

# Statistics

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# Statistics

Now we are going to cover how to perform a variety of basic statistical tests in R.

- ▶ Correlation
- ▶ T-tests
- ▶ Linear Regression
- ▶ Logistic Regression
- ▶ Proportion tests
- ▶ Chi-squared
- ▶ Fisher's Exact Test

Note: We will be glossing over the statistical theory and “formulas” for these tests. There are plenty of resources online for learning more about these tests, as well as dedicated Biostatistics series at the School of Public Health

## Correlation

`cor()` performs correlation in R

```
cor(x, y = NULL, use = "everything",
     method = c("pearson", "kendall", "spearman"))
```

Like other functions, if there are NAs, you get NA as the result. But if you specify use only the complete observations, then it will give you correlation on the non-missing data.

```
> destfile = tempfile(fileext = ".rda")
> download.file("http://www.aejaffe.com/winterR_2016/data/circ2.rda", destfile)
> load(destfile)
> cor(circ2$orangeAverage, circ2$purpleAverage)
```

```
[1] NA
```

```
> cor(circ2$orangeAverage, circ2$purpleAverage, use="complete")
```

```
[1] 0.9195356
```

## Correlation

You can also get the correlation between matrix columns

```
> signif(cor(circ2[,grep("Average",names(circ2))], use="com
```

	orangeAverage	purpleAverage	greenAverage	bannerAverage
orangeAverage	1.000	0.908	0.840	
purpleAverage	0.908	1.000	0.867	
greenAverage	0.840	0.867	1.000	
bannerAverage	0.545	0.521	0.453	

Or between columns of two matrices, column by column.

```
> signif(cor(circ2[,3:4],circ2[,5:6], use="complete.obs"),3)
```

	greenAverage	bannerAverage
orangeAverage	0.840	0.545
purpleAverage	0.867	0.521

## Correlation

You can also use `cor.test()` to test for whether correlation is significant (ie non-zero). Note that linear regression may be better, especially if you want to regress out other confounders.

```
> ct= cor.test(circ2$orangeAverage,  
+               circ2$purpleAverage, use="complete.obs")  
> ct
```

Pearson's product-moment correlation

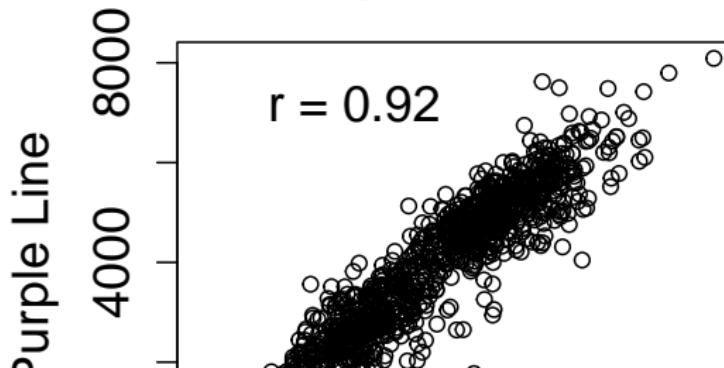
```
data: circ2$orangeAverage and circ2$purpleAverage  
t = 73.656, df = 991, p-value < 2.2e-16  
alternative hypothesis: true correlation is not equal to 0  
95 percent confidence interval:  
 0.9093438 0.9286245  
sample estimates:  
      cor  
 0.9195256
```

## Correlation

Note that you can add the correlation to a plot, via the `legend()` function.

```
> plot(circ2$orangeAverage, circ2$purpleAverage,  
+       xlab="Orange Line", ylab="Purple Line",  
+       main="Average Ridership", cex.axis=1.5,  
+       cex.lab=1.5, cex.main=2)  
> legend("topleft", paste("r =", signif(ct$estimate,3)), b
```

## Average Ridership



## Correlation

For many of these testing result objects, you can extract specific slots/results as numbers, as the ct object is just a list.

```
> # str(ct)
> names(ct)
```

```
[1] "statistic"    "parameter"    "p.value"      "estimate"
[6] "alternative"  "method"       "data.name"    "conf.int"
```

```
> ct$statistic
```

```
t
73.65553
```

```
> ct$p.value
```

```
[1] 0
```

## T-tests

The T-test is performed using the `t.test()` function, which essentially tests for the difference in means of a variable between two groups.

