# the logic of parametric tests

define the test statistic (e.g. mean)

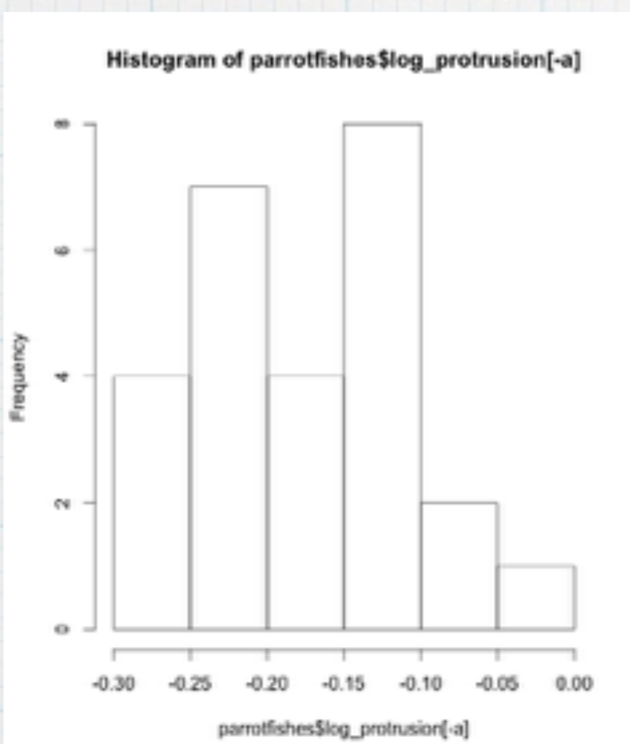
compare the observed test statistic to a distribution calculated for random samples that are drawn from a single (normal) distribution.

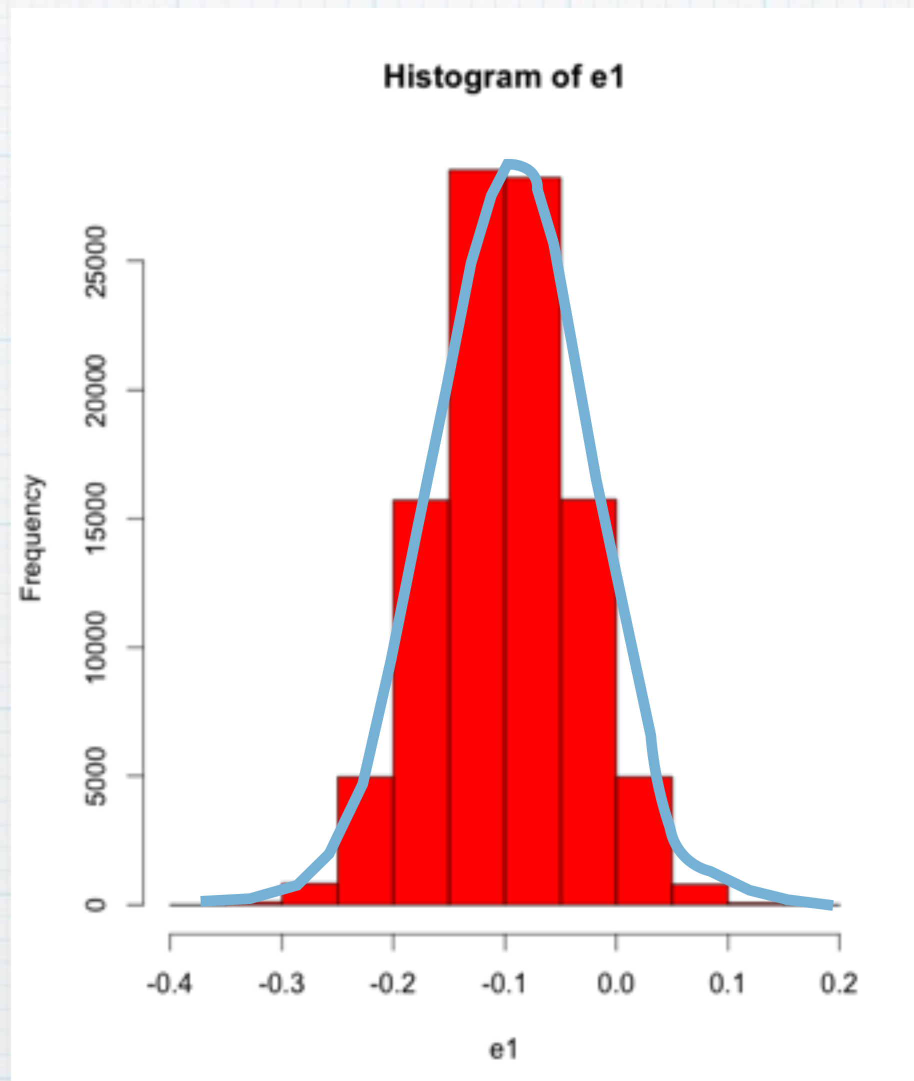
the distribution is parametrized based on your sample

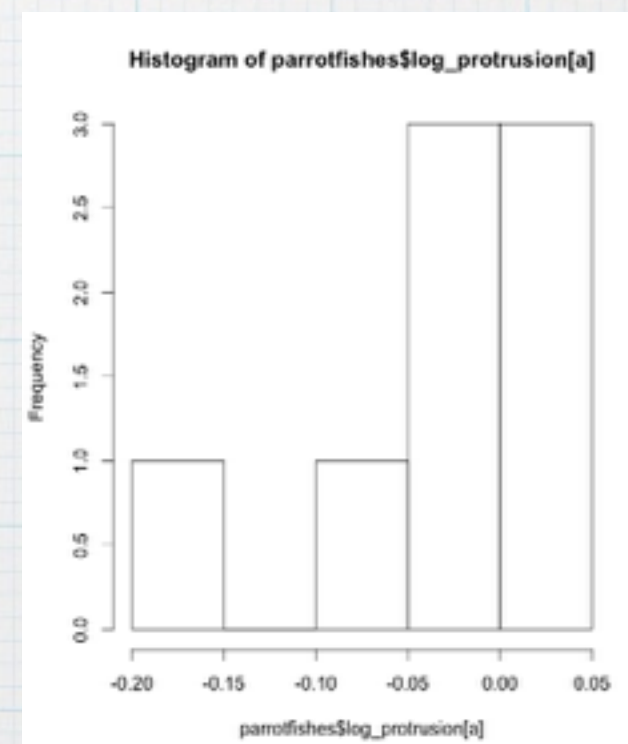
ask what is the probability of the data under the model

# the logic of parametric tests: example with a t-test

t-distribution under H0: the distribution of the test statistic calculated for 2 random samples drawn from a single (normal) distribution



