# Apply-Prep

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#### Introduction to Repeating things in R

```
estmass <- function(volume) {
  mass <- 2.65 * volume ^0.9
  return(mass)
}</pre>
```

- Make a vector and apply or map functions
- combine functions using dplyr

#### Using Vectorized functions

```
## [1] 2 4 6

volume = c(1.6, 5.6, 3.1)
estmass(volume) #already vectorized

## [1] 4.045329 12.491515 7.336204

str_to_sentence(c("dipodomys", "chartodipus")) #captilized

## [1] "Dipodomys" "Chartodipus"

genus <- c("dipodomys", "chaetodipus", "dipodomys")
species <- c("ordil", "baileyi", "spectabilis")
combine_genus_species <- function(genus, species) {
    genus_cap <- str_to_sentence(genus)
    genus_species <- paste(genus_cap, species)
    return(genus_species)
}
combine_genus_species(genus, species)</pre>
```

```
## [1] "Dipodomys ordil" "Chaetodipus baileyi" "Dipodomys spectabilis"
```

```
data <- data.frame(genus, species)
combine_genus_species(data$genus, data$species)</pre>
```

```
## [1] "Dipodomys ordil" "Chaetodipus baileyi" "Dipodomys spectabilis"
```

#### **Mapply Function**

```
estmass <- function(volume, veg_type){
  if (veg_type == "tree"){
    mass <- 2.65 * volume^0.9
  } else {
    mass <- NA
  }
  return(mass)
}
volumes <- c(1.6, 5.6, 3.1)
veg_type <- c("shrub", "tree", "tree")
mapply(FUN = estmass, volume = volumes, veg_type = veg_type)</pre>
```

## ## [1] NA 12.491515 7.336204

#### Combining functions with DPLYR

```
estmass <- function(volume, veg_type){
  if (veg_type == "tree"){
    mass <- 2.65 * volume^0.9
  } else {
    mass <- NA
  }
  return(mass)
}
estmassvectorized <- function(volume){
  mass <- 2.65 * volume^0.9
  return(mass)
}
volumes <- c(1.6, 5.6, 3.1)
veg_type <- c("shrub", "tree", "tree")
plant_data <- data.frame(volumes, veg_type)
plant_data %>% #need to use vectorized data line 82
  mutate(masses = estmassvectorized(volumes))
```

```
## volumes veg_type masses
## 1    1.6    shrub    4.045329
## 2    5.6    tree    12.491515
## 3    3.1    tree    7.336204

plant_data %>%
    rowwise() %>%
    mutate(masses = estmass(volumes, veg_type))
```

```
## # A tibble: 3 x 3
## # Rowwise:
   volumes veg_type masses
##
      <dbl> <chr> <dbl> <
##
       1.6 shrub NA
## 1
## 2
       5.6 tree
                    12.5
## 3
                     7.34
       3.1 tree
getbiomass <- function(volumes){</pre>
 masses <- estmassvectorized(volumes)</pre>
 biomass <- sum(masses)</pre>
 return(biomass)
getbiomass(volumes)
## [1] 23.87305
#with dplyr
plant_data %>%
 group_by(veg_type) %>%
 summarize(biomass = getbiomass(volumes))
## # A tibble: 2 x 2
##
   veg_type biomass
##
             <dbl>
    <chr>
               4.05
## 1 shrub
## 2 tree
              19.8
```