rightarrow \text{rejected}$



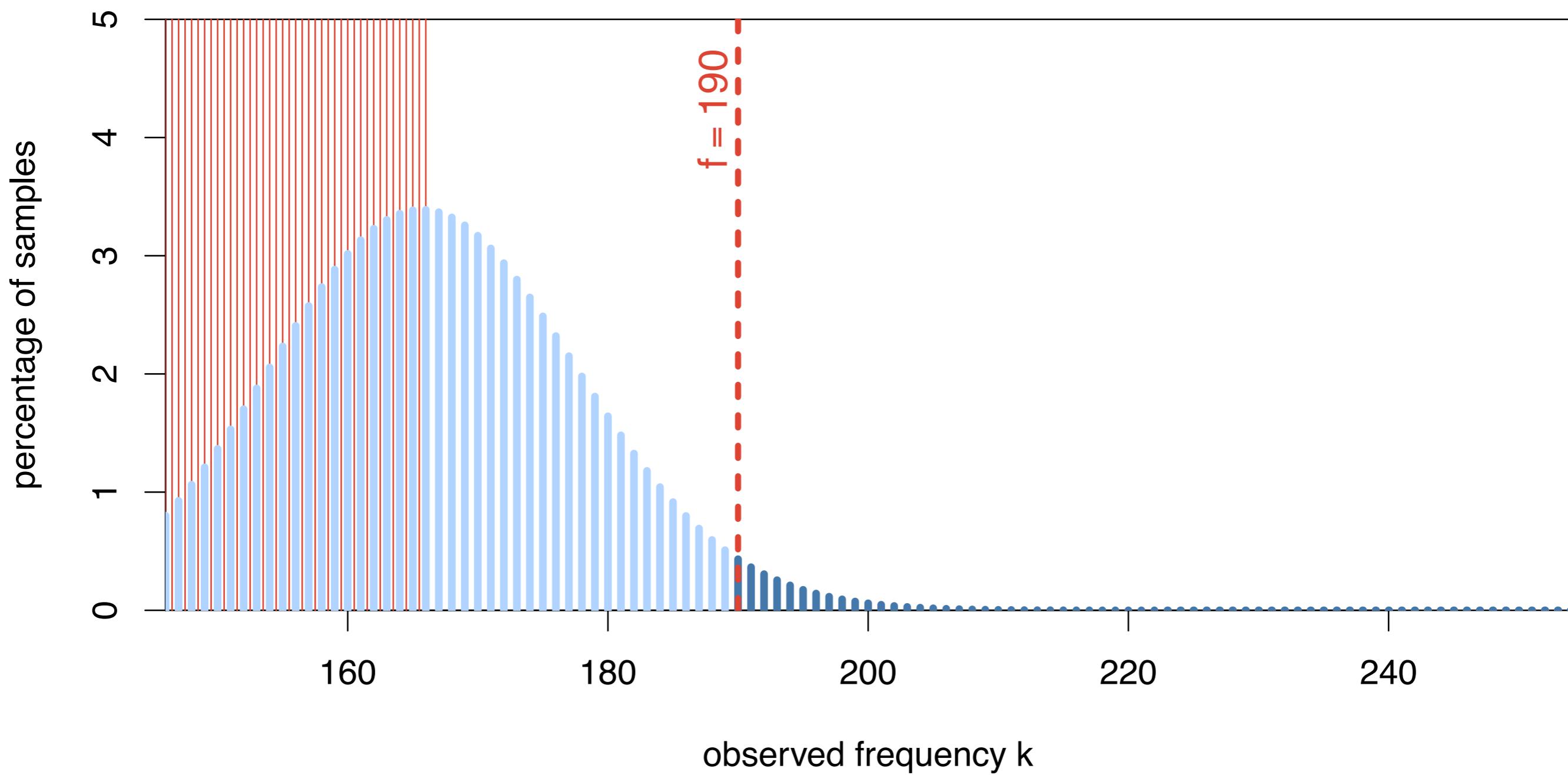
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0: \mu = 16.6\% \rightarrow \text{rejected}$



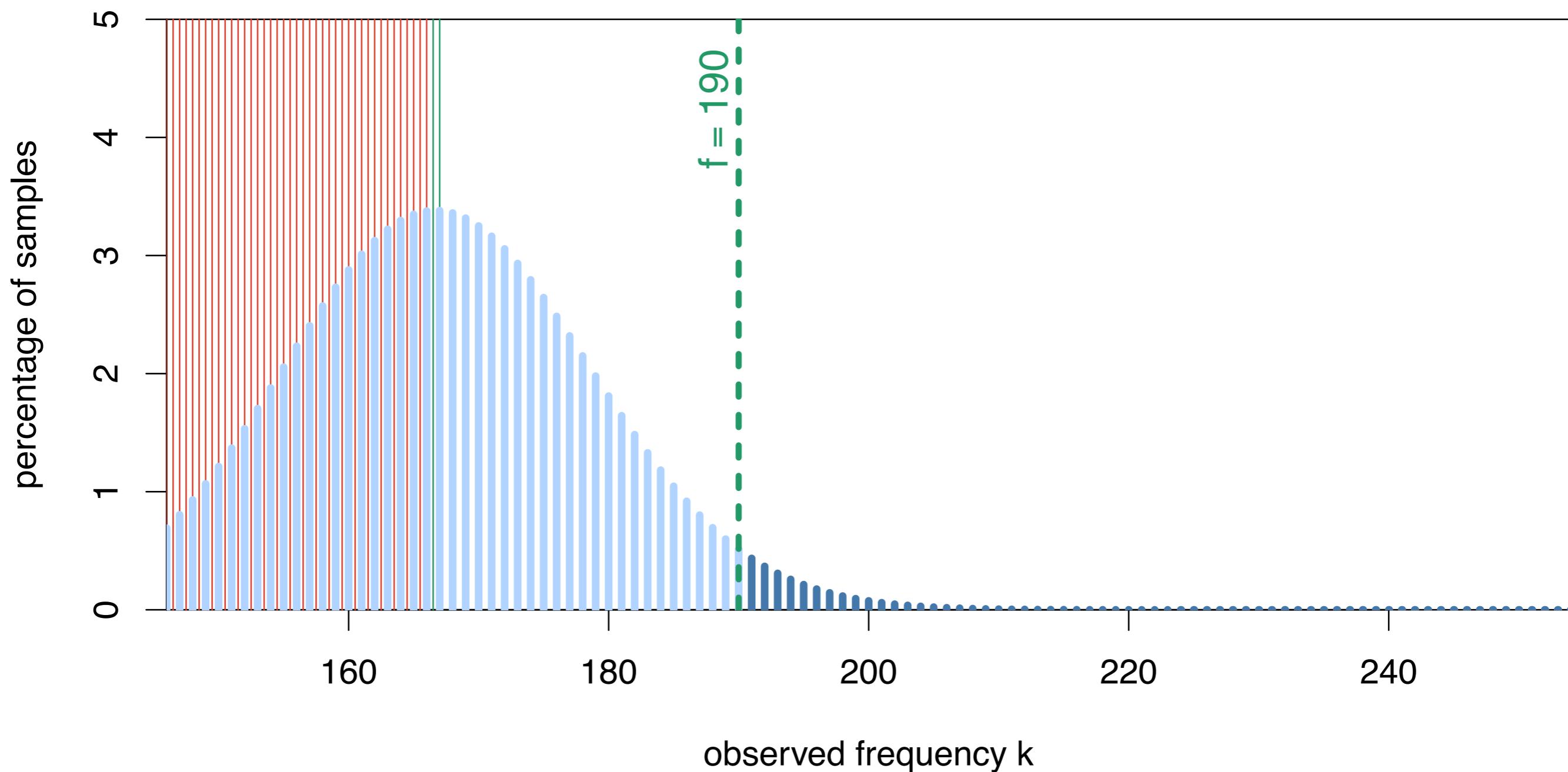
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$$H_0: \mu = 16.7\% \rightarrow \text{plausible}$$



