TUTORIAL 2
Data Manipulation

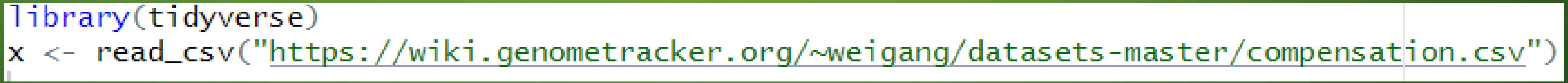
@QIU, HUNTER/CUNY

LOAD DATA

1. Download the zip file containing data sets from http://www.r4all.org/the-book/datasets
2. Upload: Files → Upload → Choose file
3. Read a data file:

```
compensation ← read_csv(“datasets-master/compensation.csv”)
```

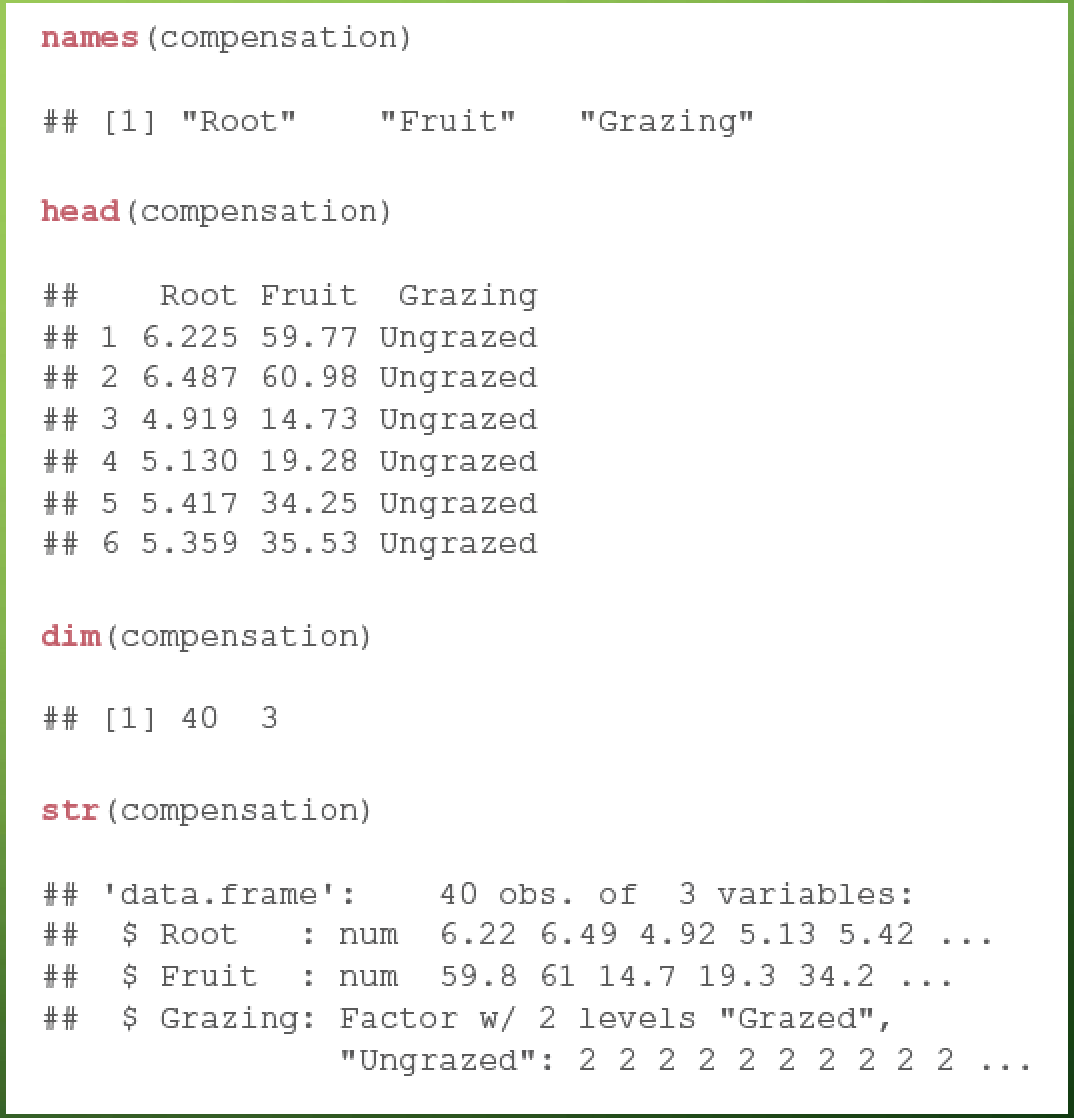
Alternatively, read from an online repository:



```
library(tidyverse)
x <- read_csv("https://wiki.genometracker.org/~weigang/datasets-master/compensation.csv")
```