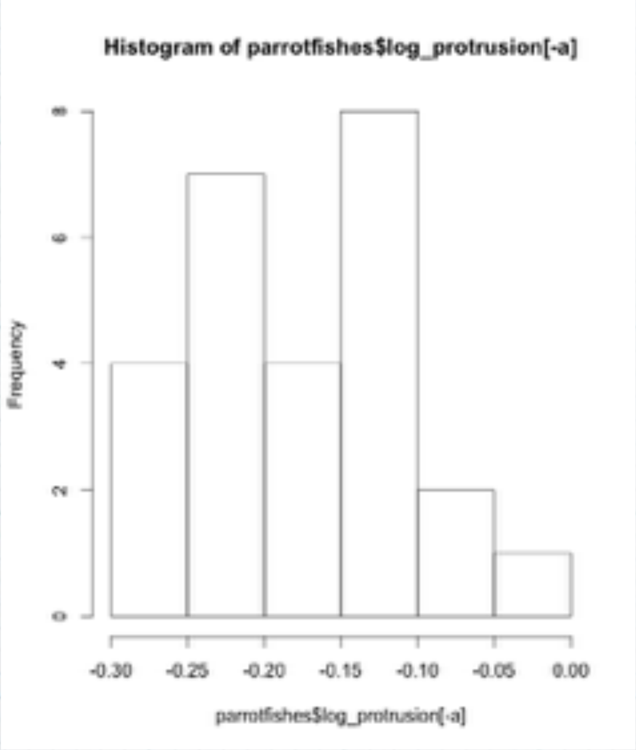

Group 0

Group 1

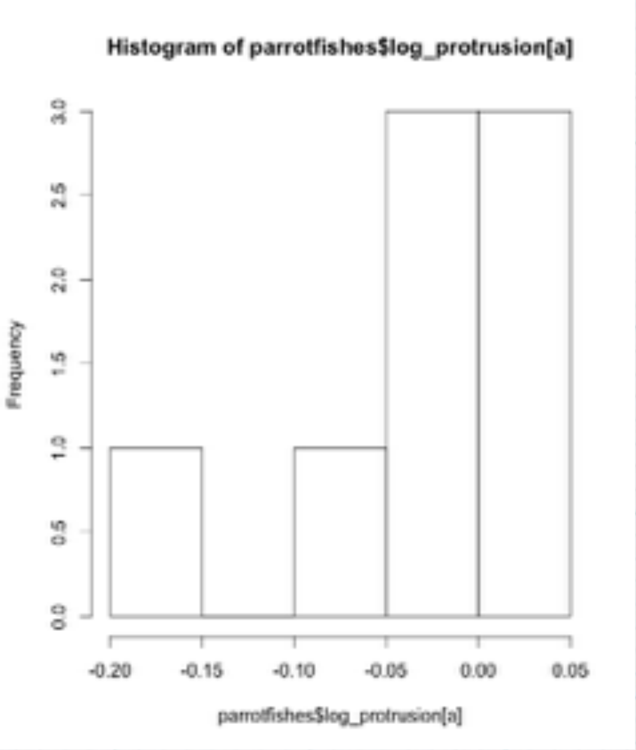
# the logic of parametric tests: example with a t-test

## step 1: extract sample data

| | mean | var | diff |
|---|---|---|---|
| group0 | -0.036 | 0.0037 | -0.134 |
| group1 | -0.17 | 0.004 | |



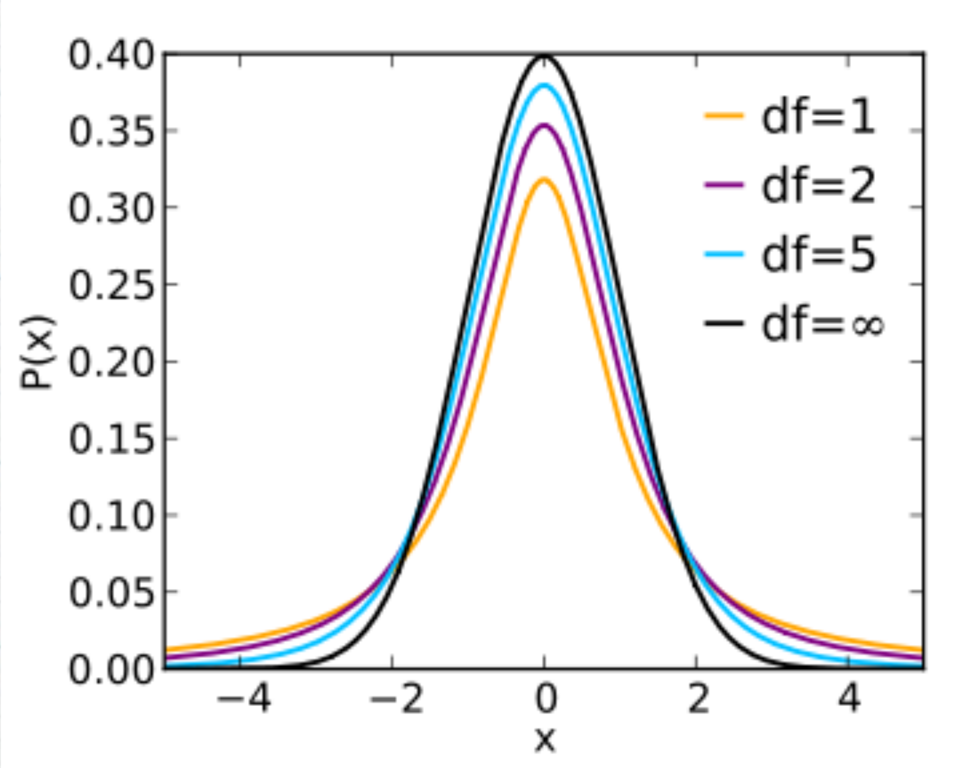

Group 0




Group 1

# the logic of parametric tests: example with a t-test

## step 2: calculate the test statistic - t




$$t = \frac{\bar{X}_1 - \bar{X}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

| | mean | var | diff |
|---|---|---|---|
| group0 | -0.036 | 0.0037 | -0.134 |
| group1 | -0.17 | 0.004 | |

# the logic of parametric tests: example with a t-test

step 2: calculate the test statistic - t

compare test statistic to a value from a theoretical distribution

| | mean | var | diff |
|---|---|---|---|
| group0 | -0.036 | 0.0037 | -0.134 |
| group1 | -0.17 | 0.004 | |

$$t = \frac{\bar{X}_1 - \bar{X}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

t = 5.4747, df = 12.119, p-value = 0.000137

# the logic of parametric tests

define the test statistic (e.g. mean)

compare the observed test statistic to a distribution calculated for random samples that are drawn from a single (normal) distribution.

ask what is the probability of the data under the model

This is where all the assumptions (normality, homogeneity of avarice) come from!

# Assumptions: t-test

1) normality of the data

2) samples are independent

its possible to test the 1st assumption using histograms, qqplot, and tests for normality (e.g. Shapiro-Wilk test)

often, the problem is lack of power due to small n

# Assumptions: ANOVA

1) normality of the data

2) samples are independent

3) homogeneity of variance (**critical**)

its possible to test the 1st assumption using histograms, qqplot, and tests for normality. power problem more extreme

its critical to test for homogeneity of variance (leveneTest in library car)

# Assumptions: regression

1) normality of the **residuals**

2) samples are independent

3) homogeneity of variance

it is generally difficult to test regression assumptions.

its possible to test the 1st assumption using histograms, qqplot, and tests for normality on residuals.

