Resampling statistics and multiple testing

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BIO5312, FALL 2017

While you wait, install the following R packages:

1. devtools

2. coin

3. modelr

4. broom

Computer-intensive methods

1. Monte Carlo simulation

2. Permutation/randomization test

3. Bootstrap
    1. Here, for computing CI and SE

Why use simulation

Test statistics have a true sampling distribution under specific conditions

- *t*-statistics from data have a *t* sampling distribution when data is normal and/or N is sufficiently large
- χ^2 statistics from data have a χ^2 sampling distribution when N is sufficiently large

We can use **simulation** to **approximate** an analytically unknown/untractable sampling distribution for given conditions

Monte Carlo simulation

Involves randomly sampling data from a probability distribution

Random sample of N=15 for *N(3.5,4)*

```
> rnorm(15, 3.5, 2)
 [1]  5.8166897  3.3402803  2.1469112  3.3038842  5.0005214  2.9234959
 [7]  4.6663932  3.1889110  6.2384465  5.8085365  1.7456411  0.3697735
[13] -1.4639567  5.8856386  8.2788721
```

Using simulation for hypothesis testing

1. Decide your test statistic
   - Make your own quantity or use a "standard" quantity (t, χ^2, etc.)
2. Generate S independent datasets under conditions of interest
3. Compute test statistic T_S for each simulated dataset
   - $T_1, T_2, T_3, \ldots T_S$ → Sampling distribution = null
4. Compute P-value by finding your test statistic in this T_S distribution

Use computers to imitate the process of repeated sampling from a population to approximate the null distribution of the test statistic.

Example simulation study

I have a sample of 10 ducks: 4 are blue, 4 are green, and 2 are purple. Are duck colors evenly distributed?

Ho: Duck colors are evenly distributed 1:1:1.
Ha: Duck colors are not evenly distributed 1:1:1

Duck color	# Observed	# expected
blue	4	3.33
green	4	3.33
purple	2	3.34

χ^2 assumption violated!

Performing the simulation study

1. Choose my test statistic, here χ^2
2. Simulate a duck group and compute the χ^2 statistic
3. Repeat **a lot** of times (1e4, 1e5)

Simulating a single group of ducks

```
### Simulate a group of ducks
> duck1 <- sample(c("blue", "green", "purple"), 10, replace=T)

### compute chi-squared statistic from duck group
> table(duck1)
duck1
  blue  green purple
     4      3      3

> e <- 10/3
> ((4-e)^2)/e + ((3-e)^2)/e + ((3-e)^2)/e
[1] 0.2
```

Do this 1e5 times to get 1e5 χ^2 test statistics

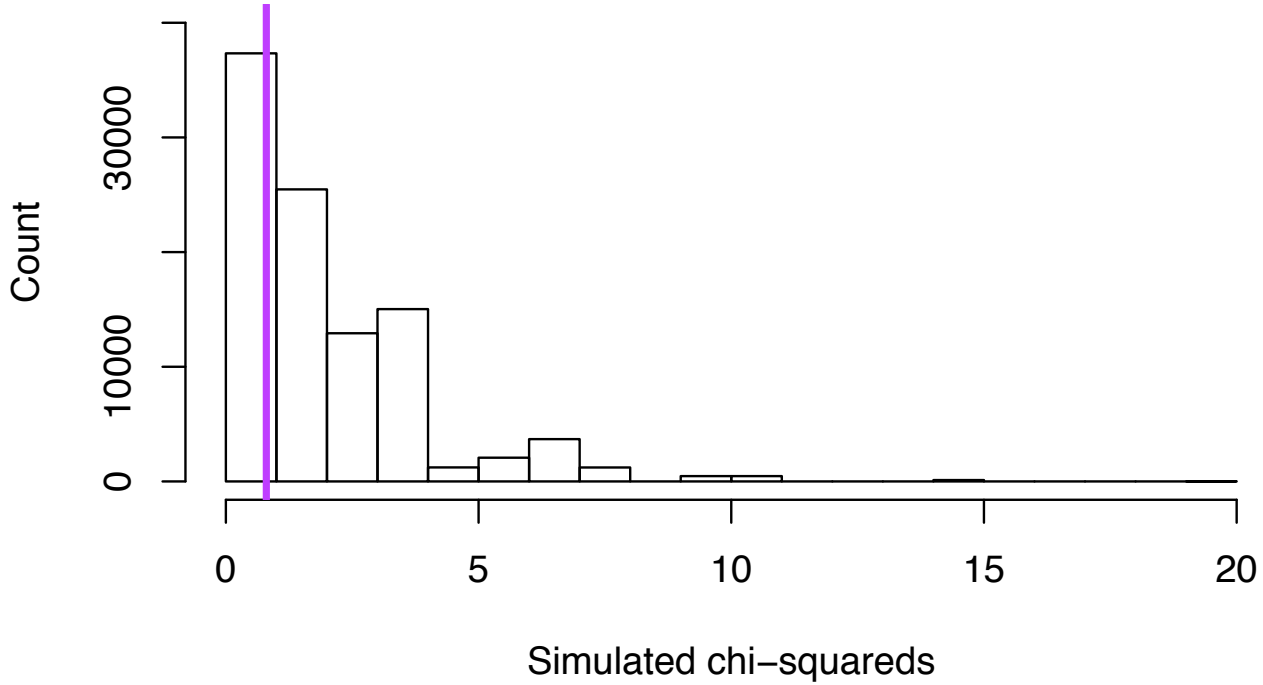
The full duck simulation

```
all.chisq <- c()
e <- 10/3
for (x in 1:1e5){
    duck <- sample(c("blue", "green", "purple"), 10, replace=T)
    b <- sum(duck == "blue")
    g <- sum(duck == "green")
    p <- sum(duck == "purple")
    chisqu <- ((b-e)^2)/e + ((g-e)^2)/e + ((p-e)^2)/e
    all.chisq <- c(all.chisq, chisqu)
}


length(all.chisq)
[1] 100000
```

Duck simulation testing

Duck color	# Observed	# expected
blue	4	3.33
green	4	3.33
purple	2	3.34

$\chi^2 = 0.8$




```
## Compute the probability of being as or more extreme as test statistic
> sum(all.chisq >= 0.8)/length(all.chisq)
[1] 0.78705
```

Duck simulation results, conclusions

With P=0.787, we fail to reject the null hypothesis. We have no evidence that duck color distributions differ from 1:1:1.