THE “compensation” DATASET

1. Numeric variable “Fruit”: production of apple (in kg)
2. Numeric variable “Root”: width of rootstock (in cm)
3. Categorical variable “Grazing”: allowing for cattle grazing or not



```
names(compensation)

## [1] "Root"    "Fruit"   "Grazing"

head(compensation)

##     Root Fruit  Grazing
## 1  6.225 59.77 Ungrazed
## 2  6.487 60.98 Ungrazed
## 3  4.919 14.73 Ungrazed
## 4  5.130 19.28 Ungrazed
## 5  5.417 34.25 Ungrazed
## 6  5.359 35.53 Ungrazed

dim(compensation)

## [1] 40  3

str(compensation)

## 'data.frame':    40 obs. of  3 variables:
##  $ Root   : num  6.22 6.49 4.92 5.13 5.42 ...
##  $ Fruit  : num  59.8 61 14.7 19.3 34.2 ...
##  $ Grazing: Factor w/ 2 levels "Grazed",
                "Ungrazed": 2 2 2 2 2 2 2 2 2 2 ...
```

TIPS FOR VARIABLE & FILE NAMES

Computer-friendly variable/file names

- camelFormatName
- worm_format_name

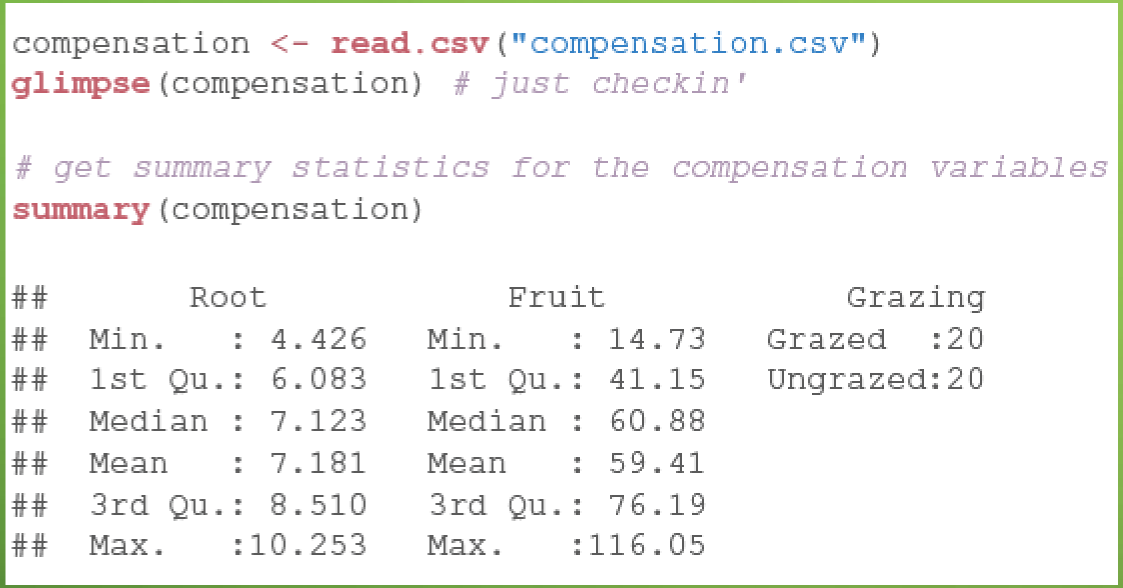
✓

Computer-unfriendly variable/file names

- “Name with spaces”
- “name-with-dashes”
- “123nameStartWithNumbers
- “a”, “b”, “c” (uninformative)

