

## Lab: Significance & p-values

### 1. Permutation test of independence

Replicate the permutation tests from slide 18 (see slide 10).

## 2. Parametric Inference

\* Recall these models from the time through the order ( $T_{TO}$ ) analysis:

$$(*) \quad y_i = \beta_1 + \beta_2 \cdot \mathbb{1}\{t_i \geq 2T_{TO}\} + \beta_3 \cdot \mathbb{1}\{t_i \geq 3T_{TO}\} \\ + \beta_{BQ} \cdot BQ_i + \beta_{PQ} \cdot PQ_i + \beta_{hand} \cdot hand_i + \beta_{home} \cdot home_i + \varepsilon_i$$

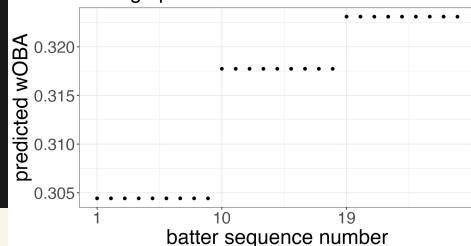
```
> m2 = lm(EVENT_WOBA_19 ~ 1 + as.numeric(ORDER_CT >= 2) + as.numeric(ORDER_CT >= 3) +
+          HAND_MATCH + BAT_HOME_IND + WOBA_FINAL_BAT_19 + WOBA_FINAL_PIT_19,
+          data=df0)
> m2
```

Call:  
 $lm(formula = EVENT_WOBA_19 \sim 1 + as.numeric(ORDER\_CT \geq 2) +$   
 $as.numeric(ORDER\_CT \geq 3) + HAND\_MATCH + BAT\_HOME\_IND + WOBA\_FINAL\_BAT\_19 +$   
 $WOBA\_FINAL\_PIT\_19, data = df0)$

Coefficients:

(Intercept)	as.numeric(ORDER_CT >= 2)	as.numeric(ORDER_CT >= 3)	HAND_MATCH
-0.299509	0.01320	0.005357	
BAT_HOME_IND	WOB_A_FINAL_BAT_19	WOB_A_FINAL_PIT_19	
0.009988	0.969370	0.962359	

handedness match, batter at home,  
average pitcher and batter



$$(*) \quad y_i = \beta_0 + \beta_1 \cdot t_i + \beta_2 \cdot \mathbb{1}\{t_i \geq 2T_{TO}\} + \beta_3 \cdot \mathbb{1}\{t_i \geq 3T_{TO}\} \\ + \beta_{BQ} \cdot BQ_i + \beta_{PQ} \cdot PQ_i + \beta_{hand} \cdot hand_i + \beta_{home} \cdot home_i + \varepsilon_i$$

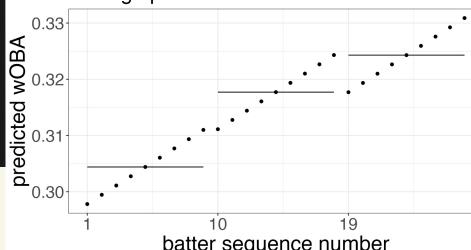
```
> m5 = lm(EVENT_WOBA_19 ~ 1 + as.numeric(ORDER_CT >= 2) + as.numeric(ORDER_CT >= 3) + BATTER_SEQ_NUM + HAND_MATCH + BAT_HOME_IND + WOBA_FINAL_BAT_19 + WOBA_FINAL_PIT_19, data=df0)
> m5
```

Call:  
 $lm(formula = EVENT_WOBA_19 \sim 1 + as.numeric(ORDER\_CT \geq 2) +$   
 $as.numeric(ORDER\_CT \geq 3) + BATTER\_SEQ\_NUM + HAND\_MATCH +$   
 $BAT\_HOME\_IND + WOBA\_FINAL\_BAT\_19 + WOBA\_FINAL\_PIT\_19, data = df0)$

Coefficients:

(Intercept)	as.numeric(ORDER_CT >= 2)	as.numeric(ORDER_CT >= 3)	BATTER_SEQ_NUM
-0.316611	-0.001528	-0.008267	0.001649
HAND_MATCH	BAT_HOME_IND	WOB_A_FINAL_BAT_19	WOB_A_FINAL_PIT_19
-0.016837	0.009994	0.999090	0.962273

handedness match, batter at home,  
average pitcher and batter



Model 1:  $\hat{\beta}_2 = 0.013, \hat{\beta}_3 = 0.0054$

Model 2:  $\hat{\beta}_2 = -0.0015, \hat{\beta}_3 = -0.0083, \hat{\beta}_1 = 0.0016$

These point estimates are a single "best guess" of the parameter value according to the model.