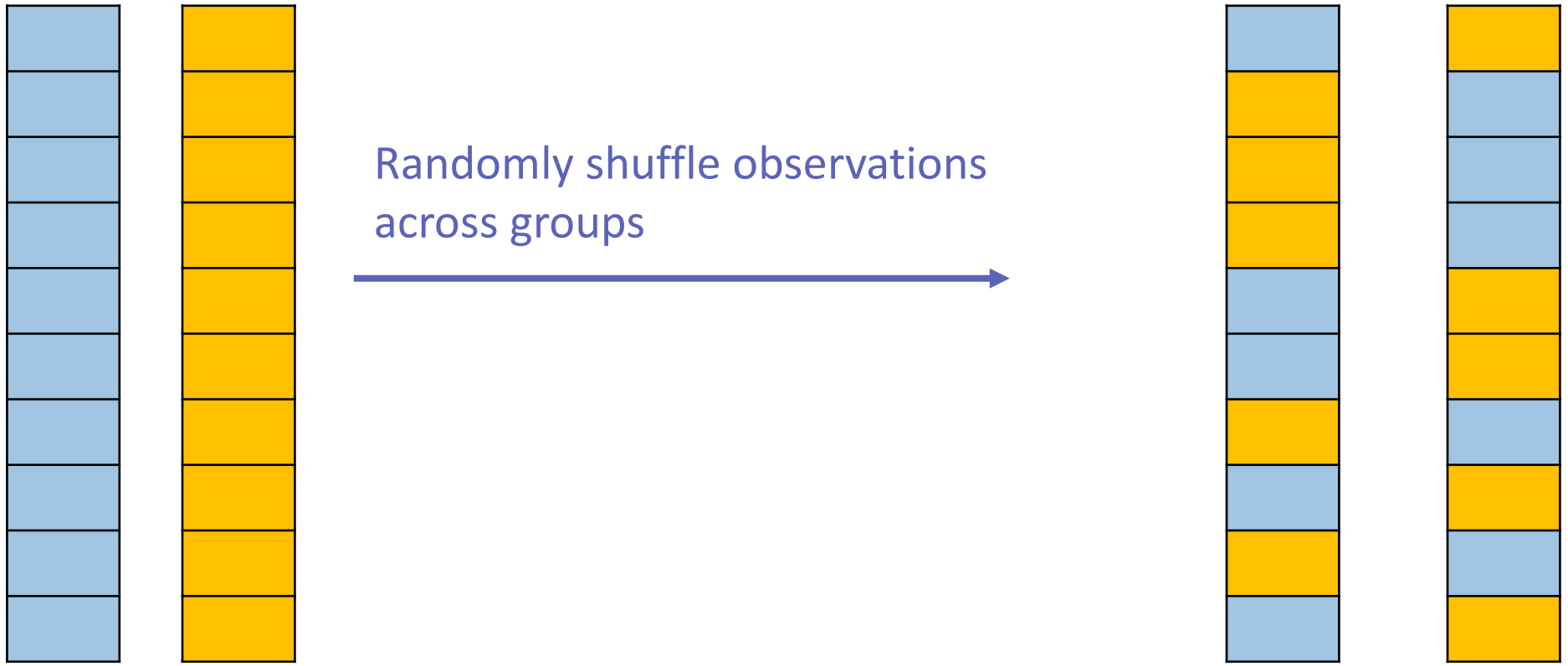
Permutation (randomization) test

A computer-intensive non-parametric approach for comparing samples

Approach:

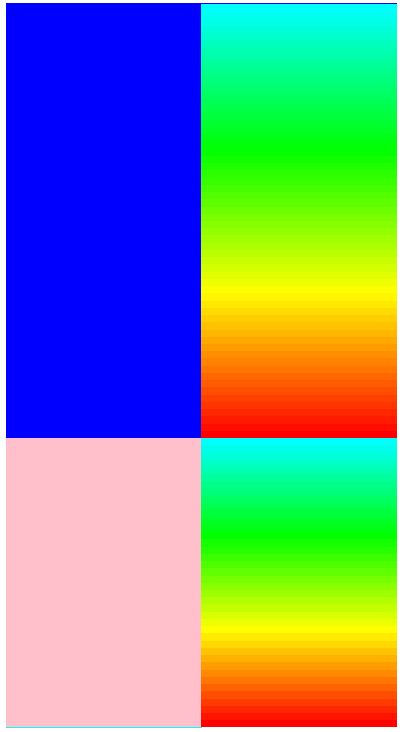
1. Choose a statistic that measures the effect you are looking for.
2. Construct the sampling distribution that this statistic would have if the effect were *not* present
3. Locate the observed statistic (i.e. from your data) on this distribution. Area to the tail = Pvalue.

Permutation tests randomize observed data

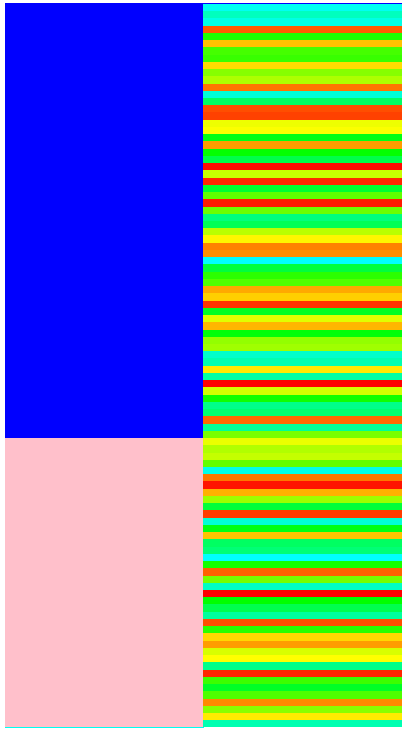


Permutation when null is true

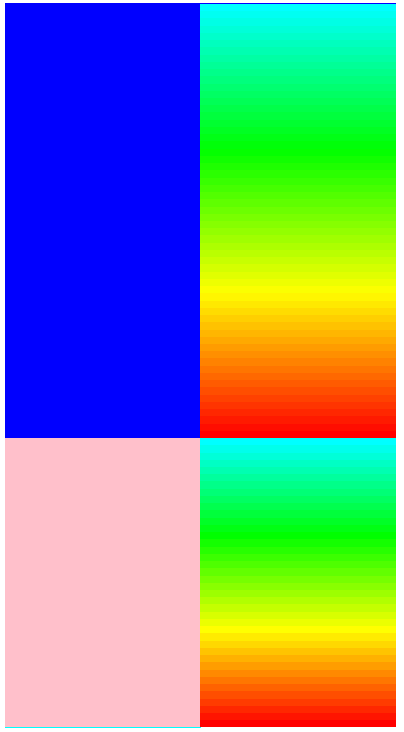
Data



Shuffling outcomes



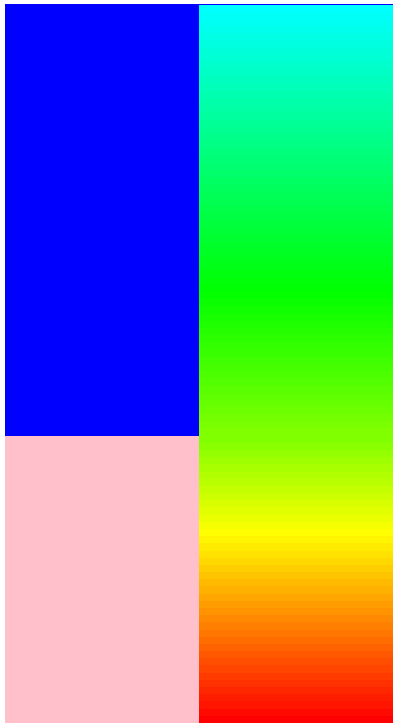
Shuffling outcomes (ordered)



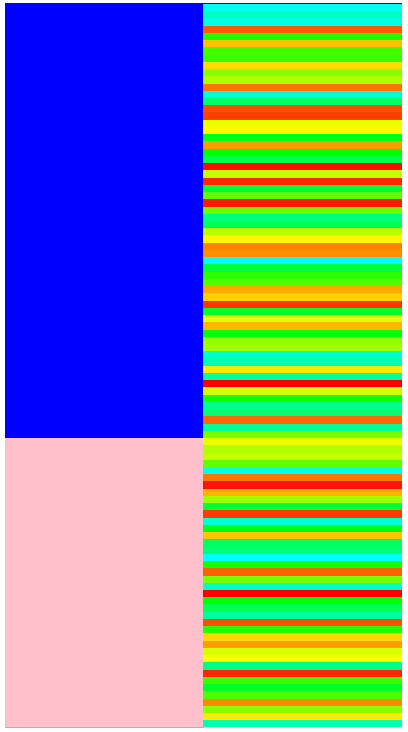
http://faculty.washington.edu/kenrice/sisg/SISG-08-06.pdf

