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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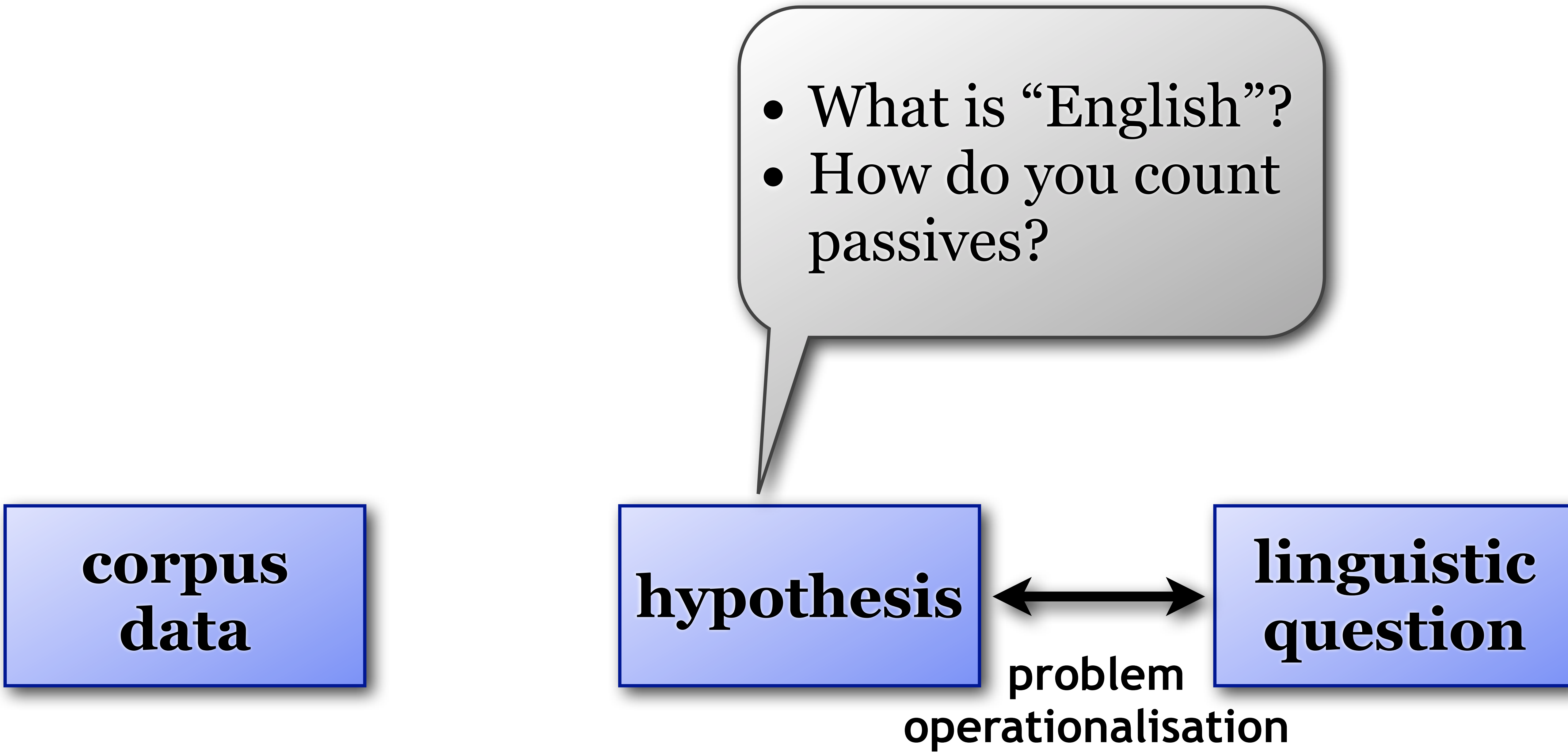

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- Here: professional writing by native speakers of AmE (⇨ target audience of style guide)

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  - **type** count: How many *different* passives are there?
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- **Absolute frequency** is not meaningful here

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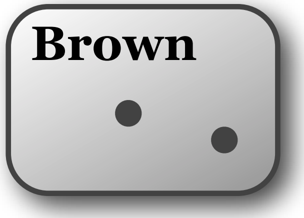

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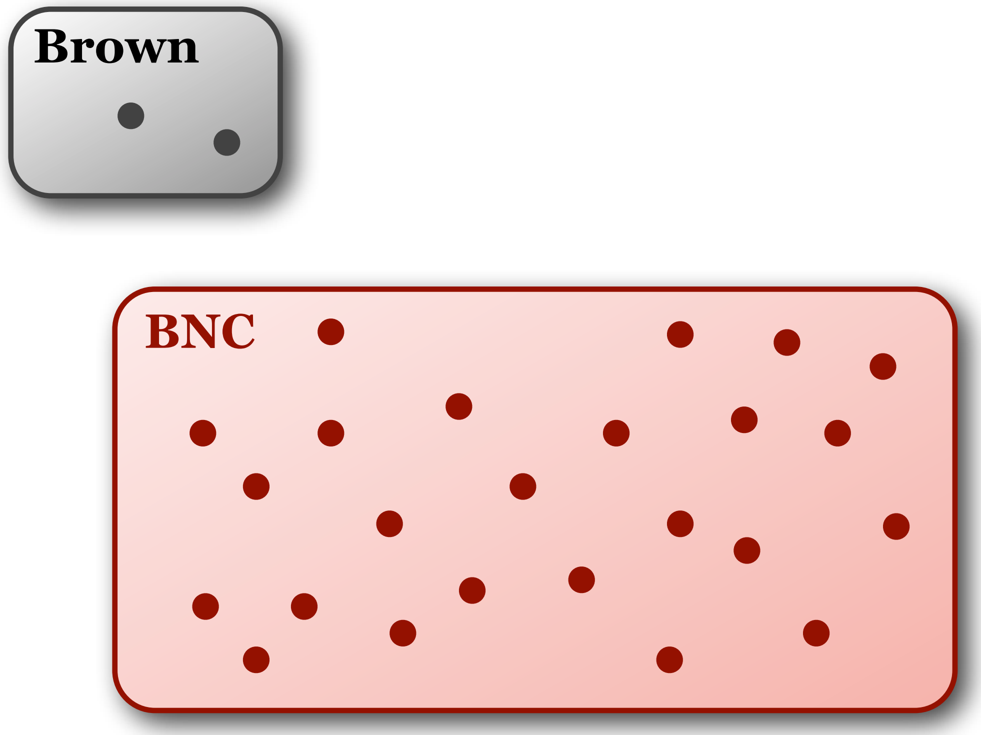
  - BNC (90M words)



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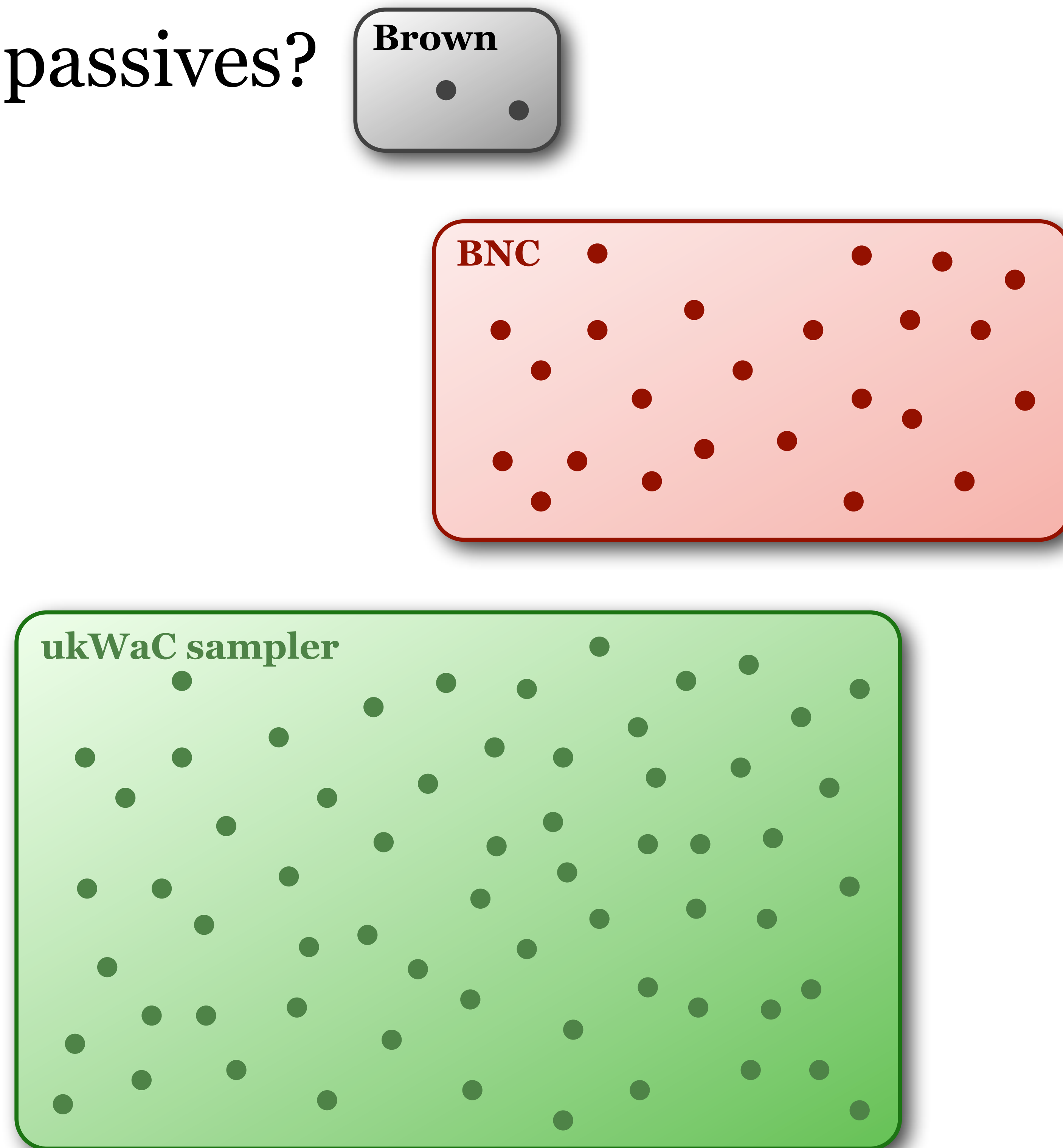
- Or 5.1 million?
  - ukWaC sampler (450M words)



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- **Relative frequency** = **proportion** π

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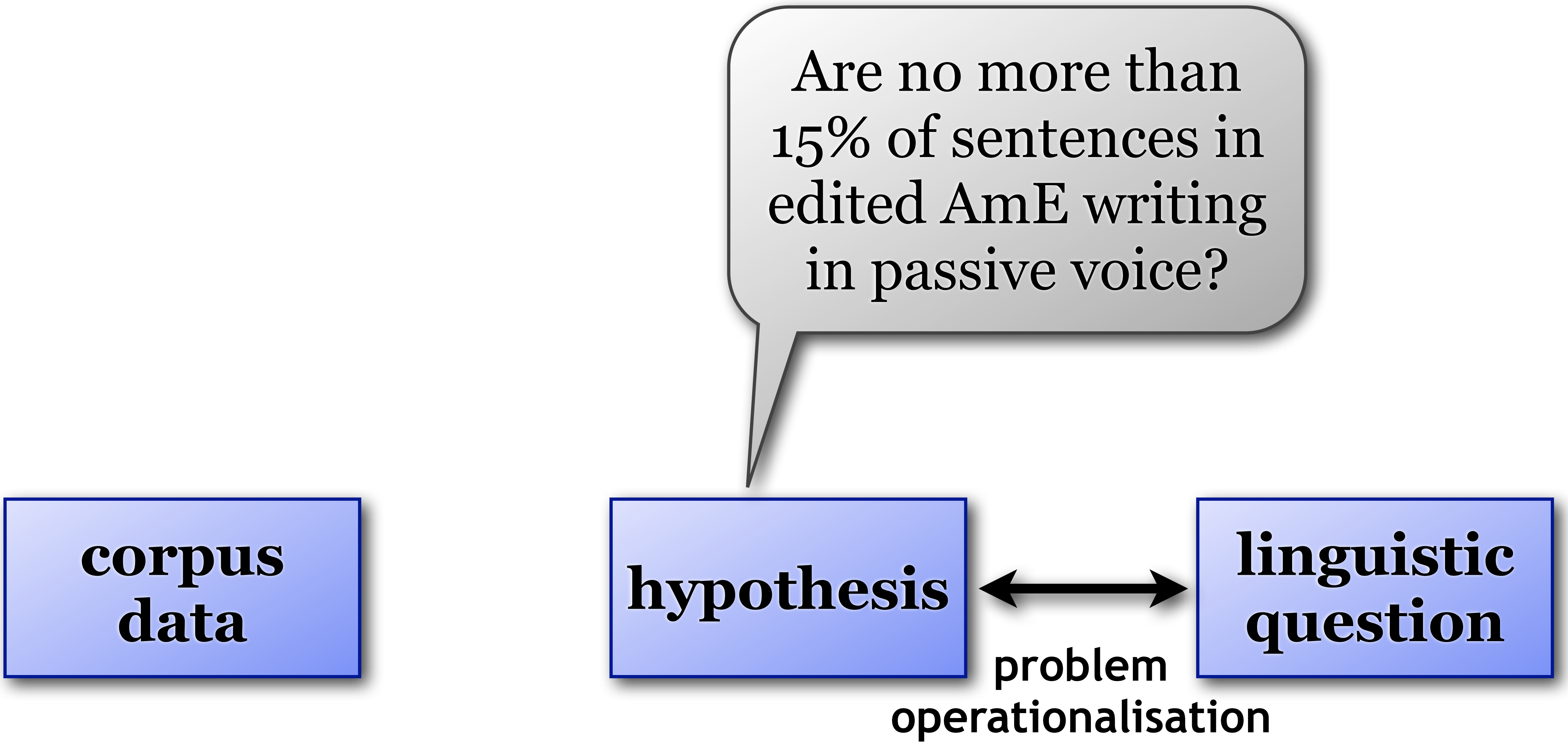

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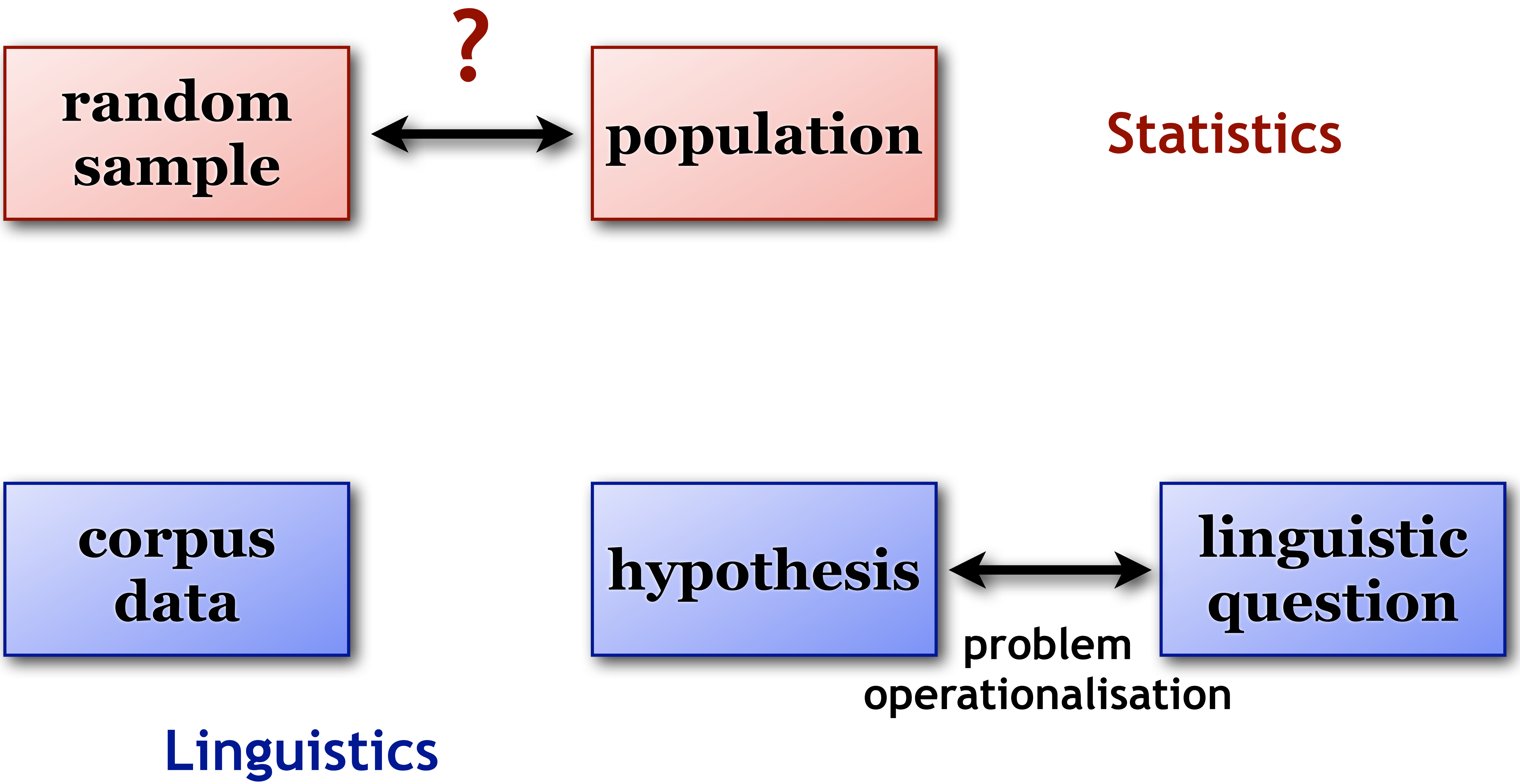

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  - this works only because of **random** sampling!
- Many statistical methods are readily available

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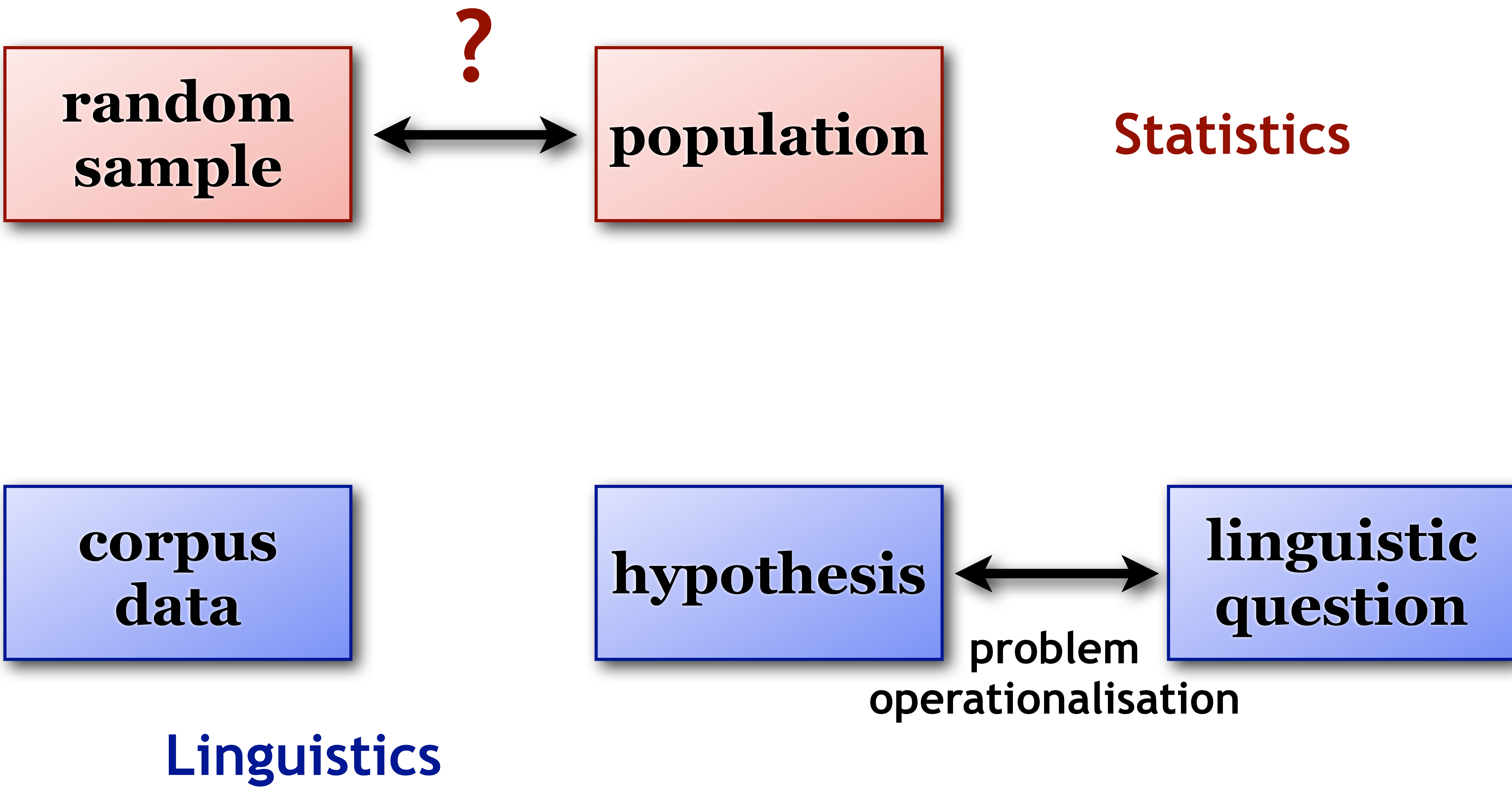

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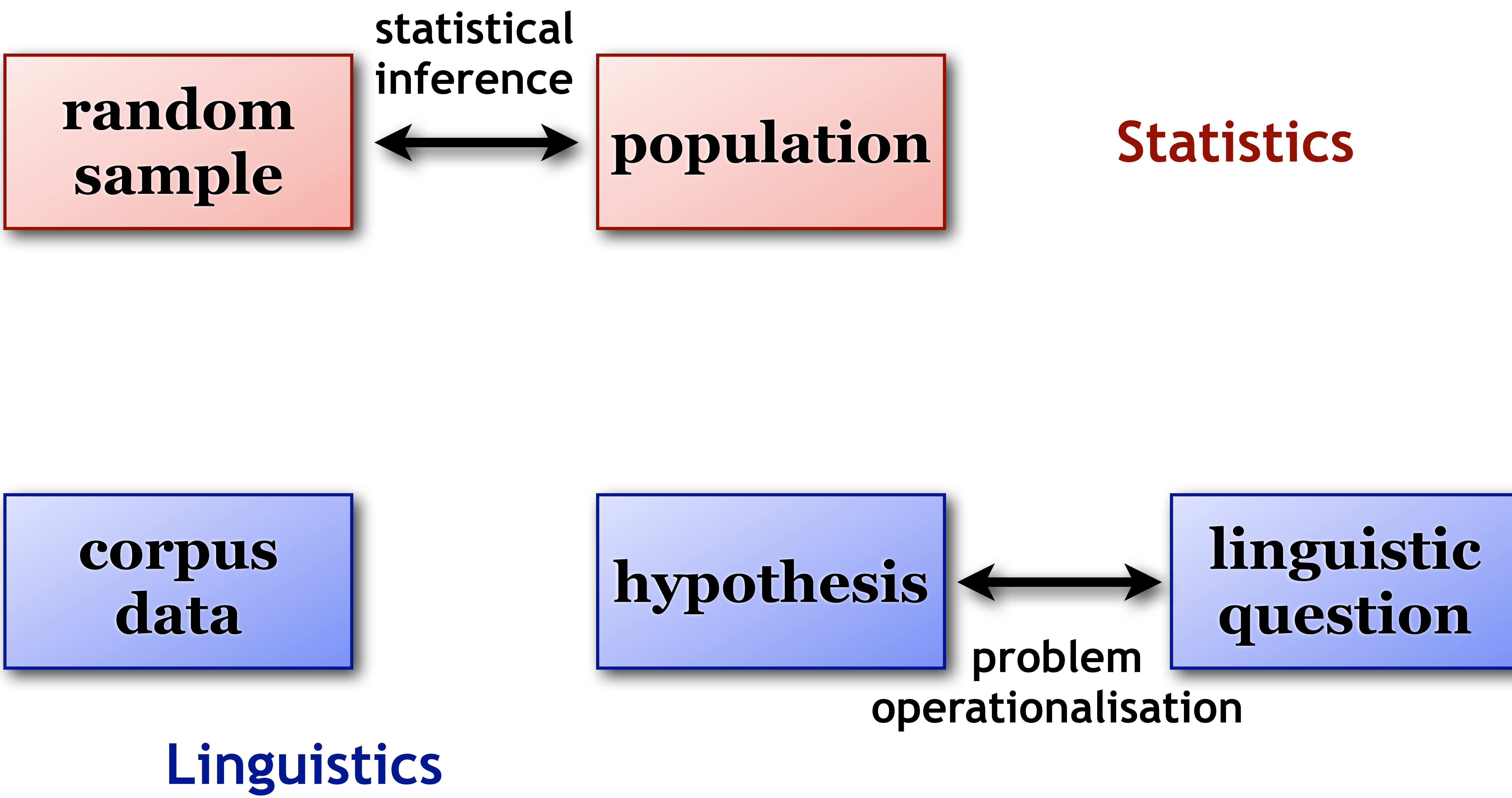

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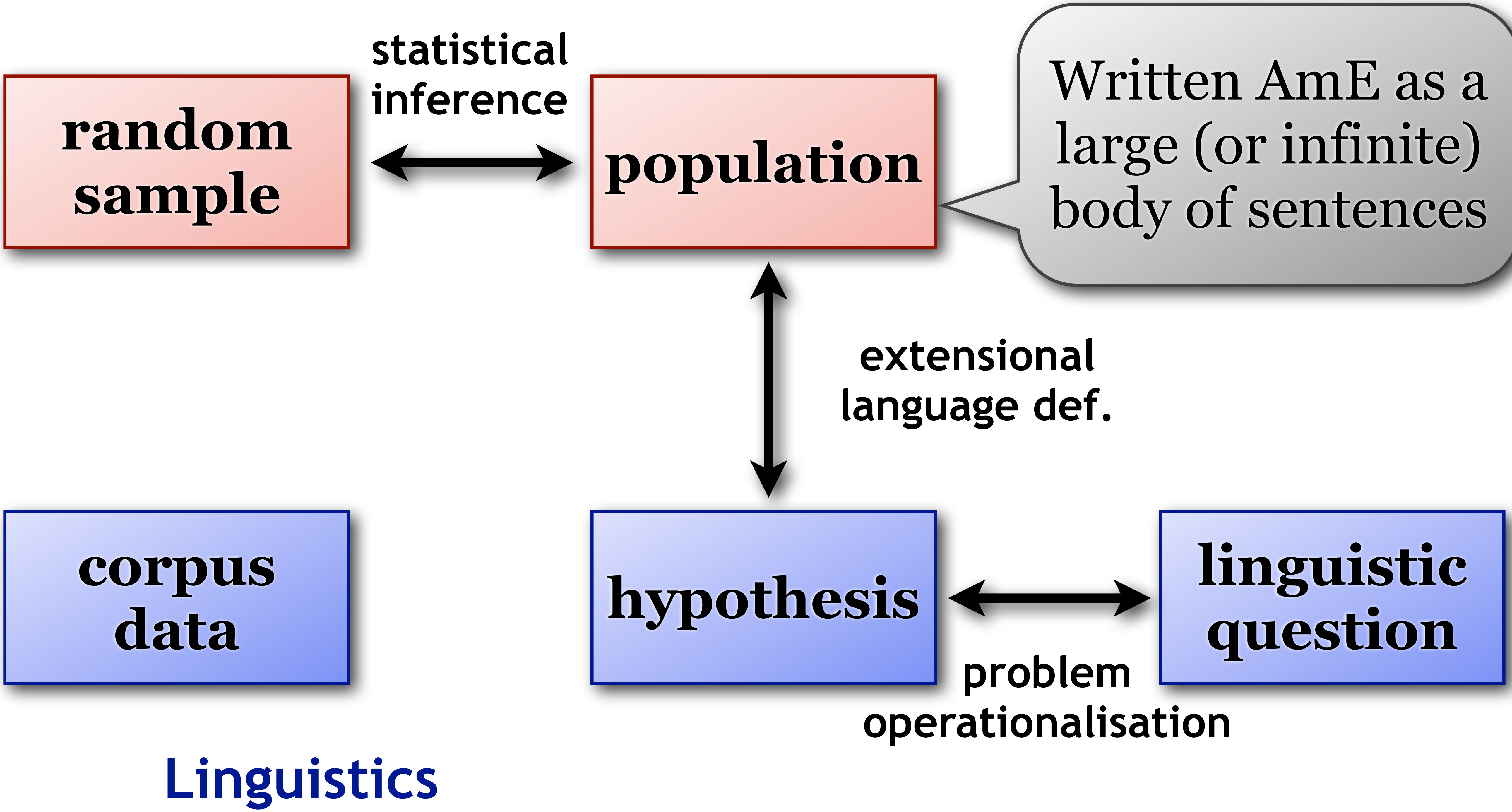

