

Intro to *data wrangling*

dplyr & tidyr workshop

Samuel Robinson, Ph.D.

November 5, 2020

Normal data manipulation in R

```
#Changes species to factor
plants$Species <- as.factor(plants$Species)
#Changes plant code to factor
plants$Plant.Code <- as.factor(plants$Plant.Code)
#Changes Seed to factor
seeds$Seed <- as.factor(seeds$Seed)
#Changes plant code to factor
seeds$Plant.Code <- as.factor(seeds$Plant.Code)
#Selects Flower, Code, Total.Germ columns
germ <- germ[,c('Flower', 'Code', 'Total.Germ')]

#Sets numerics
plants[,c(3:9)] <- as.numeric(unlist(plants[,c(3:9)]))
#Sets Dates
seeds$Collection.Date <- as.Date(seeds$Collection.Date,origin='2012-01-01')
```

- One line of code per column - lots of typing
- Lots of \$\$\$s
- Lots of room for error

Data manipulation using dplyr/tidyr

```
library(tidyverse)
#Convert factors in plants df
plants <- plants %>% mutate(across(c(Species,Plant.Code)),factor)
#Convert factors in seeds df
seeds <- seeds %>% mutate(across(c(Seed,Plant.Code)),factor)
#Select Flower, Code, and Total.Germ columns in germ df
germ <- germ %>% select(Flower,Code,Total.Germ)

#Change columns 3:9 to numeric
plants <- plants %>% mutate(across(c(3:9)),as.numeric)
#Convert Collection.Date to Date format
seeds <- seeds %>%
  mutate(Collection.Date=as.Date(Collection.Date,origin='2012-01-01'))
```

- More compact, less typing
- Easier to read
- Faster (matters for large datasets)

Things to learn today:

- Basic syntax and table verbs
- Piping
- Reshaping
- Grouping
- Exercise!



Basic Syntax

Both dplyr and tidyr work with data frames or tibbles

- data frame: similar to matrix, but with different data types for each column
- tibble: “compact” data frame, with some annoying features removed

```
head(iris) #Regular data frame
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 2	4.9	3.0	1.4	0.2	setosa
## 3	4.7	3.2	1.3	0.2	setosa
## 4	4.6	3.1	1.5	0.2	setosa
## 5	5.0	3.6	1.4	0.2	setosa
## 6	5.4	3.9	1.7	0.4	setosa

Basic Syntax

```
as_tibble(iris) #This is usually done automatically
```

```
## # A tibble: 150 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##   <dbl>         <dbl>         <dbl>         <dbl> <fct>
## 1         5.1         3.5         1.4         0.2 setosa
## 2         4.9         3         1.4         0.2 setosa
## 3         4.7         3.2         1.3         0.2 setosa
## 4         4.6         3.1         1.5         0.2 setosa
## 5         5         3.6         1.4         0.2 setosa
## 6         5.4         3.9         1.7         0.4 setosa
## 7         4.6         3.4         1.4         0.3 setosa
## 8         5         3.4         1.5         0.2 setosa
## 9         4.4         2.9         1.4         0.2 setosa
## 10        4.9         3.1         1.5         0.1 setosa
## # ... with 140 more rows
```

Basic verbs - subsetting

- **select**: returns only columns that you want

```
head(iris,3)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
```

```
#Select Petal.Length, Petal.Width, Species
irisTemp <- select(iris, Petal.Length, Petal.Width, Species)
head(irisTemp, 3)
```

```
##   Petal.Length Petal.Width Species
## 1         1.4         0.2   setosa
## 2         1.4         0.2   setosa
## 3         1.3         0.2   setosa
```

Basic verbs - subsetting

Helper functions for **select**: *colon* operator

```
irisTemp <- select(iris,Petal.Length:Species)
head(irisTemp,3) #All columns between Petal.Length and Species
```

```
##   Petal.Length Petal.Width Species
## 1          1.4          0.2  setosa
## 2          1.4          0.2  setosa
## 3          1.3          0.2  setosa
```

```
irisTemp2 <- select(iris,Petal.Length,Petal.Width,Species)
head(irisTemp2,3) #This is the same thing
```

```
##   Petal.Length Petal.Width Species
## 1          1.4          0.2  setosa
## 2          1.4          0.2  setosa
## 3          1.3          0.2  setosa
```


Basic verbs - subsetting

Helper functions for **select**: `-`, and *contains*