Permutation when null is false

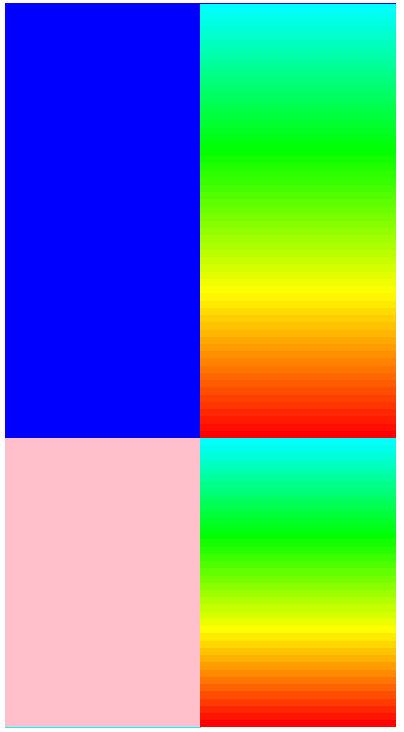
Data



Shuffling outcomes



Shuffling outcomes (ordered)



http://faculty.washington.edu/kenrice/sisg/SISG-08-06.pdf

Example permutation test

I am measuring the length of bumblebees between two species with the following data (mm):

- Species A: 4.5, 4.6, 4.1, 5.2
- Species B: 5.1, 4.7, 5.4, 4.8, 4.9

Do the bumblebee species tend to have the same lengths?

Ho: Bumblebee species A and B have the same lengths on average
Ha: Bumblebee species A and B have different lengths on average.

Some permutations of my data

Species A: 4.5, 4.6, 4.1, 5.2

Species B: 5.1, 4.7, 5.4, 4.8, 4.9

Species A: 4.5, 5.1, 4.1, 5.2

Species B: 4.6, 4.7, 5.4, 4.8, 4.9

Species A: 4.6, 4.7, 4.8, 4.9

Species B: 4.5, 4.1, 5.2, 5.4, 5.1

Testing the bee data

1. Choose my test statistic, here *t*, and compute on data

2. Create **a lot** of permuted datasets
    1. Compute *t* for each dataset to construct null sampling distribution

3. Compute P-value as probability of being as or more extreme than *t* calculated from data

Performing step 2

1. Generate your permuted data with `modelr::permute()`

2. Extract your permutations with `purrr:map()`

3. See the full permutation output with `broom::tidy()` or `broom::glance()`

Exciting detour: the `broom` package

`broom` tidies* up output from linear models and hypothesis tests

- Vignette: https://cran.r-project.org/web/packages/broom/vignettes/broom.html

Functions:

- `tidy()`
- `glance()`
- `augment()`

*groan.

Using broom in hypothesis testing

```
> versicolor <- iris %>% filter(Species == "versicolor")
> setosa <- iris %>% filter(Species == "setosa")

> my.test <- t.test(versicolor$Sepal.Length, setosa$Sepal.Length)

> tidy(my.test)
  estimate estimate1 estimate2 statistic      p.value parameter  conf.low
1     0.93     5.936     5.006  10.52099 3.746743e-17    86.538 0.7542926
  conf.high                    method alternative
1  1.105707 Welch Two Sample t-test   two.sided
```

Using broom in hypothesis testing while piping

```
> iris %>%
      filter(Species != "virginica") %>%
      do(tidy(t.test( Sepal.Length~Species, data=. )))

  estimate estimate1 estimate2 statistic      p.value parameter  conf.low
1    -0.93     5.006     5.936 -10.52099 3.746743e-17    86.538 -1.105707
   conf.high                    method alternative
1 -0.7542926 Welch Two Sample t-test   two.sided
```

Step One: compute *t* for my data

```
> bees <- tibble(species=c(rep("a", 4), rep("b", 5)),
                 lengths=c(4.5, 4.6, 4.1, 5.2, 5.1, 4.7, 5.4, 4.8, 4.9))


> t.test(lengths ~species, data=bees)
Welch Two Sample t-test


data:  lengths by species
t = -1.4673, df = 4.7391, p-value = 0.2053
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.0568836  0.2968836
sample estimates:
mean in group a mean in group b
           4.60            4.98
```

Step Two: generate permutated data

```
library(tidyverse)
library(broom)
library(modelr)

### Make 10000 permutations with permute(), from modelr
> set.seed(567)
> N <- 1e4
> bee.perms <- permute(bees, N, lengths) ## dataframe number perms, column to permute
> head(bee.perms)
# A tibble: 10,000 x 2
                perm   .id
              <list> <chr>
 1 <S3: permutation> 00001
 2 <S3: permutation> 00002
 3 <S3: permutation> 00003
 4 <S3: permutation> 00004
 5 <S3: permutation> 00005
 6 <S3: permutation> 00006
```

Step Two: Compute *t* for each permutated dataset

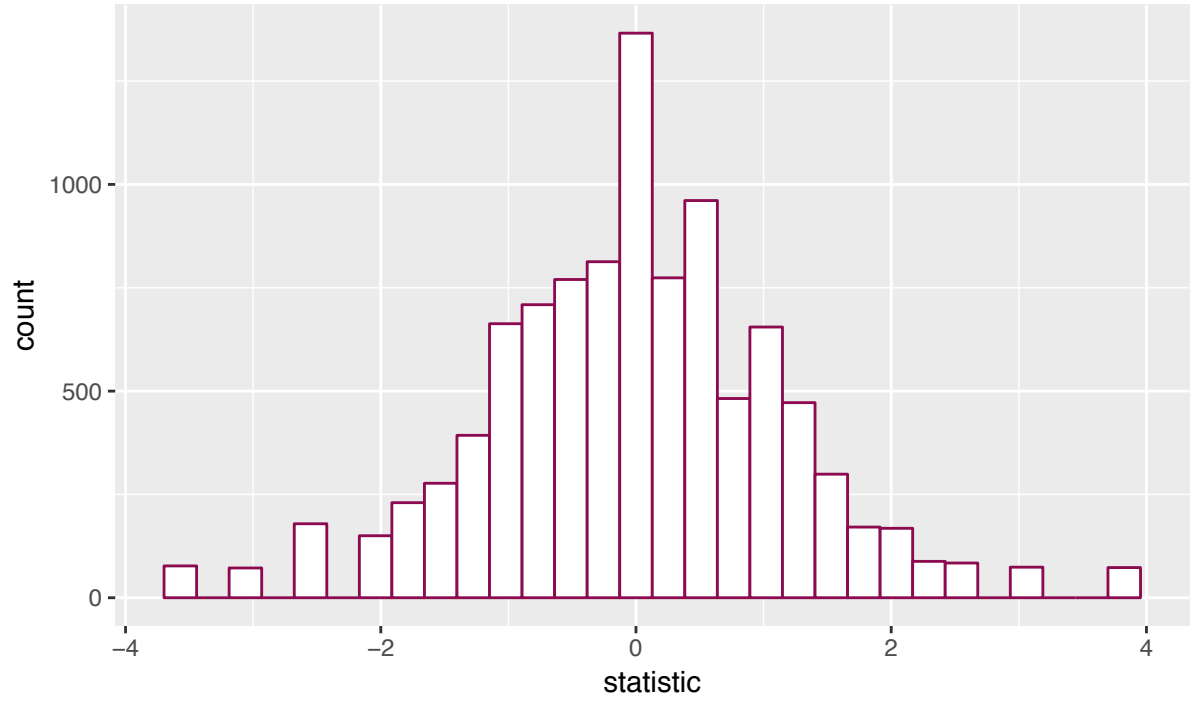
```
> bee.ttests <- map(bee.perms$perm, ~t.test(lengths~species, data=.))
> head(bee.ttests)
[[1]]

Welch Two Sample t-test

data:  lengths by species
t = -1.5636, df = 6.6843, p-value = 0.1639
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.9602378  0.2002378
sample estimates:
mean in group a mean in group b
           4.60            4.98


[[2]]

Welch Two Sample t-test

data:  lengths by species
t = -1.8074, df = 6.3713, p-value = 0.1178
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.9923401  0.1423401
sample estimates:
mean in group a mean in group b
          4.575           5.000
```

