

# **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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- evidence from frequency comparisons / estimates

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- ◆ We have doubts and want to verify this claim

# From research question to statistical analysis

**corpus  
data**

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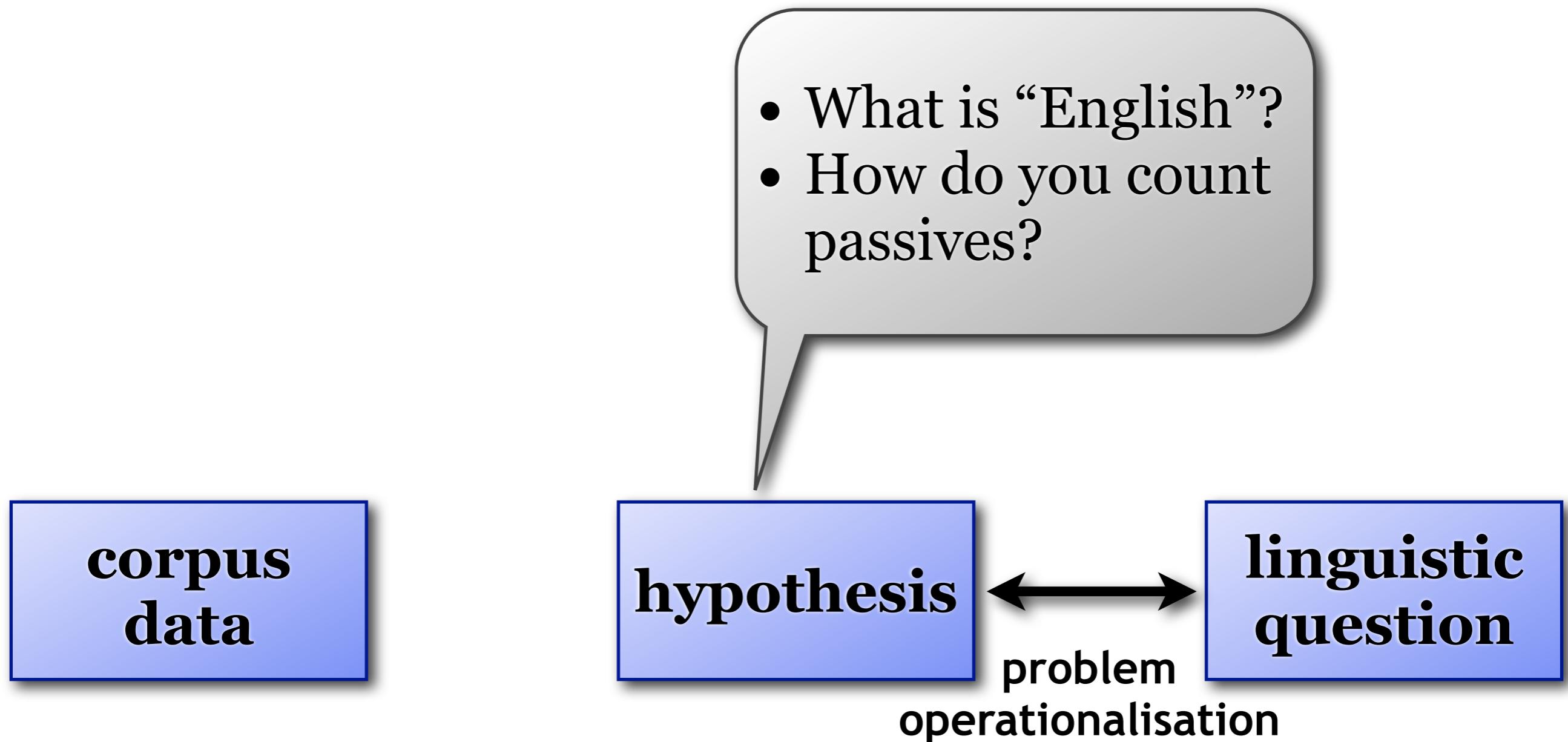
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- ◆ Here: professional writing by native speakers of AmE (⇒ target audience of style guide)

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- ◆ Types vs. tokens

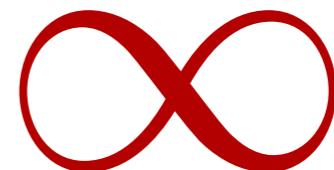
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- ◆ **Absolute frequency** is not meaningful here



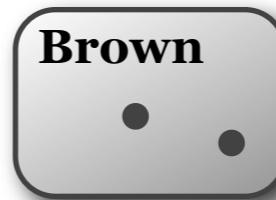
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- ◆ Are there **20,000** passives?
  - Brown (1M words)

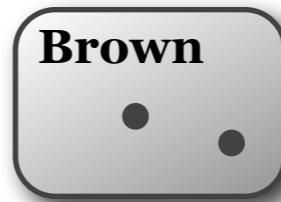
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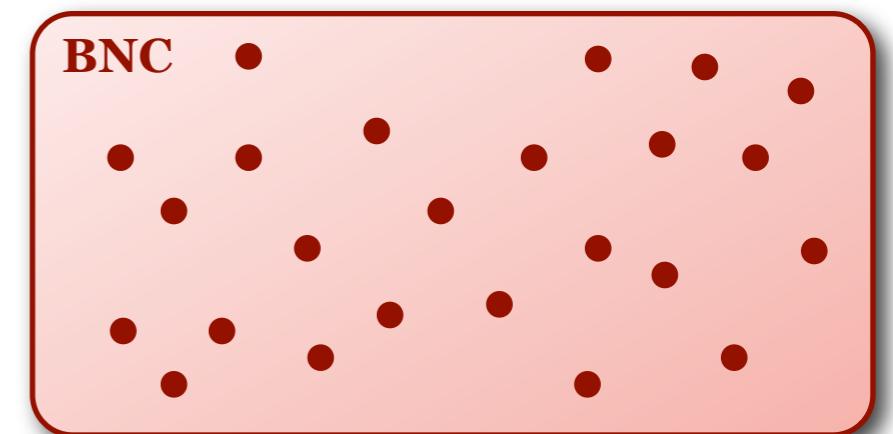
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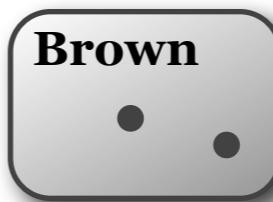
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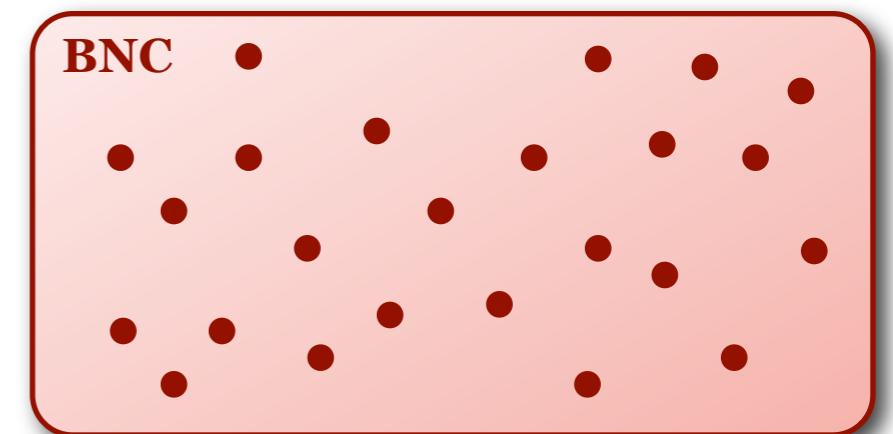
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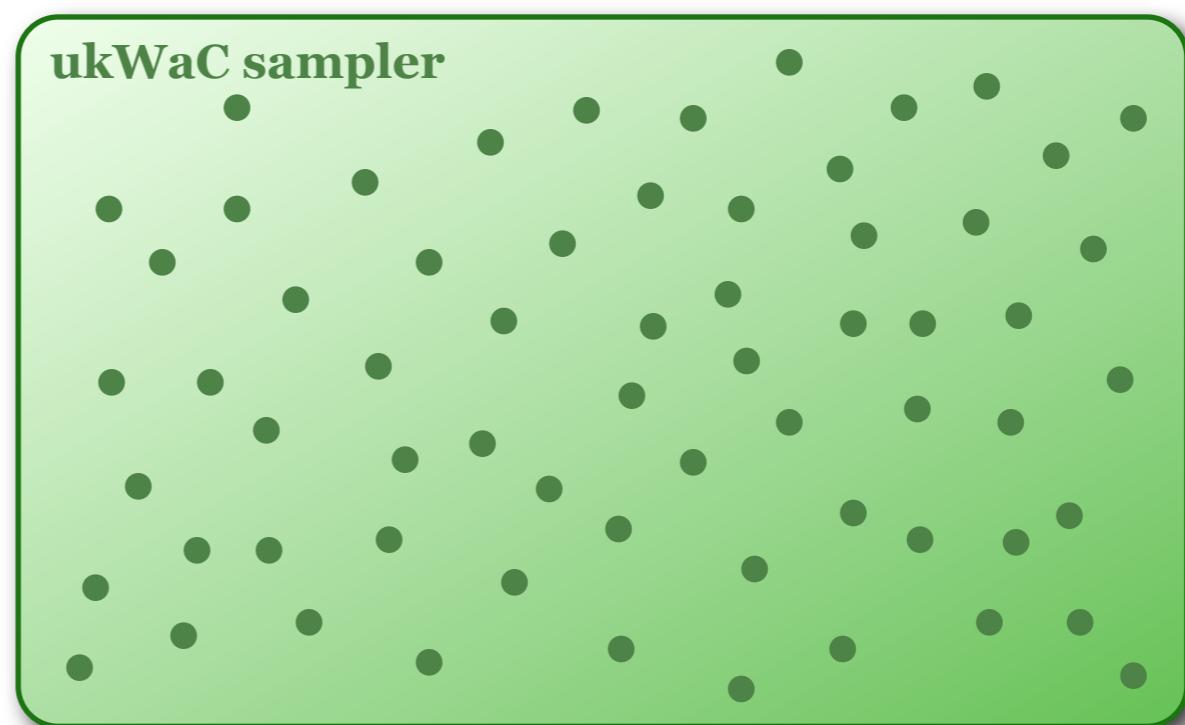
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- ◆ Or **5.1 million**?

- ukWaC sampler  
(450M words)



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- ◆ What is a sensible unit of measurement?

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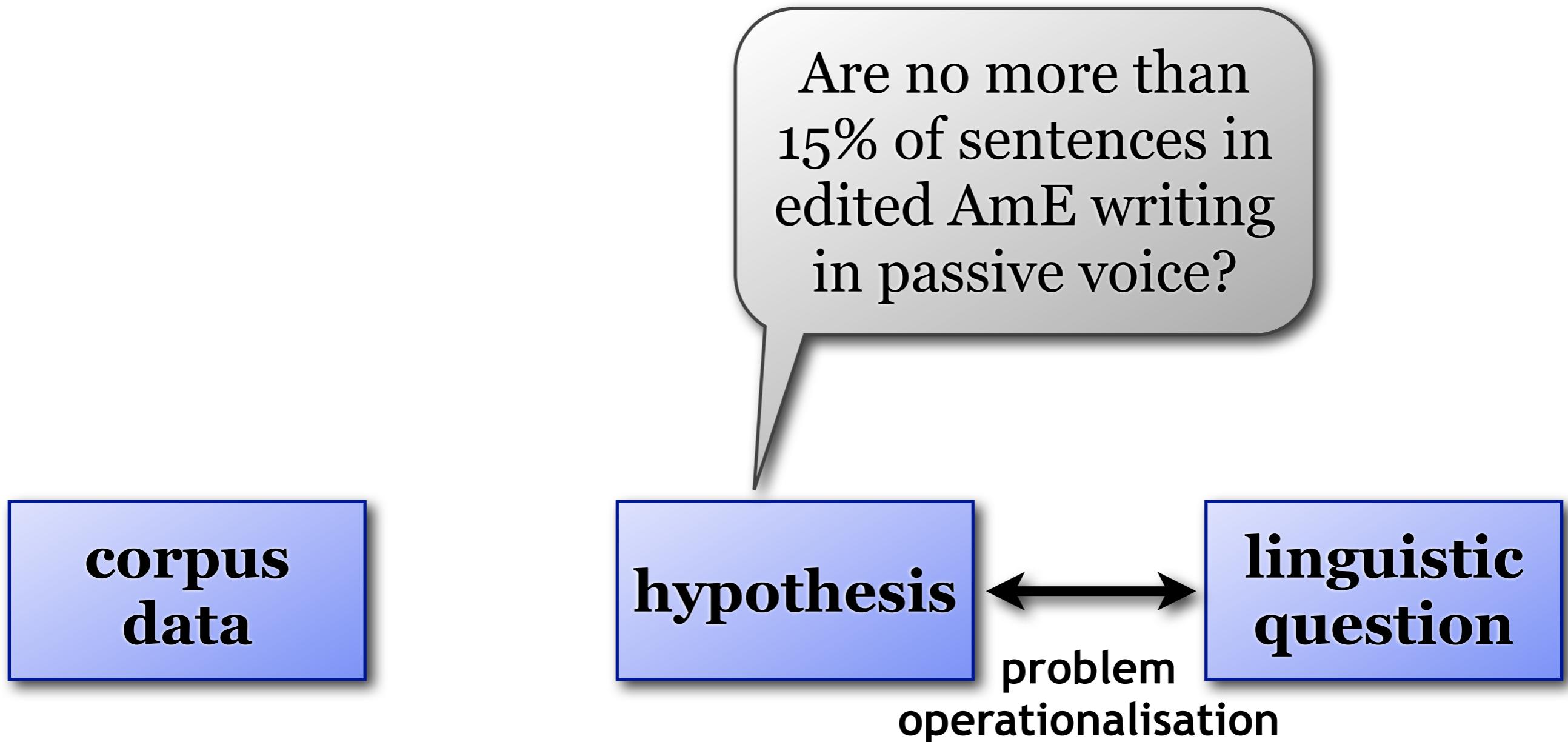
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- ◆ **Relative frequency = proportion  $\pi$**

