

Two Sample t-test

```
data: c(y1, y3) and y2
t = 0.19396, df = 18, p-value = 0.8484
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.357702  1.633892
sample estimates:
mean of x mean of y
 17.67143  17.53333
```

```
> 0.19396^2
[1] 0.03762048
> library(ISwR)
> data(red.cell.folate)
> attach(red.cell.folate)
> red.cell.folate
  folate ventilation
1    243  N20+02,24h
2    251  N20+02,24h
3    275  N20+02,24h
4    291  N20+02,24h
5    347  N20+02,24h
6    354  N20+02,24h
7    380  N20+02,24h
8    392  N20+02,24h
9    206   N20+02,op
10   210   N20+02,op
11   226   N20+02,op
12   249   N20+02,op
13   255   N20+02,op
14   273   N20+02,op
15   285   N20+02,op
16   295   N20+02,op
17   309   N20+02,op
18   241      02,24h
19   258      02,24h
20   270      02,24h
21   293      02,24h
22   328      02,24h
> summary(red.cell.folate)
      folate      ventilation
Min.   :206.0   N20+02,24h:8
1st Qu.:249.5   N20+02,op :9
Median :274.0   02,24h   :5
Mean   :283.2
3rd Qu.:305.5
Max.   :392.0
>
> anova(lm(folate~ventilation))
```

Analysis of Variance Table

Response: folate

	Df	Sum Sq	Mean Sq	F value
ventilation	2	15516	7757.9	3.7113
Residuals	19	39716	2090.3	

Pr(>F)

ventilation	0.04359	*
-------------	---------	---

Residuals

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
' ' 1

> mean(red.cell.folate[1:8,1])

[1] 316.625

> mean(red.cell.folate[9:17,1])

[1] 256.4444

> mean(red.cell.folate[18:22,1])

[1] 278

> tapply(folate,ventilation,mean)

N20+02,24h	N20+02,op	02,24h
316.6250	256.4444	278.0000

> data(juul)

> attach(juul)

> head(juul)

	age	menarche	sex	igf1	tanner	testvol
1	NA	NA	NA	90	NA	NA
2	NA	NA	NA	88	NA	NA
3	NA	NA	NA	164	NA	NA
4	NA	NA	NA	166	NA	NA
5	NA	NA	NA	131	NA	NA
6	0.17	NA	1	101	1	NA

> dim(juul)

[1] 1339 6

> anova(lm(igf1~tanner))

Analysis of Variance Table

Response: igf1

	Df	Sum Sq	Mean Sq	F value
tanner	1	10985605	10985605	686.07
Residuals	790	12649728	16012	

Pr(>F)

