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Contents

Goals

- Advanced simulation
- Practice with visualization

Advanced simulation

- Putting code into a function
- A factorial design?

Let's make it a function

- Functions help automate routines
- Parts of a function:
  - Input parameters
    - Defaults or not
  - Output(s)
- `My.function.name <- function(my.param1, my.param2 = "cool")`

```
# define global constants from prior simulation
sample.n = 200
beta0 = 36
beta1 = .33
sigma = 10
min.x = 80
max.x = 250
```

```r
Height.weight.sim <- function(sample.n = 200, beta0 = 36, beta1 = .33, sigma = 10, min.x = 80, max.x = 2
  # Calculates correlation, intercept, slope estimates for
  # linear relation between two variables

  # Args:
  #   sample.n: Number of sample poings, default is 200
  #   beta0: Intercept, default is 36 (inches)
  #   beta1: Slope, default is .33
  #   sigma: Standard deviation of error
  #   min.x: Minimum value for x (weight in lbs)
  #   max.x: Maximum value for x (weight in lbs)
  #
  # Returns:
  #   Named array with values
  #   beta0
  #   beta1
  #   beta0.lo: 2.5% quantile for intercept
  #   beta0.hi  97.5% quantile for intercept
  #   beta1.lo  2.5% quantile for slope
  #   beta1.hi  97.5% quantile for slope

  w <- runif(n = sample.n, min = min.x, max = max.x)

  h.pred <- rep(x = beta0, n = sample.n) + beta1 * w
  h <- h.pred + rnorm(n = sample.n, mean = 0, sd = sigma)
  height.weight <- data.frame(inches = h, lbs = w)

  fit <- lm(formula = inches ~ lbs, data = height.weight)
  ci <- confint(fit)

  # Create output vector with named values
  (results <- c("beta0" = beta0,
    "beta1"= beta1,
    "beta0.lo" = ci[1,1],
    "beta0.hi" = ci[1,2],
    "beta1.lo" = ci[2,1],
    "beta1.hi" = ci[2,2]))
}
```

```r
# Defaults only
Height.weight.sim()
```

```
##      beta0      beta1   beta0.lo   beta0.hi   beta1.lo   beta1.hi
## 36.0000000  0.3300000 33.9863672 43.4718002  0.2863424  0.3418117
```

```r
# Larger sample size
Height.weight.sim(sample.n = 500)
```