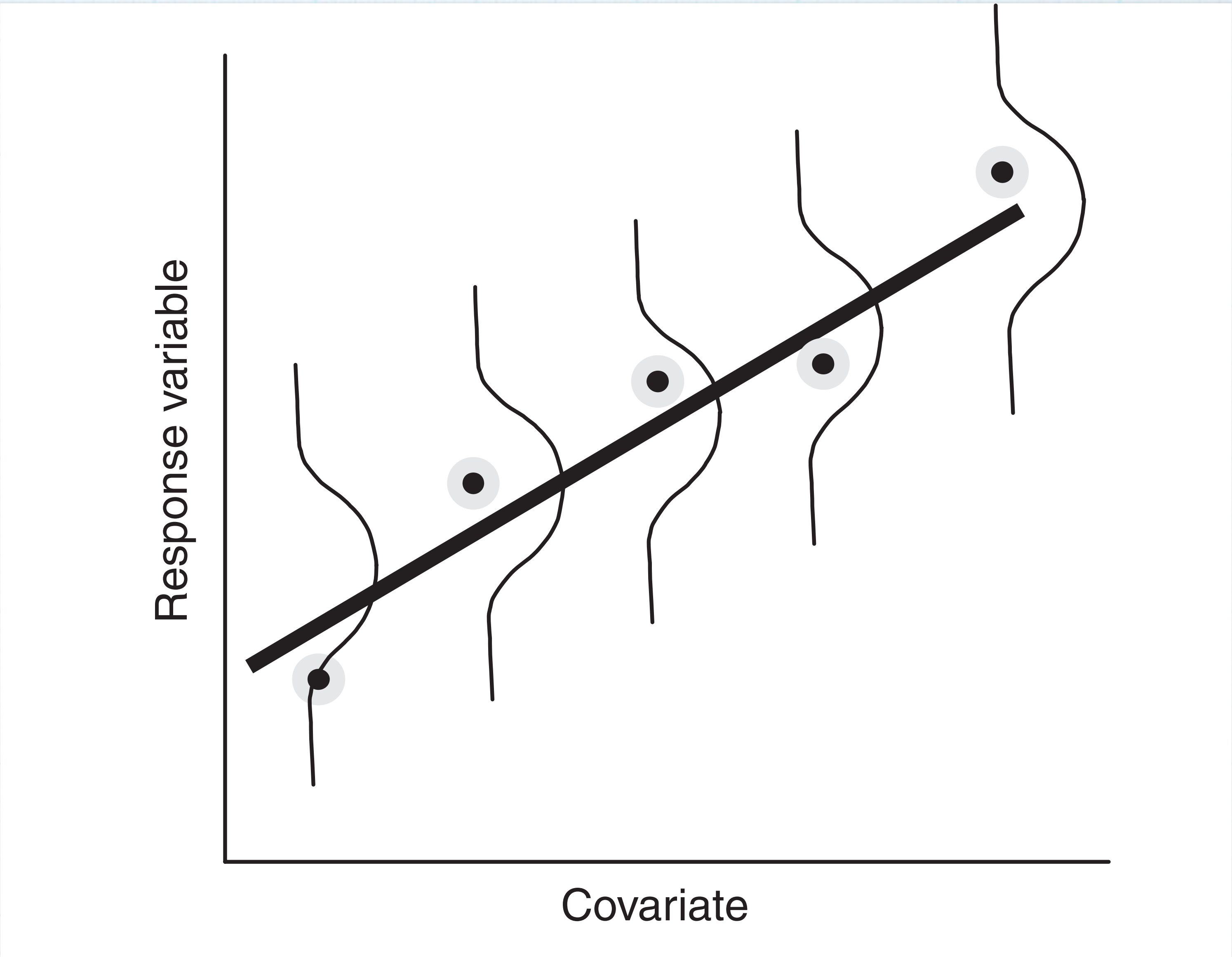
remember to think about power

# Assumptions: regression

1) normality of the **residuals**

2) samples are independent

3) homogeneity of variance

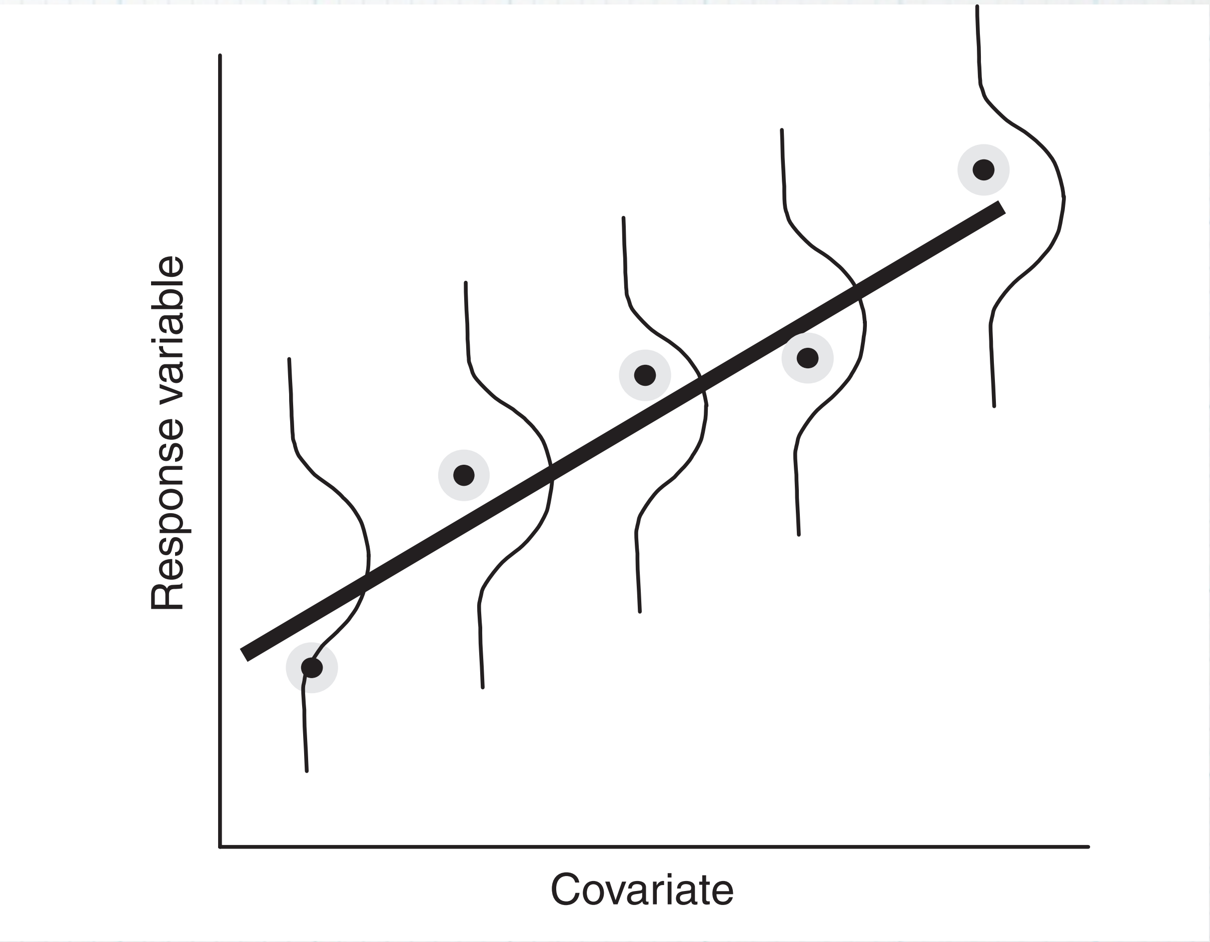


# Assumptions: regression

1) normality of the **residuals**

2) samples are independent

3) homogeneity of variance




```
model=lm(Y~X)
hist(model$residuals)
plot(model$fitted.values ,Y)
```