tanner	< 2.2e-16	***
--------	-----------	-----

Residuals

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
' ' 1

> tanner

[1] NA NA NA NA NA 1 1 1 1 1 1 1 1 1 1

[illegible]

```

[766] NA 1 NA 1 1 1 1 1 1 1 1 NA 1 1 1
[781] 1 1 1 1 NA NA 1 1 1 1 1 1 1 1
[796] 1 NA 1 1 NA 1 1 1 1 1 1 1 1 1
[811] NA 1 1 NA NA 1 1 1 1 1 1 1 NA 1 1
[826] 1 1 NA 1 NA 2 NA 1 NA 2 NA 1 1 1 1
[841] 1 1 2 2 1 2 1 NA 1 NA 1 1 1 1 2
[856] 1 1 1 2 NA 1 1 NA NA NA 1 NA 1 2 2
[871] 3 2 1 3 1 2 2 1 1 1 2 1 2 2 NA
[886] 1 2 1 NA 1 3 NA NA 3 2 NA 1 NA 1 NA
[901] 1 2 1 2 1 NA 1 2 NA 1 2 3 NA NA 1
[916] 3 3 3 4 1 1 3 1 2 NA 2 3 3 3 1
[931] 1 2 3 3 1 2 3 1 2 2 2 NA 3 4 NA
[946] 2 3 NA 3 2 NA 2 3 NA 1 4 2 3 NA 1
[961] 1 1 1 3 3 5 NA 3 2 3 2 NA 2 2 4
[976] 5 2 2 3 NA 4 4 4 5 3 4 5 NA 4 5
[991] NA 3 3 5 4 2 5 5 2 4 4 NA 5 4 2
[1006] 5 NA 3 5 2 5 1 4 2 5 5 3 2 5 5
[1021] 2 4 4 3 4 3 5 5 5 4 3 4 5 4 NA
[1036] 4 2 2 3 5 5 5 4 4 3 NA NA 5 4 4
[1051] 4 5 5 3 NA 5 5 NA 4 4 NA 4 NA 4 5
[1066] 5 4 4 4 4 NA 5 NA 5 NA 5 3 NA NA 4
[1081] NA NA 5 NA NA 5 5 5 5 5 5 5 5 NA
[1096] 5 5 NA NA 5 NA 5 NA 5 5 NA 4 5 NA NA
[1111] 3 NA 5 5 5 5 5 5 NA 5 4 5 5 5 5
[1126] 5 4 NA 5 5 5 5 5 5 5 5 5 5 4 5
[1141] 5 5 NA 5 5 5 5 5 5 5 5 5 5 NA 5
[1156] 5 NA 5 5 5 5 5 5 5 5 NA 5 5 5 5
[1171] NA 5 5 5 5 5 5 5 5 5 5 5 5 5 5
[1186] 5 5 5 5 5 4 5 5 5 5 5 5 5 5 5
[1201] 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
[1216] 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
[1231] 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
[1246] 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
[1261] 5 5 5 5 5 5 NA 5 NA NA NA NA NA NA
[1276] NA NA NA 5 NA NA NA NA NA NA NA NA NA
[1291] NA NA NA NA NA NA NA 5 5 NA NA NA NA NA
[1306] NA NA NA NA NA NA NA NA 5 NA NA NA 5 NA 5
[1321] NA NA NA NA 5 5 NA NA 5 NA NA NA NA 5 5
[1336] NA NA NA NA

```

```

> juul<-transform(juul,tanner=factor(tanner,
+ labels=c("one","two","three","four","five")))

```

```

>
> anova(lm(juul$igf1~juul$tanner))
Analysis of Variance Table

```

Response: juul\$igf1

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
juul\$tanner	4	12696217	3174054	228.35	< 2.2e-16
Residuals	787	10939116	13900		

```
juul$tanner ***
```

```
Residuals
```

```
---
```

```
Signif. codes:
```

```
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> data(juul)
```

```
> anova(lm(juul$igf1~juul$tanner))
```

```
Analysis of Variance Table
```

```
Response: juul$igf1
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
juul\$tanner	1	10985605	10985605	686.07	< 2.2e-16
Residuals	790	12649728	16012		

```
juul$tanner ***
```

```
Residuals
```

```
---
```

```
Signif. codes:
```

```
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> juul$tanner<-
```

```
+ factor(juul$tanner,labels=c("one","two","three","four","five"))
```

```
> anova(lm(juul$igf1~juul$tanner))
```

```
Analysis of Variance Table
```

```
Response: juul$igf1
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
juul\$tanner	4	12696217	3174054	228.35	< 2.2e-16
Residuals	787	10939116	13900		

```
juul$tanner ***
```

```
Residuals
```

```
---
```

```
Signif. codes:
```

```
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> red.cell.folate
```

	folate	ventilation
1	243	N20+02,24h
2	251	N20+02,24h
3	275	N20+02,24h
4	291	N20+02,24h
5	347	N20+02,24h
6	354	N20+02,24h
7	380	N20+02,24h
8	392	N20+02,24h
9	206	N20+02,op
10	210	N20+02,op
11	226	N20+02,op
12	249	N20+02,op
13	255	N20+02,op
14	273	N20+02,op

```

15    285    N20+02,op
16    295    N20+02,op
17    309    N20+02,op
18    241      02,24h
19    258      02,24h
20    270      02,24h
21    293      02,24h
22    328      02,24h