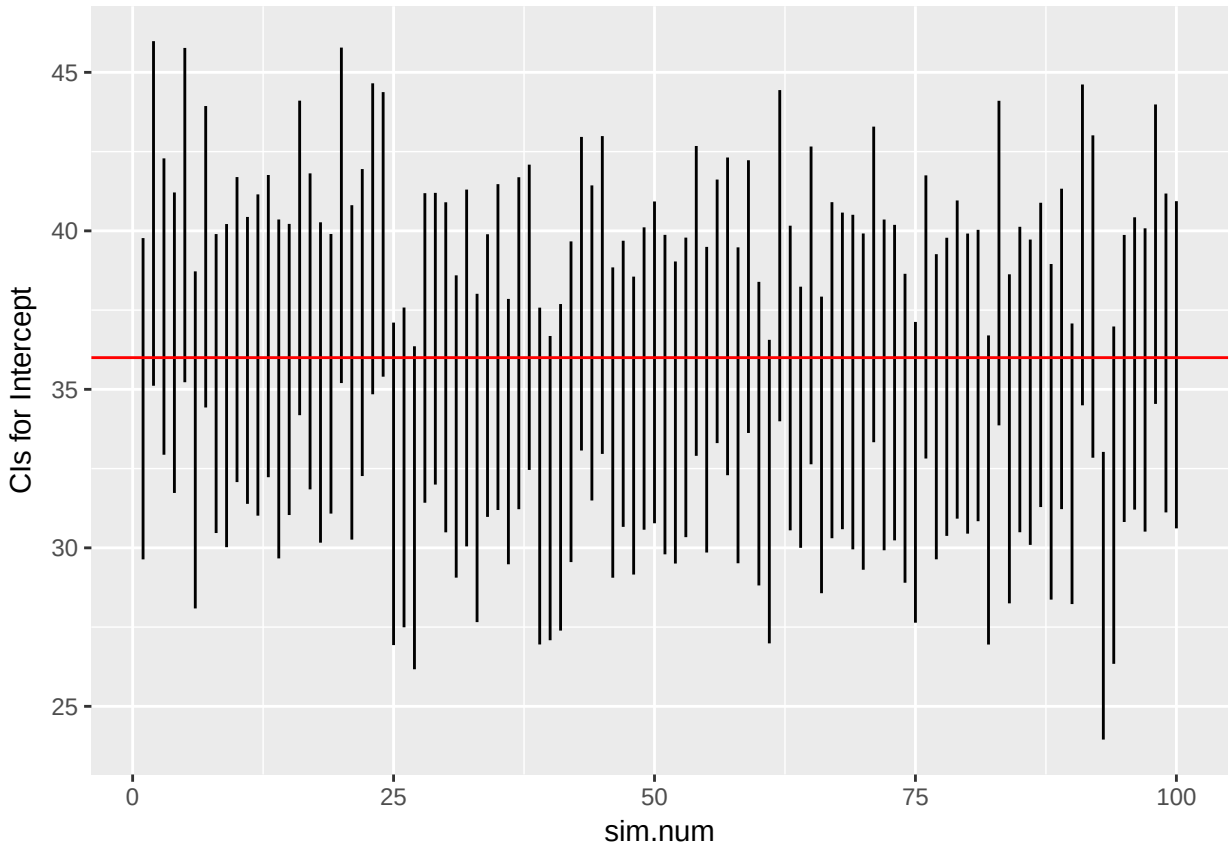
```
##      beta0      beta1   beta0.lo   beta0.hi   beta1.lo   beta1.hi
## 36.0000000  0.3300000 34.0626272 40.3748579  0.3024982  0.3389162
```