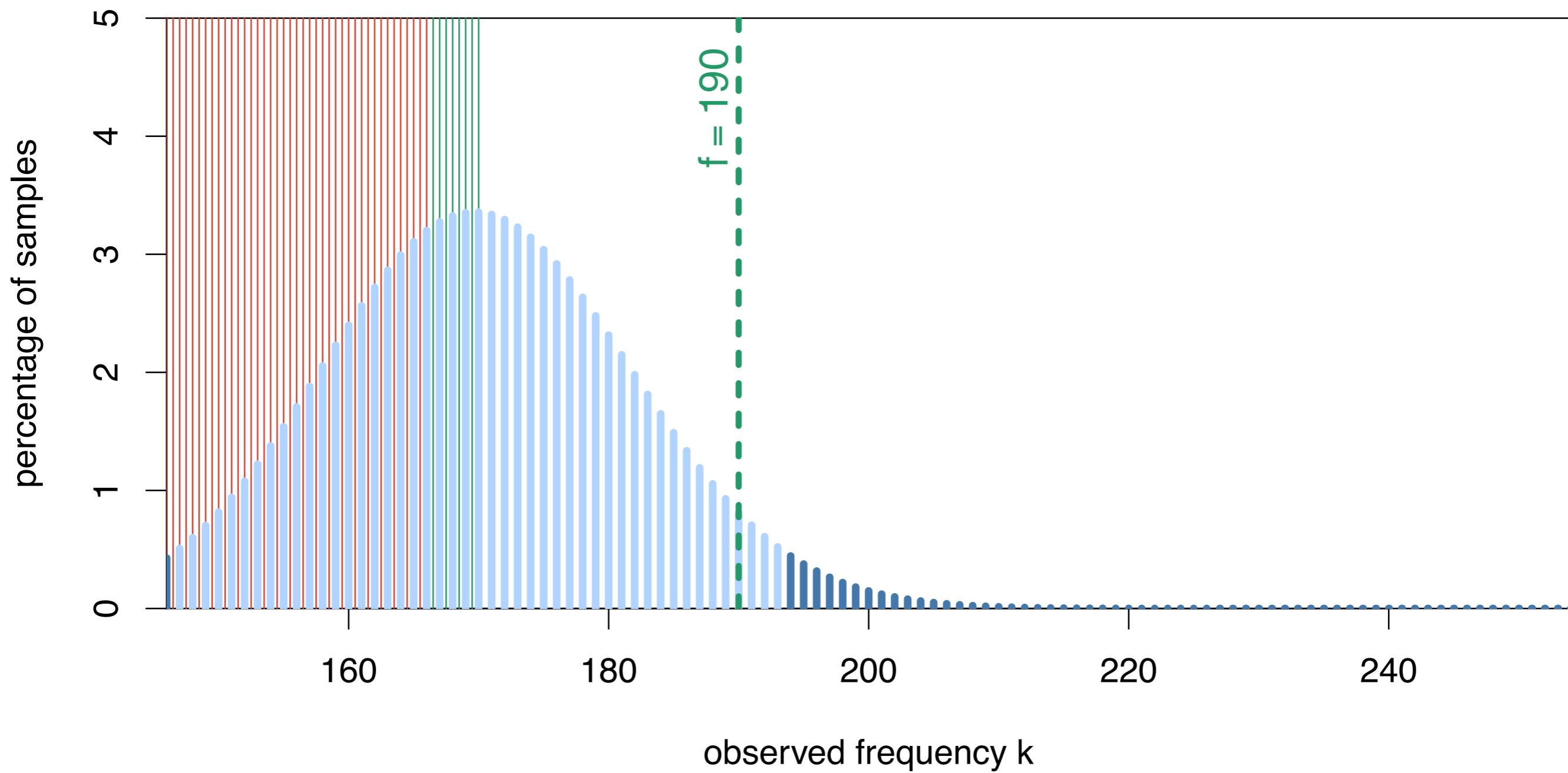
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0: \mu = 17\% \rightarrow \text{plausible}$



Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0: \mu = 18\% \rightarrow \text{plausible}$

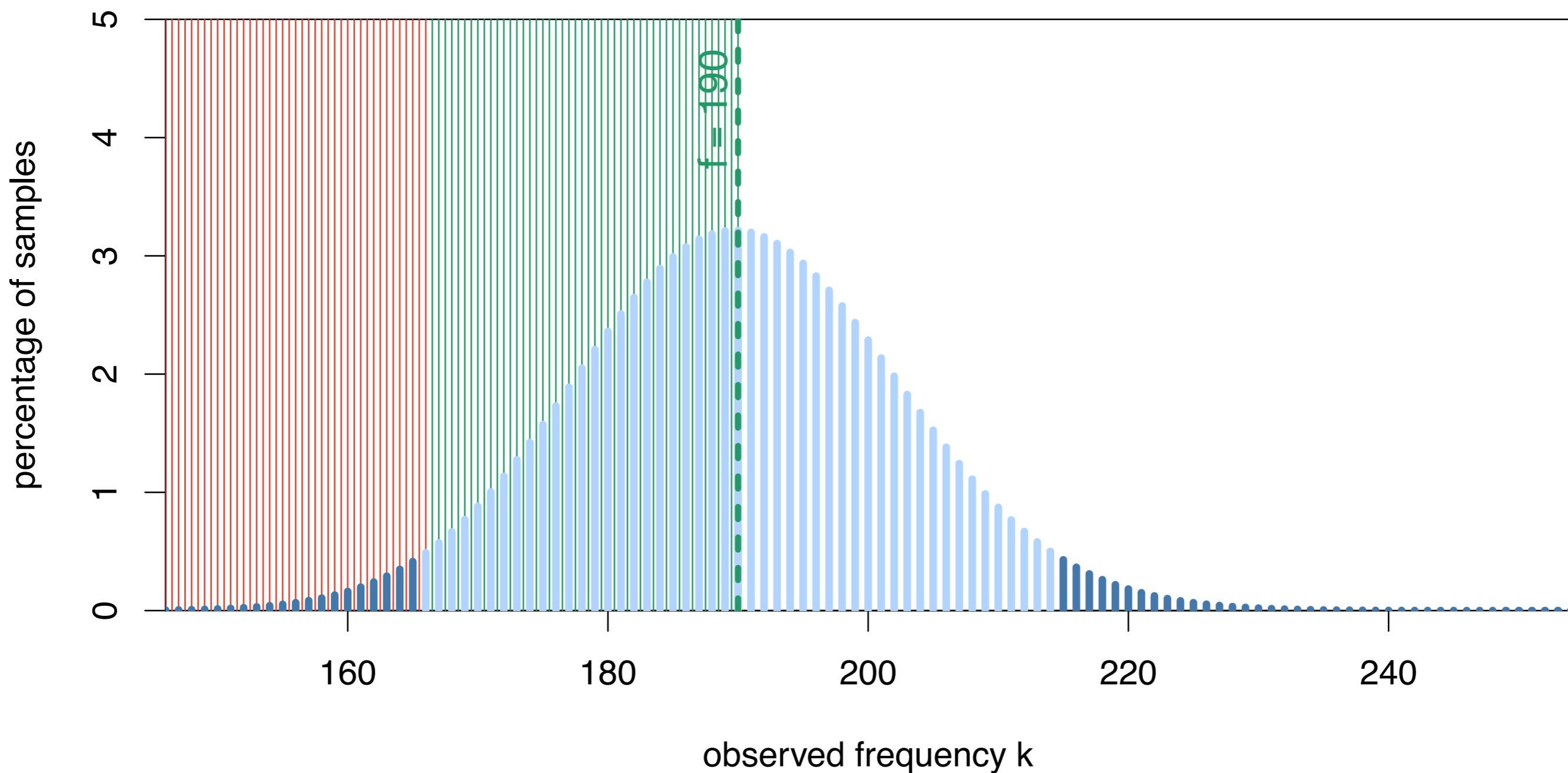
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0: \mu = 19\% \rightarrow \text{plausible}$



