

Reproducible Research with Table Data

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```
require(moonBook)
require(ztable)
require(webr)
require(ggplot2)
options(ztable.type='latex')
```

mytable

```
result= mytable(sex~.,data=acs)
print(ztable(result,longtable=TRUE),type='latex')
```

	Female (N=287)	Male (N=570)	P
age	68.7 ± 10.7	60.6 ± 11.2	0.000
cardiogenicShock			0.136
No	275 (95.8%)	530 (93.0%)	
Yes	12 (4.2%)	40 (7.0%)	
entry			0.035
Femoral	119 (41.5%)	193 (33.9%)	
Radial	168 (58.5%)	377 (66.1%)	
Dx			0.012
NSTEMI	50 (17.4%)	103 (18.1%)	
STEMI	84 (29.3%)	220 (38.6%)	
Unstable Angina	153 (53.3%)	247 (43.3%)	
EF	56.3 ± 10.1	55.6 ± 9.4	0.387
height	153.8 ± 6.2	167.9 ± 6.1	0.000
weight	57.2 ± 9.3	68.7 ± 10.3	0.000
BMI	24.2 ± 3.6	24.3 ± 3.2	0.611
obesity			0.580
No	194 (67.6%)	373 (65.4%)	
Yes	93 (32.4%)	197 (34.6%)	
TC	188.9 ± 51.1	183.3 ± 45.9	0.124
LDLC	117.8 ± 41.2	116.0 ± 41.1	0.561
HDLC	39.0 ± 11.5	37.8 ± 10.9	0.145
TG	119.9 ± 76.2	127.9 ± 97.3	0.195
DM			0.077
No	173 (60.3%)	380 (66.7%)	
Yes	114 (39.7%)	190 (33.3%)	
HBP			0.000
No	83 (28.9%)	273 (47.9%)	
Yes	204 (71.1%)	297 (52.1%)	
smoking			0.000
Ex-smoker	49 (17.1%)	155 (27.2%)	
Never	209 (72.8%)	123 (21.6%)	
Smoker	29 (10.1%)	292 (51.2%)	

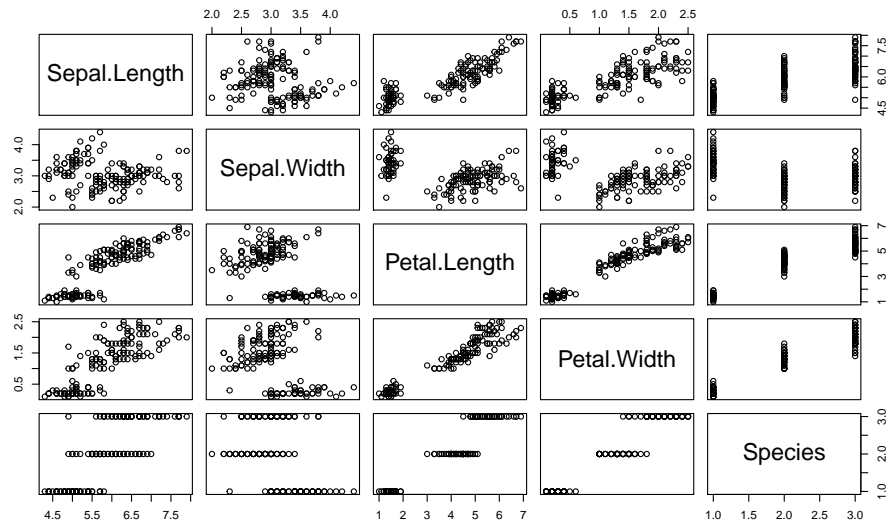
head(iris)

```
print(ztable( head(iris) ,longtable=TRUE),type='latex')
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.10	3.50	1.40	0.20	setosa
2	4.90	3.00	1.40	0.20	setosa
3	4.70	3.20	1.30	0.20	setosa
4	4.60	3.10	1.50	0.20	setosa
5	5.00	3.60	1.40	0.20	setosa
6	5.40	3.90	1.70	0.40	setosa

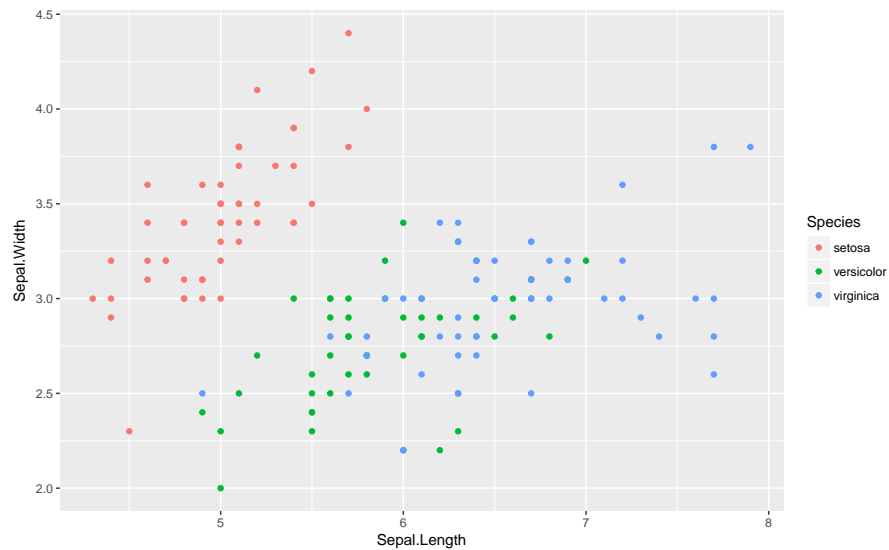
plot

```
plot(iris)
```



ggplot

```
ggplot(iris,aes(x=Sepal.Length,y=Sepal.Width,color=Species))+geom_point()
```