Step Two: Compute *t* for each permutated dataset

```
> bee.ttests <- map(bee.perms$perm, ~t.test(lengths~species, data=.))
> tidied.bees <- map_df(bee.ttests, tidy, .id = "id")
> head(tidied.bees)
  id estimate estimate1 estimate2  statistic   p.value parameter   conf.low
1  1   -0.380     4.600      4.98 -1.5635521 0.1639062  6.684311 -0.9602378
2  2   -0.425     4.575      5.00 -1.8074200 0.1178304  6.371305 -0.9923401
3  3    0.160     4.900      4.74  0.6064784 0.5637055  6.865079 -0.4663247
4  4   -0.065     4.775      4.84 -0.2156013 0.8386887  4.518027 -0.8655244
5  5   -0.245     4.675      4.92 -0.8733769 0.4214981  5.123589 -0.9609000
6  6   -0.335     4.625      4.96 -1.3358210 0.2245809  6.799964 -0.9315602
   conf.high                    method alternative
1 0.2002378 Welch Two Sample t-test   two.sided
2 0.1423401 Welch Two Sample t-test   two.sided
3 0.7863247 Welch Two Sample t-test   two.sided
4 0.7355244 Welch Two Sample t-test   two.sided
5 0.4709000 Welch Two Sample t-test   two.sided
6 0.2615602 Welch Two Sample t-test   two.sided
```

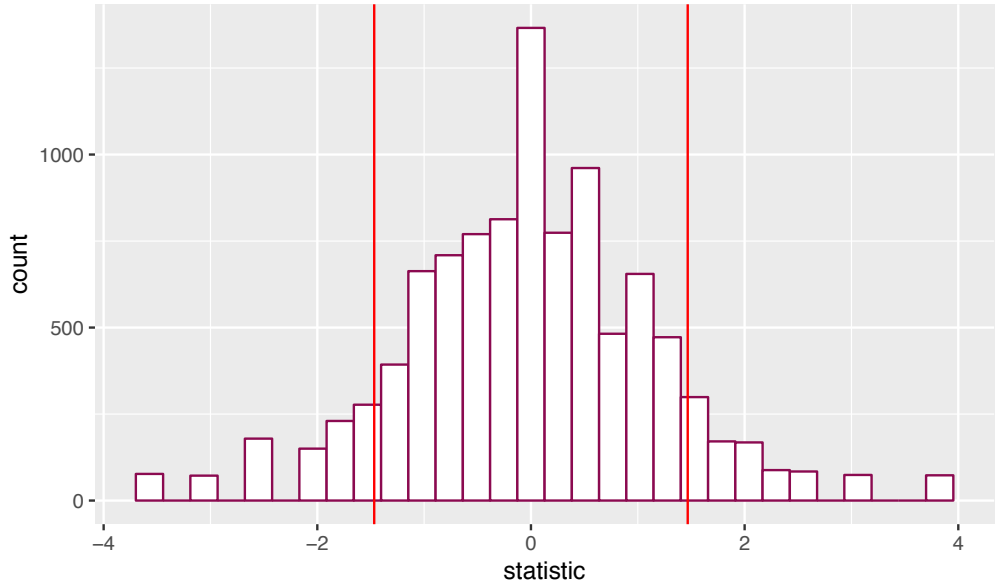
Visualize the null constructed with permutation

```
ggplot(tidied.bees,aes(x = statistic)) +
       geom_histogram(fill="white", color="deeppink4")
```



Visualize the null constructed with permutation

```
ggplot(tidied.bees,aes(x = statistic)) +
       geom_histogram(fill="white", color="deeppink4") +
       geom_vline(xintercept = -1.4673, color="red") +
       geom_vline(xintercept = 1.4673, color="red")
```



Step Three: calculate our Pvalue

```
> t.from.data <- -1.4673

> sum(tidied.bees$statistic >= abs(t.from.data)) -> upper.tail

> sum(tidied.bees$statistic <= -1*abs(t.from.data)) -> lower.tail

> (upper.tail + lower.tail) / nrow(tidied.bees)
[1] 0.1942
```

With P=0.1942, we fail to reject the null hypothesis. We have no evidence that bumblebee species a and b have different lengths.

Pop Quiz: P-values for a permutation test can never be 0. Why?

Note on computations shown here

```
bee.ttests <- map(bee.perms$perm, ~t.test(lengths~species, data=.))

bee.results <- map(bee.perms$perm, ~<only certain functions> )
```

Note the R package coin…

Pre-dated the tidyverse but **very** convenient for simple tests

```
library(coin)
### Permutation test for two arbitrary samples
independence_test(b ~ a, data)


independence_test(lengths ~ species, data = bees)

Asymptotic General Independence Test

data:  lengths by species (a, b)
Z = -1.4337, p-value = 0.1517
alternative hypothesis: two.sided
```

coin for contingency tables

```
> sparrows %>% group_by(Sex, Survival) %>% tally() -> sex.survival
     Sex Survival     n
1 Female    Alive    21
2 Female     Dead    28
3   Male    Alive    51
4   Male     Dead    36
> xtabs(n ~ Sex + Survival, data = sex.survival) -> sex.survival.table
        Survival
Sex      Alive Dead
  Female    21   28
  Male      51   36

>independence_test(sex.survival.table)
Asymptotic General Independence Test

data:  Survival by Sex (Female, Male)
Z = -1.7617, p-value = 0.07813
alternative hypothesis: two.sided
```