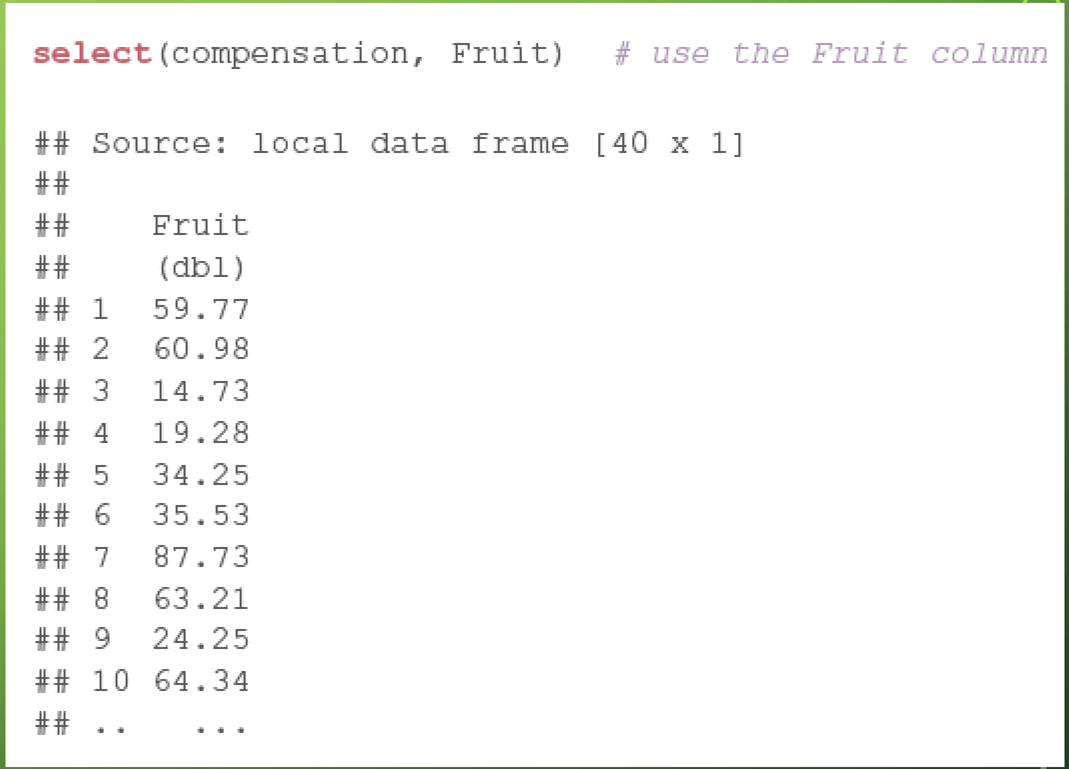
✗

summary(): statistics



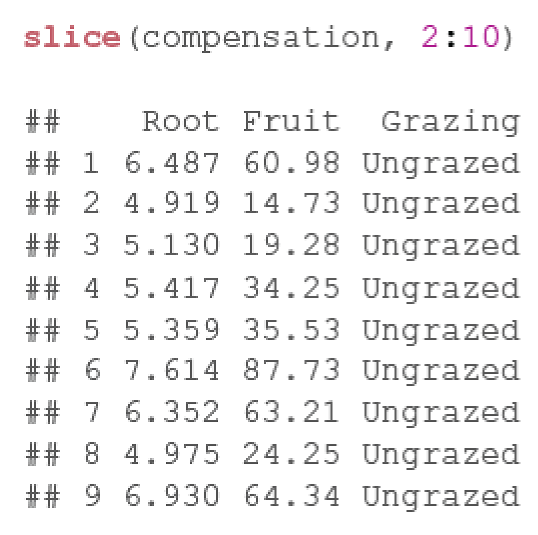
```
compensation <- read.csv("compensation.csv")
glimpse(compensation) # just checkin'

# get summary statistics for the compensation variables
summary(compensation)

##       Root             Fruit             Grazing
##  Min.   : 4.426   Min.   : 14.73   Grazed  :20
##  1st Qu.: 6.083   1st Qu.: 41.15   Ungrazed:20
##  Median : 7.123   Median : 60.88
##  Mean   : 7.181   Mean   : 59.41
##  3rd Qu.: 8.510   3rd Qu.: 76.19
##  Max.   :10.253   Max.   :116.05
```