points in extreme x values have strong leverage

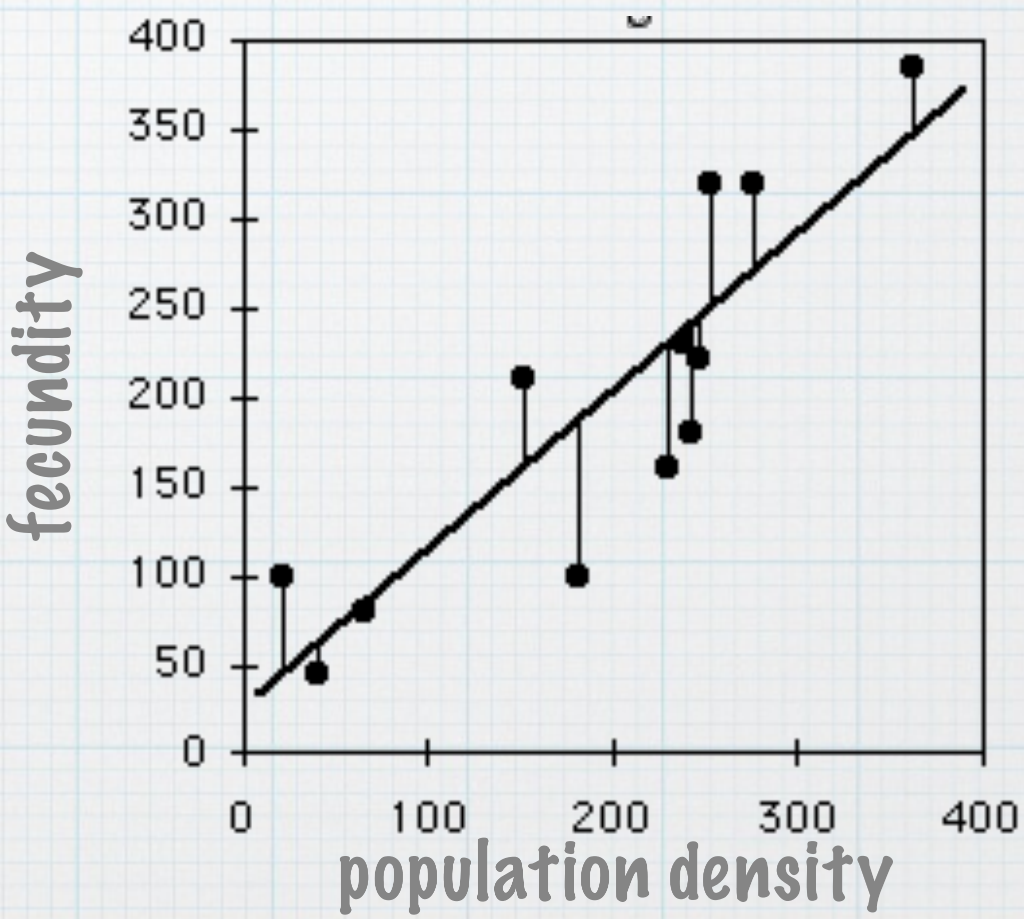
# More assumptions: regression

1) normality of the residuals

2) samples are independent

3) homogeneity of variance

4) X is known with no error




```
library(lmodel2)
lmodel2(density~ fecundity, data=data, nperm=99)
```

# More assumptions: regression

```
Call: lmodel2(formula = Predicted_by_model ~ Survival, data =
mod2ex1, nperm = 99)

n = 54   r = 0.8387315   r-square = 0.7034705
Parametric P-values:   2-tailed = 2.447169e-15    1-tailed = 1.223585e-15
Angle between the two OLS regression lines = 9.741174 degrees

Permutation tests of OLS, MA, RMA slopes: 1-tailed, tail corresponding to sign
A permutation test of r is equivalent to a permutation test of the OLS slope
P-perm for SMA = NA because the SMA slope cannot be tested

Regression results
  Method Intercept     Slope  Angle (degrees)  P-perm (1-tailed)
1    OLS 0.6852956 0.6576961         33.33276               0.01
2     MA 0.4871990 0.7492103         36.84093               0.01
3    SMA 0.4115541 0.7841557         38.10197                 NA

Confidence intervals
  Method  2.5%-Intercept 97.5%-Intercept  2.5%-Slope 97.5%-Slope
1    OLS       0.4256885       0.9449028  0.5388717   0.7765204
2     MA       0.1725753       0.7633080  0.6216569   0.8945561
3    SMA       0.1349629       0.6493905  0.6742831   0.9119318

Eigenvalues: 0.1332385 0.01090251

H statistic used for computing C.I. of MA: 0.007515993
```

library(lmodel2)
lmodel2(density~ fecundity, data=data, nperm=99)

# More assumptions: regression

For species data, samples cannot be truly considered independent, because they share a common history

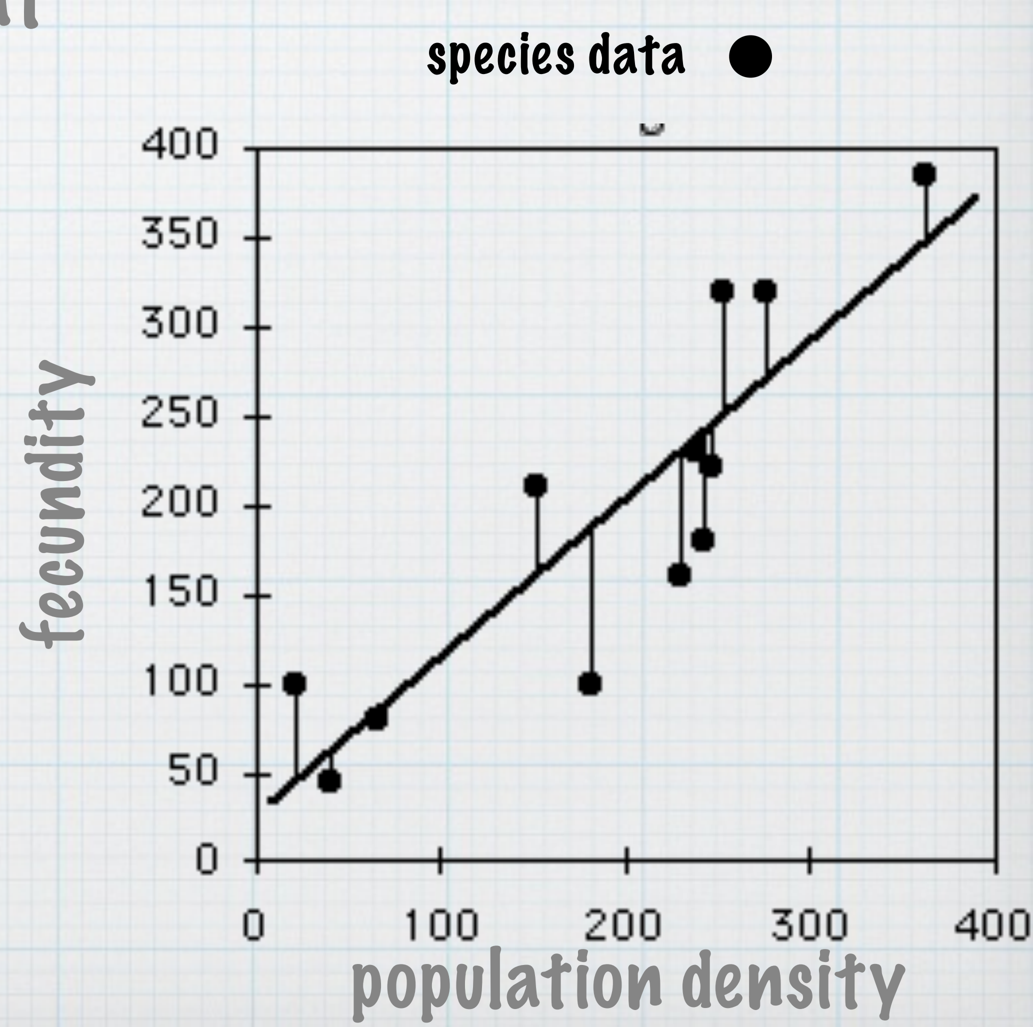
its possible to account for this correlation if phylogenetic information is available

If this is applicable for your data, learn more at

http://en.wikipedia.org/ wiki/Phylogenetic_comparative_methods

or here

http://bodegaphylo.wikispot.org/Phylogenetic_Comparative_Methods



What if my assumptions are invalid?