Doing a series of simulations

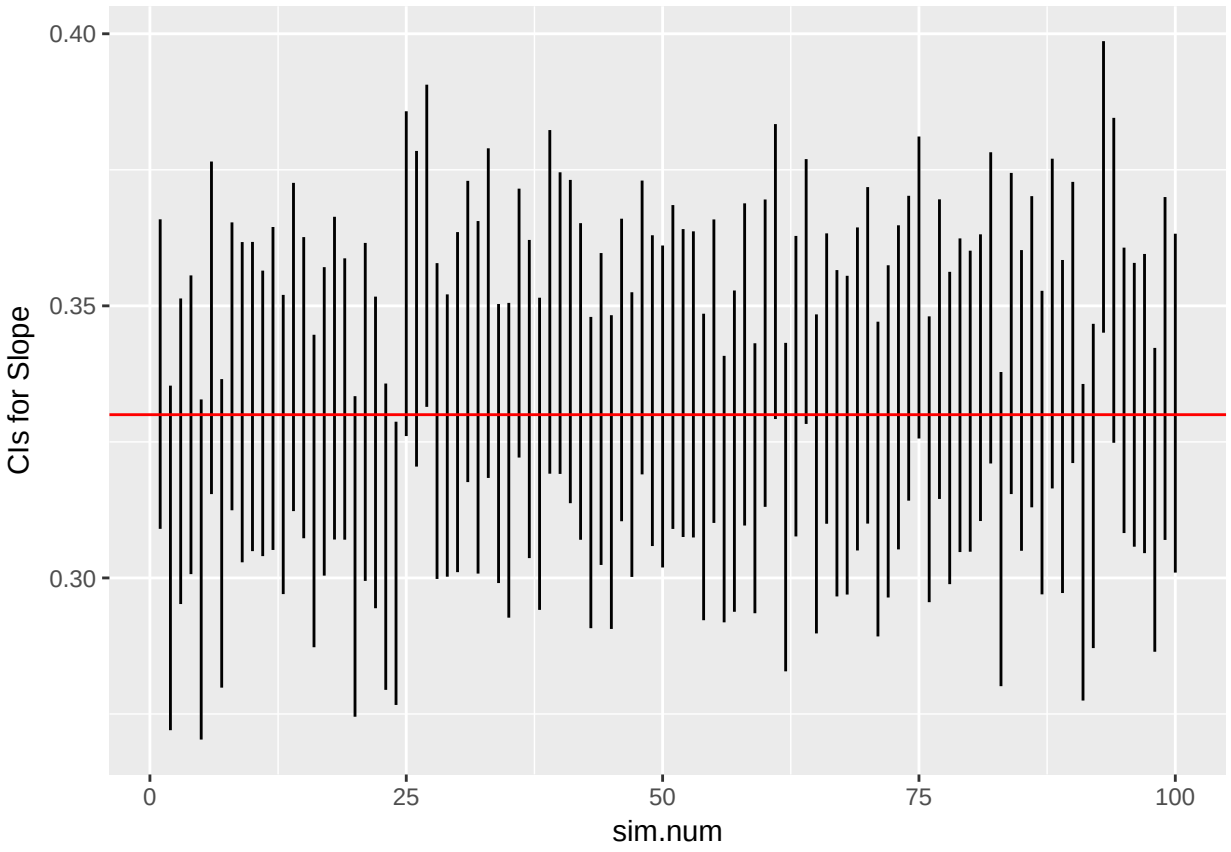
- Goal: run our function a number of times, collect the results

```
n.simulations = 100
n.vars = 6 # variables Height.weight.sim() outputs

# initialize output array
height.weight.sim.data <- array(0, dim=c(n.simulations, n.vars))

# Repeat Height.weight.sim() n.simulations times
for (i in 1:n.simulations) {
  height.weight.sim.data[i,] <- Height.weight.sim()
  }
```

```
# Easier to make simulation data a data frame
ht.wt.sims <- as.data.frame(height.weight.sim.data)

# rename variables to be more easily read
names(ht.wt.sims) <- c("beta0", "beta1",
                       "beta0.lo", "beta0.hi",
                       "beta1.lo", "beta1.hi")

# Add a variable to index the simulation number
ht.wt.sims$sim.num <- 1:n.simulations

# Plot beta0 min and max (now called V3, V4)
ggplot(data = ht.wt.sims) +
  aes(x = sim.num) +
  geom_linerange(mapping = aes(ymin=beta0.lo,
                               ymax=beta0.hi)) +
  ylab("CIs for Intercept") +
  geom_hline(yintercept = beta0, color = "red")
```




```
# Plot beta1 min and max (now called V5, V6)
ggplot(data = ht.wt.sims) +
  aes(x = sim.num) +
  geom_linerange(mapping = aes(ymin=beta1.lo,
                               ymax=beta1.hi)) +
  ylab("CIs for Slope") +
  geom_hline(yintercept = beta1, color = "red")
```