select(): choose columns

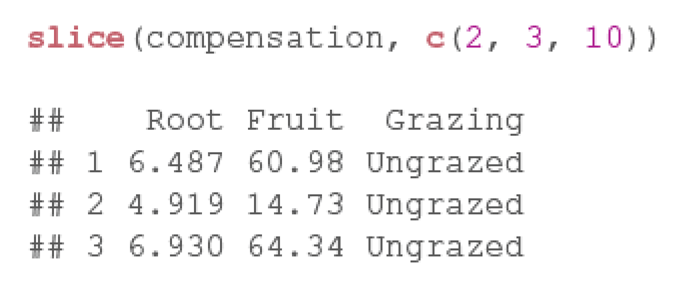


```
select(compensation, Fruit)  # use the Fruit column

## Source: local data frame [40 x 1]
##
##    Fruit
##    (dbl)
## 1  59.77
## 2  60.98
## 3  14.73
## 4  19.28
## 5  34.25
## 6  35.53
## 7  87.73
## 8  63.21
## 9  24.25
## 10 64.34
## ..   ...
```

slice(): choose rows

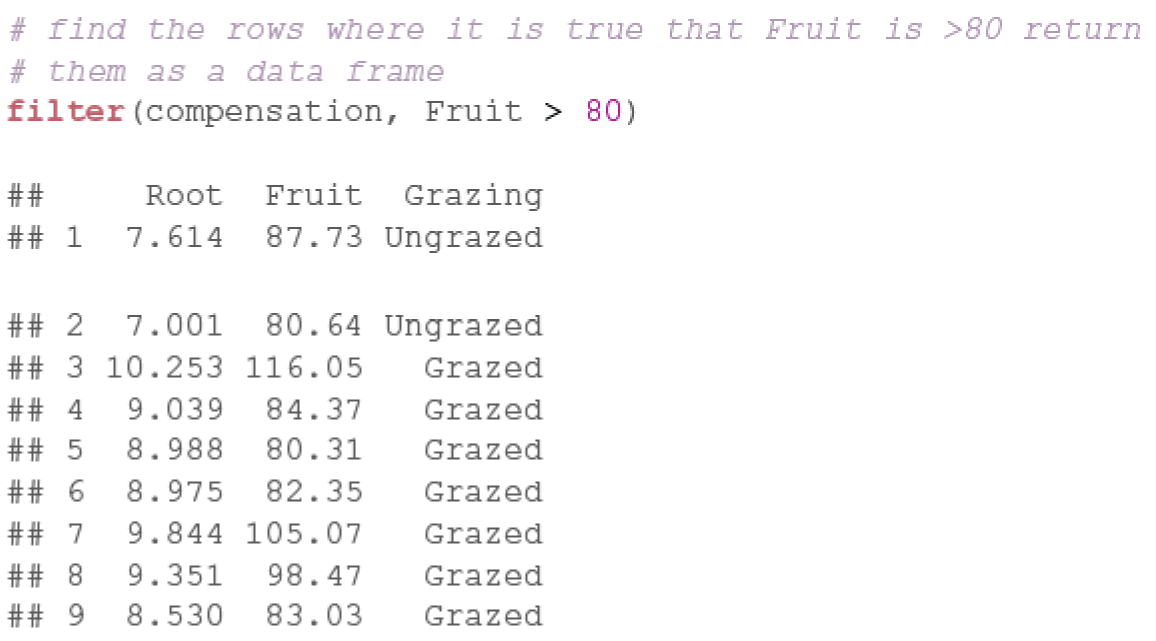


```
slice(compensation, 2:10)

##    Root Fruit  Grazing
## 1 6.487 60.98 Ungrazed
## 2 4.919 14.73 Ungrazed
## 3 5.130 19.28 Ungrazed
## 4 5.417 34.25 Ungrazed
## 5 5.359 35.53 Ungrazed
## 6 7.614 87.73 Ungrazed
## 7 6.352 63.21 Ungrazed
## 8 4.975 24.25 Ungrazed
## 9 6.930 64.34 Ungrazed
```