## the logic of parametric tests

define the test statistic (e.g. mean)

compare the observed test statistic to a distribution calculated for random samples that are drawn from a single (normal) distribution.

ask what is the probability of the data under the model

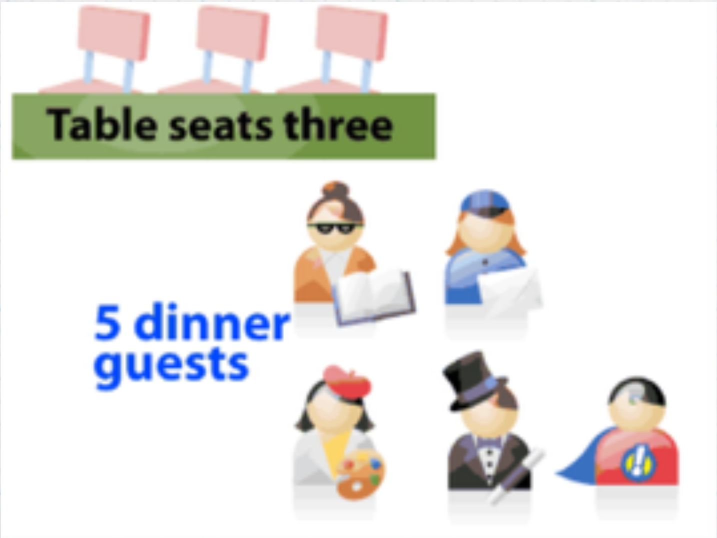
**Can I compare my data to another distribution?**

## Permutation, Montecarlo, and bootstrap: what's the deal?

Permutation & randomization tests: generating the probability of test statistics from the data, rather than a theoretical distribution

Montecarlo: generating the probability of test statistics from the process, rather than a theoretical distribution

Bootstrap, Jackknife: estimating bias and precision of estimates from the data, rather than a theoretical distribution





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# the logic of randomisation tests

define the test statistic (e.g. mean)

shuffle the data, extract test statistic

repeat for all possible permutations (permutation test) or a sub-sample of them (randomization)

ask what is the probability of the observed test statistics under the generated distribution

# the logic of randomisation tests: example with a t-test

## step 1: extract sample data

| | mean | var | diff |
|---|---|---|---|
| group0 | -0.036 | 0.0037 | -0.134 |
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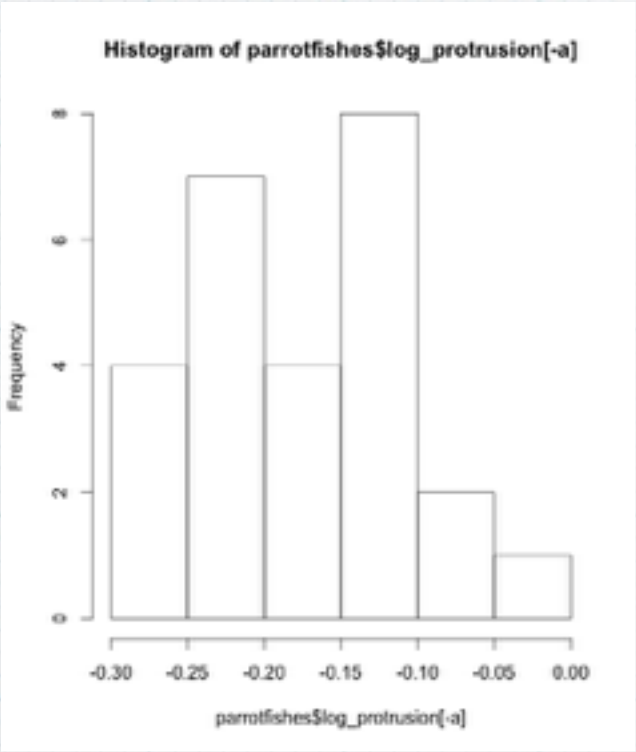
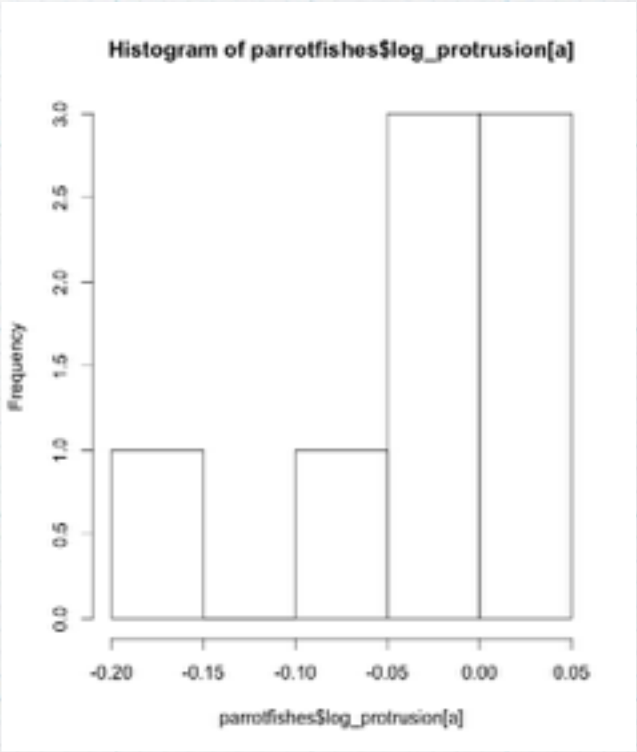