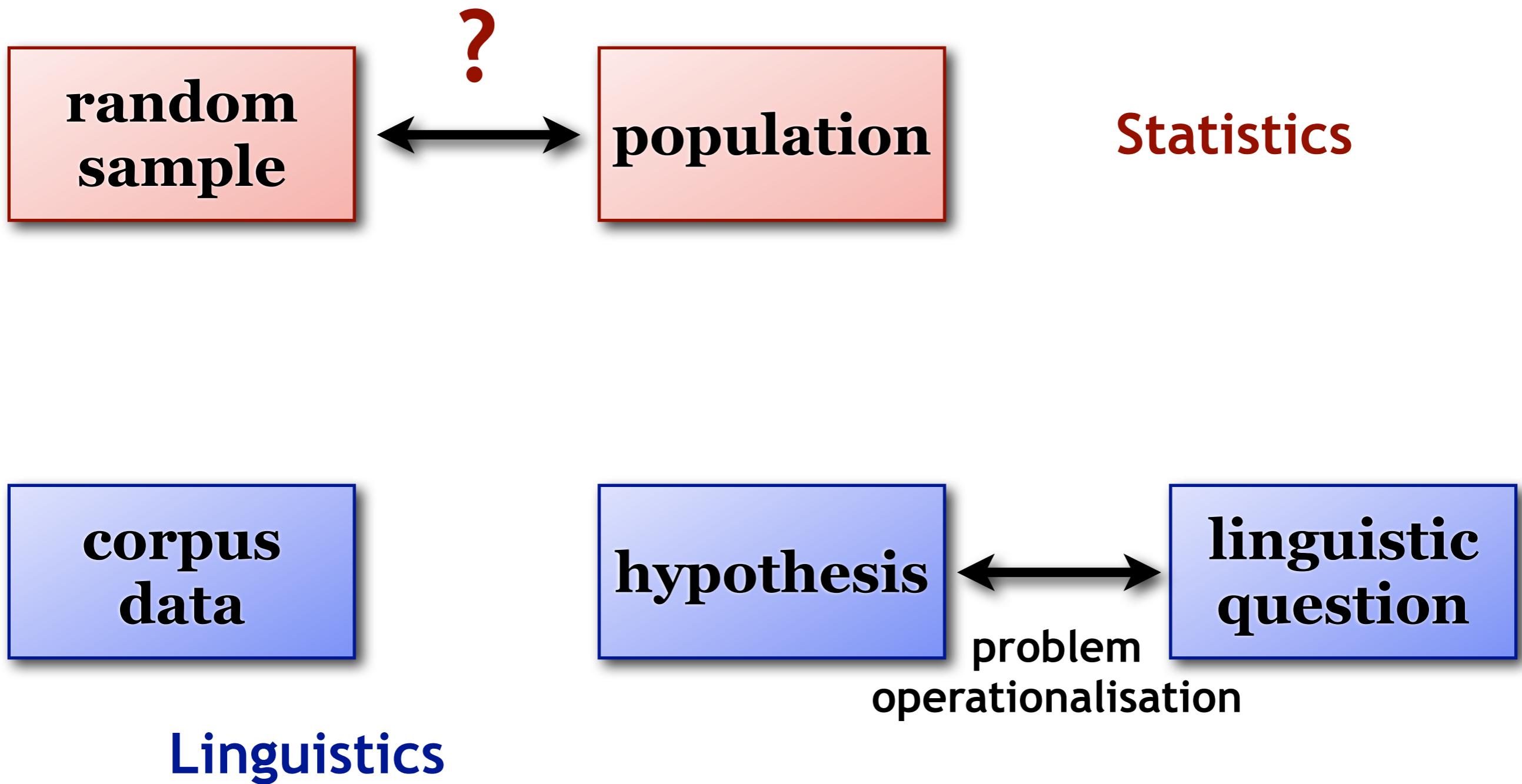
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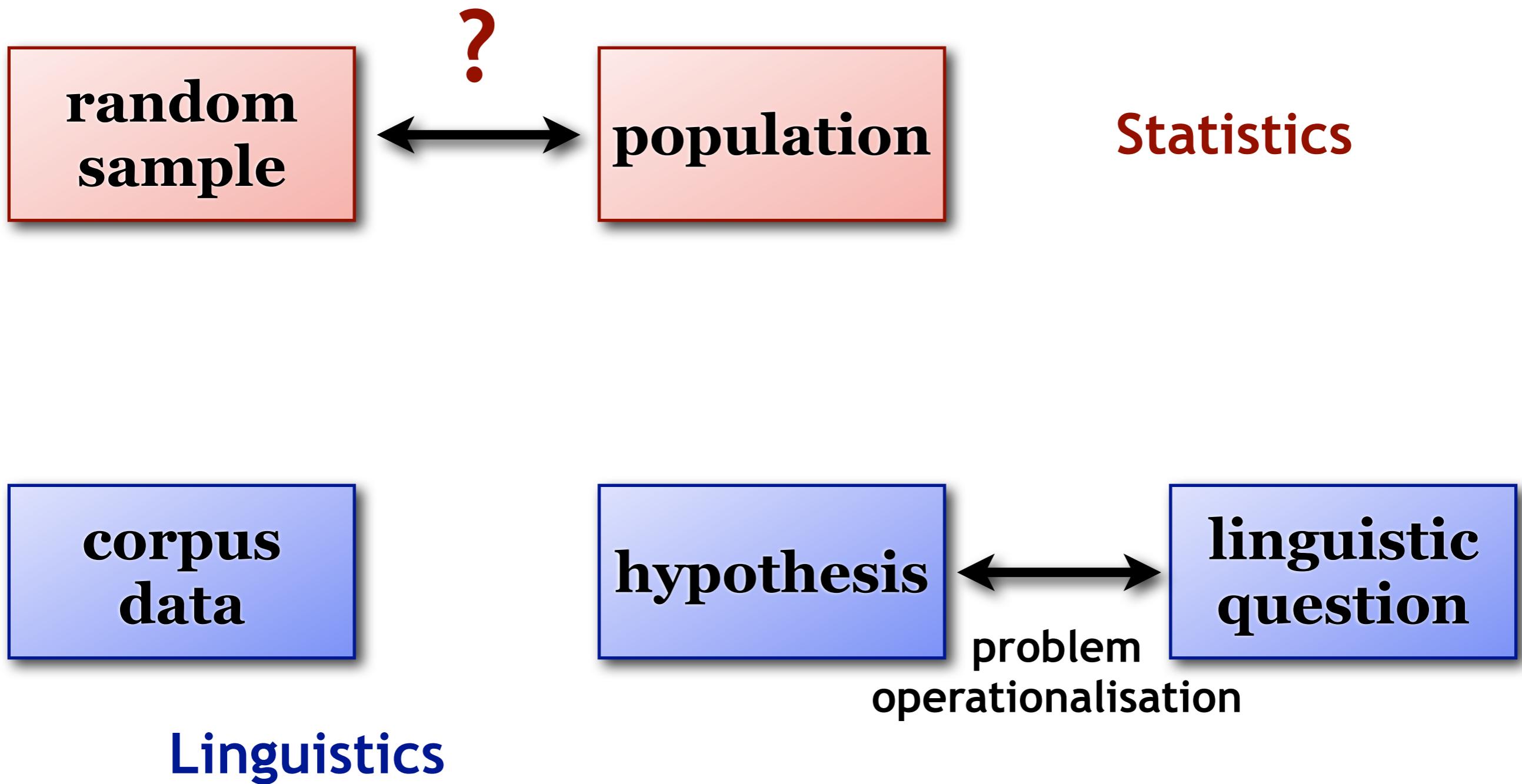
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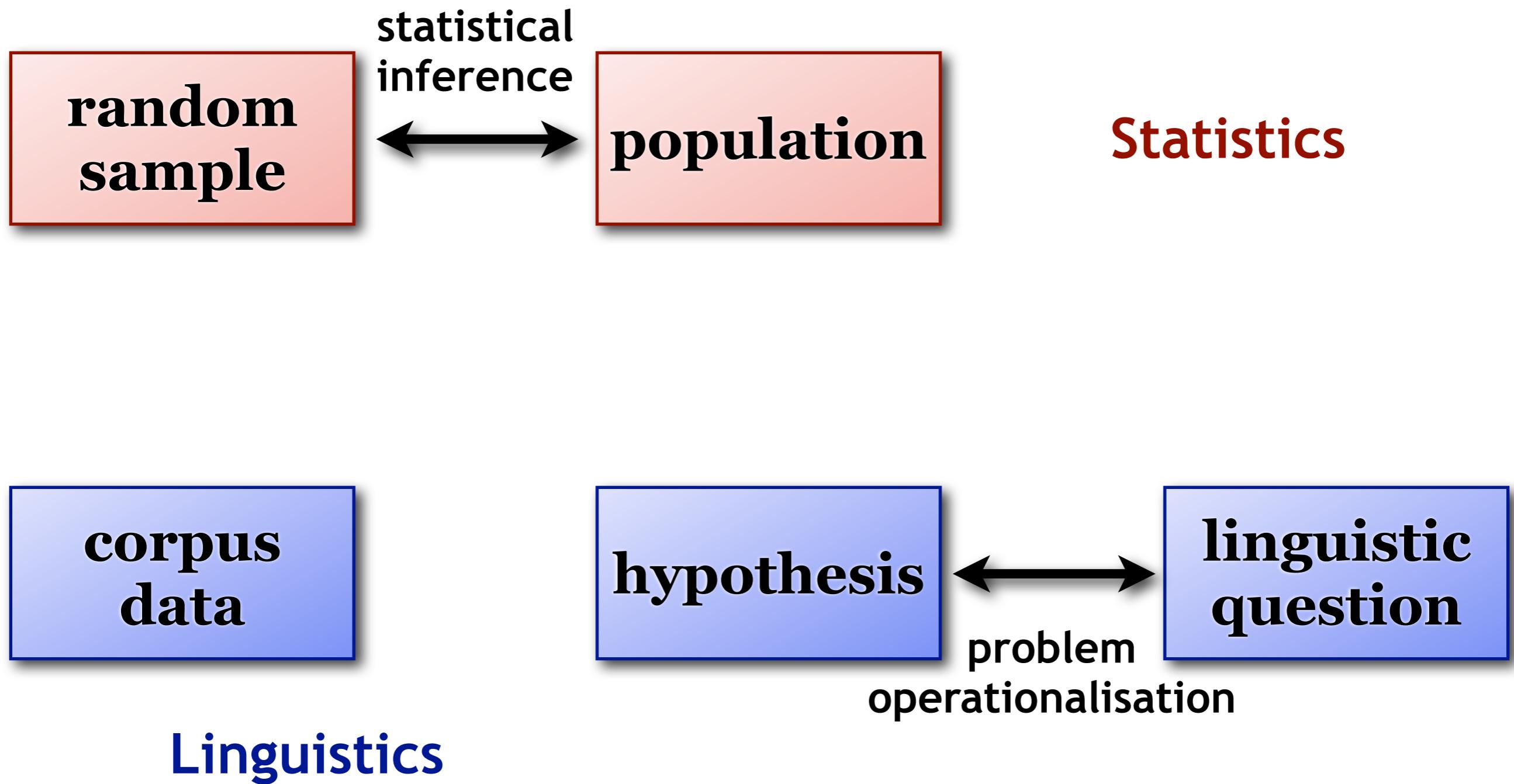
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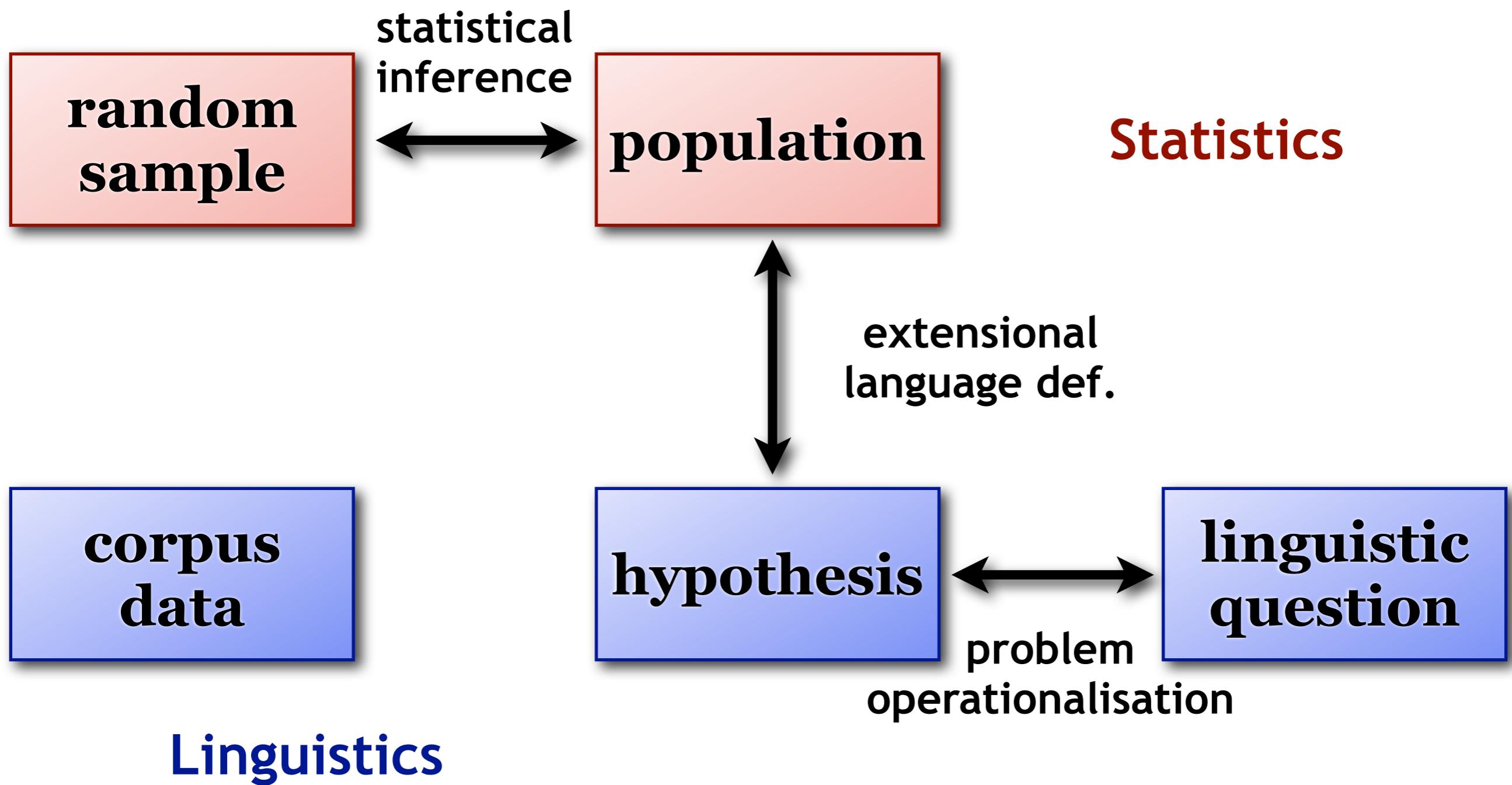
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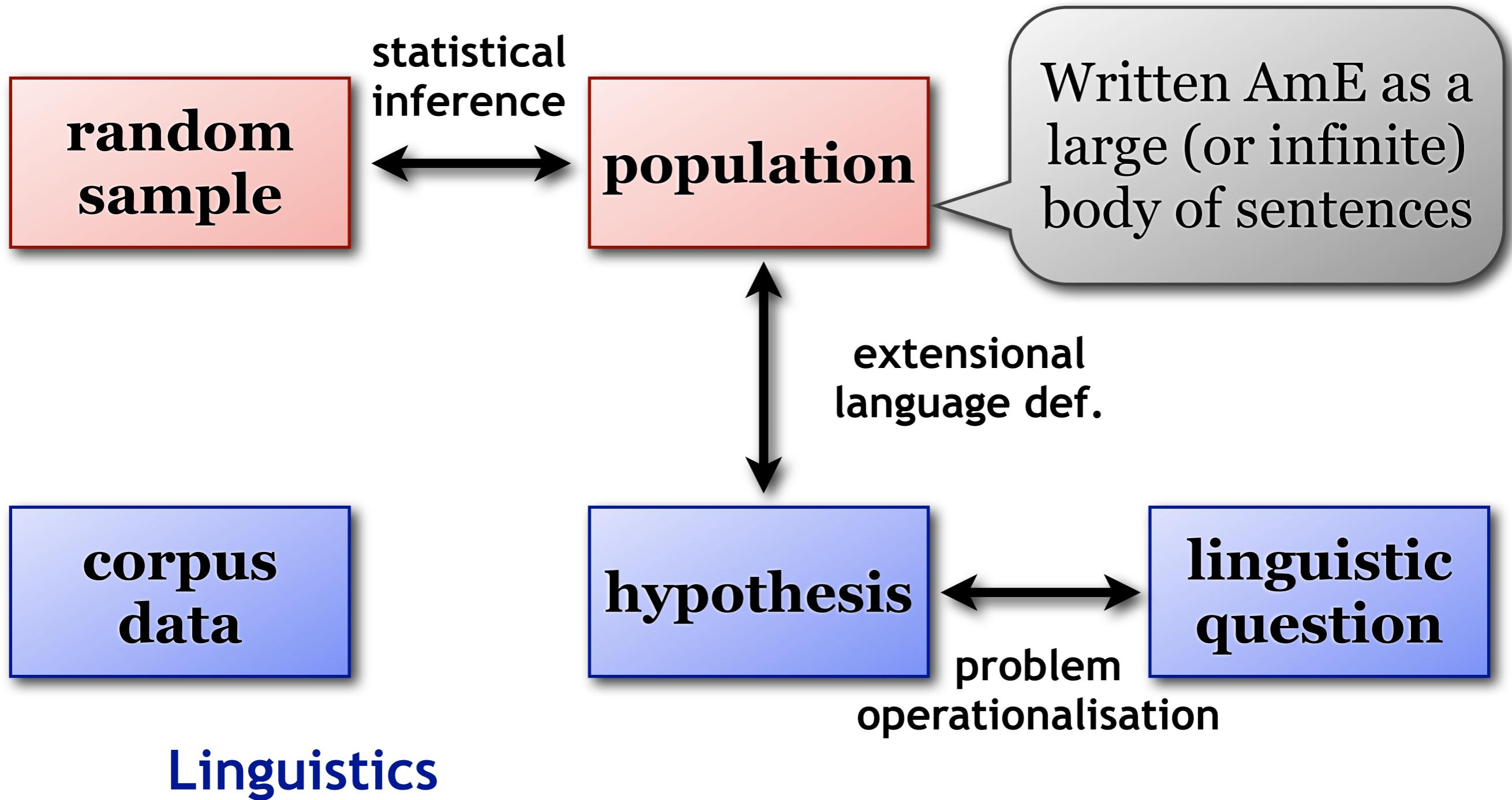
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# The library metaphor

