浙江大学爱丁堡大学联合学院

ZJU-UoE Institute

Bootstrapping

ADS2, Lecture 2.14

Dr Rob Young – robert.young@ed.ac.uk

Semester 2, 2023/24

Pre-lecture version

This lecture contains questions that I will ask you to think about before class. Providing the answers beforehand would defeat that purpose.

Therefore, the version of the slides available to you before the lecture will not contain all of the information that is presented in the lecture.

A complete version will be uploaded to Blackboard Learn after the lecture. In the meantime, here is a famous Scottish design by the artist Charles Rennie Mackintosh.

We've talked a lot about assumptions in ADS2…

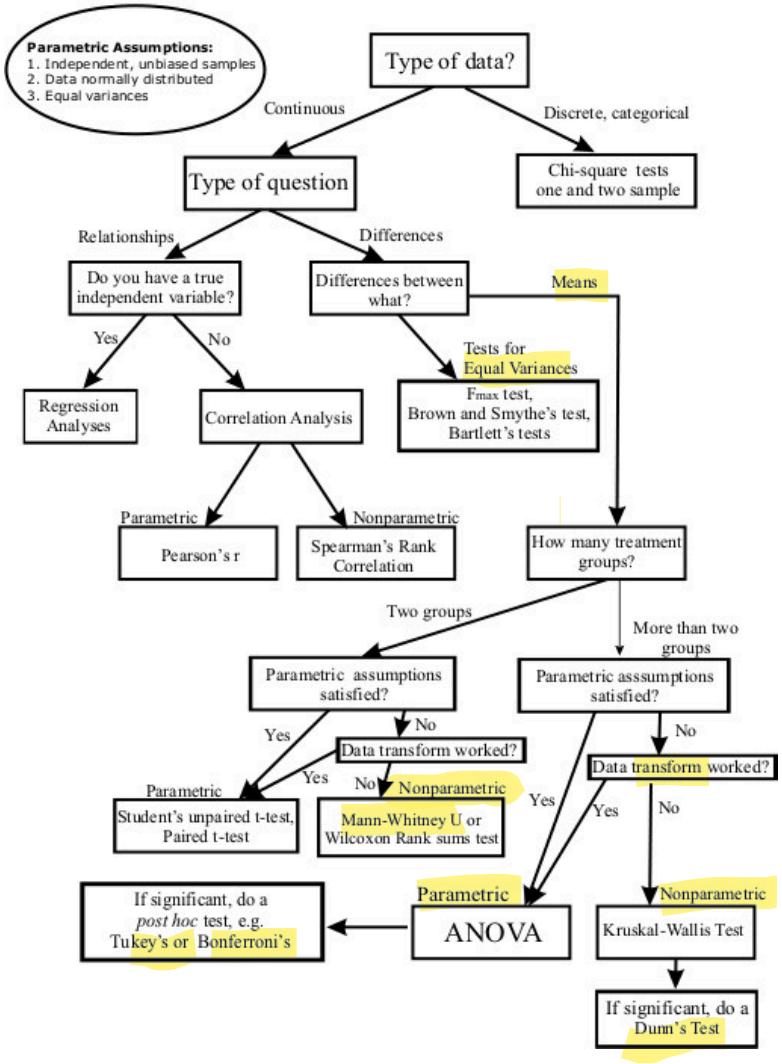
T-tests

Correlation and regression

Categorical data

ANOVA

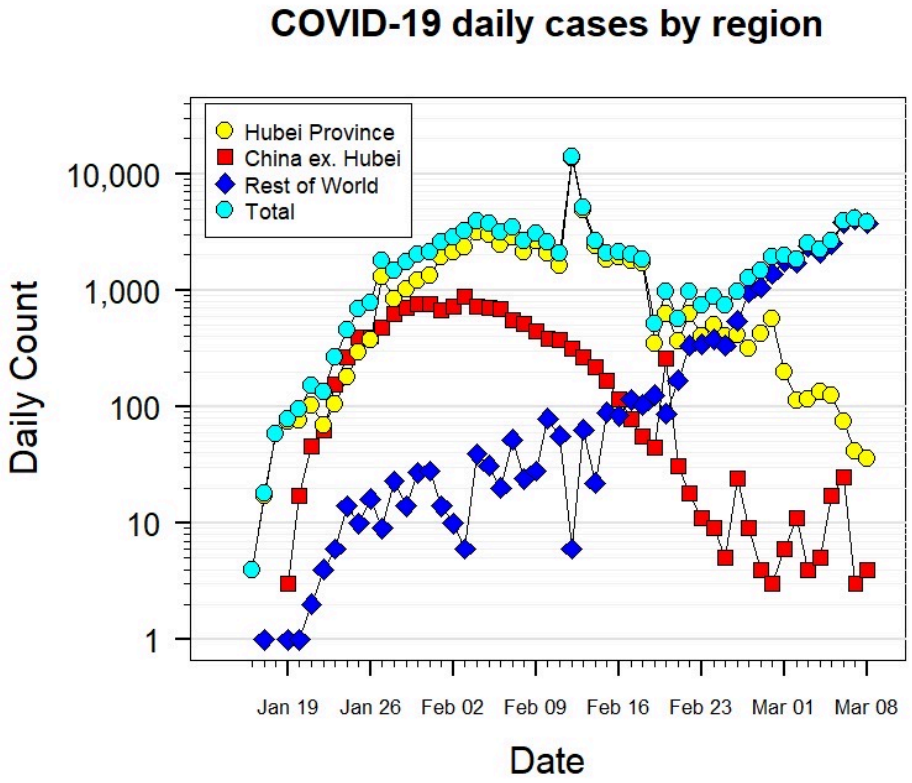
We talk a lot about assumptions in statistics generally…

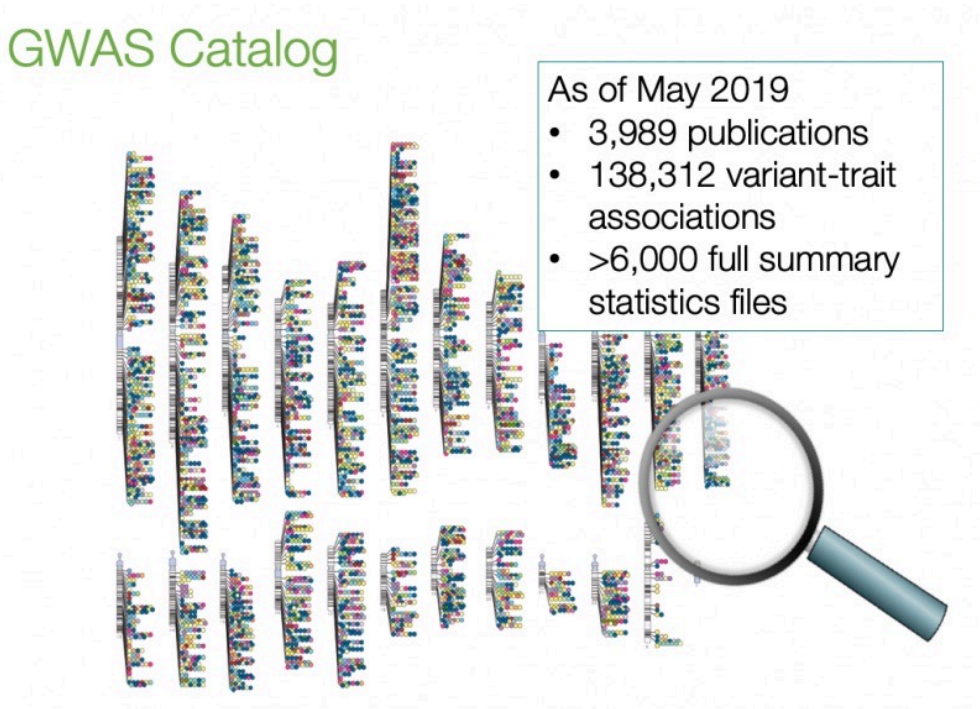


…but what if your data doesn't fit any of these?!

