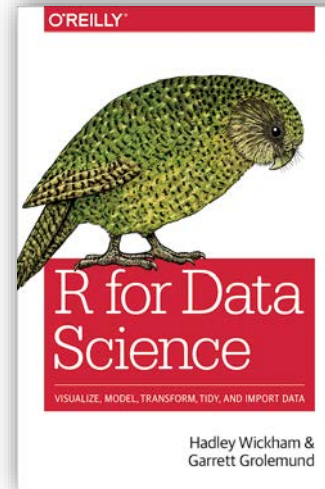
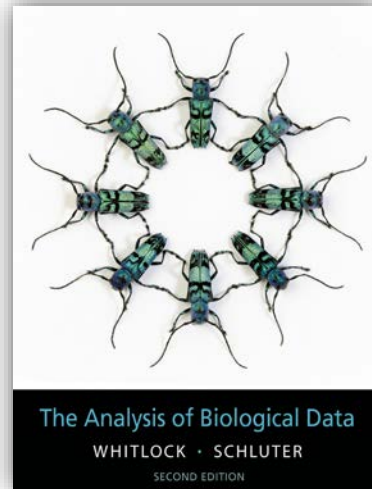


Data Science in Bioinformatics

Palle Villesen & Thomas Bataillon



Outline for week 05

- Any questions from last week ?
- Chapter 6
 - Open discussion & Exercises
- Thursday
 - Who will be responsible

Hypothesis testing

4 basic steps

- State null hypothesis
- Compute test statistic
- Determine p value
- Conclude

Why statistical tests?

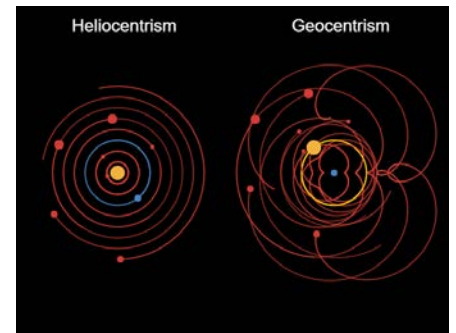
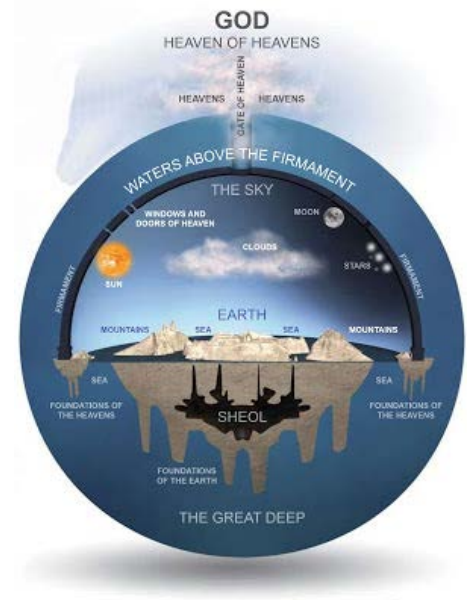
- One use of hypothesis testing is deciding whether experimental results contain enough information to **cast doubt on conventional wisdom**
 - That means reject the null hypothesis

Null hypothesis

A good null hypothesis is a statement that would be interesting to reject

Examples

- H0: Tomato plants do not exhibit a higher rate of growth when planted in compost rather than soil.
- H0: World is Flat
- H0: The Geocentric Model: Earth is the centre of the Universe and it is Spherical
- H0: The Heliocentric Model: Sun is the centre of the universe



Discuss

- How do you formulate a null-hypothesis, if you have absolutely no idea about the expected parameter value, and how do you judge if a null-hypothesis is "good" or not, if there's no data - or theory based assumptions of the true parameter value.

Polio vaccine – what is the H0?

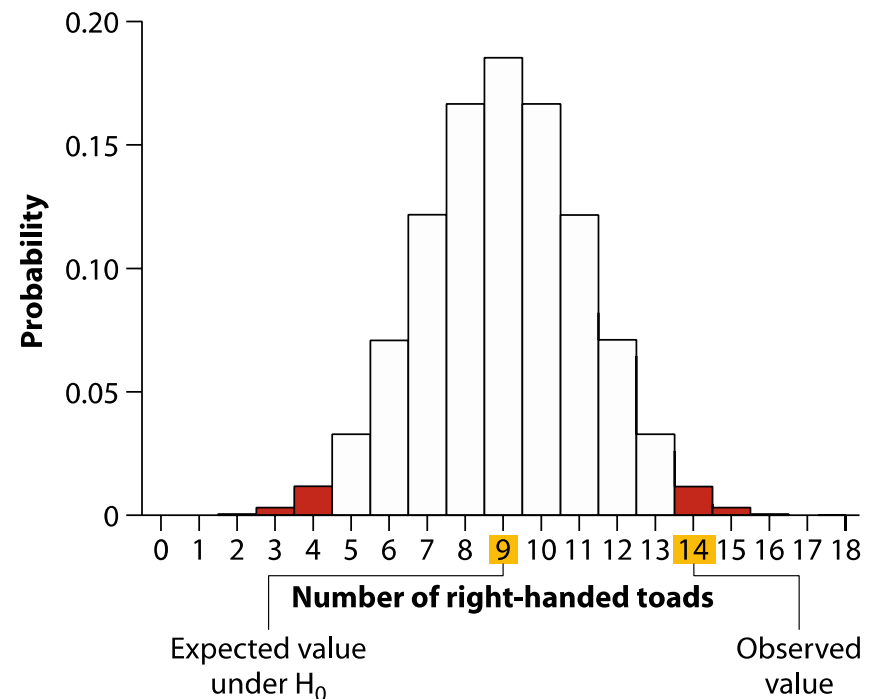
- 401974 students in two groups
- 0.016% got polio with vaccine
 - 33/200987
- 0.057% got polio without vaccine
 - 115/200987

Null distribution

The null distribution is the sampling distribution of outcomes for a test statistic under the assumption that the null hypothesis is true

H0 and its null distribution

- Distribution arising under the null hypothesis
- A null hypothesis (H_0):
a (precise) statement about a property of a population
- Test of an hypothesis:
How unlikely is my observation under H_0 ?
If unlikely enough \rightarrow reject H_0
If not \rightarrow do not reject H_0 ...
does it mean accepting it ?



