

brains

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brains

reference: McElreath, Statistical Rethinking, chap 6, pp.165-207

```
library(rethinking)
library(ggplot2)
```

hominid brains

data

```
## R code 6.1
sppnames <- c( "afarensis", "africanus", "habilis", "boisei",
              "rudolfensis", "ergaster", "sapiens" )
brainvolcc <- c( 438 , 452 , 612, 521, 752, 871, 1350 )
masskg <- c( 37.0 , 35.5 , 34.5 , 41.5 , 55.5 , 61.0 , 53.5 )
d <- data.frame( species=sppnames , brain=brainvolcc , mass=masskg )
str(d)

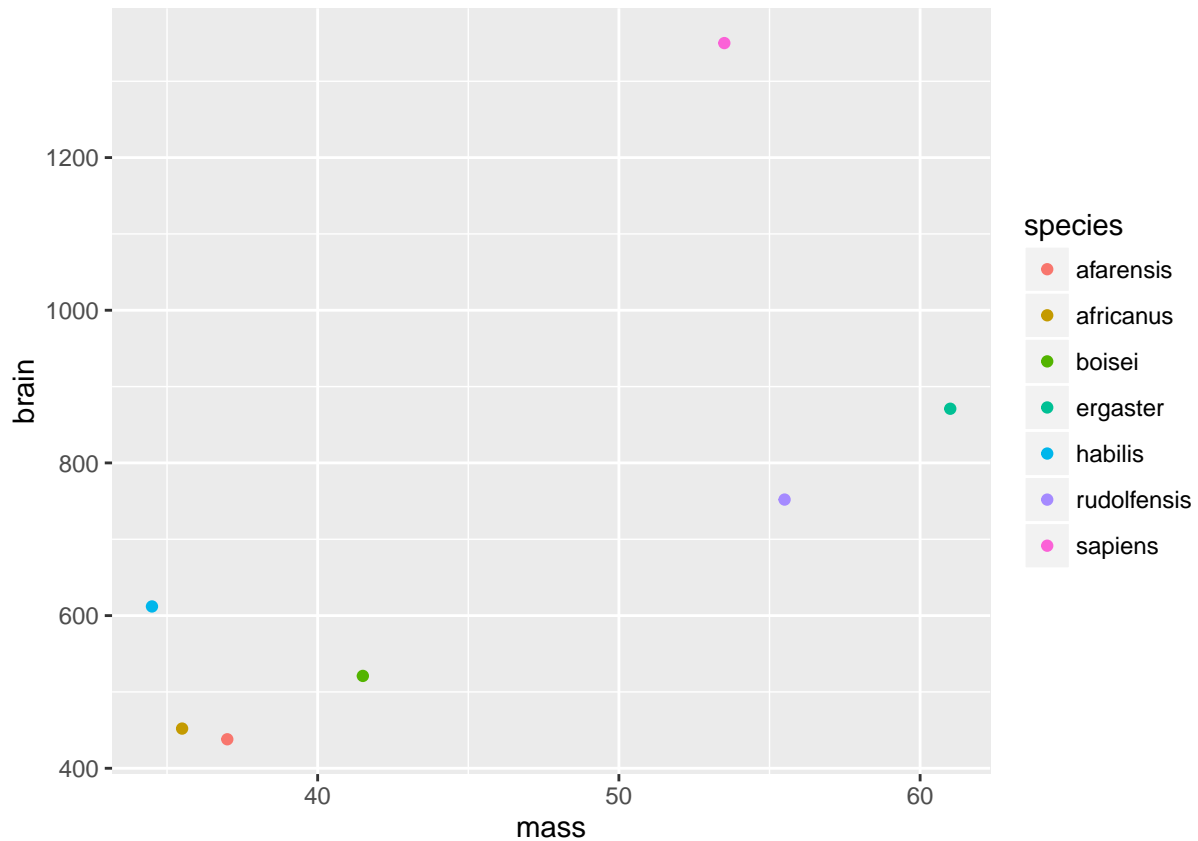
## 'data.frame': 7 obs. of 3 variables:
## $ species: Factor w/ 7 levels "afarensis","africanus",...: 1 2 5 3 6 4 7
## $ brain : num 438 452 612 521 752 871 1350
## $ mass : num 37 35.5 34.5 41.5 55.5 61 53.5
```

exploratory data analysis

```
d2 <- d
d2$species <- factor(d2$species)
str(d2)

## 'data.frame': 7 obs. of 3 variables:
## $ species: Factor w/ 7 levels "afarensis","africanus",...: 1 2 5 3 6 4 7
## $ brain : num 438 452 612 521 752 871 1350
## $ mass : num 37 35.5 34.5 41.5 55.5 61 53.5

ggplot(d2, aes(x = mass, y = brain, color = species)) +
  geom_point(shape = 19)
```



models

```
## R code 6.2
m6.1 <- lm( brain ~ mass , data=d )
options(show.signif.stars = FALSE)
summary(m6.1)
```

```
##
## Call:
## lm(formula = brain ~ mass, data = d)
##
## Residuals:
##      1      2      3      4      5      6      7
## -99.86 -54.83 125.86 -109.96 -168.60 -163.39  470.77
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -227.629    439.794  -0.518  0.6268
## mass         20.689     9.436   2.192  0.0798
##
## Residual standard error: 252.1 on 5 degrees of freedom
## Multiple R-squared:  0.4902, Adjusted R-squared:  0.3882
## F-statistic: 4.807 on 1 and 5 DF, p-value: 0.07985
```

```
## R code 6.3
1 - var(resid(m6.1))/var(d$brain)
```

```

## [1] 0.490158
## R code 6.4
m6.2 <- lm( brain ~ mass + I(mass^2) , data=d )

## R code 6.5
m6.3 <- lm( brain ~ mass + I(mass^2) + I(mass^3) , data=d )
m6.4 <- lm( brain ~ mass + I(mass^2) + I(mass^3) + I(mass^4) ,
  data=d )
m6.5 <- lm( brain ~ mass + I(mass^2) + I(mass^3) + I(mass^4) +
  I(mass^5) , data=d )
m6.6 <- lm( brain ~ mass + I(mass^2) + I(mass^3) + I(mass^4) +
  I(mass^5) + I(mass^6) , data=d )

## R code 6.6
m6.7 <- lm( brain ~ 1 , data=d )

## R code 6.7
# d.new <- d[ -i , ]

## R code 6.8
plot( brain ~ mass , d , col="slateblue" )
for ( i in 1:nrow(d) ) {
  d.new <- d[ -i , ]
  m0 <- lm( brain ~ mass, d.new )
  abline( m0 , col=col.alpha("black",0.5) )
}

```