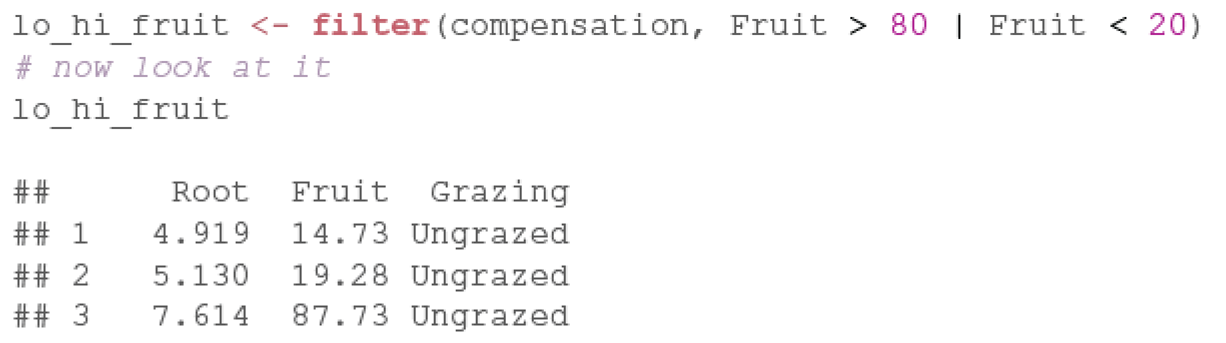


```
slice(compensation, c(2, 3, 10))

##    Root Fruit  Grazing
## 1 6.487 60.98 Ungrazed
## 2 4.919 14.73 Ungrazed
## 3 6.930 64.34 Ungrazed
```