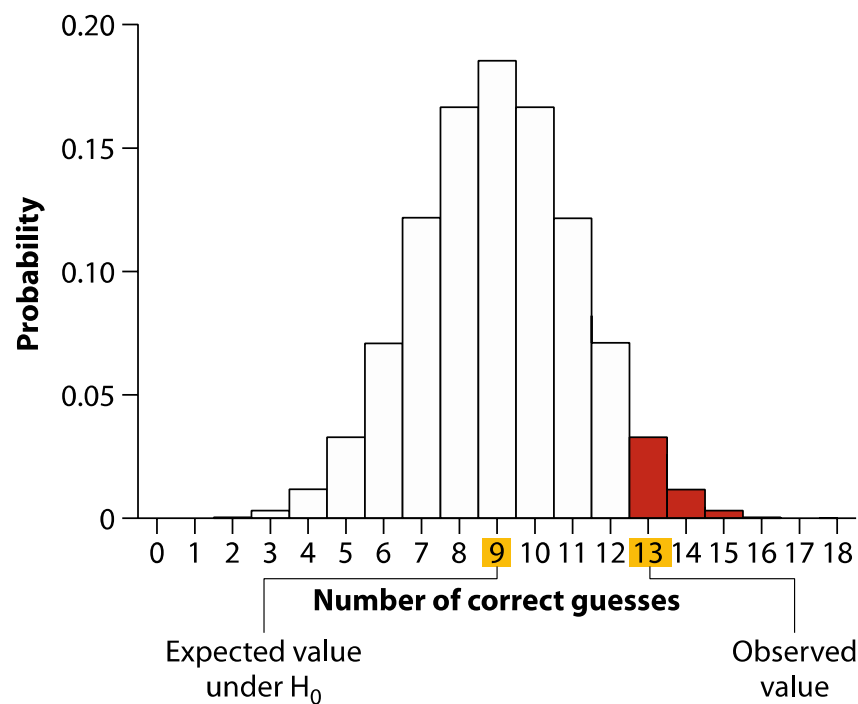
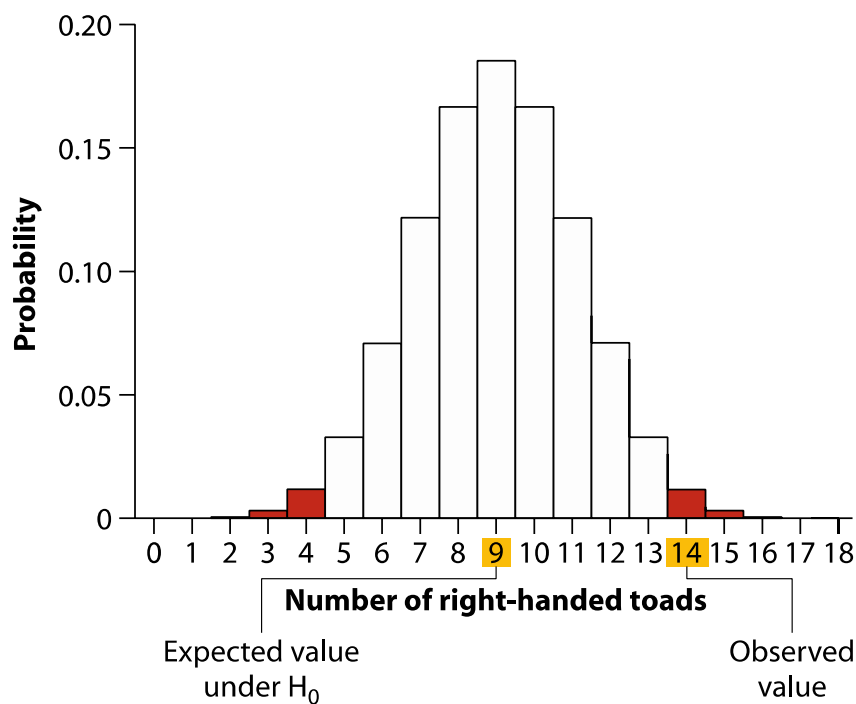
P values

Compare the observed test statistic
to the null distribution

What is a P-value?

The probability of obtaining outcomes as extremes or more extreme than the observed data at hand under the hypothesis H_0

How do we define “extreme”?

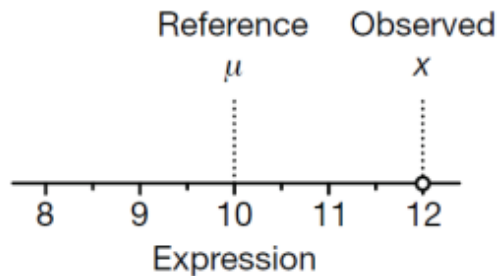


“Two sided” or “one sided”?

How to obtain p

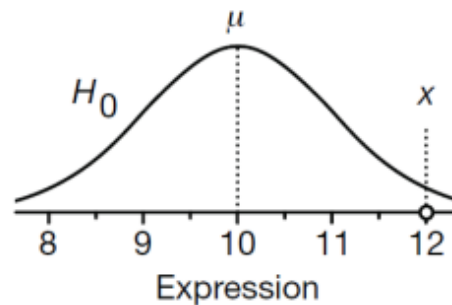
a

Experimental
observation



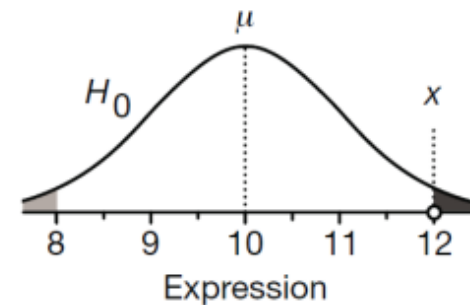
b

Distribution of reference
expression values



c

Probability of observing
a more extreme value



P value

- A p value is not a measure of how right you are, or how significant the difference is; it's a measure of ***how surprised you should be*** if there is no actual difference between the groups, but you got data suggesting there is. A bigger difference, or one backed up by more data, suggests more surprise and a smaller p value.

But there are limitations

- The p value is a measure of surprise, not a measure of the size of the effect. I can get a tiny p value by either measuring a huge effect – “this medicine makes people live four times longer” – or by measuring a tiny effect with great certainty.
- **Statistical significance does not mean your result has any *practical* significance.**

Significance

- In statistics, a result is called statistically significant if it is **unlikely to have occurred by chance alone**, according to a pre-determined threshold probability, the significance level.

The big issue

- There's no mathematical tool to tell you if your hypothesis is true; you can only see whether it is consistent with the data, and if the data is sparse or unclear, your conclusions are uncertain.
- But we can't let that stop us.
- www.statisticsonewrong.com

Type I and Type II errors

	H0 is TRUE	H0 is False
DECISION (based on D)		
Reject H0	Type I error (α)	Correct
Do not reject H0	Correct	Type II error (β)

Choosing a significance level (α) for a P-value sets the type I error rate at α .