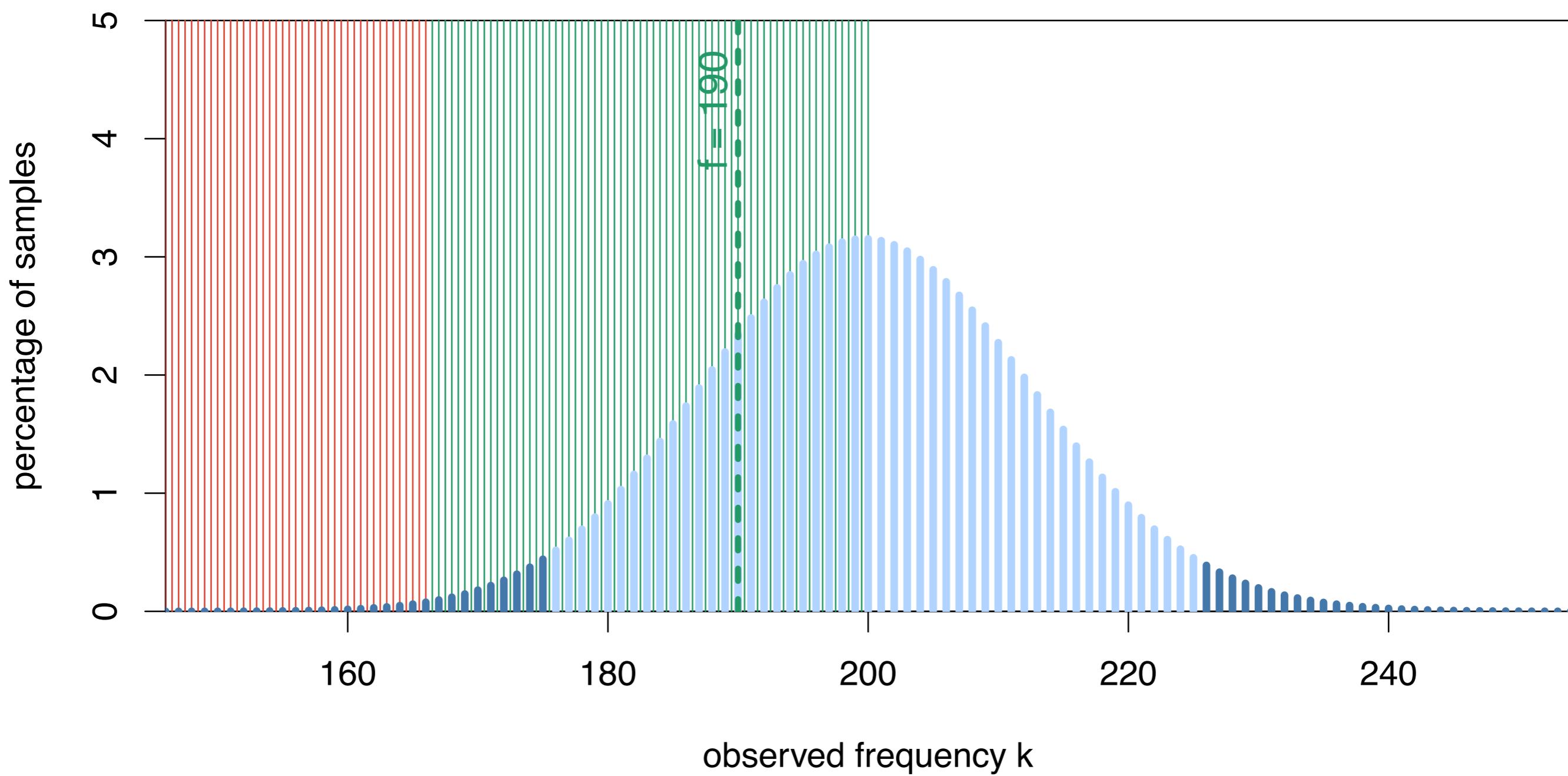
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0: \mu = 20\% \rightarrow \text{plausible}$



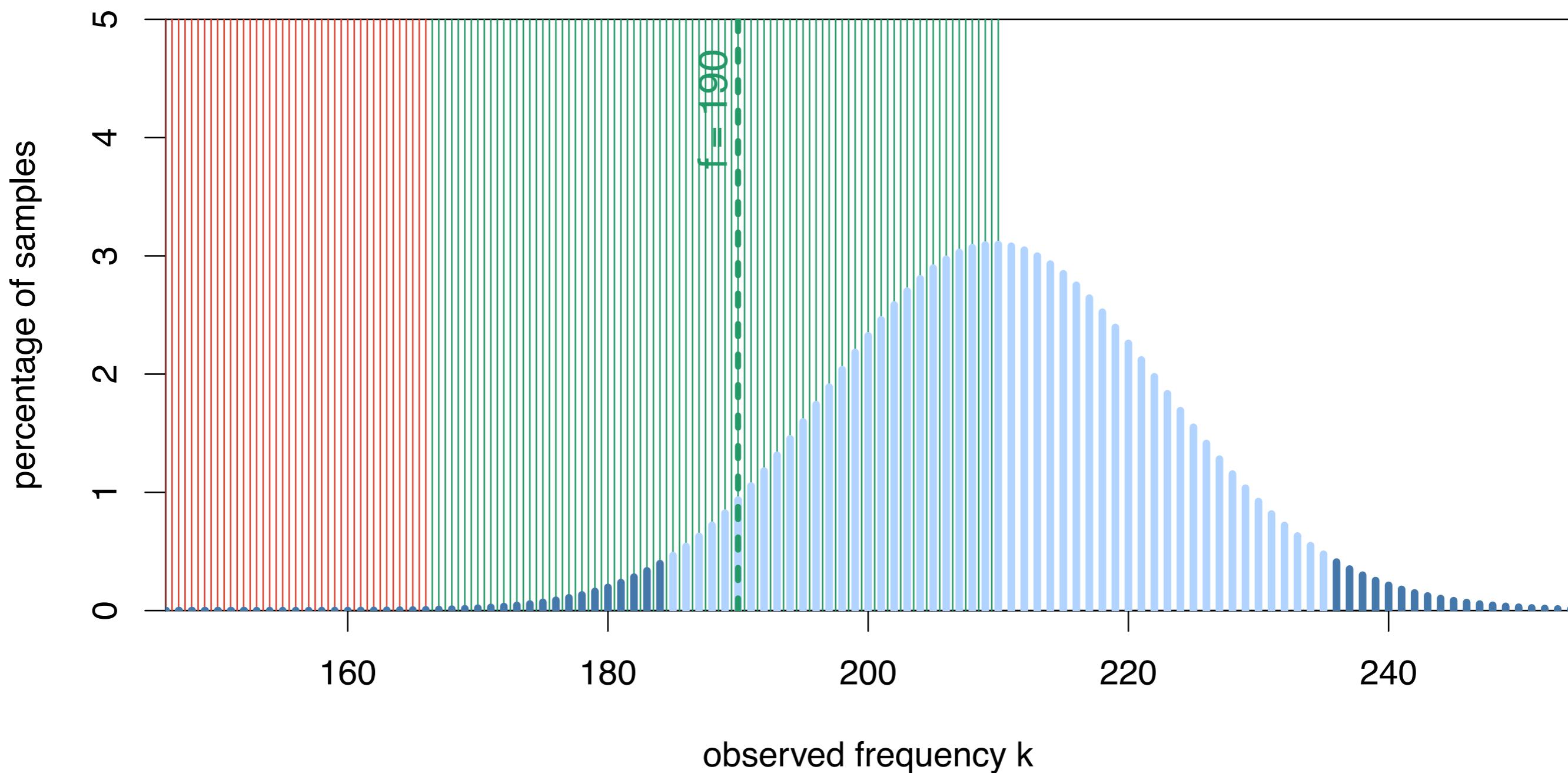
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0: \mu = 21\% \rightarrow \text{plausible}$