…but what if your data doesn't fit any of these?!

Many biomedical datasets have a complex distribution





Learning objectives

After this lecture, you should be able to:

- Explain the concept of bootstrapping.
- Recognise situations where bootstrapping is useful.

Lecture outline

1. R function `sample`
2. Bootstrapping for hypothesis testing
3. Bootstrapping to generate confidence intervals
4. Reflection on bootstrapping

Bonus content: No equations, only a function

- Sampling from a set: `sample()`

  e.g. draw 10 samples from your dataset without replacement:
  `sample(dataset, 10, replace=FALSE)`

- Can you explore this function yourself in R?
- What do you think might be the most useful parameters?

Drawing random numbers in R

- Sampling from a set: `sample()`, e.g. draw 10 samples from your dataset with replacement: `sample(dataset, 10, replace=FALSE)`

If your dataset contains 50 data points, what is the maximal sample size for sampling without replacement? How about with replacement?

Drawing random numbers in R

- Sampling from a set: `sample()`, e.g. draw 10 samples from your dataset with replacement: `sample(dataset, 10, replace=FALSE)`

If your datasets contains 50 data points, what is the maximal sample size for sampling without replacement? How about with replacement?

- Normally distributed random numbers: `rnorm()`, e.g. draw 100 numbers from a normal distribution with mean 4 and standard deviation 2: `rnorm(100,4,2)`

What will the histogram look like?

Drawing random numbers in R

- Sampling from a set: `sample()`, e.g. draw 10 samples from your dataset with replacement: `sample(dataset, 10, replace=FALSE)`

If your datasets contains 50 data points, what is the maximal sample size for sampling without replacement? How about with replacement?

- Normally distributed random numbers: `rnorm()`, e.g. draw 100 numbers from a normal distribution with mean 4 and standard deviation 2: `rnorm(100,4,2)`

What will the histogram look like?

- Uniformly distributed random numbers: `runif()`, e.g. draw 100 numbers between 0 and 10: `runif(100,0,10)`

What will the histogram look like?

Lecture outline

1. R function `sample`
2. Bootstrapping for hypothesis testing
3. Bootstrapping to generate confidence intervals

Bootstrapping

Problem:

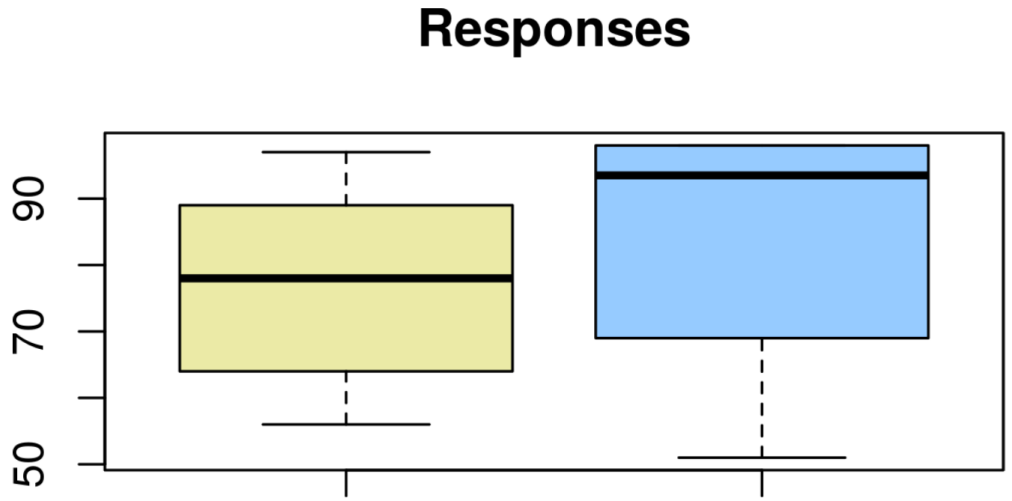
- We do not know or fully understand the population distribution.