Varying α will have consequences for the rate of type II error and statistical power

Power = $1 - \beta$

IF your test is well behaved/ calibrated and p-value well calculated THEN you will reject

Wrongly H0 a proportion α of the time when making a test

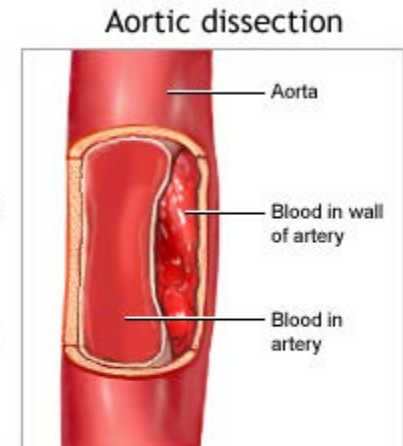
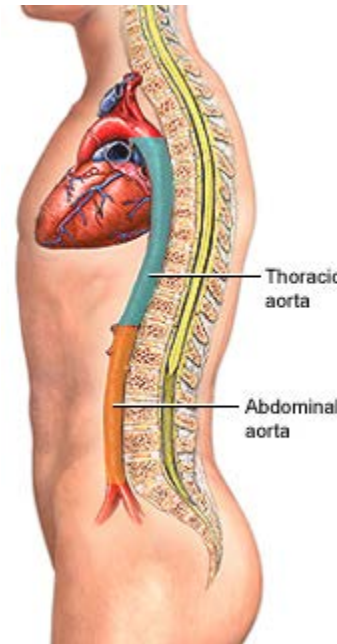
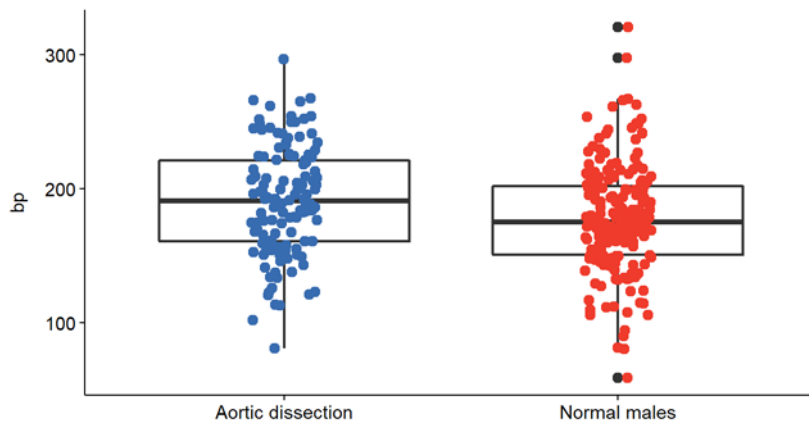
What about H_0 ?

- When do we know that H_0 is true?
- H_0 : HPV vaccine is not harmful
- H_a : HPV vaccine causes serious side effects

Statistics in three different ways

- Using known test with known distribution
 - Compare test statistic to known distribution of H_0
 - E.g. t-test
- **Simulating** test statistic "under H_0 "
 - Compare test statistic to simulated distribution of H_0
- **Permute** data → test statistic "under H_0 "
 - Compare test statistic to permuted distribution of H_0

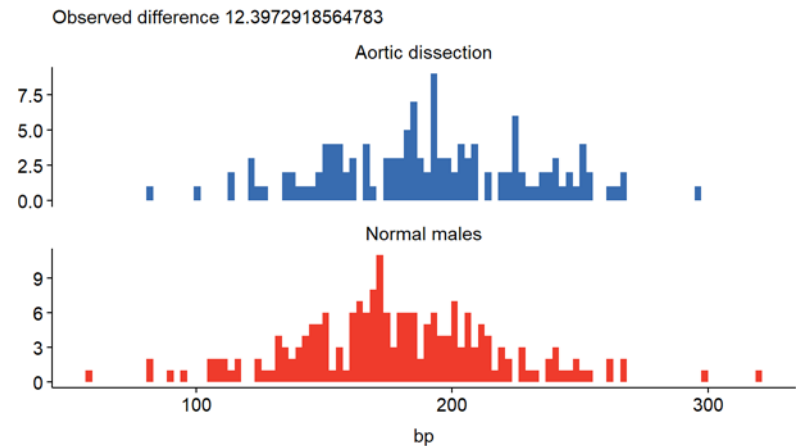
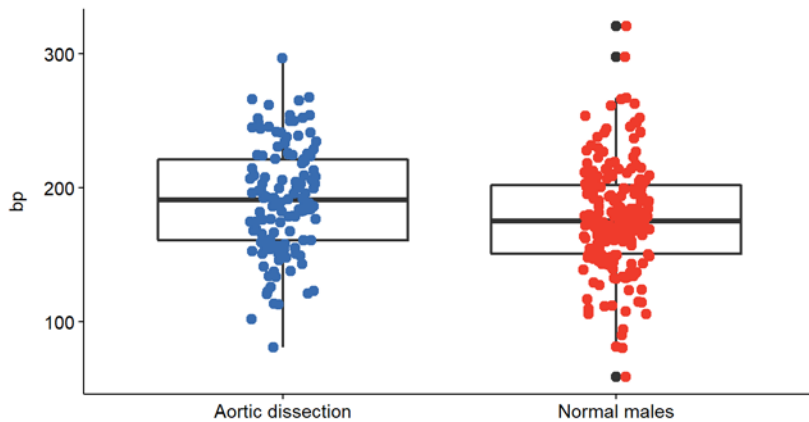
Do the poor guys on the left have higher blood pressure?



My own test statistic

$ts = \text{abs}(\text{mean}(g1) - \text{mean}(g2))$

Measures difference between two groups



Is the observed difference significant?