The library metaphor

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- 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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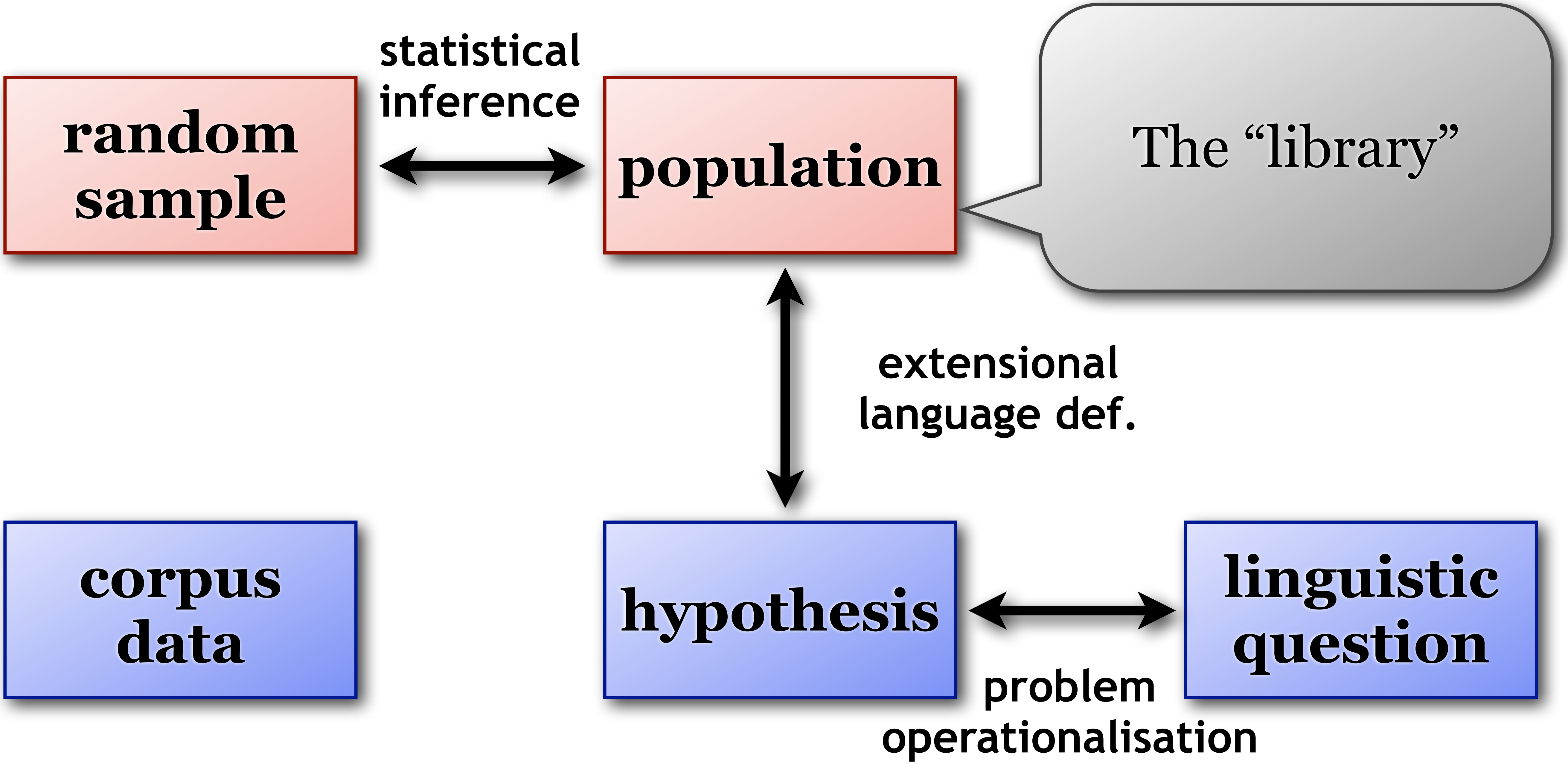

Linguistics

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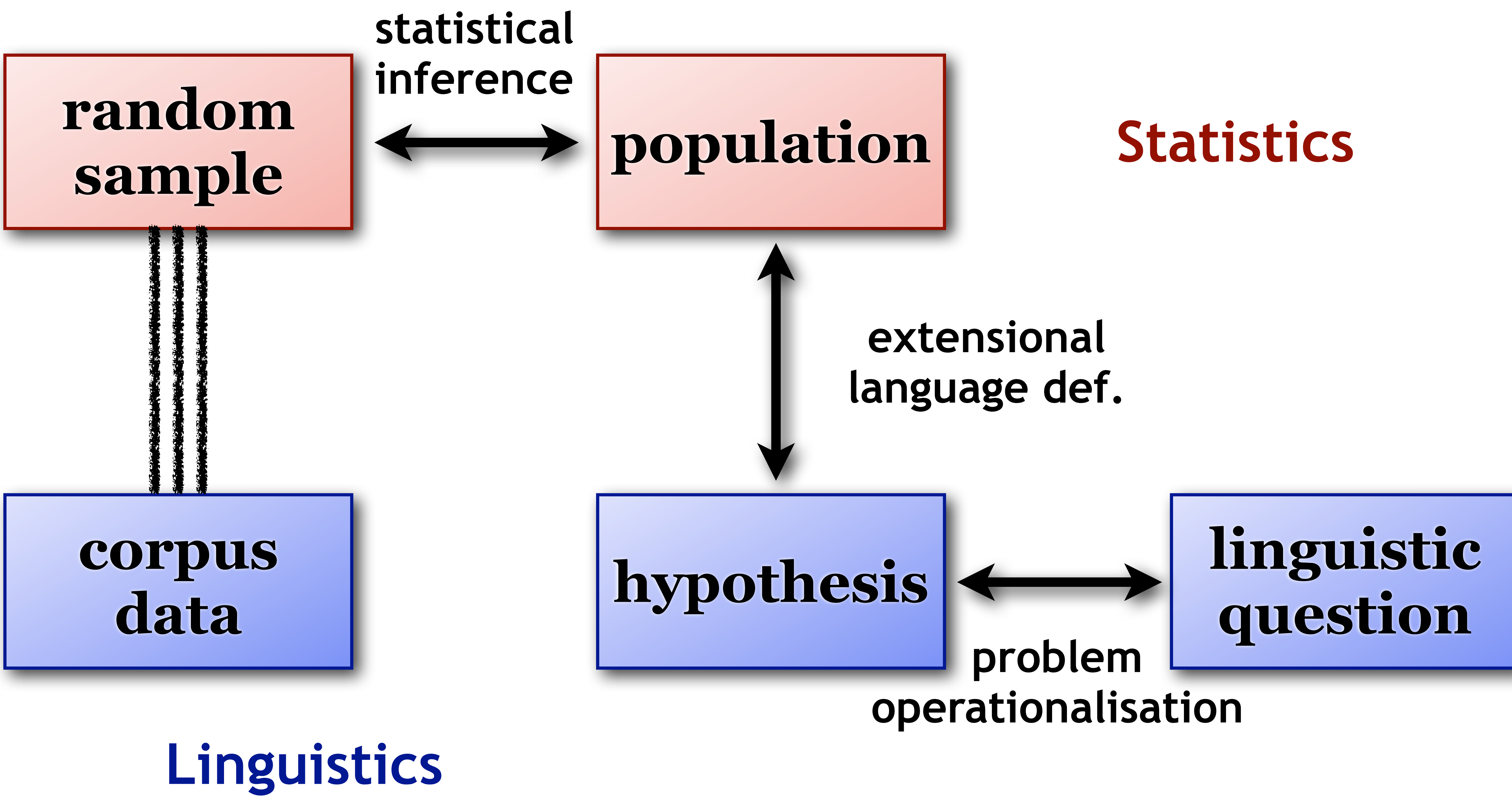

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- Objects = whatever **unit of measurement** the proportions of interest are based on
  - we need to take a random sample of such units

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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 $\{t_1, \ldots, t_n\}$ = proportion of tokens t_i that belong to this type

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

frequency of type

sample size

- Compare relative sample frequency $\boldsymbol{p}$ against (hypothesised) population proportion $\boldsymbol{\pi}$

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

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  - style guide → population proportion $\pi = 15\%$
  - $p > \pi$ → 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?

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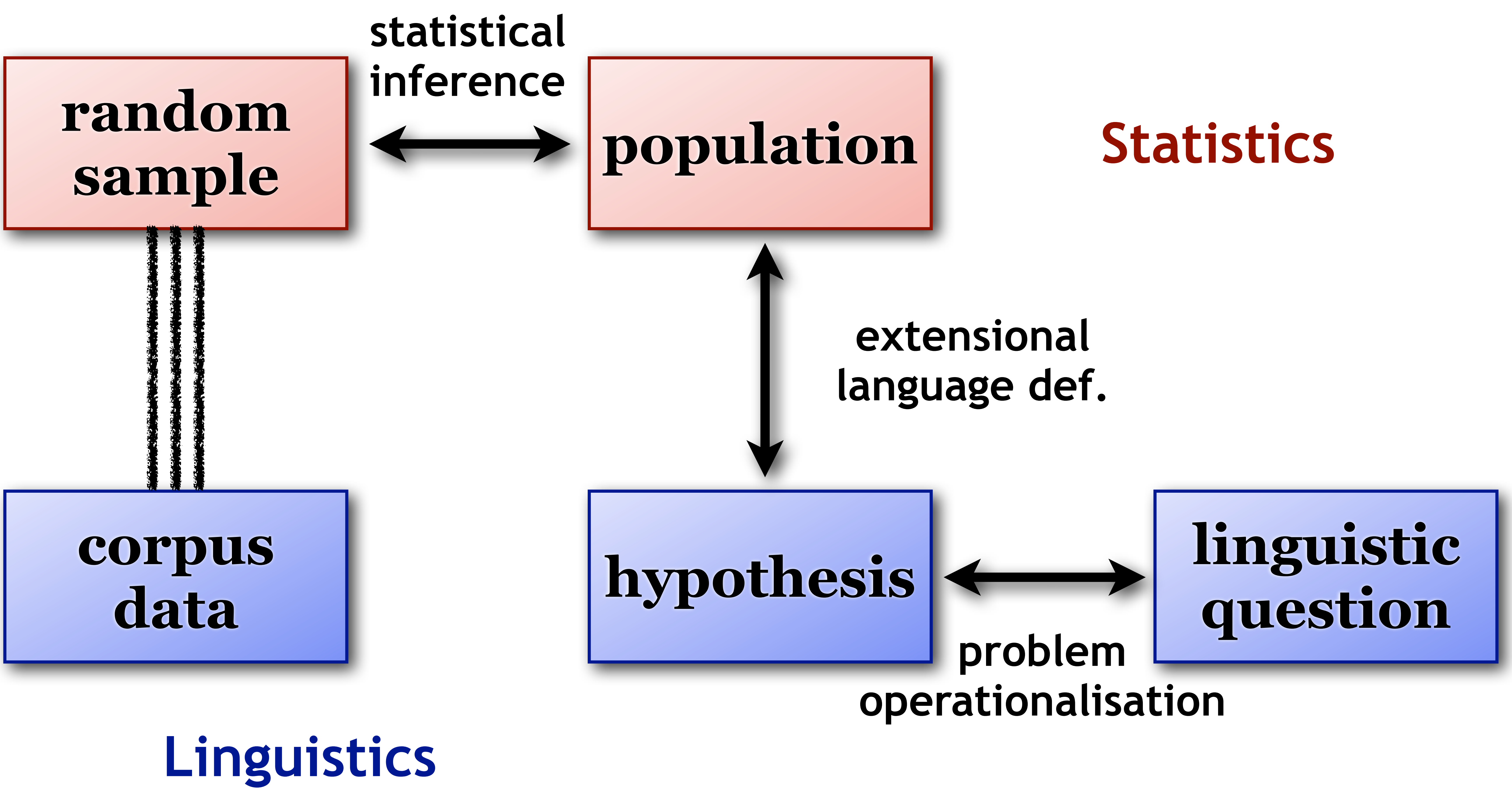
- But it also means that for every sample we will get a different value because of chance effects → **sampling variation**
  - problem: erroneous rejection of style guide's claim results in publication of a false result
- The main purpose of statistical methods is to estimate & correct for sampling variation
  - that's all there is to inferential statistics, really

Reminder: The role of statistics



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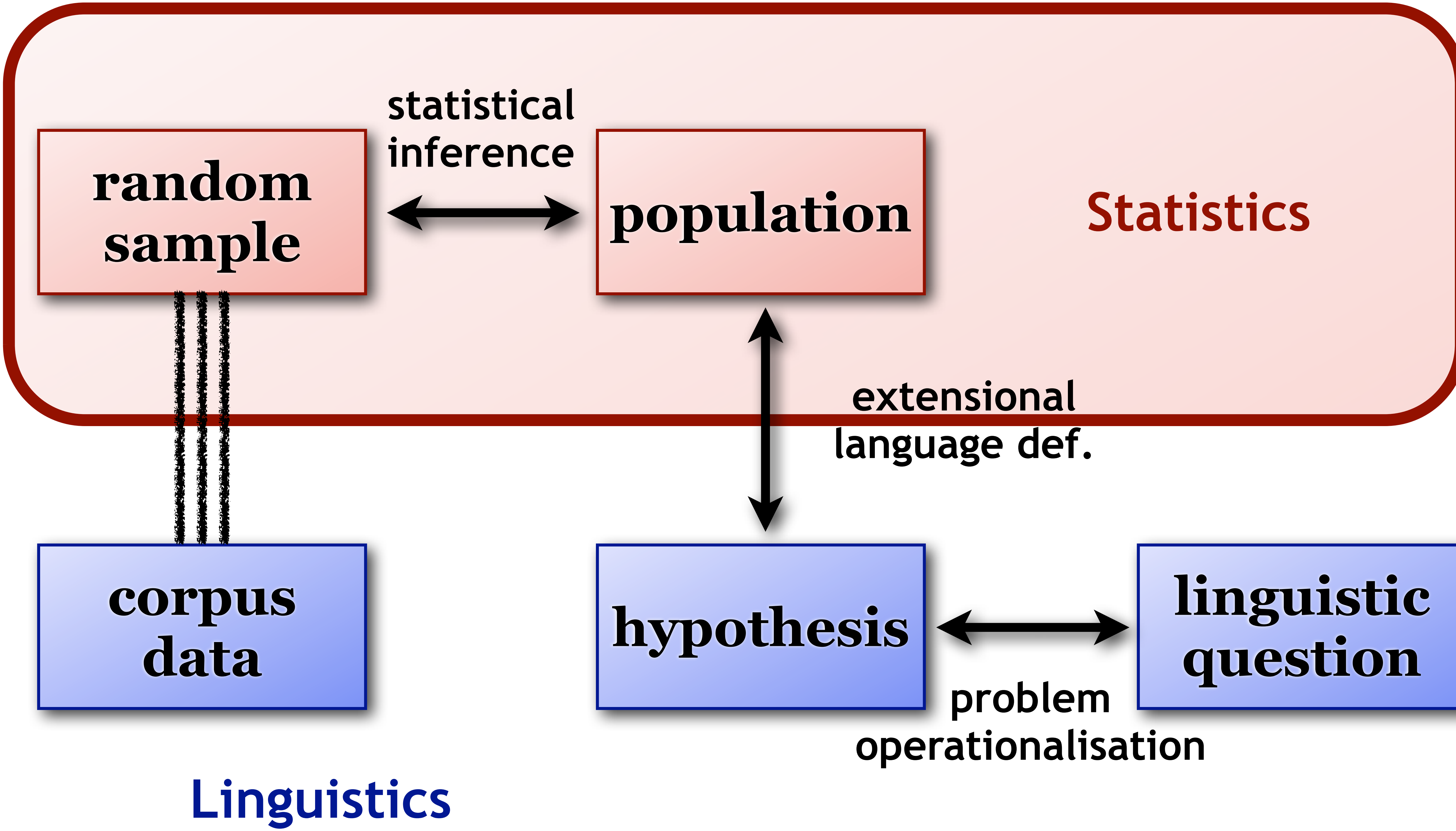

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- Need to control risk of a type I error

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  - 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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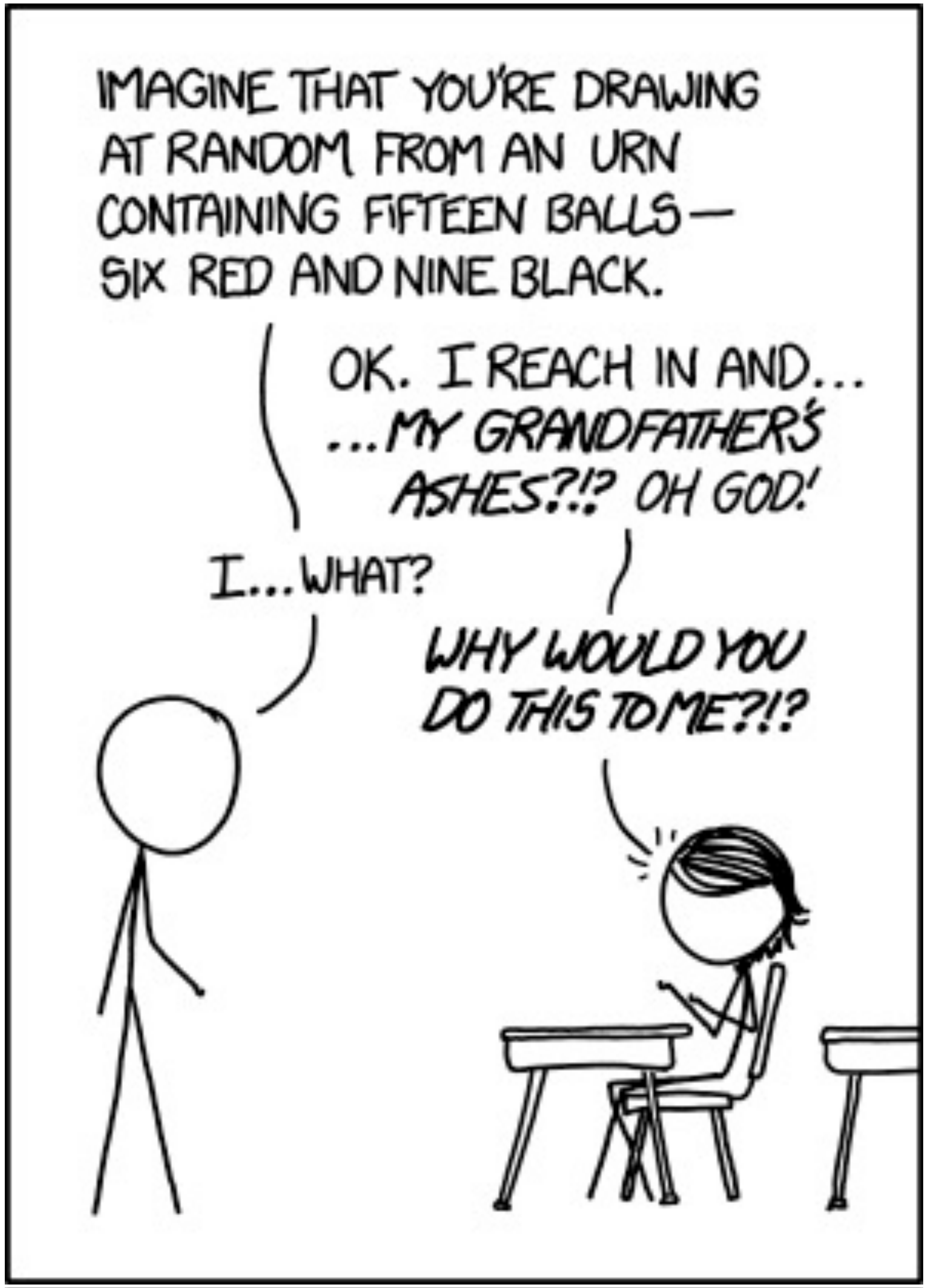
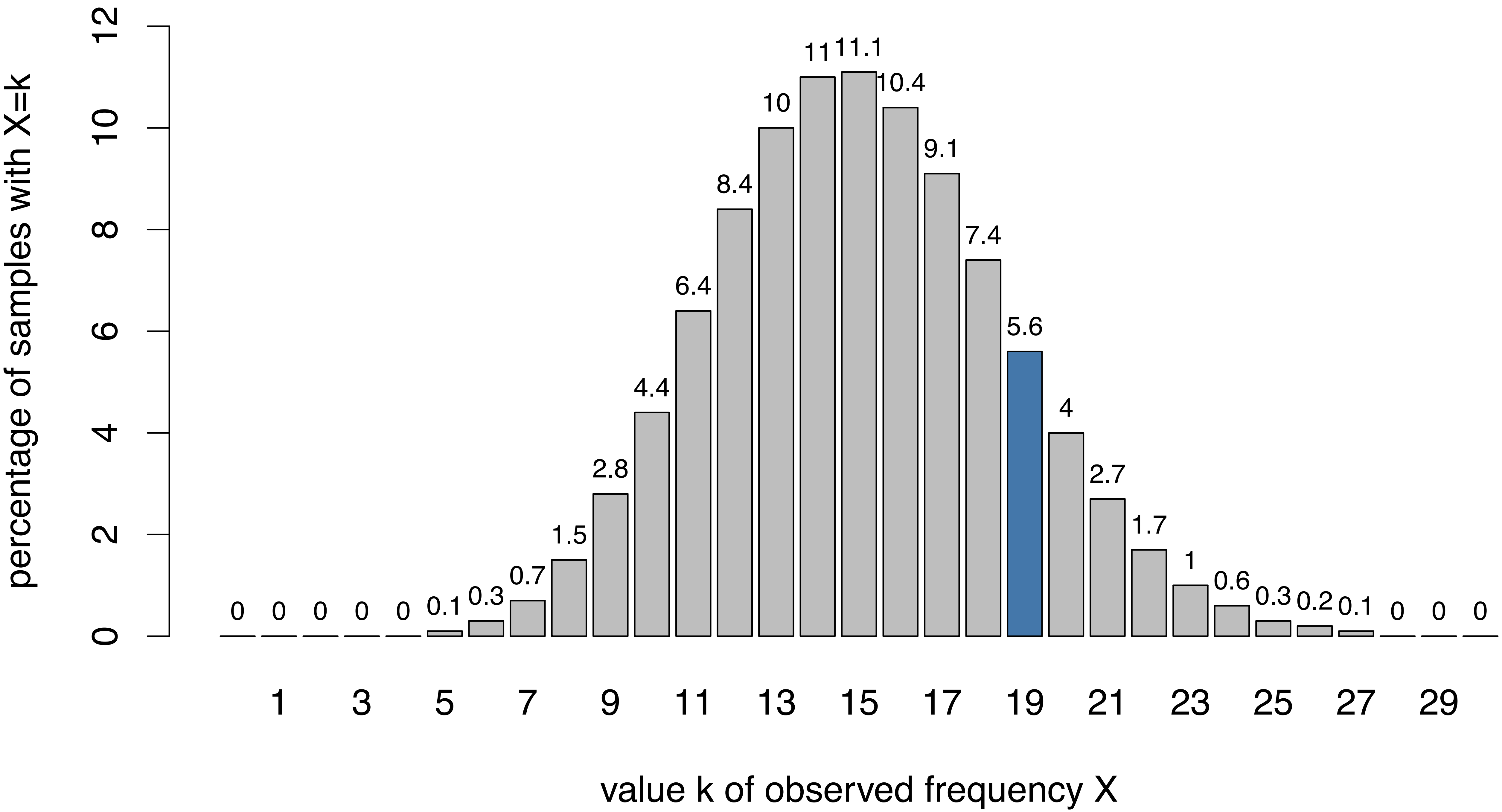
percentage of samples = **probability**



http://xkcd.com/1374/

Comic relief

Binomial sampling distribution



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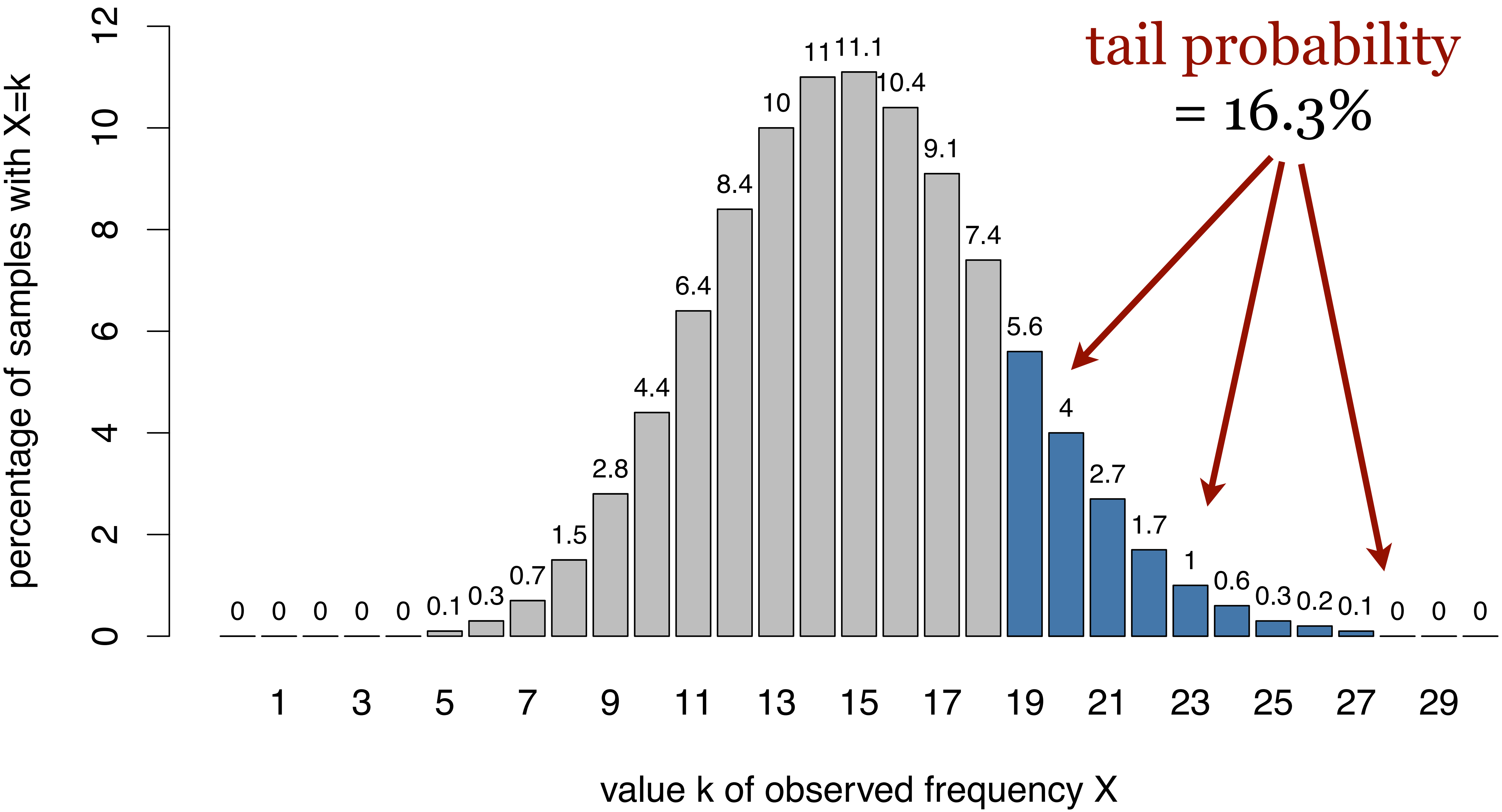

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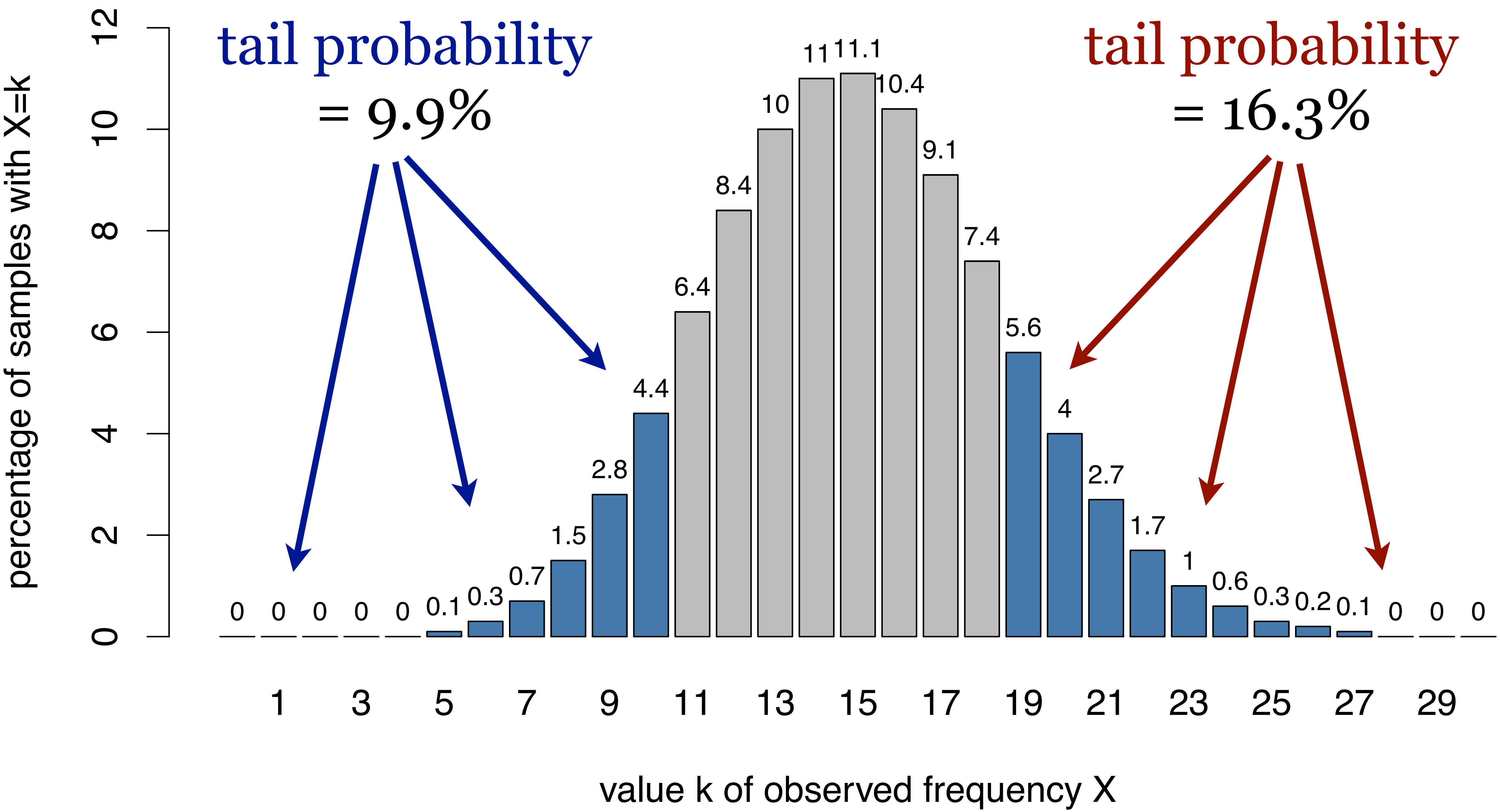
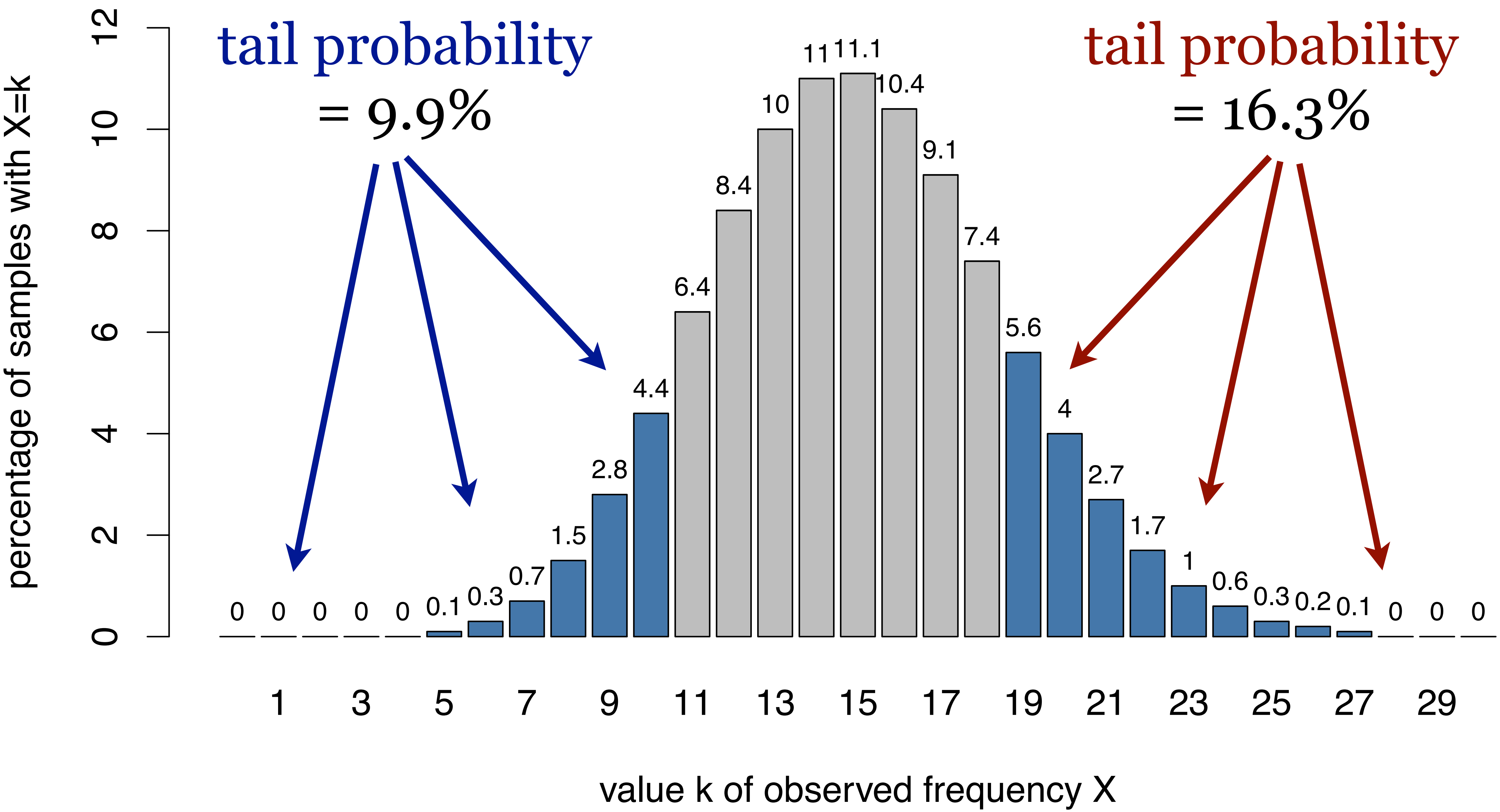