However:

We have *some* information about the underlying distribution: the data! We use the data itself as the basis for our randomisation. This is called **bootstrapping**. We create a **bootstrap sample** by sampling (with replacement) from the data, and repeat this procedure many times.

Example: How do groups respond to a drug?

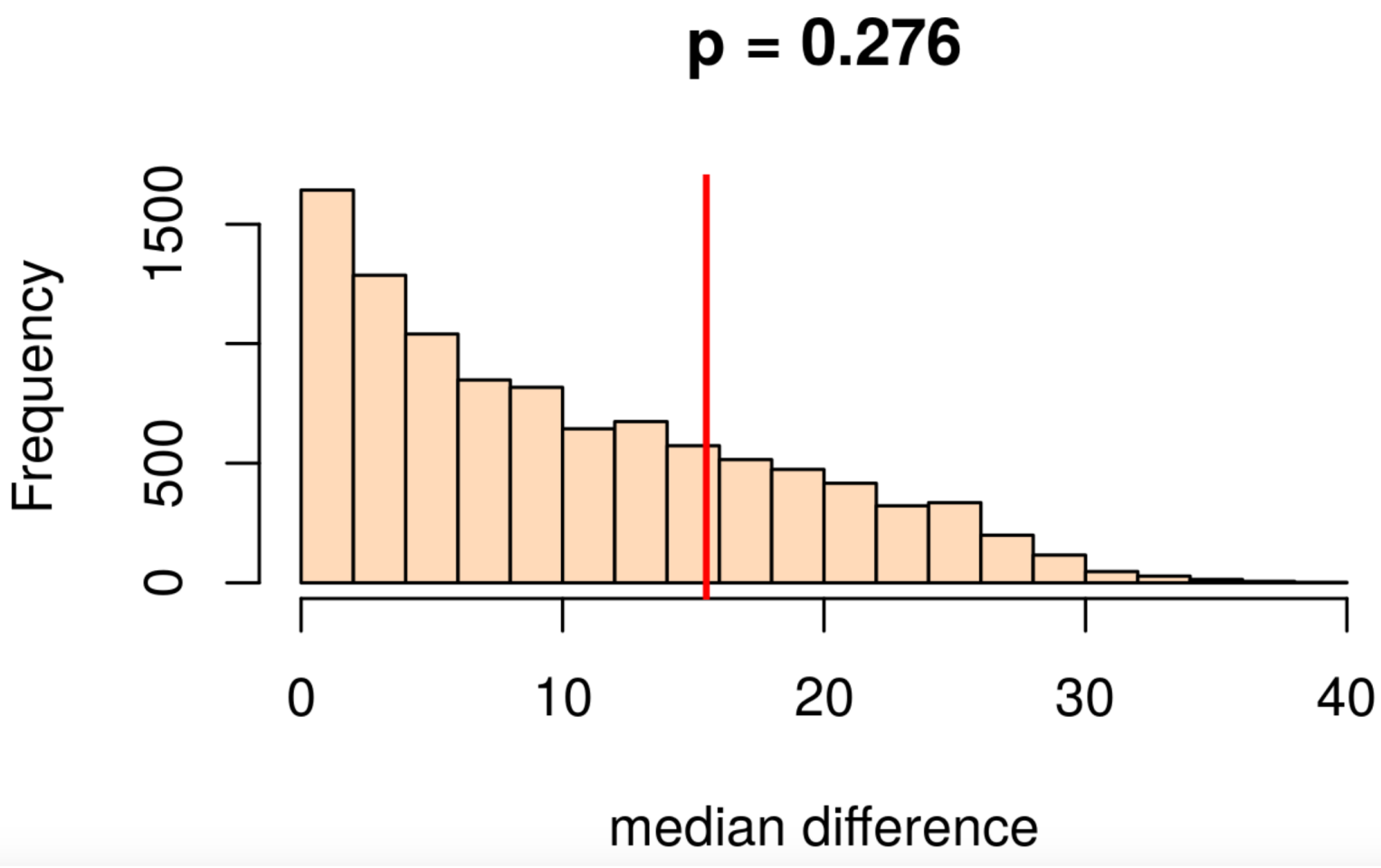
A lab tests response to a cancer drug in two cell lines with different genetic backgrounds. Response is measured as survival rate (in percent) per sample. 10 samples were tested for each condition. Researchers would like to know whether the median response rate differs between both groups. What test would you use?