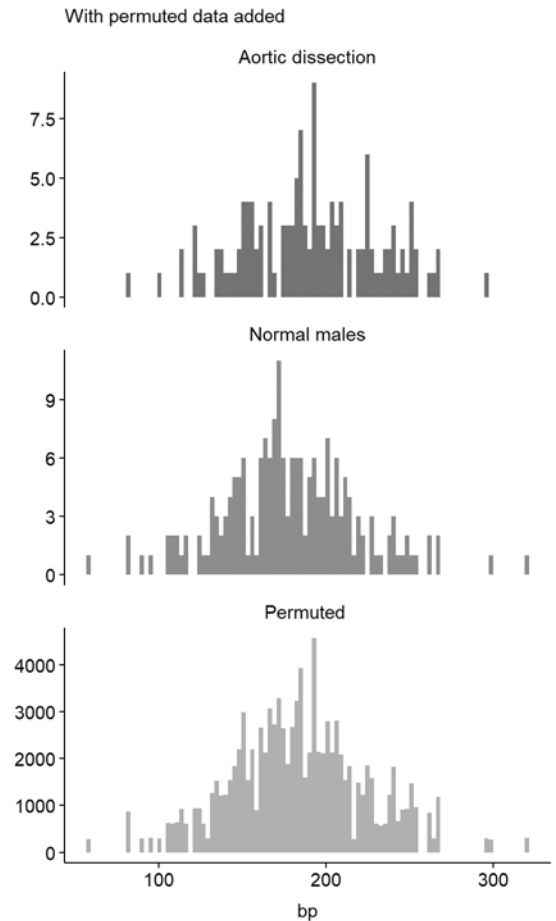
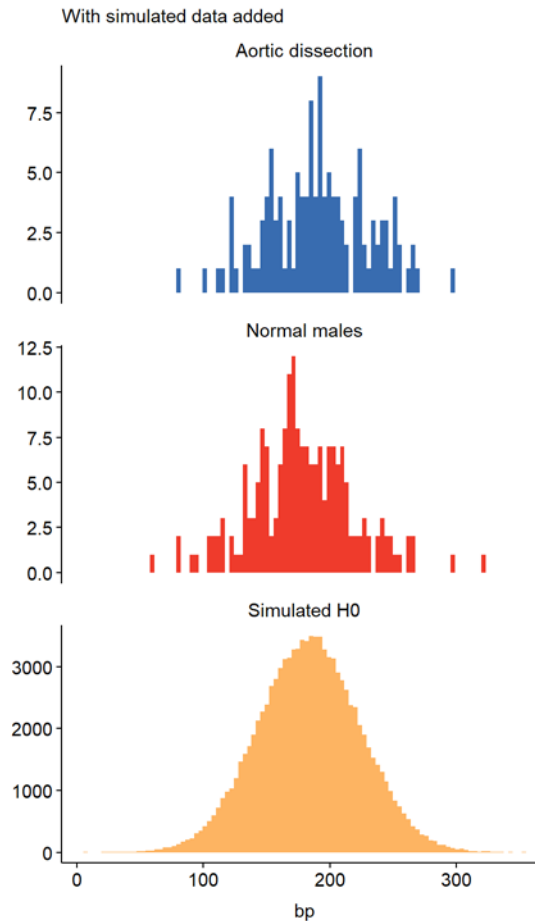
Normally we use a "distribution of ts under H_0 "
– but what does that even mean?

Statistical test: did sick and normal come from the same population?

H0 = Sick comes from the blue "population"

H0 = Normal comes from the blue population

H0 = Sick and Normal are the same



Simulating the null distribution

- H0: Only one **population** = one mean
- Draw two **samples** from that H0 **population** (H0: same mean)
- Calculate the test-statistic between the two **samples**
- Repeat 100000 times

Simulating data to get H0 distribution

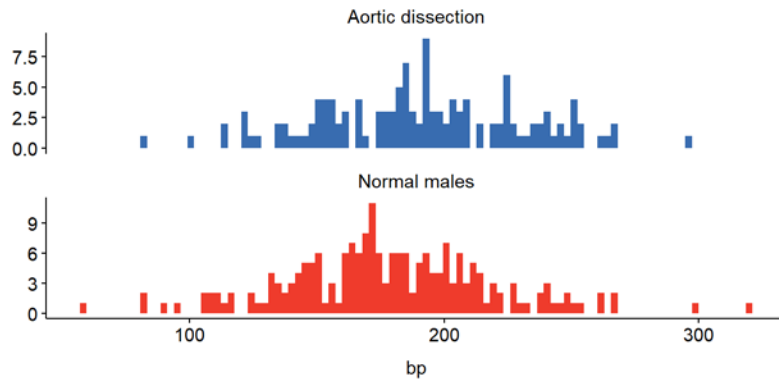
```
d = read.table("Aortic_dissection.tsv")
g1 = d$bp[d$group != "Normal males"]
g2 = d$bp[d$group == "Normal males"]

mean_h0 = mean(d$bp)
sd_h0    = sd(d$bp)

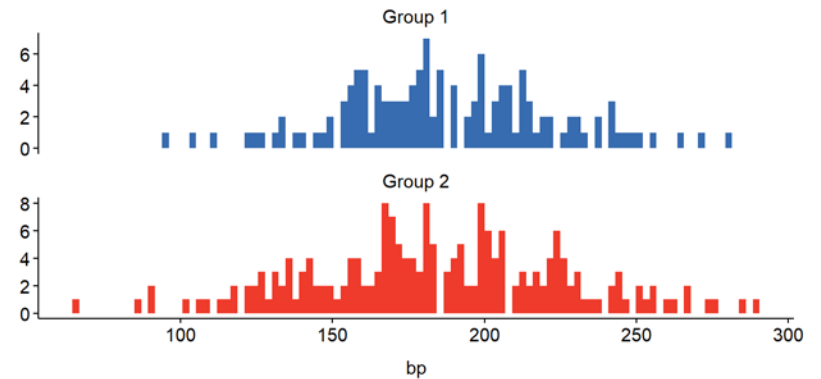
ts = rep(0,100000)
for (i in 1:length(ts)) {
  ng1    = rnorm(length(g1), mean=mean_h0, sd=sd_h0)
  ng2    = rnorm(length(g1), mean=mean_h0, sd=sd_h0)
  ts[i] = abs(mean(ng1)-mean(ng2))
}
```

Simulations

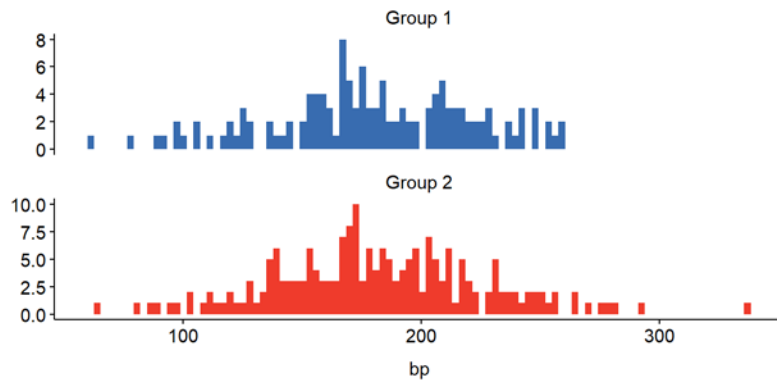
The observed data
Difference in means= 12.3972918564783