```

```

> anova(lm(folate~ventilation))
Analysis of Variance Table

```

Response: folate

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ventilation	2	15516	7757.9	3.7113	0.04359 *
Residuals	19	39716	2090.3		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

> summary(lm(folate~ventilation))

```

Call:

```

lm(formula = folate ~ ventilation)

```

Residuals:

Min	1Q	Median	3Q	Max
-73.625	-35.361	-4.444	35.625	75.375

Coefficients:

	Estimate	Std. Error	t value
(Intercept)	316.62	16.16	19.588
ventilationN20+02,op	-60.18	22.22	-2.709
ventilation02,24h	-38.62	26.06	-1.482

Pr(>|t|)

(Intercept)	4.65e-14 ***
ventilationN20+02,op	0.0139 *
ventilation02,24h	0.1548

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 45.72 on 19 degrees of freedom

Multiple R-squared: 0.2809, Adjusted R-squared: 0.2052

F-statistic: 3.711 on 2 and 19 DF, p-value: 0.04359

```

> summary(lm(folate~ventilation))

```

Call:

```

lm(formula = folate ~ ventilation)

```

Residuals:

Min	1Q	Median	3Q	Max
-73.625	-35.361	-4.444	35.625	75.375

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	316.62	16.16	19.588	4.65e-14
ventilationN20+02,op	-60.18	22.22	-2.709	0.0139
ventilation02,24h	-38.62	26.06	-1.482	0.1548

(Intercept) ***
ventilationN20+02,op *
ventilation02,24h

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 45.72 on 19 degrees of freedom
Multiple R-squared: 0.2809, Adjusted R-squared: 0.2052
F-statistic: 3.711 on 2 and 19 DF, p-value: 0.04359

> pairwise.t.test(folate,ventilation,p.adj="bonferroni")

Pairwise comparisons using t tests with pooled SD

data: folate and ventilation

	N20+02,24h	N20+02,op
N20+02,op	0.042	-
02,24h	0.464	1.000

P value adjustment method: bonferroni

> pairwise.t.test(folate,ventilation)

Pairwise comparisons using t tests with pooled SD

data: folate and ventilation

	N20+02,24h	N20+02,op
N20+02,op	0.042	-
02,24h	0.310	0.408

P value adjustment method: holm

> anova(lm(juul\$igf1~juul\$tanner))

Analysis of Variance Table

Response: juul\$igf1

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
juul\$tanner	4	12696217	3174054	228.35	< 2.2e-16 ***
Residuals	787	10939116	13900		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> pairwise.t.test(juul$igf1,juul$tanner,p.adj="bonferroni")
```

Pairwise comparisons using t tests with pooled SD

data: juul\$igf1 and juul\$tanner

	one	two	three	four
two	< 2e-16	-	-	-
three	< 2e-16	9.9e-08	-	-
four	< 2e-16	5.5e-13	1.000	-
five	< 2e-16	1.3e-11	1.000	0.048

P value adjustment method: bonferroni

```
> summary(lm(juul$igf1,juul$tanner))
```

Error in formula.default(object, env = baseenv()) : invalid formula

```
> summary(lm(juul$igf1~juul$tanner))
```

Call:

```
lm(formula = juul$igf1 ~ juul$tanner)
```

Residuals:

Min	1Q	Median	3Q	Max
-365.33	-71.37	-10.24	61.53	448.67

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	207.473	6.685	31.034	<2e-16 ***
juul\$tannertwo	145.199	15.597	9.309	<2e-16 ***
juul\$tannerthree	275.750	18.804	14.665	<2e-16 ***
juul\$tannerfour	305.545	16.863	18.120	<2e-16 ***
juul\$tannerfive	257.862	9.477	27.208	<2e-16 ***

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 117.9 on 787 degrees of freedom
(547 observations deleted due to missingness)

Multiple R-squared: 0.5372, Adjusted R-squared: 0.5348

F-statistic: 228.4 on 4 and 787 DF, p-value: < 2.2e-16

```
> pairwise.t.test(juul$igf1,juul$tanner)
```