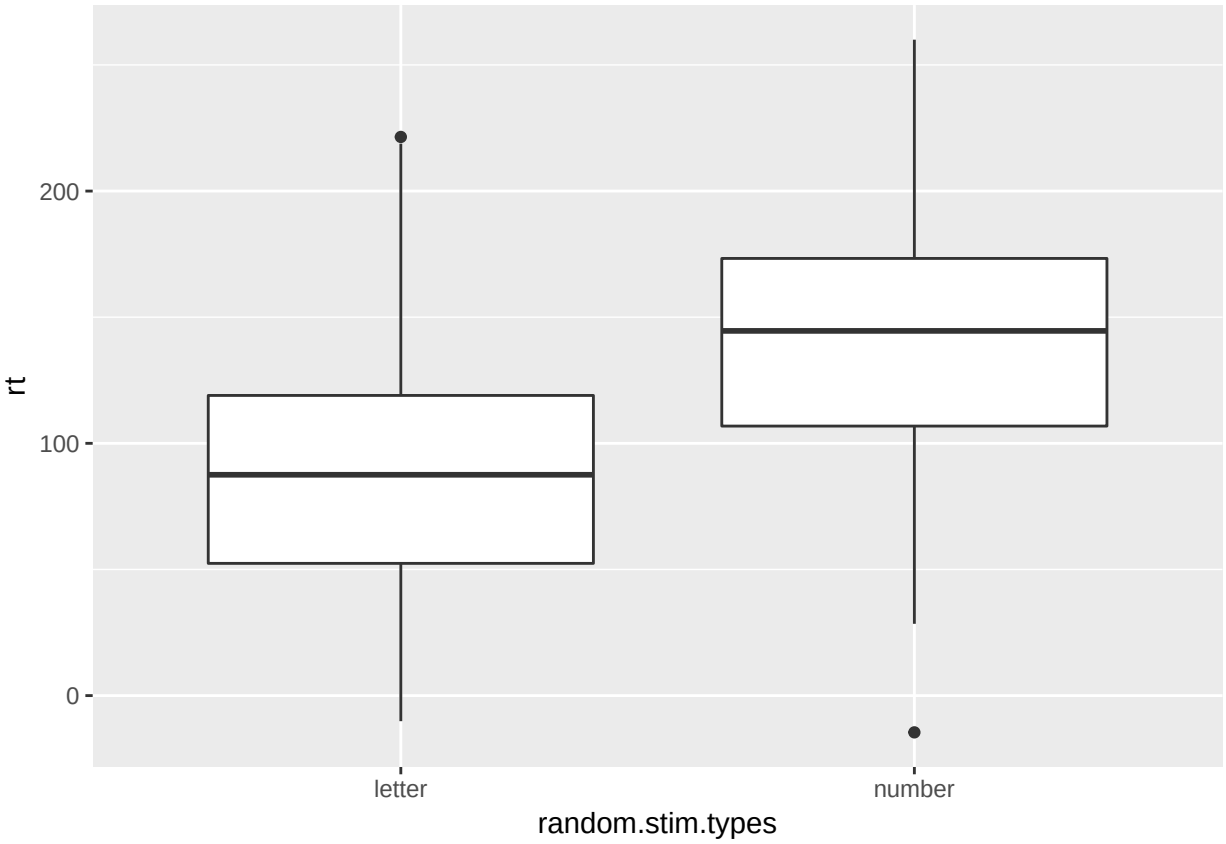


How about a factorial design?

- Dependent variable: RT
- Independent variables
  - Fixed
    - Symbol type: {letter, number}
  - Random
    - Subject mean RT
- Hypothesis:
  - RT to detect numbers is lower than for letters
  - There is no order effect
- Rick wishes he'd found this first: https://www.r-bloggers.com/design-of-experiments-%E2%80%93-full-factorial-designs/

```
# Simulation parameters
n.subs = 30
trials.per.cond = 100

letters.numbers.rt.diff = 50 # ms
rt.mean.across.subs = 35
sigma = 50
cond.labels = c("letter", "number")
cond.rts <- c("letter" = 0, "number" = letters.numbers.rt.diff)

stim.types <- factor(x = rep(x = c(1,2), trials.per.cond), labels = cond.labels)
```

```r
#sample(factor(x=rep(c("letter", "number"), 100)), 200)
random.stim.types <- sample(stim.types, trials.per.cond*length(cond.labels))

mean.sub.rt <- rnorm(n = 1, mean = rt.mean.across.subs, sd = sigma)
trial.rt <- array(0, dim = length(random.stim.types))

# Generate RTs based on trial, condition
for (t in 1:length(random.stim.types)) {
  trial.rt[t] <- mean.sub.rt + cond.rts[random.stim.types[t]] + rnorm(n = 1, mean = 0, sd = sigma)
}

# Make data frame
letter.number.df <- data.frame(trial = 1:length(random.stim.types), stim = random.stim.types, rt = trial

ggplot(data = letter.number.df, aes(x = random.stim.types, y = rt)) + geom_boxplot()
```