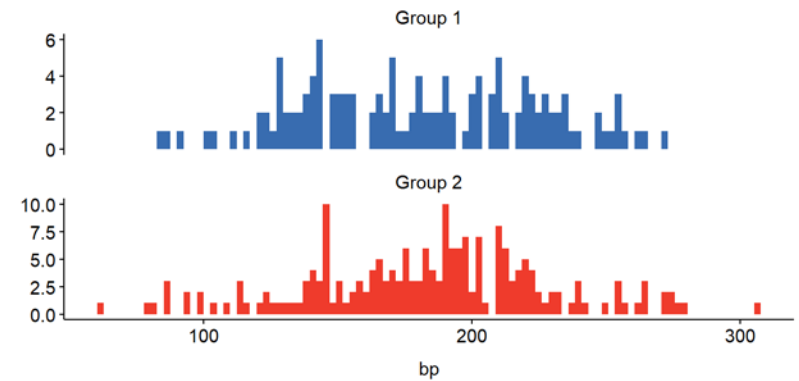
Simulation 1
Difference in means= 3.163021



Simulation 2
Difference in means= 2.546546

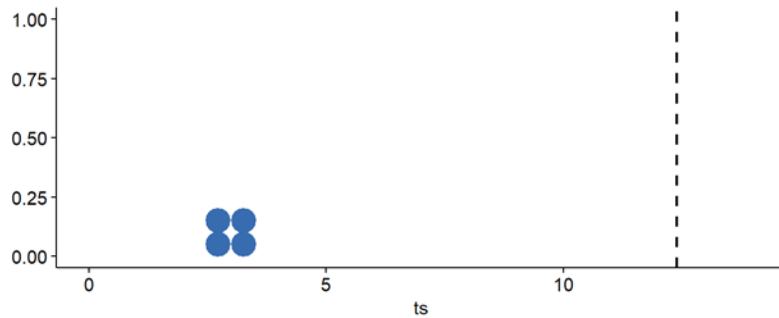


Simulation 3
Difference in means= 2.884519

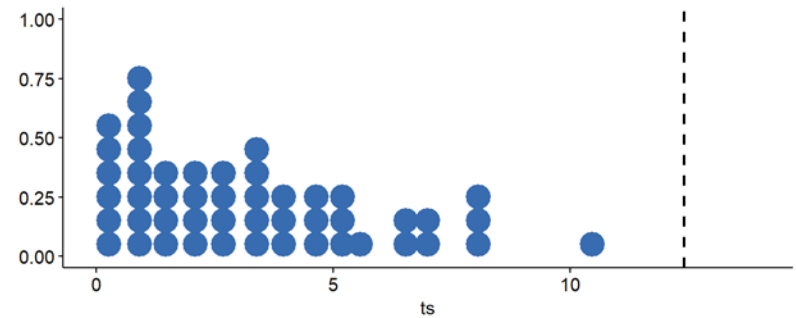


$$p = \frac{n_{\text{more extreme}} + 1}{n_{\text{simulations}} + 1}$$

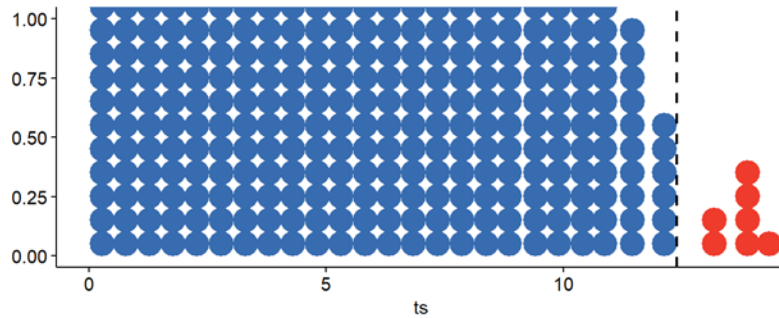
The first 4 test values
Number of observations > 12.3972918564783 = 0
Estimated p < 0.2



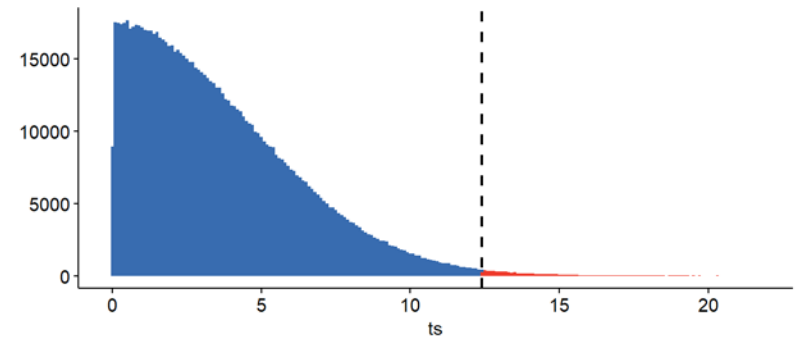
The first 49 test values
Number of observations > 12.3972918564783 = 0
Estimated p < 0.02



The first 1999 test values
Number of observations > 12.3972918564783 = 9
Estimated p < 0.005



Number of extreme values: 6348 of 1000000
Simulated H0 p < 0.00634899365100635



If you can't get the probability distribution (like the chi-square) and can't simulate it – because your data doesn't “behave nicely”

PERMUTATION TESTS (RANDOMIZATION)

