apply-prep

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Introduction to repeating things in R

```r
estmass <- function(volume) {
  mass <- 2.65 * volume ^0.9
  return(mass)
}
#make a vector
# apply or map functions
#combining function using dplyr
```

Using vectorized functions

```r
c(1,2,3) * 2
```

```
## [1] 2 4 6
```

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

```
## [1]  4.045329 12.491515  7.336204
```

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

```
## [1] "Dipodomys"    "Chartodipus"
```

```r
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)
```

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

```r
data <- data.frame(genus, species)
combine_genus_species(data$genus, data$species)
```

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

apply functions

```r
#estmass <- function(volume) {
  #if (volume > 5){
  #mass <- 2.65 * volume ^0.9
  #} else {
    #mass <- NA
  #}
  #return(mass)
#}
#volumes <- c(1.6, 5.6, 3.1)
#estmass(volume)
#sapply(volumes, estmass) #adding l would give l and s gives vecetor
```

mapply function

```r
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) # multiple arguments
```

```
## [1]       NA 12.491515  7.336204
```

combining functions with dplyr

```r
estmass <- function(volume, veg_type){
  if (veg_type == "tree"){
    mass <- 2.65 * volume^0.9
  } else {
    mass <- NA
  }
  return(mass)
```

```r
}
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
```

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

```
## # A tibble: 3 x 3
## # Rowwise:
##   volumes veg_type masses
##     <dbl> <chr>     <dbl>
## 1     1.6 shrub        NA
## 2     5.6 tree       12.5
## 3     3.1 tree        7.34
```

```r
getbiomass <- function(volumes){
  masses <- estmassvectorized(volumes)
  biomass <- sum(masses)
  return(biomass)
}
getbiomass(volumes)
```

```
## [1] 23.87305
```

```r
#with dplyr
plant_data %>%
  group_by(veg_type) %>%
  summarize(biomass = getbiomass(volumes))
```

```
## # A tibble: 2 x 2
##   veg_type biomass
##   <chr>      <dbl>
## 1 shrub       4.05
## 2 tree       19.8
```