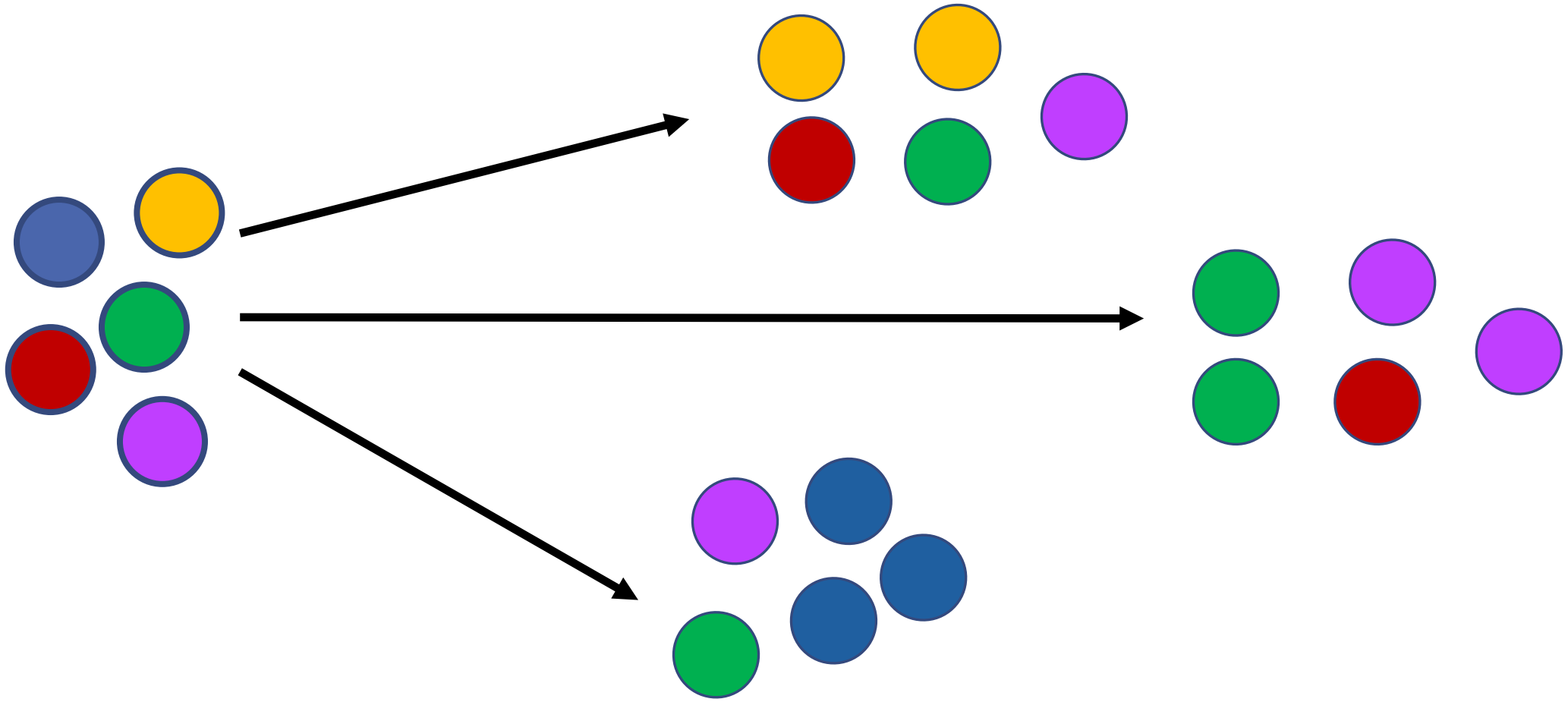
Exercise break

Bootstrapping

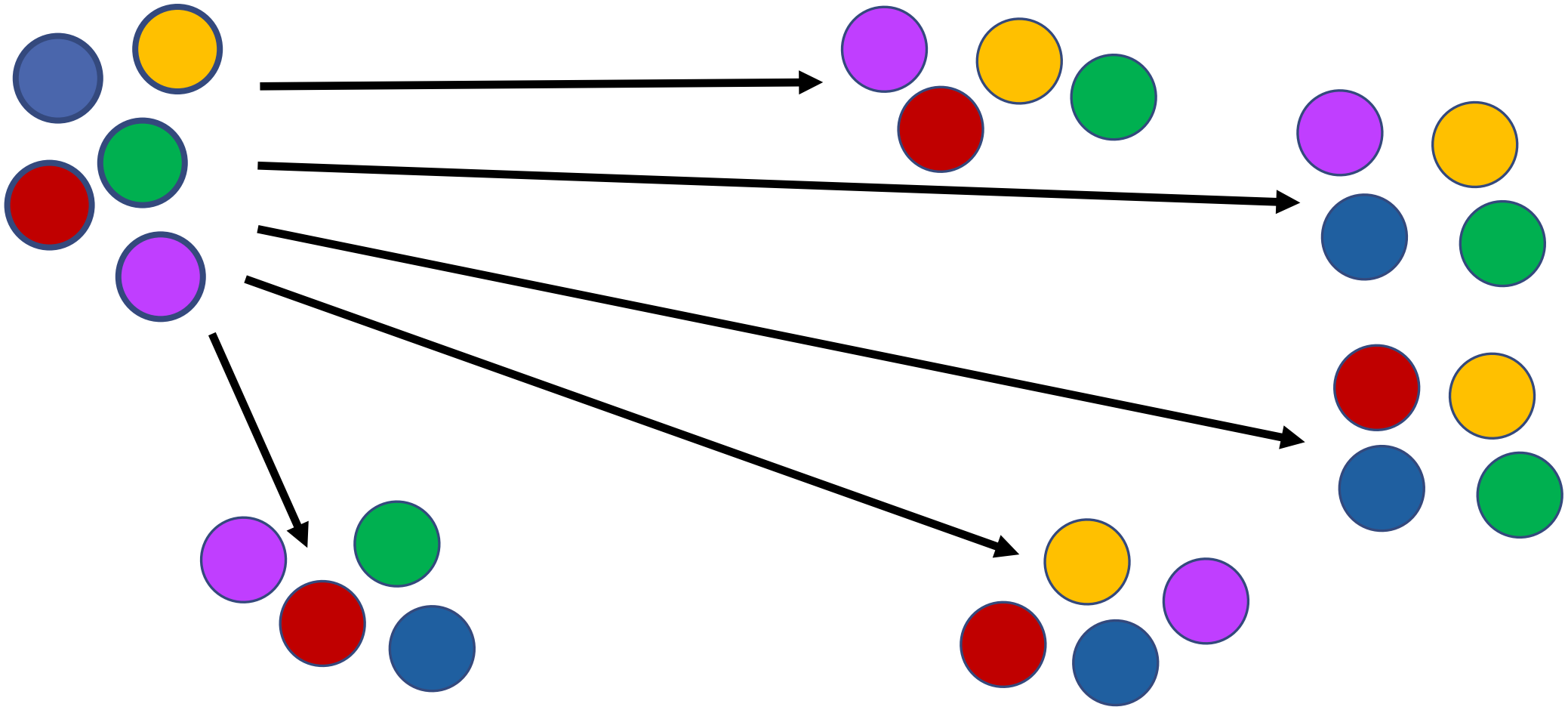
Bootstrapping uses resampling from the data with replacement to approximate the sampling distribution of an estimate

Use bootstrapping to calculate CI and standard error

What is bootstrapping?