Binomial sampling distribution

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



Statistical hypothesis testing

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  - control the risk of false rejection (**type I error**) to a "socially acceptable level" (**significance level** α)
  - **p-value** = risk of type I error given observation, interpreted as amount of evidence against H_0

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- 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

extrapolate to [ ] items

Clear fields

Calculate

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

Clear fields

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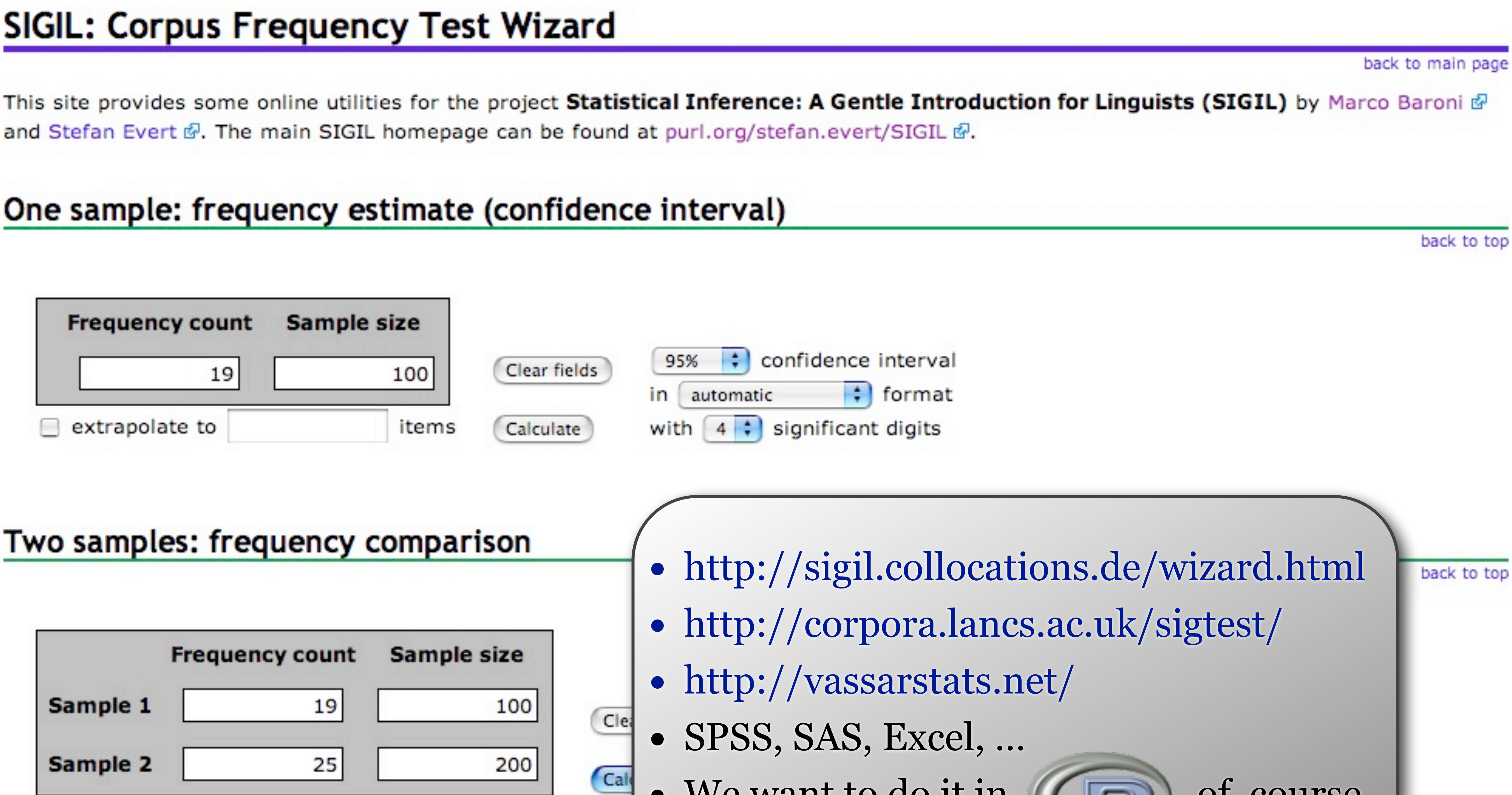
Hypothesis tests in practice



- http://sigil.collocations.de/wizard.html
- http://corpora.lancs.ac.uk/sigtest/
- http://vassarstats.net/
- SPSS, SAS, Excel, …
- We want to do it in R, of course

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- 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

```
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   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
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sample estimates:
probability of success
                  0.19
```

Rejection criterion & significance level

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- Type II error = failure to reject incorrect H_0
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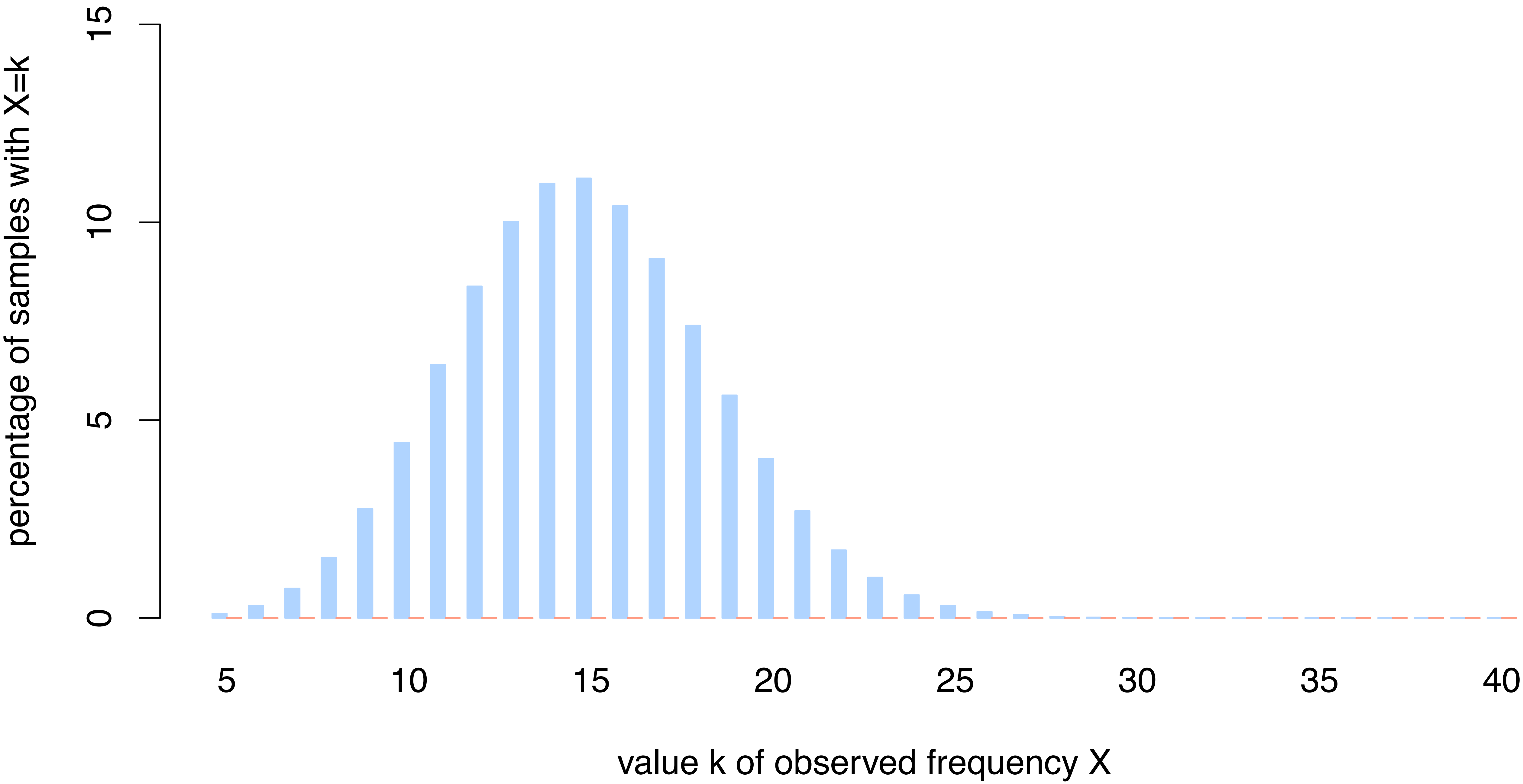
    → rejection correct, non-rejection is an error
- What is the risk of a type II error?
  - depends on unknown true population proportion π
  - intuitively, risk of type II error will be low if the difference $\delta = \pi - \pi_0$ (the **effect size**) is large enough

Type II errors



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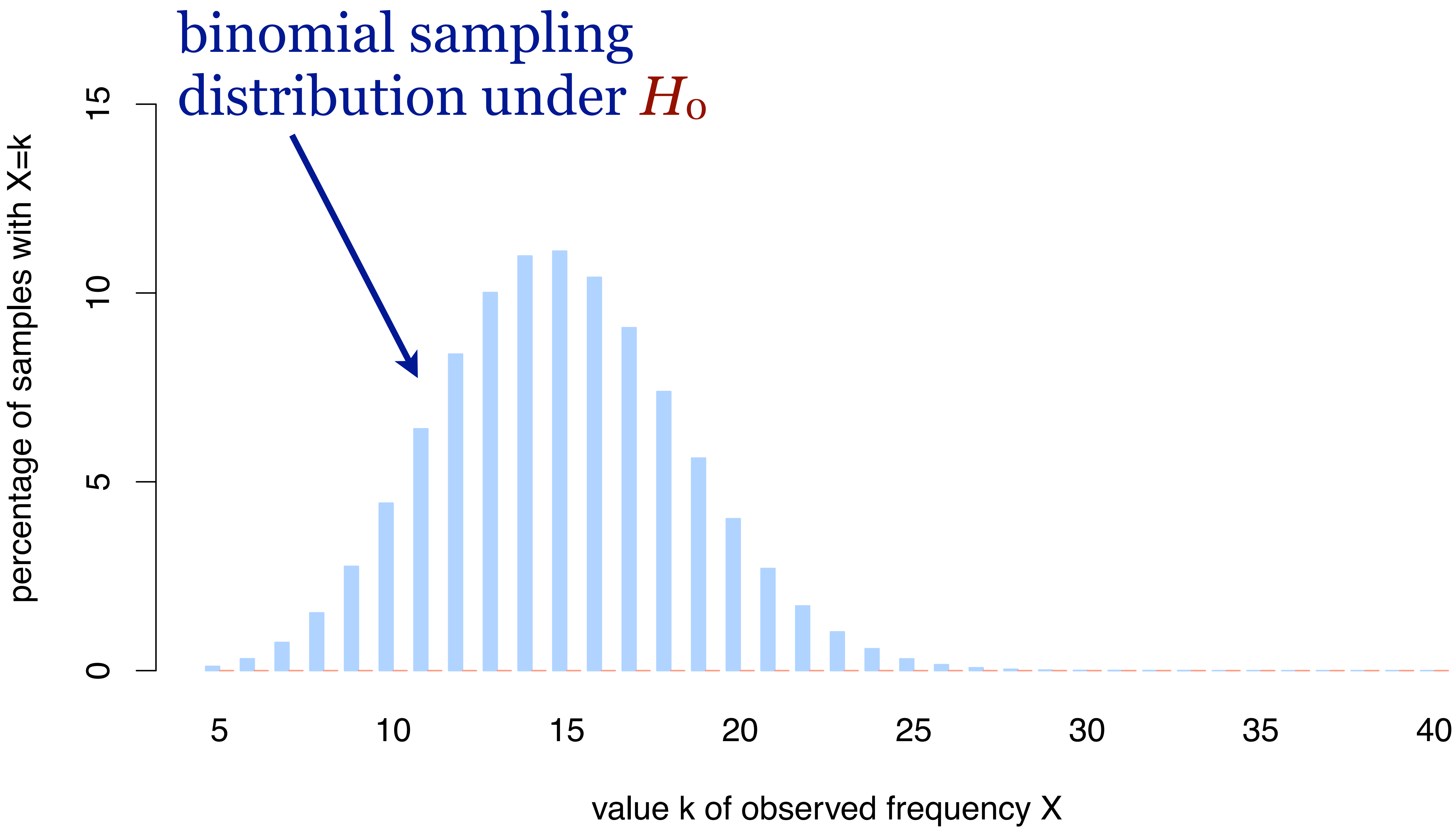

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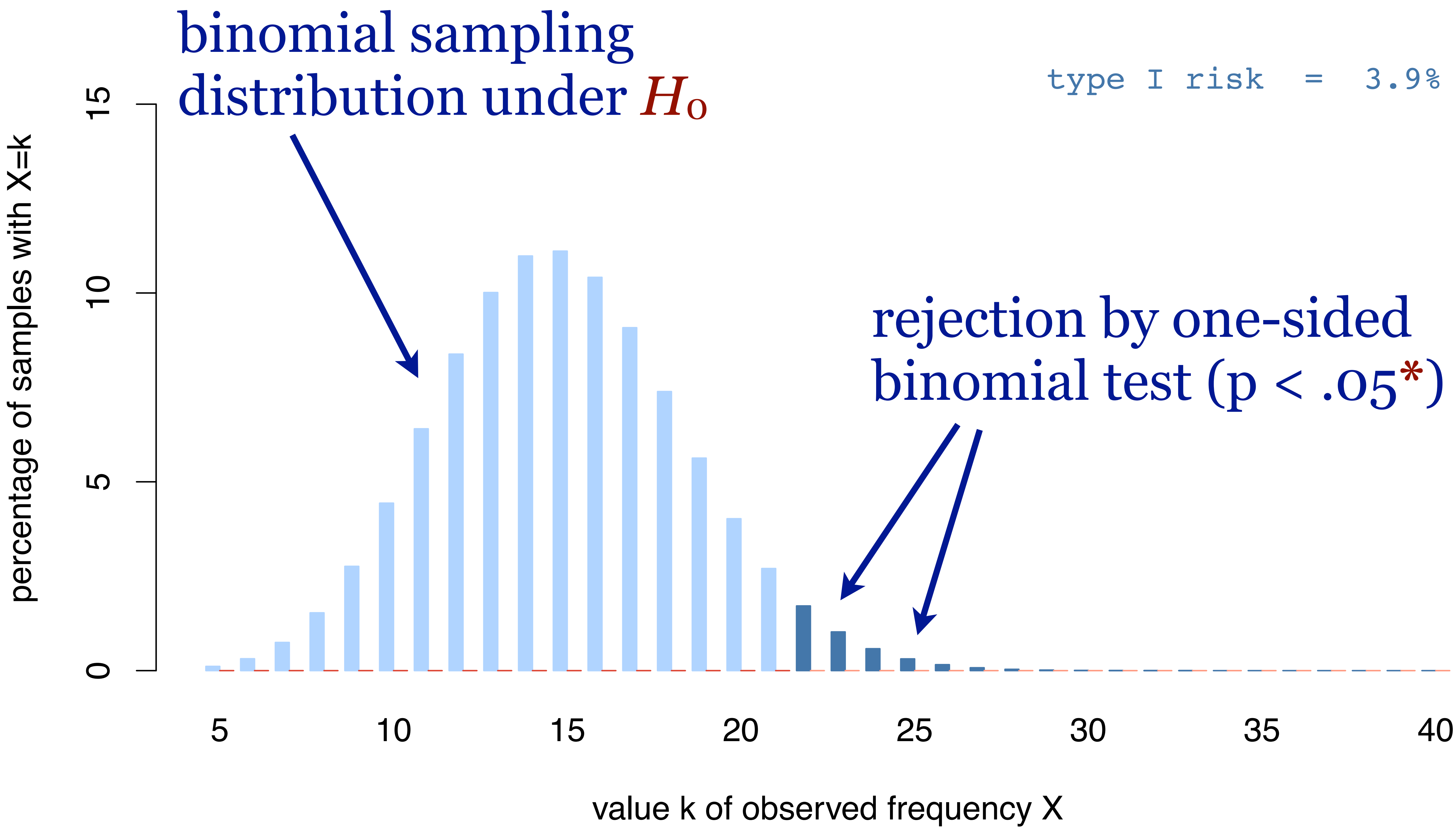

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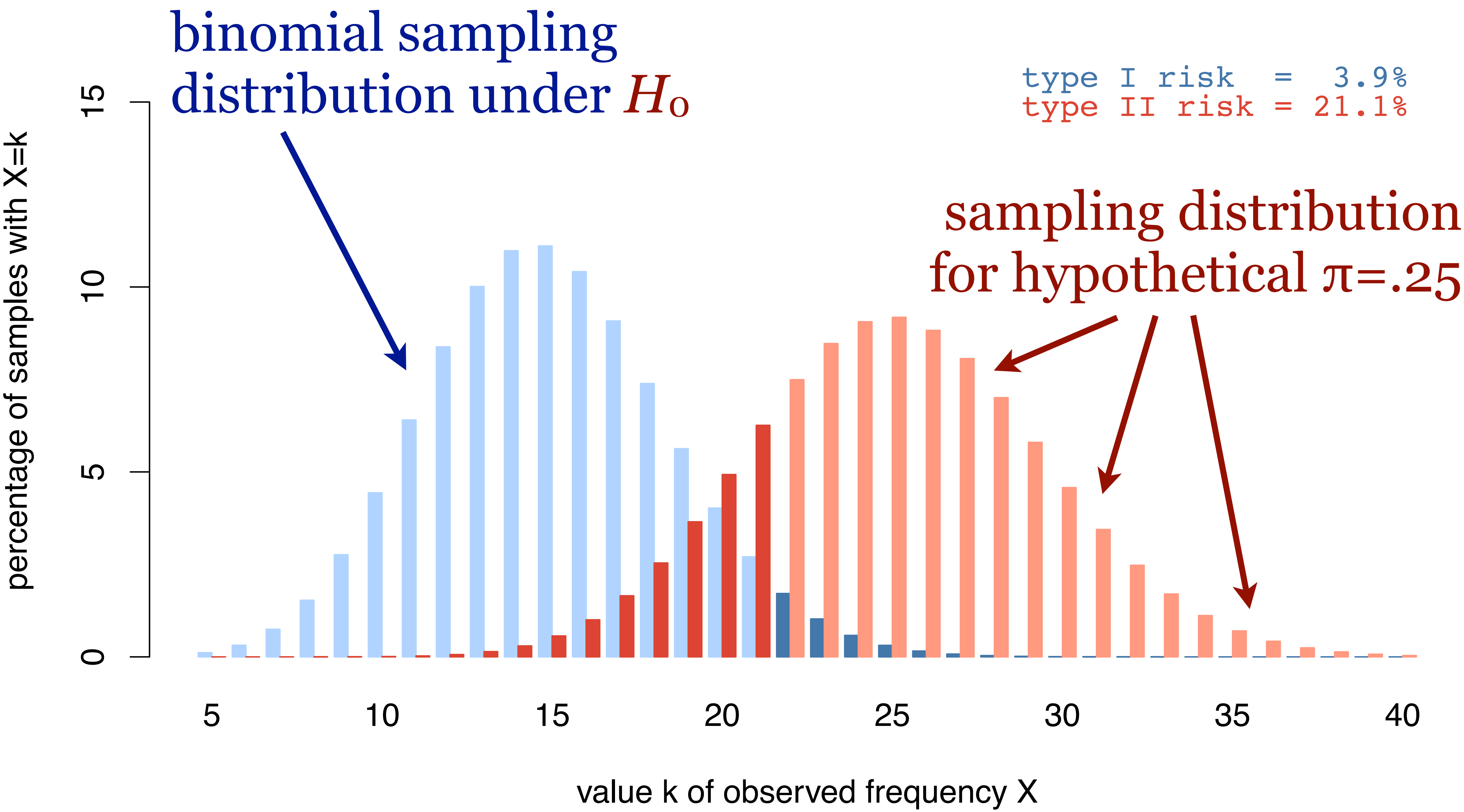

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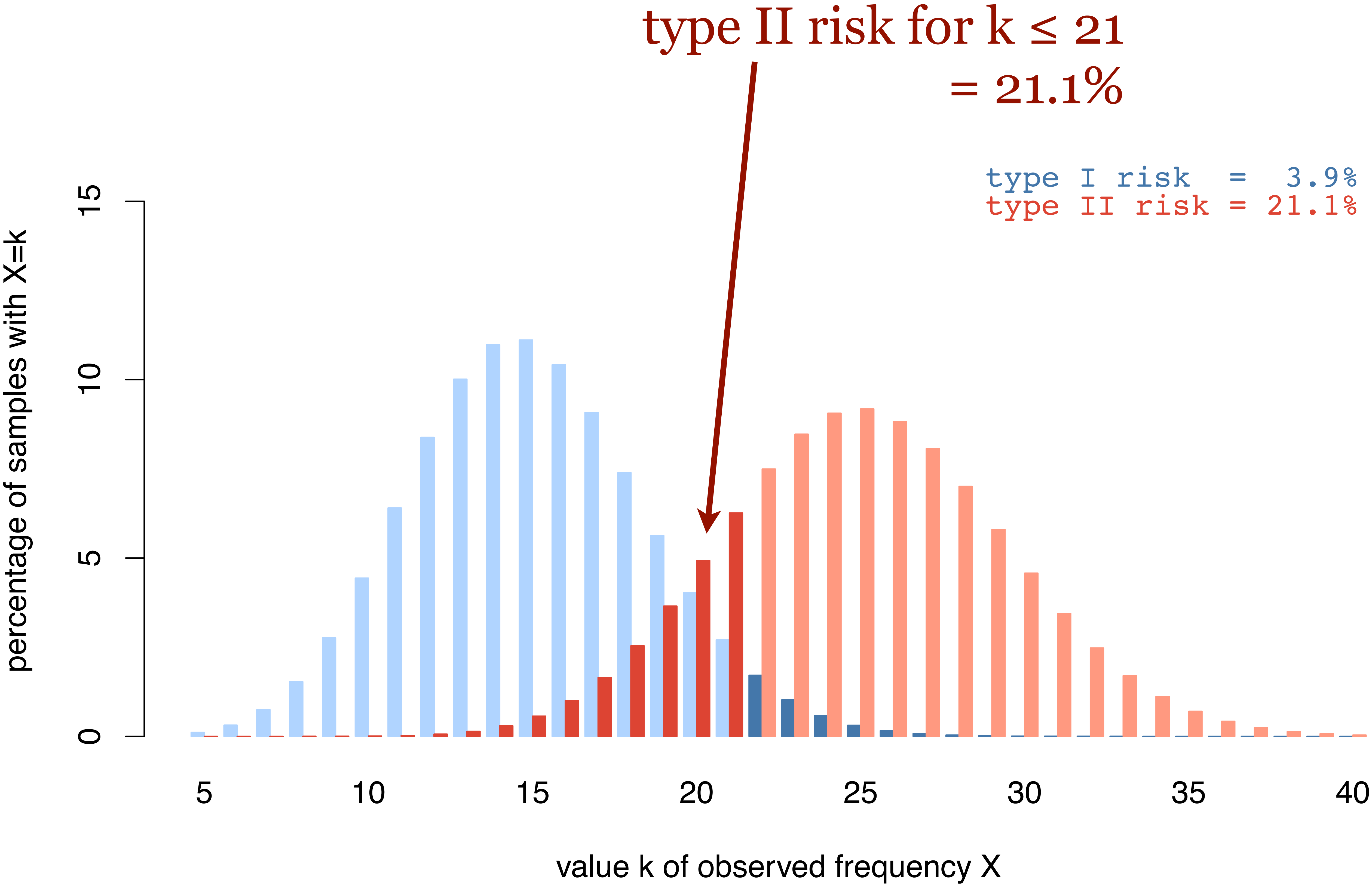
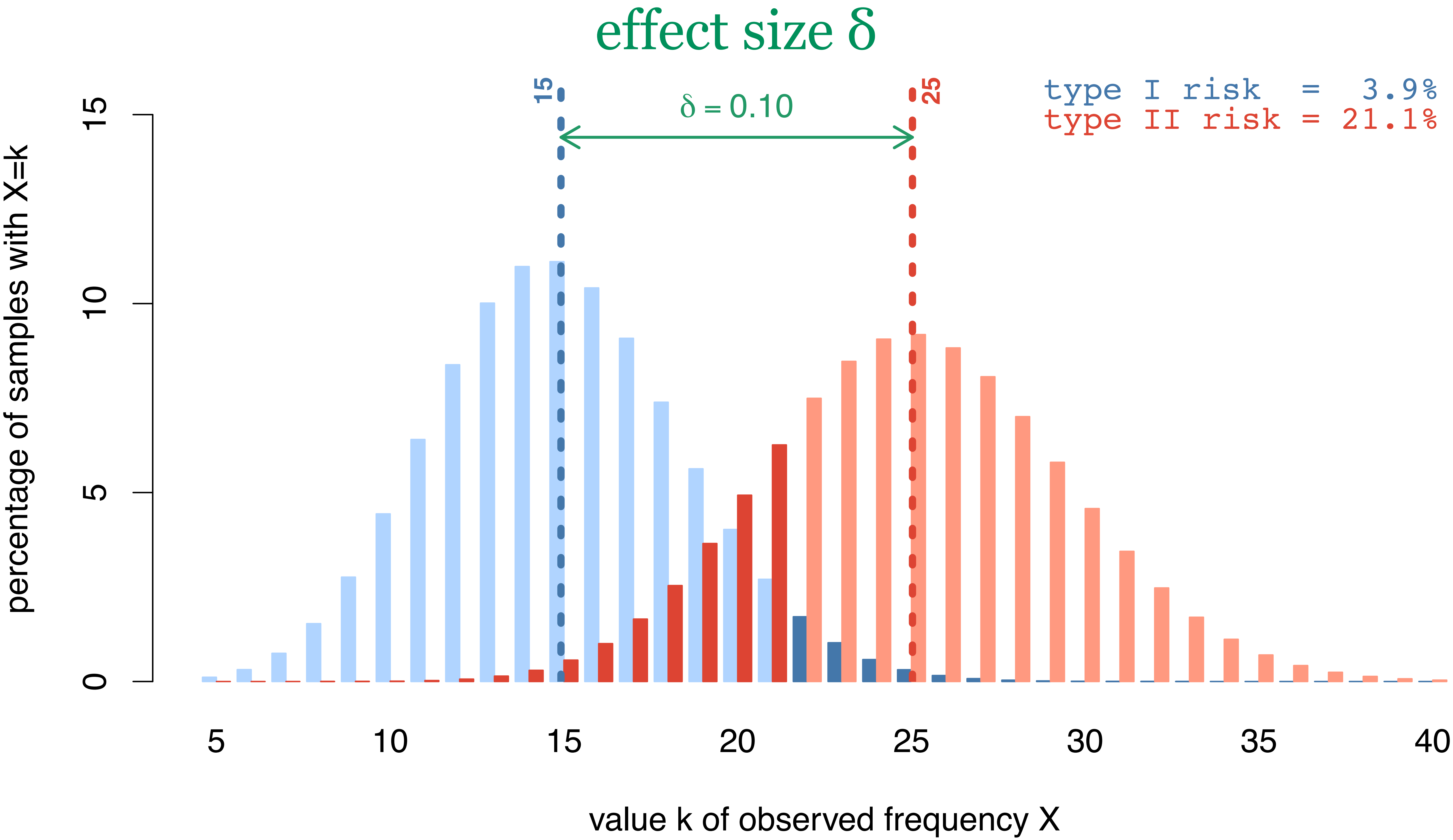