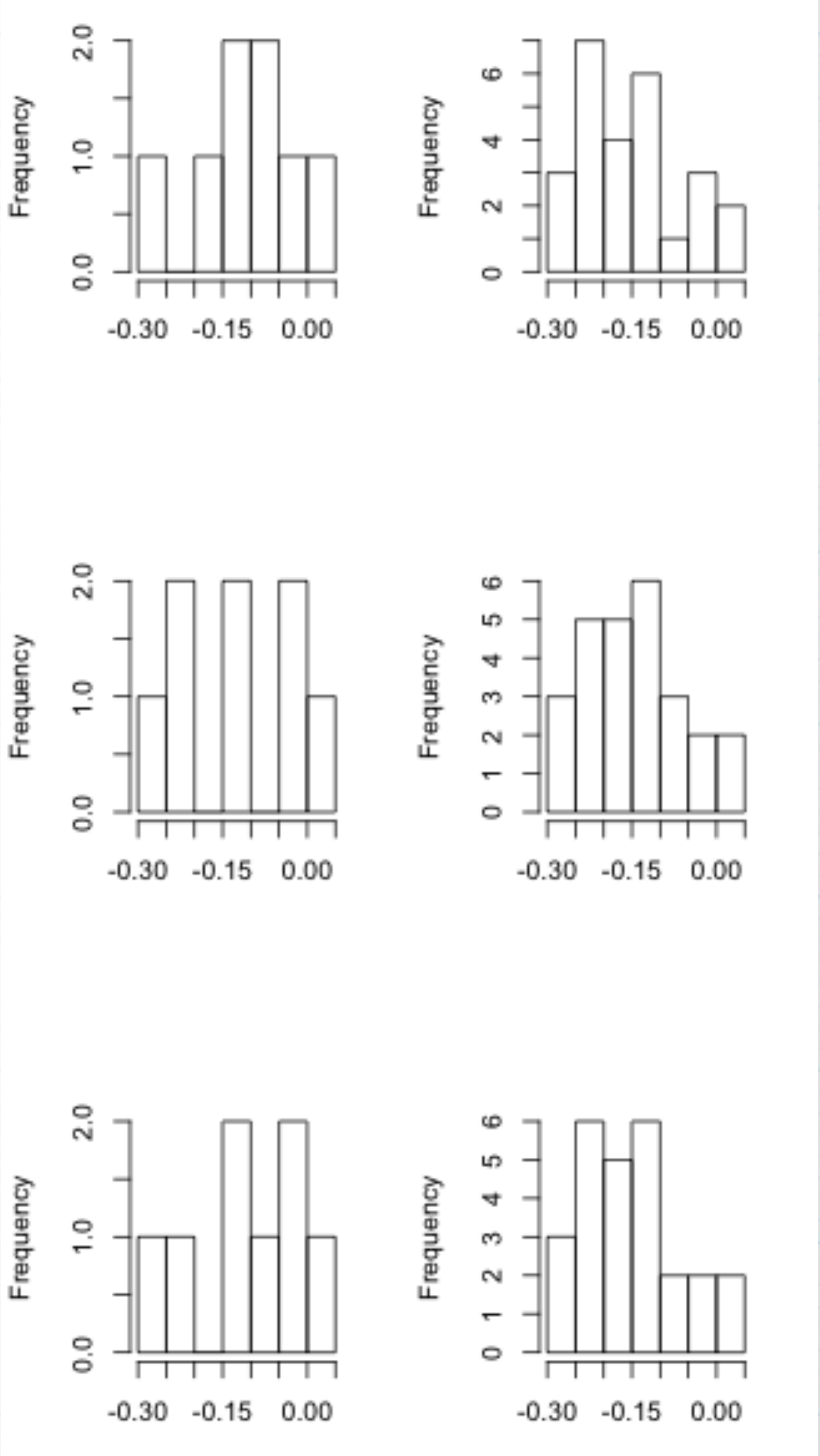

Group 0

Group 1

# the logic of randomisation tests: example with a t-test

## step 2: shuffle the data, extract the test statistic. repeat.

| | group0 | group1 | diff |
|---|---|---|---|
| iteration 1 | 0.8023 | 0.2460 | 0.5563 |
| iteration 2 | 0.3252 | 0.9017 | -0.5764 |
| iteration 3 | 0.6556 | 0.7817 | -0.1261 |
| iteration 4 | 0.9292 | 0.2860 | 0.6432 |
| iteration 5 | 0.9953 | 0.9452 | 0.0501 |
| iteration 6 | 0.2650 | 0.8852 | -0.6201 |
| iteration 7 | 0.8313 | 0.9650 | -0.1336 |
| iteration 8 | 0.4534 | 0.6516 | -0.1981 |
| iteration 1000 | 0.8300 | 0.7998 | 0.0301 |



# the logic of parametric tests

ask what is the probability of the observed test statistics under the generated distribution

Min. :-0.1198963

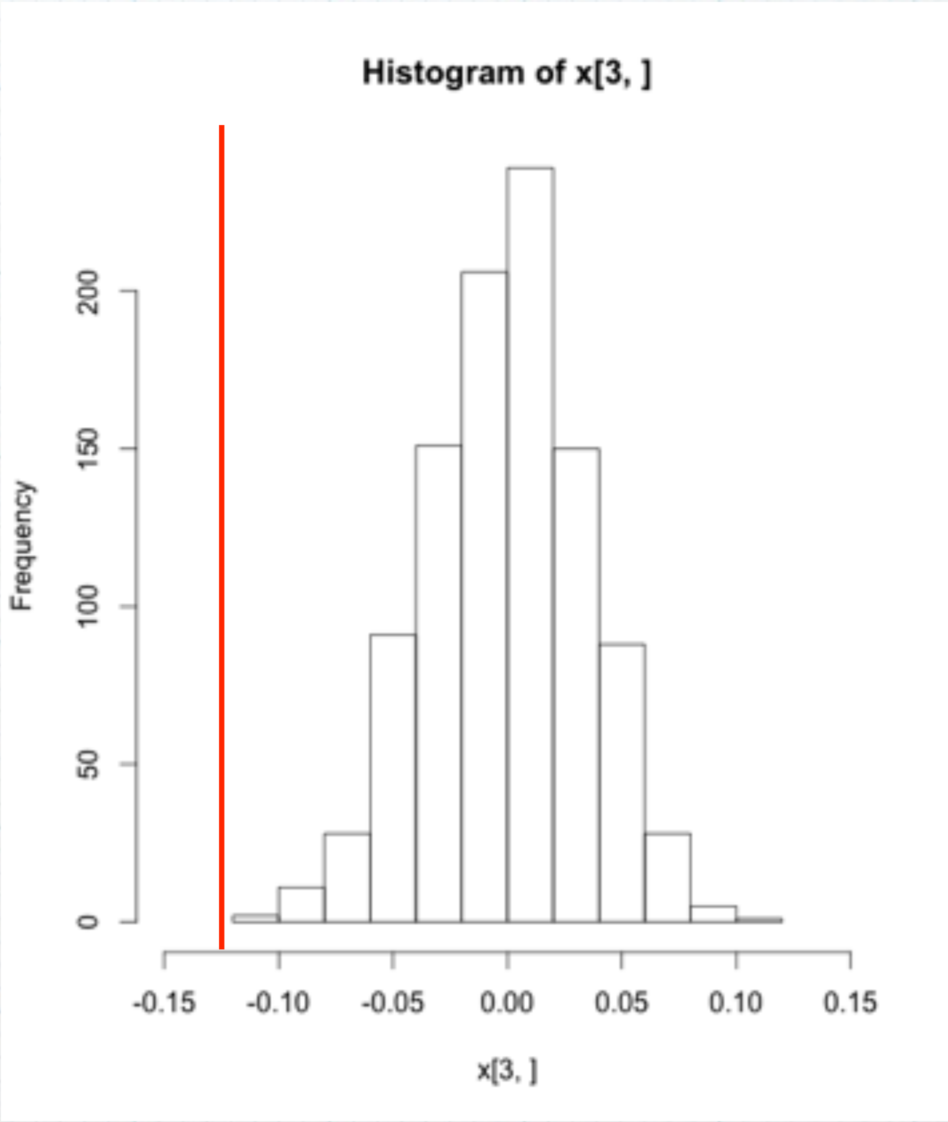
1st Qu.:-0.0235121

Median : 0.0010862

Mean :-0.0003389

3rd Qu.: 0.0223127

Max. : 0.1062735



# the logic of randomisation tests: example with a t-test

define the test statistic (e.g. mean)

shuffle the data, extract test statistic

repeat for all possible permutations (permutation test) or a sub-sample of them (randomization)

ask what is the probability of the observed test statistics under the generated distribution

No assumptions regarding the distribution of population

# the logic of randomisation tests: example with a t-test

## step 1: extract sample data

```
real.diff=(data$dependent[group0]-data$dependent[group1])
```

# the logic of randomisation tests: example with a t-test

## step 2: shuffle the data, extract the test statistic.

```
randomvector=sample(n)
mock.data=data$dependent[randomvector]
mock.diff=(data$dependent[group0]-data$dependent[group0])
```

# the logic of randomisation tests: example with a t-test

## step 2: shuffle the data, extract the test statistic. repeat

```
all.diff=matrix(NA,1000,1)

for (i in 1:1000){

randomvector=sample(n)
mock.data=data$dependent[randomvector]
mock.diff=(data$dependent[group0]-data$dependent[group0])
all.diff[i]=mock.diff
}
```

# the logic of randomisation tests: example with a t-test

ask what is the probability of the observed test statistics under the generated distribution

```
p=(length(which(all.diff > real.diff)) + length(which(all.diff < -real.diff)))/1000
```

# the logic of randomisation tests: example with a t-test

$\boxed{\text{define the test statistic (e.g. mean)}}$

shuffle the data, extract test statistic

repeat for all possible permutations (permutation test) or a sub-sample of them (randomization)

ask what is the probability of the observed test statistics under the generated distribution

possible to choose other statistics e.g. (t) or (f)

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## the logic of randomisation tests: example using Lloyd's index

define the test statistic (e.g. Lloyd's index)

model the process. for example, place "organisms" randomly on a grid, with parameters (density) matching your's