```
irisTemp <- select(iris,-Species)
head(irisTemp,3) #Selects all columns EXCEPT Species
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1         5.1         3.5         1.4         0.2
## 2         4.9         3.0         1.4         0.2
## 3         4.7         3.2         1.3         0.2
```

```
irisTemp2 <- select(iris,contains('Petal'))
head(irisTemp2,3) #Selects columns with names containing 'Petal'
```

```
##   Petal.Length Petal.Width
## 1         1.4         0.2
## 2         1.4         0.2
## 3         1.3         0.2
```

Basic verbs - subsetting

- **filter**: returns only rows that you want

```
head(iris,3)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1          3.5          1.4          0.2 setosa
## 2          4.9          3.0          1.4          0.2 setosa
## 3          4.7          3.2          1.3          0.2 setosa
```

```
irisTemp <- filter(iris,Sepal.Length<5,Species=='versicolor')
head(irisTemp,3) #Chooses rows matching logical criteria
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          4.9          2.4          3.3          1 versicolor
```

Basic verbs - make new variables

- **mutate**: add variables or alter existing ones

```
head(iris,3)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1          3.5           1.4          0.2 setosa
## 2          4.9          3.0           1.4          0.2 setosa
## 3          4.7          3.2           1.3          0.2 setosa
```

```
irisTemp <- mutate(iris,P.Width2=Petal.Width^2)
head(irisTemp,3) #Squares Petal.Width
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width Species P.Width2
## 1          5.1          3.5           1.4          0.2 setosa    0.04
## 2          4.9          3.0           1.4          0.2 setosa    0.04
## 3          4.7          3.2           1.3          0.2 setosa    0.04
```

Basic verbs - make new variables

```
head(irisTemp,3)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	P.Width2
## 1	5.1	3.5	1.4	0.2	setosa	0.04
## 2	4.9	3.0	1.4	0.2	setosa	0.04
## 3	4.7	3.2	1.3	0.2	setosa	0.04

```
irisTemp <- mutate(iris,P.Width2=(Petal.Width^2)*2)  
head(irisTemp,3) #Alters variable in place
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	P.Width2
## 1	5.1	3.5	1.4	0.2	setosa	0.08
## 2	4.9	3.0	1.4	0.2	setosa	0.08
## 3	4.7	3.2	1.3	0.2	setosa	0.08

Basic verbs - make new variables

- **across:** uses the function on a number of columns
 - Must be used *inside* verbs

```
head(iris,3)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
```

```
# "~" is called a lambda (similar to a function)
# "." means "data from column", so...
# "~.^2" means "square anything in this column"
irisTemp <- mutate(iris, across(c(Sepal.Length,Petal.Width), ~.^2))
head(irisTemp,3)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1        26.01         3.5         1.4         0.04   setosa
## 2        24.01         3.0         1.4         0.04   setosa
## 3        22.09         3.2         1.3         0.04   setosa
```

Basic verbs - make new variables

- rename & transmute

```
irisTemp <- rename(iris, PWidth=Petal.Width, PLength=Petal.Length)
head(irisTemp,3) #Renames columns
```

```
## Sepal.Length Sepal.Width PLength PWidth Species
## 1      5.1      3.5      1.4      0.2 setosa
## 2      4.9      3.0      1.4      0.2 setosa
## 3      4.7      3.2      1.3      0.2 setosa
```

```
irisTemp2 <- transmute(iris, P.Width2=(Petal.Width^2))
head(irisTemp2,3) #Same as mutate, but drops other columns
```

```
## P.Width2
## 1      0.04
## 2      0.04
## 3      0.04
```

Exercises!

Using the iris dataset:

- Filter only rows with “virginica”
- Make 2 new “area” columns, which are length \times width of Petals and Sepals
- Get rid of all columns except “Species” + 2 new columns

```
##      Species P.Area S.Area
## 1 virginica  15.00  20.79
## 2 virginica   9.69  15.66
## 3 virginica  12.39  21.30
## 4 virginica  10.08  18.27
## 5 virginica  12.76  19.50
## 6 virginica  13.86  22.80
## 7 virginica   7.65  12.25
## 8 virginica  11.34  21.17
## 9 virginica  10.44  16.75
## 10 virginica  15.25  25.92
```

Piping - %>%

- Takes data from one verb and passes it to the next one
- Allows you to string together complex operations