Pairwise comparisons using t tests with pooled SD

data: juul\$igf1 and juul\$tanner

	one	two	three	four
two	< 2e-16	-	-	-


```
three < 2e-16 3.9e-08 - -
four  < 2e-16 3.3e-13 0.407 -
five  < 2e-16 6.3e-12 0.407 0.015
```

```
P value adjustment method: holm
> oneway.test(folate~ventilation)
```

One-way analysis of means (not assuming equal variances)

```
data: folate and ventilation
F = 2.9704, num df = 2.000, denom df = 11.065,
p-value = 0.09277
```

```
> red.cell.folate
```

	folate	ventilation
1	243	N20+02,24h
2	251	N20+02,24h
3	275	N20+02,24h
4	291	N20+02,24h
5	347	N20+02,24h
6	354	N20+02,24h
7	380	N20+02,24h
8	392	N20+02,24h
9	206	N20+02,op
10	210	N20+02,op
11	226	N20+02,op
12	249	N20+02,op
13	255	N20+02,op
14	273	N20+02,op
15	285	N20+02,op
16	295	N20+02,op
17	309	N20+02,op
18	241	02,24h
19	258	02,24h
20	270	02,24h
21	293	02,24h
22	328	02,24h

```
> pairwise.t.test(folate,ventilation,pool.sd=F)
```

Pairwise comparisons using t tests with non-pooled SD

```
data: folate and ventilation
```

	N20+02,24h	N20+02,op
N20+02,op	0.087	-
02,24h	0.321	0.321

```
P value adjustment method: holm
> bartlett.test(folate~ventilation)
```

Bartlett test of homogeneity of variances

data: folate by ventilation

Bartlett's K-squared = 2.0951, df = 2, p-value = 0.3508

```
> xbar<-tapply(folate,ventilation,mean) s<-
tapply(folate,ventilation,sd) n<-tapply(folate,ventilation,length)
Error: unexpected symbol in "xbar<-tapply(folate,ventilation,mean) s"
> sem<-s/sqrt(n)
Error: object 's' not found
> xbar<-tapply(folate,ventilation,mean) ;s<-
tapply(folate,ventilation,sd) ;n<-tapply(folate,ventilation,length)
> sem<-s/sqrt(n)
>
stripchart(folate~ventilation,vert=T,pch=16 ,method="jitter") ;arrows(
1:3,xbar+sem,1:3,xbar-
sem,angle=90,code=3,length=0.1) ;lines(1:3,xbar,pch=4,type="b",cex=2)
>
> pain = c(4, 5, 4, 3, 2, 4, 3, 4, 4, 6, 8, 4, 5, 4, 6, 5, 8, 6, 6, 7,
6, 6, 7, 5, 6, 5, 5)
> drug = c(rep("A",9), rep("B",9), rep("C",9))
> migraine = data.frame(pain,drug);migraine
  pain drug
1     4   A
2     5   A
3     4   A
4     3   A
5     2   A
6     4   A
7     3   A
8     4   A
9     4   A
10    6   B
11    8   B
12    4   B
13    5   B
14    4   B
15    6   B
16    5   B
17    8   B
18    6   B
19    6   C
20    7   C
21    6   C
22    6   C
23    7   C
24    5   C
25    6   C
```

```

26    5    C
27    5    C
> plot(pain ~ drug, data=migraine)
> anova(lm(pain~drug, data=migraine))
Analysis of Variance Table

```

```

Response: pain
      Df Sum Sq Mean Sq F value
drug    2  28.222   14.111   11.906
Residuals 24  28.444    1.1852
      Pr(>F)
drug    0.0002559 ***
Residuals
---

```

```

Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'
  0.1 ' ' 1

```

```

> summary(aov(pain~drug, data=migraine))
      Df Sum Sq Mean Sq F value
drug    2  28.22   14.111   11.91
Residuals 24  28.44    1.185
      Pr(>F)
drug    0.000256 ***
Residuals
---