filter(): conditional row filtering

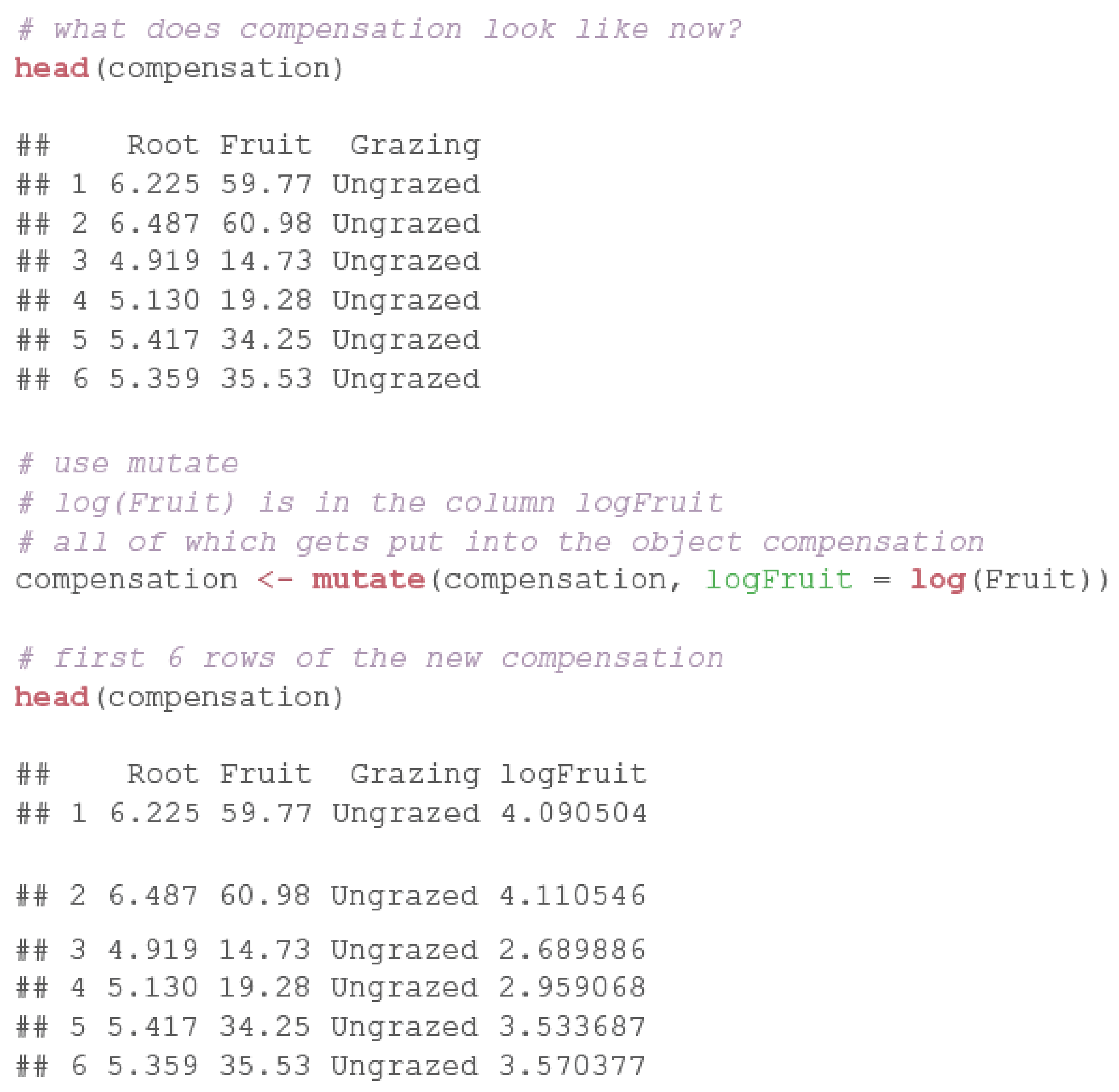


```
# find the rows where it is true that Fruit is >80 return
# them as a data frame
filter(compensation, Fruit > 80)

##      Root  Fruit  Grazing
## 1   7.614  87.73 Ungrazed

## 2   7.001  80.64 Ungrazed
## 3 10.253 116.05   Grazed
## 4   9.039  84.37   Grazed
## 5   8.988  80.31   Grazed
## 6   8.975  82.35   Grazed
## 7   9.844 105.07   Grazed
## 8   9.351  98.47   Grazed
## 9   8.530  83.03   Grazed
```



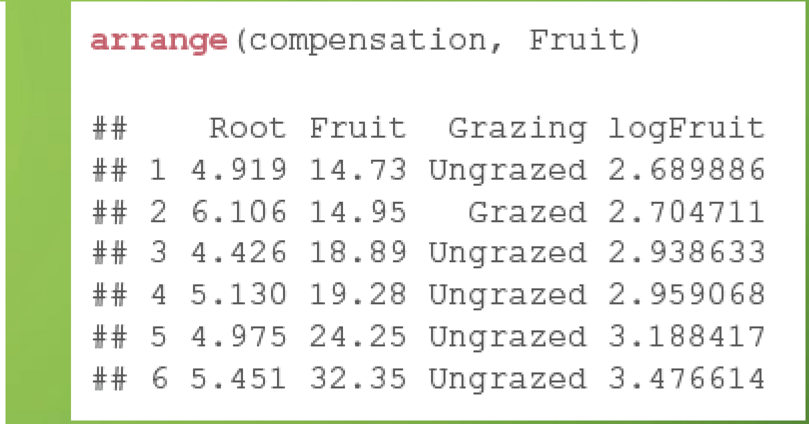
```
lo_hi_fruit <- filter(compensation, Fruit > 80 | Fruit < 20)
# now look at it
lo_hi_fruit

##       Root  Fruit  Grazing
## 1    4.919  14.73 Ungrazed
## 2    5.130  19.28 Ungrazed
## 3    7.614  87.73 Ungrazed
```