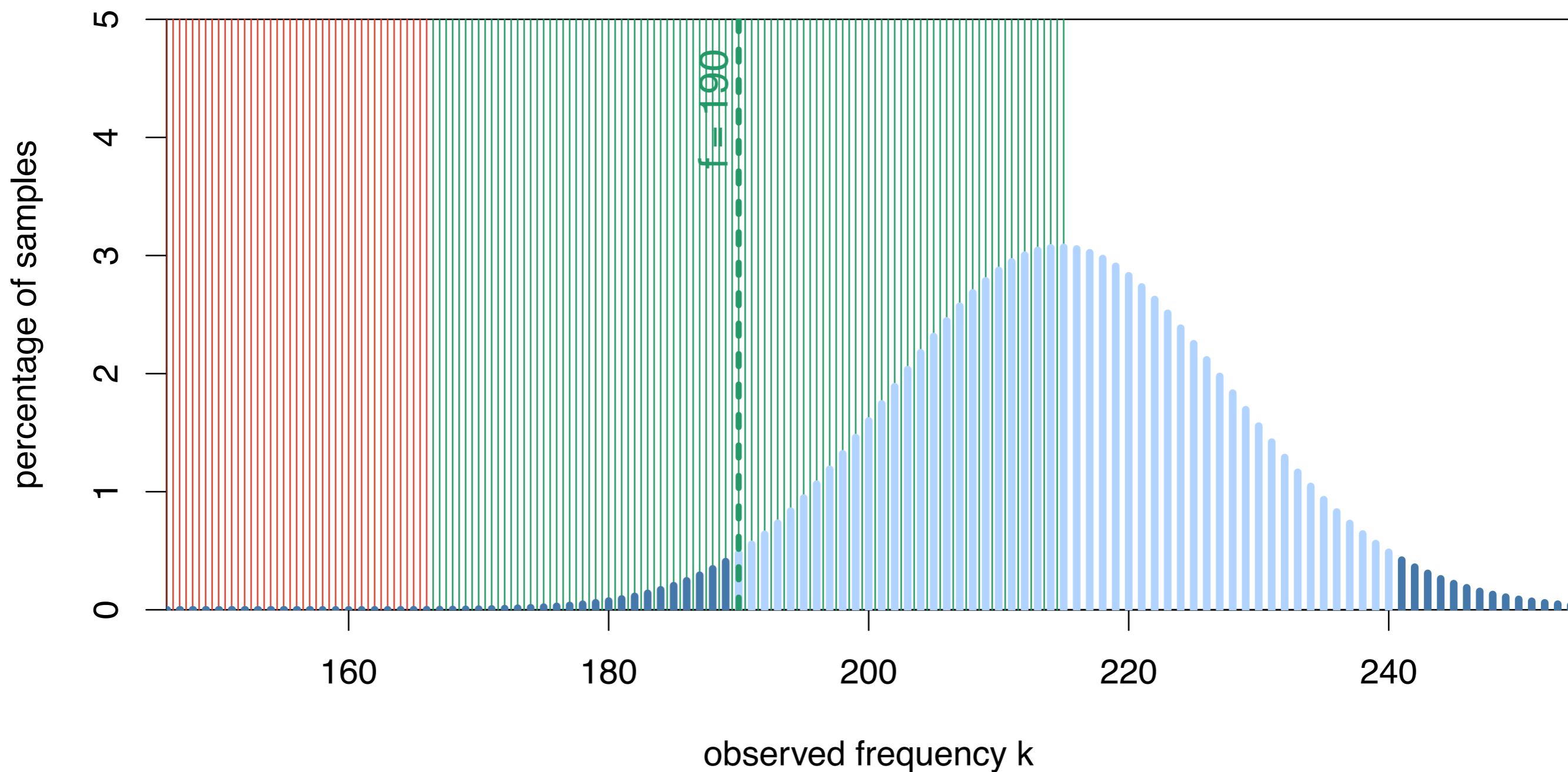
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
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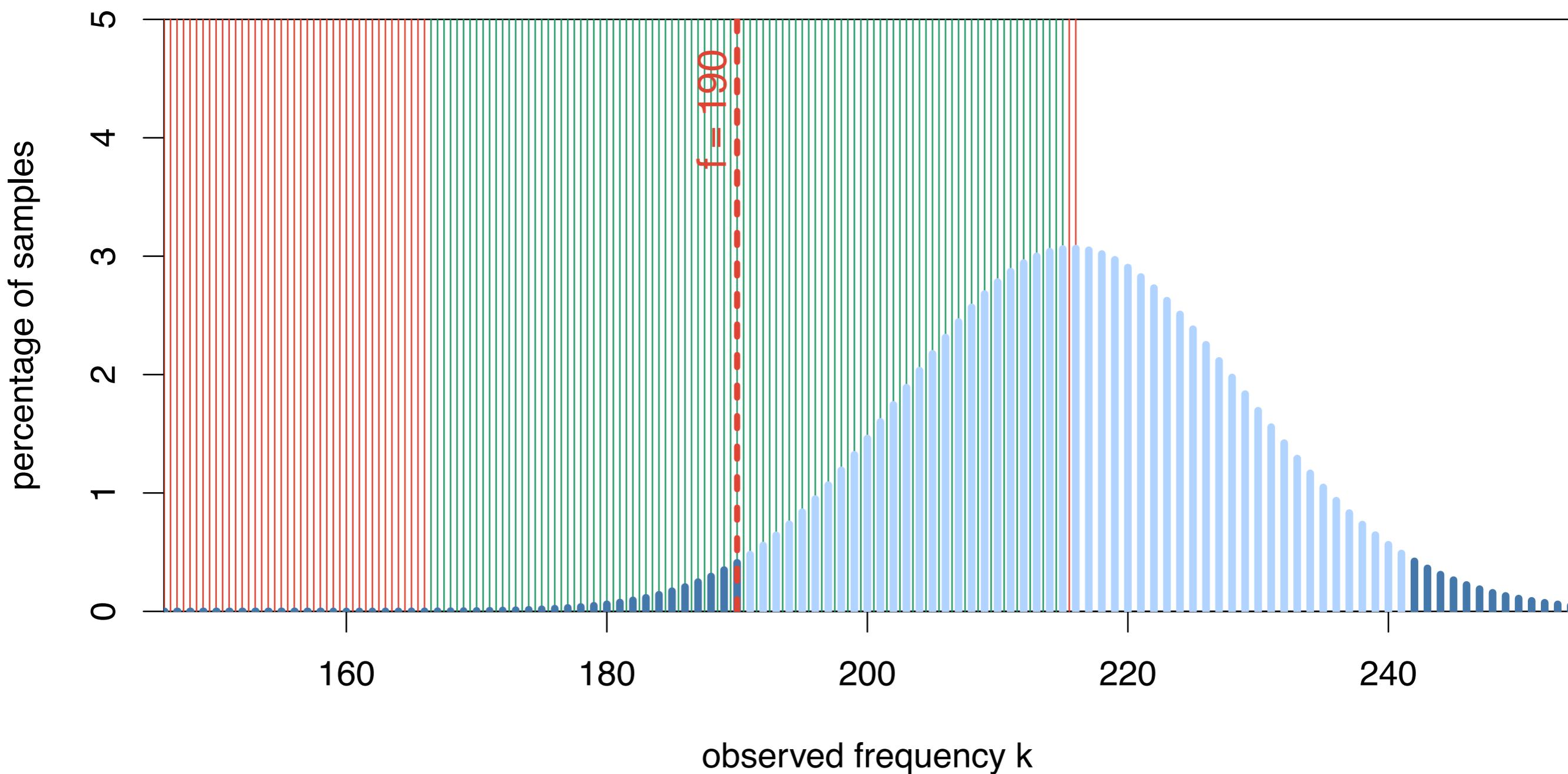
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0: \mu = 21.6\% \rightarrow \text{rejected}$



