

2 Data Import and Wrangling

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1 Chapter 2: Data Import and Data Wrangling

1.1 Agenda

- **Part 1 (30 mins)** – Data Import and Data Wrangling (Reading Different Types of Data)
 - **Part 2 (40 mins)** – Data Cleaning and Manipulation using `dplyr`
 - **Part 3 (30 mins)** – Handling Missing Data
 - **Part 4 (20 mins)** – Practice and Q&A
-

1.2 Part 1: Reading Different Types of Data (30 mins)

We can also check our working directory using the command `getwd()`.

1.2.1 CSV File Example: Iris Dataset

```
# We can import csv file using the base library using the command read.csv
iris_data <- read.csv("../data/Iris.csv")

# Or we can use readr library using the command read_csv to import csv
library(readr)
iris_data_r <- read_csv("../data/Iris.csv")
```

Rows: 150 Columns: 6

-- Column specification -----

Delimiter: ","

chr (1): Species

dbl (5): Id, SepalLengthCm, SepalWidthCm, PetalLengthCm, PetalWidthCm

i Use ``spec()`` to retrieve the full column specification for this data.

i Specify the column types or set ``show_col_types = FALSE`` to quiet this message.

```
# View column names
names(iris_data)
```

```
[1] "Id"          "SepalLengthCm" "SepalWidthCm"  "PetalLengthCm"
[5] "PetalWidthCm" "Species"
```

```
# View first few rows
head(iris_data)
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	1	5.1	3.5	1.4	0.2	Iris-setosa
2	2	4.9	3.0	1.4	0.2	Iris-setosa
3	3	4.7	3.2	1.3	0.2	Iris-setosa
4	4	4.6	3.1	1.5	0.2	Iris-setosa
5	5	5.0	3.6	1.4	0.2	Iris-setosa
6	6	5.4	3.9	1.7	0.4	Iris-setosa

```
# Check structure
str(iris_data)
```

```
'data.frame':  150 obs. of  6 variables:
 $ Id      : int  1 2 3 4 5 6 7 8 9 10 ...
 $ SepalLengthCm: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ SepalWidthCm : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ PetalLengthCm: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ PetalWidthCm : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species      : chr  "Iris-setosa" "Iris-setosa" "Iris-setosa" "Iris-
setosa" ...
```

1.2.2 Understanding the Difference: read.csv() vs read_csv()

```
# Base R: read.csv()
class(iris_data)      # Returns "data.frame"
```

```
[1] "data.frame"
```

```
# readr: read_csv()
class(iris_data_r)    # Returns "spec_tbl_df" "tbl_df" "tbl" "data.frame"
```

```
[1] "spec_tbl_df" "tbl_df"      "tbl"        "data.frame"
```

```
# Both work, but read_csv() is generally faster and has better defaults
```

1.2.3 Quick Data Exploration

```
# Dimensions  
dim(iris_data)
```

```
[1] 150  6
```

```
# Summary statistics  
summary(iris_data)
```

Id	SepalLengthCm	SepalWidthCm	PetalLengthCm
Min. : 1.00	Min. :4.300	Min. :2.000	Min. :1.000
1st Qu.: 38.25	1st Qu.:5.100	1st Qu.:2.800	1st Qu.:1.600
Median : 75.50	Median :5.800	Median :3.000	Median :4.350
Mean : 75.50	Mean :5.843	Mean :3.054	Mean :3.759
3rd Qu.:112.75	3rd Qu.:6.400	3rd Qu.:3.300	3rd Qu.:5.100
Max. :150.00	Max. :7.900	Max. :4.400	Max. :6.900

PetalWidthCm	Species
Min. :0.100	Length:150
1st Qu.:0.300	Class :character
Median :1.300	Mode :character
Mean :1.199	
3rd Qu.:1.800	
Max. :2.500	

```
# View in RStudio  
# View(iris_data)
```

1.3 Part 2: Data Cleaning and Manipulation using dplyr (40 mins)

1.3.1 Load Required Packages

```
library(dplyr)
```

```
Attaching package: 'dplyr'
```

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

1.3.2 The Pipe Operator: %>%

The pipe operator %>% makes code more readable by chaining operations together.