The thing is, you can fit a model to any dataset and get estimated coefficients.

You ought to wonder: what if the model is shit? In our case, we've done enough validating of our model (via plotting) to be convinced it's not completely shit. And, "shit" is vague.

A more refined question is: are the values of these estimated coefficients due to a real trend in the data or due to noise and random chance?

Since we're interested in whether these coefficients are zero or not, we ask: is there enough evidence in the data to include that the coefficient is highly likely nonzero (i.e., significantly nonzero)?

These questions underly parametric inference: we'd like to infer whether a parameter in a model is nonzero.

$$\left\{ \begin{array}{ll} \text{Null hypothesis } H_0: \beta = 0 \\ \text{Alt hypothesis } H_1: \beta \neq 0 \\ \text{Test statistic } t = \hat{\beta} / SE(\hat{\beta}) \end{array} \right.$$

$SE(\hat{\beta})$  is the standard error of  $\hat{\beta}$ , which is an estimate of the standard deviation of  $\hat{\beta}$ .

Since  $\hat{\beta}$  is computed from the data  $(X, y)$  and  $y$  is generated from model  $y = X\beta + \epsilon$ ,  $y$  is a random variable and hence  $\hat{\beta}$  is a random variable and hence  $\hat{\beta}$  has a standard deviation which we estimate,  $SE(\hat{\beta}) = \sqrt{\text{var}(\hat{\beta})}$ .

optional math HW: derive  $SE(\hat{\beta})$  in multivariable linear regression.

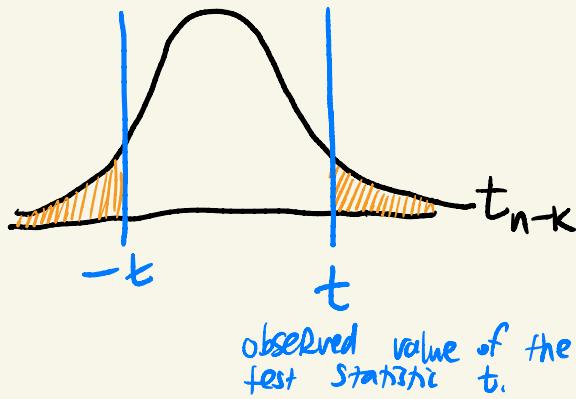
Theorem: Suppose  $\epsilon_i \stackrel{iid}{\sim} N(0, \sigma^2)$ .

Suppose  $H_0$  is true, so  $\beta = 0$ .

Then the test statistic  $t$  has distribution  $t \sim t_{n-k}$ , the  $t$  distribution with  $n-k$  degrees of freedom ( $n = \# \text{ datapoints}$ ,  $k = \# \text{ predictors}$ ).

optional math HW: prove this

Under our assumptions, the test statistic  $t$  has a  $t_{n-k}$  distribution, which is nearly Normal when  $n$  is large,



The **p-value** is the orange area to the Right of  $t$  and left of  $-t$  Under the  $t_{n-k}$  density curve. It is, assuming the null  $H_0$  is true, the probability of observing a test statistic as extreme as the one we actually observed, where the randomness here is over the sampling distribution (generating  $y$  from  $x$ ).

Theorem: the **p-value**  $P = P_{H_0}(|t_{n-k}| > t)$  has distribution  $p \sim \text{Unif}[0, 1]$ .

optional math HW: prove this

If the null  $H_0$  is true, we are unlikely to observe a  $|t|$  in the far tails of the distribution, and so we are unlikely to observe a **p-value** that is small.