```
irisTemp <- select(iris,Sepal.Length,Species) %>% #Selects Sepal.Length & Species
  filter(Sepal.Length>5,Species=='versicolor') %>% #Filters using dataframe from above
  mutate(SLength2=Sepal.Length^2) #Mutates using dataframe from above
head(irisTemp)
```

##	Sepal.Length	Species	SLength2
## 1	7.0	versicolor	49.00
## 2	6.4	versicolor	40.96
## 3	6.9	versicolor	47.61
## 4	5.5	versicolor	30.25
## 5	6.5	versicolor	42.25
## 6	5.7	versicolor	32.49

Reshaping - i.e. “data gymnastics”

- This is very tedious to do in base R and Excel
- Reshaping operations in `tidyr` make this much easier
- Four main commands:
 - ① `pivot_longer` - gather columns into rows ('long format')
 - ② `pivot_wider` - spread rows into columns ('wide format')
 - ③ `unite` - unite many columns into one (similar to `paste`)
 - ④ `separate` - separates one column into many (similar to `strsplit`)

Reshaping - *pivot_longer*: columns to rows

- Some data in a “wide” format

```
#Some data to work with
```

```
(bats <- data.frame(bat=letters[1:3], weight = seq(1,3,1),  
                  height=seq(2.5,5.5,length=3), wings=rep(2,3)))
```

```
##   bat weight height wings  
## 1   a      1    2.5      2  
## 2   b      2    4.0      2  
## 3   c      3    5.5      2
```

Reshaping - *pivot_longer*: columns to rows

- Change “wide” dataframe to “long” dataframe

```
(longBats <- bats %>% pivot_longer(cols=weight:wings, #Columns to be made into 2  
  names_to='trait', #Name of "naming" column  
  values_to='meas')) #Name of "value" column
```

```
## # A tibble: 9 x 3  
##   bat   trait   meas  
##   <fct> <chr>   <dbl>  
## 1 a     weight    1  
## 2 a     height   2.5  
## 3 a     wings     2  
## 4 b     weight    2  
## 5 b     height    4  
## 6 b     wings     2  
## 7 c     weight    3  
## 8 c     height   5.5  
## 9 c     wings     2
```

Reshaping - *pivot_wider*: rows to columns

- This is the inverse of *pivot_longer*

```
longBats %>% pivot_wider(names_from=trait, #Names of new columns
                        values_from=meas) #Values to go into new columns
```

```
## # A tibble: 3 x 4
##   bat   weight height wings
##   <fct> <dbl>   <dbl> <dbl>
## 1 a         1     2.5     2
## 2 b         2     4       2
## 3 c         3     5.5     2
```

#Note: this must have unique row identifiers

Reshaping - *unite*: many columns into one

- Useful when combined with other reshaping functions

```
irisTemp <- iris %>% unite(newCol,Sepal.Length:Petal.Width,sep='_')  
head(irisTemp,10)
```

```
##           newCol Species  
## 1  5.1_3.5_1.4_0.2  setosa  
## 2   4.9_3.1_1.4_0.2  setosa  
## 3  4.7_3.2_1.3_0.2  setosa  
## 4  4.6_3.1_1.5_0.2  setosa  
## 5   5.3_6.1_4.0_0.2  setosa  
## 6  5.4_3.9_1.7_0.4  setosa  
## 7  4.6_3.4_1.4_0.3  setosa  
## 8   5.3_4.1_1.5_0.2  setosa  
## 9  4.4_2.9_1.4_0.2  setosa  
## 10 4.9_3.1_1.5_0.1  setosa
```

Reshaping - *separate*: one column into many

```
irisTemp %>% separate(newCol, c('SLength', 'SWidth', 'PLength', 'PWidth'), sep='_') %>%  
  head(10)
```

	SLength	SWidth	PLength	PWidth	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 2	4.9	3	1.4	0.2	setosa
## 3	4.7	3.2	1.3	0.2	setosa
## 4	4.6	3.1	1.5	0.2	setosa
## 5	5	3.6	1.4	0.2	setosa
## 6	5.4	3.9	1.7	0.4	setosa
## 7	4.6	3.4	1.4	0.3	setosa
## 8	5	3.4	1.5	0.2	setosa
## 9	4.4	2.9	1.4	0.2	setosa
## 10	4.9	3.1	1.5	0.1	setosa

Reshaping - combinations of reshaping functions

Say we wanted lengths and widths in separate columns, split by Petal & Sepal

```
irisTemp <- iris %>% unite(col=sepals,contains('Sepal'),sep='_') %>%  
  unite(col=petals,contains('Petal'),sep='_')  
head(irisTemp,10)
```