Type II errors
& effect size



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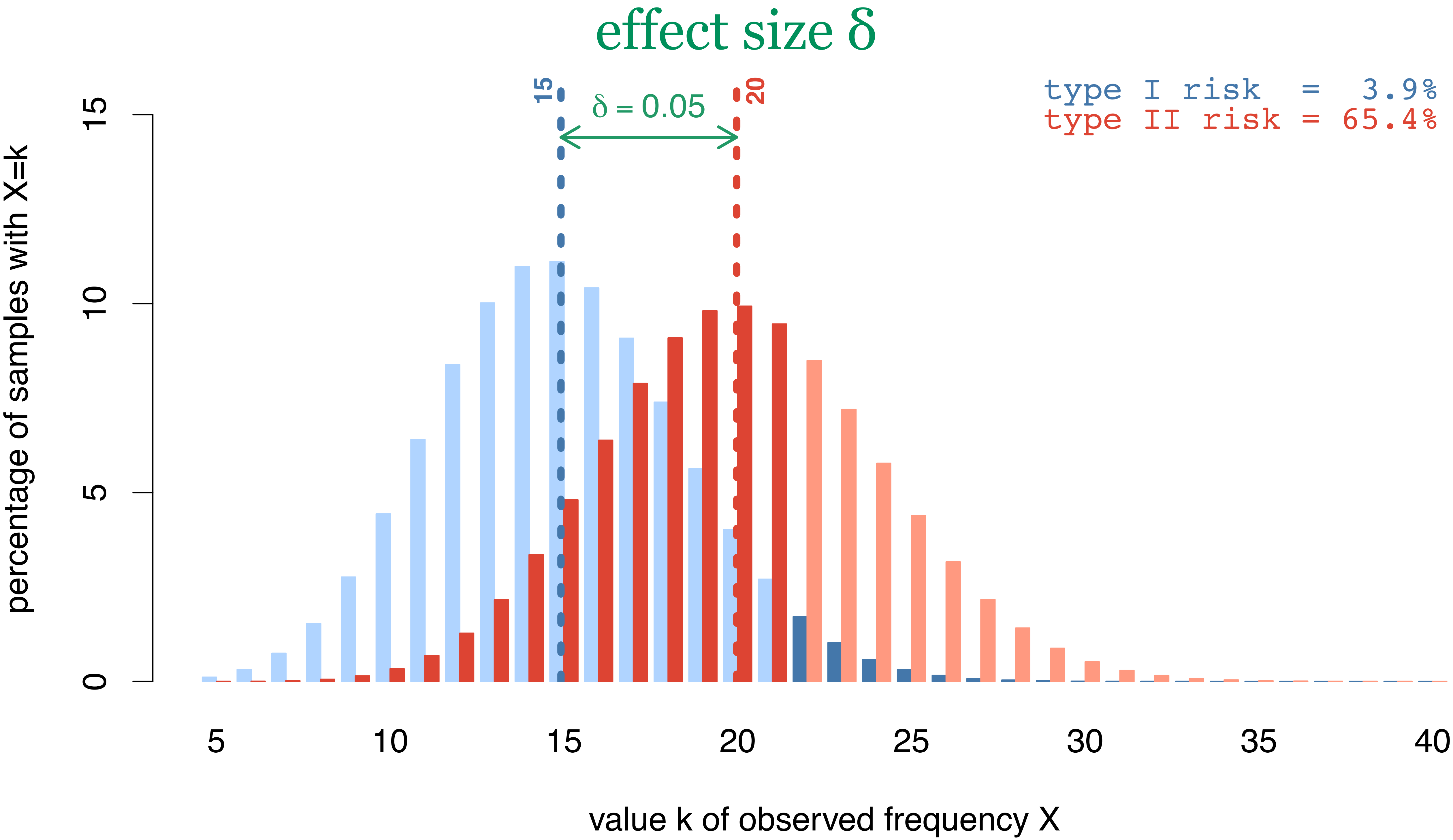

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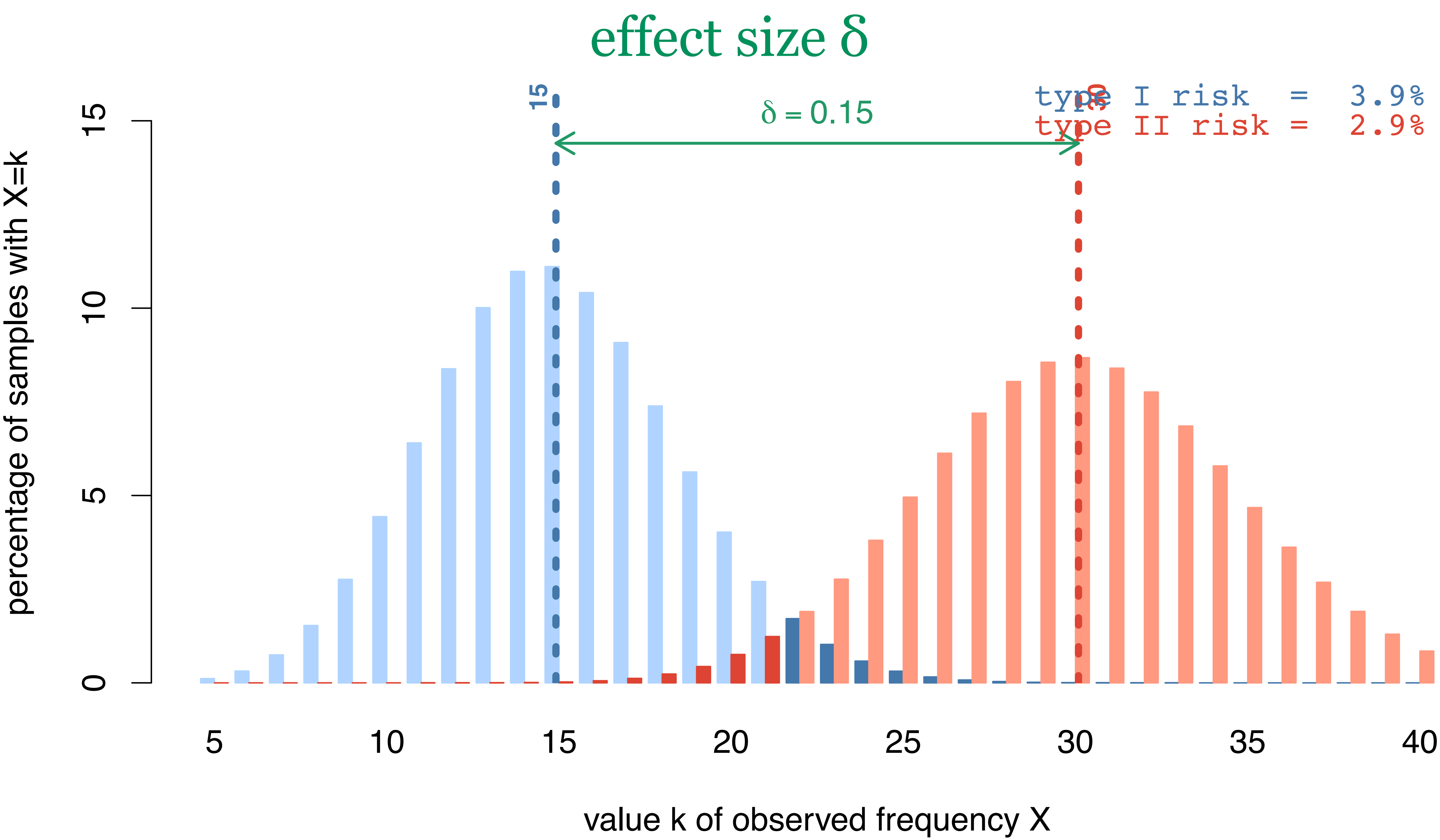

Type II errors
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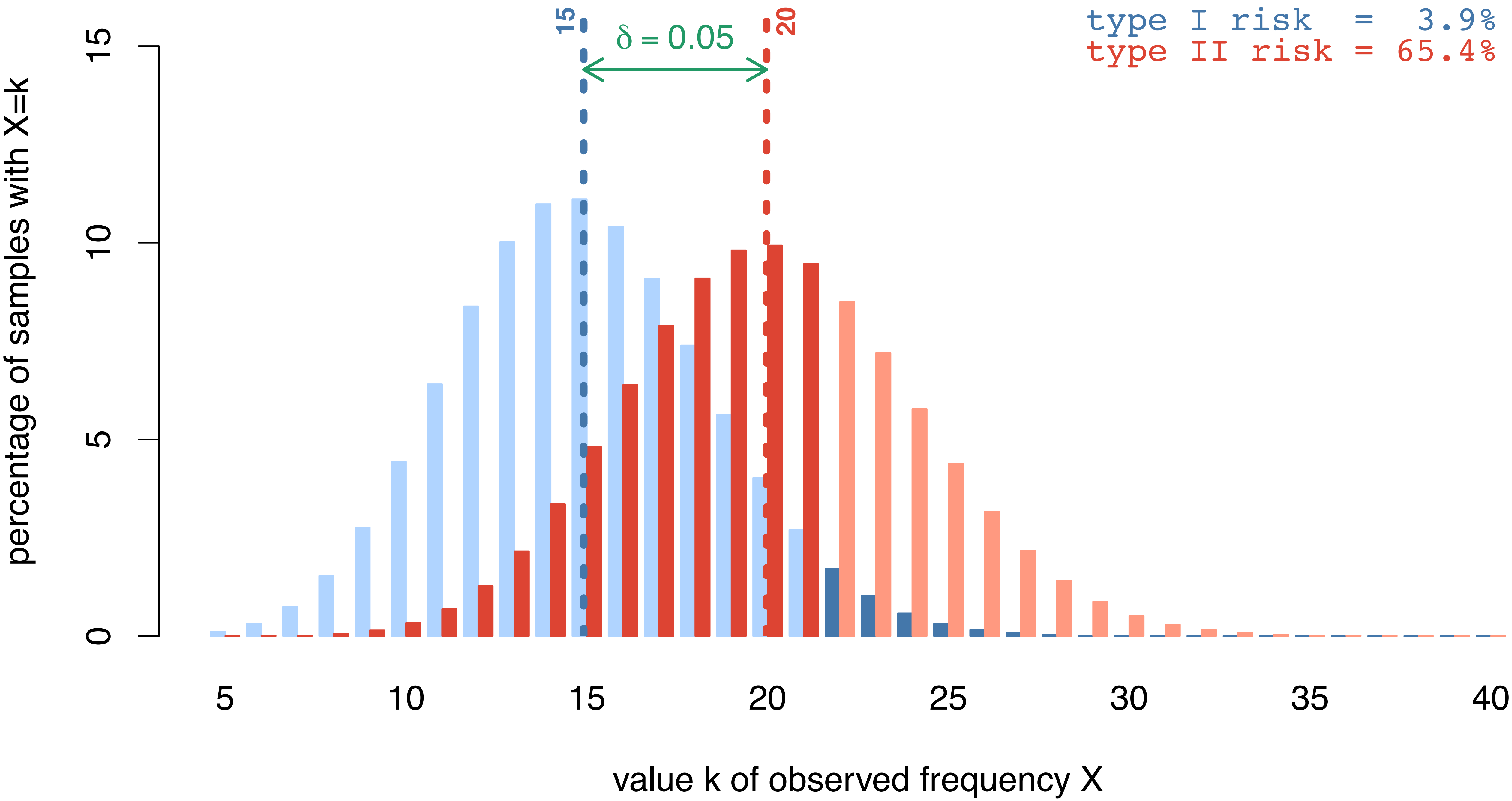

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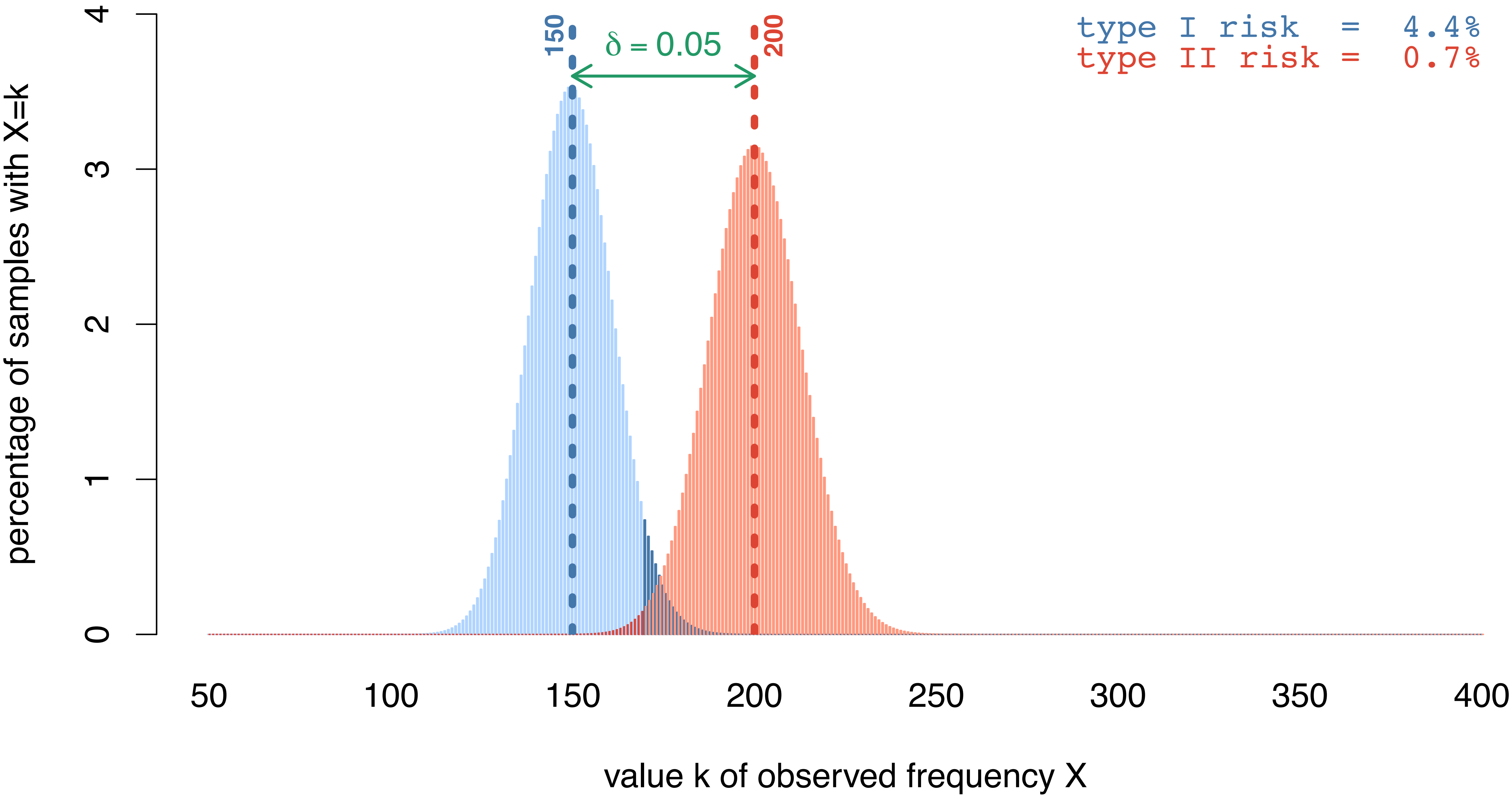

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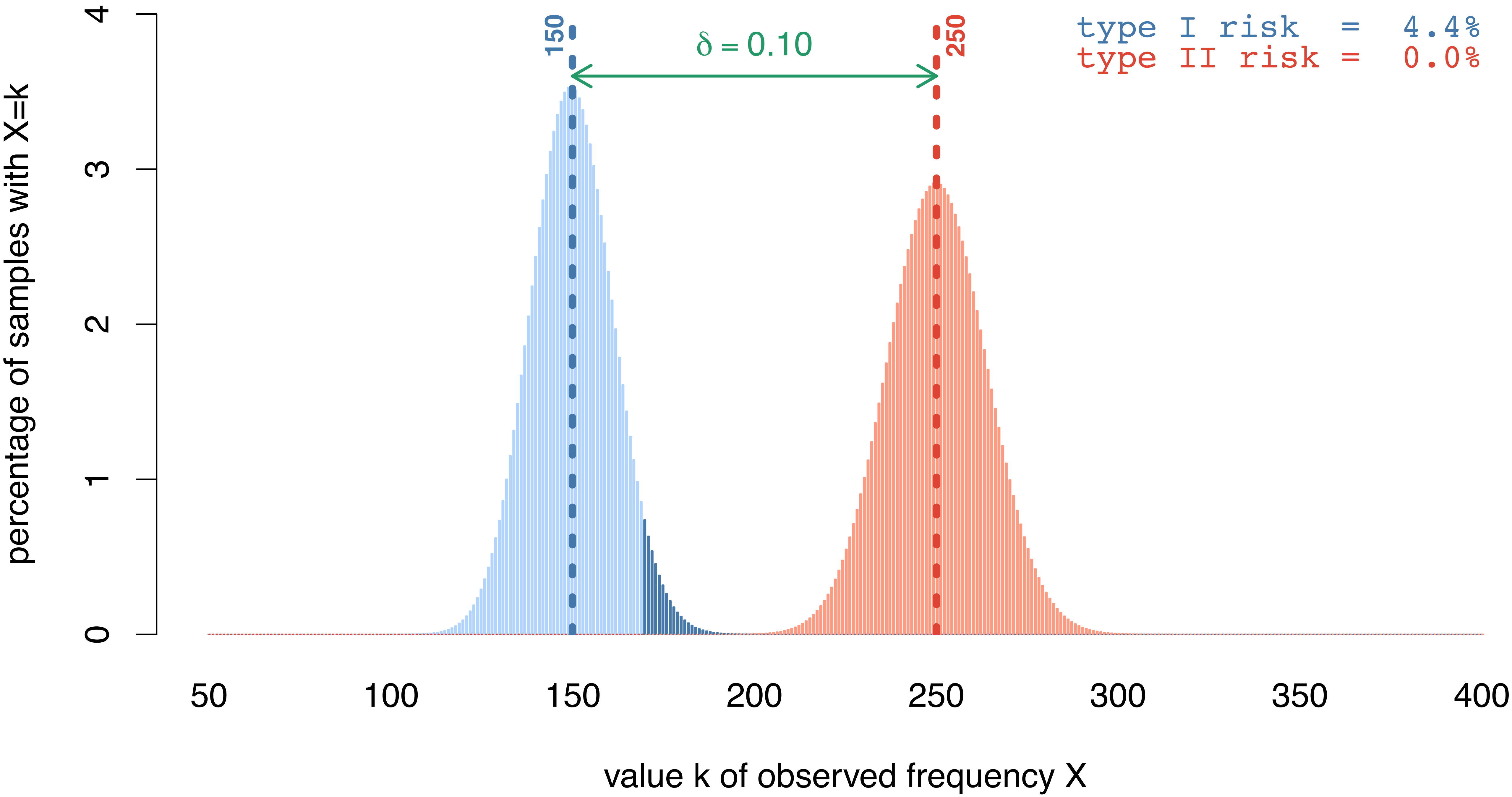

Power

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- Type II error = failure to reject incorrect H_o
  - the larger the difference between H_o and the true population proportion, the more likely it is that H_o can be rejected based on a given sample
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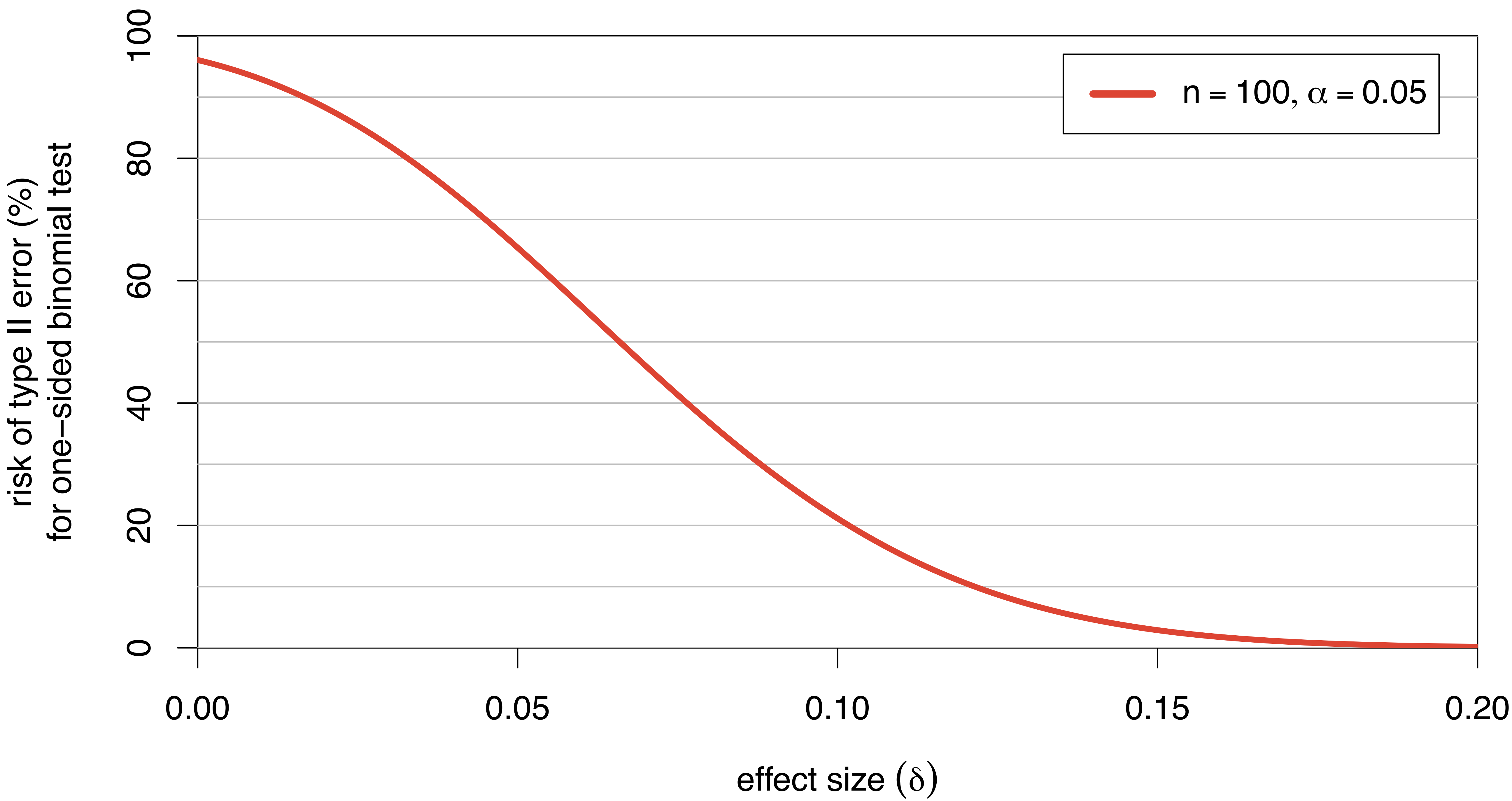
  - power analysis explores the relationship between effect size and risk of type II error
- Key insight: larger sample = more power
  - relative sampling variation becomes smaller
  - power also depends on significance level

Power analysis for binomial test



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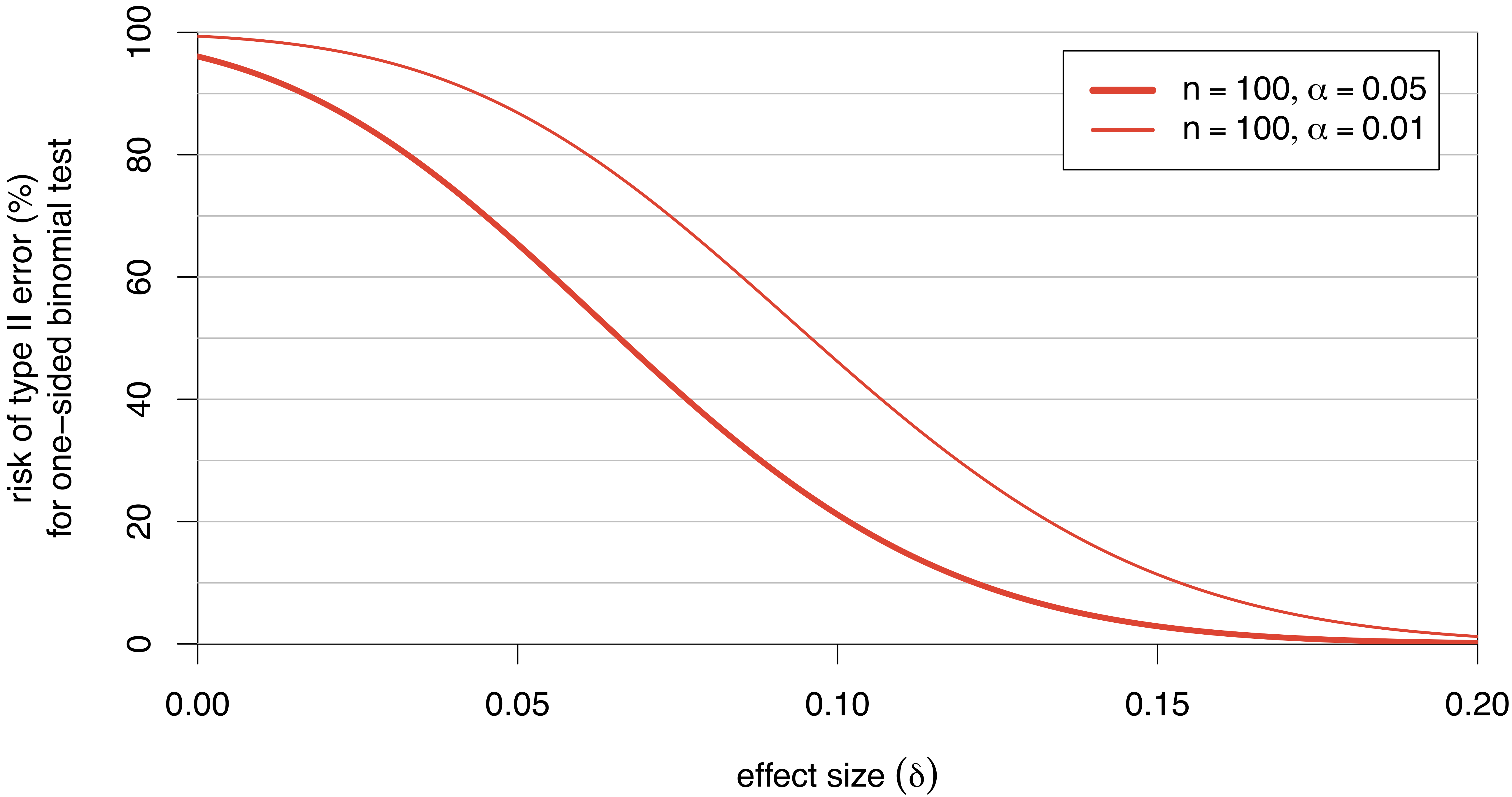

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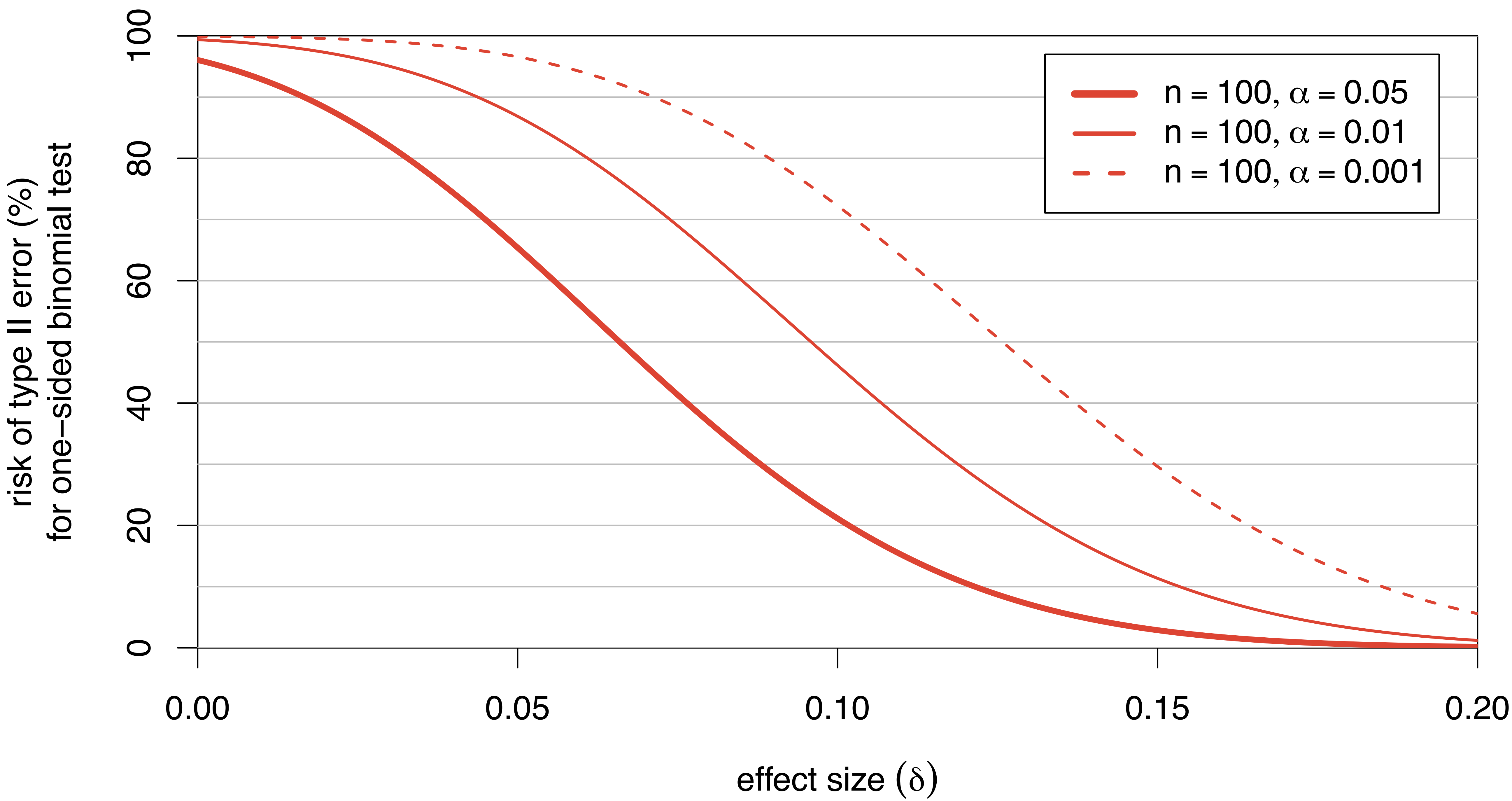