```

```

Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'
  0.1 ' ' 1

```

```

> pairwise.t.test(pain, drug, p.adjust="bonferroni")

```

Pairwise comparisons using t tests with pooled SD

data: pain and drug

```

  A      B
B 0.00119 -
C 0.00068 1.00000

```

P value adjustment method: bonferroni

```

> pairwise.t.test(pain, drug)

```

Pairwise comparisons using t tests with pooled SD

data: pain and drug

```

  A      B
B 0.00079 -
C 0.00068 0.83042

```

P value adjustment method: holm

```
> results = aov(pain ~ drug, data=migraine)
> TukeyHSD(results, conf.level = 0.95)
  Tukey multiple comparisons of means
    95% family-wise confidence level
```

```
Fit: aov(formula = pain ~ drug, data = migraine)
```

```
$drug
      diff      lwr      upr    p adj
B-A 2.111111 0.8295028 3.392719 0.0011107
C-A 2.222222 0.9406139 3.503831 0.0006453
C-B 0.111111 -1.1704972 1.392719 0.9745173
```

```
> TukeyHSD(results, conf.level = 0.9)
  Tukey multiple comparisons of means
    90% family-wise confidence level
```

```
Fit: aov(formula = pain ~ drug, data = migraine)
```

```
$drug
      diff      lwr      upr    p adj
B-A 2.111111 1.0053515 3.216871 0.0011107
C-A 2.222222 1.1164627 3.327982 0.0006453
C-B 0.111111 -0.9946485 1.216871 0.9745173
```

```
> plot(TukeyHSD(results, conf.level = 0.95))
> plot(TukeyHSD(results, conf.level = 0.9))
> plot(TukeyHSD(results, conf.level = 0.999))
> plot(TukeyHSD(results, conf.level = 0.999999))
> heart.rate <- data.frame(hr = c(96,110,89,95,128,100,72,79,100,
92,106,86,78,124,98,68,75,106,86,108,85,78,118,100,67,74, 104,
92,114,83,83,118,94,71,74,102),
+ subj=gl(9,1,36), time=gl(4,9,36,labels=c(0,30,60,120)))
> heart.rate
```

```
   hr subj time
1   96    1    0
2  110    2    0
3   89    3    0
4   95    4    0
5  128    5    0
6  100    6    0
7   72    7    0
8   79    8    0
9  100    9    0
10  92    1   30
11 106    2   30
12  86    3   30
13  78    4   30
14 124    5   30
15  98    6   30
```

```

16 68 7 30
17 75 8 30
18 106 9 30
19 86 1 60
20 108 2 60
21 85 3 60
22 78 4 60
23 118 5 60
24 100 6 60
25 67 7 60
26 74 8 60
27 104 9 60
28 92 1 120
29 114 2 120
30 83 3 120
31 83 4 120
32 118 5 120
33 94 6 120
34 71 7 120
35 74 8 120
36 102 9 120
> c(1:9,1:9,1:9,1:9)
[1] 1 2 3 4 5 6 7 8 9 1 2 3 4 5 6 7 8 9 1 2
[21] 3 4 5 6 7 8 9 1 2 3 4 5 6 7 8 9
> gl(9,1,36)
[1] 1 2 3 4 5 6 7 8 9 1 2 3 4 5 6 7 8 9 1 2
[21] 3 4 5 6 7 8 9 1 2 3 4 5 6 7 8 9
Levels: 1 2 3 4 5 6 7 8 9
> gl(9,1,37)
[1] 1 2 3 4 5 6 7 8 9 1 2 3 4 5 6 7 8 9 1 2
[21] 3 4 5 6 7 8 9 1 2 3 4 5 6 7 8 9 1
Levels: 1 2 3 4 5 6 7 8 9
> c(rep(0,9),rep(30,9),rep(60,9),rep(120,9))
[1] 0 0 0 0 0 0 0 0 0 30
[11] 30 30 30 30 30 30 30 30 30 60
[21] 60 60 60 60 60 60 60 60 120 120
[31] 120 120 120 120 120 120
> gl(4,9,36,labels=c(0,30,60,120))
[1] 0 0 0 0 0 0 0 0 0 30
[11] 30 30 30 30 30 30 30 30 60 60
[21] 60 60 60 60 60 60 60 120 120 120
[31] 120 120 120 120 120 120
Levels: 0 30 60 120
> gl(4,9,36)
[1] 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 3 3
[21] 3 3 3 3 3 3 3 4 4 4 4 4 4 4 4 4
Levels: 1 2 3 4
> gl(4,9,36,labels=c(0,30,60,120))
[1] 0 0 0 0 0 0 0 0 0 30
[11] 30 30 30 30 30 30 30 30 60 60