```
# Without pipe (hard to read)
head(filter(iris_data, SepalLengthCm > 6))
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	51	7.0	3.2	4.7	1.4	Iris-versicolor
2	52	6.4	3.2	4.5	1.5	Iris-versicolor
3	53	6.9	3.1	4.9	1.5	Iris-versicolor
4	55	6.5	2.8	4.6	1.5	Iris-versicolor
5	57	6.3	3.3	4.7	1.6	Iris-versicolor
6	59	6.6	2.9	4.6	1.3	Iris-versicolor

```
# With pipe (easier to read)
iris_data %>%
  filter(SepalLengthCm > 6) %>%
  head()
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	51	7.0	3.2	4.7	1.4	Iris-versicolor
2	52	6.4	3.2	4.5	1.5	Iris-versicolor
3	53	6.9	3.1	4.9	1.5	Iris-versicolor
4	55	6.5	2.8	4.6	1.5	Iris-versicolor
5	57	6.3	3.3	4.7	1.6	Iris-versicolor
6	59	6.6	2.9	4.6	1.3	Iris-versicolor

Keyboard shortcut: Ctrl + Shift + M (Windows) or Cmd + Shift + M (Mac)

1.3.3 Basic Wrangling Examples

1.3.3.1 Selecting Columns with `select()`

```
# Select specific columns
iris_data %>%
  select(Species, SepalLengthCm, PetalLengthCm) %>%
  head()
```

	Species	SepalLengthCm	PetalLengthCm
1	Iris-setosa	5.1	1.4
2	Iris-setosa	4.9	1.4
3	Iris-setosa	4.7	1.3
4	Iris-setosa	4.6	1.5
5	Iris-setosa	5.0	1.4
6	Iris-setosa	5.4	1.7

```
# Select columns using patterns
iris_data %>%
  select(starts_with("Petal")) %>%
  head()
```

	PetalLengthCm	PetalWidthCm
1	1.4	0.2
2	1.4	0.2
3	1.3	0.2
4	1.5	0.2
5	1.4	0.2
6	1.7	0.4

```
iris_data %>%
  select(ends_with("Cm")) %>%
  head()
```

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm
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
4	4.6	3.1	1.5	0.2
5	5.0	3.6	1.4	0.2
6	5.4	3.9	1.7	0.4

```
# Exclude columns with minus sign
iris_data %>%
  select(-Id) %>%
  head()
```

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	5.1	3.5	1.4	0.2	Iris-setosa
2	4.9	3.0	1.4	0.2	Iris-setosa
3	4.7	3.2	1.3	0.2	Iris-setosa
4	4.6	3.1	1.5	0.2	Iris-setosa
5	5.0	3.6	1.4	0.2	Iris-setosa
6	5.4	3.9	1.7	0.4	Iris-setosa

1.3.3.2 Filtering Rows with filter()

```
# Filter for setosa species only
iris_data %>%
  filter(Species == "Iris-setosa") %>%
  head()
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	1	5.1	3.5	1.4	0.2	Iris-setosa
2	2	4.9	3.0	1.4	0.2	Iris-setosa
3	3	4.7	3.2	1.3	0.2	Iris-setosa
4	4	4.6	3.1	1.5	0.2	Iris-setosa
5	5	5.0	3.6	1.4	0.2	Iris-setosa
6	6	5.4	3.9	1.7	0.4	Iris-setosa

```
# Filter flowers with long petals
iris_data %>%
  filter(PetalLengthCm > 5) %>%
  head()
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	84	6.0	2.7	5.1	1.6	Iris-versicolor
2	101	6.3	3.3	6.0	2.5	Iris-virginica
3	102	5.8	2.7	5.1	1.9	Iris-virginica
4	103	7.1	3.0	5.9	2.1	Iris-virginica
5	104	6.3	2.9	5.6	1.8	Iris-virginica
6	105	6.5	3.0	5.8	2.2	Iris-virginica

```
# Multiple conditions with AND (&)
iris_data %>%
  filter(Species == "Iris-virginica" & SepalLengthCm > 6.5) %>%
  head()
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	103	7.1	3.0	5.9	2.1	Iris-virginica
2	106	7.6	3.0	6.6	2.1	Iris-virginica
3	108	7.3	2.9	6.3	1.8	Iris-virginica
4	109	6.7	2.5	5.8	1.8	Iris-virginica
5	110	7.2	3.6	6.1	2.5	Iris-virginica
6	113	6.8	3.0	5.5	2.1	Iris-virginica

```
# Multiple conditions with OR (|)
iris_data %>%
  filter(PetalLengthCm > 6 | PetalWidthCm > 2) %>%
  head()
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	101	6.3	3.3	6.0	2.5	Iris-virginica
2	103	7.1	3.0	5.9	2.1	Iris-virginica
3	105	6.5	3.0	5.8	2.2	Iris-virginica
4	106	7.6	3.0	6.6	2.1	Iris-virginica
5	108	7.3	2.9	6.3	1.8	Iris-virginica
6	110	7.2	3.6	6.1	2.5	Iris-virginica

