#### **Statistical Inference**

Lecture 11a

ANU - RSFAS

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- We will consider two types of tests:
  - permutation/randomization tests
  - bootstrap tests

- Permutation tests are a computer-intensive approach introduced in the 1930s by R.A. Fisher.
- We will consider a two sample problem (the idea can easily be extended)
- Suppose we observe the following two data sets drawn from two potentially different probability distribution F and G:

$$F \rightarrow \mathbf{y} = (y_1, \dots, y_n)$$
  
 $G \rightarrow \mathbf{x} = (x_1, \dots, x_m)$ 

 Data: 16 mice were randomly assigned to a treatment and control group. The survival times, in days, following a test surgery were recorded.

```
treat <- c(94, 197, 16, 38, 99, 141, 23)
n <- length(treat)
control <- c(52, 104, 146, 10, 51, 30, 40, 27, 46)
m <- length(control)</pre>
```

Consider testing whether:

```
H_0: F(\text{treatment}) = G(\text{control})

H_1: \text{The distributions are not equal}
```

• Under  $H_0$  the assignment (label) of each data point can be permuted. Whether a data point was a "treatment" or "control" is the same!

Now we need a test statistic. Consider:

$$\theta = \bar{T} - \bar{C}$$

- Note: For our alternative we are stating the distributions are not the same. But we can consider one or two-sided tests for our alternative.
- For the data we have:

```
theta <- mean(treat) - mean(control)
theta</pre>
```

```
## [1] 30.63492
```

• Under  $H_0$  we can permute the labels of the data and calculate our test statistic:

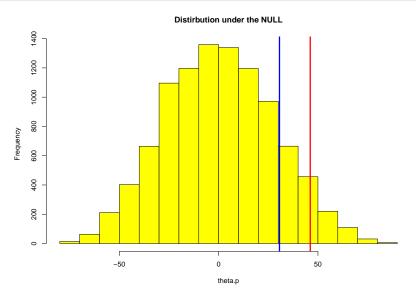
```
data <- c(treat, control)</pre>
data.p <- sample(data)</pre>
treat.p <- data.p[1:n]</pre>
control.p \leftarrow data.p[(n+1):(n+m)]
treat.p
## [1] 27 94 10 141 38 146 40
control.p
## [1] 16 30 52 51 23 99 104 197 46
theta.p <- mean(treat.p) - mean(control.p)</pre>
theta.p
```

## [1] 2.190476

• Let's repeat this process B = 10000:

```
set.seed(1001)
B <- 10000
theta.p \leftarrow rep(0, B)
for(b in 1:B){
  data.p <- sample(data)</pre>
  treat.p <- data.p[1:n]</pre>
  control.p \leftarrow data.p[(n+1):(n+m)]
  theta.p[b] <- mean(treat.p) - mean(control.p)</pre>
  }
```

```
hist(theta.p, col="yellow",
     main="Distirbution under the NULL")
## determine the critical value for alpha = 0.05
qu <- quantile(theta.p, 0.95)
abline(v=qu, lwd=3, col="red")
## add the statistic based on the
## original data (non permuted)
abline(v=theta, lwd=3, col="blue")
```



- Let's consider a one sided upper tail test.
- We see that our original test statistic (based on the non permuted data) does not cross into the rejection region. Thus we do not reject  $H_0$ .
- Let's calculate the p-value:

$$P(T(\boldsymbol{X}, \boldsymbol{Y}) \geq T(\boldsymbol{x}, \boldsymbol{y}))$$

```
p.value <- mean(theta.p > theta)
p.value
```

## [1] 0.142

• Permutation tests: How many possible ways are there to permute? Let N=n+m:

$$\boldsymbol{z} = \{y_1, \dots, y_n, x_1, \dots, x_m\}$$

$$\frac{N!}{n!m!} = \binom{N}{n}$$

If we construct our test based on every possible permutation, then we have a permutation test and an exact p-value!

• If we randomly sample from the  $\binom{N}{n}$  possible permutations then we have a randomization test and the p-value is approximate.

 We can also consider hypothesis testing for our two sample problem via the bootstrap.

$$H_0: F(\text{treatment}) = G(\text{control})$$

 $H_1$ : The distirbutions are not equal

$$\mathbf{z} = \{y_1, \ldots, y_n, x_1, \ldots, x_m\}$$

- **1.** Draw B samples of size N = n + m with replacement from z. Call the first n observations  $y^*$  and the remaining m observations  $x^*$ .
- **2.** Evaluate the test statistic  $t(\cdot)$  on each bootstrap sample:

$$t(\boldsymbol{y}^*,\boldsymbol{x}^*)=\bar{y}^*-\bar{x}^*$$

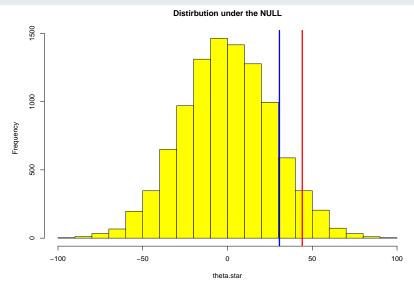
**3.** Construct an approximate p-value:

p-value 
$$\approx \#\{t(\boldsymbol{X}^*, \boldsymbol{Y}^*) \geq t_{obs}\}/B$$

• Let's conduct a bootstrap test with B = 10000:

```
set.seed(1001)
B <- 10000
theta.star \leftarrow rep(0, B)
N < - n + m
theta <- mean(treat) - mean(control)
for(b in 1:B){
  data.star <- sample(data, N, replace=TRUE)</pre>
  treat.star <- data.star[1:n]</pre>
  control.star <- data.star[-c(1:n)]
  theta.star[b] <- mean(treat.star) - mean(control.star)</pre>
```

```
hist(theta.star, col="yellow",
     main="Distirbution under the NULL")
## determine the critical value for alpha = 0.05
qu <- quantile(theta.star, 0.95)
abline(v=qu, lwd=3, col="red")
## add the statistic based on the original data (non permuted)
abline(v=theta, lwd=3, col="blue")
p.value <- mean(theta.star > theta)
p.value
```



## [1] 0.1216 <sub>16/32</sub>

• While permutation/randomization tests are very useful, the bootstrap approach is a little more flexible. Consider testing

$$H_0: \mu_{treat} = 129$$

 There is no permutation/randomization test available. They require the idea of label switching and here we only have one label.

 Let's use the following test statistic (t-statistic) based on a two-sided alternative:

$$H_1: \mu_{treat} \neq 129.0$$

$$|t(\mathbf{y})| = \left|\frac{\bar{y} - \mu_0}{s/\sqrt{7}}\right| = \left|\frac{86.9 - 129.0}{66.8/\sqrt{7}}\right| = \left|-1.67\right| = 1.67$$

```
y <- treat
mean(y)</pre>
```

```
## [1] 86.85714
```

sd(y)

## [1] 66.76683

- Now we need a way to construct a distribution of  $t(\cdot)$  under the Null hypothesis.
- We need to recenter our data:

$$\tilde{y}_i = y_i - \bar{y} + 129 = y_i - 86.9 + 129.0 = y_i + 42.1$$

• Now we resample with replacement for  $i=1,\ldots,7$  to get  $\tilde{y}_i^*$ :

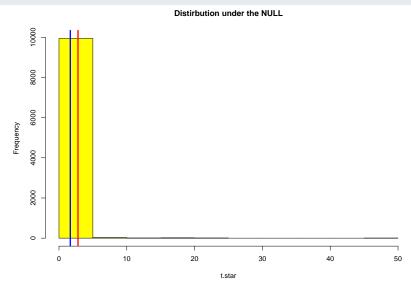
$$\tilde{y}_i^* = y_i^* + 42.1$$

$$|t(\boldsymbol{\tilde{y}}^*)| = \Big|rac{ar{ ilde{y}}^* - \mu_0}{ ilde{s}^*/\sqrt{7}}\Big| = \Big|rac{ar{ ilde{y}}^* - 129.0}{ ilde{s}^*/\sqrt{7}}\Big|$$

• Let's conduct a bootstrap test with B = 10000:

```
set.seed(1001)
B <- 10000
m <- length(y)
t.obs <- abs( (mean(y) - 129)/(sd(y)/sqrt(7)))
t.star \leftarrow rep(0, B)
for(b in 1:B){
y.star <- sample(y, m, replace=TRUE)</pre>
y.tilde.star <- y.star + 42.1
t.star[b] <- abs( (mean(y.tilde.star) - 129)/
                      (sd(y.tilde.star)/sqrt(7)))
```

```
hist(t.star, col="yellow",
     main="Distirbution under the NULL")
## determine the critical value for alpha = 0.05
qu <- quantile(t.star, 0.95)
abline(v=qu, lwd=3, col="red")
## add the statistic based on the original data
abline(v=t.obs, lwd=3, col="blue")
p.value <- mean(t.star > t.obs)
p.value
```



## [1] 0.1501

• Based on either the p-value or examination based on the critical region, we see that we do not reject  $H_0$ .