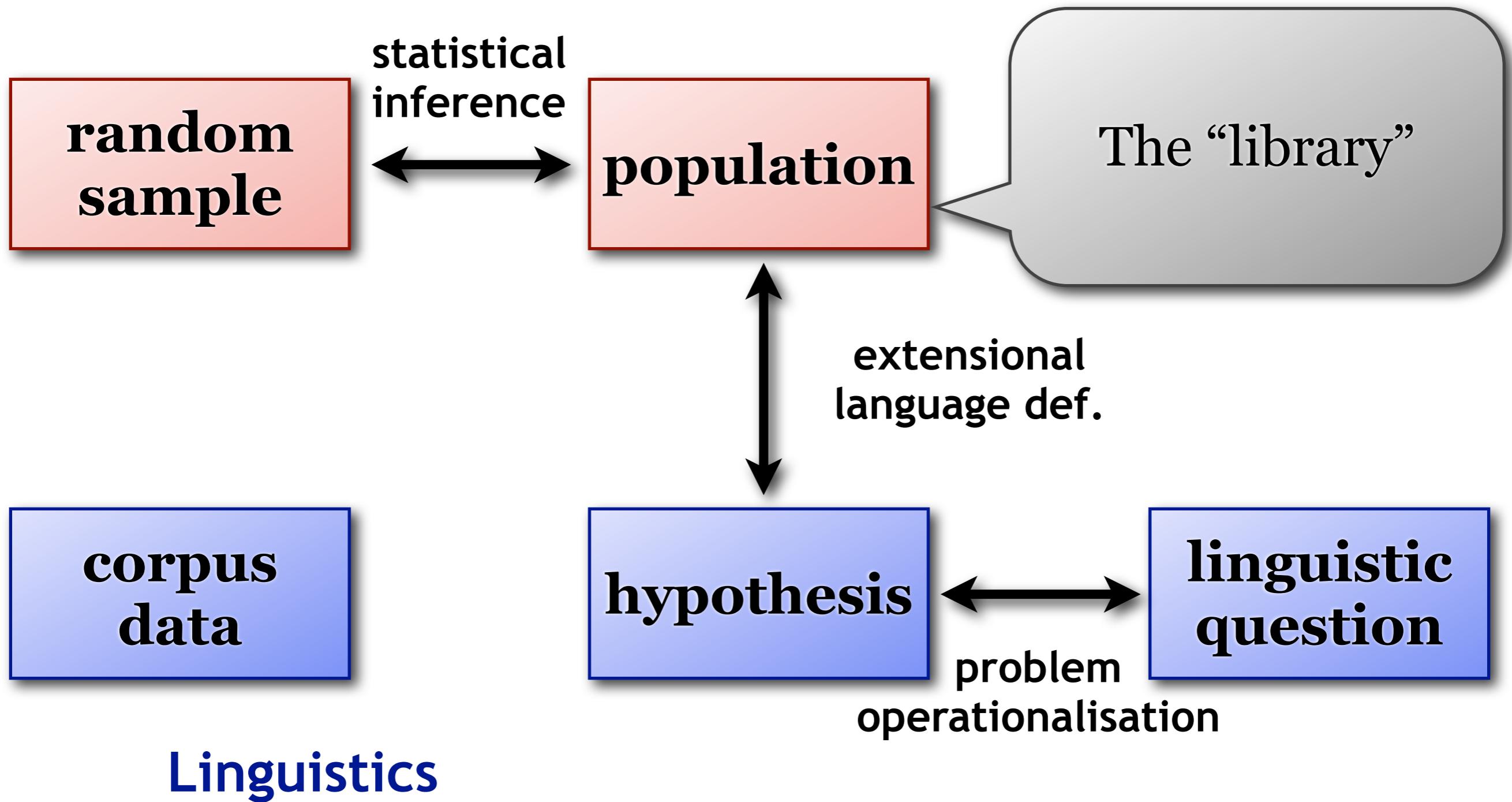
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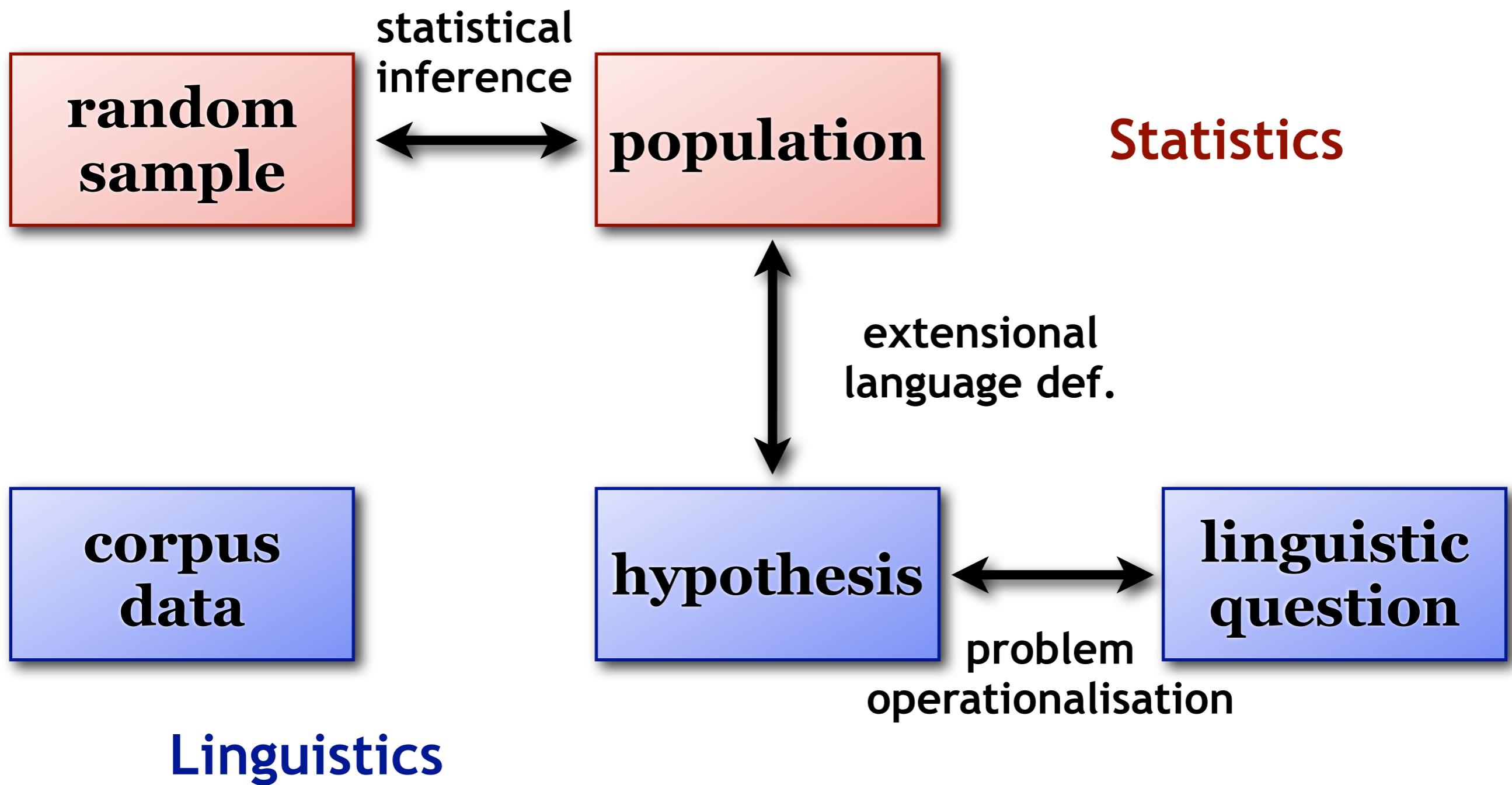
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- ◆ Extensional definition of a language:  
“All utterances made by speakers of the language under appropriate conditions, plus all utterances they *could* have made”
  - ◆ Imagine a huge library with all the books written in a language, as well as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