```
# Using %in% operator for multiple values
iris_data %>%
  filter(Species %in% c("Iris-setosa", "Iris-versicolor")) %>%
  head()
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	1	5.1	3.5	1.4	0.2	Iris-setosa
2	2	4.9	3.0	1.4	0.2	Iris-setosa
3	3	4.7	3.2	1.3	0.2	Iris-setosa
4	4	4.6	3.1	1.5	0.2	Iris-setosa
5	5	5.0	3.6	1.4	0.2	Iris-setosa
6	6	5.4	3.9	1.7	0.4	Iris-setosa

1.3.3.3 Creating New Variables with mutate()

```
# Calculate areas
iris_data <- iris_data %>%
  mutate(
    SepalArea = SepalLengthCm * SepalWidthCm,
    PetalArea = PetalLengthCm * PetalWidthCm
  )

head(iris_data)
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	1	5.1	3.5	1.4	0.2	Iris-setosa
2	2	4.9	3.0	1.4	0.2	Iris-setosa
3	3	4.7	3.2	1.3	0.2	Iris-setosa
4	4	4.6	3.1	1.5	0.2	Iris-setosa
5	5	5.0	3.6	1.4	0.2	Iris-setosa
6	6	5.4	3.9	1.7	0.4	Iris-setosa

	SepalArea	PetalArea
1	17.85	0.28
2	14.70	0.28
3	15.04	0.26
4	14.26	0.30
5	18.00	0.28
6	21.06	0.68

```
# Create categorical variables
iris_data <- iris_data %>%
  mutate(
    SizeCategory = ifelse(PetalLengthCm > 4, "Large", "Small"),
    SepalRatio = SepalLengthCm / SepalWidthCm
  )

head(iris_data)
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	1	5.1	3.5	1.4	0.2	Iris-setosa
2	2	4.9	3.0	1.4	0.2	Iris-setosa
3	3	4.7	3.2	1.3	0.2	Iris-setosa
4	4	4.6	3.1	1.5	0.2	Iris-setosa
5	5	5.0	3.6	1.4	0.2	Iris-setosa

6	6	5.4	3.9	1.7	0.4	Iris-setosa
	SepalArea	PetalArea	SizeCategory	SepalRatio		
1	17.85	0.28	Small	1.457143		
2	14.70	0.28	Small	1.633333		
3	15.04	0.26	Small	1.468750		
4	14.26	0.30	Small	1.483871		
5	18.00	0.28	Small	1.388889		
6	21.06	0.68	Small	1.384615		

```
# Using case_when() for multiple conditions
iris_data <- iris_data %>%
  mutate(
    PetalSize = case_when(
      PetalLengthCm < 2 ~ "Small",
      PetalLengthCm < 5 ~ "Medium",
      TRUE ~ "Large"
    )
  )
head(iris_data)
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	1	5.1	3.5	1.4	0.2	Iris-setosa
2	2	4.9	3.0	1.4	0.2	Iris-setosa
3	3	4.7	3.2	1.3	0.2	Iris-setosa
4	4	4.6	3.1	1.5	0.2	Iris-setosa
5	5	5.0	3.6	1.4	0.2	Iris-setosa
6	6	5.4	3.9	1.7	0.4	Iris-setosa

	SepalArea	PetalArea	SizeCategory	SepalRatio	PetalSize
1	17.85	0.28	Small	1.457143	Small
2	14.70	0.28	Small	1.633333	Small
3	15.04	0.26	Small	1.468750	Small
4	14.26	0.30	Small	1.483871	Small
5	18.00	0.28	Small	1.388889	Small
6	21.06	0.68	Small	1.384615	Small

1.3.3.4 Sorting Rows with arrange()