In this syntax, `x` and `y` are the column of data for each group.

```
> tt = t.test(circ2$orangeAverage, circ2$purpleAverage)  
> tt
```

Welch Two Sample t-test

```
data: circ2$orangeAverage and circ2$purpleAverage  
t = -17.076, df = 1984, p-value < 2.2e-16  
alternative hypothesis: true difference in means is not equal to zero  
95 percent confidence interval:  
 -1096.7602 -870.7867  
sample estimates:  
mean of x mean of y
```

## T-tests

`t.test` saves a lot of information: the difference in means estimate, confidence interval for the difference `conf.int`, the p-value `p.value`, etc.

```
> names(tt)
```

```
[1] "statistic"    "parameter"    "p.value"        "conf.int"  
[6] "null.value"   "alternative"  "method"         "data.name"
```

## T-tests

You can also use the 'formula' notation. In this syntax, it is  $y \sim x$ , where  $x$  is a factor with 2 levels or a binary variable and  $y$  is a vector of the same length.

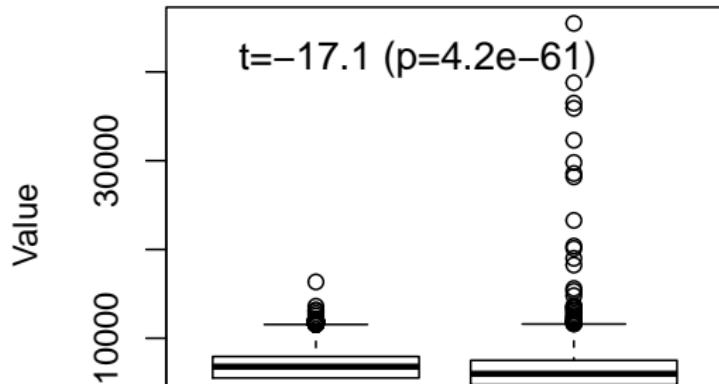
```
> http_data_dir = "http://www.aejaffe.com/winterR_2016/data"
>
> cars = read.csv(paste0(http_data_dir, "kaggleCarAuction.csv"))
+           as.is=TRUE)
> tt2 = t.test(VehBCost~IsBadBuy, data=cars)
> tt2$estimate
```

mean in group 0	mean in group 1
6797.077	6259.274

## T-tests

You can add the t-statistic and p-value to a boxplot.

```
> boxplot(VehBCost~IsBadBuy, data=cars,
+           xlab="Bad Buy", ylab="Value")
> leg = paste("t=", signif(tt$statistic,3),
+             " (p=", signif(tt$p.value,3),")", sep="")
> legend("topleft", leg, cex=1.2, bty="n")
```



# Linear Regression

Now we will briefly cover linear regression. I will use a little notation here so some of the commands are easier to put in the proper context.

$$y_i = \alpha + \beta x_i + \varepsilon_i$$

where:

- ▶  $y_i$  is the outcome for person i
- ▶  $\alpha$  is the intercept
- ▶  $\beta$  is the slope
- ▶  $x_i$  is the predictor for person i
- ▶  $\varepsilon_i$  is the residual variation for person i

# Linear Regression

The R version of the regression model is:

$$y \sim x$$

where:

- ▶  $y$  is your outcome
- ▶  $x$  is/are your predictor(s)

# Linear Regression

For a linear regression, when the predictor is binary this is the same as a t-test:

```
> fit = lm(VehBCost~IsBadBuy, data=cars)  
> fit
```

Call:

```
lm(formula = VehBCost ~ IsBadBuy, data = cars)
```

Coefficients:

(Intercept)	IsBadBuy
6797.1	-537.8

'(Intercept)' is  $\alpha$

'IsBadBuy' is  $\beta$

## Linear Regression

The `summary` command gets all the additional information (p-values, t-statistics, r-square) that you usually want from a regression.

```
> sfit = summary(fit)
> print(sfit)
```

Call:

```
lm(formula = VehBCost ~ IsBadBuy, data = cars)
```

Residuals:

Min	1Q	Median	3Q	Max
-6258	-1297	-27	1153	39210

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	6797.077	6.953	977.61	<2e-16 ***
IsBadBuy	-537.803	19.826	-27.13	<2e-16 ***