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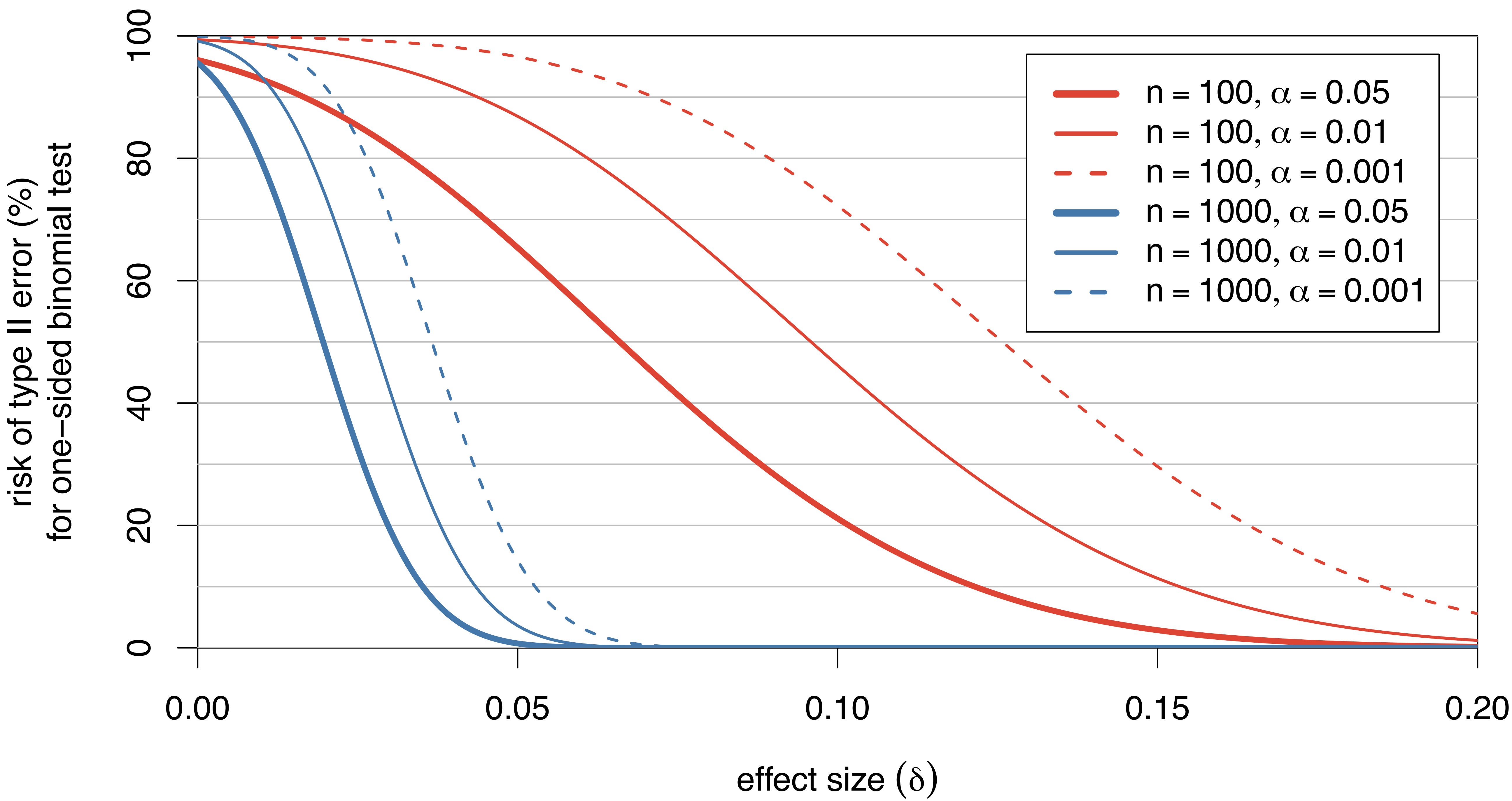

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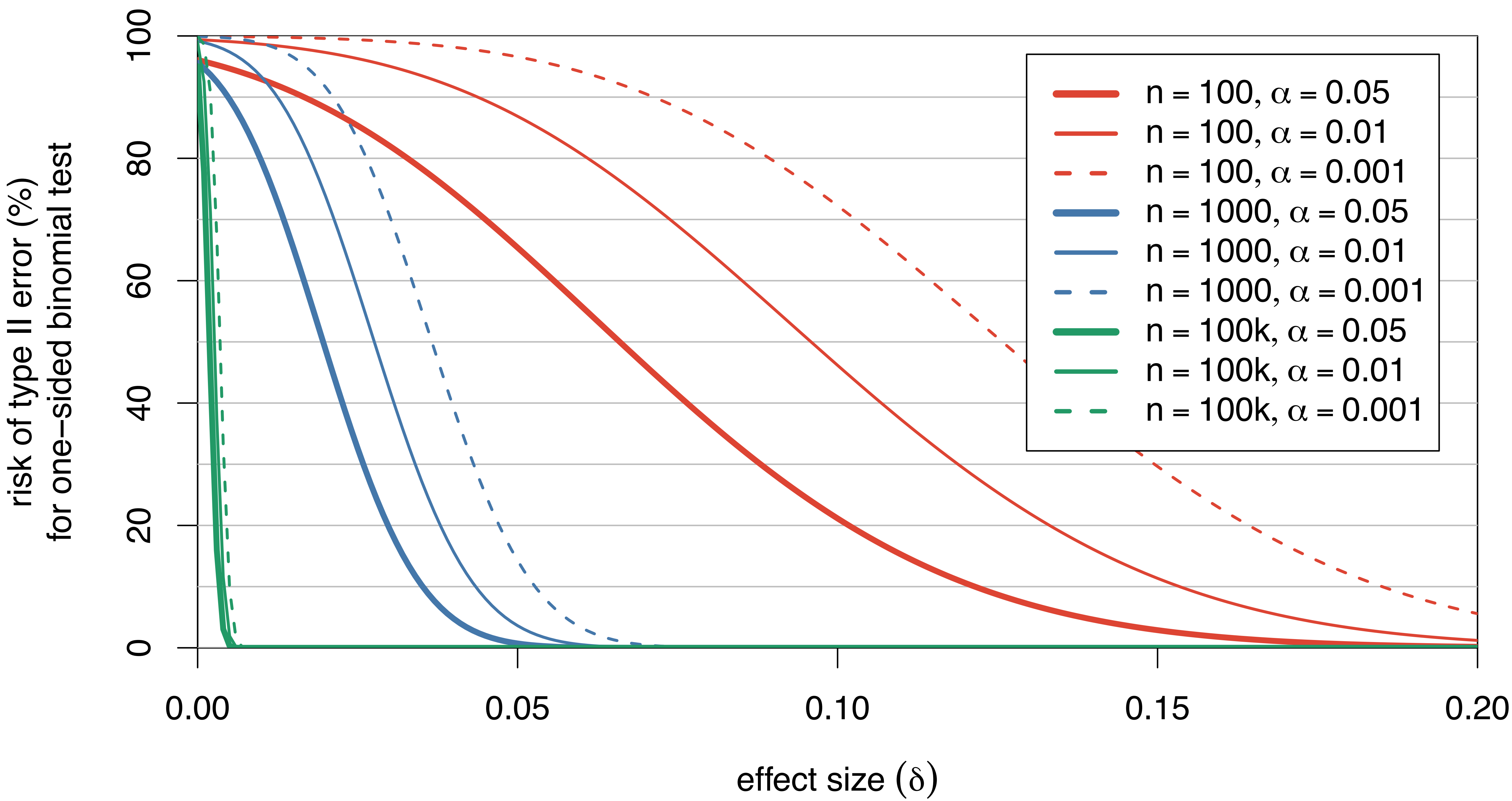

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- Influence of hypothesis test procedure
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  - parametric tests more powerful than non-parametric
  - statisticians look for "uniformly most powerful" test
- Tests can become too powerful!
  - reject 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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- Significance level
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- Conservative tests
  - put more weight on avoiding type I errors $\rightarrow$ weaker
  - most non-parametric methods are conservative

Confidence interval

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- But what if we do not have an obvious null hypothesis to start with?
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- 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:
$k = 190$ / $n = 1000$

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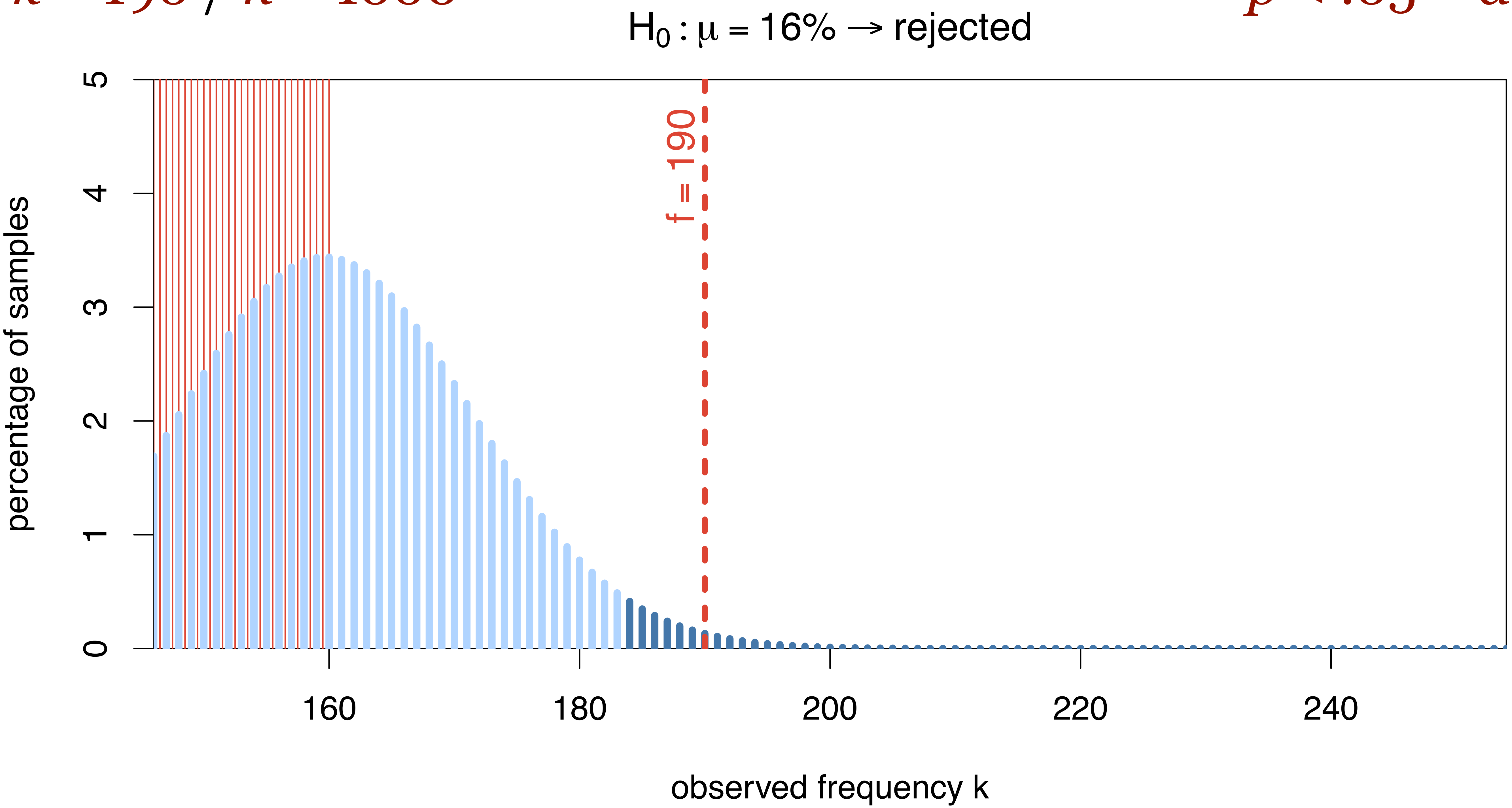
95% confidence
$p < .05 = \alpha$



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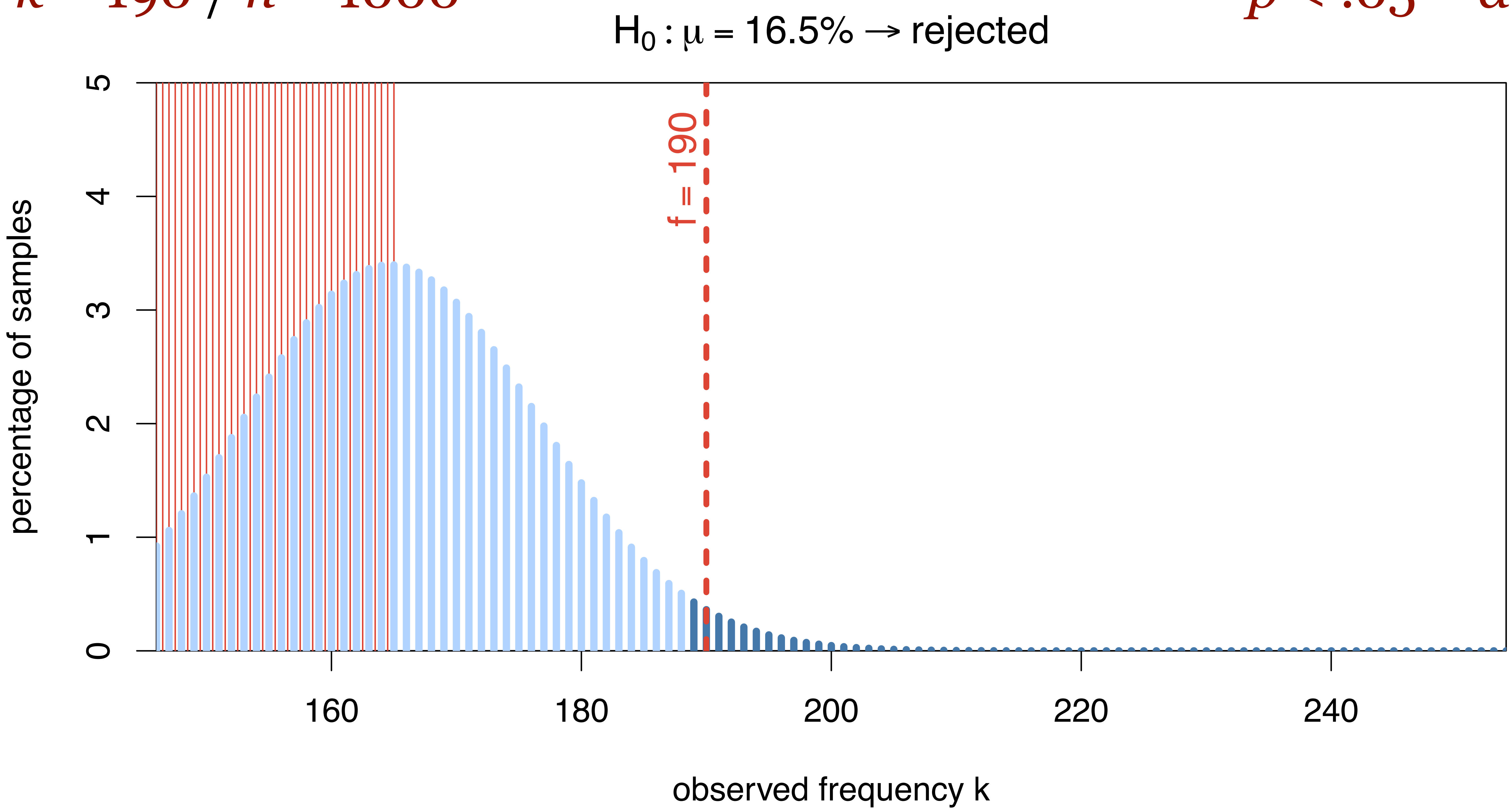

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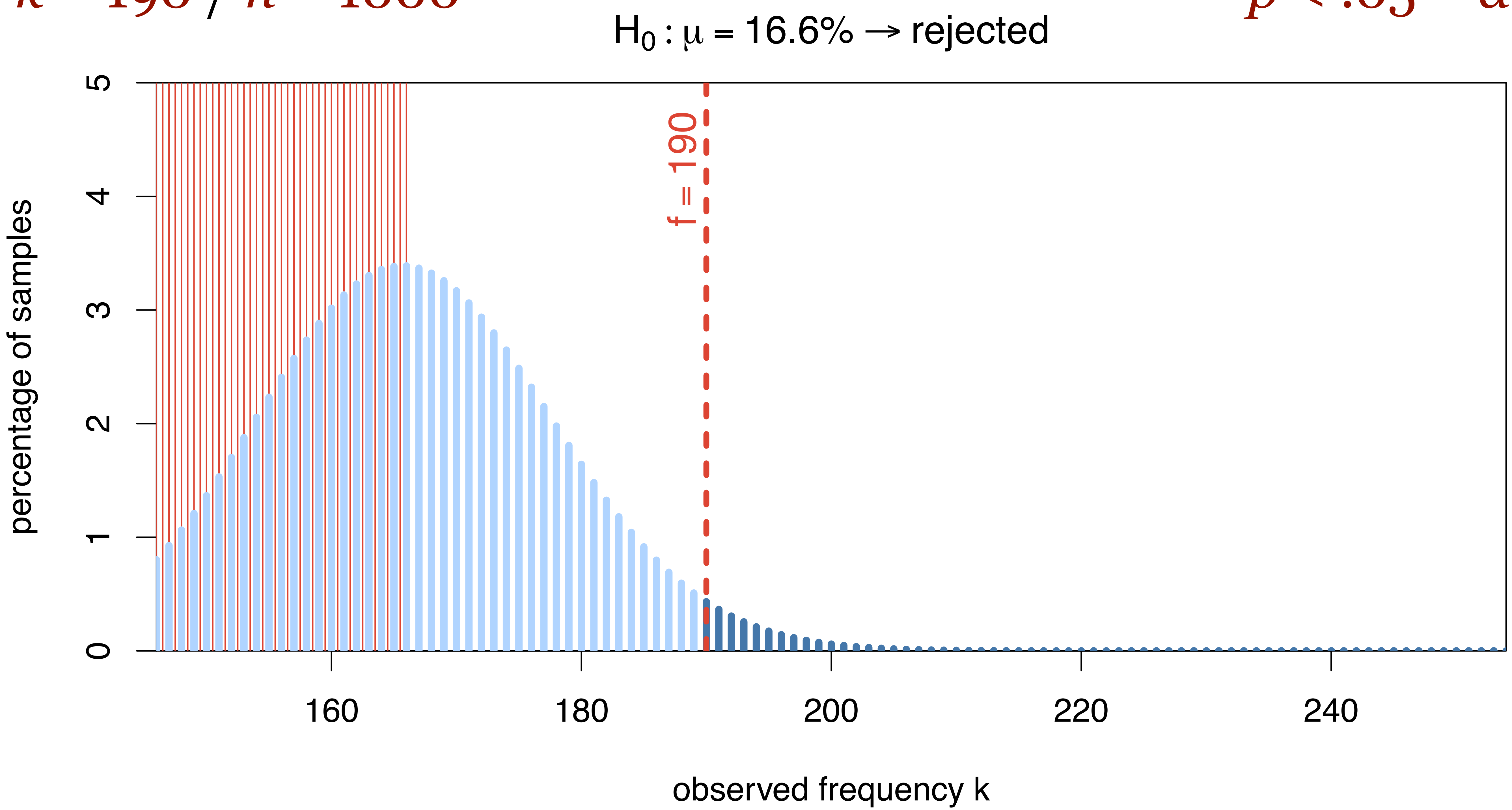

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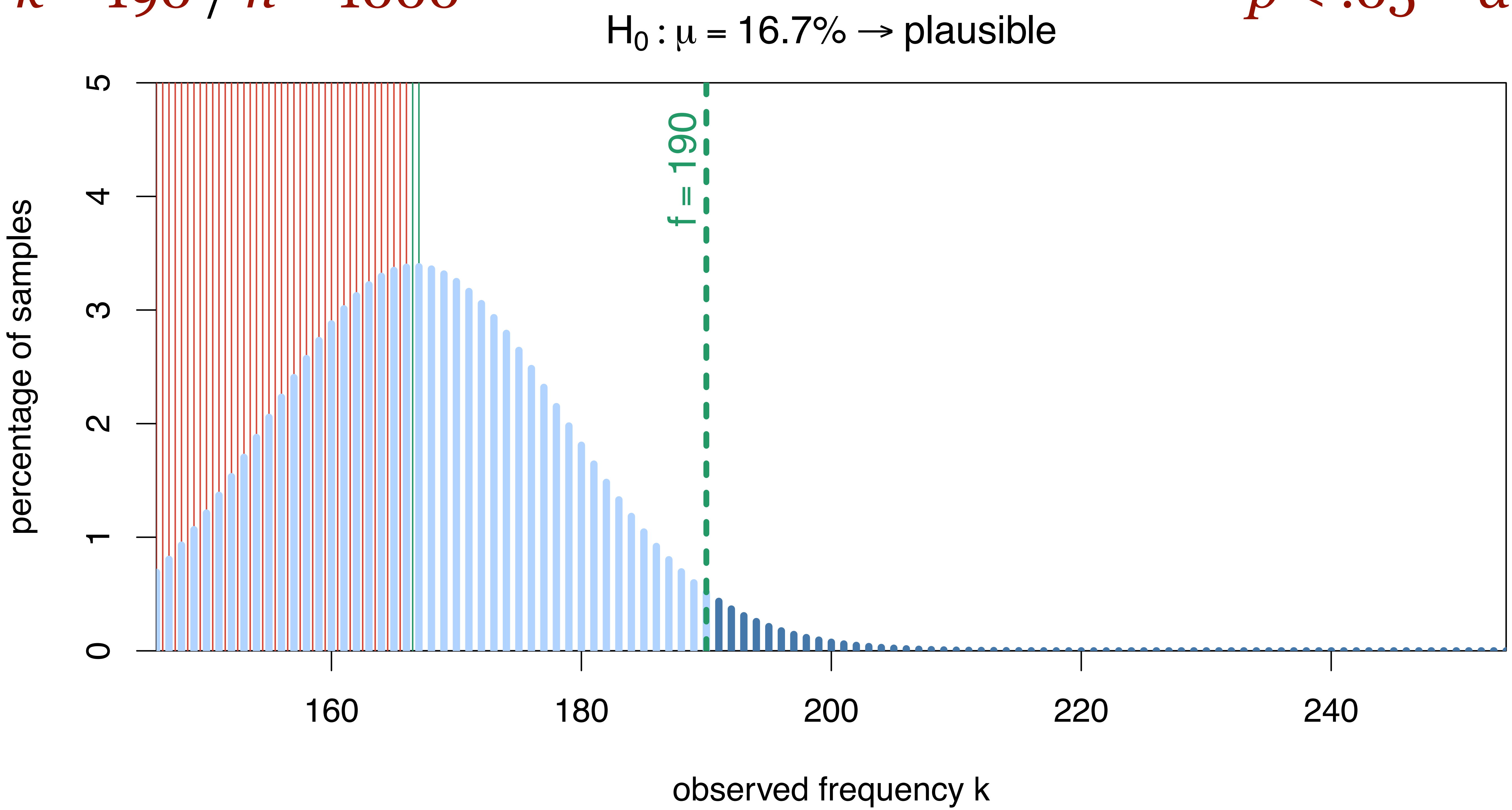

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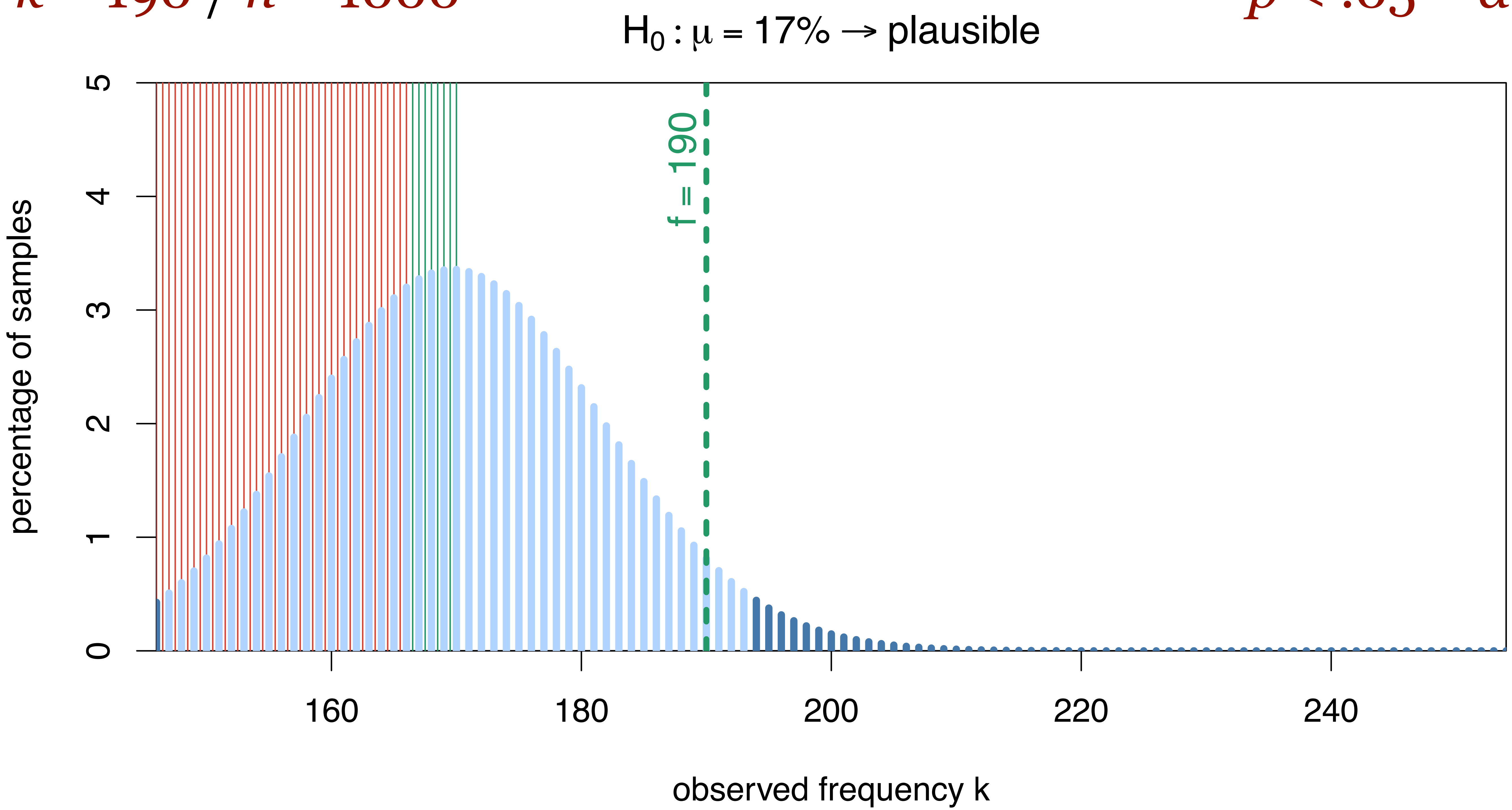

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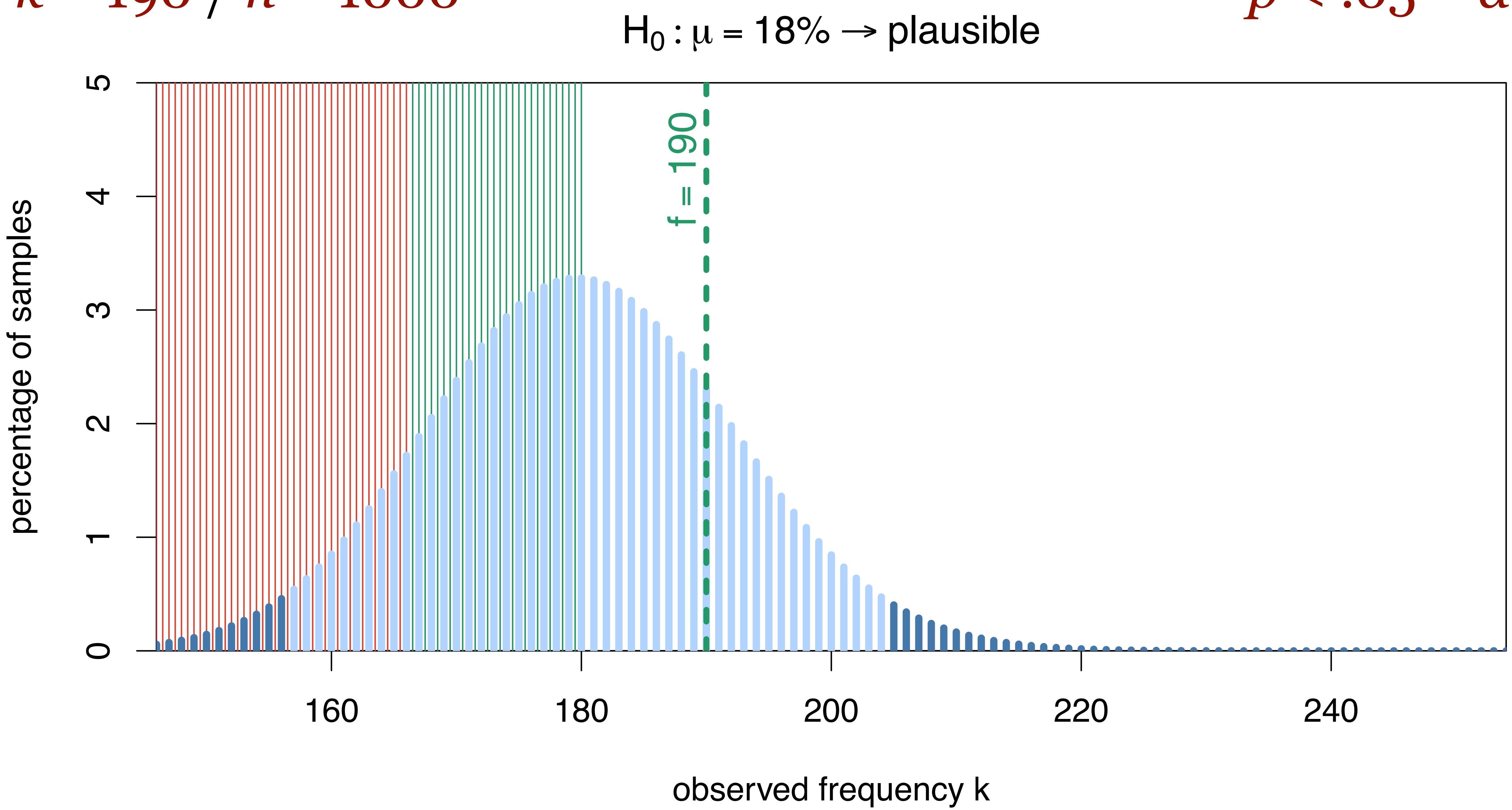