Basic idea of permutations

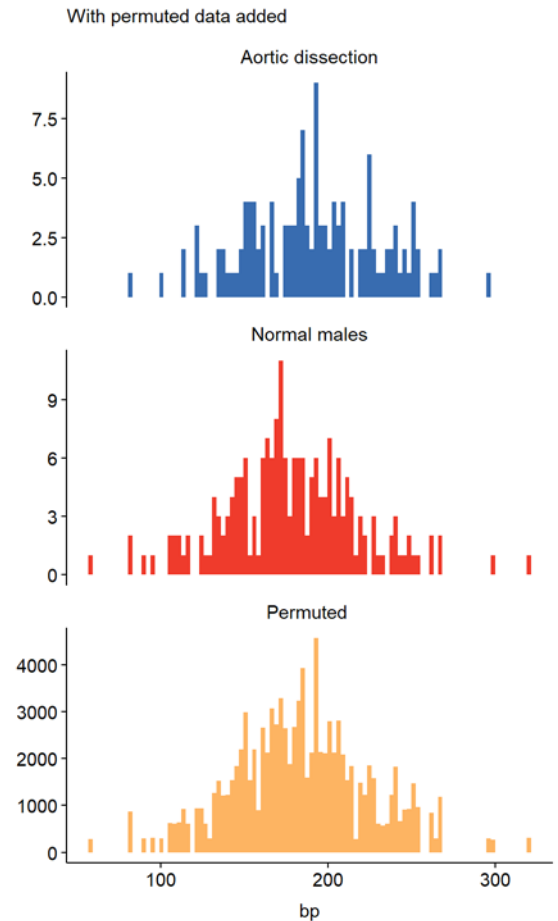
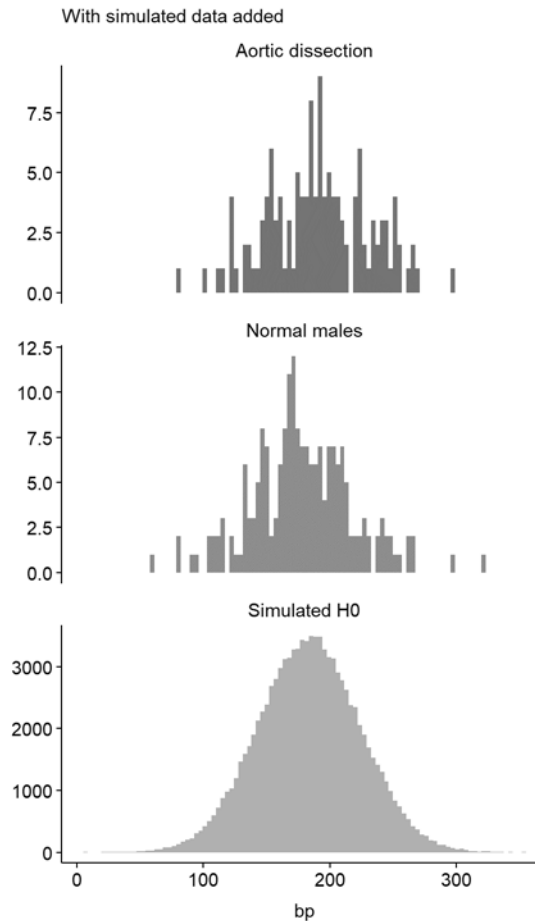
- We use the data to generate **permuted datasets – that are expected to follow the H_0**
- For patients/control – we **randomly switch patients and controls**
- Before:
 - Calculate test statistic of observed data
- Loop:
 - Permute data
 - Calculate test statistic of permuted data
- P-value:
 - How many permutations were more extreme than the observed

Statistical test: did sick and normal come from the same population?

H0 = Sick comes from the blue "population"

H0 = Normal comes from the blue population

H0 = Sick and Normal are the same



Permuting data to get H0

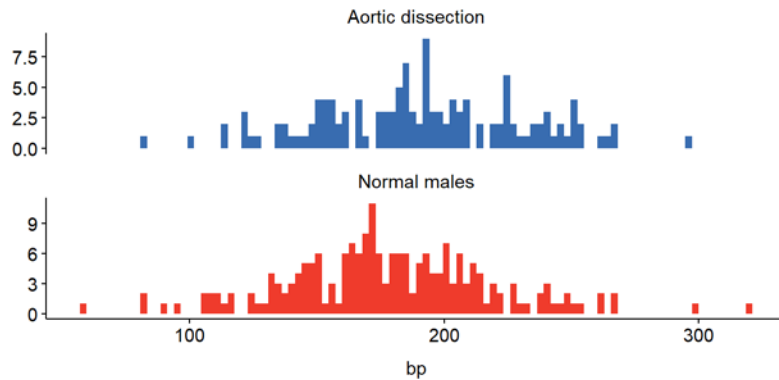
```
set.seed(1)
permutations = 100000
ts = rep(NA, permutations)

for (i in 1:length(ts)) {
  pmg = sample(d$group)          # Mix samples between groups
  ng1 = d$bp[pmg != "Normal males"] # The values from the sick group
  ng2 = d$bp[pmg == "Normal males"]  # The values from the normal group
  ts[i] = abs(mean(ng1) - mean(ng2)) # Test statistic (H0 is true)
  if(i %% 1000==0) {
    cat(i, "\n")
    flush.console()
  }
}

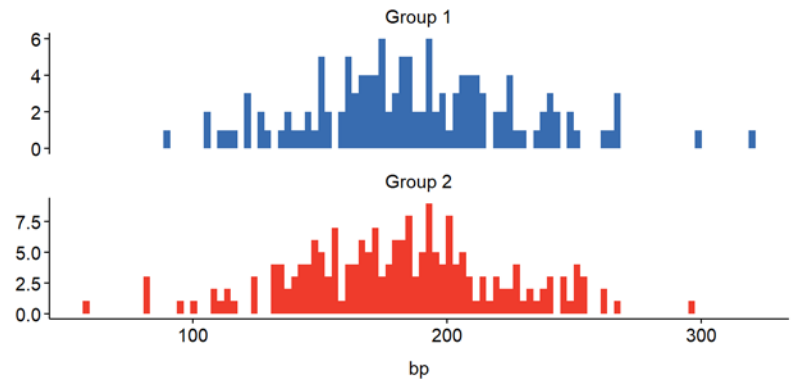
extreme_values = sum(ts >= observed_difference)
pval_estimated = extreme_values/length(ts)
```

Permutations

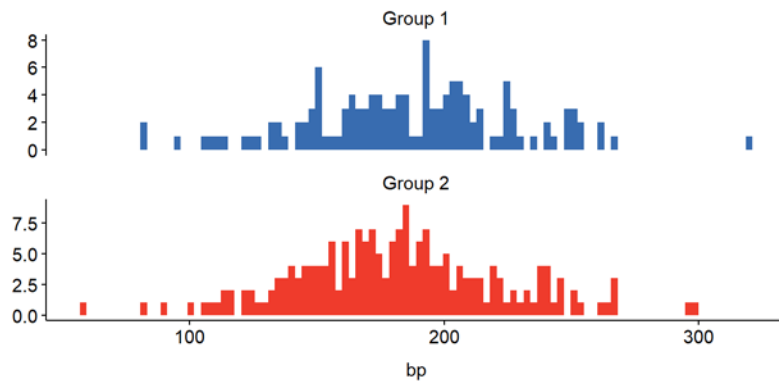
The observed data
Difference in means= 12.3972918564783