```

```

[21] 60 60 60 60 60 60 60 120 120 120
[31] 120 120 120 120 120 120
Levels: 0 30 60 120
> anova(lm(hr~subj+time))
Error in eval(predvars, data, env) : object 'hr' not found
> attach(heart.rate)
> anova(lm(hr~subj+time))
Analysis of Variance Table

```

```

Response: hr
      Df Sum Sq Mean Sq F value
subj    8 8966.6  1120.82  90.6391
time    3  151.0    50.32   4.0696
Residuals 24  296.8    12.37
      Pr(>F)
subj 4.863e-16 ***
time 0.01802  *
Residuals
---

```

```

Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.'
  0.1 ' ' 1

```

```

> anova(lm(hr~subj+time))
Analysis of Variance Table

```

```

Response: hr
      Df Sum Sq Mean Sq F value      Pr(>F)
subj    8 8966.6  1120.82  90.6391 4.863e-16 ***
time    3  151.0    50.32   4.0696 0.01802  *
Residuals 24  296.8    12.37
---

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

> interaction.plot(time,subj,hr)
> data(thuesen)
> attach(thuesen)
> thuesen

```

```

      blood.glucose short.velocity
1          15.3          1.76
2          10.8          1.34
3           8.1          1.27
4          19.5          1.47
5           7.2          1.27
6           5.3          1.49
7           9.3          1.31
8          11.1          1.09
9           7.5          1.18
10         12.2          1.22
11           6.7          1.25
12           5.2          1.19
13         19.0          1.95

```

```

14          15.1          1.28
15          6.7          1.52
16          8.6          NA
17          4.2          1.12
18         10.3          1.37
19         12.5          1.19
20         16.1          1.05
21         13.3          1.32
22          4.9          1.03
23          8.8          1.12
24          9.5          1.70
> lm.velo<-lm(short.velocity~blood.glucose); summary(lm.velo)

Call:
lm(formula = short.velocity ~ blood.glucose)

Residuals:
    Min       1Q   Median       3Q      Max
-0.40141 -0.14760 -0.02202  0.03001  0.43490

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.09781    0.11748   9.345 6.26e-09 ***
blood.glucose  0.02196    0.01045   2.101  0.0479 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2167 on 21 degrees of freedom
(1 observation deleted due to missingness)
Multiple R-squared:  0.1737,    Adjusted R-squared:  0.1343
F-statistic: 4.414 on 1 and 21 DF,  p-value: 0.0479

>
> anova(lm.velo)
Analysis of Variance Table

Response: short.velocity
              Df Sum Sq Mean Sq F value Pr(>F)
blood.glucose  1  0.20727  0.207269    4.414 0.0479 *
Residuals     21  0.98610  0.046957
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> 2.101^2
[1] 4.414201
> 0.20727/(0.20727+0.98610)
[1] 0.1736846
> sqrt(0.046957)
[1] 0.2166956
> Drug = c(rep("Placebo",6), rep("5mg",6),rep("10mg",6))
> Drug