Example: How do groups respond to a drug?

How would you bootstrap this?

Results



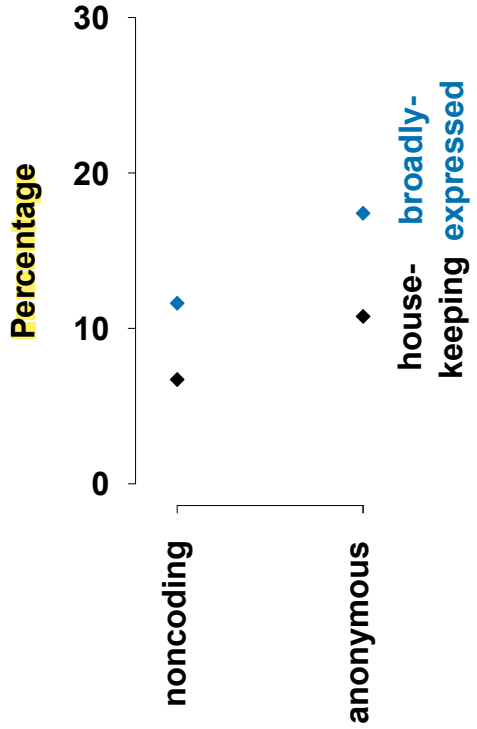
Lecture outline

1. R function `sample`
2. Bootstrapping for hypothesis testing
3. Bootstrapping to generate confidence intervals
4. Reflection on bootstrapping

The frequent evolutionary birth and death of functional promoters in mouse and human

GENOME RESEARCH

Robert S. Young,[1] Yoshihide Hayashizaki,[2] Robin Andersson,[3] Albin Sandelin,[3] Hideya Kawaji,[2,4] Masayoshi Itoh,[2,4] Timo Lassmann,[4] Piero Carninci,[4] The FANTOM Consortium, Wendy A. Bickmore,[1] Alistair R. Forrest,[4,5] and Martin S. Taylor[1]

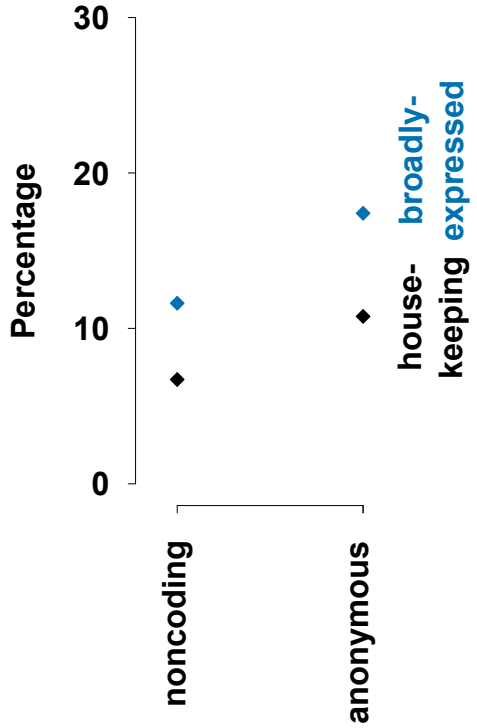


- Do the percentage of different types of noncoding and anonymous promoters differ?