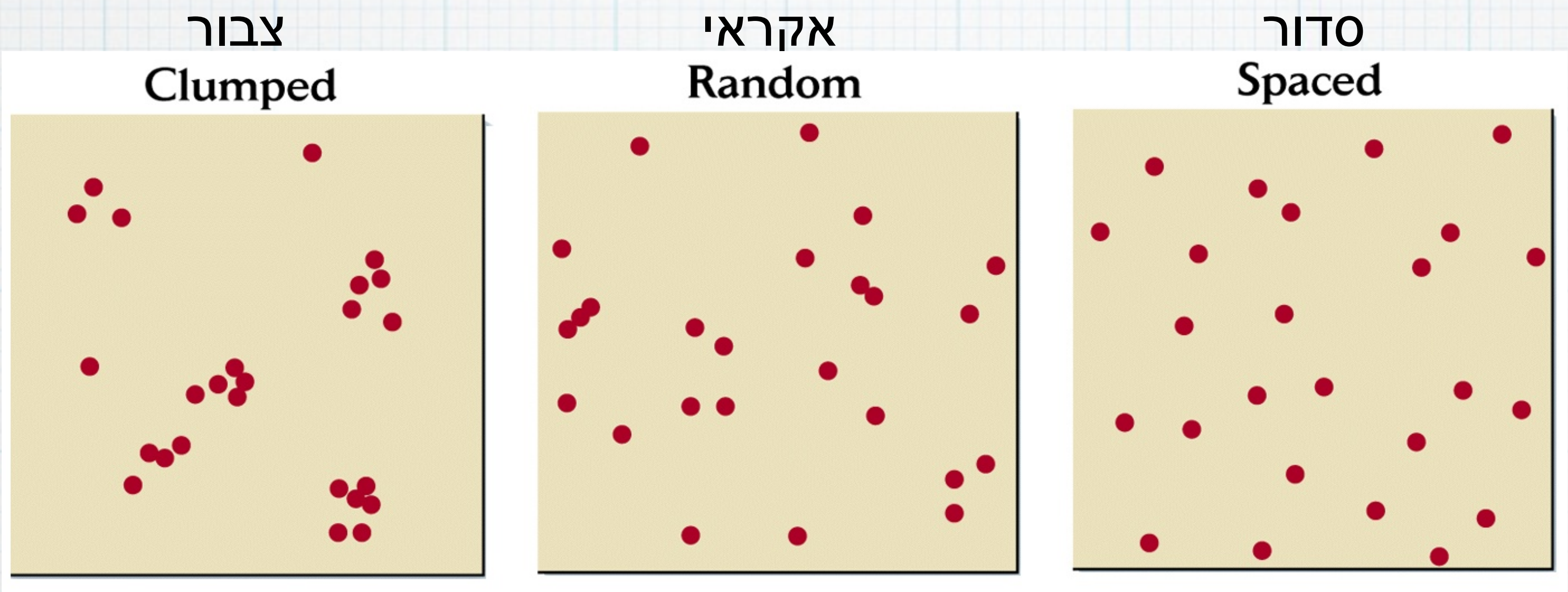
calculate the test statistic (Lloyd's index)

repeat multiple times

ask what is the probability of the observed test statistics under the generated distribution

# the logic of randomisation tests: example using Lloyd's index

## define the test statistic (e.g. Lloyd's index)

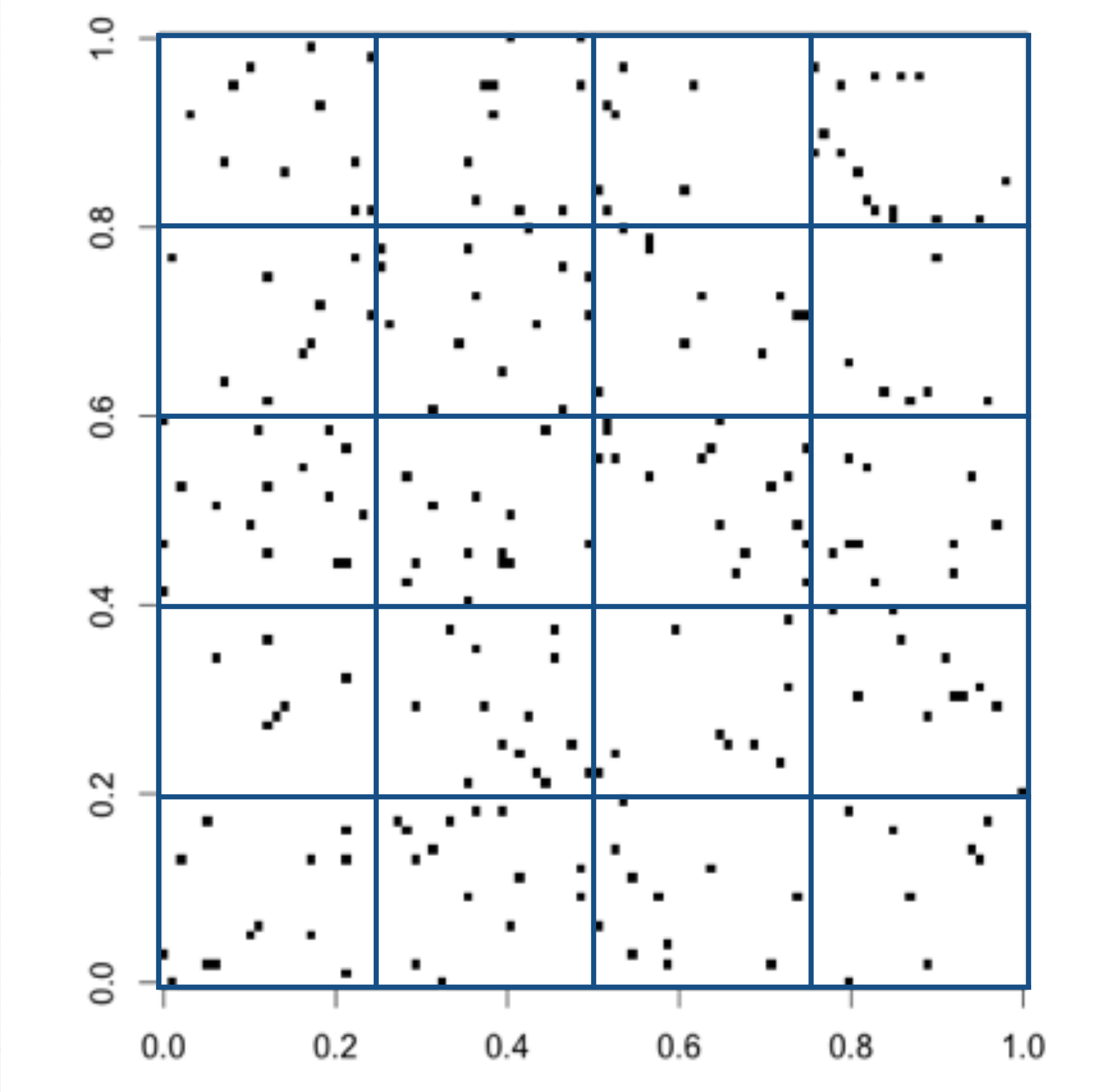



$$L = \frac{V}{\overline{X}^2} + 1 - \frac{1}{\overline{X}}$$

# the logic of randomisation tests: example using Lloyd's index

define the test statistic (e.g. Lloyd's index)

place "organisms" randomly on a grid, with parameters (density) matching yours. calculate Lloyd's




