

R Examples from BIOST 514/517

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November 21, 2014

Difference in Means

FEV data

Default in R assumes variances unequal Can use `t.test()` (stats) or `ttest()` (uwIntroStats). You can set `var.eq=T` for equal variances
Make sure to load all of the required packages and data

```
smoke <- SMOKE
sex <- SEX

## ttest for difference in means
height <- HEIGHT
ttest(height, by=sex)
```

Call:
`ttest.default(var1 = height, by = sex)`

Two-sample t-test allowing for unequal variances :

Summary:

	Group	Obs	Missing	Mean	Std. Err.	Std. Dev.	95% CI
sex = 2	336	0	62.03	0.345	6.33	[61.346, 62.7]	
sex = 1	318	0	60.21	0.269	4.79	[59.683, 60.74]	
Difference	654	0	1.81	0.438	<NA>	[0.954, 2.67]	

Ho: difference in means = 0 ;
Ha: difference in means != 0
t = 4.144 , df = 622
Pr(|T| > t) = 3.88659e-05

Proportions

FEV data

Calculate the confidence interval by yourself! Use the `qt()` to get t quantiles, and `qbinom()` for binomial quantiles

Comparing Proportions

FEV data

`prop.test()` function

Gives us a two-sided test by default (change with alternative option). Tests equality of the proportions

```
## difference of proportions
is_smoker <- smoke==1
successMale <- smoke==1 & sex==1
table(successMale)
prop1 <- 26
## recall that we already know the observations from the t-test above
obs1 <- 336
successFemale <- smoke==1 & sex==2
prop2 <- 39
obs2 <- 318
prop.test(c(prop1, prop2), c(obs1, obs2), correct=FALSE)
```

2-sample test for equality of proportions without continuity correction

```
data:  c(prop1, prop2) out of c(obs1, obs2)
X-squared = 3.739, df = 1, p-value = 0.05316
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.0912611312  0.0007400171
sample estimates:
   prop 1    prop 2 
0.07738095 0.12264151
```

Odds Ratios and Risk Ratios

Download the `epitools` package, or calculate by hand
The `riskratio` and `oddsratio` functions will calculate for
entered counts

One-sample t-test

Given count data, use the `ttesti()` function from `uwIntroStats`

```
ttesti(25, 220, 46, null.hyp=211)
```

One-sample t-test

	Obs	Mean	Std. Error	SD	95 %CI
x	25	220	9.2	46	[201.01, 238.99]

t-statistic = 0.978 , df = 24

Ho: mean = 211

Ha: mean != 211 , $\Pr(|T| > |t|) = 1.6623$

```
ttest(sbp, by=dibpat)
```

Call:

```
ttest.default(var1 = sbp, by = dibpat)
```

Two-sample t-test allowing for unequal variances :

Summary:

	Group	Obs	Missing	Mean	Std. Err.	Std. Dev.	95% CI
dibpat = A1,A2		1589	0	129.78	0.394	15.7	[129.01, 130.55]
dibpat = B3,B4		1565	0	127.47	0.365	14.4	[126.75, 128.18]
Difference		3154	0	2.32	0.537	<NA>	[1.26, 3.37]

Ho: difference in means = 0 ;

Ha: difference in means != 0

t = 4.317 , df = 3137

Pr(|T| > t) = 1.62861e-05

Shoulder Pain Data

Use the `matched=TRUE` option!

Can also run a one-sample t-test as above

```
ttest(pain[time==1], pain[time==6], matched=TRUE)
```

Call:

```
ttest.default(var1 = pain[time == 1], var2 = pain[time == 6],  
              matched = TRUE)
```

Two-sample (matched) t-test :

Summary:

	Group	Obs	Missing	Mean	Std. Err.	Std. Dev.	95% CI
pain[time == 1]		41	0	1.098	0.206	1.319	[0.681, 1.514]
pain[time == 6]		41	0	0.585	0.131	0.836	[0.322, 0.849]
Difference		41	0	0.512	0.185	1.17	[0.138, 0.886]

Ho: difference in means = 0 ;

Ha: difference in means != 0

t = 2.766 , df = 40

Pr(|T| > t) = 0.00855172

Use the tabulate function

Use the same function in the PBC data set examples

```
tabulate(grade, bss)
```

Call:

```
tabulate.default(grade, bss)
```

	bss.1	bss.2	bss.3	bss.NA	bss.NotNA	bss.ALL
grade.1	1	3	6	0	10	10
grade.2	2	4	9	0	15	15
grade.3	2	4	9	1	15	16
grade.NA	0	2	6	1	8	9
grade.NotNA	5	11	24	1	40	41
grade.ALL	5	13	30	2	48	50

	Point Estimate	Test Statistic	df	95% CI	p-value	Warnings
Chi-squared		4.3115	16		0.99825	

Fisher's Exact Test

Use the `fisher.test()` function, or the `tabulate()` function with the `tests="fisher"` option

Create a `Surv` variable, plot the curve with confidence interval
To plot cumulative hazard function, use the `fun="cumhaz"` option
To compare survival times, use the `survdiff` function from the `survival` package

```
relapse <- ifelse(inrem=="no", 1, 0)
atrisk <- Surv(obstime, relapse)
survFit <- survfit(atrisk~1)
plot(survFit)
```