```

```

[1] "Placebo" "Placebo" "Placebo" "Placebo"
[5] "Placebo" "Placebo" "5mg"      "5mg"
[9] "5mg"      "5mg"      "5mg"      "5mg"
[13] "10mg"     "10mg"     "10mg"     "10mg"
[17] "10mg"     "10mg"
> Age = c(rep(c(rep("young",3), rep("old",3)),3))
> Age
[1] "young" "young" "young" "old"   "old"
[6] "old"   "young" "young" "young" "old"
[11] "old"   "old"   "young" "young" "young"
[16] "old"   "old"   "old"
> Value = c(4, 3, -1, 2, 1, -2, 4, 5, 7, 3, 3, 4, 9, 12, 10, 7, 8, 7)
> data<-data.frame(Drug, Age, Value);data
  Drug Age Value
1 Placebo young    4
2 Placebo young    3
3 Placebo young   -1
4 Placebo  old     2
5 Placebo  old     1
6 Placebo  old    -2
7      5mg young    4
8      5mg young    5
9      5mg young    7
10     5mg  old     3
11     5mg  old     3
12     5mg  old     4
13    10mg young    9
14    10mg young   12
15    10mg young   10
16    10mg  old     7
17    10mg  old     8
18    10mg  old     7
> par(mfrow=c(1,2))
> plot(Value ~ Drug + Age, data=data)
Hit <Return> to see next plot:
> interaction.plot(data$Age, data$Drug, data$Value)
> interaction.plot(data$Drug, data$Age, data$Value)
> anova(lm(Value ~ Drug + Age +Drug*Age, data=data)
+ )

```

Analysis of Variance Table

Response: Value

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Drug	2	178.111	89.056	32.06	1.535e-05
Age	1	22.222	22.222	8.00	0.01522
Drug:Age	2	1.444	0.722	0.26	0.77529
Residuals	12	33.333	2.778		

```

Drug    ***
Age      *

```


Drug:Age
Residuals

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova(lm(Value ~ Drug + Age, data=data))

Analysis of Variance Table

Response: Value

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Drug	2	178.111	89.056	35.8498	3.105e-06
Age	1	22.222	22.222	8.9457	0.009725
Residuals	14	34.778	2.484		

Drug ***

Age **

Residuals

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> anova(lm(Value ~ Drug + Age +Drug*Age, data=data))

Analysis of Variance Table

Response: Value

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Drug	2	178.111	89.056	32.06	1.535e-05
Age	1	22.222	22.222	8.00	0.01522
Drug:Age	2	1.444	0.722	0.26	0.77529
Residuals	12	33.333	2.778		

Drug ***

Age *

Drug:Age

Residuals

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> prop.test(39, 215, 0.15)

1-sample proportions test with continuity
correction

data: 39 out of 215, null probability 0.15

X-squared = 1.425, df = 1, p-value = 0.2326

alternative hypothesis: true p is not equal to 0.15

95 percent confidence interval:

0.1335937 0.2408799

sample estimates:

p

0.1813953

```

> (39-215*0.15)/sqrt(215*0.15*0.85)
[1] 1.289227
> ((39-215*0.15)/sqrt(215*0.15*0.85))^2
[1] 1.662107
> ((38.5-215*0.15)/sqrt(215*0.15*0.85))^2
[1] 1.424989
> 39/215
[1] 0.1813953
> binom.test(39, 215, 0.15)

```

Exact binomial test

```

data: 39 and 215
number of successes = 39, number of trials =
215, p-value = 0.2135
alternative hypothesis: true probability of success is not equal to
0.15
95 percent confidence interval:
 0.1322842 0.2395223
sample estimates:
probability of success
 0.1813953

