# Linear regression

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# Let’s do some actual analysis!

Now that we’ve got the hang of some R commands, let’s do some real analysis

# Linear regression:

- explains the linear relationship between dependent (Y) and independent (X) variables
- “line of best fit” to data
- a “simple” linear regression is equivalent to a correlation
- can be considered *supervised* machine learning technique (see here)
  - the model learns from known data, and can be used to predict
  - sometimes we are looking for trends and don’t care about predictions

# Linear regression

linear regression takes the linear equation of:

$$Y = mX + b$$

But we're going to use it more like:

$$\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i + \epsilon_i$$

where:
$\hat{y}_i =$ predicted response for expeimental unit $i$
$x_i =$ predictor (or independent variable) of experimental unit $i$
$\hat{\beta}_0 =$ is expected value when $x_i = 0$ (intercept)
$\hat{\beta}_1 =$ slope
$\epsilon =$ some error, because models are never perfect!

# $\beta_0$ and $\beta_1$

$\beta_0$ and $\beta_1$ are unknown.
We will estimate these coefficients from known data. To do this, we need to estimate a line of best fit than minimizes error

# An example: Does head size predict brain size?

```r
library(data.table)
# we've already loaded this package...
head_brain <- fread(
  'http://www.stat.ufl.edu/~winner/data/brainhead.dat')
head(head_brain)
```

```
##    V1 V2   V3   V4
## 1:  1  1 4512 1530
## 2:  1  1 3738 1297
## 3:  1  1 4261 1335
## 4:  1  1 3777 1282
## 5:  1  1 4177 1590
## 6:  1  1 3585 1300
```

# Brain and head size data

Columns are:

1. gender (1 = male, 2 = female)
2. age (1 = 20-46, 2 = 46+)
3. head size ($cm^3$)
4. brain weight (g)

```r
# name columns to reflect what they are
colnames(head_brain) = c("gender", "age", "head", "brain")
```

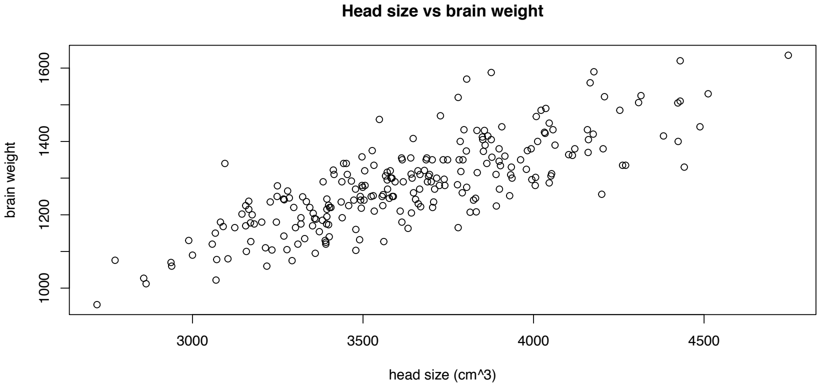
# Change data type

```r
head_brain <- as.data.frame(head_brain)

head_brain$gender <- as.factor(head_brain$gender)
head_brain$age <- as.factor(head_brain$age)
head_brain$head <- as.numeric(head_brain$head)
head_brain$brain <- as.numeric(head_brain$brain)
```

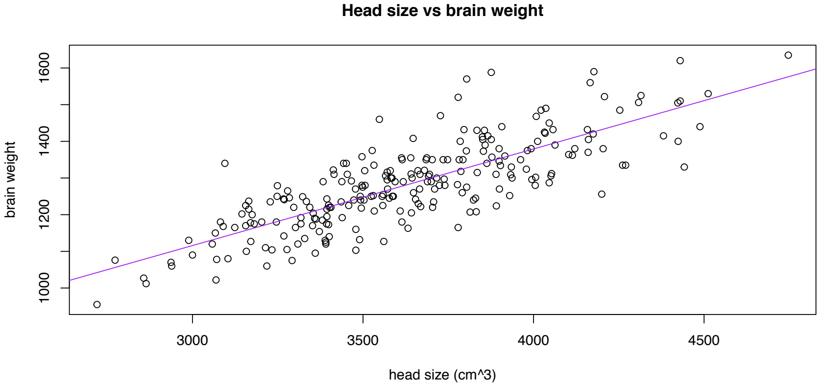
# Plot data

```r
plot(head_brain$head, head_brain$brain,
     main="Head size vs brain weight",
     xlab = "head size (cm^3)", ylab = "brain weight")
```



# How to do a linear regression

```r
set.seed(519)
lm1 = lm(brain ~ head, data=head_brain)
plot(head_brain$head, head_brain$brain,
     main="Head size vs brain weight",
     xlab = "head size (cm^3)", ylab = "brain weight")
abline(lm1, col="purple")
```



# Summary of the linear regression

Here's a good explanation of the summary in MUCH more detail.

```r
summary(lm1)
```

```
##
## Call:
## lm(formula = brain ~ head, data = head_brain)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -175.98  -49.76   -1.76   46.60  242.34
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 325.57342   47.14085   6.906 4.61e-11 ***
## head          0.26343    0.01291  20.409  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 72.43 on 235 degrees of freedom
## Multiple R-squared:  0.6393, Adjusted R-squared:  0.6378
## F-statistic: 416.5 on 1 and 235 DF,  p-value: < 2.2e-16
```

# Summary output gives a lot of information

1. Info about distrubution of residuals (errors)
2. The estimates of our coefficients
3. Standard error of coefficient estimates
   - square root of the variance
   - $\sqrt{\sigma}^2$
4. t-values (coefficient estimates/standard error)
5. $R^2 =$ (want closer to 1)
6. p-values (yuck!)
   - testing if your coefficient $= 0$

# Quick residual check

What is a residual?

```
Residuals

Min      1Q  Median      3Q     Max  -175.98  -49.76
-1.76   46.60  242.34
```

- Median should be around 0
- 1Q and 3Q should be roughly of same absolute magnitube

# Linear equation with coefficients

- $\beta_0$ = intercept = 325.57
- $\beta_1$ = head size coefficient = 0.26

$$\hat{y}_i = 325.57 + 0.26x_i + \epsilon_i$$

What does this mean in actual words?