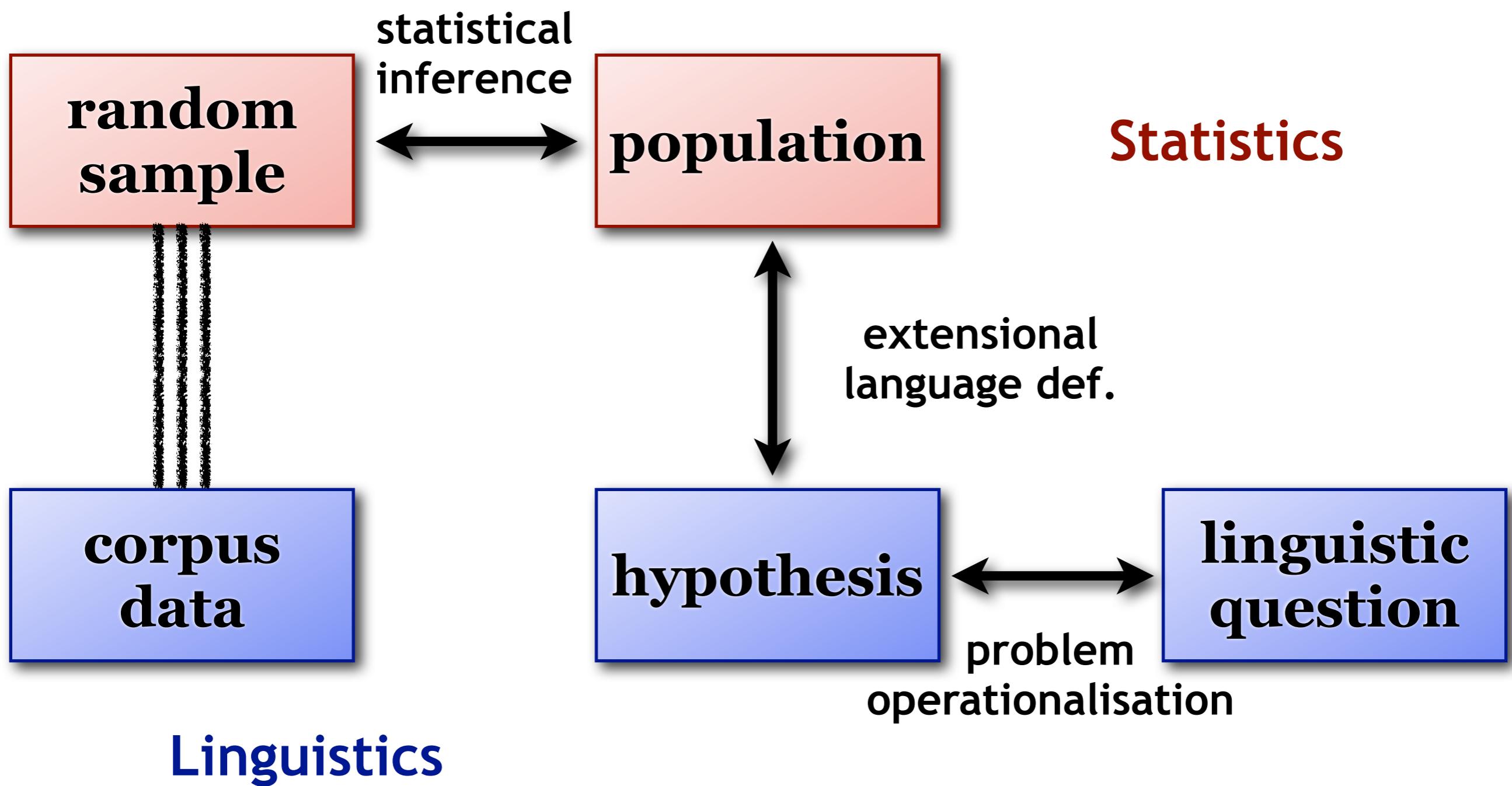
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- ◆ Objects = whatever **unit of measurement** the proportions of interest are based on
  - we need to take a random sample of such units

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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  
= 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  $\pi$  of type

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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?

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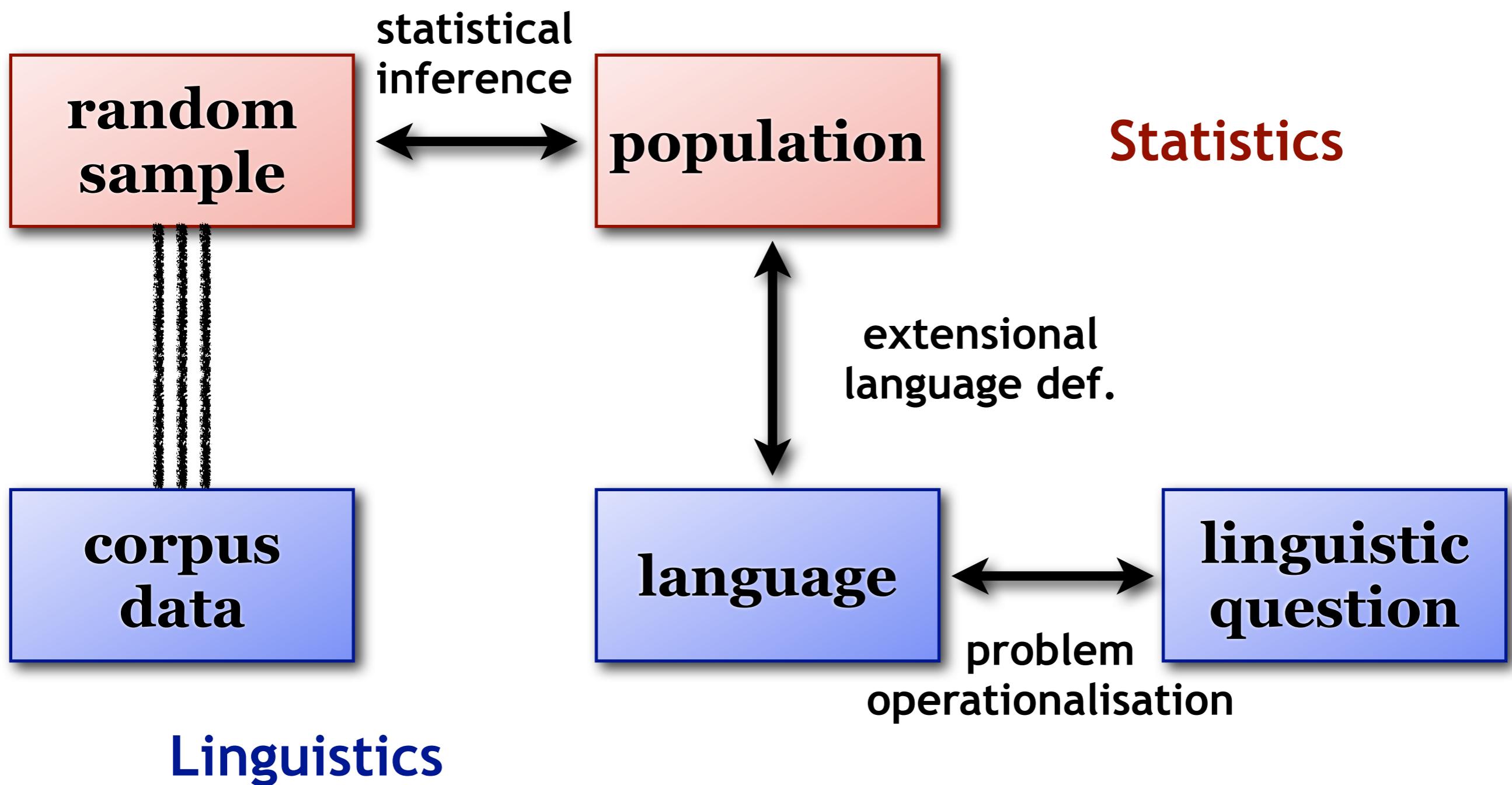
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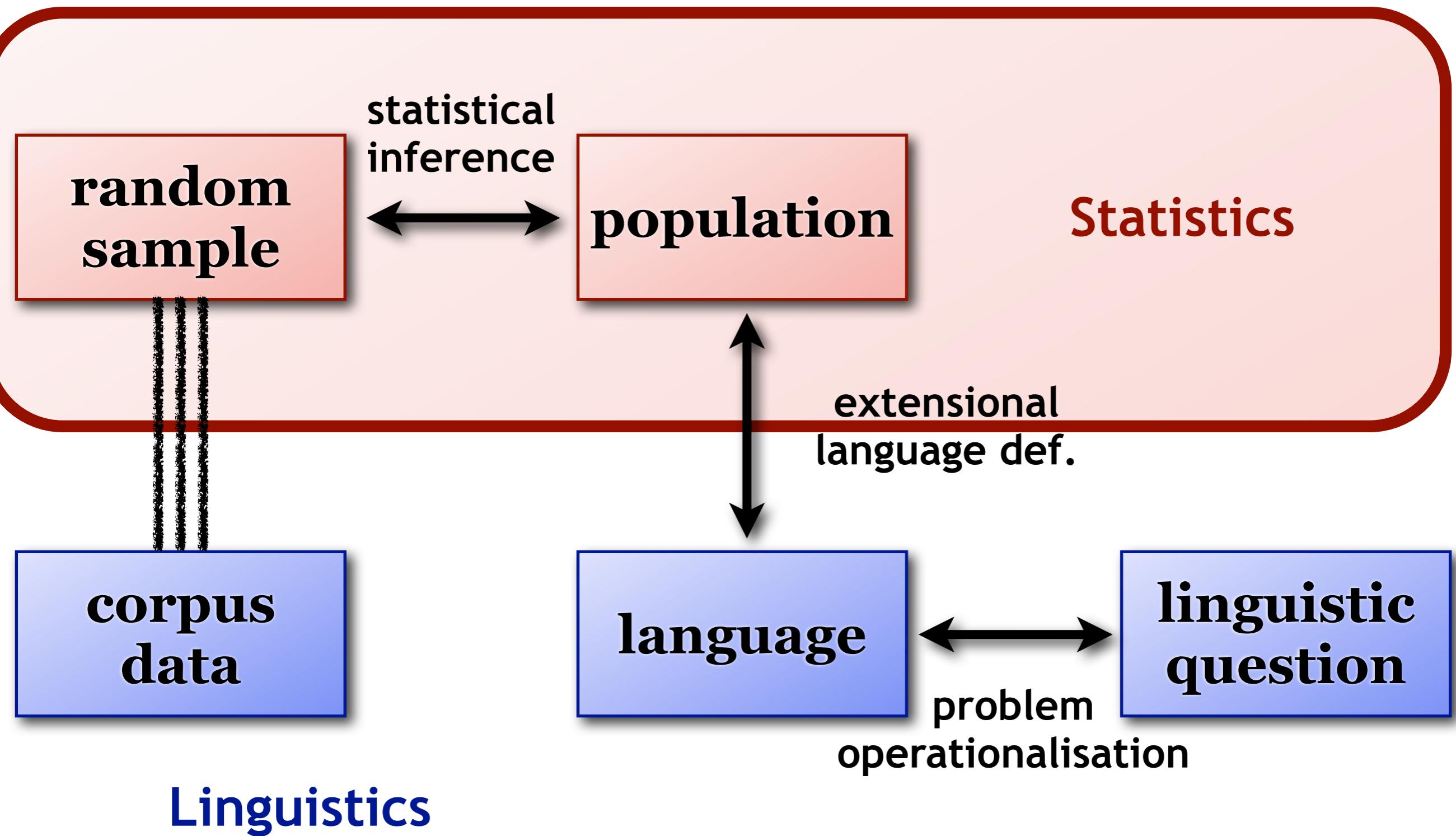
- ◆ Random choice of sample ensures proportions are the same on average in sample & population
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→ **sampling variation**
- ◆ The main purpose of statistical methods is to estimate & correct for sampling variation
  - that's all there is to inferential statistics, really



# Reminder: The role of statistics



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- we also refer to  $\pi_0 = .15$  as the **null proportion**
- ◆ Many corpus linguists set out to test  $H_0$ 
  - 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.?