The frequent evolutionary birth and death of functional promoters in mouse and human

GENOME RESEARCH

Robert S. Young,[1] Yoshihide Hayashizaki,[2] Robin Andersson,[3] Albin Sandelin,[3] Hideya Kawaji,[2,4] Masayoshi Itoh,[2,4] Timo Lassmann,[4] Piero Carninci,[4] The FANTOM Consortium, Wendy A. Bickmore,[1] Alistair R. Forrest,[4,5] and Martin S. Taylor[1]

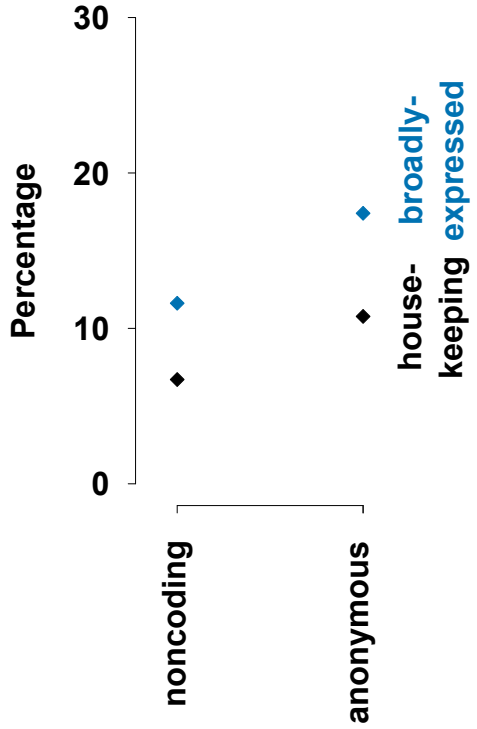


- 21/313 noncoding promoters are housekeeping (6.7%).

The frequent evolutionary birth and death of functional promoters in mouse and human

GENOME RESEARCH

Robert S. Young,[1] Yoshihide Hayashizaki,[2] Robin Andersson,[3] Albin Sandelin,[3] Hideya Kawaji,[2,4] Masayoshi Itoh,[2,4] Timo Lassmann,[4] Piero Carninci,[4] The FANTOM Consortium, Wendy A. Bickmore,[1] Alistair R. Forrest,[4,5] and Martin S. Taylor[1]



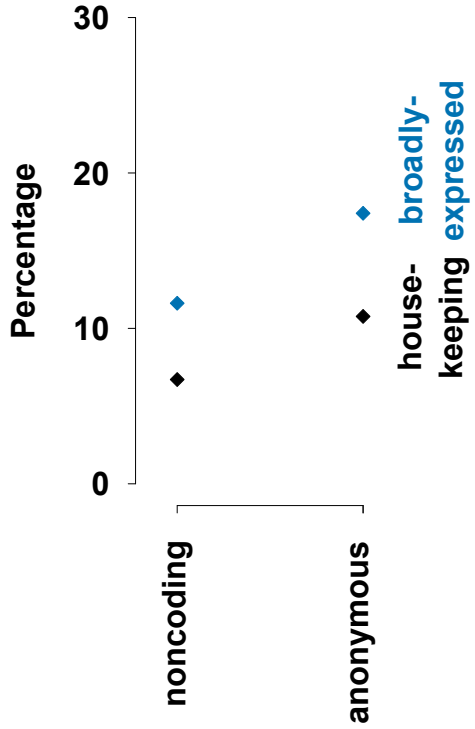
- 21/313 noncoding promoters are housekeeping (6.7%).

```
> summary(as.factor(noncoding))
house other
   21   292
> sample1<-sample(noncoding, size = length(noncoding), replace = T)
> summary(as.factor(sample1))
house other
   18   295
> sample2<-sample(noncoding, size = length(noncoding), replace = T)
> summary(as.factor(sample2))
house other
   21   292
```