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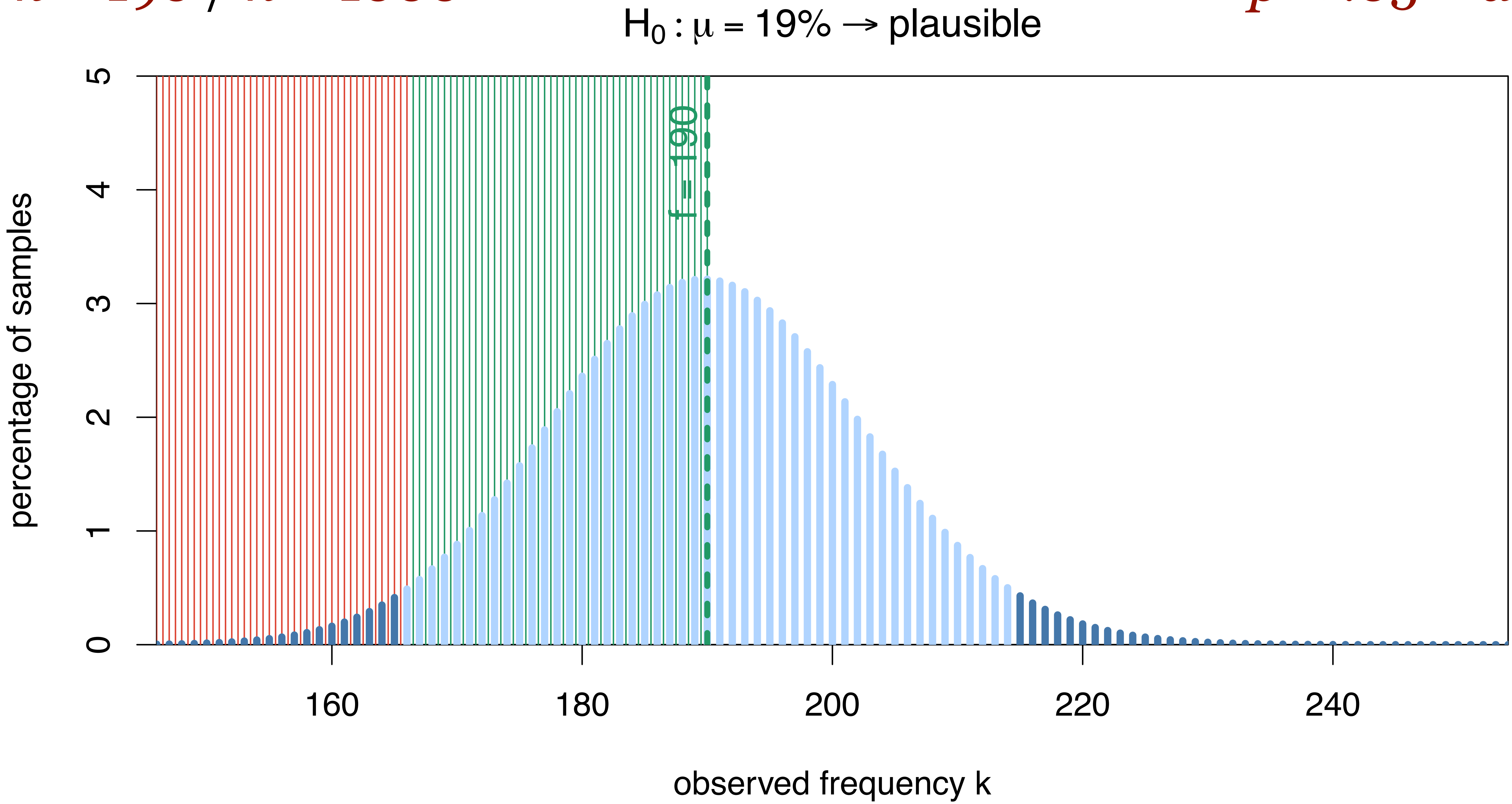

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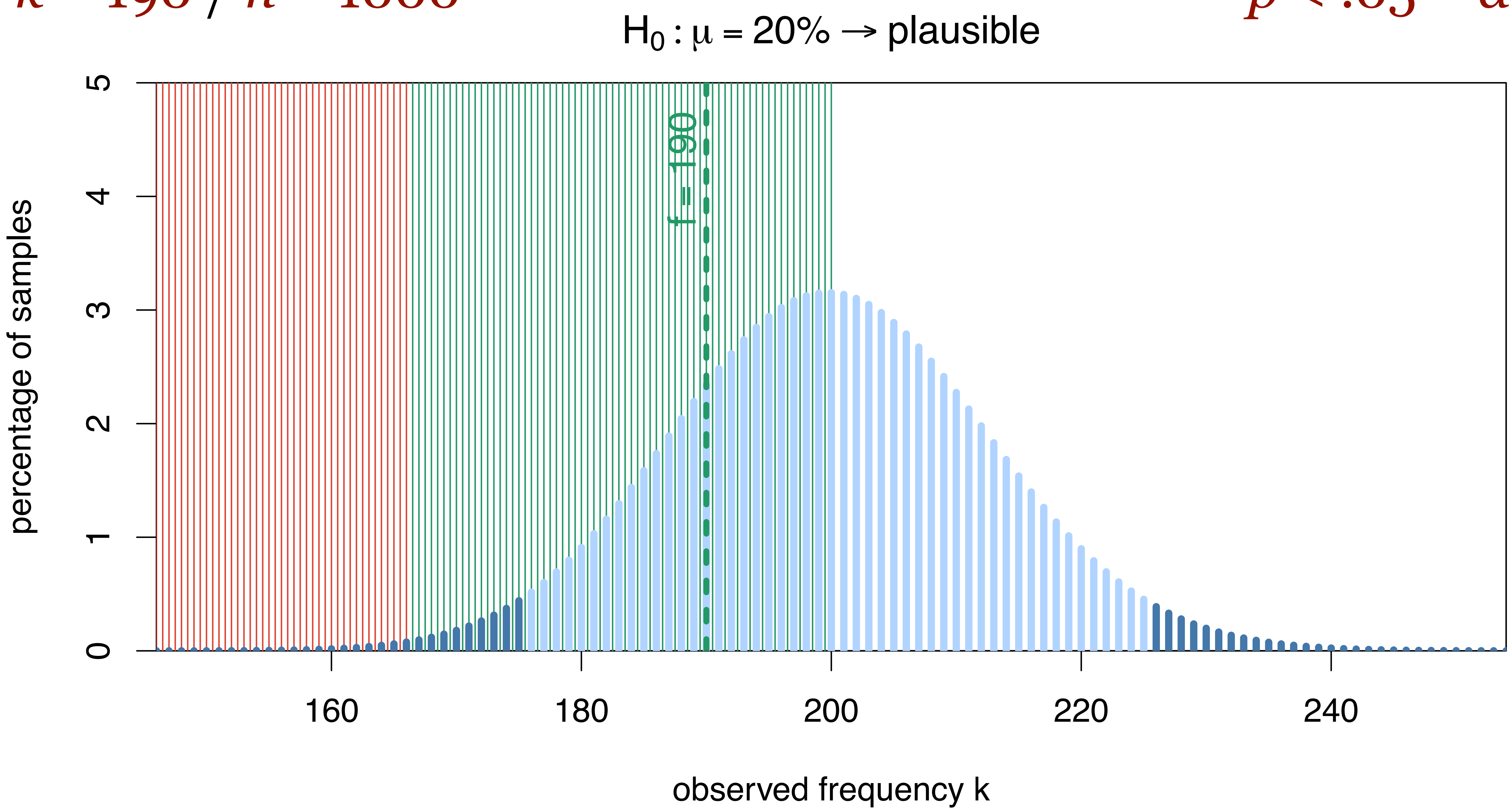

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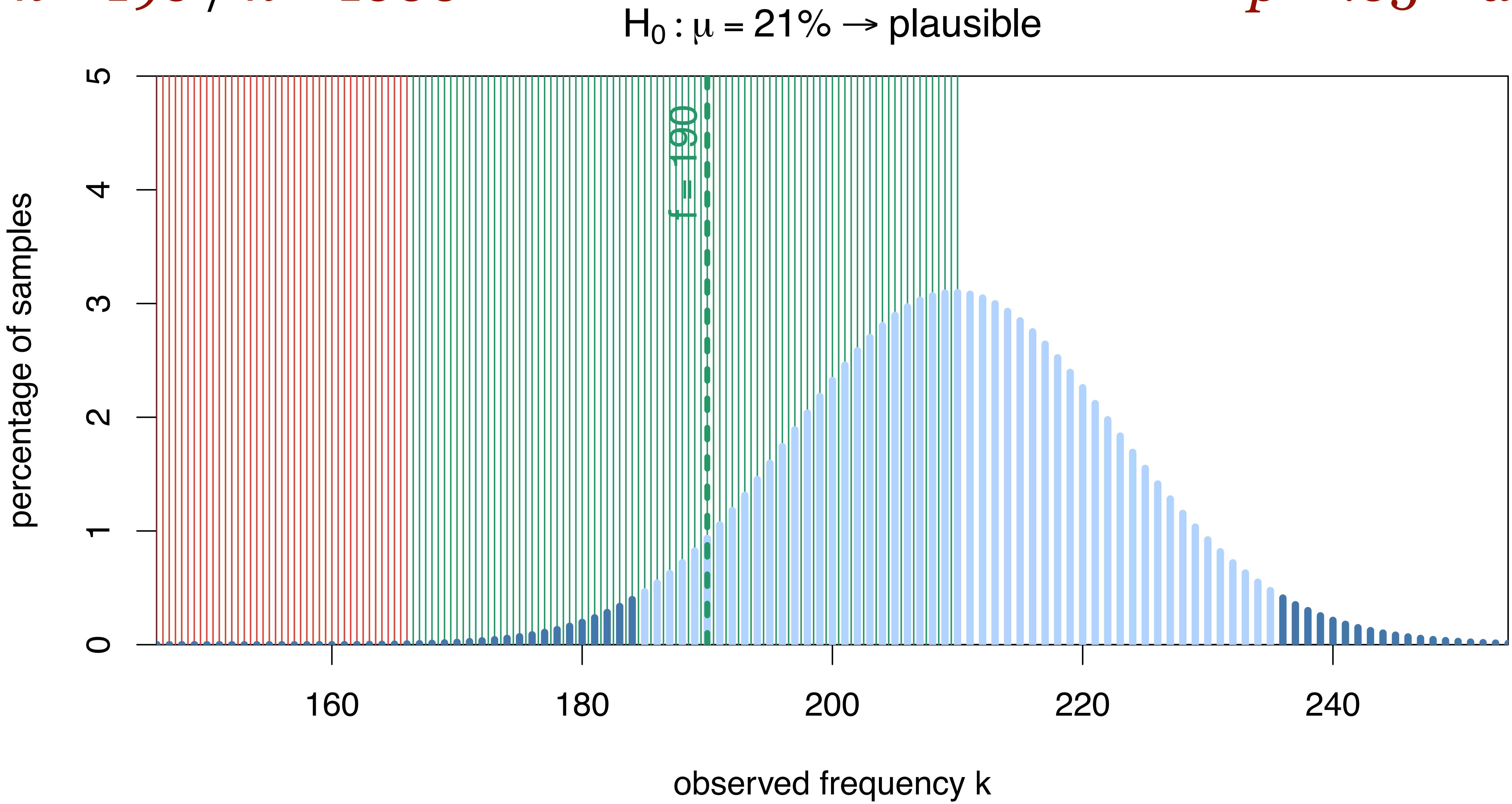

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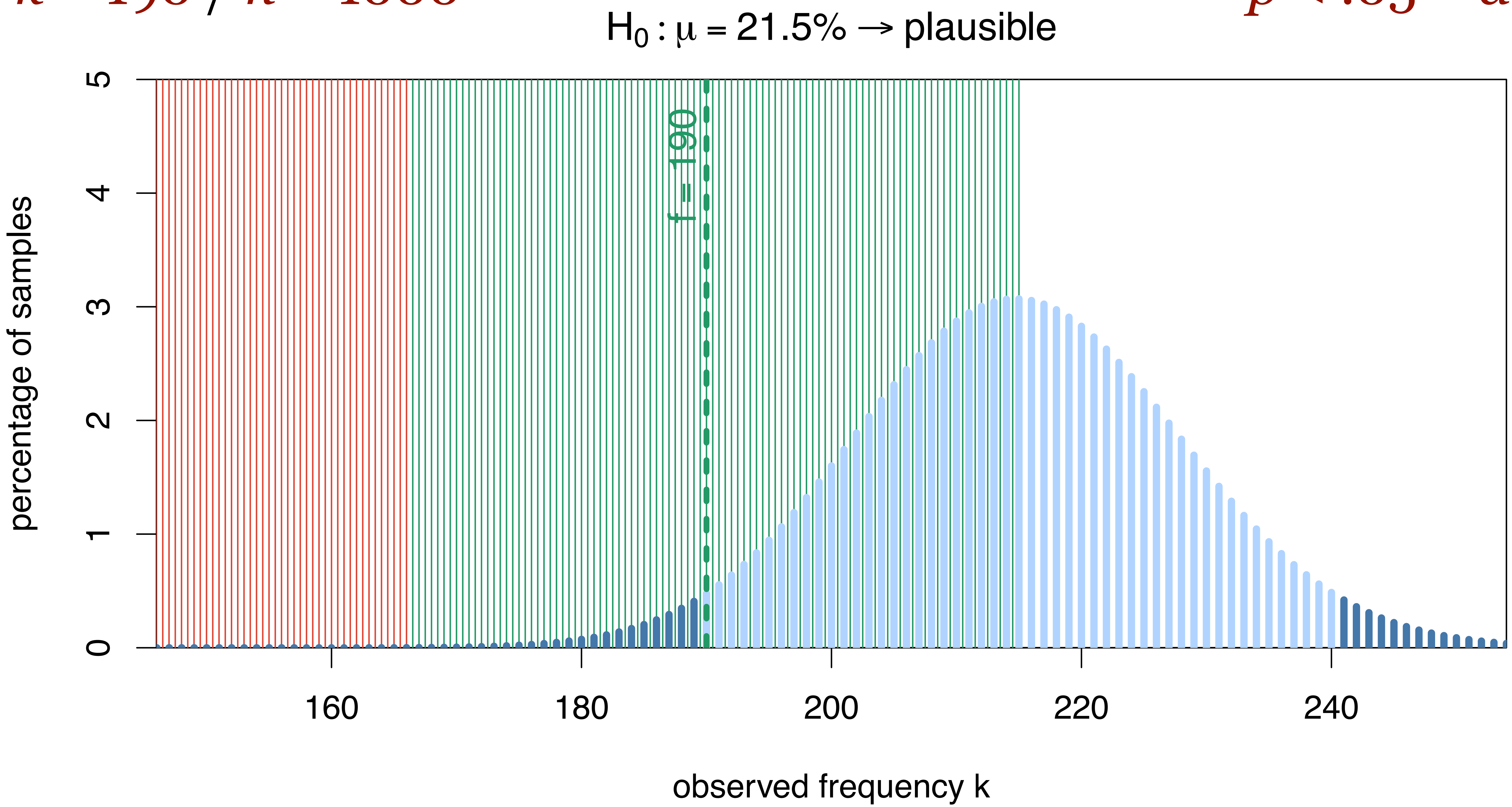

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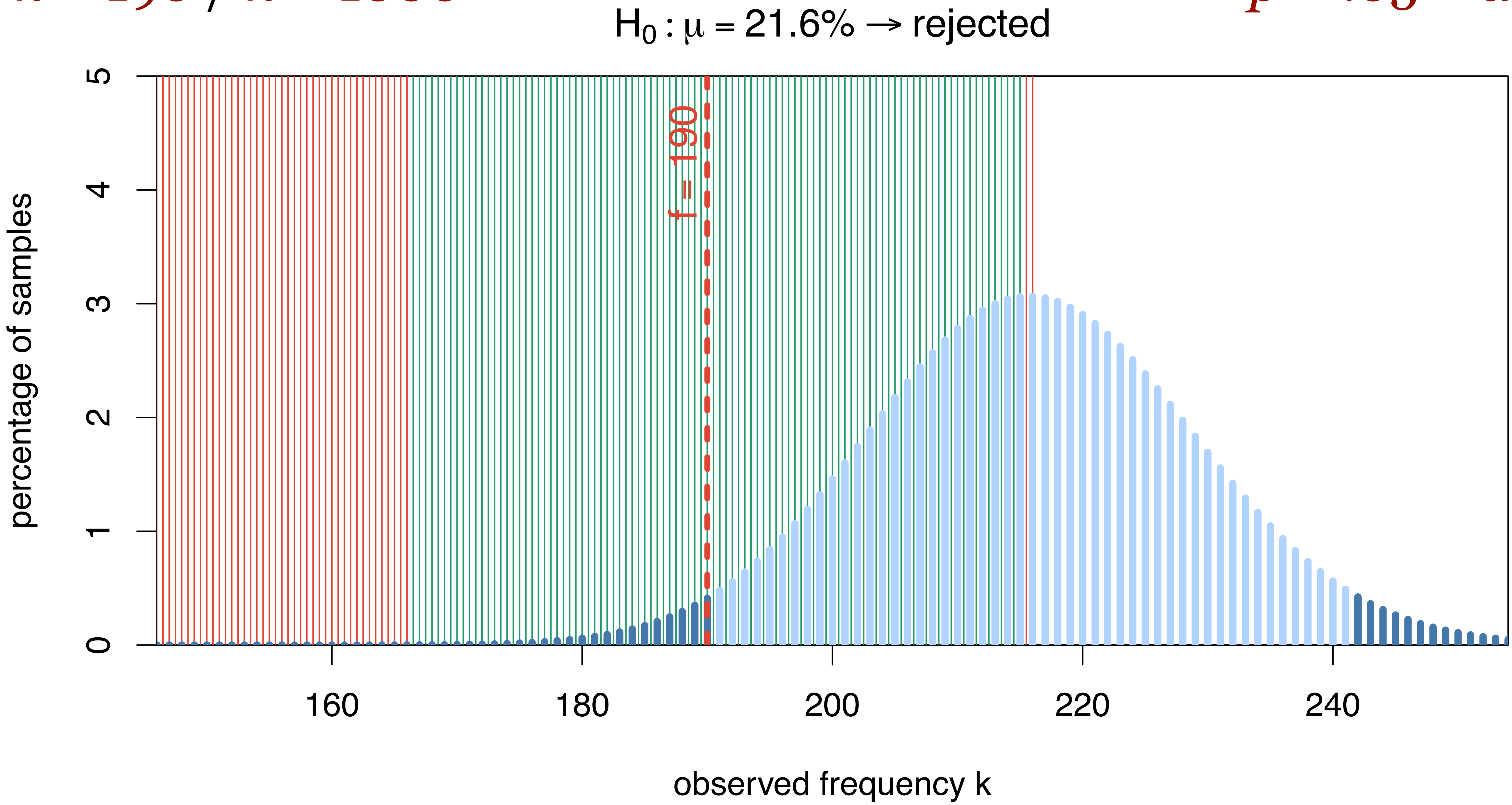

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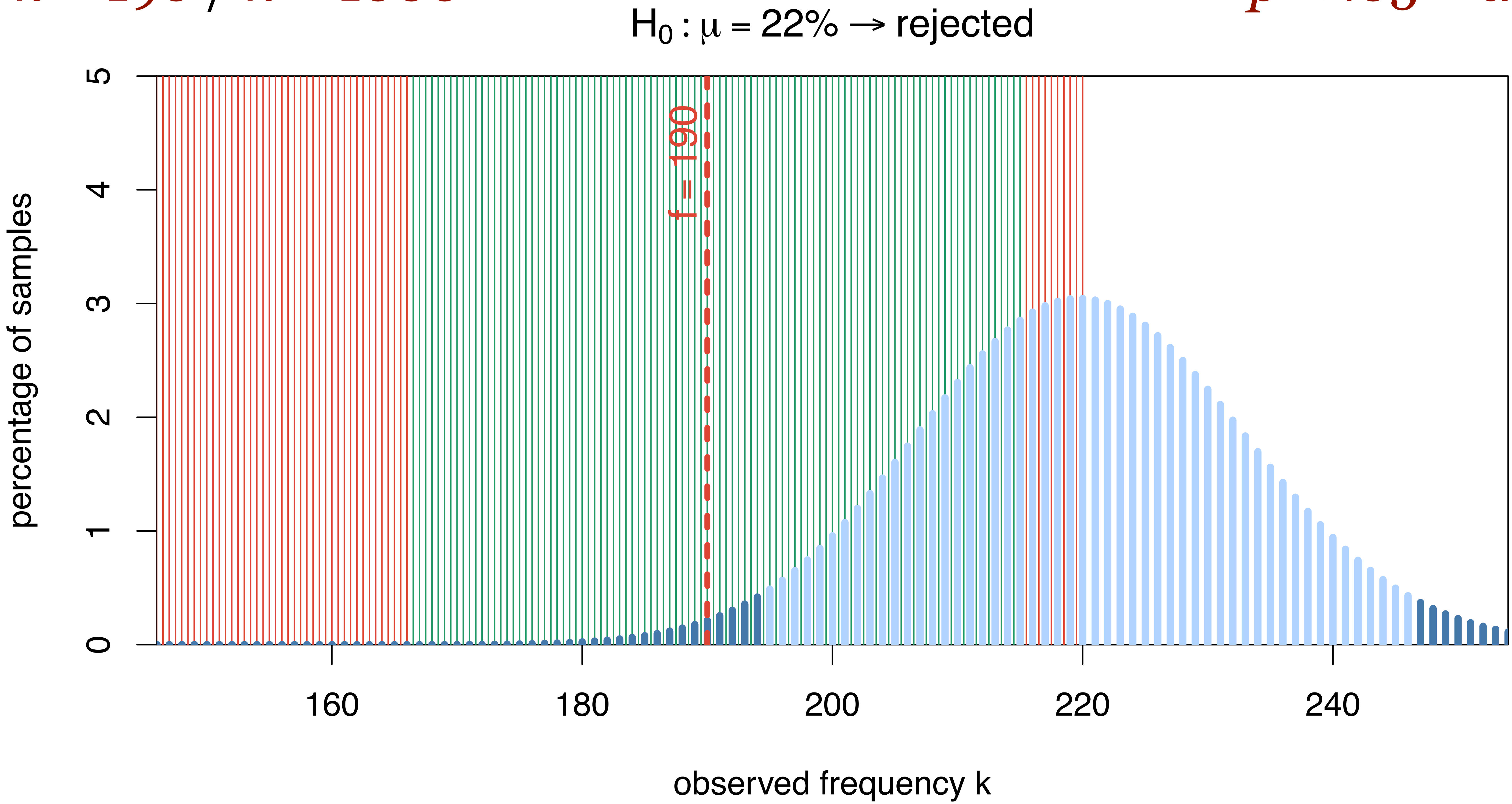

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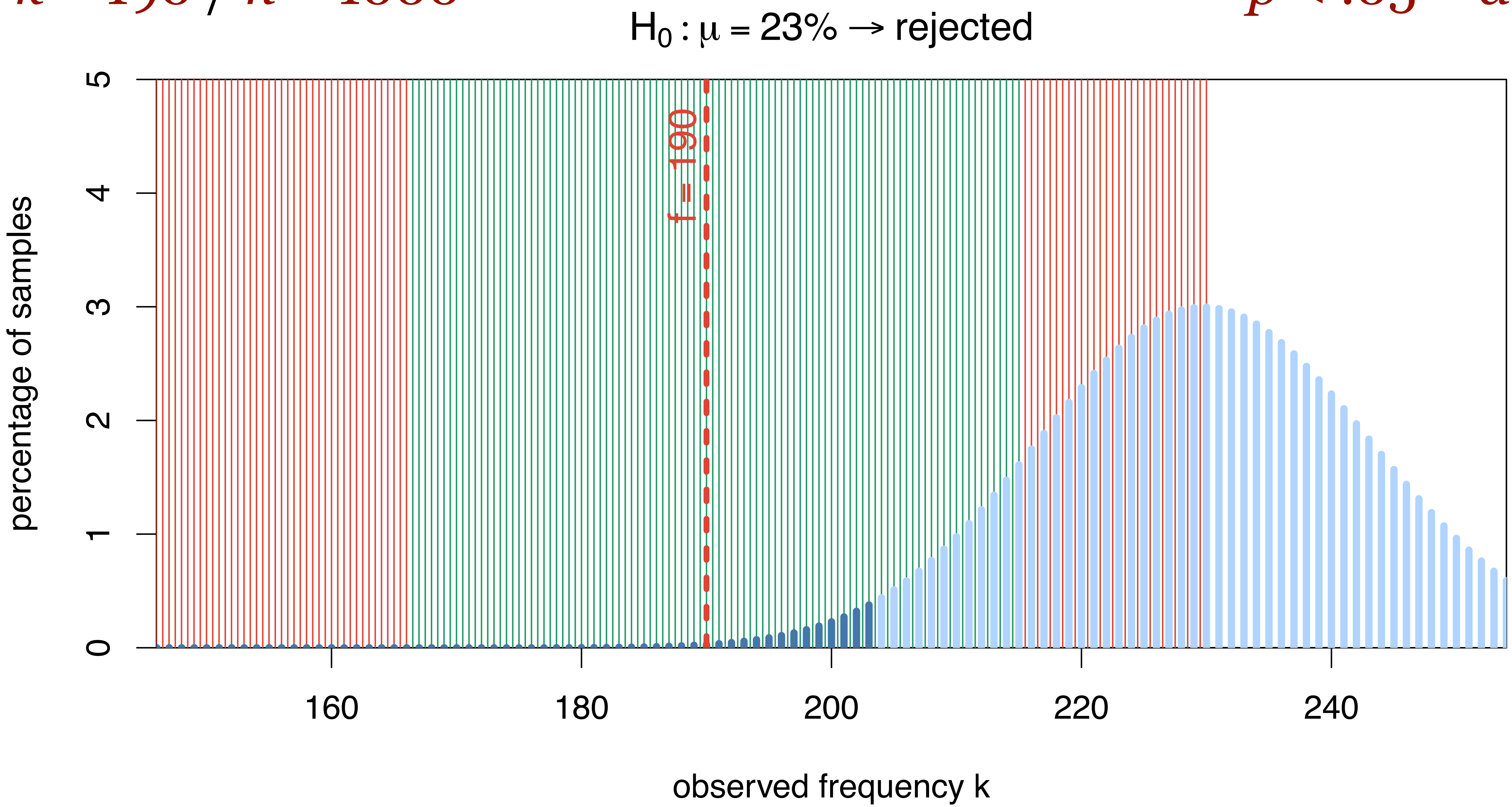

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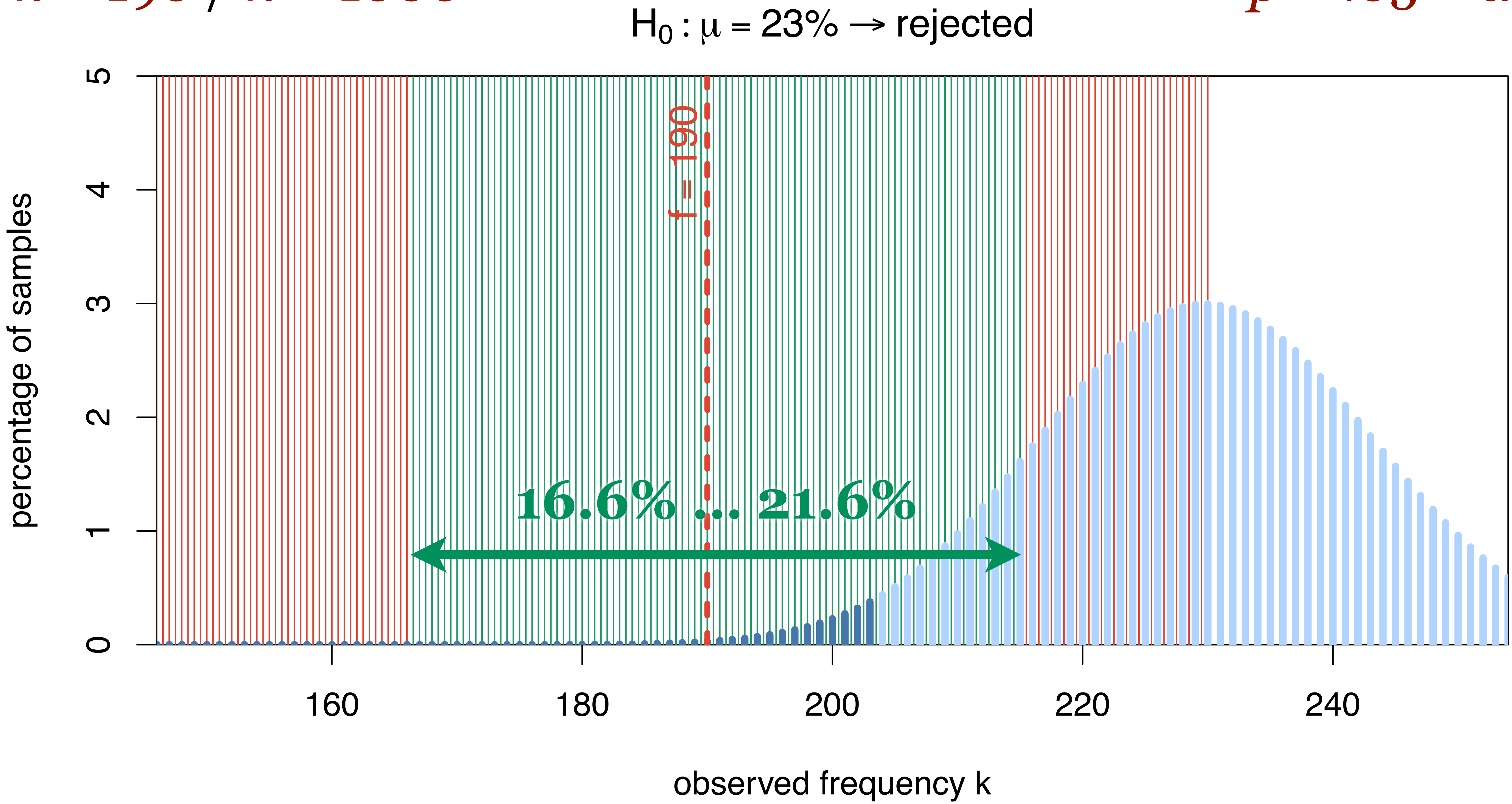