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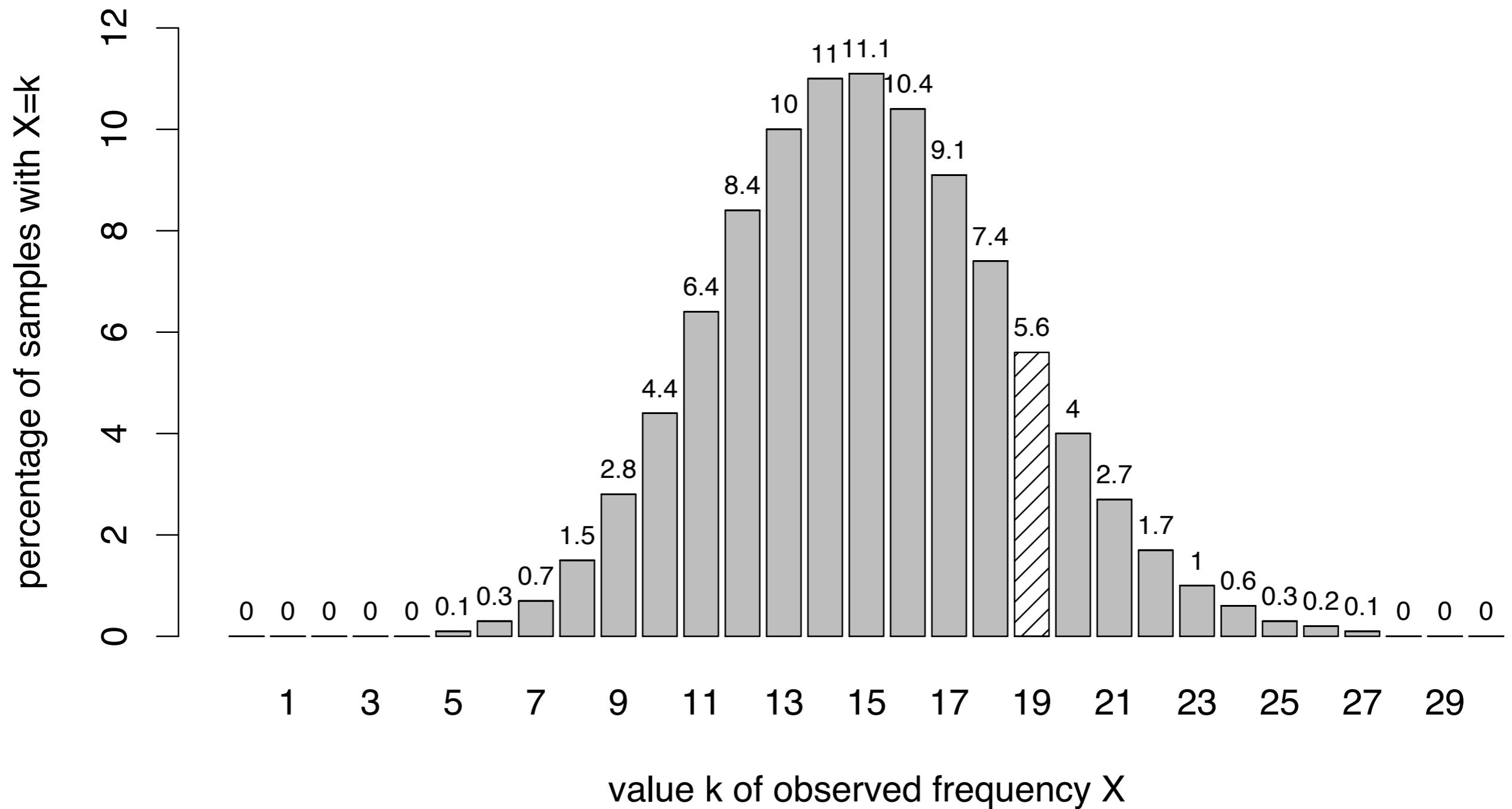
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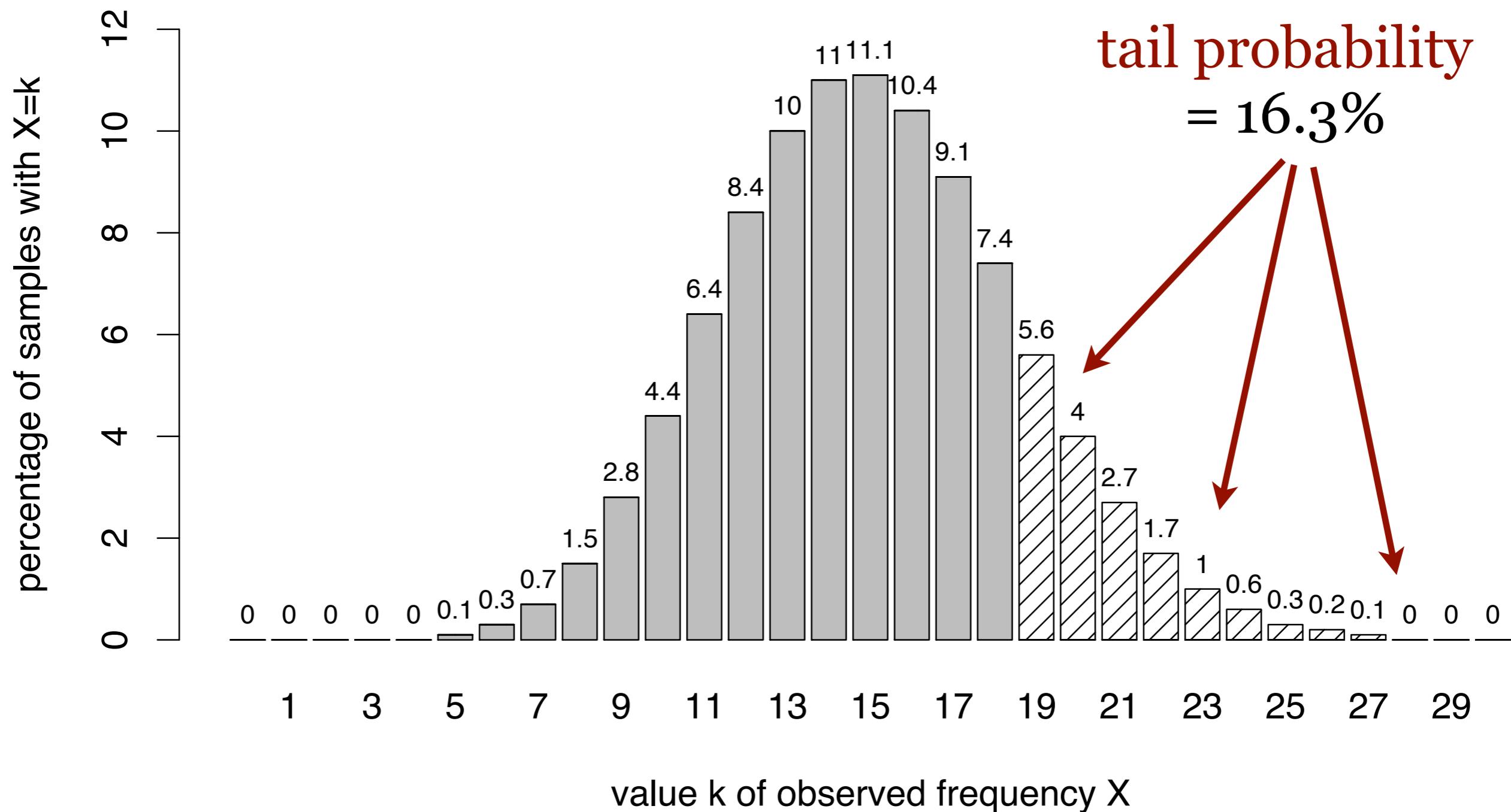
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**percentage** of samples = **probability**

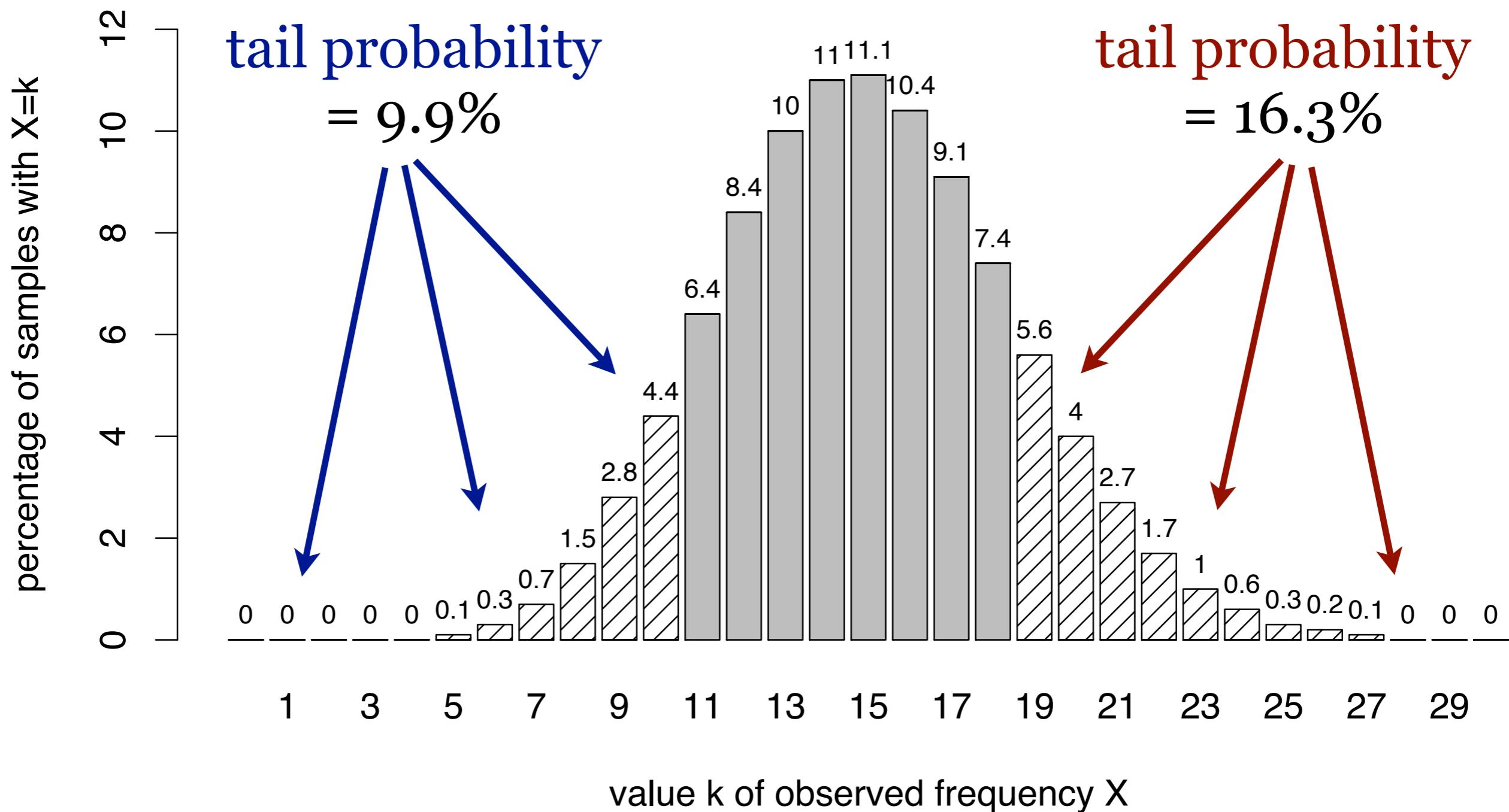
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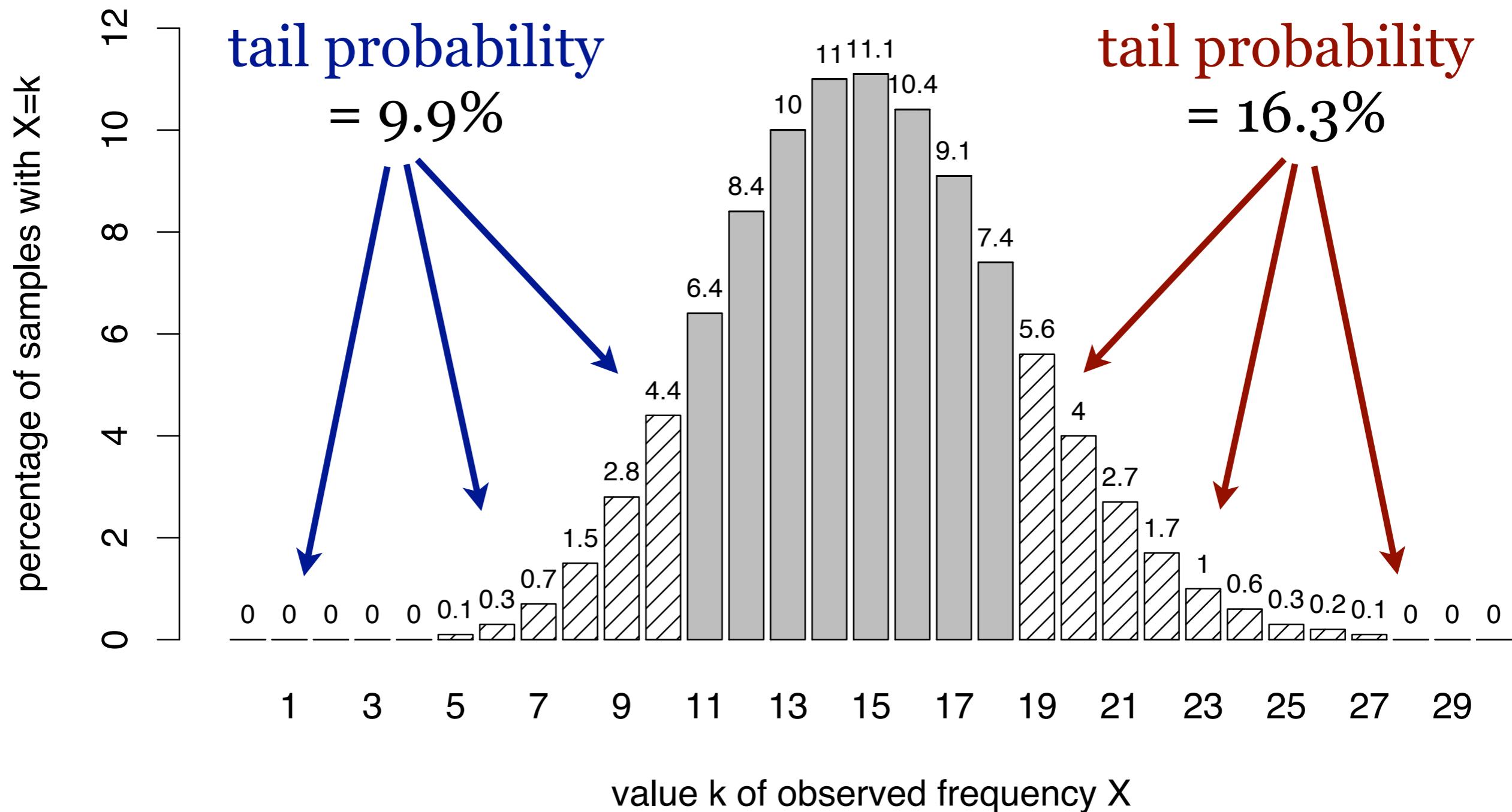


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→ risk of false rejection = **p-value** = 26.2%



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- ◆ Two-sided vs. one-sided tests
  - in general, two-sided tests should be preferred
  - 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](http://purl.org/stefan.evert/SIGIL).

### One sample: frequency estimate (confidence interval)

[back to top](#)

<b>Frequency count</b>	<b>Sample size</b>
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](#)

<b>Frequency count</b>	<b>Sample size</b>
<b>Sample 1</b>	19
	100
<b>Sample 2</b>	25
	200

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- <http://sigil.collocations.de/wizard.html>
- <http://faculty.vassar.edu/lowry/VassarStats.html>
- SPSS, SAS, Excel, ...
- We want to do it in , of course

### Two samples: frequency comparison

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

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# Binomial hypothesis test in R

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  - **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

# Binomial hypothesis test in R

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

```
[1] 0.2622728
```

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

```
[1] 0.03430725
```

```
> binom.test(190, 1000, p=.15)$p.value
```

```
[1] 0.0006356804
```

# Power

# Power

- ◆ Type II error = failure to reject incorrect  $H_o$ 
  - the larger the discrepancy between  $H_o$  and the true situation, the more likely it will be rejected
  - e.g. if the true proportion of passives is  $\pi = .25$ , then most samples provide enough evidence to reject; but true  $\pi = .16$  makes rejection very difficult
  - a **powerful** test has a low type II error

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  - a **powerful** test has a low type II error
- ◆ Basic insight: larger sample = more power
  - relative sampling variation becomes smaller
  - might become powerful enough to reject for  $\pi = 15.1\%$

# Parametric vs. non-parametric

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  - not just those assuming a normal distribution
  - binomial test: strong random sampling assumption  
→ might be considered a parametric test in this sense!