```

```

> caff.marital <-matrix(c(652,1537,598,242,36,46,38,21,218,327,
106,67), nrow=3,byrow=T)
> colnames(caff.marital) <- c("0","1-150","151-300", ">300")
rownames(caff.marital) <- c("Married","Prev.married","Single")
Error: unexpected symbol in "colnames(caff.marital) <-
c("0","1-150","151-300", ">300") rownames"
> caff.marital
      [,1] [,2] [,3] [,4]
[1,]  652 1537  598  242
[2,]   36  46  38  21
[3,]  218 327 106  67
> caff.marital <-matrix(c(652,1537,598,242,36,46,38,21,218,327,
106,67), nrow=3,byrow=T)
> ;colnames(caff.marital) <-
c("0","1-150","151-300", ">300") ;rownames(caff.marital) <-
c("Married","Prev.married","Single")
Error: unexpected ';' in ";"
> caff.marital
      [,1] [,2] [,3] [,4]
[1,]  652 1537  598  242
[2,]   36  46  38  21
[3,]  218 327 106  67
> caff.marital <-matrix(c(652,1537,598,242,36,46,38,21,218,327,
106,67), nrow=3,byrow=T);colnames(caff.marital) <-
c("0","1-150","151-300", ">300") ;rownames(caff.marital) <-
c("Married","Prev.married","Single")

```

```

> ;caff.marital
Error: unexpected ';' in ";"
> caff.marital<-matrix(c(652,1537,598,242,36,46,38,21,218,327,
106,67), nrow=3,byrow=T);colnames(caff.marital)<-
c("0","1-150","151-300",">300");rownames(caff.marital) <-
c("Married","Prev.married","Single");caff.marital
      0 1-150 151-300 >300
Married      652  1537      598  242
Prev.married  36   46       38   21
Single       218  327      106   67
> chisq.test(caff.marital)

      Pearson's Chi-squared test

data:  caff.marital
X-squared = 51.656, df = 6, p-value =
2.187e-09

> chisq.test(caff.marital)$expected
      0      1-150    151-300
Married    705.83179 1488.01183 578.06533
Prev.married 32.85648  69.26698 26.90895
Single     167.31173 352.72119 137.02572
      >300
Married     257.09105
Prev.married 11.96759
Single       60.94136
> chisq.test(caff.marital)$observed
      0 1-150 151-300 >300
Married    652  1537      598  242
Prev.married 36   46       38   21
Single     218  327      106   67
> caf.marital[,1]
Error: object 'caf.marital' not found
> caff.marital[,1]
      Married Prev.married      Single
      652      36      218
> sum(caff.marital[,1])
[1] 906
> sum(caff.marital[1,])
[1] 3029
> sum(caff.marital)
[1] 3888
> sum(caff.marital[1,])*sum(caff.marital[1,])/ sum(caff.marital)
[1] 2359.784
> sum(caff.marital[1,])*sum(caff.marital[,1])/ sum(caff.marital)
[1] 705.8318
> sum(caff.marital[3,])*sum(caff.marital[,2])/ sum(caff.marital)
[1] 352.7212
> E <- chisq.test(caff.marital)$expected

```

```

> 0 <- chisq.test(caff.marital)$observed
> (0-E)^2/E

```

	0	1-150	151-300
Married	4.1055981	1.612783	0.6874502
Prev.married	0.3007537	7.815444	4.5713926
Single	15.3563704	1.875645	7.0249243

```

> sum((0-E)^2/E)
[1] 51.65564
> dim(caff.marital)
[1] 3 4
> data(juul)
> head(juul)

```

	age	menarche	sex	igf1	tanner	testvol
1	NA	NA	NA	90	NA	NA
2	NA	NA	NA	88	NA	NA
3	NA	NA	NA	164	NA	NA
4	NA	NA	NA	166	NA	NA
5	NA	NA	NA	131	NA	NA
6	0.17	NA	1	101	1	NA

```

> chisq.test(tanner,sex)

```

Pearson's Chi-squared test

```

data:  tanner and sex
X-squared = 28.867, df = 4, p-value =
8.318e-06

```

```

objc[600]: Class FIFinderSyncExtensionHost is implemented in both /
System/Library/PrivateFrameworks/FinderKit.framework/Versions/A/
FinderKit (0x7fff949aec90) and /System/Library/PrivateFrameworks/
FileProvider.framework/OverrideBundles/
FinderSyncCollaborationFileProviderOverride.bundle/Contents/MacOS/
FinderSyncCollaborationFileProviderOverride (0x110e2ccd8). One of the
two will be used. Which one is undefined.
>

```