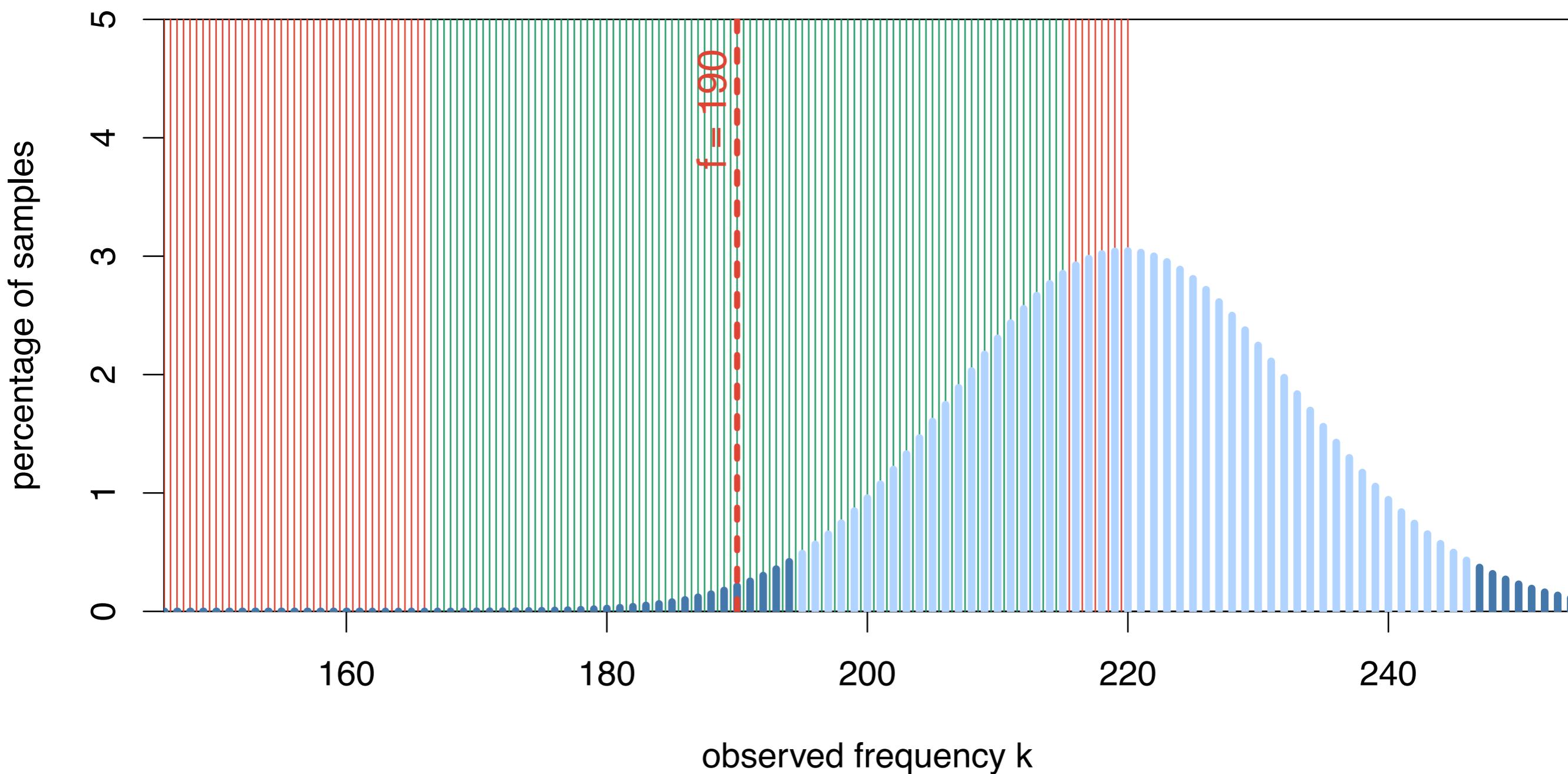
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0 : \mu = 22\% \rightarrow \text{rejected}$