Regression Analysis

```
fit=lm(mpg~wt*hp,data=mtcars)
summary(fit)
```

Call:

```
lm(formula = mpg ~ wt * hp, data = mtcars)
```

Residuals:

Min	1Q	Median	3Q	Max
-3.0632	-1.6491	-0.7362	1.4211	4.5513

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	49.80842	3.60516	13.816	5.01e-14 ***
wt	-8.21662	1.26971	-6.471	5.20e-07 ***
hp	-0.12010	0.02470	-4.863	4.04e-05 ***
wt:hp	0.02785	0.00742	3.753	0.000811 ***

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

Residual standard error: 2.153 on 28 degrees of freedom

Multiple R-squared: 0.8848, Adjusted R-squared: 0.8724

F-statistic: 71.66 on 3 and 28 DF, p-value: 2.981e-13

Summary

```
summary(mtcars)
```

mpg	cyl	disp	hp
Min. :10.40	Min. :4.000	Min. : 71.1	Min. : 52.0
1st Qu.:15.43	1st Qu.:4.000	1st Qu.:120.8	1st Qu.: 96.5
Median :19.20	Median :6.000	Median :196.3	Median :123.0

Mean :20.09	Mean :6.188	Mean :230.7	Mean :146.7
3rd Qu.:22.80	3rd Qu.:8.000	3rd Qu.:326.0	3rd Qu.:180.0
Max. :33.90	Max. :8.000	Max. :472.0	Max. :335.0
drat	wt	qsec	vs
Min. :2.760	Min. :1.513	Min. :14.50	Min. :0.0000
1st Qu.:3.080	1st Qu.:2.581	1st Qu.:16.89	1st Qu.:0.0000
Median :3.695	Median :3.325	Median :17.71	Median :0.0000
Mean :3.597	Mean :3.217	Mean :17.85	Mean :0.4375
3rd Qu.:3.920	3rd Qu.:3.610	3rd Qu.:18.90	3rd Qu.:1.0000
Max. :4.930	Max. :5.424	Max. :22.90	Max. :1.0000
am	gear	carb	
Min. :0.0000	Min. :3.000	Min. :1.000	
1st Qu.:0.0000	1st Qu.:3.000	1st Qu.:2.000	
Median :0.0000	Median :4.000	Median :2.000	
Mean :0.4062	Mean :3.688	Mean :2.812	
3rd Qu.:1.0000	3rd Qu.:4.000	3rd Qu.:4.000	
Max. :1.0000	Max. :5.000	Max. :8.000	

Text

This document is an example of reproducible research using webr package.

The home page of this project is github.com/cardiomoon/webr.

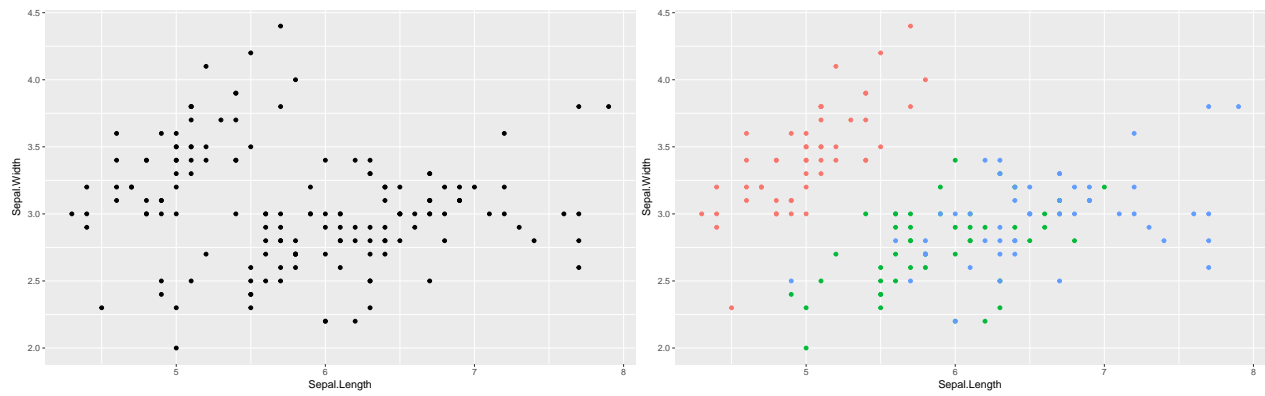
table

```
result= df2flectable(head(mtcars))
df=result$body$dataset
df=html2latex(df)
class(df)='data.frame'
print(ztable(df,longtable=TRUE),type='latex')
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.00	6.00	160.00	110.00	3.90	2.62	16.46	0.00	1.00	4.00	4.00
Mazda RX4 Wag	21.00	6.00	160.00	110.00	3.90	2.88	17.02	0.00	1.00	4.00	4.00
Datsun 710	22.80	4.00	108.00	93.00	3.85	2.32	18.61	1.00	1.00	4.00	1.00
Hornet 4 Drive	21.40	6.00	258.00	110.00	3.08	3.21	19.44	1.00	0.00	3.00	1.00
Hornet Sportabout	18.70	8.00	360.00	175.00	3.15	3.44	17.02	0.00	0.00	3.00	2.00
Valiant	18.10	6.00	225.00	105.00	2.76	3.46	20.22	1.00	0.00	3.00	1.00

Two ggplots

```
ggplot(iris,aes(Sepal.Length,Sepal.Width))+geom_point()
ggplot(iris,aes(Sepal.Length,Sepal.Width,colour=Species))+geom_point()+guides(colour=FALSE)
```



Two plots

```
hist(rnorm(1000))
plot(1:10)
```