```
# Sort by Petal Length (ascending)
iris_data %>%
  arrange(PetalLengthCm) %>%
  head()
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	23	4.6	3.6	1.0	0.2	Iris-setosa
2	14	4.3	3.0	1.1	0.1	Iris-setosa
3	15	5.8	4.0	1.2	0.2	Iris-setosa
4	36	5.0	3.2	1.2	0.2	Iris-setosa
5	3	4.7	3.2	1.3	0.2	Iris-setosa
6	17	5.4	3.9	1.3	0.4	Iris-setosa

	SepalArea	PetalArea	SizeCategory	SepalRatio	PetalSize
1	16.56	0.20	Small	1.277778	Small
2	12.90	0.11	Small	1.433333	Small
3	23.20	0.24	Small	1.450000	Small
4	16.00	0.24	Small	1.562500	Small
5	15.04	0.26	Small	1.468750	Small
6	21.06	0.52	Small	1.384615	Small

```
# Sort by Petal Length (descending)
iris_data %>%
  arrange(desc(PetalLengthCm)) %>%
  head()
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	119	7.7	2.6	6.9	2.3	Iris-virginica
2	118	7.7	3.8	6.7	2.2	Iris-virginica
3	123	7.7	2.8	6.7	2.0	Iris-virginica
4	106	7.6	3.0	6.6	2.1	Iris-virginica
5	132	7.9	3.8	6.4	2.0	Iris-virginica
6	108	7.3	2.9	6.3	1.8	Iris-virginica

	SepalArea	PetalArea	SizeCategory	SepalRatio	PetalSize
1	20.02	15.87	Large	2.961538	Large
2	29.26	14.74	Large	2.026316	Large
3	21.56	13.40	Large	2.750000	Large
4	22.80	13.86	Large	2.533333	Large
5	30.02	12.80	Large	2.078947	Large
6	21.17	11.34	Large	2.517241	Large

```
# Sort by multiple columns
iris_data %>%
  arrange(Species, desc(SepalLengthCm)) %>%
  head()
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
--	----	---------------	--------------	---------------	--------------	---------

1	15	5.8	4.0	1.2	0.2	Iris-setosa
2	16	5.7	4.4	1.5	0.4	Iris-setosa
3	19	5.7	3.8	1.7	0.3	Iris-setosa
4	34	5.5	4.2	1.4	0.2	Iris-setosa
5	37	5.5	3.5	1.3	0.2	Iris-setosa
6	6	5.4	3.9	1.7	0.4	Iris-setosa

	SepalArea	PetalArea	SizeCategory	SepalRatio	PetalSize
1	23.20	0.24	Small	1.450000	Small
2	25.08	0.60	Small	1.295455	Small
3	21.66	0.51	Small	1.500000	Small
4	23.10	0.28	Small	1.309524	Small
5	19.25	0.26	Small	1.571429	Small
6	21.06	0.68	Small	1.384615	Small

1.3.3.5 Summarizing with group_by() and summarize()

```
# Overall summary
iris_data %>%
  summarize(
    avg_sepal_length = mean(SepalLengthCm, na.rm = TRUE),
    avg_petal_length = mean(PetalLengthCm, na.rm = TRUE),
    total_flowers = n()
  )
```

	avg_sepal_length	avg_petal_length	total_flowers
1	5.843333	3.758667	150

```
# Summary by species
iris_data %>%
  group_by(Species) %>%
  summarize(
    avg_sepal_length = mean(SepalLengthCm, na.rm = TRUE),
    avg_sepal_width = mean(SepalWidthCm, na.rm = TRUE),
    avg_petal_length = mean(PetalLengthCm, na.rm = TRUE),
    avg_petal_width = mean(PetalWidthCm, na.rm = TRUE),
    count = n()
  )
```

```
# A tibble: 3 x 6
  Species      avg_sepal_length avg_sepal_width avg_petal_length avg_petal_width
  <chr>          <dbl>          <dbl>          <dbl>          <dbl>
```

1	Iris-setosa	5.01	3.42	1.46	0.244
2	Iris-versic~	5.94	2.77	4.26	1.33
3	Iris-virgin~	6.59	2.97	5.55	2.03

i 1 more variable: count <int>

```
# Summary by multiple groups
iris_data %>%
  group_by(Species, SizeCategory) %>%
  summarize(
    avg_sepal_length = mean(SepalLengthCm, na.rm = TRUE),
    count = n(),
    .groups = 'drop'
  )
```

```
# A tibble: 4 x 4
  Species      SizeCategory avg_sepal_length count
  <chr>        <chr>          <dbl>   <int>
1 Iris-setosa   Small             5.01     50
2 Iris-versicolor Large          6.15     34
3 Iris-versicolor Small          5.49     16
4 Iris-virginica Large          6.59     50
```