```
##      sepals  petals Species  
## 1  5.1_3.5  1.4_0.2  setosa  
## 2    4.9_3  1.4_0.2  setosa  
## 3  4.7_3.2  1.3_0.2  setosa  
## 4  4.6_3.1  1.5_0.2  setosa  
## 5    5_3.6  1.4_0.2  setosa  
## 6  5.4_3.9  1.7_0.4  setosa  
## 7  4.6_3.4  1.4_0.3  setosa  
## 8    5_3.4  1.5_0.2  setosa  
## 9  4.4_2.9  1.4_0.2  setosa  
## 10 4.9_3.1  1.5_0.1  setosa
```

Reshaping - combinations of reshaping functions

- Now that measurements are *united*, we *pivot_longer* and then *separate* them

```
irisTemp %>% pivot_longer(cols=sepals:petals,names_to='Type',values_to='Measurement') %>%  
  separate(Measurement,c('Length','Width'),sep='_',convert=T) %>%  
  head(10)
```

```
## # A tibble: 10 x 4  
##   Species Type    Length Width  
##   <fct>  <chr>    <dbl> <dbl>  
## 1 setosa sepals     5.1   3.5  
## 2 setosa petals     1.4   0.2  
## 3 setosa sepals     4.9   3  
## 4 setosa petals     1.4   0.2  
## 5 setosa sepals     4.7   3.2  
## 6 setosa petals     1.3   0.2  
## 7 setosa sepals     4.6   3.1  
## 8 setosa petals     1.5   0.2  
## 9 setosa sepals     5     3.6  
## 10 setosa petals     1.4   0.2
```


Exercises!

Using the *CO2* dataset:

- Select only *non-chilled* plants from *Quebec*
- Pipe data frame to next command
- Change the uptake dataset from long to wide format (each plant should have its own column), with a column at the beginning showing concentration
- Hint: *filter* rows and *select* columns you need, then *pivot_wide* to wide format

```
## # A tibble: 7 x 4
##   conc   Qn1   Qn2   Qn3
##   <dbl> <dbl> <dbl> <dbl>
## 1    95    16   13.6  16.2
## 2   175   30.4  27.3  32.4
## 3   250   34.8  37.1  40.3
## 4   350   37.2  41.8  42.1
## 5   500   35.3  40.6  42.9
## 6   675   39.2  41.4  43.9
## 7  1000   39.7  44.3  45.5
```

Grouping

- Often, we want to perform operations only on groups within data frames
- For example, what is the average of each species' *Petal.width*?

```
with(iris,tapply(Petal.Width,Species,mean)) #Using tapply
```

```
##      setosa versicolor  virginica  
##      0.246      1.326      2.026
```

```
aggregate(Petal.Width~Species,data=iris,mean) #Using aggregate
```

```
##      Species Petal.Width  
## 1      setosa      0.246  
## 2 versicolor      1.326  
## 3  virginica      2.026
```

Grouping

- How can this be done in dplyr/tidyr?

```
iris %>% group_by(Species) %>% #Group by species
  summarize(meanPWidth=mean(Petal.Width), #Mean of Petal.Width
            sdPWidth=sd(Petal.Width)) #SD of Petal.Width
```

```
## # A tibble: 3 x 3
##   Species    meanPWidth sdPWidth
##   <fct>         <dbl>    <dbl>
## 1 setosa         0.246     0.105
## 2 versicolor    1.33      0.198
## 3 virginica     2.03      0.275
```

- Apply *grouping*, then use `summarize` function
 - Breaks dataframe into “mini-dataframes” before applying the function
- Data frame can be fed into other functions after summarizing

Grouping - Examples

```
iris %>% group_by(Species) %>% #Group by species
  summarize(count=n(), #Number of rows
            med=median(Petal.Width), #Median
            iqr=IQR(Petal.Width)) #Inter-quartile range
```

```
## # A tibble: 3 x 4
##   Species    count  med   iqr
##   <fct>      <int> <dbl> <dbl>
## 1 setosa         50   0.2  0.100
## 2 versicolor    50   1.3   0.3
## 3 virginica     50   2    0.500
```

- n is empty, because it uses the length of the subsetted data frame

Grouping - Examples

- Also useful for applying functions to subsets of data, *without* summarizing

```
iris %>% group_by(Species) %>%  
  mutate(ID=1:n()) %>% #Makes ID column, with numbers 1-N  
  filter(ID<4) #Selects ID 1-3 from each group
```