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- ◆ Parametric tests make stronger assumptions
  - not just those assuming a normal 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
  - i.e. between **significance** and **power**

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  - determines trade-off point
  - low significance level (p-value) → low power

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  - i.e. between **significance** and **power**
- ◆ Significance level
  - determines trade-off point
  - low significance level (p-value) → low power
- ◆ Conservative tests
  - put more weight on avoiding type I errors → weaker
  - most non-parametric methods are conservative

# Confidence interval

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- ◆ 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

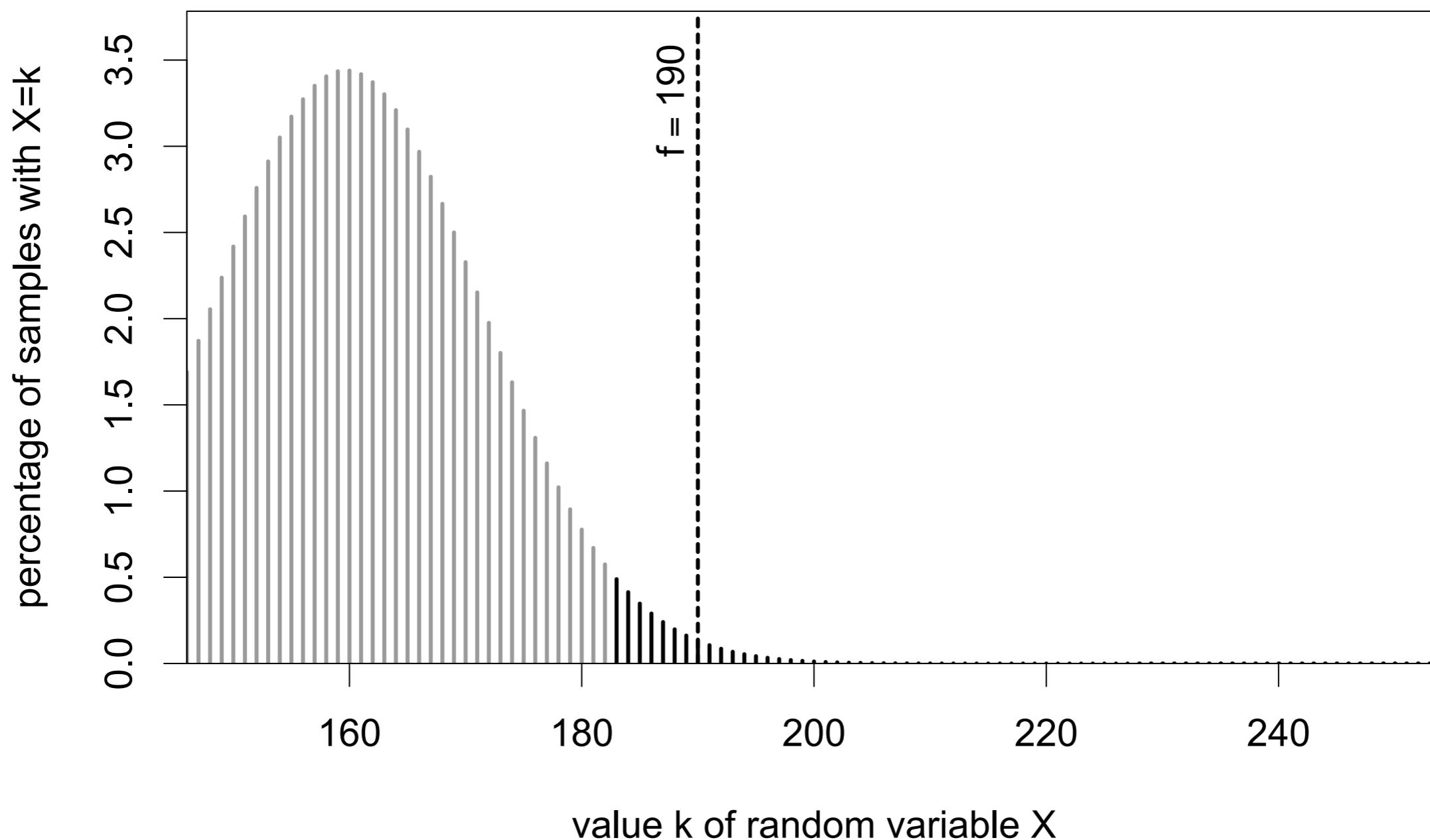
# Confidence interval

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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