L= 1.06

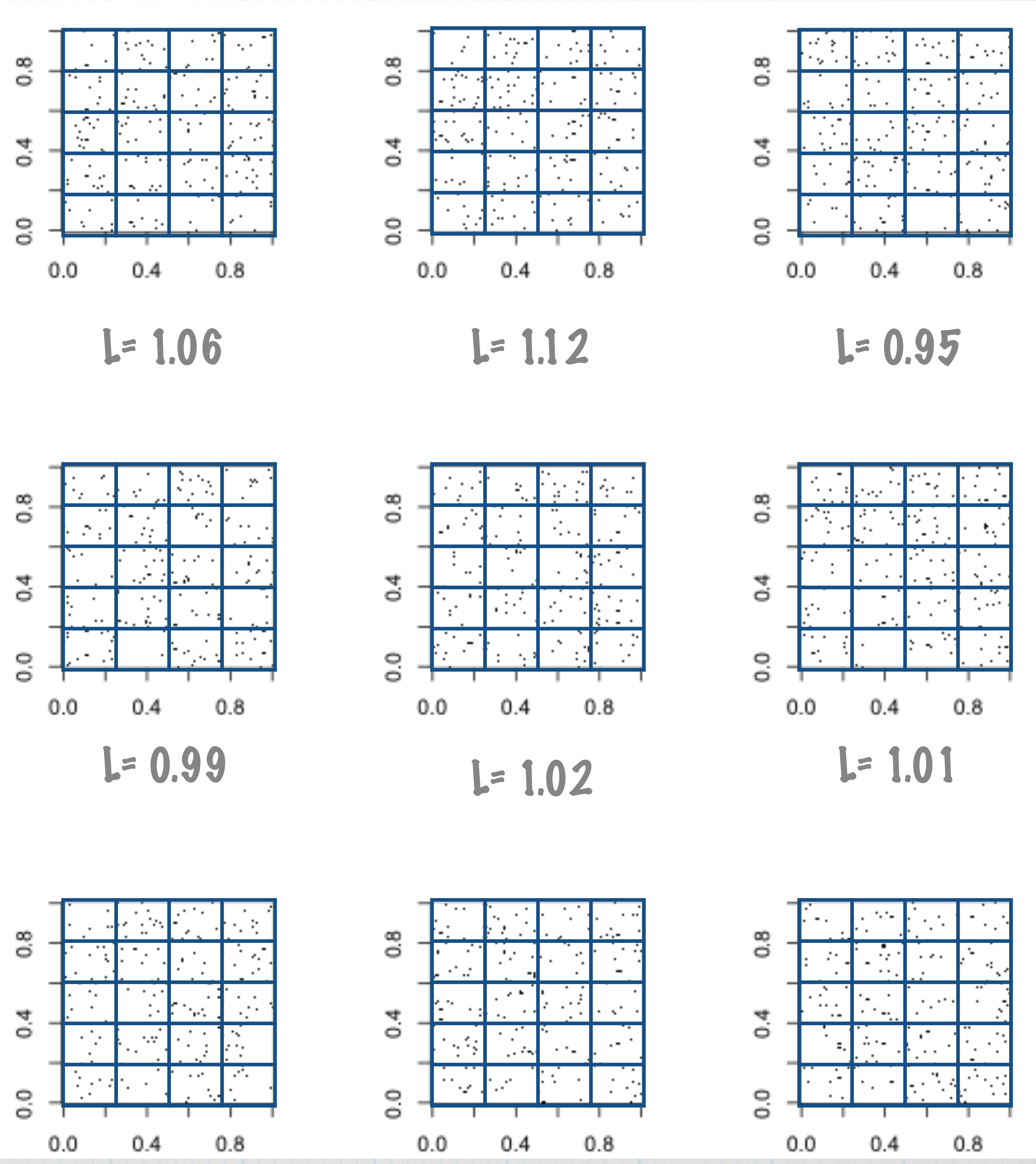
# the logic of randomisation tests: example using Lloyd's index

define the test statistic (e.g. Lloyd's index)

place "organisms" randomly on a grid, with parameters (density) matching your's

calculate Lloyd's index

**repeat multiple times**



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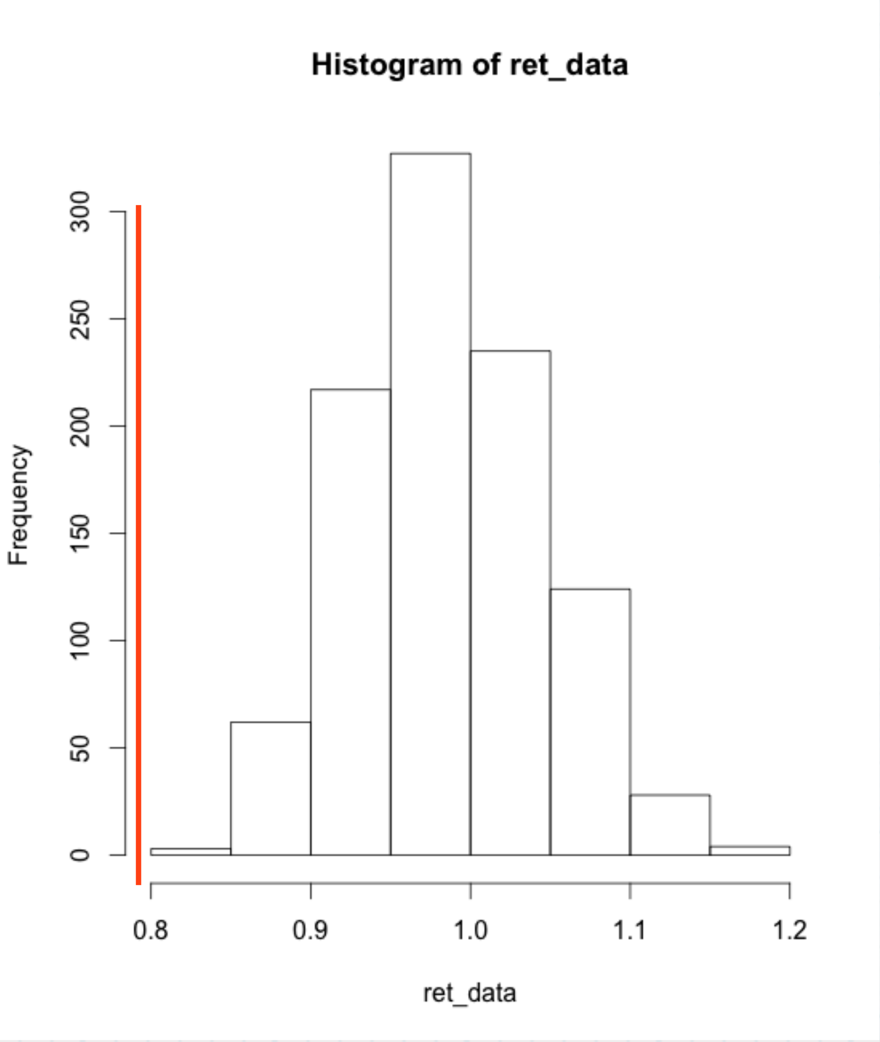
model the process. for example, place "organisms" randomly on a grid, with parameters (density) matching your's

calculate the test statistic (Lloyd's index)

repeat multiple times

**ask what is the probability of the observed test statistics under the generated distribution**



# the logic of randomisation tests: example using Lloyd's index

define the test statistic (e.g. Lloyd's index)

model the process. for example, place "organisms" randomly on a grid, with parameters (density) matching your's

calculate the test statistic (Lloyd's index)

repeat multiple times

ask what is the probability of the observed test statistics under the generated distribution

one can make more complex models, i.e. place organisms that have an interaction between them

## Permutation, Montecarlo, and bootstrap: what's the deal?

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Bootstrap, Jackknife: estimating bias and precision of parameters from the data, rather than a theoretical distribution

# the logic of bootstrap

compute the parameter of interest (e.g. number of species) from your n samples. the sample estimate is $\hat{s}$.

sample (with replacement) n samples from your original dataset

calculate the parameter of interest: $\hat{s}_b$

repeat B times (For SE and bias estimation 50-100, For CI calculation 1000)

Use the results to generate an empirical sampling distribution of $\hat{s}$.

# the logic of bootstrap

The bootstrap estimate of the parameter

$$\hat{S}_{bs} = \frac{1}{B}\sum_{i=1}^{B}\hat{S}_i$$

The bootstrap standard error (i.e. the standard deviation of the bootstrap estimate)

$$s.e._{bs}(\hat{S}) = \sqrt{\frac{1}{B-1}\sum_{i=1}^{B}(\hat{S}_i - \hat{S}_{bs})}$$

The bootstrap estimate of the bias:

$$b_{bs} = \hat{S}_{bs} - \hat{S}$$

The bias corrected estimate:

$$\hat{S} - (\hat{S}_{bs} - \hat{S}) = 2\hat{S} - \hat{S}_{bs}$$

Definition: Bias=S_hat - S; where S is the true parameter. Hence, S=S_hat - bias where the bias is estimated by (S_hat_bs - S_hat)