```
## # A tibble: 9 x 6  
## # Groups:   Species [3]  
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species      ID  
##         <dbl>      <dbl>      <dbl>      <dbl> <fct>    <int>  
## 1         5.1        3.5        1.4        0.2 setosa      1  
## 2         4.9         3         1.4        0.2 setosa      2  
## 3         4.7        3.2        1.3        0.2 setosa      3  
## 4         7         3.2        4.7        1.4 versicolor  1  
## 5         6.4        3.2        4.5        1.5 versicolor  2  
## 6         6.9        3.1        4.9        1.5 versicolor  3  
## 7         6.3        3.3         6         2.5 virginica  1  
## 8         5.8        2.7        5.1        1.9 virginica  2  
## 9         7.1         3         5.9        2.1 virginica  3
```

Grouping

- Another way of doing the same thing

```
iris %>% group_by(Species) %>%  
  slice(1:3) #Selects rows 1-3 from each group
```

```
## # A tibble: 9 x 5  
## # Groups:   Species [3]  
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species  
##         <dbl>         <dbl>         <dbl>         <dbl> <fct>  
## 1         5.1          3.5           1.4           0.2 setosa  
## 2         4.9          3            1.4           0.2 setosa  
## 3         4.7          3.2           1.3           0.2 setosa  
## 4          7          3.2           4.7           1.4 versicolor  
## 5         6.4          3.2           4.5           1.5 versicolor  
## 6         6.9          3.1           4.9           1.5 versicolor  
## 7         6.3          3.3           6            2.5 virginica  
## 8         5.8          2.7           5.1           1.9 virginica  
## 9         7.1          3            5.9           2.1 virginica
```

- You can use most of the subset and window functions across groups

Exercises!

Using the *InsectSprays* dataset:

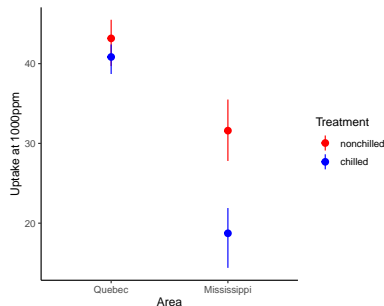
- Find the mean and SD of each type of spray type
- Reshape dataframe so that each spray has its own column, with mean and SD in separate rows
- Hint: get summary stats first, then `pivot_longer` and `pivot_wider`

```
## # A tibble: 2 x 7
##   stat      A      B      C      D      E      F
##   <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 mean  14.5  15.3   2.08  4.92   3.5   16.7
## 2 sd    4.72  4.27   1.98  2.50   1.73  6.21
```

Final remarks

- dplyr & tidyr interface well with other parts of the tidyverse

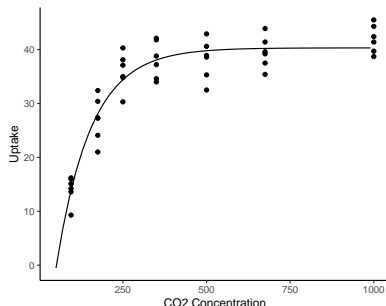
```
library(ggplot2)
#Code for dplyr begins here
C02 %>% filter(conc==1000) %>%
  group_by(Type,Treatment) %>%
  summarize(meanUp=mean(uptake),
             maxUp=max(uptake),
             minUp=min(uptake)) %>%
  #Code for ggplot begins here
  ggplot(aes(x=Type,col=Treatment))+
  geom_pointrange(aes(y=meanUp,
                     ymax=maxUp,
                     ymin=minUp))+
  labs(x='Area',y='Uptake at 1000ppm')+
  scale_colour_manual(values=c('red','blue'))
```



Final remarks

- dplyr & tidyr can pass data frames to and from other functions: use ' ' operator

```
co2mod <- CO2 %>%  
  filter(Type=='Quebec') %>%  
  #Code for nls begins here  
  nls(uptake~SSasympt(conc,A,B,C),  
      start=list(A=30,B=-15,C=-5),data=.)  
  
data.frame(conc=seq(50,1000,20)) %>%  
  predict(co2mod,newdata=.) %>%  
  data.frame(conc=seq(50,1000,20),predUp=.) %>%  
  #Code for ggplot begins here  
  ggplot(aes(conc,predUp))+  
  geom_line()+  
  geom_point(data=filter(CO2,Type=='Quebec'),  
            aes(conc,uptake))+  
  labs(x='CO2 Concentration',y='Uptake')
```



Happy wrangling! Yee-haw!