Put this in a function

```r
Simulate.sub.rt <- function(trials.per.cond = 100,
                            letters.numbers.rt.diff = 50,
                            rt.mean.across.subs = 350,
                            sigma = 50) {

  cond.rts <- c("letter" = 0, "number" = letters.numbers.rt.diff)
  stim.types <- factor(x = rep(x = c(1,2), trials.per.cond), labels = c("letter", "number"))
```

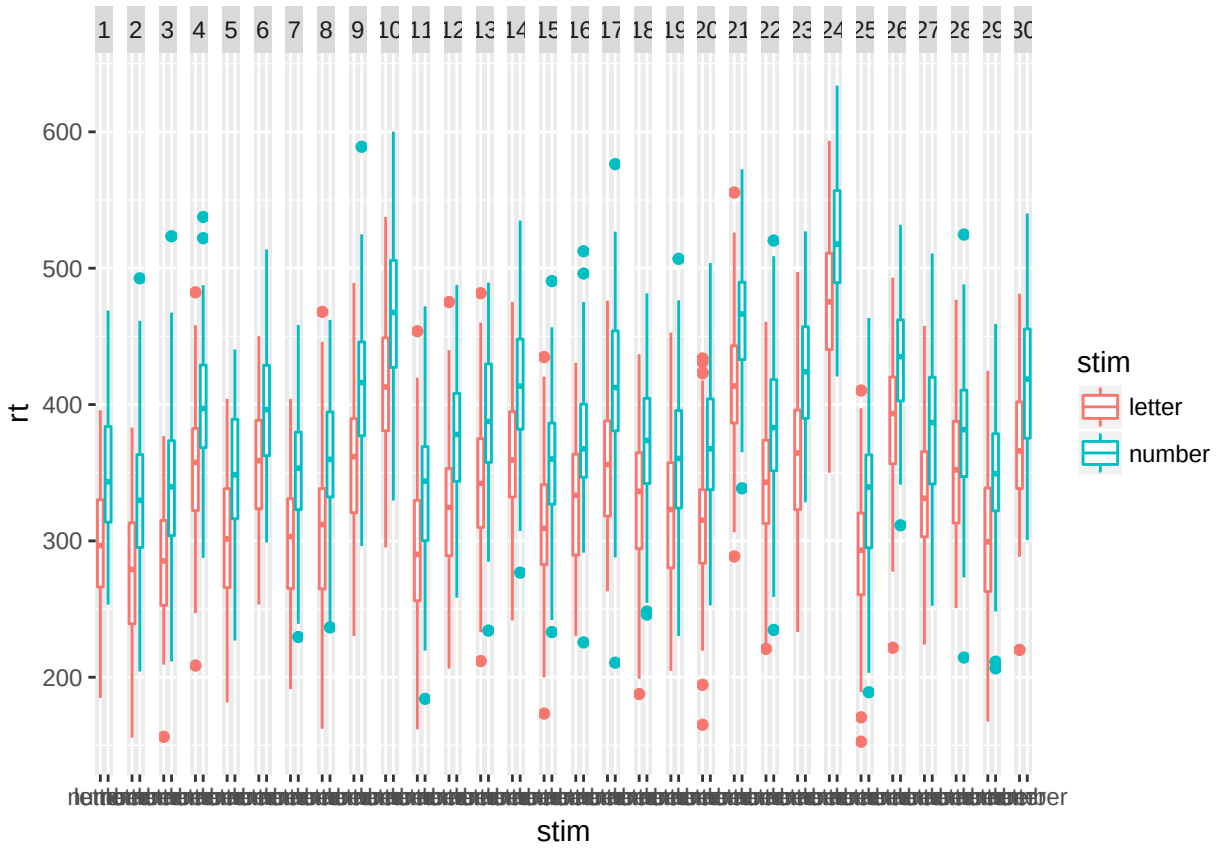
```
  random.stim.types <- sample(stim.types, 200)

  mean.sub.rt <- rnorm(n = 1, mean = rt.mean.across.subs, sd = sigma)
  trial.rt <- array(0, dim = length(random.stim.types))

  # Generate RTs based on trial, condition
  for (t in 1:length(random.stim.types)) {
    trial.rt[t] <- mean.sub.rt + cond.rts[random.stim.types[t]] +
      rnorm(n = 1, mean = 0, sd = sigma)
    }

  # Make data frame
  letter.number.df <- data.frame(trial = 1:length(random.stim.types),
                                 stim = random.stim.types,
                                 rt = trial.rt)
}
```