# Use confidence intervals instead of p-values

```r
confint(lm1, level=0.95) #95% confidence interval
```

```
##                   2.5 %      97.5 %
## (Intercept) 232.7007553 418.4460868
## head          0.2380003   0.2888584
```

# We have more information than just head size!

We also have age range and sex!
We can use this information to potentially improve our regression by using a multiple linear regression model.

Here's a good tutorial.

# Multiple linear regression

First, let's change out age and sex categories into 0s and 1s. (This is the convention in programming)

```r
head_brain$gender = as.factor(ifelse(head_brain$gender == 1, 1, 0))
# if head_brain$gender[i] == 1
#     head_brain$gender[i] == 1
# else
#     head_brain$gender[i] == 0
head_brain$age = as.factor(ifelse(head_brain$age == 1, 1, 0))
```

# Does age have an effect on brain size?

We have some options on possible formulas for the linear regression:

- brain ∼ head + age
  - $\hat{brain}_i = \hat{\beta}_0 + \hat{\beta}_1 head_i + \hat{\beta}_2 age_i + \epsilon_i$
- brain ∼ head:age
  - $\hat{brain}_i = \hat{\beta}_0 + \hat{\beta}_2 age_i head_i + \epsilon_i$
- brain ∼ head*age = brain ∼ head + age + head x age
  - $\hat{brain}_i = \hat{\beta}_0 + \hat{\beta}_1 head_i + \hat{\beta}_2 age_i + \hat{\beta}_2 age_i head_i + \epsilon_i$

```r
lm2 = lm(brain ~ head + age, data=head_brain)
lm3 = lm(brain ~ head:age, data=head_brain)
lm4 = lm(brain ~ head * age, data=head_brain)
```

# How can we interpret this?

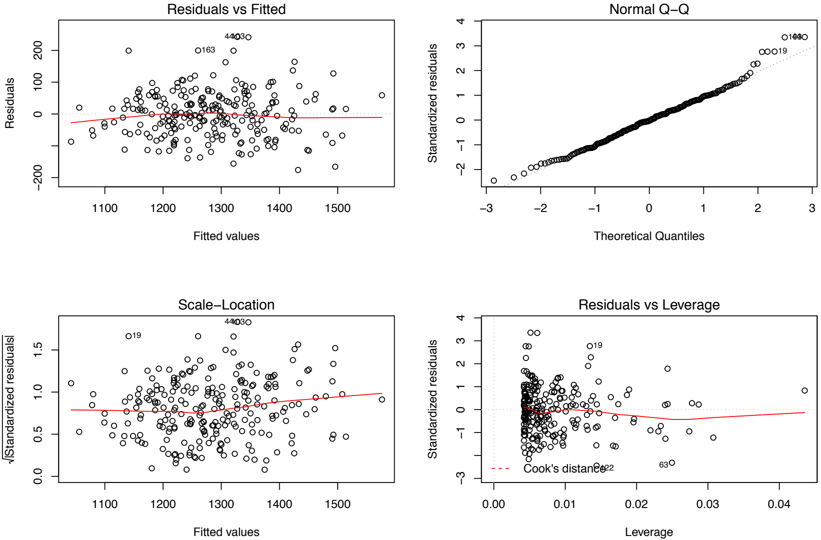
Interactions mean that slopes is different for each age category and each head size.

# Evaluate

How can we evaluate these models?

# Do these models meet the asumptions of linear models?

```r
par(mfrow=c(2,2))
plot(lm1)
```



# Diagnostic plot

- Residuals vs. Fitted
  - look for residuals randomly distributed around 0.
- Q-Q plot
  - used to look for normality of residuals
  - want the points to follow the diagonal line.
- Scale-Location plot
  - Similar to residuals vs fitted.
- Residuals vs. Leverage plot
  - Was our model driven by outliers?
    - Cook's distance lines would be visible (they aren't right now)
    - Data points driving the model would be labeled
    - If this happens, try removing the outliers.

*PS. http://data.library.virginia.edu/diagnostic-plots/ is helpful for interpretting these plots.*

# Predictions

What if we are given new data, and want to make predictions from our models?

```r
new_data = data.frame(gender = as.factor(c(1,1,0,0)),
                      age = as.factor(c(0,1,0,1)),
                      head = as.numeric(c(2265, 999, 2775, 9275)))
print(new_data)
```

```
##   gender age head
## 1      1   0 2265
## 2      1   1  999
## 3      0   0 2775
## 4      0   1 9275
```

# Predictions

```
lm1_pred <- predict(lm1,newdata=new_data,
                    interval="confidence", level=.95)
lm2_pred <- predict(lm2,newdata=new_data,
                    interval="confidence", level=.95)
lm3_pred <- predict(lm3,newdata=new_data,
                    interval="confidence", level=.95)
lm4_pred<- predict(lm4,newdata=new_data,
                   interval="confidence", level=.95)
```

# Predictions

To see our predictions...

How do they compare?

```
print(lm1_pred)
print(lm2_pred)
print(lm3_pred)
print(lm4_pred)
```

# Can we test which model has the best predictions?

How can we do this?

# Acknowledgements

This document was inspired by: this tutorial