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- Can also compute one-sided confidence interval
  - controlled by `alternative` parameter
  - two-sided confidence intervals strongly recommended

Confidence intervals in R

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   Exact binomial test

data:  190 and 1000

number of successes = 190, number of
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alternative hypothesis: true probability of
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99 percent confidence interval:
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sample estimates:
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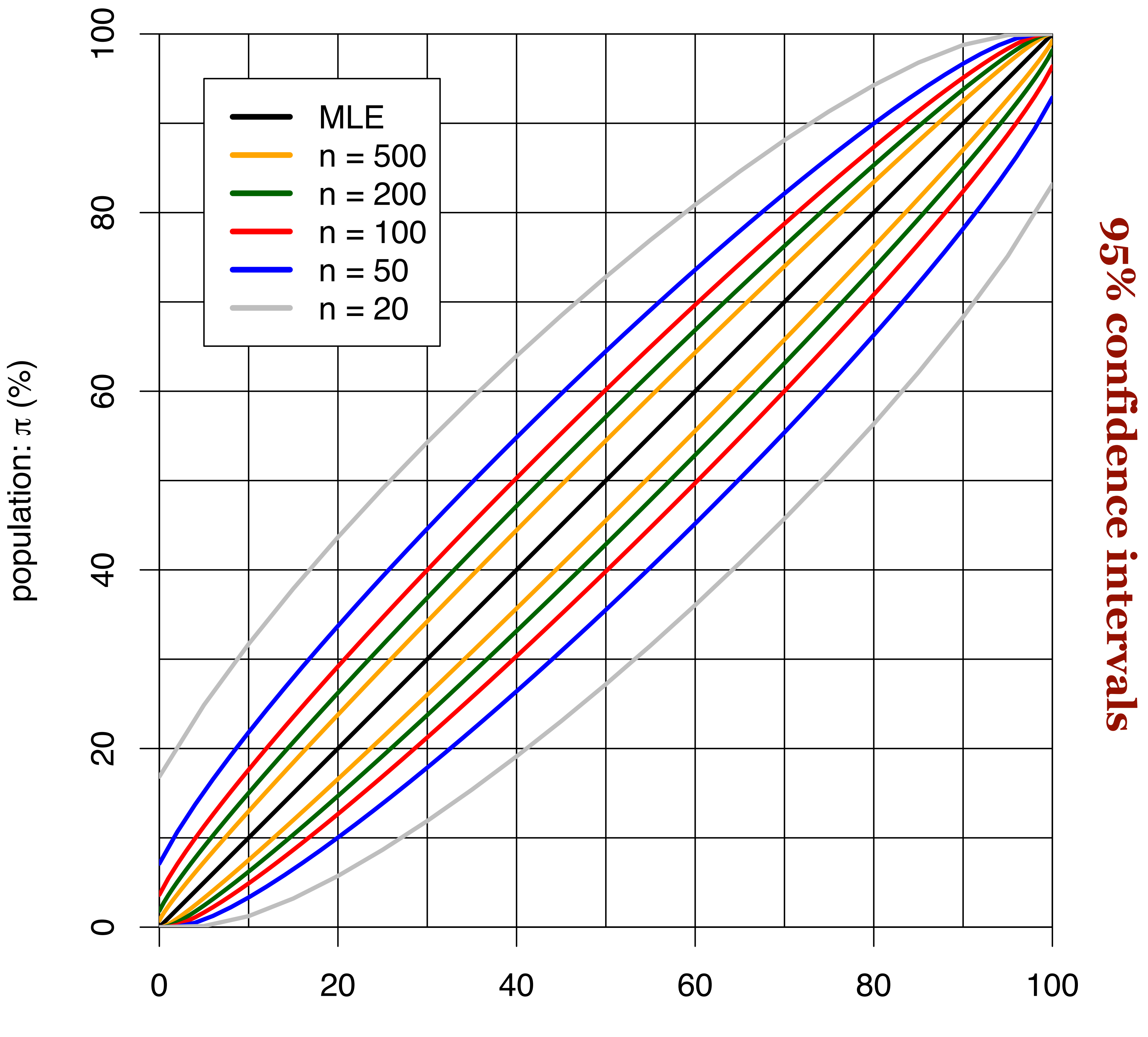

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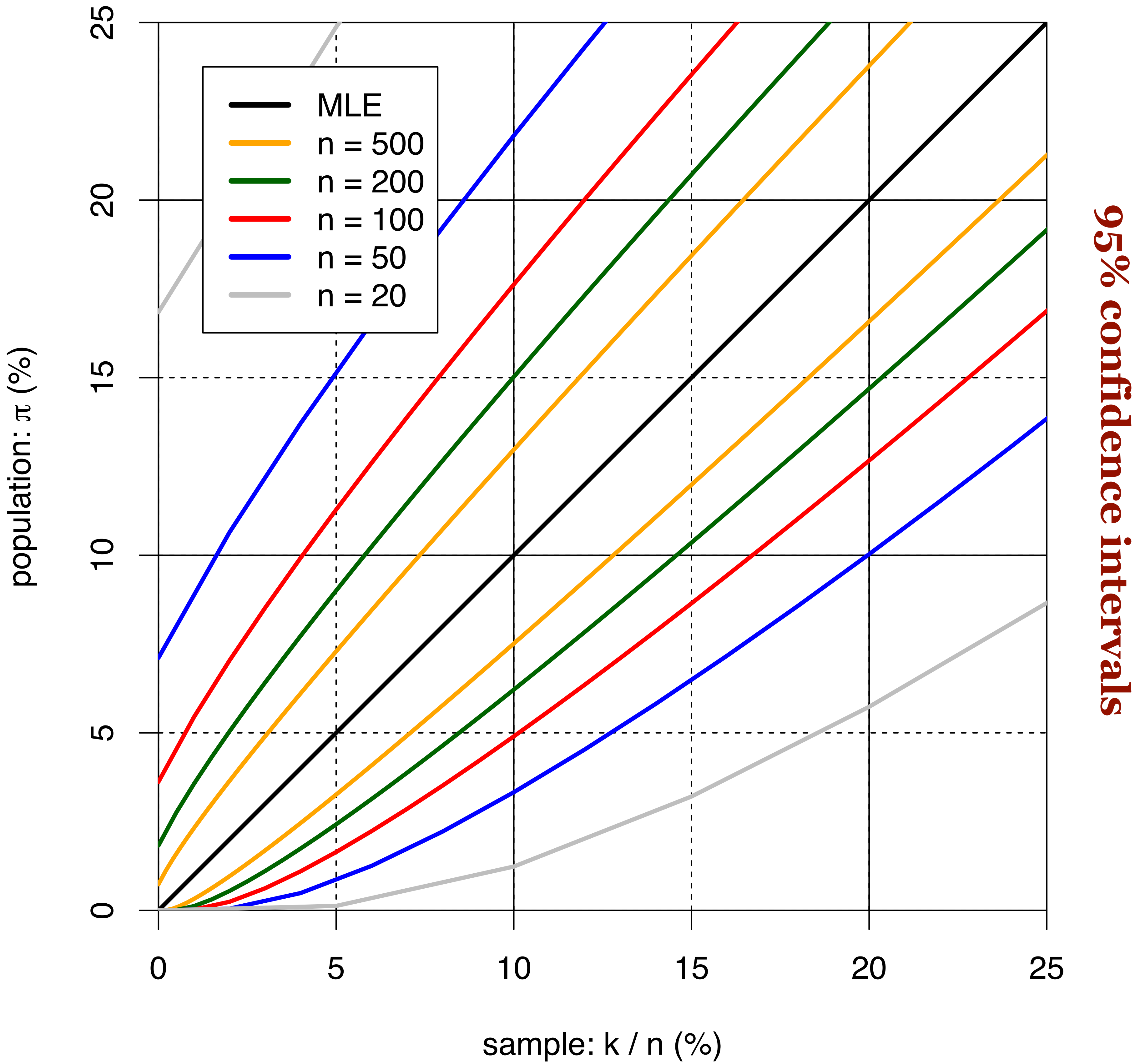

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- The `corpora` package has a vectorised function

```
> library(corpora)
> prop.cint(190, 1000, conf.level=.99)
> ?prop.cint  # “conf. intervals for proportions”
```

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- Compare observed frequencies in two samples

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- 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: $\delta = 0$)

Frequency comparison in R

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- Frequency comparison test: `prop.test()`
  - observed data: counts k_i and sample sizes n_i
  - also computes confidence interval for effect size

Frequency comparison in R

- Frequency comparison test: `prop.test()`
  - observed data: counts k_i and sample sizes n_i
  - 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

```
> 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
	n_1	n_2

19	25
81	175
100	200

- 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
  - generalization to larger tables possible

Tests for contingency tables

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  - computationally expensive, mostly for small samples

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  - X^2 can be translated into corresponding p-value
  - suitable for large samples and small balanced samples

Tests for contingency tables

- **Fisher's exact test** = generalization of binomial test to contingency tables
  - computationally expensive, mostly for small samples
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  - larger value of $X^2 \rightarrow$ less likely under H_0
  - X^2 can be translated into corresponding p-value
  - suitable for large samples and small balanced samples
- **Likelihood-ratio test** based on statistic G^2
  - popular in collocation and keyword identification
  - suitable for highly skewed data

Tests for contingency tables

- Can easily carry out chi-squared (`chisq.test`) and Fisher's exact test (`fisher.test`) in R
  - likelihood ratio test not included 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)
```

19	**25**
81	**175**

Significance vs. relevance

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- Much focus on significant p-value, but …

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  - large differences may be non-significant if sample size is too small (e.g. 10/80 = 12.5% vs. 20/80 = 25%)

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Significance vs. relevance

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  - increase sample size for more powerful/sensitive test
  - 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)

Significance vs. relevance

- Much focus on significant p-value, but …
  - large differences may be non-significant if sample size is too small (e.g. 10/80 = 12.5% vs. 20/80 = 25%)
  - increase sample size for more powerful/sensitive test
  - 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

Effect size in contingency tables

- Simple effect size measure: **difference of proportions**

$$\delta = \pi_1 - \pi_2$$

- H₀: $\delta = 0$

- Issues
  - depends on scale of π_1 and π_2
  - small effects for lexical freq's

π_1	π_2
$1-\pi_1$	$1-\pi_2$

population equivalent of a contingency table, which determines the multinomial sampling distribution

$$\hat{\pi}_1 = \frac{k_1}{n_1}$$

$$\hat{\pi}_2 = \frac{k_2}{n_2}$$

Effect size in contingency tables

- Effect size measure:
  (log) **relative risk**

$$r = \frac{\pi_1}{\pi_2}$$

- H_0: $r = 1$

- Issues
  - can be inflated for small π_2
  - mathematically inconvenient

π_1	π_2
$1-\pi_1$	$1-\pi_2$

population equivalent of a contingency table, which determines the multinomial sampling distribution

$$\hat{\pi}_1 = \frac{k_1}{n_1}$$

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Effect size in contingency tables

- Effect size measure: (log) **odds ratio**

$$\theta = \frac{\frac{\pi_1}{1-\pi_1}}{\frac{\pi_2}{1-\pi_2}} = \frac{\pi_1(1-\pi_2)}{\pi_2(1-\pi_1)}$$

- H_0: $\theta = 1$

π_1	π_2
$1-\pi_1$	$1-\pi_2$

population equivalent of a contingency table, which determines the multinomial sampling distribution

- Issues
  - can be inflated for small π_2
  - interpretation not very intuitive

$$\hat{\pi}_1 = \frac{k_1}{n_1}$$

$$\hat{\pi}_2 = \frac{k_2}{n_2}$$

Effect size in contingency tables

- Effect size measure:
  φ coefficient / Cramér *V*

$$\phi = \sqrt{\frac{X^2}{n}}$$

- H₀: ???

$$n = n_1 + n_2$$

π_1	π_2
$1-\pi_1$	$1-\pi_2$

population equivalent of a contingency table, which determines the multinomial sampling distribution

- Issues
  - this is a property of the sample rather than the population!

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$$\hat{\pi}_2 = \frac{k_2}{n_2}$$

Effect size in contingency tables

- Effect size measure:
  φ coefficient / Cramér *V*

$$\phi = \frac{\pi_1(1-\pi_2) - \pi_2(1-\pi_1)}{\sqrt{(r_1\pi_1 + r_2\pi_2)(1 - r_1\pi_1 - r_2\pi_2)/r_1 r_2}}$$

π_1	π_2
$1-\pi_1$	$1-\pi_2$

population equivalent of a contingency table, which determines the multinomial sampling distribution

- H_0: $\varphi = 0$

$$n = n_1 + n_2$$

$$r_1 = n_1 / n$$

$$r_2 = n_2 / n$$

- Issues
  - depends on relative sample sizes
  - interpretation entirely unclear

$$\hat{\pi}_1 = \frac{k_1}{n_1}$$

$$\hat{\pi}_2 = \frac{k_2}{n_2}$$

Effect size in contingency tables

π_1	π_2
$1-\pi_1$	$1-\pi_2$

population equivalent of a contingency table, which determines the multinomial sampling distribution

$$\hat{\pi}_1 = \frac{k_1}{n_1}$$

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Effect size in contingency tables

- We can estimate effect sizes by inserting sample values k_i/n_i

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$1-\pi_1$	$1-\pi_2$

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Effect size in contingency tables

- We can estimate effect sizes by inserting sample values k_i/n_i
- But such point estimates are meaningless!

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population equivalent of a contingency table, which determines the multinomial sampling distribution

$$\hat{\pi}_1 = \frac{k_1}{n_1}$$

$$\hat{\pi}_2 = \frac{k_2}{n_2}$$

Effect size in contingency tables

- We can estimate effect sizes by inserting sample values k_i/n_i
- But such point estimates are meaningless!
- Confidence intervals available only for some effect measures
  - approximate interval for δ from proportions test
  - exact interval for odds ratio θ from Fisher's test
  - φ computed from chi-square statistic is still a point estimate!

π_1	π_2
$1-\pi_1$	$1-\pi_2$

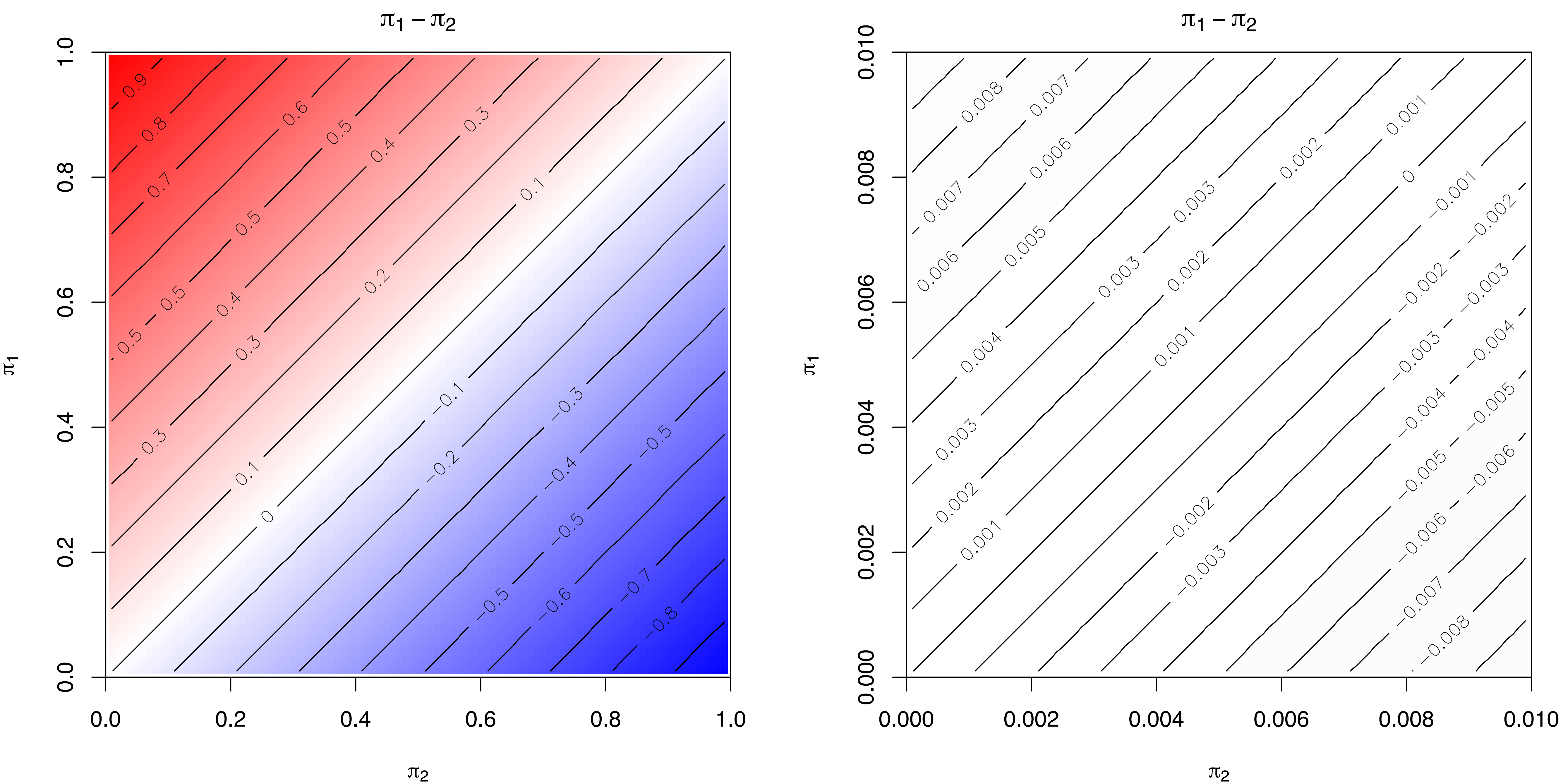
population equivalent of a contingency table, which determines the multinomial sampling distribution