mutate(): data transformation



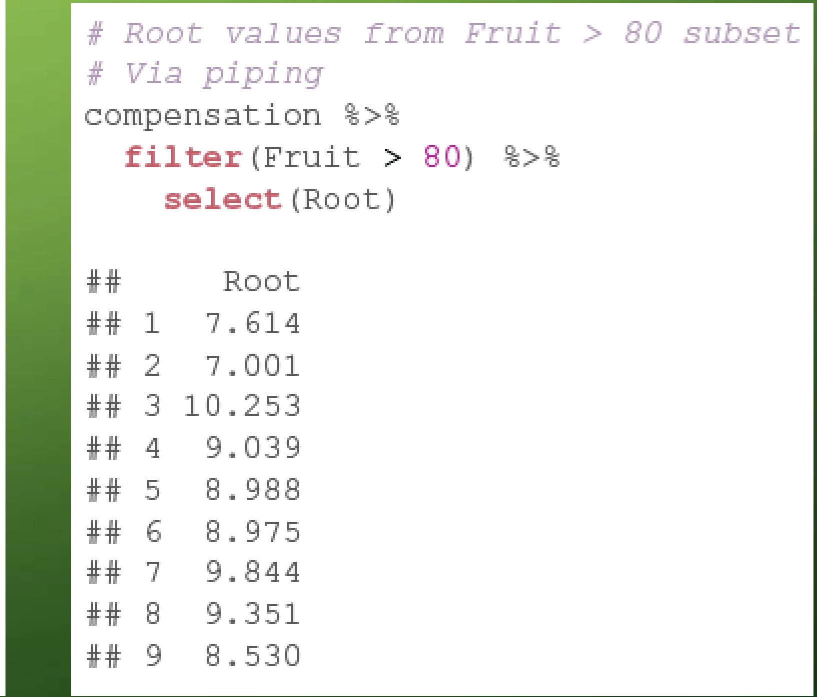
```
# what does compensation look like now?
head(compensation)

##    Root Fruit  Grazing
## 1 6.225 59.77 Ungrazed
## 2 6.487 60.98 Ungrazed
## 3 4.919 14.73 Ungrazed
## 4 5.130 19.28 Ungrazed
## 5 5.417 34.25 Ungrazed
## 6 5.359 35.53 Ungrazed

# use mutate
# log(Fruit) is in the column logFruit
# all of which gets put into the object compensation
compensation <- mutate(compensation, logFruit = log(Fruit))

# first 6 rows of the new compensation
head(compensation)

##    Root Fruit  Grazing logFruit
## 1 6.225 59.77 Ungrazed 4.090504

## 2 6.487 60.98 Ungrazed 4.110546
## 3 4.919 14.73 Ungrazed 2.689886
## 4 5.130 19.28 Ungrazed 2.959068
## 5 5.417 34.25 Ungrazed 3.533687
## 6 5.359 35.53 Ungrazed 3.570377
```

arrange(): sort rows



```
arrange(compensation, Fruit)

##    Root Fruit  Grazing logFruit
## 1 4.919 14.73 Ungrazed 2.689886
## 2 6.106 14.95   Grazed 2.704711
## 3 4.426 18.89 Ungrazed 2.938633
## 4 5.130 19.28 Ungrazed 2.959068
## 5 4.975 24.25 Ungrazed 3.188417
## 6 5.451 32.35 Ungrazed 3.476614
```