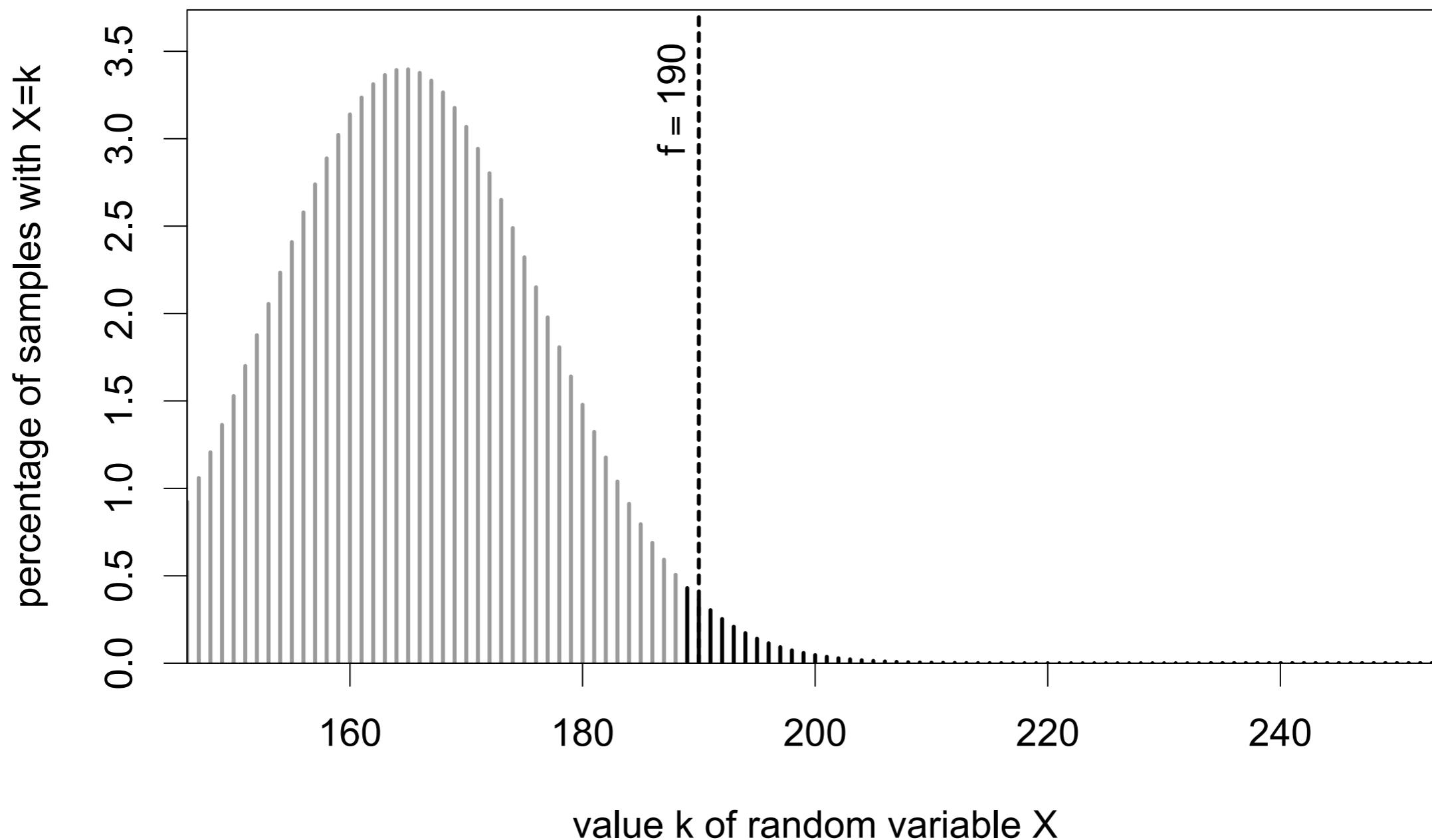
# Confidence interval

$\pi = 16\% \rightarrow H_0$  is rejected



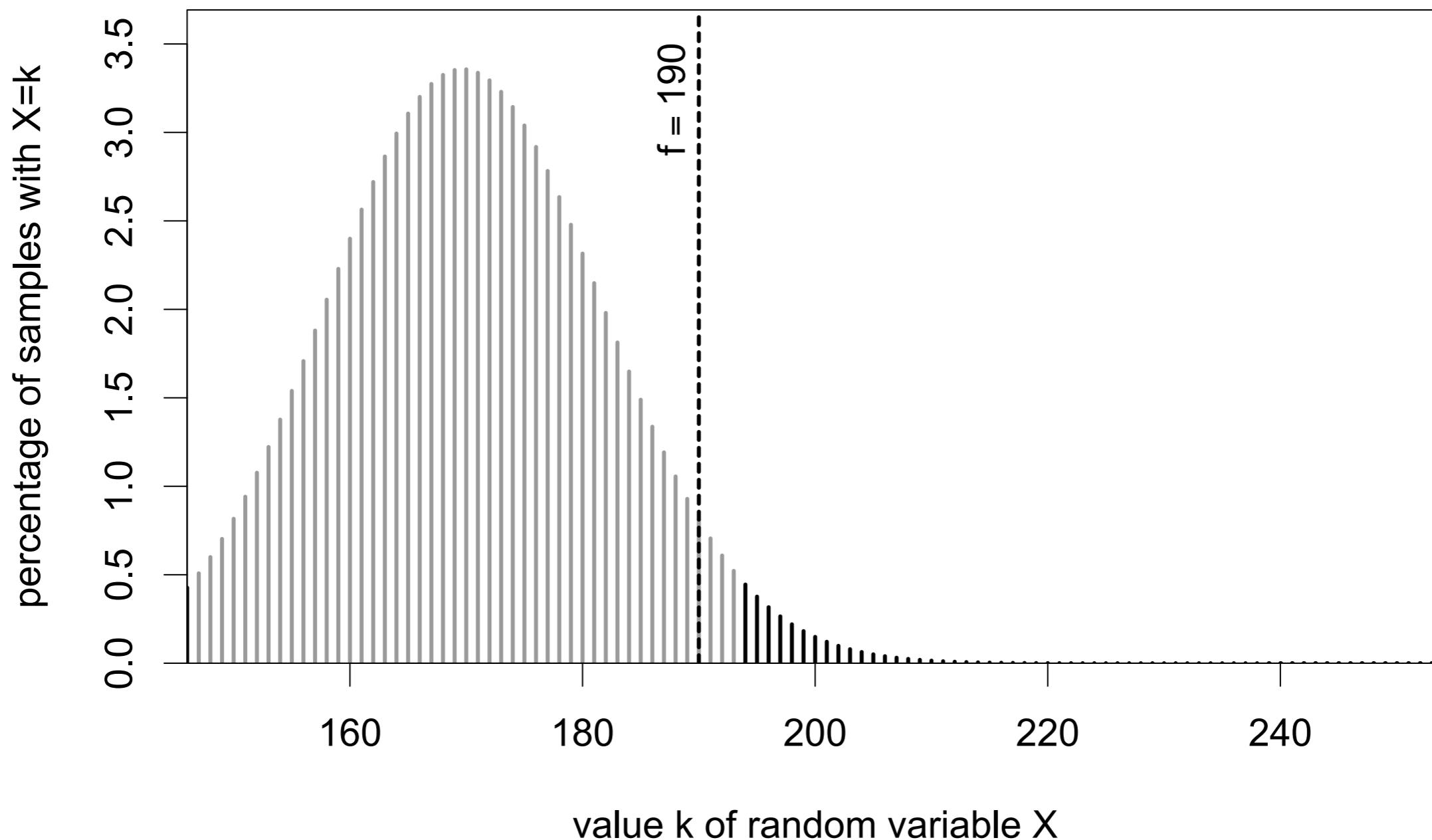
# Confidence interval

$\pi = 16.5\% \rightarrow H_0 \text{ is rejected}$



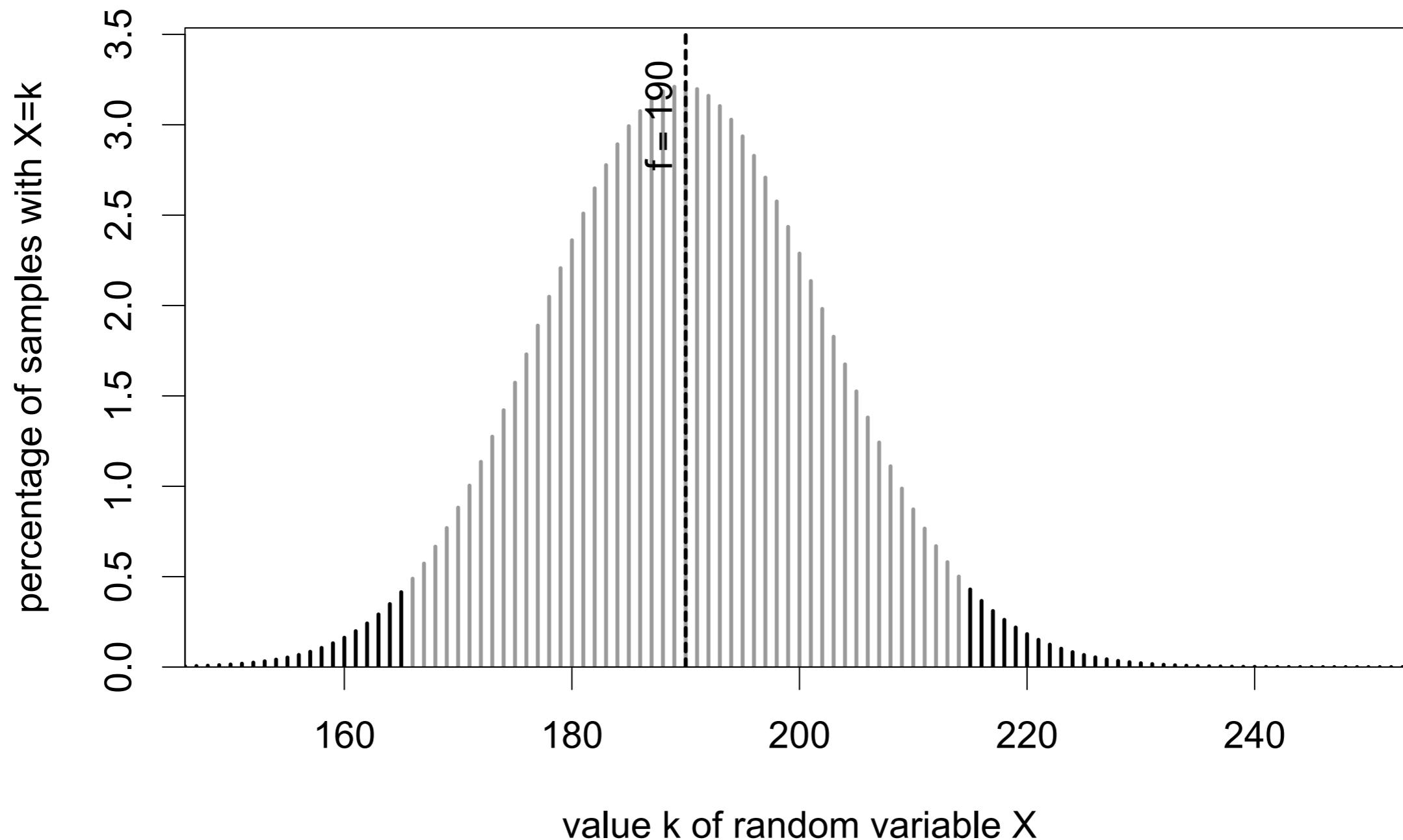
# Confidence interval

$\pi = 17\% \rightarrow H_0$  is not rejected



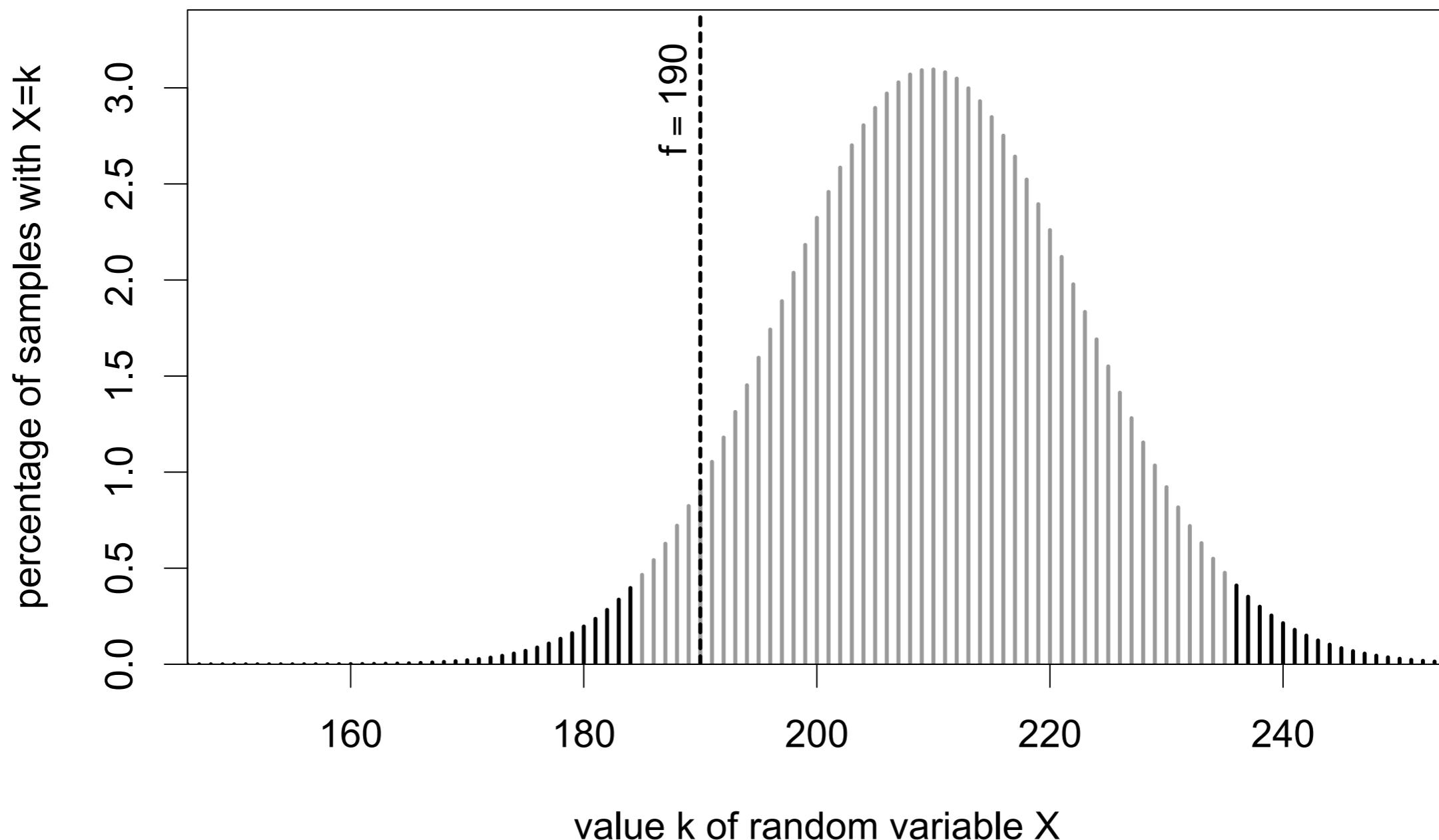
# Confidence interval

$\pi = 19\% \rightarrow H_0$  is not rejected



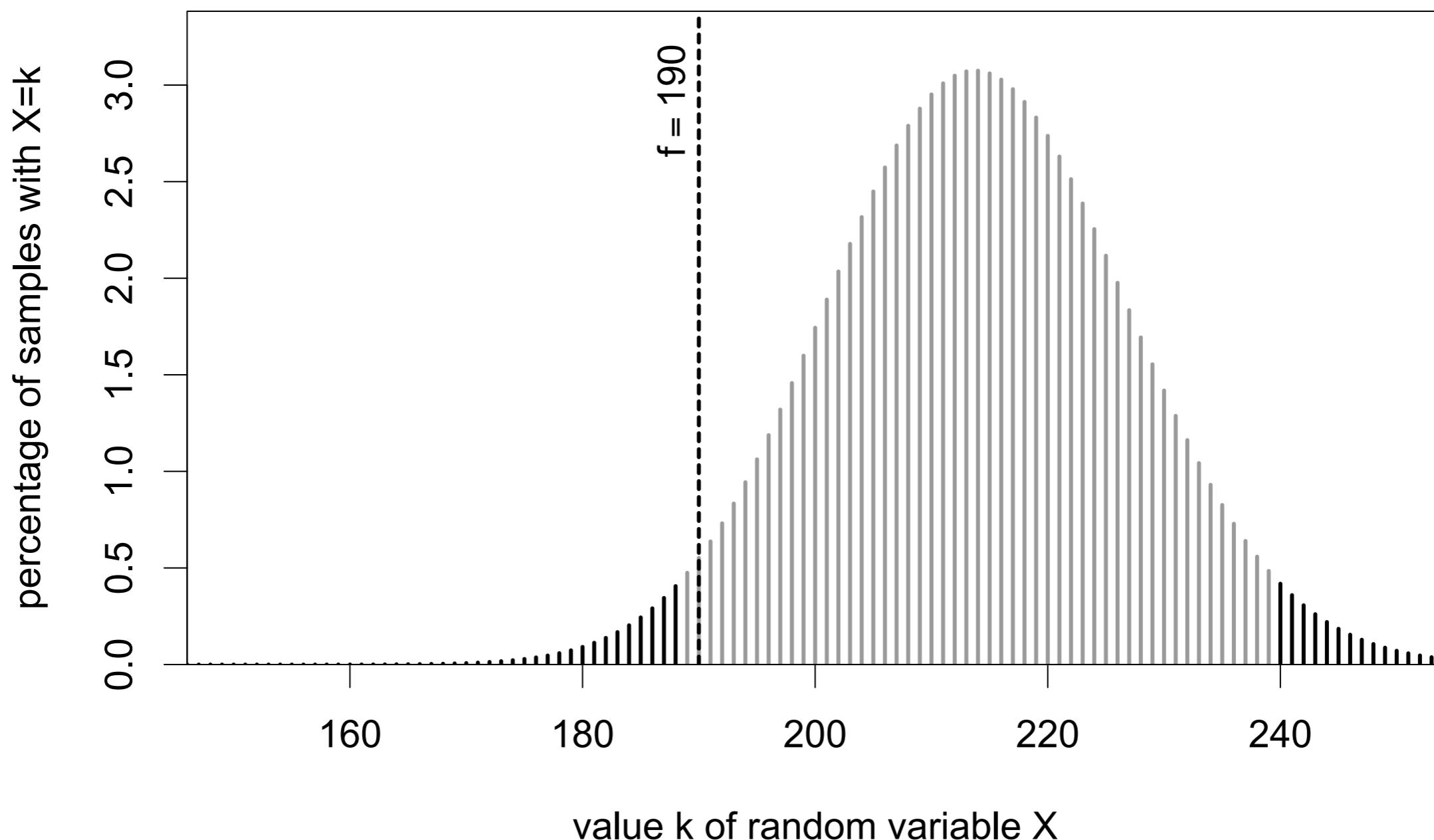
# Confidence interval

$\pi = 21\% \rightarrow H_0$  is not rejected



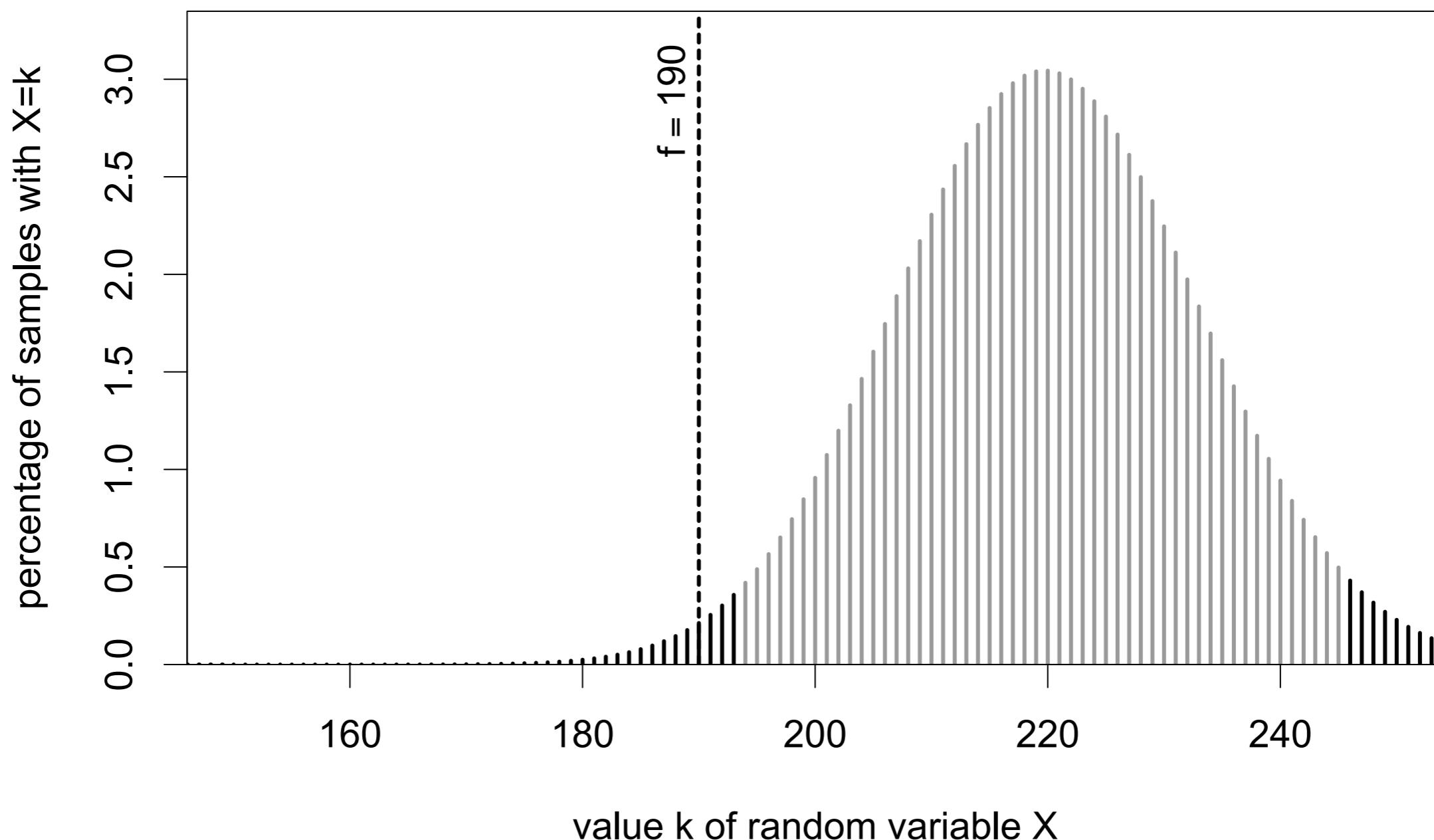
# Confidence interval

$\pi = 21.4\% \rightarrow H_0$  is not rejected



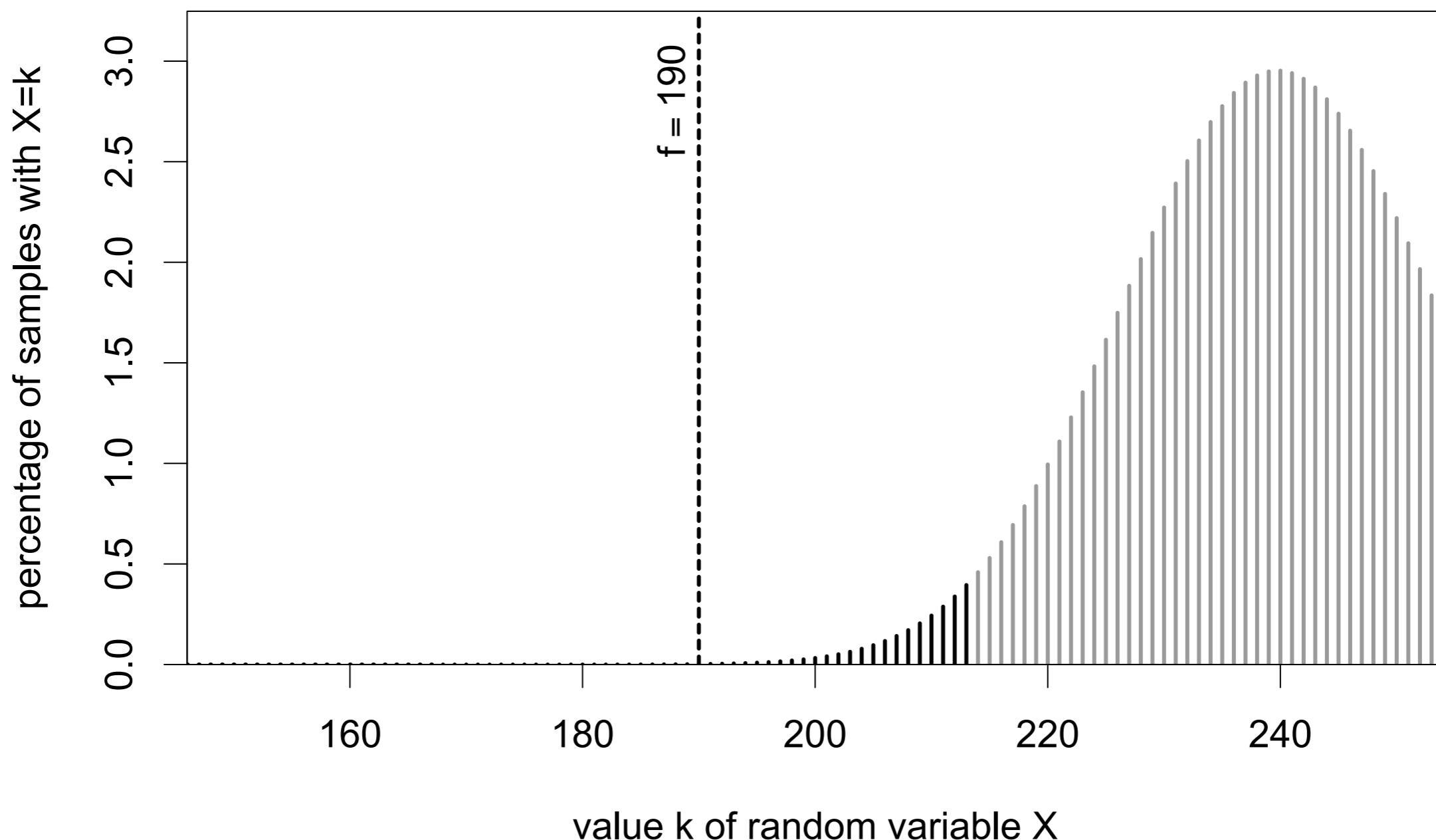
# Confidence interval

$\pi = 22\% \rightarrow H_0 \text{ is rejected}$



# Confidence interval

$\pi = 24\% \rightarrow H_0 \text{ is rejected}$



# Confidence intervals

- ◆ Confidence interval = range of plausible values for true population proportion
- ◆ Size of confidence interval depends on sample size and the significance level of the test

	$n = 100$ $k = 19$	$n = 1,000$ $k = 190$	$n = 10,000$ $k = 1,900$
$\alpha = .05$	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 an interval)

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  - expressed as confidence, e.g. `conf.level=.95` for significance level  $\alpha = .05$ , i.e. 95% confidence

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- ◆ 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:

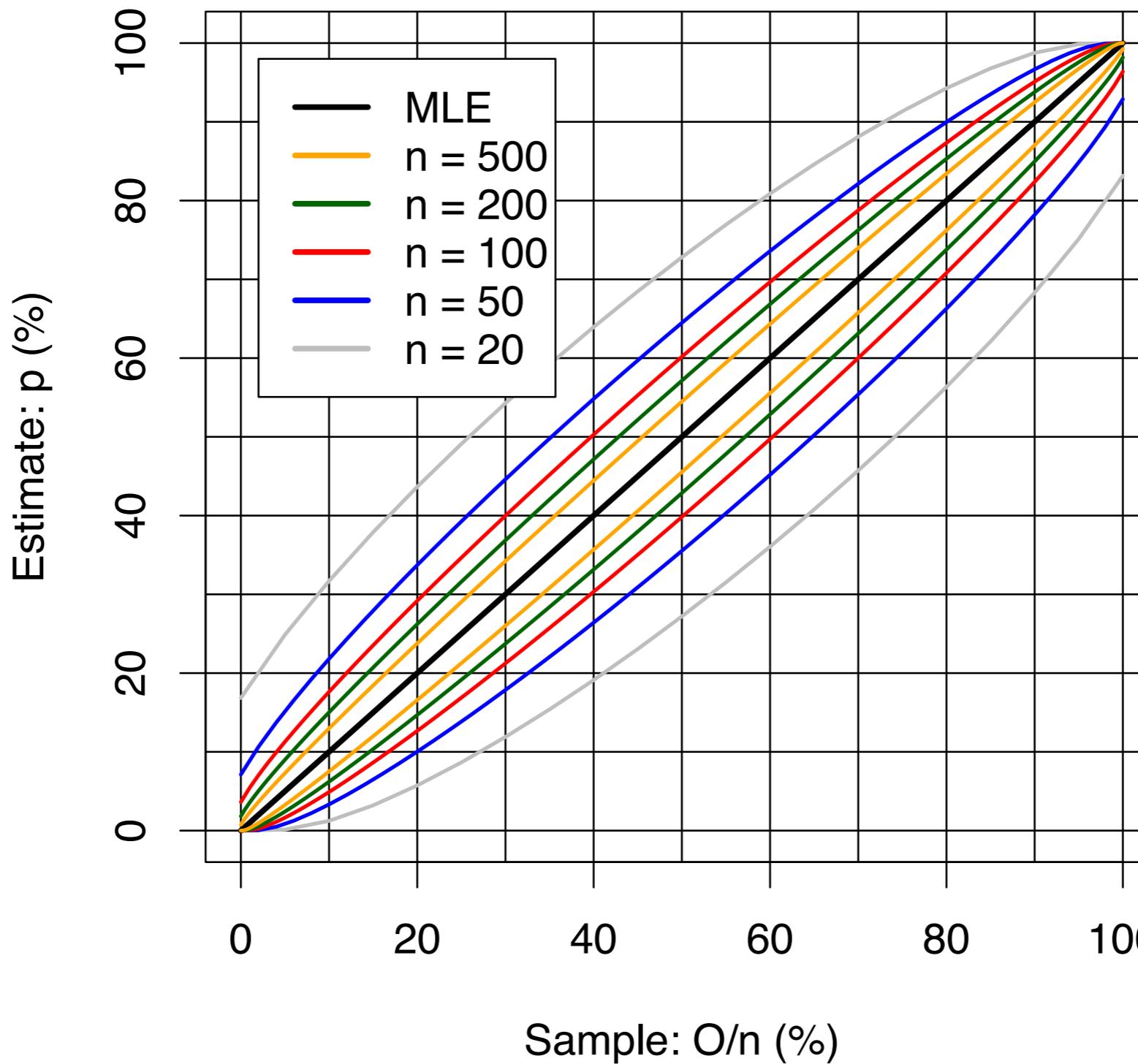
probability of success

0.19

# Choosing sample size

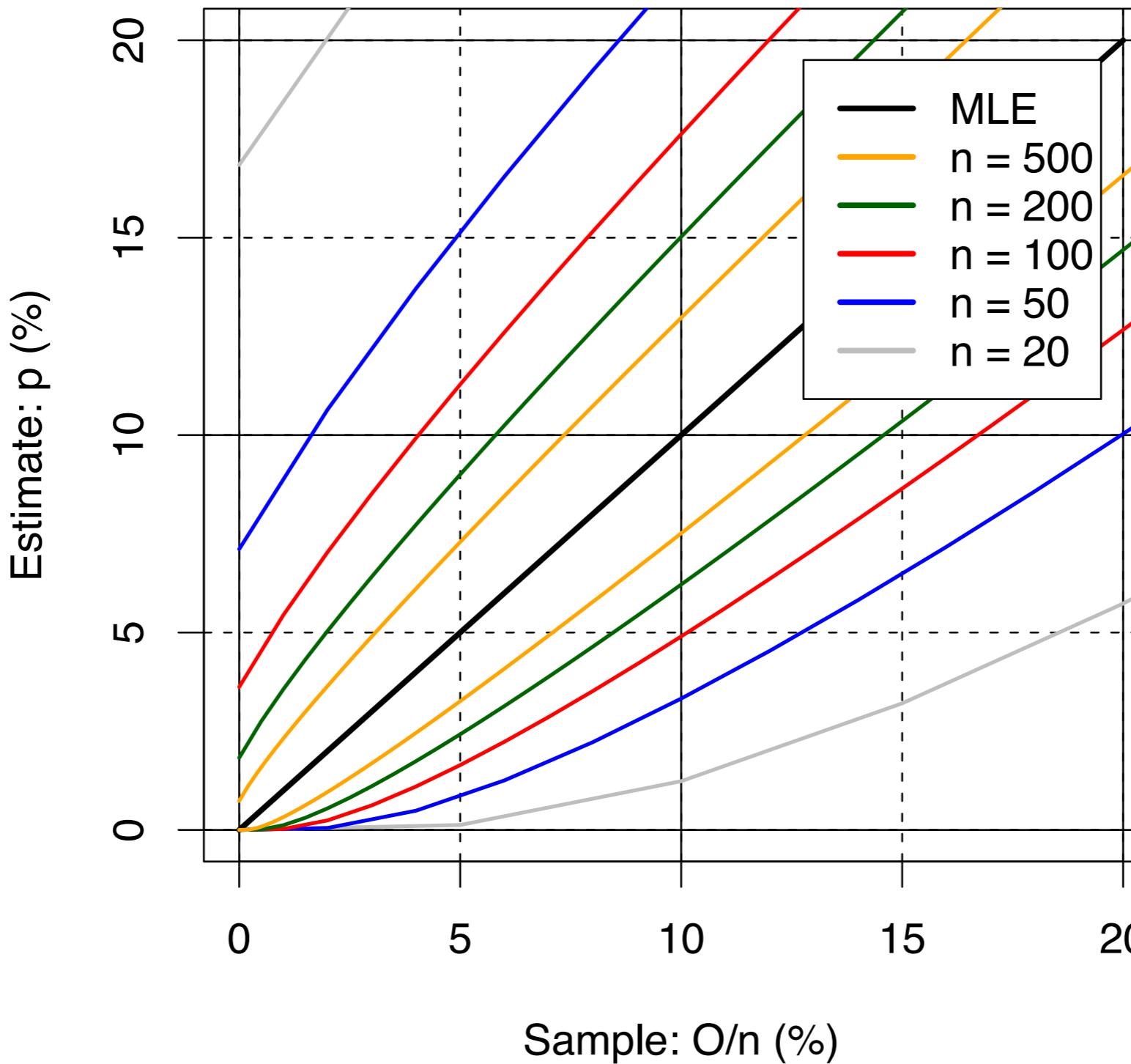
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95% confidence intervals

# Using R to choose sample size

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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”`

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  - Do speakers prefer *I couldn't agree more* over alternative compositional realisations?
- ◆ Compare observed frequencies in two samples

# Frequency comparison

$k_1$	$k_2$
$n_1 - k_1$	$n_2 - k_2$

19	25
81	175

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81	175

- ◆ Contingency table for frequency comparison
  - e.g. samples of sizes  $n_1 = 100$  and  $n_2 = 200$ , containing 19 and 25 passives
  - $H_0$ : same proportion in both underlying populations

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  - $H_0$ : same proportion in both underlying populations
- ◆ Chi-squared  $X^2$ , likelihood ratio  $G^2$ , Fisher's test
  - based on same principles as binomial test

# Frequency comparison

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- ◆ Chi-squared, log-likelihood and Fisher are appropriate for different (numerical) situations