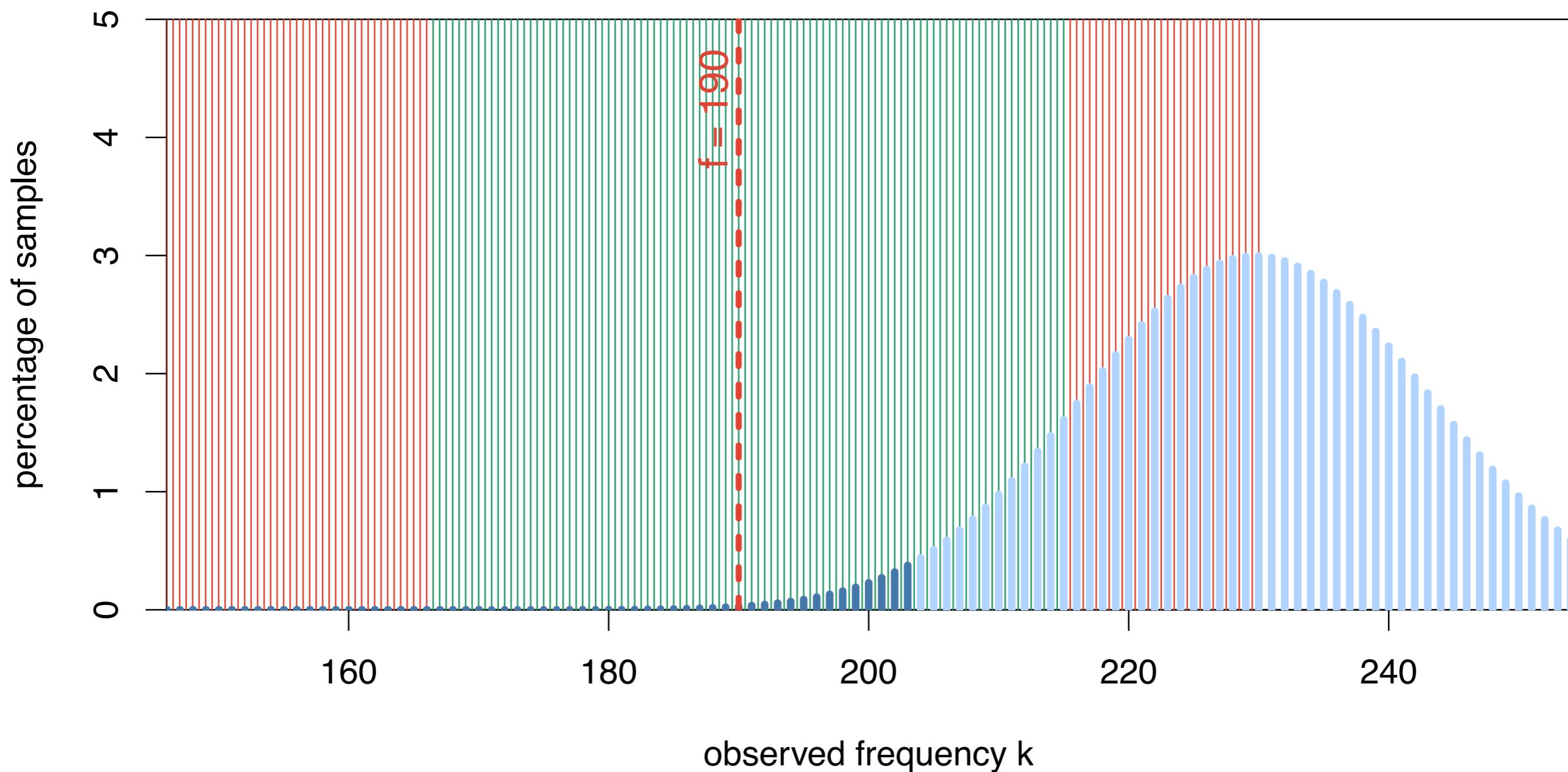
Confidence interval

observed data:

$$k = 190 / n = 1000$$

95% confidence
 $p < .05 = \alpha$

$H_0 : \mu = 23\% \rightarrow \text{rejected}$



Confidence interval

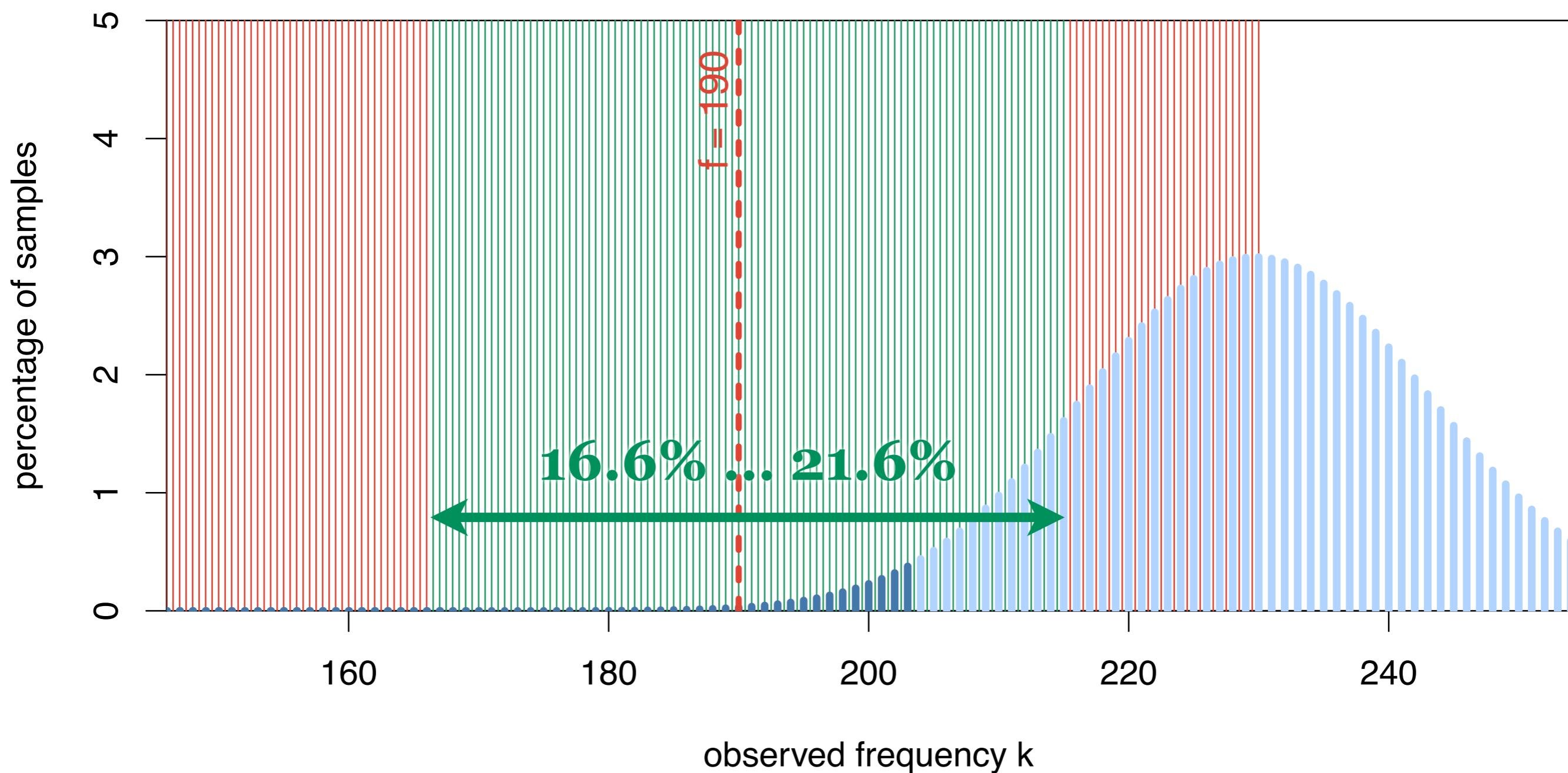
observed data:

$$k = 190 / n = 1000$$

95% confidence

$$p < .05 = \alpha$$

$H_0 : \mu = 23\% \rightarrow \text{rejected}$



Confidence intervals

- ◆ Confidence interval = range of plausible values for true population proportion
 - H_0 rejected by test iff π_0 is outside confidence interval
- ◆ Size of confidence interval depends on power of the test (i.e. sample size and significance level)

	$n = 100$ $k = 19$	$n = 1,000$ $k = 190$	$n = 10,000$ $k = 1,900$
$\alpha = .05$	11.8% ... 28.1%	16.6% ... 21.6%	18.2% ... 19.8%
$\alpha = .01$	10.1% ... 31.0%	15.9% ... 22.4%	18.0% ... 20.0%
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I'm cheating
here a tiny little
bit (not always
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Confidence intervals in R

- ◆ Most hypothesis tests in R also compute a confidence interval (including `binom.test()`)
 - omit H_0 if only interested in confidence interval
- ◆ Significance level of underlying hypothesis test is controlled by `conf.level` parameter
 - expressed as confidence, e.g. `conf.level = .95` for significance level $\alpha = .05$, i.e. 95% confidence
- ◆ Can also compute one-sided confidence interval
 - controlled by `alternative` parameter
 - two-sided confidence intervals strongly recommended

Confidence intervals in R

```
> binom.test(190, 1000, conf.level=.99)
```

Exact binomial test

data: 190 and 1000

number of successes = 190, number of trials = 1000, p-value < 2.2e-16

alternative hypothesis: true probability of success is not equal to 0.5

99 percent confidence interval:

0.1590920 0.2239133

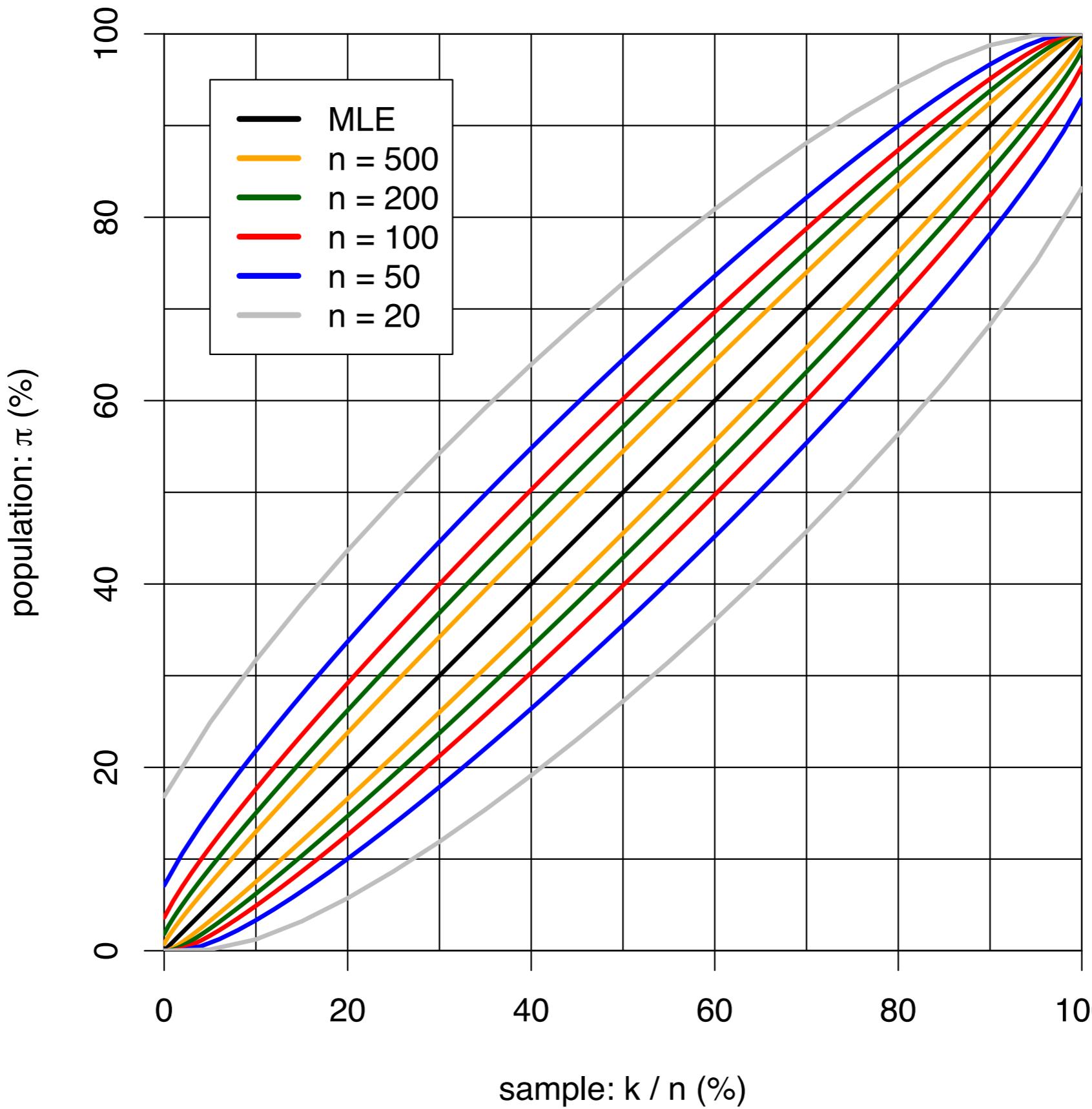
sample estimates:

probability of success

0.19

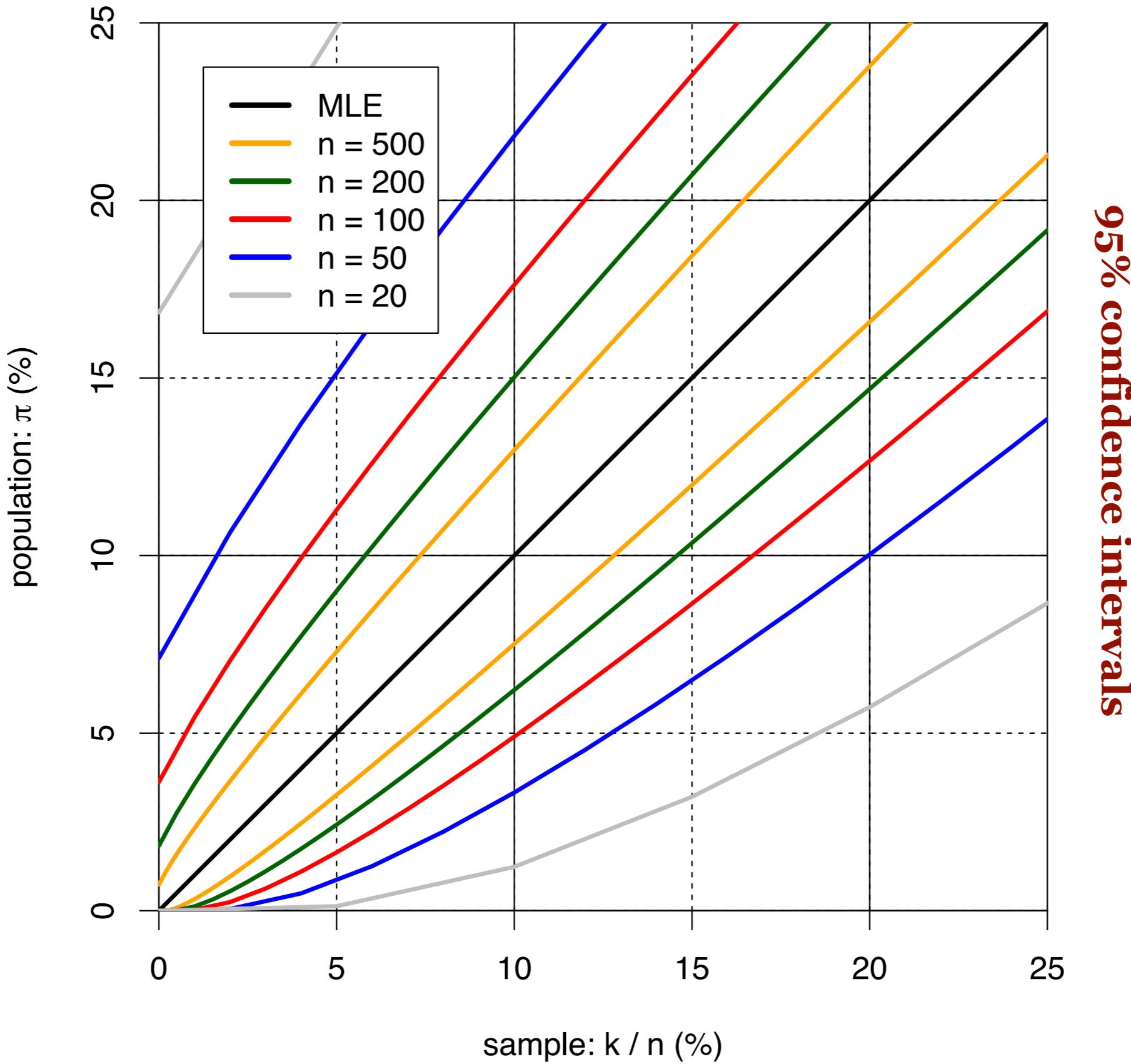
Choosing sample size

Choosing sample size



95% confidence intervals

Choosing sample size



Using R to choose sample size

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 - requires calculation of large number of hypothetical confidence intervals
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Using R to choose sample size

- ◆ Call `binom.test()` with hypothetical values
- ◆ Plots on previous slides also created with R
 - requires calculation of large number of hypothetical confidence intervals
 - `binom.test()` is both inconvenient and inefficient
- ◆ The `corpora` package has a vectorised function
 - > `library(corpora)`
 - > `prop.cint(190, 1000, conf.level=.99)`
 - > `?prop.cint # “conf. intervals for proportions”`