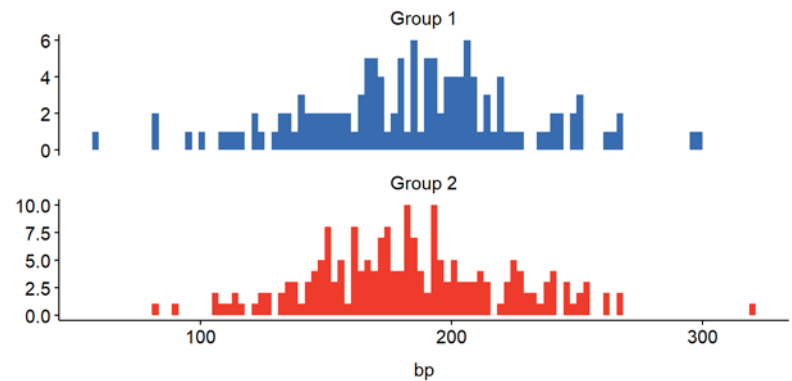
Permutation 1
Difference in means= 6.345061



Permutation 2
Difference in means= 5.060732

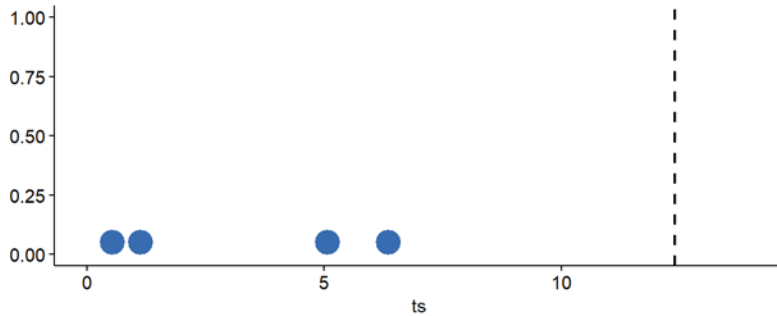


Permutation 3
Difference in means= 0.5258341

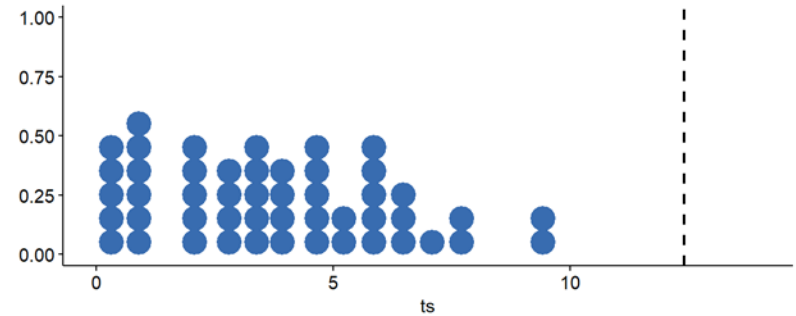


$$p = \frac{n_{\text{more extreme}} + 1}{n_{\text{simulations}} + 1}$$

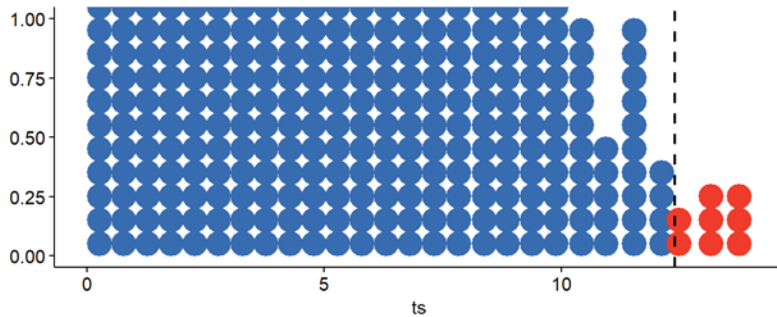
The first 4 test values
Number of observations > 12.3972918564783 = 0
Estimated p < 0.2



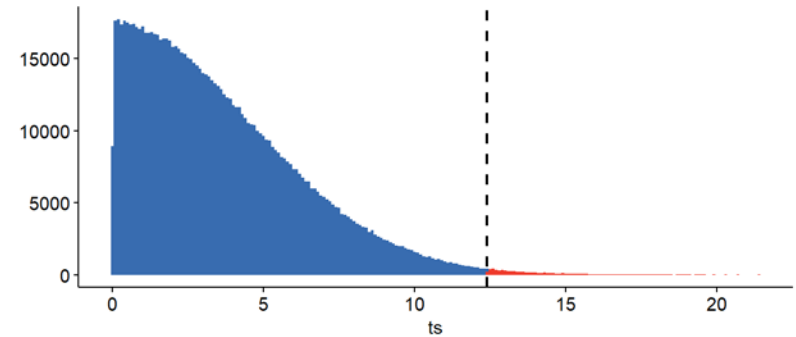
The first 49 test values
Number of observations > 12.3972918564783 = 0
Estimated p < 0.02



The first 1999 test values
Number of observations > 12.3972918564783 = 12
Estimated p < 0.0065



Number of extreme values: 6182 of 1000000
Permuted H0 p < 0.00618299381700618



t.test(g1,g2, var.equal=T)

Welch Two Sample t-test

data: g1 and g2

t = 2.7555, df = 281.6, p-value = **0.006242**

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

3.541172 21.253411

sample estimates:

mean of x mean of y

190.8181 178.4208

Statistics in three different ways

- T.test
 - $P = 0.006242$
- Simulating test statistic "under H_0 "
 - $P = 0.00635$
- Permute data \rightarrow test statistic "under H_0 "
 - $P = 0.00619$

What was wrong?

- Is my test statistic good or bad?
- $ts = \text{abs}(\text{mean}(g1) - \text{mean}(g2))$
- Number of observations?
 - "Sample size"
- Variation of sample?
 - "Variance" or "standard deviation"

T test (wikipedia)

Independent two-sample *t*-test [\[edit \]](#)

Equal sample sizes, equal variance [\[edit \]](#)

This test is only used when both:

- . The two sample sizes (that is, the number, n , of participants of each group) are equal;
- . It can be assumed that the two distributions have the same variance.

Violations of these assumptions are discussed below.