Chaining with “%>%” or “|>”



```
# Root values from Fruit > 80 subset
# Via piping
compensation %>%
  filter(Fruit > 80) %>%
    select(Root)

##      Root
## 1   7.614
## 2   7.001
## 3  10.253
## 4   9.039
## 5   8.988
## 6   8.975
## 7   9.844
## 8   9.351
## 9   8.530
```

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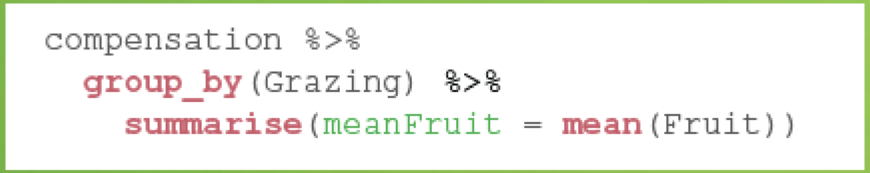
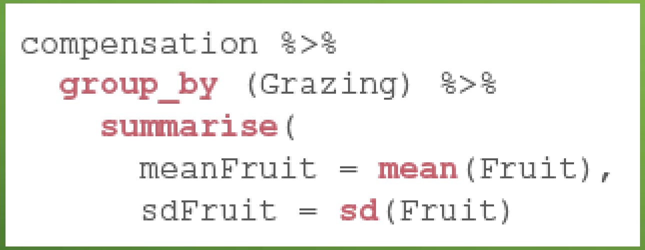
Summarize by groups

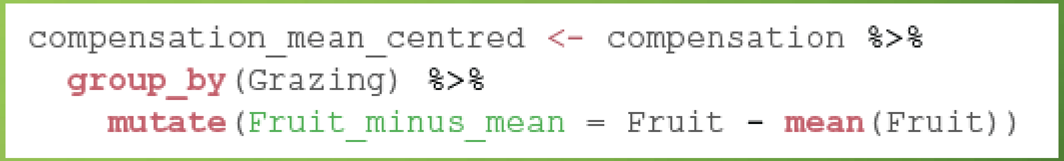


```
compensation %>%
  group_by(Grazing) %>%
    summarise(meanFruit = mean(Fruit))
```



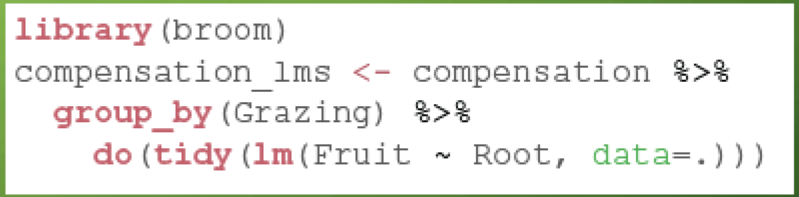
```
compensation %>%
  group_by (Grazing) %>%
    summarise(
      meanFruit = mean(Fruit),
      sdFruit = sd(Fruit)
```

Transform by groups



```
compensation_mean_centred <- compensation %>%
  group_by(Grazing) %>%
    mutate(Fruit_minus_mean = Fruit - mean(Fruit))
```

Regression by groups



```
library(broom)
compensation_lms <- compensation %>%
  group_by(Grazing) %>%
    do(tidy(lm(Fruit ~ Root, data=.)))
```

PRACTICE #2

Load the “iris” dataset with `data(“iris")` & answer the following questions:

1. Fine the dimensions of the dataset
2. List the variables and their data types (Hint: run `glimpse(“iris")`)
3. Summarize the variables (Hint: run `summary(“iris")`)
4. Get the last 10 observations of the dataset
5. Select only the first four columns (remove the “`species`” column)
6. Filter rows by species, retain only rows from one species (e.g., “`setosa`”)
7. Filter rows by a cutoff value (e.g., “`Sepal.Length >= 4`”)
8. Add a column by taking the log10 of “`Sepal.Lengh`”
9. What are the medians of the variable “`Sepal.Length`” for each species?
10. Count how many samples for each species
11. Save all commands in a file “practice-2.R”