• Consider testing:

$$H_0: \theta \in \Theta_0$$
 vs.  $H_1: \theta \in \Theta_1$ 

- The classical statistician considers  $\theta$  a fixed unknown, thus a hypothesis test is true or false. Either  $\theta$  is in  $\Theta_0$  or  $\Theta_1$ !
- ullet Bayesians however consider heta to be random and it is quite natural to consider:

$$P(\theta \in \Theta_0 | \mathbf{x})$$
 vs.  $P(\theta \in \Theta_1 | \mathbf{x})$ 

• One approach to Bayesian testing is to reject  $H_0$  if:

$$P(\theta \in \Theta_1|\mathbf{x}) > P(\theta \in \Theta_0|\mathbf{x})$$

**Example 8.2.7:**  $X_1, \ldots, X_n \stackrel{\text{iid}}{\sim} \operatorname{normal}(\theta, \sigma^2)$ . Let  $\theta \sim \operatorname{normal}(\mu, \tau^2)$ , where  $\sigma^2, \mu, \tau^2$  are known. Consider testing:

$$H_0: \theta \leq \theta_0 \quad \text{ vs. } \quad H_1: \theta > \theta_0$$

$$[\theta | \mathbf{x}] \sim \operatorname{normal}\left(\frac{\sigma^2 \mu + n\tau^2 \bar{\mathbf{x}}}{\sigma^2 + n\tau^2}, \frac{\sigma^2 \tau^2}{\sigma^2 + n\tau^2}\right)$$

To compare we simply examine:

$$\int_{-\infty}^{\theta_0} p(\theta|\mathbf{x}) d\theta \quad \text{vs.} \quad \int_{\theta_0}^{\infty} p(\theta|\mathbf{x}) d\theta$$

 Based on this Bayesian approach to hypothesis testing, what if we wanted to test:

$$H_0: \theta = \theta_0$$
 vs.  $H_1: \theta \neq \theta_0$ 

$$[\theta | \mathbf{x}] \sim \operatorname{normal}\left(\frac{\sigma^2 \mu + n\tau^2 \bar{\mathbf{x}}}{\sigma^2 + n\tau^2}, \frac{\sigma^2 \tau^2}{\sigma^2 + n\tau^2}\right)$$

•  $[\theta | \mathbf{x}]$  is a continuous distribution, so the probability of any single point (such as  $\theta_0$ ) is zero. This approach does not seem to work.

- Notice that when we test through a Bayesian approach, we model the parameter of interest (i.e. we put a prior on it).
- If our scientific question concerns whether a parameter can be exactly  $\theta_0$  or not, then we should model that:

$$\theta \sim p \mathbf{1}_{\theta=\theta_0} + (1-p) \operatorname{normal}(\mu, \tau^2)$$

where  $0 \le p \le 1$ .

• In a regression or GLM setting many times we are interested in testing whether  $\beta=0$  vs.  $\beta\neq0$  and these priors or variants on them can be quite useful.

• Another approach that does allow for consideration of  $\beta=0$  is Bayes factors. Let's rephrase hypothesis testing as choosing between competing models:

Model 1 (
$$M_1$$
):  $y_i = \alpha + \epsilon_i$   $\epsilon_i \stackrel{\text{iid}}{\sim} \operatorname{normal}(0, \sigma^2); \quad \theta_1 = \{\alpha, \sigma^2\}$   
Model 2 ( $M_2$ ):  $y_i = \alpha + \beta x_i + \epsilon_i$   $\epsilon_i \stackrel{\text{iid}}{\sim} \operatorname{normal}(0, \sigma^2); \quad \theta_2 = \{\alpha, \beta, \sigma^2\}$ 

• Let's figure out the posterior probability for a given model i:

$$\pi(M_i|\mathbf{x}) = \frac{f(\mathbf{x}|M_i)\pi(M_i)}{m(\mathbf{x})}$$

$$f(\mathbf{x}|M_i) = \int_{\theta} f(\mathbf{x}|\theta, M_i)\pi(\theta|M_i)d\theta_i$$

$$m(\mathbf{x}) = \sum_{i=1}^{2} f(\mathbf{x}|M_i)\pi(M_i)$$

• Now consider the following ratio of the posterior model probabilities:

$$\frac{\pi(M_2|\mathbf{x})}{\pi(M_1|\mathbf{x})} = \frac{f(\mathbf{x}|M_2)}{f(\mathbf{x}|M_1)} \times \frac{\pi(M_2)}{\pi(M_1)}$$
$$= BF(M_2; M_1) \times \frac{\pi(M_2)}{\pi(M_1)}$$

Where  $BF(M_2; M_1)$  is called the Bayes factor.

- Typically  $\pi(M_2) = \pi(M_1)$ , so the ratio of the posterior probabilities is the Bayes factor.
- The Bayes factor looks like a likelihood ratio. However, the difference is that  $\theta$  has been integrated out in both the numerator and denominator, so we have the marginal distribution of the data given the model.

- If  $f(\mathbf{x}|M_2) > f(\mathbf{x}|M_1)$  or  $\frac{f(\mathbf{x}|M_2)}{f(\mathbf{x}|M_1)} > 1$  then we have support for  $M_2$  against  $M_1$ .
- Jeffreys, H. (1961 appendix B) suggested the following:

$BF(M_2;M_1)=B_{21}$	Evidence against model $1 (H_0)$
1 to 3.2	Not worth more than a bare mention
3.2 to 10	Substantial
10 to 100	Strong
> 100	Decisive