The t statistic to test whether the means are different can be calculated as follows:

$$t = \frac{\bar{X}_1 - \bar{X}_2}{s_{X_1X_2} \cdot \sqrt{\frac{1}{n}}}$$

where

$$s_{X_1X_2} = \sqrt{s_{X_1}^2 + s_{X_2}^2}$$

Here $s_{X_1X_2}$ is the grand [standard deviation](#) (or [pooled standard deviation](#)), 1 = group one, 2 = group two. $s_{X_1}^2$ and $s_{X_2}^2$ are the [unbiased estimators](#) of the [variances](#) of the two samples. The denominator of t is the [standard error](#) of the difference between two means.

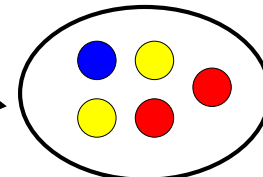
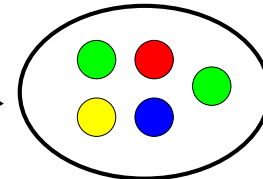
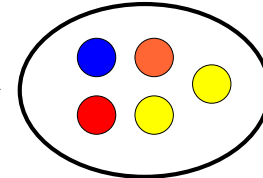
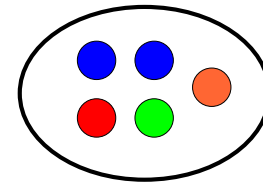
For significance testing, the [degrees of freedom](#) for this test is $2n - 2$ where n is the number of participants in each group.

Population UNKNOWN

- Virtually infinite
- Parameters
- Probability distribution

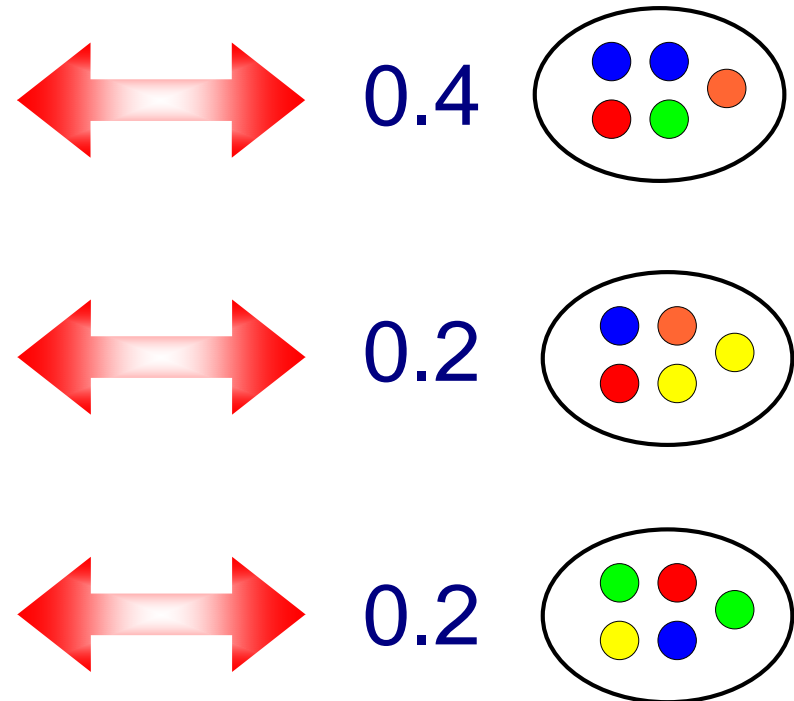
VS sample KNOWN

- n obs: x_1, x_2, \dots, x_n
- Parameter estimates
- Sampling distribution



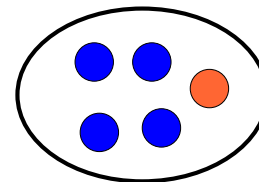
Estimating with uncertainty

- Estimates of parameters are based on a finite sample from the population.
- **Sampling error** is chance-induced variation between the estimate and the true parameter.



Hypothesis testing

- From sample to general knowledge about population
- **Sampling error** is chance-induced variation between the estimate and the true parameter
- Is the sample more blue than expected?
- H_0 : it is a random sample, $\text{frequency}(\text{blue}) = 0.23$

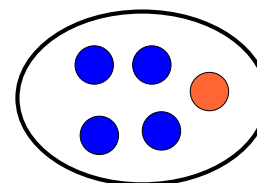
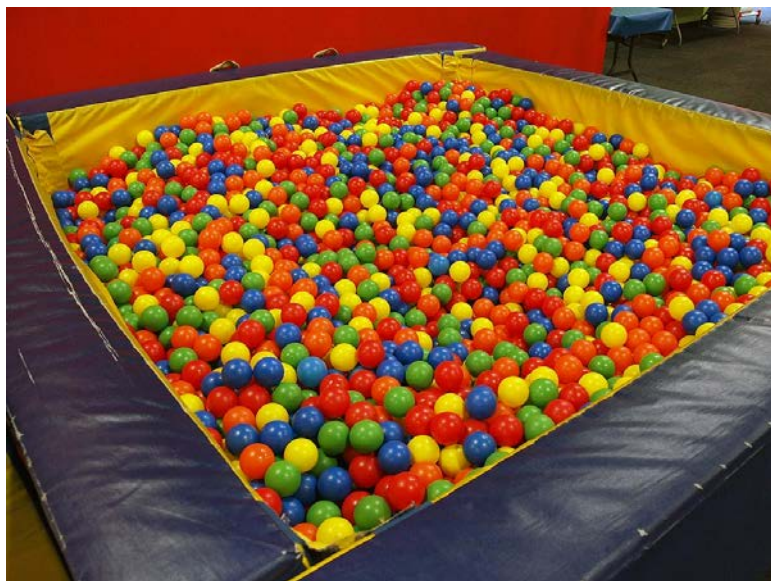


Think binomial

- What is the chance of “blue” (under H_0)
- What is the chance of “not blue” (under H_0)
- What is the chance of BBBBN ? BBNBB ? NBBBB
- What is more extreme than the observed?
- What is the chance of 5 blues (under H_0)?
- What is the total chance of same or more extreme than the observed?

Hypothesis testing

- H_0 : our sample is from the pool, frequency(blue) = 0.23
- H_A : ?
- Formulate and discuss the test of this sample
- What is the observed? What is more extreme?
- What is the frequency of more extreme = pvalue?



Questions to think about

Imagine that you make 1000 test using the threshold α for significance of each test,

Define a random variable X as the number of false positive (type I errors)?

How is X distributed?

How many type I errors do you expect?

4 basic steps

- State hypothesis
- Compute test statistic
- Determine p value
 - Compare TS with null
- Conclude
 - $P < 0.05$? 0.001? 0.00001?
 - Number of tests

Presenting thursday