# Linear Regression

The coefficients from a summary are the coefficients, standard errors, t-statistics, and p-values for all the estimates.

```
> names(sfit)
```

```
[1] "call"           "terms"          "residuals"       "coefficients"  
[5] "aliased"        "sigma"          "df"              "r.squared"  
[9] "adj.r.squared"  "fstatistic"     "cov.unscaled"
```

```
> sfit$coef
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	6797.0774	6.952728	977.61299	0.00000e+00
IsBadBuy	-537.8033	19.825525	-27.12681	3.01661e-161

# Linear Regression

We'll look at vehicle odometer value by vehicle age:

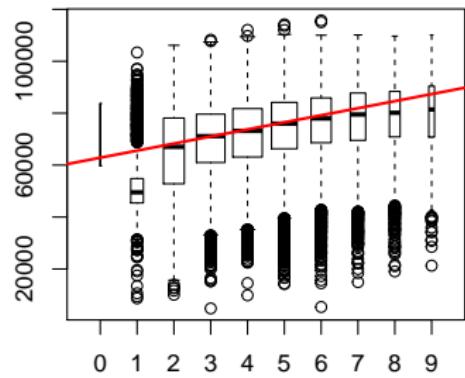
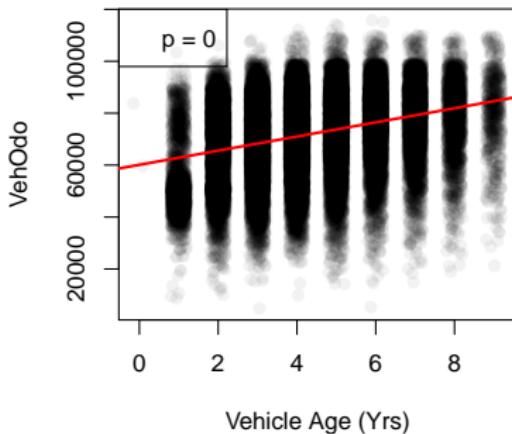
```
fit = lm(VehOdo~VehicleAge, data=cars)
print(fit)
```

```
##
## Call:
## lm(formula = VehOdo ~ VehicleAge, data = cars)
##
## Coefficients:
## (Intercept)  VehicleAge
##           60127          2723
```

# Linear Regression

We can visualize the vehicle age/odometer relationship using scatter plots or box plots (with regression lines). The function `abline` will plot the regression line on the plot.

```
> library(scales) # we need this for the alpha command - m  
> par(mfrow=c(1,2))  
> plot(VehOdo ~ jitter(VehicleAge,amount=0.2), data=cars, p  
+       col = alpha("black",0.05), xlab="Vehicle Age (Yrs)")  
> abline(fit, col="red",lwd=2)  
> legend("topleft", paste("p =",summary(fit)$coef[2,4]))  
> boxplot(VehOdo ~ VehicleAge, data=cars, varwidth=TRUE)  
> abline(fit, col="red",lwd=2)
```



## Linear Regression

Note that you can have more than 1 predictor in regression models. The interpretation for each slope is change in the predictor corresponding to a one-unit change in the outcome, holding all other predictors constant.

```
> fit2 = lm(VehOdo ~ IsBadBuy + VehicleAge, data=cars)  
> summary(fit2)
```

Call:

```
lm(formula = VehOdo ~ IsBadBuy + VehicleAge, data = cars)
```

Residuals:

Min	1Q	Median	3Q	Max
-70856	-9490	1390	10311	41193

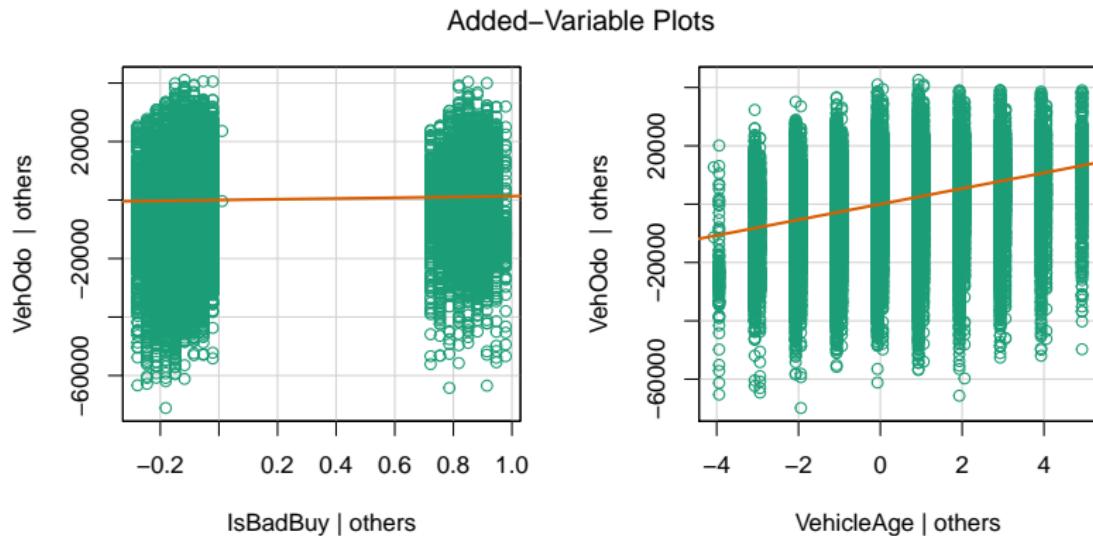
Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
--	----------	------------	---------	----------

# Linear Regression

Added-Variable plots can show you the relationship between a variable and outcome after adjusting for other variables. The function `avPlots` from the `car` package can do this:

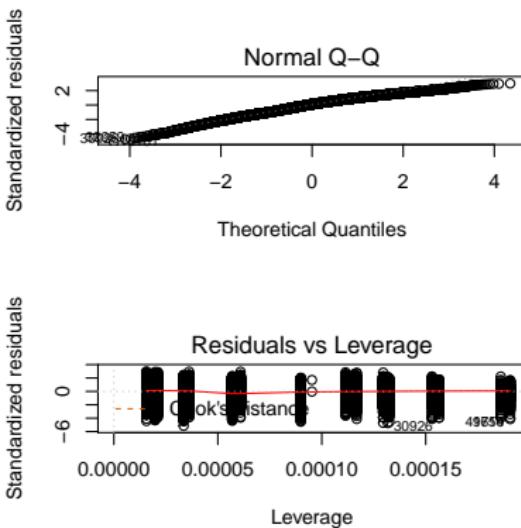
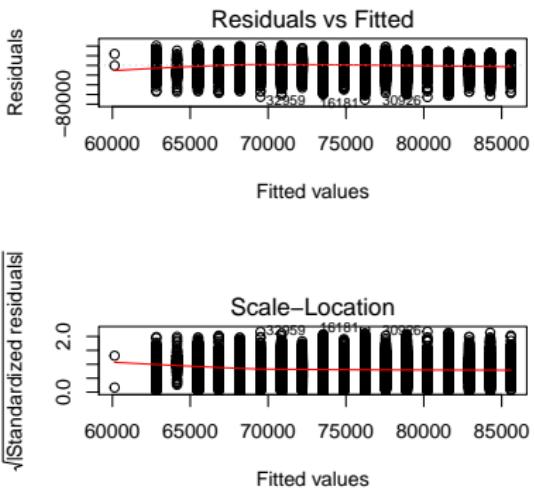
```
> library(car)  
> avPlots(fit2)
```



# Linear Regression

Plot on an `lm` object will do diagnostic plots. Residuals vs. Fitted should have no discernable shape (the red line is the smoother), the qqplot shows how well the residuals fit a normal distribution, and Cook's distance measures the influence of individual points.

```
> par(mfrow=c(2,2))  
> plot(fit2, ask= FALSE)
```



## Linear Regression

Factors get special treatment in regression models - lowest level of the factor is the comparison group, and all other factors are relative to its values.

```
> fit3 = lm(VehOdo ~ factor(TopThreeAmericanName), data=car)
> summary(fit3)
```

Call:

```
lm(formula = VehOdo ~ factor(TopThreeAmericanName), data =
```

Residuals:

Min	1Q	Median	3Q	Max
-71947	-9634	1532	10472	45936

Coefficients:

	Estimate	Std. Error	t value
(Intercept)	68248.48	92.98	733.9
factor(Ford) (Intercept)	1762.42	172.87	10.1

## Logistic Regression and GLMs

Generalized Linear Models (GLMs) allow for fitting regressions for non-continuous/normal outcomes. The `glm` has similar syntax to the `lm` command. Logistic regression is one example.

```
> glmfit = glm(IsBadBuy ~ VehOdo + VehicleAge, data=cars,  
> summary(glmfit)
```

Call:

```
glm(formula = IsBadBuy ~ VehOdo + VehicleAge, family = binomial,  
     data = cars)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.9943	-0.5481	-0.4534	-0.3783	2.6318

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	3.776	0.324	11.654	0.000
VehOdo	-0.003	0.001	-2.500	0.013
VehicleAge	-0.001	0.001	-0.833	0.409

# Logistic Regression

Note the coefficients are on the original scale, we must exponentiate them for odds ratios:

```
> exp(coef(glmfit))
```

(Intercept)	VehOdo	VehicleAge
0.02286316	1.00000834	1.30748911

## Proportion tests

`prop.test()` can be used for testing the null that the proportions (probabilities of success) in several groups are the same, or that they equal certain given values.

```
prop.test(x, n, p = NULL,  
          alternative = c("two.sided", "less", "greater"),  
          conf.level = 0.95, correct = TRUE)
```

```
> prop.test(x=15, n =32)
```