Create code to a set of participants and create one merged data frame

```
Make.sub.rt.df <- function(sub.id) {
  sub.rt.df <- Simulate.sub.rt()
  sub.rt.df$sub.id <- sub.id
  sub.rt.df
}

# Use lapply to make separate data frames for all subs
sub.rt.df.list <- lapply(1:n.subs, Make.sub.rt.df)

# Use Reduce() with the merge function to make one big file
sub.rt.df.merged <- Reduce(function(x, y) merge(x, y, all=TRUE), sub.rt.df.list)
```

Now, want to see what we have?

```
ggplot(data = sub.rt.df.merged) +
  aes(x=stim, y=rt, color=stim) +
  geom_boxplot() +
  facet_grid(facets = . ~ as.factor(sub.id))
```



And, just for fun

```
library(lme4)
```

```
## Loading required package: Matrix
```

```
fit1 <- lmer(formula = rt ~ stim + (1|sub.id), data = sub.rt.df.merged)
summary(fit1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: rt ~ stim + (1 | sub.id)
##    Data: sub.rt.df.merged
##
## REML criterion at convergence: 64077.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.9789 -0.6664  0.0138  0.6735  3.7634
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  sub.id   (Intercept) 1948     44.14
##  Residual             2485     49.85
## Number of obs: 6000, groups:  sub.id, 30
##
## Fixed effects:
```

```
##             Estimate Std. Error t value
## (Intercept)  338.257      8.110   41.71
## stimnumber    48.695      1.287   37.83
##
## Correlation of Fixed Effects:
##            (Intr)
## stimnumber -0.079
```

Or

```
fit2 <- aov(formula = rt ~ stim + Error(as.factor(sub.id)), data = sub.rt.df.merged)
summary(fit2)
```

```
##
## Error: as.factor(sub.id)
##           Df   Sum Sq Mean Sq F value Pr(>F)
## Residuals 29 11372227  392146
##
## Error: Within
##              Df   Sum Sq Mean Sq F value Pr(>F)
## stim          1  3556876 3556876    1431 <2e-16 ***
## Residuals 5969 14834969    2485
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Practice with visualization

- Work through the Wickham & Grolemund chapter on your own.
  - http://r4ds.had.co.nz/data-visualisation.html

Learning by example

```
# Installing packages
list.of.packages <- c("xlsx", "ggplot2","nlme", "foreign", "gplots", "stats", "psych" , "ISwR", "ggm" , "ca
new.packages <- list.of.packages[!(list.of.packages %in% installed.packages()[,"Package"])]
if(length(new.packages)) install.packages(new.packages)

# Loading packages
lapply(list.of.packages, require, character.only = TRUE)
```

https://github.com/psu-psych-511-2017-spring/liu_yushuang/blob/master/output.Rmd

A syntax I like

```
my.data <- data.frame(x.var = ..., y.var = ...)

my.data %>%
  ggplot() +      # pipe %>% operator feeds it my.data
  aes(x=x.var, y=y.var) + # plus + operator 'adds' to plot
  geom_point() -> # assign -> operator saves output
  my.scatter.plot # variable containing plot
```

```
my.scatter.plot # prints it
```

- Uses 'pipe' `%>%` operator and 'assign' `->` operator
- Easy to follow flow of what's going on

Assignment (due Monday, Feburary 20)

- Create your own simulated data set for a real or proposed study.
  - You may adapt or build upon the examples used in class.
- Plot the results of your simulation using ggplot2 commands.