{ So, a large  $|t|$  value and small **p-value** is associated with less evidence of  $\beta$  being zero.

The convention is to set a **significance level**, typically  $\alpha = 0.05$ , and then

{ Reject  $H_0$  if  $P < \alpha$  else do not Reject.

But this  $\alpha$  is arbitrary and 0.05 is still a pretty big number.

P-values should be treated as a spectrum and not a strict cutoff.

R automatically runs this t-test for every coefficient.  
 You can do this by `summary(m)`  
 $m \leftarrow lm(\cdot)$  is the object that stores  
 the linear model.

```
> summary(m2)

Call:
lm(formula = EVENT_WOBA_19 ~ 1 + as.numeric(ORDER_CT >= 2) +
   as.numeric(ORDER_CT >= 3) + HAND_MATCH + BAT_HOME_IND + WOBA_FINAL_BAT_19 +
   WOBA_FINAL_PIT_19, data = df0)

Residuals:
    Min      1Q  Median      3Q     Max 
-1.0089 -0.3351 -0.2762  0.3995  1.8396 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -0.295909  0.010110 -29.626 < 2e-16 ***
as.numeric(ORDER_CT >= 2) 0.013320  0.002481  5.370 7.89e-08 ***
as.numeric(ORDER_CT >= 3) 0.005357  0.002922  1.833  0.0668 .  
HAND_MATCH   -0.016306  0.002206 -7.392 1.45e-13 ***
BAT_HOME_IND 0.009988  0.002183  4.575 4.77e-06 ***
WOBA_FINAL_BAT_19 0.969370  0.017123 56.613 < 2e-16 ***
WOBA_FINAL_PIT_19 0.962359  0.026573 36.215 < 2e-16 *** 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5053 on 214379 degrees of freedom
Multiple R-squared:  0.0222, Adjusted R-squared:  0.02218 
F-statistic: 811.3 on 6 and 214379 DF, p-value: < 2.2e-16
```

t Statistic  
 for each regression coefficient

```
> summary(m5)

Call:
lm(formula = EVENT_WOBA_19 ~ 1 + as.numeric(ORDER_CT >= 2) +
   as.numeric(ORDER_CT >= 3) + BATTER_SEQ_NUM + HAND_MATCH +
   BAT_HOME_IND + WOBA_FINAL_BAT_19 + WOBA_FINAL_PIT_19, data = df0)

Residuals:
    Min      1Q  Median      3Q     Max 
-1.0133 -0.3348 -0.2761  0.3995  1.8391 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -0.3166112  0.0113189 -27.972 < 2e-16 ***
as.numeric(ORDER_CT >= 2) -0.0015278  0.0050680 -0.301 0.763064
as.numeric(ORDER_CT >= 3) -0.0082619  0.0049974 -1.653 0.098285 .
BATTER_SEQ_NUM 0.0016491  0.0004909  3.360 0.000781 ***
HAND_MATCH    -0.0168367  0.0022114 -7.613 2.68e-14 ***
BAT_HOME_IND   0.0099937  0.0021831  4.578 4.70e-06 ***
WOBA_FINAL_BAT_19 0.9909002  0.0192728 51.839 < 2e-16 ***
WOBA_FINAL_PIT_19 0.9622731  0.0265726 36.213 < 2e-16 *** 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5053 on 214378 degrees of freedom
Multiple R-squared:  0.02225, Adjusted R-squared:  0.02222 
F-statistic: 697 on 7 and 214378 DF, p-value: < 2.2e-16
```

p-Value  
 for each regression coefficient

- Fit the two models (\*) and (\*\*).  
In the first model, is pitcher decline from one time through the order to the next significant? Explain.  
Think carefully about how you'll explain it.

- \* I don't really like parametric inference.  
The theorems are based on strict mathematical assumptions like  $\epsilon_i \stackrel{iid}{\sim} N(0, \sigma^2)$  that are often unreasonable.  
There are other better ways to do inference, which we will discuss:  
Bootstrapping & Bayesian statistics.  
But it is still good that y'all got an overview.