Frequency comparison

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 - Does *meow* occur more often in the vicinity of *cat* than elsewhere in the text?
 - Do speakers prefer *I couldn't agree more* over alternative realisations such as *I agree completely*?
- ◆ Compare observed frequencies in two samples

Frequency comparison

$$H_0 : \pi_1 = \pi_2$$

Frequency comparison

- ◆ Null hypothesis for frequency comparison

$$H_0 : \pi_1 = \pi_2$$

- no assumptions about the precise value $\pi_1 = \pi_2 = \pi$

Frequency comparison

- ◆ Null hypothesis for frequency comparison

$$H_0 : \pi_1 = \pi_2$$

- no assumptions about the precise value $\pi_1 = \pi_2 = \pi$
- ◆ Observed data
 - target count k_i and sample size n_i for each sample i
 - e.g. $k_1 = 19 / n_1 = 100$ passives vs. $k_2 = 25 / n_2 = 200$

Frequency comparison

- ◆ Null hypothesis for frequency comparison

$$H_0 : \pi_1 = \pi_2$$

- no assumptions about the precise value $\pi_1 = \pi_2 = \pi$
- ◆ Observed data
 - target count k_i and sample size n_i for each sample i
 - e.g. $k_1 = 19 / n_1 = 100$ passives vs. $k_2 = 25 / n_2 = 200$
- ◆ Effect size: difference of proportions
 - effect size $\delta = \pi_1 - \pi_2$ (and thus $H_0: \delta = 0$)

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 - also computes confidence interval for effect size
 - ◆ E.g. for 19 passives out of 100 / 25 out of 200
 - parameters `conf.level` and `alternative` can be used in the familiar way
- ```
> prop.test(c(19, 25), c(100, 200))
```

# Frequency comparison in R

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> prop.test(c(19,25), c(100,200))

 2-sample test for equality of proportions with
continuity correction

data: c(19, 25) out of c(100, 200)
X-squared = 1.7611, df = 1, p-value = 0.1845
alternative hypothesis: two.sided

95 percent confidence interval:
-0.03201426 0.16201426

sample estimates:
prop 1 prop 2
0.190 0.125
```

# Contingency tables

|         | sample 1    | sample 2    |
|---------|-------------|-------------|
| passive | $k_1$       | $k_2$       |
| active  | $n_1 - k_1$ | $n_2 - k_2$ |
|         | 19          | 25          |
|         | 81          | 175         |

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- ◆ Data can also be given as a **contingency table**
  - e.g.  $k_1 = 19 / n_1 = 100$  passives vs.  $k_2 = 25 / n_2 = 200$
  - represents a cross-classification of  $n = 300$  items
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- ◆ Chi-squared  $X^2$ , likelihood ratio  $G^2$ , Fisher's test

# Contingency tables

- ◆ Can easily carry out chi-squared (`chisq.test`) and Fisher's exact test (`fisher.test`) in R
  - likelihood ratio test not in R standard library
- ◆ Table for 19 / 100 vs. 25 / 200

```
> ct <- cbind(c(19,81),
+ c(25,175))

> chisq.test(ct)

> fisher.test(ct)
```

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→ approx. confidence interval from proportions test
  - **relative risk**     $r = \pi_1 / \pi_2$
  - **odds ratio**       $\theta = \pi_1 (1 - \pi_2) / \pi_2 (1 - \pi_1)$   
→ exact confidence interval from Fisher's test

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  - very large samples lead to highly significant p-values for minimal and irrelevant differences (e.g. 1M tokens with  $150,000 = 15\%$  vs.  $151,000 = 15.1\%$  occurrences)
- ◆ It is important to assess both **significance** and **relevance** (= effect size) of frequency data!
  - confidence intervals combine both aspects

# A case study: passives

- ◆ As a case study, we will compare the frequency of passives in Brown (AmE) and LOB (BrE)
  - pooled data
  - separately for each genre category
- ◆ Data files provided in CSV format
  - **passives.brown.csv** & **passives.lob.csv**
  - cat = genre category, passive = number of passives, n\_w = number of word, n\_s = number of sentences, name = description of genre category

# Preparing the data

```
> Brown <- read.csv("passives.brown.csv")
> LOB <- read.csv("passives.lob.csv")

> library(SIGIL) # also included in SIGIL package
> Brown <- BrownPassives
> LOB <- LOBPassives

now take a look at the two tables: what info do they provide?

pooled data for entire corpus = column sums (col. 2 ... 4)
> Brown.all <- colSums(Brown[, 2:4])
> LOB.all <- colSums(LOB[, 2:4])
```

# Frequency tests for pooled data

```
proportions test reports p-value is based on chi-squared test
and approximate confidence interval for effect size δ
> prop.test(c(10123, 10934), c(49576, 49742))

> ct <- cbind(c(10123, 49576-10123), # Brown
 c(10934, 49742-10934)) # LOB

> ct # contingency table for chi-squared / Fisher

> fisher.test(ct) # exact confidence interval for odds ratio θ

we could in principle do the same for all 15 genres ...
```

# Automation: user functions

```
user function do.test() executes proportions test for samples
k_1/n_1 and k_2/n_2 , and summarizes relevant results in compact form
> do.test <- function (k1, n1, k2, n2) {

 # res contains results of proportions test (list = data structure)
 res <- prop.test(c(k1, k2), c(n1, n2))

 # data frames are a nice way to display summary tables
 fmt <- data.frame(p=res$p.value,
 lower=res$conf.int[1], upper=res$conf.int[2])

 fmt # return value of function = last expression
}

> do.test(10123, 49576, 10934, 49742) # pooled data
> do.test(146, 975, 134, 947) # humour genre
```

# A nicer user function

```
nicer version of user function with genre category labels
> do.test <- function (k1, n1, k2, n2, cat="") {
 res <- prop.test(c(k1, k2), c(n1, n2))
 data.frame(
 p=res$p.value,
 lower=100*res$conf.int[1], # scaled to % points
 upper=100*res$conf.int[2],
 row.names=cat # add genre as row label
) # return data frame directly without local variable fmt
}
```

```
extract relevant information directly from data frames
> do.test(Brown$passive[15], Brown$n_s[15],
 LOB$passive[15], LOB$n_s[15],
 cat=Brown$name[15])
```

# Ad-hoc functions & loops

```
ad-hoc convenience function to reduce typing/editing
(works only if global Brown/L0B variables are set correctly!)
quick.test <- function (i) {
 do.test(k1=Brown$passive[i], n1=Brown$n_s[i],
 k2=L0B$passive[i], n2=L0B$n_s[i],
 cat=Brown$name[i])
}
quick.test(15) # easy to repeat for different genres now
quick.test(9)

loop over all 15 categories (more general: 1:nrow(Brown))
for (i in 1:15) {
 print(quick.test(i))
}
```

# R wizardry: working with lists

```
our code only works if rows of Brown/LOB are in the same order!
> all(Brown$cat == LOB$cat)

it would be nice to collect all these results in a single overview table
for this, we need a little bit of R wizardry ...

apply function quick.test() to each number 1, ..., 15
res.list <- lapply(1:15, quick.test)

pass res.list as individual arguments to rbind()
(think of this as an idiom you just have to remember ...)
res <- do.call(rbind, res.list)

res # data frame with one row for each genre
round(res, 3) # rounded values are easier to read
```

# It's your turn now ...

- ◆ Questions:

- Which differences are significant?
- Are the effect sizes linguistically relevant?

- ◆ A different approach:

- You can construct a list of contingency tables with the `cont.table()` function from the `corpora` package
- Apply `fisher.test()` or `chisq.test()` directly to each table in the list using the `lapply()` function
- Try to extract relevant information with `sapply()`