As aside, this is jackknifing



WA acidic rain estimation, the "regular way"

```
> rain <- tibble(pH = c(4.73, 5.28, 5.06, 5.16, 5.25, 5.11, 4.79))


> mean(rain$pH)
[1] 5.054286

## 95% CI as estimate +- t_0.025*SE
> se <- sd(rain$pH)/sqrt(nrow(rain))
> df <- nrow(rain) -1
> qt(0.025,df) * se
[1] -0.1992792
```

Estimate for WA rain acidity is 5.05 +- 0.199

BUT our assumptions for this approach were not met, so we should use the bootstrap

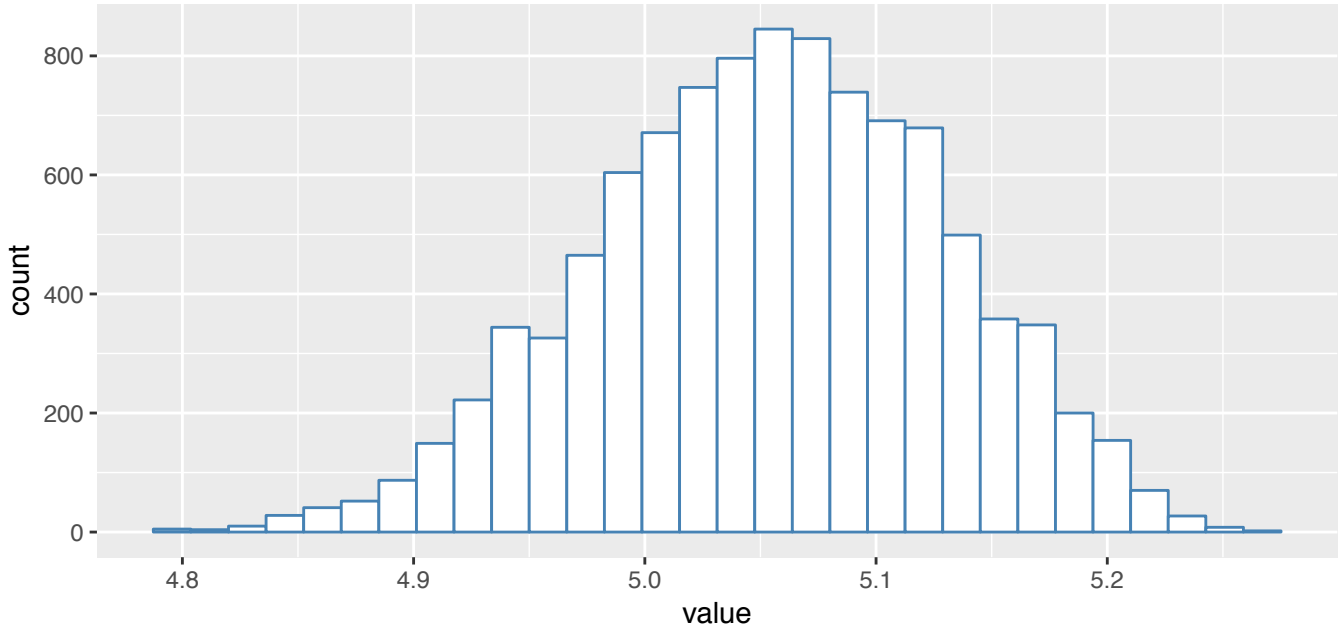
Using the bootstrap to estimate rain pH

```
> set.seed(199)
> devtools::install_github('jtleek/slipper')

> rain.boot <- slipper(rain, mean(pH), B=10000)
> head(rain.boot)
       type    value
1  observed 5.054286
2 bootstrap 5.090000
3 bootstrap 5.115714
4 bootstrap 4.984286
5 bootstrap 5.015714
6 bootstrap 5.164286

> rain.boot %>% filter(type == "bootstrap") %>% summarize(mean(value))
  mean(value)
1    5.054452
```

https://github.com/jtleek/slipper

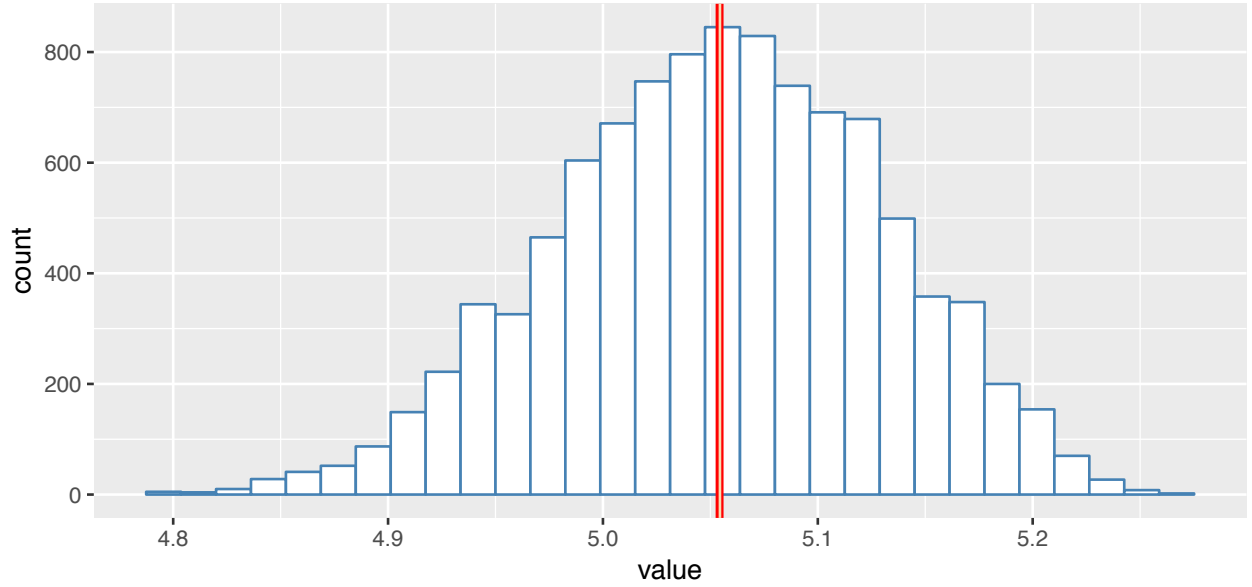
Visualizing the bootstrap sampling distribution of the mean

```
> rain.boot %>%
      filter(type == "bootstrap") %>%
      ggplot(aes(x = value)) + geom_histogram(fill = "white", color ="steelblue")
```



Visualizing the bootstrap sampling distribution of the mean

```
> rain.boot %>%
      filter(type == "bootstrap") %>%
      ggplot(aes(x = value)) + geom_histogram(fill = "white", color ="steelblue")+
      geom_vline(xintercept=5.054286, color="red", size=1.5) +
      geom_vline(xintercept=5.054452, color="wheat")
```



All together, computing the bootstrap estimates

```
rain %>%
       slipper(mean(pH),B=10000) %>%
       filter(type=="bootstrap") %>%
       summarize(mean = mean(value),
                 ci_low = quantile(value,0.025),
                 ci_high = quantile(value,0.975))

      mean   ci_low  ci_high
1 5.053425 4.894286 5.192857
```

Our bootstrap estimate: pH has a mean of 5.053 with a 95% CI of [4.89, 5.19]

"Regular" bootstrap was 5.05 with 95% CI of [4.85, 5.24]

What might we want to estimate from the bee data?