1.3.4 Combining Multiple Operations

```
# Complex pipeline: Find large virginica flowers and their stats
iris_data %>%
  filter(Species == "Iris-virginica", PetalLengthCm > 6) %>%
  select(Species, SepalLengthCm, PetalLengthCm, SepalArea, PetalArea) %>%
  arrange(desc(PetalArea)) %>%
  head(10)
```

	Species	SepalLengthCm	PetalLengthCm	SepalArea	PetalArea
1	Iris-virginica	7.7	6.9	20.02	15.87
2	Iris-virginica	7.2	6.1	25.92	15.25
3	Iris-virginica	7.7	6.7	29.26	14.74
4	Iris-virginica	7.7	6.1	23.10	14.03
5	Iris-virginica	7.6	6.6	22.80	13.86
6	Iris-virginica	7.7	6.7	21.56	13.40
7	Iris-virginica	7.9	6.4	30.02	12.80
8	Iris-virginica	7.4	6.1	20.72	11.59
9	Iris-virginica	7.3	6.3	21.17	11.34

1.3.5 Additional Useful Functions

1.3.5.1 Count rows with count()

```
# Count flowers by species
iris_data %>%
  count(Species)
```

```
      Species  n
1  Iris-setosa 50
2 Iris-versicolor 50
3  Iris-virginica 50
```

```
# Count with sorting
iris_data %>%
  count(Species, sort = TRUE)
```

```
      Species  n
1  Iris-setosa 50
2 Iris-versicolor 50
3  Iris-virginica 50
```

```
# Count by multiple variables
iris_data %>%
  count(Species, SizeCategory)
```

```
      Species SizeCategory  n
1  Iris-setosa      Small  50
2 Iris-versicolor      Large 34
3 Iris-versicolor      Small 16
4  Iris-virginica      Large 50
```

1.3.5.2 Get unique values with distinct()

```
# Get unique species
iris_data %>%
  distinct(Species)
```

```

      Species
1    Iris-setosa
2 Iris-versicolor
3  Iris-virginica

```

```

# Get unique combinations
iris_data %>%
  distinct(Species, PetalSize)

```

```

      Species PetalSize
1    Iris-setosa    Small
2 Iris-versicolor  Medium
3 Iris-versicolor   Large
4  Iris-virginica   Large
5  Iris-virginica  Medium

```

1.4 Part 3: Handling Missing Data (30 mins)

1.4.1 Checking Missing Values

```

# Load nanian for missing data visualization
library(nanian)

# Check for missing values
miss_var_summary(iris_data)

```

```

# A tibble: 11 x 3
  variable      n_miss pct_miss
  <chr>         <int>   <num>
1 Id           0         0
2 SepalLengthCm 0         0
3 SepalWidthCm  0         0
4 PetalLengthCm 0         0
5 PetalWidthCm  0         0
6 Species       0         0
7 SepalArea     0         0
8 PetalArea     0         0

```

```

 9 SizeCategory      0      0
10 SepalRatio        0      0
11 PetalSize         0      0

```

```

# Check if any values are missing
any(is.na(iris_data))

```

```
[1] FALSE
```

```

# Count NAs in each column
colSums(is.na(iris_data))

```

```

      Id SepalLengthCm SepalWidthCm PetalLengthCm PetalWidthCm
      0              0             0             0             0
Species      SepalArea      PetalArea SizeCategory      SepalRatio
      0              0             0             0             0
PetalSize
      0

```

1.4.2 Creating Sample Data with Missing Values

For demonstration, let's introduce some missing values:

```

# Create a copy with missing values
iris_missing <- iris_data
set.seed(123) # For reproducibility

# Randomly introduce NAs
iris_missing$SepalLengthCm[sample(1:nrow(iris_missing), 10)] <- NA
iris_missing$PetalWidthCm[sample(1:nrow(iris_missing), 15)] <- NA

# Check missing data
miss_var_summary(iris_missing)

```

```

# A tibble: 11 x 3
  variable      n_miss pct_miss
  <chr>         <int>   <num>
1 PetalWidthCm     15     10
2 SepalLengthCm    10     6.67
3 Id              0      0

```


4	SepalWidthCm	0	0
5	PetalLengthCm	0	0
6	Species	0	0
7	SepalArea	0	0
8	PetalArea	0	0
9	SizeCategory	0	0
10	SepalRatio	0	0
11	PetalSize	0	0