  - Fisher: computationally expensive, small samples;  
 $X^2$ : small balanced samples;  $G^2$ : highly skewed data

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- ◆ Frequency comparison in practice
  - all relevant tests can be performed in



# Frequency comparison in R

- ◆ Frequency comparison with `prop.test()`
  - easy to use: specify counts  $k_i$  and sample sizes  $n_i$
  - uses chi-squared test “behind the scenes”
  - also computes confidence interval for difference of population proportions
- ◆ E.g. for 19 passives out of 100 vs. 25 out of 200
  - > `prop.test(c(19, 25), c(100, 200))`
  - parameters `conf.level` and `alternative` can be used in the familiar way

# 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
```

# Frequency comparison in R

- ◆ Can also carry out chi-squared (`chisq.test`) and Fisher's exact test (`fisher.test`)
  - requires full contingency table as  $2 \times 2$  matrix
  - NB: likelihood ratio test not in standard library
- ◆ Table for 19 out of 100 vs. 25 out of 200

```
> ct <- cbind(c(19,81),  
+               c(25,175))  
> chisq.test(ct)  
> fisher.test(ct)
```

19	25
81	175

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  - very large samples lead to highly significant p-values for minimal and irrelevant differences (e.g.  $1M$  tokens with  $100,000 = 10\%$  vs.  $101,000 = 10.1\%$  occurrences)

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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  $100,000 = 10\%$  vs.  $101,000 = 10.1\%$  occurrences)
- ◆ It is important to assess both **significance** and **relevance** of frequency data!
  - confidence intervals combine both aspects

# Some fine print

- ◆ Convenient `cont.table` function for building contingency tables in `corpora` package
  - > `library(corpora)`
  - > `ct <- cont.table(19, 100, 25, 200)`
- ◆ Difference of proportions no always suitable as **measure of effect size**
  - especially if proportions can have different magnitudes (e.g. for lexical frequency data)
  - more intuitive: ratio of proportions (**relative risk**)
  - Conf. int. for similar **odds ratio** from Fisher's test

# 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")

> Brown      # take a first look at the data tables
> LOB

# 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

```
> ct <- cbind(c(10123, 49576-10123), # Brown  
               c(10934, 49742-10934)) # LOB  
  
> ct          # contingency table for chi-squared / Fisher  
> fisher.test(ct)  
  
# proportions test provides more interpretable effect size  
> prop.test(c(10123, 10934), c(49576, 49742))  
  
# 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 relies on same ordering of genres in Brown/LOB!
> 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()`