Estimate for *difference of means*

Confidence interval for *difference of means*

Generate bootstraps when data frame has multiple samples

```
> bees %>% filter(species == "a") -> bees.a
> bees.a %>%
     slipper(mean(lengths), B=1e4) %>%
     mutate(species = "a") -> a.boot
        type value species
1   observed 4.600       a
2  bootstrap 4.575       a
3  bootstrap 4.200       a
4  bootstrap 4.650       a
...
```

```
> bees %>% filter(species == "b") -> bees.b
> bees.b %>%
     slipper(mean(lengths), B=1e4) %>%
     mutate(species = "b") -> b.boot
       type value species
1  observed  4.98       b
2 bootstrap  5.10       b
3 bootstrap  4.84       b
4 bootstrap  4.88       b
...
```

con't

```
full.boot <- rbind(a.boot, b.boot)
head(full.boot)
       type value species
1  observed 4.600       a
2 bootstrap 4.750       a
3 bootstrap 4.450       a

full.boot %>%
    filter(type == "bootstrap") %>%
    group_by(species) %>%       ### Add unique ID per group line
    mutate(n = 1:n()) %>%       ### ""
    spread(species, value)
          type     n     a     b
        <fctr> <int> <dbl> <dbl>
    1 bootstrap     1 4.750  5.10
    2 bootstrap     2 4.450  4.84
    3 bootstrap     3 4.500  4.88
```

con't

```
full.boot %>%
    filter(type == "bootstrap") %>%
    group_by(species) %>%        ### Add unique ID per group line
    mutate(n = 1:n()) %>%        ### ""
    spread(species, value) %>%
    mutate(value = a - b) %>%
    summarize(mean = mean(value),
              ci_low = quantile(value,0.025),
              ci_high = quantile(value,0.975))

   # A tibble: 1 x 3
           mean ci_low ci_high
          <dbl>  <dbl>   <dbl>
   1 -0.3816805 -0.815    0.07
```

The bootstrap difference in mean bee lengths is -0.382 with a 95% bootstrap CI of [-0.815, 0.07]

Pop quiz! Recall our permutation test gave P=0.19. Is the bootstrap consistent?

Exercise break

Multiple testing

https://xkcd.com/882/

Run tests until you get a significant result = **no.**

- Data dredging
- P-hacking
- Data fishing
- Data snooping

False positive rate increases with more tests

Single test

P(false positive) = α

P(not false positive) = 1- α

N tests

P(no false positives) = $(1 - \alpha)^N$

P(at least 1 false positive) = $1 - (1 - \alpha)^N$

For N=20 and α=0.05, P(at least 1 false positive) = 65%

For N=100 and α=0.05, P(at least 1 false positive) = 99%

Example: Many tests on iris

```
versicolor <- iris %>% filter(Species == "versicolor")
virginica<- iris %>% filter(Species == "virginica")
setosa <- iris %>% filter(Species == "setosa")
```

```
> t.test(versicolor$Sepal.Length, virginica$Sepal.Length)$p.value
[1] 1.866144e-07
> t.test(versicolor$Sepal.Length, setosa$Sepal.Length)$p.value
[1] 3.746743e-17
> t.test(virginica$Sepal.Length, setosa$Sepal.Length)$p.value
[1] 3.966867e-25

> t.test(versicolor$Sepal.Width, virginica$Sepal.Width)$p.value
[1] 0.001819483
> t.test(versicolor$Sepal.Width, setosa$Sepal.Width)$p.value
[1] 2.484228e-15
> t.test(virginica$Sepal.Width, setosa$Sepal.Width)$p.value
[1] 4.570771e-09
```

```
> t.test(versicolor$Petal.Length, virginica$Petal.Length)$p.value
[1] 4.900288e-22
> t.test(versicolor$Petal.Length, setosa$Petal.Length)$p.value
[1] 9.934433e-46
> t.test(virginica$Petal.Length, setosa$Petal.Length)$p.value
[1] 9.269628e-50

> t.test(versicolor$Petal.Width, virginica$Petal.Width)$p.value
[1] 2.111534e-25
> t.test(versicolor$Petal.Width, setosa$Petal.Width)$p.value
[1] 2.717008e-47
> t.test(virginica$Petal.Width, setosa$Petal.Width)$p.value
[1] 2.437136e-48
```

Two broad types of error rates

Family-wise error rate (FWER)

- Probability of having at least one false positive among all tests
- Probability of rejecting at least one true null
- Corrections control FWER <= α

False discovery rate (FDR)

- Expected proportion of false positives among rejected hypotheses
- Rate that false discoveries occur
- FP / (FP + TP)
- Corrections control FDR <= α

Controlling the FWER

Bonferroni correction is the most common

- For *m* tests, change α → α/m and assess significance

My 6 tests gave P = {0.01, 0.03, 0.004, 0.027, 0.0006, 0.048}

- 0.05 → 0.05/6 → My new α is 0.0083
- P = {0.01, 0.03, 0.004, 0.027, 0.0006, 0.048}

Can alternatively multiply P-values by *m* and use original α (0.05)

- raw P = {0.01, 0.03, 0.004, 0.027, 0.0006, 0.048}
- **corrected P** = {0.06, 0.18, 0.024, 0.162 0.0036, ~~2.88~~ 1.0}

The Holm (BH) method uses a *stepwise* procedure to control FWER

Uses a *stepwise* (step-down) procedure to control FWER

1. Order P-values from *m* tests from smallest to largest and rank *k*
2. For a given α, find the **smallest** *k* where $P_k > \alpha/(m+1-k)$
3. Reject Ho for all $P_1 \ldots P_{k-1}$
    1. Fail to reject Ho for all $P_k \ldots P_m$

Holm (Bonferroni-Holm) FWER correction

P = {0.01, 0.03, 0.004, 0.027, 0.0006, 0.048}

Raw P	***α/(m-k+1)***	
0.0006	0.05/(6-1+1) = 0.0083	**P** is smaller, continue
0.004	0.05/(6-2+1) = 0.01	**P** is smaller, continue
0.01	0.05/(6-3+1) = 0.0125	**P** is smaller, continue
0.027	0.05/(6-4+1) = 0.0125	**P** is greater, **STOP**
0.03		
0.048		

P = {0.01, 0.03, 0.004, 0.027, 0.0006, 0.048}

Holm FWER correction with corrected P

$P_{corrected} = m * p_{k,}$ k=1

$= \max[\ p_{(k-1)}, p_k * (m-k+1)\ ],$ k>1

Raw P	Holm-corrected P
0.0006	0.0006 * 6 = **0.0036**
0.004	0.004 * (6-2+1) = 0.02 max(0.0036, 0.02) = **0.02**
0.01	0.01 * (6-3+1) = 0.04 max(0.02, 0.04) = **0.04**
0.027	0.027 * (6-4+1) = 0.081 max(0.04, 0.081) = **0.081**
0.03	0.03 * (6-5+1) = 0.06 max(0.081, 0.06) = **0.081**
0.048	0.048 * (6-6+1) = 0.048 max(0.081, 0.048) = **0.081**

Controlling error with FDR

FWER control procedures are **highly conservative**

- Bonferroni is the most severe
- Guarantees low false positive rate at the cost of a high false negative rate

FDR control procedures are much more powerful

- You end up with more significant results, at the cost of a higher false positive rate
- Invented as a response to the severe conservatism of Bonferroni, etc.