1.4.3 Removing Missing Values

```
# Remove rows with any missing values
iris_complete <- na.omit(iris_missing)

cat("Original rows:", nrow(iris_missing), "\n")
```

Original rows: 150

```
cat("After removing NAs:", nrow(iris_complete), "\n")
```

After removing NAs: 127

```
# Remove only if specific column has NA
iris_filtered <- iris_missing %>%
  filter(!is.na(SepalLengthCm))

cat("After filtering SepalLengthCm:", nrow(iris_filtered), "\n")
```

After filtering SepalLengthCm: 140

1.4.4 Replacing Missing Values

```
# Replace NAs with mean
iris_mean <- iris_missing %>%
  mutate(
    SepalLengthCm = ifelse(is.na(SepalLengthCm),
                          mean(SepalLengthCm, na.rm = TRUE),
```

```

        SepalLengthCm),
    PetalWidthCm = ifelse(is.na(PetalWidthCm),
                          mean(PetalWidthCm, na.rm = TRUE),
                          PetalWidthCm)
  )

# Verify
miss_var_summary(iris_mean)

# A tibble: 11 x 3
  variable      n_miss pct_miss
  <chr>         <int>    <num>
1 Id             0         0
2 SepalLengthCm  0         0
3 SepalWidthCm   0         0
4 PetalLengthCm  0         0
5 PetalWidthCm   0         0
6 Species        0         0
7 SepalArea      0         0
8 PetalArea       0         0
9 SizeCategory   0         0
10 SepalRatio     0         0
11 PetalSize      0         0

# Replace with median (more robust to outliers)
iris_median <- iris_missing %>%
  mutate(
    SepalLengthCm = ifelse(is.na(SepalLengthCm),
                          median(SepalLengthCm, na.rm = TRUE),
                          SepalLengthCm),
    PetalWidthCm = ifelse(is.na(PetalWidthCm),
                          median(PetalWidthCm, na.rm = TRUE),
                          PetalWidthCm)
  )

# Replace with species-specific mean (group imputation)
iris_group_mean <- iris_missing %>%
  group_by(Species) %>%
  mutate(
    SepalLengthCm = ifelse(is.na(SepalLengthCm),
                          mean(SepalLengthCm, na.rm = TRUE),

```

```

        SepalLengthCm),
  PetalWidthCm = ifelse(is.na(PetalWidthCm),
                        mean(PetalWidthCm, na.rm = TRUE),
                        PetalWidthCm)
) %>%
ungroup()

miss_var_summary(iris_group_mean)

```

```

# A tibble: 11 x 3
  variable      n_miss pct_miss
  <chr>         <int>   <num>
1 Id             0         0
2 SepalLengthCm  0         0
3 SepalWidthCm   0         0
4 PetalLengthCm  0         0
5 PetalWidthCm   0         0
6 Species        0         0
7 SepalArea      0         0
8 PetalArea      0         0
9 SizeCategory   0         0
10 SepalRatio    0         0
11 PetalSize     0         0

```

1.4.5 Handling NAs During Analysis

```

# Without na.rm - returns NA
mean(iris_missing$SepalLengthCm)

```

```
[1] NA
```

```

# With na.rm = TRUE - ignores NAs
mean(iris_missing$SepalLengthCm, na.rm = TRUE)

```

```
[1] 5.855714
```

```
# Summary with NA handling
iris_missing %>%
  summarize(
    mean_sepal = mean(SepalLengthCm, na.rm = TRUE),
    median_sepal = median(SepalLengthCm, na.rm = TRUE),
    count_non_na = sum(!is.na(SepalLengthCm)),
    count_na = sum(is.na(SepalLengthCm))
  )
```

```
mean_sepal median_sepal count_non_na count_na
1 5.855714 5.8 140 10
```