The frequent evolutionary birth and death of functional promoters in mouse and human

GENOME RESEARCH

Robert S. Young,[1] Yoshihide Hayashizaki,[2] Robin Andersson,[3] Albin Sandelin,[3] Hideya Kawaji,[2,4] Masayoshi Itoh,[2,4] Timo Lassmann,[4] Piero Carninci,[4] The FANTOM Consortium, Wendy A. Bickmore,[1] Alistair R. Forrest,[4,5] and Martin S. Taylor[1]



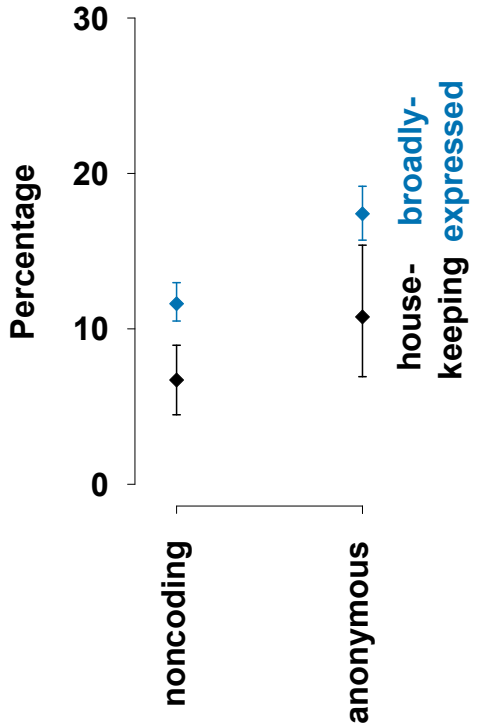
- 21/313 noncoding promoters are housekeeping (6.7%).

```
> house_samples<-vector()
> for (rep in 1:1000){
+     sample1<-sample(noncoding, size = length(noncoding), replace = T)
+     house_length<-length(subset(sample1, sample1=="house"))
+     house_samples<-c(house_samples, house_length)
+ }
> summary(house_samples)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    8.0    18.0    21.0    20.9    24.0    36.0
> quantile(house_samples, probs = c(0.025,0.975))
 2.5% 97.5%
   13    30
> lower<-13/313
> lower
[1] 0.04153355
> upper<-30/313
> upper
[1] 0.09584665
```

The frequent evolutionary birth and death of functional promoters in mouse and human

GENOME RESEARCH

Robert S. Young,[1] Yoshihide Hayashizaki,[2] Robin Andersson,[3] Albin Sandelin,[3] Hideya Kawaji,[2,4] Masayoshi Itoh,[2,4] Timo Lassmann,[4] Piero Carninci,[4] The FANTOM Consortium, Wendy A. Bickmore,[1] Alistair R. Forrest,[4,5] and Martin S. Taylor[1]



- Do the percentage of different types of noncoding and anonymous promoters differ?
- Error bars represent the 95% confidence interval of 1,000 samplings → why with replacement?
- Can we reject the H_0?

Lecture outline

1. R function `sample`
2. Bootstrapping for hypothesis testing
3. Bootstrapping to generate confidence intervals
4. Reflection on bootstrapping

Does bootstrapping make you uncomfortable?

Learning objectives

After this lecture, you should be able to:

- Explain the concept of bootstrapping.
- Recognise situations where bootstrapping is useful.

浙江大学爱丁堡大学联合学院

ZJU-UoE Institute

Bootstrapping
Any questions?

ADS2, Lecture 2.14

Dr Rob Young – robert.young@ed.ac.uk

Semester 2, 2023/24