Controlling FDR with Benjamini-Hotchberg ("BH")

This is also a stepwise ("step-up") procedure

1. Determine the FDR you are willing to live with with, *Q*
2. Order P-values from *m* tests from smallest to largest and rank
3. For a given Q, find the **largest** *k* where $P_k \leq Q * k/m$
4. Reject all Ho for $P_1 \ldots P_k$
    1. Fail to reject Ho for $P_{k+1} \ldots P_m$

BH FDR procedure

P = {0.01, 0.03, 0.004, 0.027, 0.0006, 0.048}

Raw P	***α * k/m***
0.0006	
0.004	
0.027	
0.03	
0.01	
0.048	0.05 * 6/6 = 0.05

P is smaller, **STOP**

P = {0.01, 0.03, 0.004, 0.027, 0.0006, 0.048}

FDR correction with corrected P

$P_{corrected} = p_{k,}$ k=m

$= \min[\ p_{(k+1)}, p_k*(m/k)\ ],$ k<m

Raw P	FDR-corrected P
0.0006	0.0006 * 6/1 = 0.0036 min(0.012, 0.0036) = **0.0036**
0.004	0.004 * 6/2 = 0.012 min(0.02, 0.012) = **0.012**
0.01	0.01 * 6/3 = 0.02 min(0.036, 0.02) = **0.02**
0.027	0.027 * 6/4 = 0.0405 min(0.036, 0.0405) = **0.036**
0.03	0.03 * 6/5 = 0.036 min(0.048, 0.036) = **0.036**
0.048	**0.048**

R makes it **super easy**

```
p.values <- c(0.0006, 0.004, 0.01, 0.027, 0.03, 0.048)

### Holm is default
p.adjust(p.values)
[1] 0.0036 0.0200 0.0400 0.0810 0.0810 0.0810

### Specify Bonferroni
p.adjust(p.values, method = "bonferroni")
[1] 0.0036 0.0240 0.0600 0.1620 0.1800 0.2880

### Specify as bonf for when you can't remember if 2 r's or 2 n's
p.adjust(p.values, method = "bonf")
[1] 0.0036 0.0240 0.0600 0.1620 0.1800 0.2880

### Specify FDR
p.adjust(p.values, method = "fdr")
[1] 0.0036 0.0120 0.0200 0.0360 0.0360 0.0480
```

Use sum() to determine number of significant results

```
p.values <- c(0.0006, 0.004, 0.01, 0.027, 0.03, 0.048)
alpha <- 0.05

### Holm
sum( p.adjust(p.values) <= alpha )
[1] 3

### Bonferroni
sum( p.adjust(p.values, method = "bonf") <= alpha)
[1] 2

### FDR
sum( p.adjust(p.values, method = "fdr") <= alpha)
[1] 6
```

Running multiple tests in R

```
pairwise.t.test(response, grouping)
pairwise.wilcox.test(response, grouping)
```

```
> pairwise.t.test(iris$Sepal.Width, iris$Species)

Pairwise comparisons using t tests with pooled SD

data:  iris$Sepal.Width and iris$Species

           setosa  versicolor
versicolor < 2e-16 -
virginica  9.1e-10 0.0031

P value adjustment method: holm
```

Specify correction with "p.adj"

```
> pairwise.t.test(iris$Sepal.Width, iris$Species, p.adj = "fdr" )


Pairwise comparisons using t tests with pooled SD

data:  iris$Sepal.Width and iris$Species


           setosa  versicolor
versicolor < 2e-16 -
virginica  6.8e-10 0.0031

P value adjustment method: fdr
```

The triumphant return of broom!

```
> pairwise.t.test(iris$Sepal.Width, iris$Species, p.adj = "fdr") %>% tidy()

       group1     group2      p.value
1 versicolor     setosa 5.497468e-17
2  virginica     setosa 6.808435e-10
4  virginica versicolor 3.145180e-03

### How many are significant at 0.05?
pairwise.t.test(iris$Sepal.Width, iris$Species, p.adj = "fdr") %>%
       tidy() %>%
       mutate(sig = p.value <= 0.05) %>%
       group_by(sig) %>% tally()
        sig     n
      <lgl> <int>
   1  TRUE     3
```

ENTIFIC REPORTS

Genome-wide association study of aggressive behaviour in chicken

Zhenhui Li[1,2], Ming Zheng[1,2], Bahareldin Ali Abdalla[1,2], Zhe Zhang[1,2], Zhenqiang Xu[1,2,3], Qiao Ye[1,2], Haiping Xu[1,2], Wei Luo[1,2], Qinghua Nie[1,2] & Xiquan Zhang[1,2]

The thrilling age of GWAS

Abbreviation	Phenotype Description	Classification	Mean ± SD
T1	Number of fighting times during the whole recording period (16 days)	Fighting times	14.69 ± 11.24
T2	Number of fighting times in days with frequencies not less than 4 times per day		4.64 ± 8.63
T3	Number of days for chicken showed fighting	Fighting days	7.28 ± 3.53
T4	Number of days for chicken showed fighting with frequencies not less than 4 times per day		0.89 ± 3.53

Table 1. Four aggressive-behaviour phenotypes measured traits in male chickens.

The age of GWAS

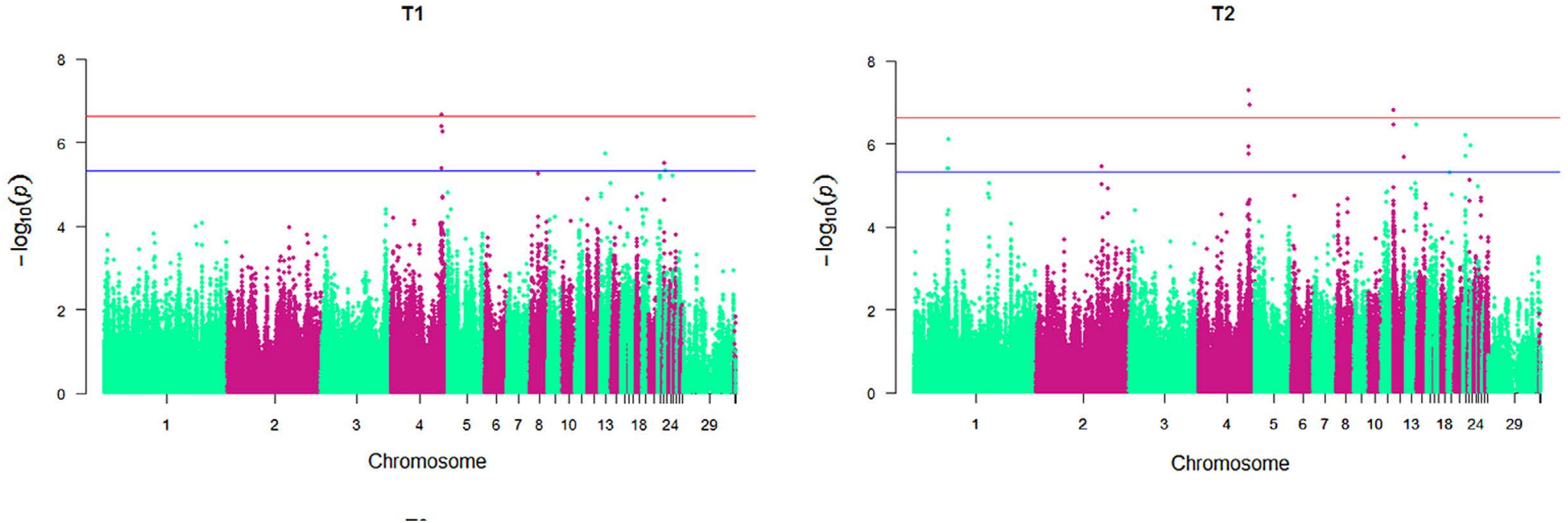


Figure 1. Manhattan plots of genome-wide association study on chicken aggressive-behaviour measured traits from T1 to T4 for all the SNPs.
The associated values (in terms of −log10P) are shown by chromosomes.
The blue highlighted line indicates genome-wide association (*P* = 4.6E-6),
and the red highlighted line indicates significance with a *P*-value threshold of the 5% Bonferroni genome-wide significance (*P* = 2.3E-7).

Exercise break