1.5 Part 4: Practice and Q&A (20 mins)

1.5.1 Practice Tasks (based on iris data)

1.5.1.1 Task 1: Import and Explore

- Import the iris dataset
- Display the first 10 rows
- Check the number of rows and columns

```
# Solution
iris_practice <- read.csv("../data/Iris.csv")
head(iris_practice, 10)
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	1	5.1	3.5	1.4	0.2	Iris-setosa
2	2	4.9	3.0	1.4	0.2	Iris-setosa
3	3	4.7	3.2	1.3	0.2	Iris-setosa
4	4	4.6	3.1	1.5	0.2	Iris-setosa
5	5	5.0	3.6	1.4	0.2	Iris-setosa
6	6	5.4	3.9	1.7	0.4	Iris-setosa
7	7	4.6	3.4	1.4	0.3	Iris-setosa
8	8	5.0	3.4	1.5	0.2	Iris-setosa
9	9	4.4	2.9	1.4	0.2	Iris-setosa
10	10	4.9	3.1	1.5	0.1	Iris-setosa

```
dim(iris_practice)
```

```
[1] 150   6
```

1.5.1.2 Task 2: Filter and Select

- Select only Iris-virginica flowers with PetalLengthCm > 6
- Show only Species, SepalLengthCm, and PetalLengthCm columns

```
# Solution
iris_practice %>%
  filter(Species == "Iris-virginica", PetalLengthCm > 6) %>%
  select(Species, SepalLengthCm, PetalLengthCm)
```

	Species	SepalLengthCm	PetalLengthCm
1	Iris-virginica	7.6	6.6
2	Iris-virginica	7.3	6.3
3	Iris-virginica	7.2	6.1
4	Iris-virginica	7.7	6.7
5	Iris-virginica	7.7	6.9
6	Iris-virginica	7.7	6.7
7	Iris-virginica	7.4	6.1
8	Iris-virginica	7.9	6.4
9	Iris-virginica	7.7	6.1

1.5.1.3 Task 3: Create New Variables

- Create a variable for PetalRatio = PetalLengthCm / PetalWidthCm
- Create a variable for SepalRatio = SepalLengthCm / SepalWidthCm

```
# Solution
iris_practice <- iris_practice %>%
  mutate(
    PetalRatio = PetalLengthCm / PetalWidthCm,
    SepalRatio = SepalLengthCm / SepalWidthCm
  )

head(iris_practice)
```

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
1	1	5.1	3.5	1.4	0.2	Iris-setosa
2	2	4.9	3.0	1.4	0.2	Iris-setosa
3	3	4.7	3.2	1.3	0.2	Iris-setosa
4	4	4.6	3.1	1.5	0.2	Iris-setosa
5	5	5.0	3.6	1.4	0.2	Iris-setosa
6	6	5.4	3.9	1.7	0.4	Iris-setosa

	PetalRatio	SepalRatio
1	7.00	1.457143
2	7.00	1.633333
3	6.50	1.468750
4	7.50	1.483871
5	7.00	1.388889
6	4.25	1.384615

1.5.1.4 Task 4: Group and Summarize

- Group by Species
- Calculate average SepalLengthCm, PetalLengthCm, and count per species

```
# Solution
iris_practice %>%
  group_by(Species) %>%
  summarize(
    avg_sepal_length = mean(SepalLengthCm, na.rm = TRUE),
    avg_petal_length = mean(PetalLengthCm, na.rm = TRUE),
    count = n()
  )
```

```
# A tibble: 3 x 4
  Species      avg_sepal_length avg_petal_length count
  <chr>          <dbl>          <dbl> <int>
1 Iris-setosa      5.01            1.46     50
2 Iris-versicolor  5.94            4.26     50
3 Iris-virginica   6.59            5.55     50
```

1.5.1.5 Task 5: Complex Pipeline

- Filter for flowers with SepalLengthCm > 6
- Create a new variable TotalLength = SepalLengthCm + PetalLengthCm
- Group by Species

- Calculate average TotalLength
- Sort by average TotalLength descending

```
# Solution
iris_practice %>%
  filter(SepalLengthCm > 6) %>%
  mutate(TotalLength = SepalLengthCm + PetalLengthCm) %>%
  group_by(Species) %>%
  summarize(
    avg_total_length = mean(TotalLength, na.rm = TRUE),
    count = n()
  ) %>%
  arrange(desc(avg_total_length))
```

```
# A tibble: 2 x 3
  Species      avg_total_length count
  <chr>          <dbl>   <int>
1 Iris-virginica      12.5     41
2 Iris-versicolor     11.0     20
```

1.6 Further Resources (for Data Import & Wrangling)

- Tidyverse Documentation: <https://www.tidyverse.org/packages/>
- Importing Data in R: <https://r4ds.hadley.nz/data-import.html>
- Data Transformation Cheatsheet: <https://posit.co/resources/cheatsheets/>