1-sample proportions test with continuity correction

```
data: 15 out of 32, null probability 0.5  
X-squared = 0.03125, df = 1, p-value = 0.8597  
alternative hypothesis: true p is not equal to 0.5  
95 percent confidence interval:  
 0.2951014 0.6496695
```

## Chi-squared tests

`chisq.test()` performs chi-squared contingency table tests and goodness-of-fit tests.

```
chisq.test(x, y = NULL, correct = TRUE,  
           p = rep(1/length(x), length(x)), rescale.p = FAI  
           simulate.p.value = FALSE, B = 2000)
```

```
> tab = table(cars$IsBadBuy, cars$IsOnlineSale)  
> tab
```

	0	1
0	62375	1632
1	8763	213

## Chi-squared tests

You can also pass in a table object (such as tab here)

```
> cq=chisq.test(tab)  
> cq
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: tab  
X-squared = 0.92735, df = 1, p-value = 0.3356
```

```
> names(cq)
```

```
[1] "statistic" "parameter" "p.value"      "method"       "data.name"  
[7] "expected"   "residuals"  "stdres"
```

```
> cq$p.value
```

## Chi-squared tests

Note that does the same test as prop.test, for a 2x2 table.

```
> chisq.test(tab)
```

Pearson's Chi-squared test with Yates' continuity corre

data: tab

X-squared = 0.92735, df = 1, p-value = 0.3356

```
> prop.test(tab)
```

2-sample test for equality of proportions with continuity correction

data: tab

X-squared = 0.92735, df = 1, p-value = 0.3356

## Fisher's Exact test

`fisher.test()` performs contingency table test using the hypogeometric distribution (used for small sample sizes).

```
fisher.test(x, y = NULL, workspace = 200000, hybrid = FALSE,
            control = list(), or = 1, alternative = "two.sided",
            conf.int = TRUE, conf.level = 0.95,
            simulate.p.value = FALSE, B = 2000)
```

```
> fisher.test(tab)
```

Fisher's Exact Test for Count Data

```
data: tab
p-value = 0.3324
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
0.8001727 1.0742114
sample estimates:
```

# Probability Distributions

Sometimes you want to generate data from a distribution (such as normal), or want to see where a value falls in a known distribution. R has these distributions built in:

- ▶ Normal
- ▶ Binomial
- ▶ Beta
- ▶ Exponential
- ▶ Gamma
- ▶ Hypergeometric
- ▶ etc

# Probability Distributions

Each has 4 options:

- ▶ r for random number generation [e.g. `rnorm()`]
- ▶ d for density [e.g. `dnorm()`]
- ▶ p for probability [e.g. `pnorm()`]
- ▶ q for quantile [e.g. `qnorm()`]

```
> rnorm(5)
```

```
[1] 0.03555676 -1.30063209 1.24466236 0.30948683 0.9268
```

# Sampling

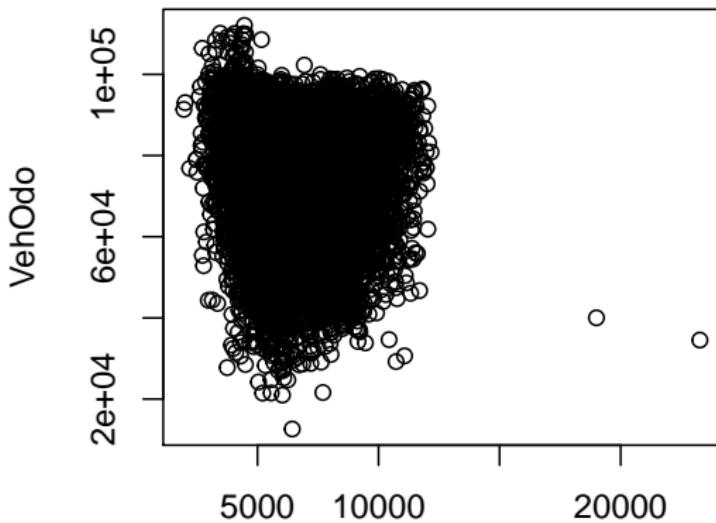
The `sample()` function is pretty useful for permutations

```
> sample(1:10, 5, replace=FALSE)
```

```
[1] 6 4 1 10 5
```

Also, if you want to only plot a subset of the data (for speed/time or overplotting)

```
> samp.cars <- cars[ sample(nrow(cars), 10000), ]  
> plot(VehODO ~ jitter(VehBCost, amount=0.3), data= samp.cars)
```



jitter(VehBCost, amount = 0.3)