$$\hat{\pi}_1 = \frac{k_1}{n_1}$$

$$\hat{\pi}_2 = \frac{k_2}{n_2}$$

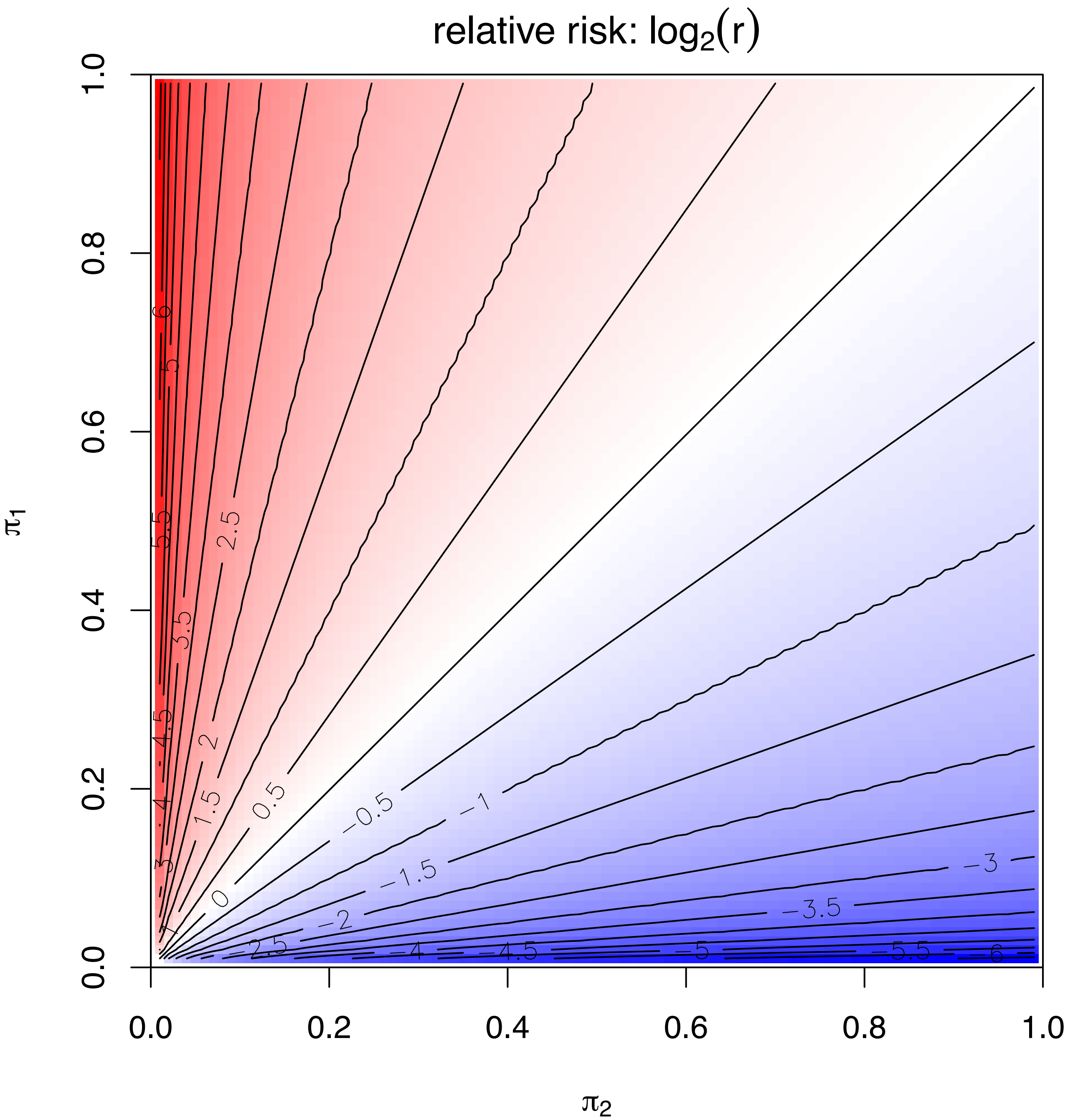
Visualizing effect size measures

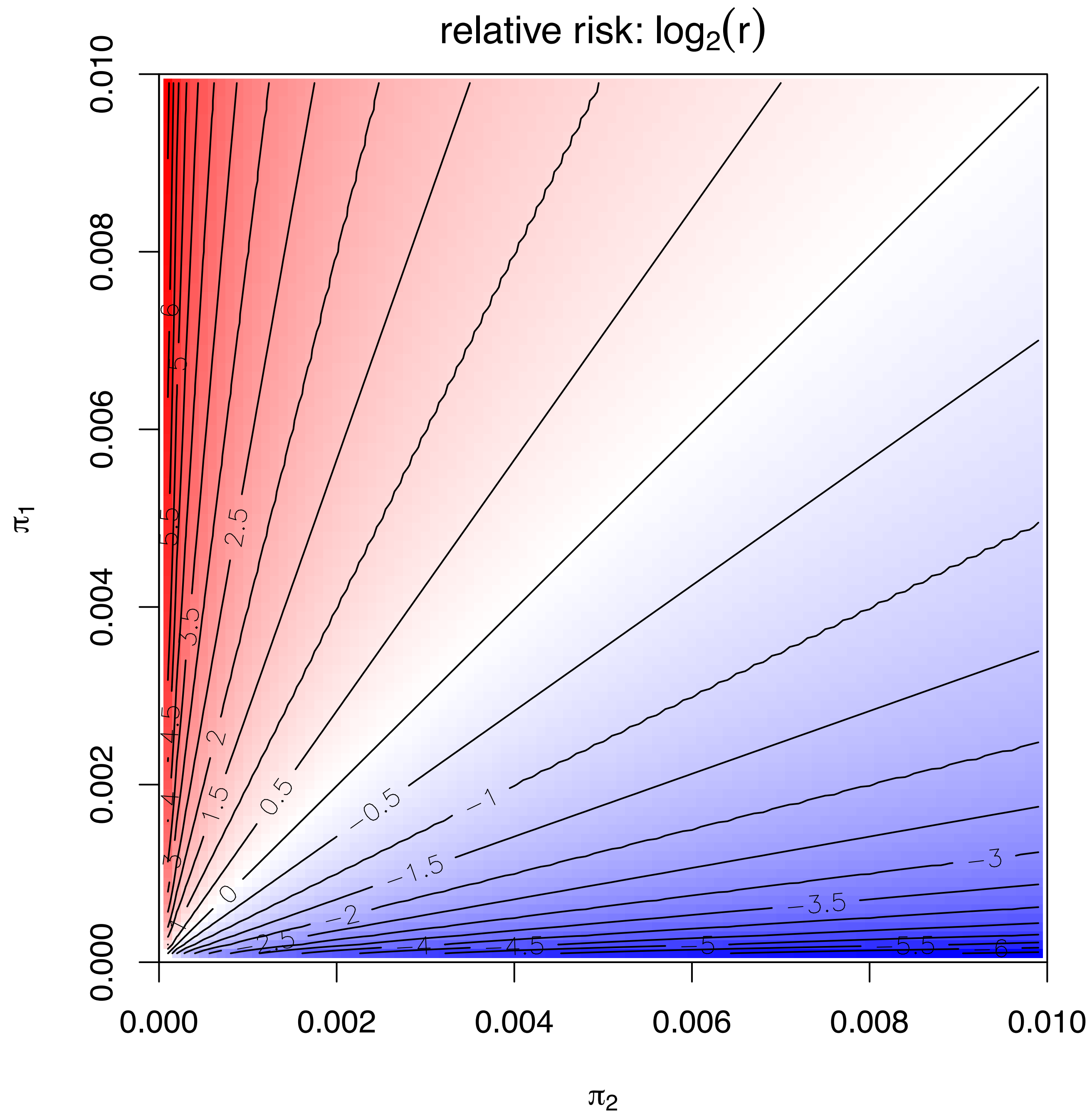
difference of proportions



Visualizing effect size measures

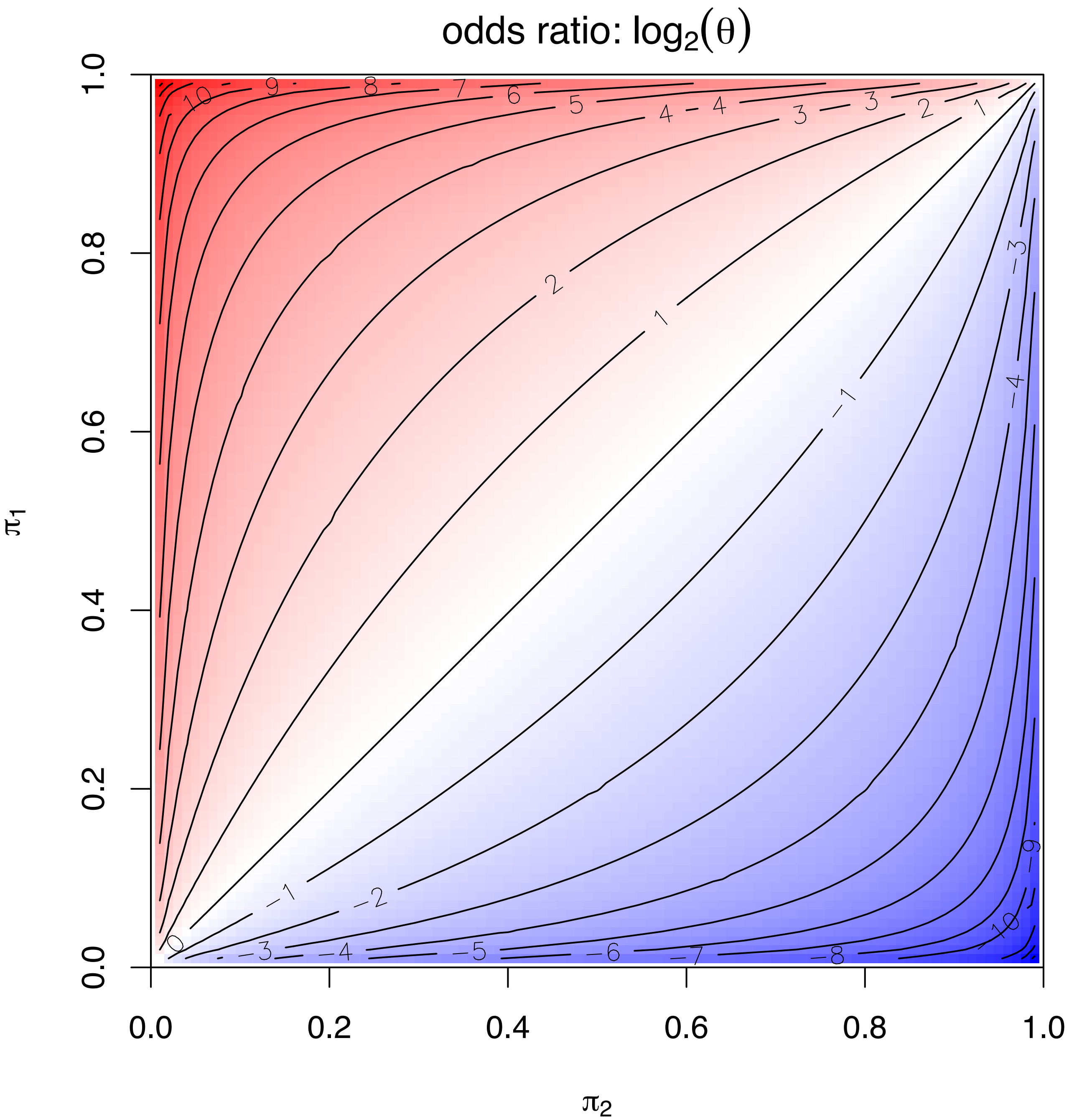
(log) relative risk

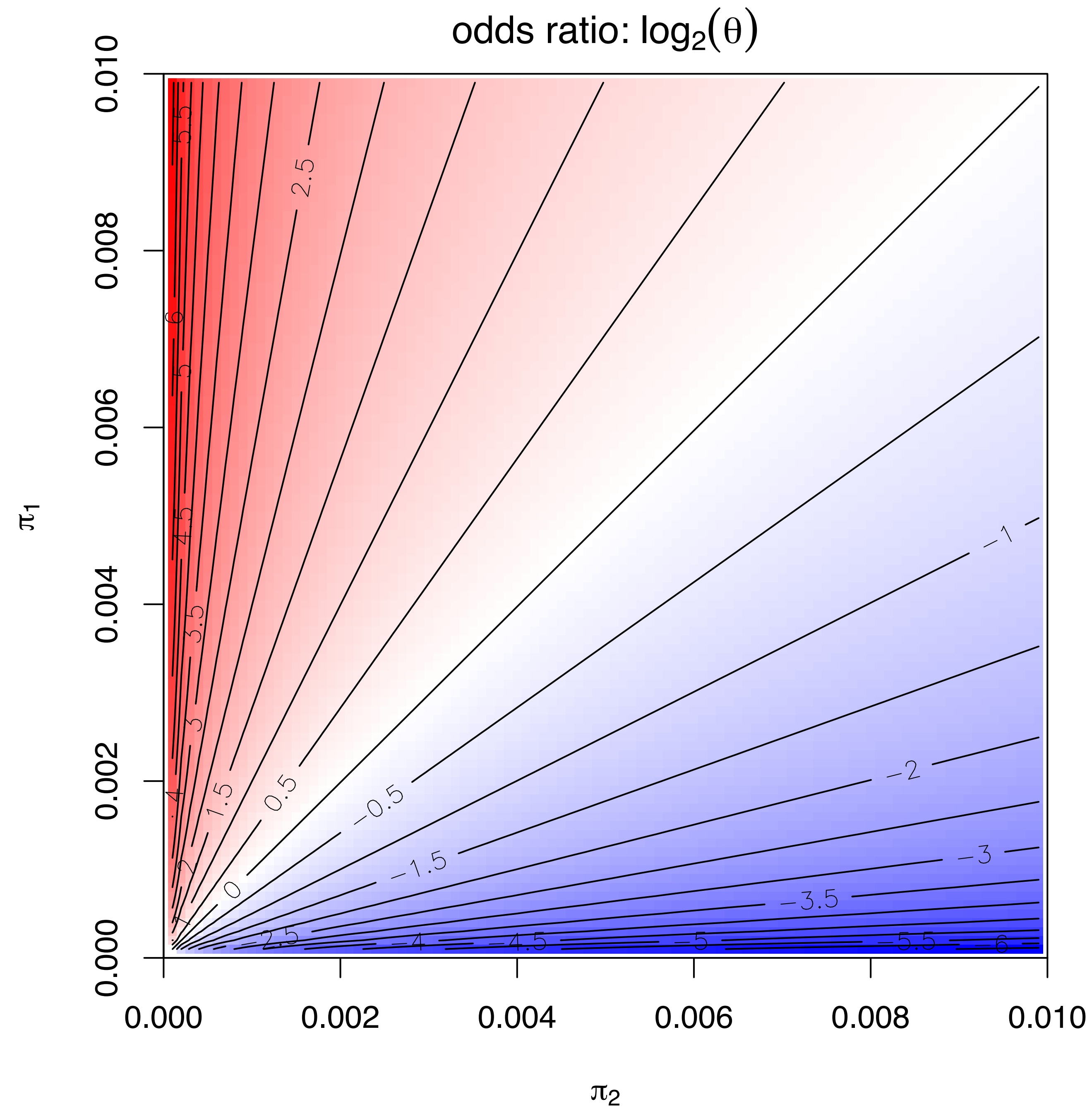




Visualizing effect size measures

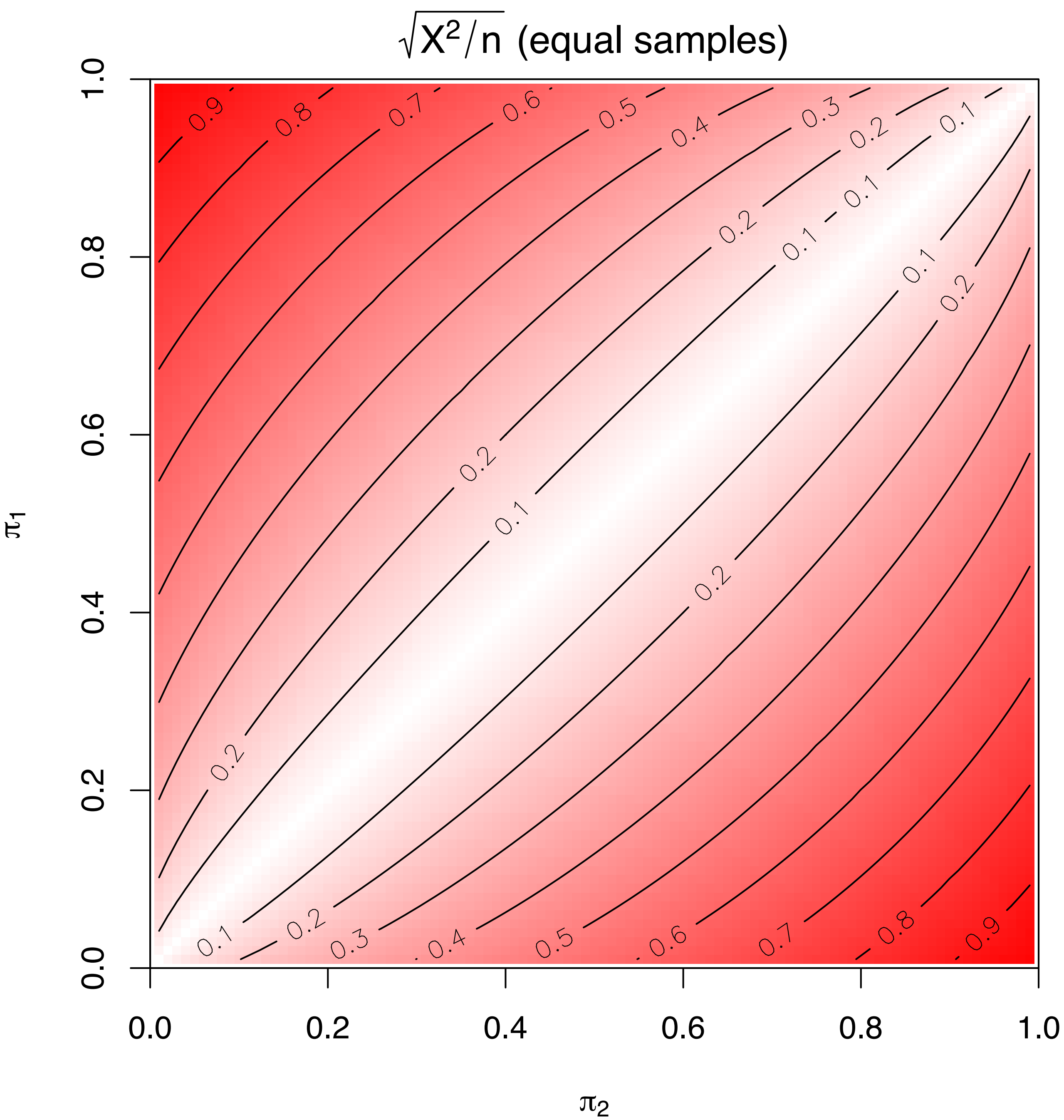
(log) odds ratio

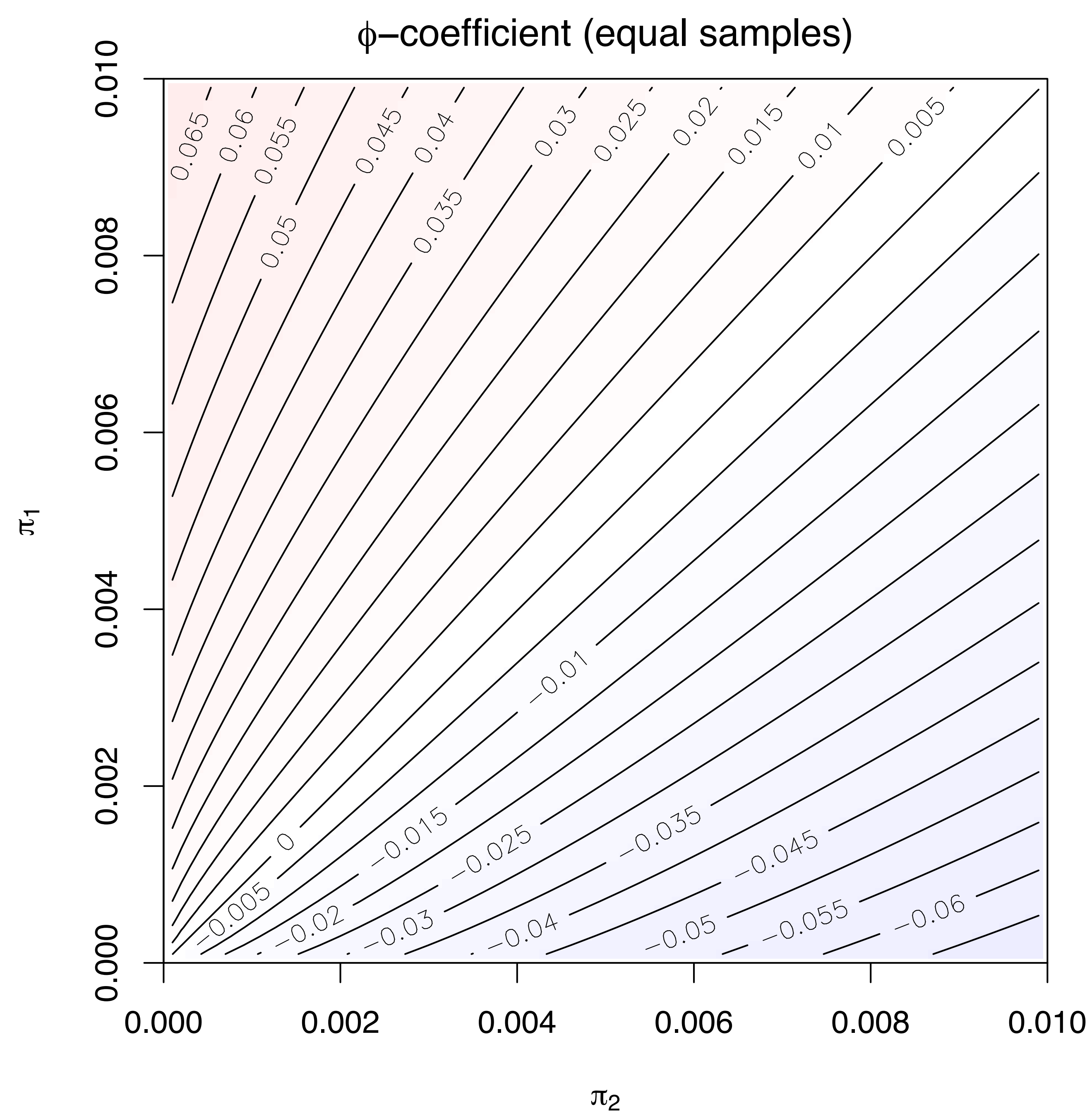




Visualizing effect size measures

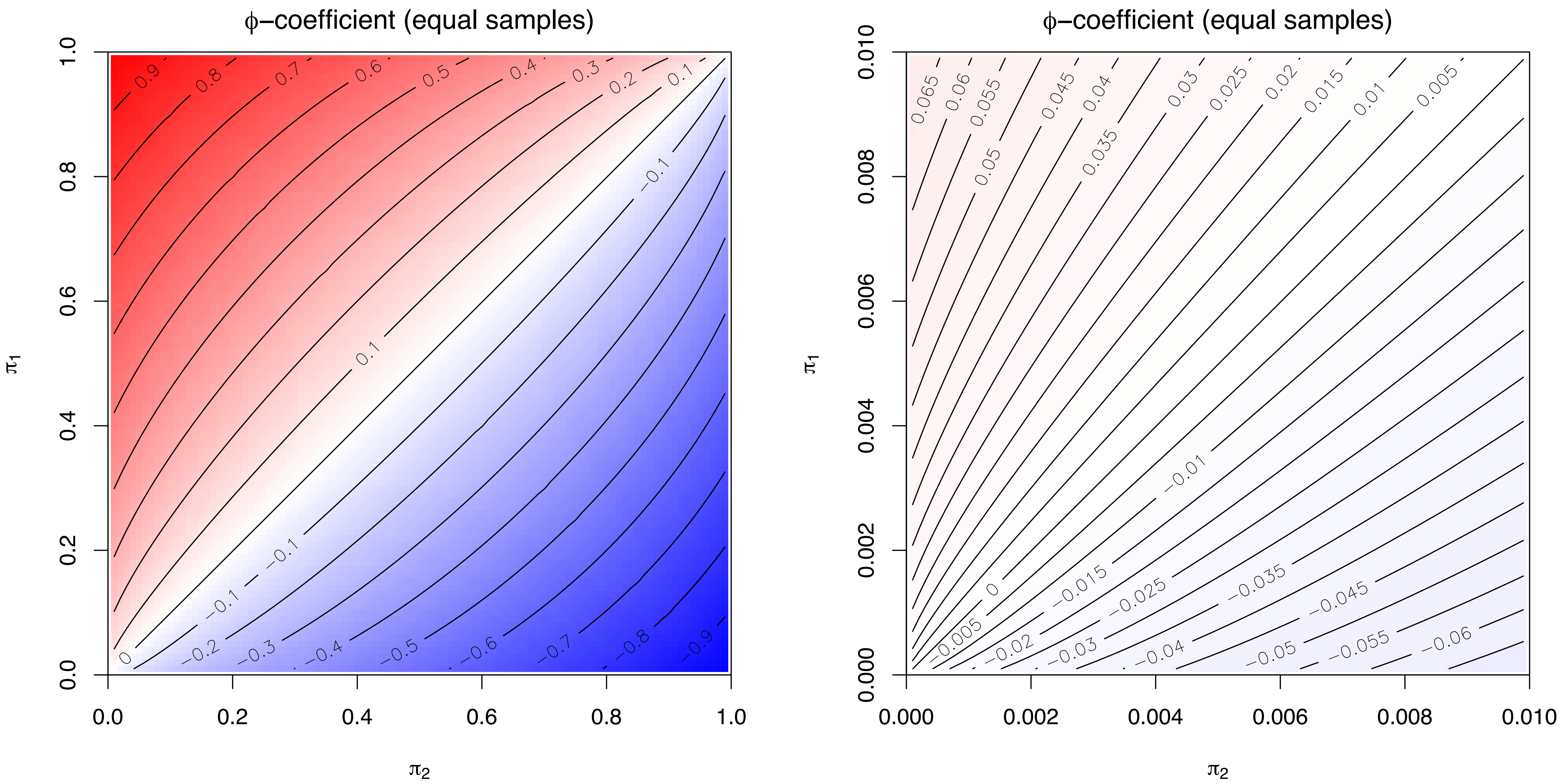
φ coefficient (1 : 1)





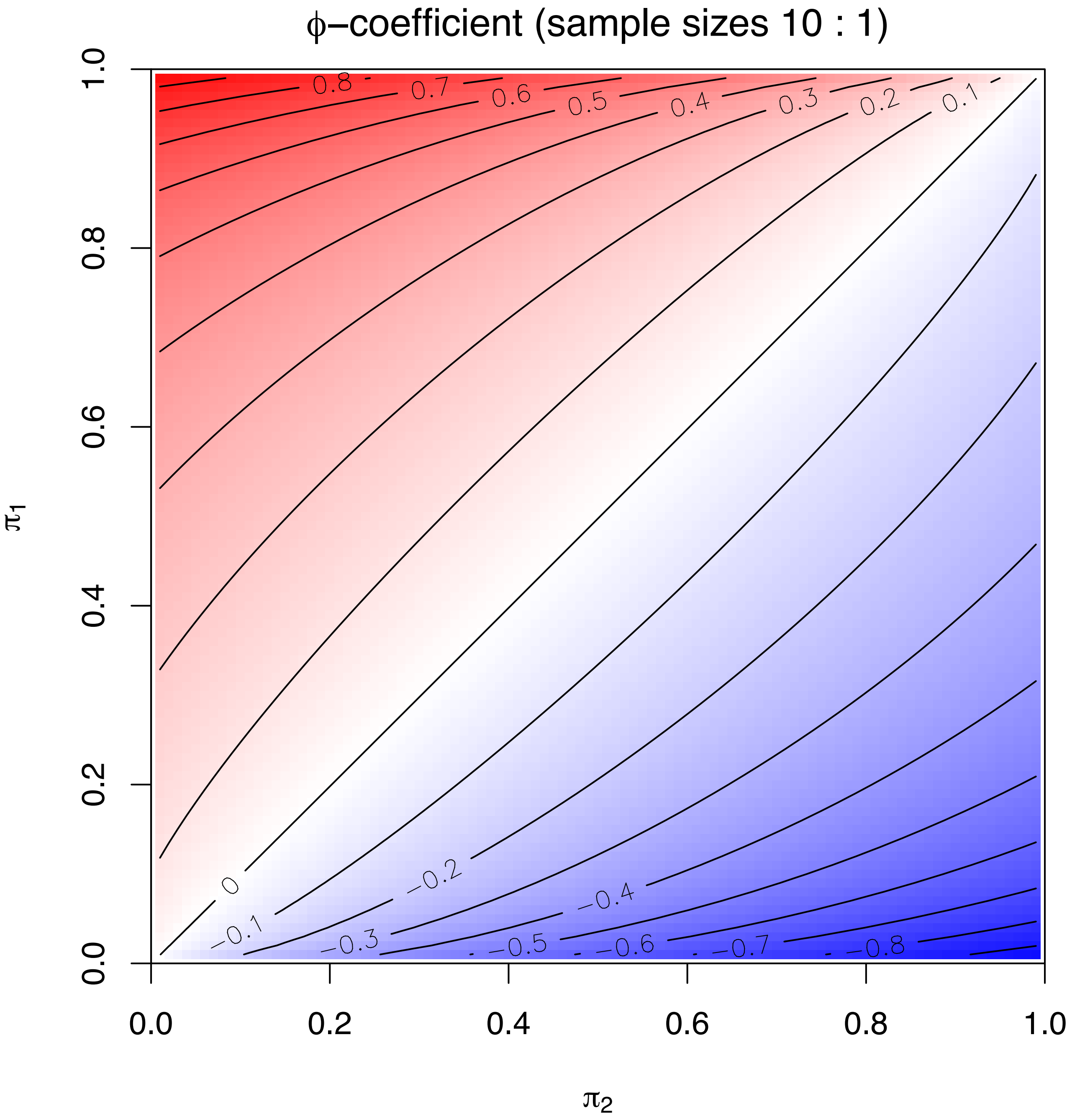
Visualizing effect size measures

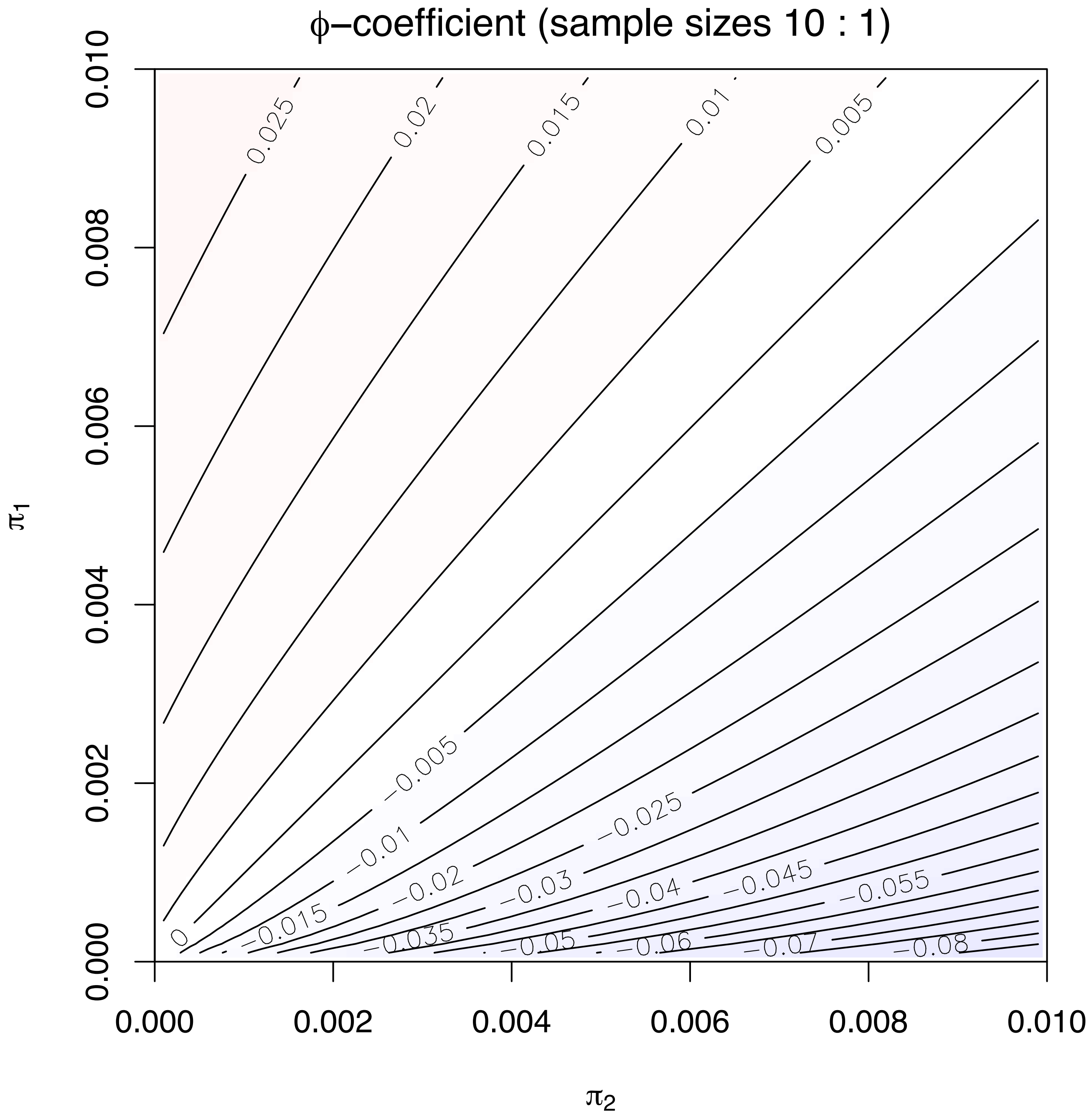
φ coefficient (1 : 1)



Visualizing effect size measures

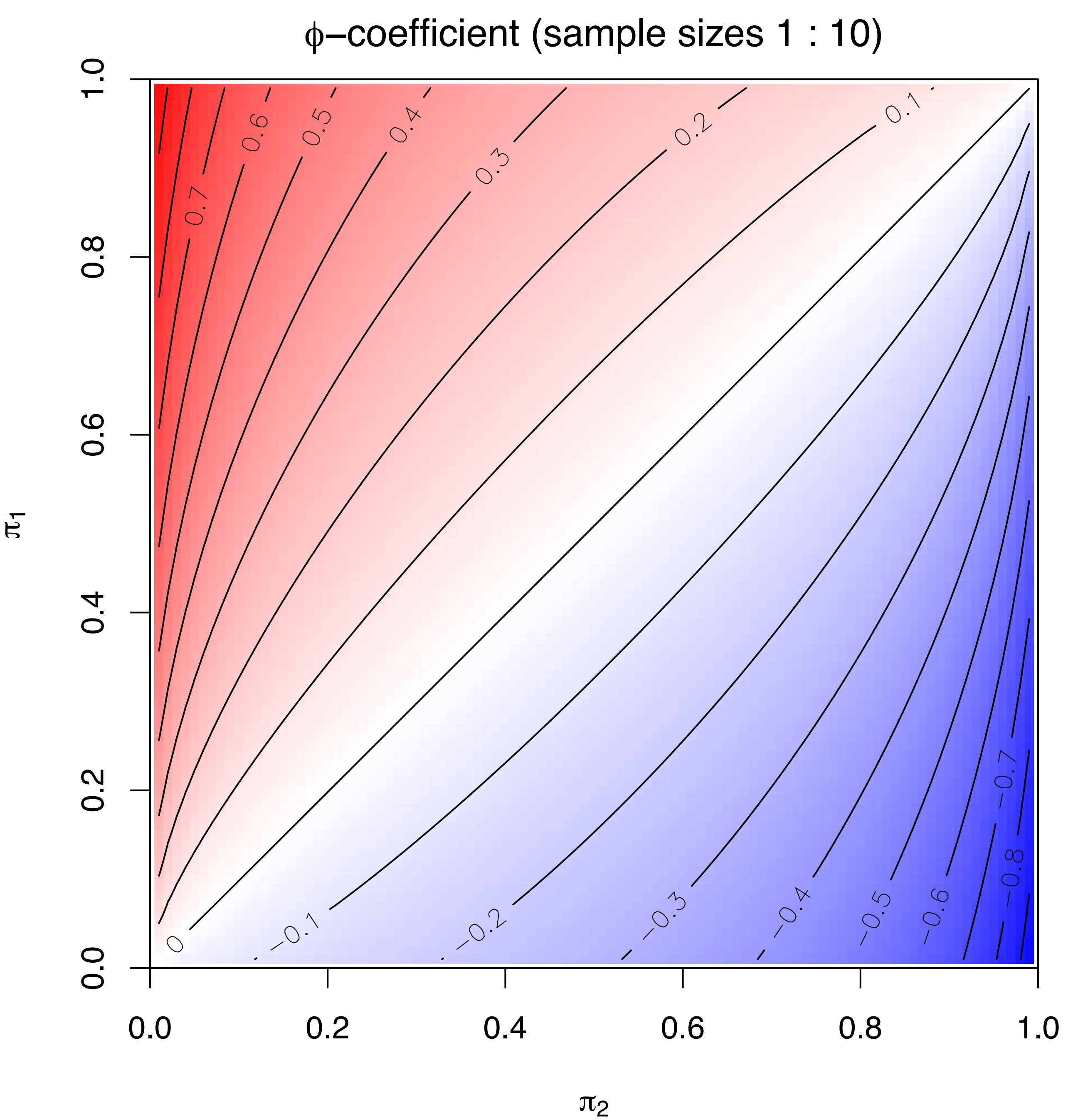
φ coefficient (10 : 1)

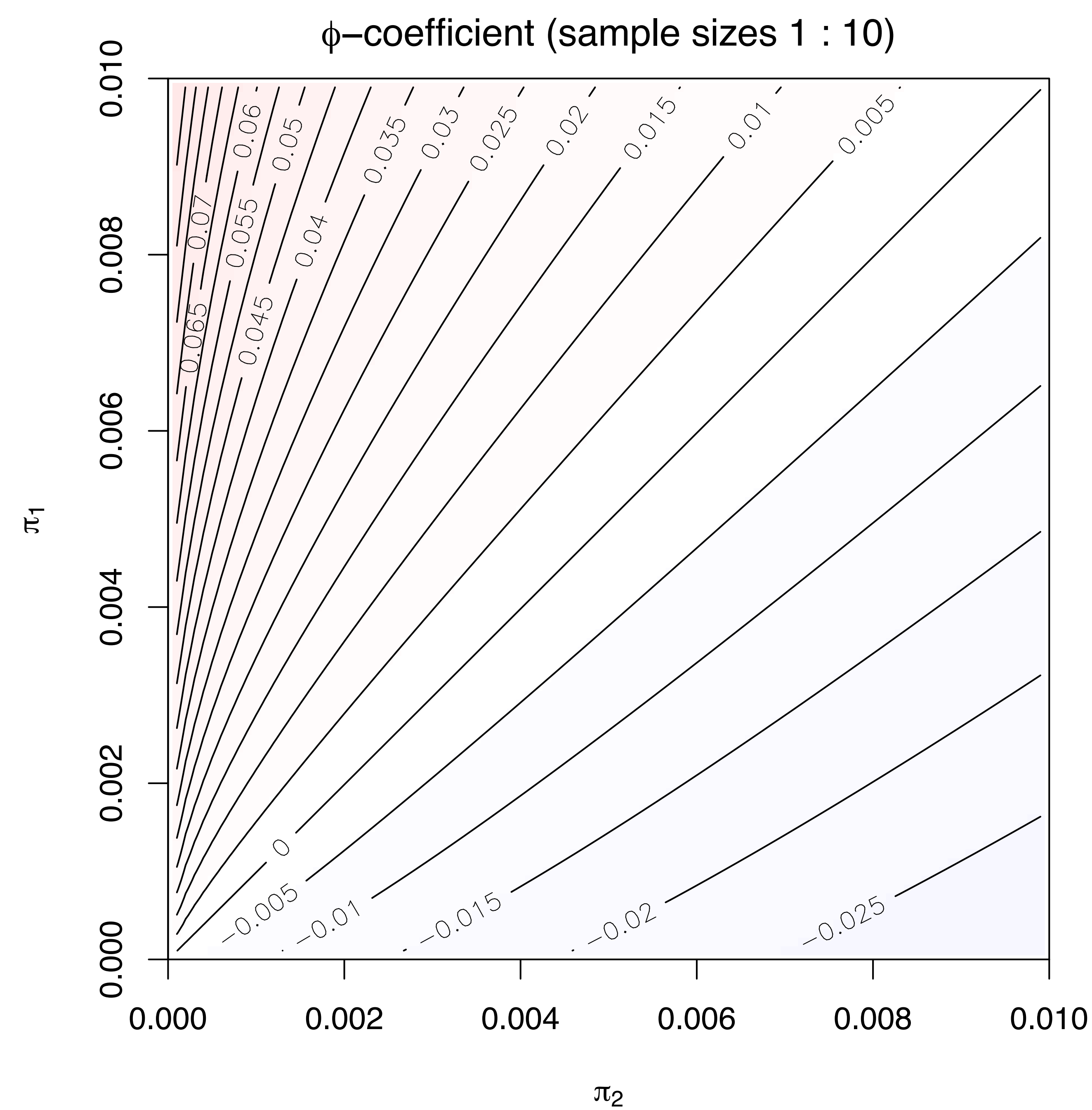




Visualizing effect size measures

φ coefficient (1 : 10)





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)  # or use versions 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
# k1/n1 and k2/n2, 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/LOB variables are set correctly!)
quick.test <- function (i) {
  do.test(k1=Brown$passive[i], n1=Brown$n_s[i],
          k2=LOB$passive[i], n2=LOB$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()`