



## 1.3.4: Missing Data and Sampling Weights (brief intro) (In Person)

### Session Objectives (*updated*)

1. Identify, summarize and visualize missing data.
  2. Missing Data Mechanisms (bias mechanisms or models)
  3. Missing Data Handling and Imputation Methods (brief intro)
  4. Impact of Sampling Weights for Survey Data (brief intro)
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### 0. Prework - Before You Begin

#### A. Install packages

If you do not have them already, install the following packages from CRAN (using the RStudio Menu “Tools/Install” Packages interface):

- [VIM](#) and [VIM package website](#)
- (Optional) [skimr](#) and [skimr website](#)
- (Optional) [modelsummary](#) and [modelsummary website](#)
- (Optional) [summarytools](#) and [summarytools on Github](#)
- [palmerpenguins](#) and [palmerpenguins website](#)
- [ggplot2](#) and [ggplot2 website](#)
- [naniar](#) and [naniar website](#)
- [dplyr](#) and [dplyr website](#)
- [gtsummary](#) and [gtsummary website](#)
- [Hmisc](#) and [Hmisc website](#)
- [mice](#) and [mice website](#)



**B. Review these online Book Chapters:**

- [BOOK: Flexible Imputation of Missing Data, 2nd ed., by Stef van Buuren \(mice package author\) - Chapter 1 “Introduction”, Sections 1.1-1.4](#)
- [BOOK: The Epidemiologist R Handbook - Chapter 20 “Missing Data”](#)

**C. Open/create an RStudio project for this lesson**

Let's start with the `myfirstRproject` RStudio project you created in [Module 1.3.2 - part 1](#). If you have not yet created this `myfirstRproject` RStudio project, go ahead and create a new RStudio Project for this lesson. *Feel free to name your project whatever you want, it does not need to be named `myfirstRproject`.*

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## 1. Identify, summarize and visualize missing data

### Find Missing Data in Your Dataset.

One simple way to find missing data is to open it in the Data Viewer window and sort the data.

For example, load the VIM package and take a look at the `sleep` dataset provided within this package.

```
library(VIM)
data("sleep")
```

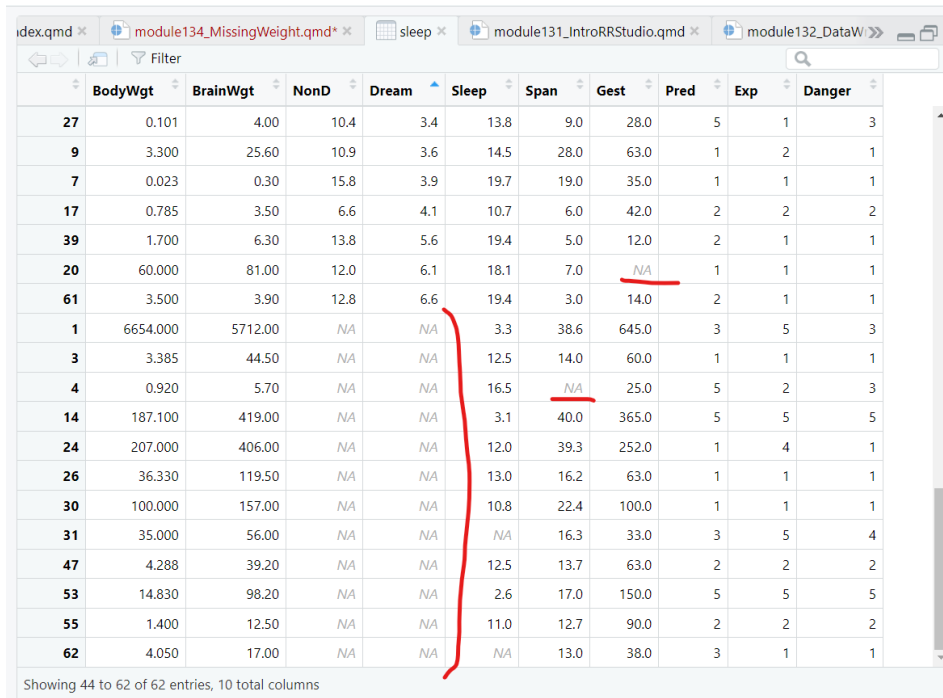
Click on the `sleep` dataset to open it in the data viewer:

	BodyWgt	BrainWgt	NonD	Dream	Sleep	Span	Gest	Pred	Exp	Danger
1	6654.000	5712.00	NA	NA	3.3	38.6	645.0	3	5	3
2	1.000	6.60	6.3	2.0	8.3	4.5	42.0	3	1	3
3	3.385	44.50	NA	NA	12.5	14.0	60.0	1	1	1
4	0.920	5.70	NA	NA	16.5	NA	25.0	5	2	3
5	2547.000	4603.00	2.1	1.8	3.9	69.0	624.0	3	5	4
6	10.550	179.50	9.1	0.7	9.8	27.0	180.0	4	4	4
7	0.023	0.30	15.8	3.9	19.7	19.0	35.0	1	1	1
8	160.000	169.00	5.2	1.0	6.2	30.4	392.0	4	5	4
9	3.300	25.60	10.9	3.6	14.5	28.0	63.0	1	2	1
10	52.160	440.00	8.3	1.4	9.7	50.0	230.0	1	1	1
11	0.425	6.40	11.0	1.5	12.5	7.0	112.0	5	4	4
12	465.000	423.00	3.2	0.7	3.9	30.0	281.0	5	5	5
13	0.550	2.40	7.6	2.7	10.3	NA	NA	2	1	2
14	187.100	419.00	NA	NA	3.1	40.0	365.0	5	5	5
15	0.075	1.20	6.3	2.1	8.4	3.5	42.0	1	1	1
16	3.000	25.00	8.6	0.0	8.6	50.0	28.0	2	2	2
17	0.785	3.50	6.6	4.1	10.7	6.0	42.0	2	2	2
18	0.200	5.00	9.5	1.2	10.7	10.4	120.0	2	2	2
19	1.410	17.50	4.8	1.3	6.1	34.0	NA	1	2	1

Showing 1 to 20 of 62 entries, 10 total columns

Notice the light grey NAs shown for the missing data spots in this dataset.

If we click on the column for the `Dream` variable and sort these values, notice that the NAs all now show up at the bottom of the viewer window. It does not matter if you sort ascending or descending, the NAs are always at the bottom of the viewer.



	BodyWgt	BrainWgt	NonD	Dream	Sleep	Span	Gest	Pred	Exp	Danger
27	0.101	4.00	10.4	3.4	13.8	9.0	28.0	5	1	3
9	3.300	25.60	10.9	3.6	14.5	28.0	63.0	1	2	1
7	0.023	0.30	15.8	3.9	19.7	19.0	35.0	1	1	1
17	0.785	3.50	6.6	4.1	10.7	6.0	42.0	2	2	2
39	1.700	6.30	13.8	5.6	19.4	5.0	12.0	2	1	1
20	60.000	81.00	12.0	6.1	18.1	7.0	NA	1	1	1
61	3.500	3.90	12.8	6.6	19.4	3.0	14.0	2	1	1
1	6654.000	5712.00	NA	NA	3.3	38.6	645.0	3	5	3
3	3.385	44.50	NA	NA	12.5	14.0	60.0	1	1	1
4	0.920	5.70	NA	NA	16.5	NA	25.0	5	2	3
14	187.100	419.00	NA	NA	3.1	40.0	365.0	5	5	5
24	207.000	406.00	NA	NA	12.0	39.3	252.0	1	4	1
26	36.330	119.50	NA	NA	13.0	16.2	63.0	1	1	1
30	100.000	157.00	NA	NA	10.8	22.4	100.0	1	1	1
31	35.000	56.00	NA	NA	NA	16.3	33.0	3	5	4
47	4.288	39.20	NA	NA	12.5	13.7	63.0	2	2	2
53	14.830	98.20	NA	NA	2.6	17.0	150.0	5	5	5
55	1.400	12.50	NA	NA	11.0	12.7	90.0	2	2	2
62	4.050	17.00	NA	NA	NA	13.0	38.0	3	1	1

This method is ok for a small dataset with not too many variables or rows of data. But let's look at other ways to summarize the amounts of missing data in your dataset.

**Describe Missing Data.****Built-in summary() function**

As we saw back in [Module 1.3.2, Section 5](#), we can use the `summary()` function to get some basic statistics for each variable in the dataset, including the number of NAs.

```
summary(sleep)
```

BodyWgt		BrainWgt		NonD		Dream	
Min.	: 0.005	Min.	: 0.14	Min.	: 2.100	Min.	:0.000
1st Qu.:	0.600	1st Qu.:	4.25	1st Qu.:	6.250	1st Qu.:	0.900
Median :	3.342	Median :	17.25	Median :	8.350	Median :	1.800
Mean :	198.790	Mean :	283.13	Mean :	8.673	Mean :	1.972
3rd Qu.:	48.203	3rd Qu.:	166.00	3rd Qu.:	11.000	3rd Qu.:	2.550
Max.	:6654.000	Max.	:5712.00	Max.	:17.900	Max.	:6.600
				NA's	:14	NA's	:12
Sleep		Span		Gest		Pred	
Min.	: 2.60	Min.	: 2.000	Min.	: 12.00	Min.	:1.000
1st Qu.:	8.05	1st Qu.:	6.625	1st Qu.:	35.75	1st Qu.:	2.000
Median :	10.45	Median :	15.100	Median :	79.00	Median :	3.000
Mean :	10.53	Mean :	19.878	Mean :	142.35	Mean :	2.871
3rd Qu.:	13.20	3rd Qu.:	27.750	3rd Qu.:	207.50	3rd Qu.:	4.000
Max.	:19.90	Max.	:100.000	Max.	:645.00	Max.	:5.000
NA's	:4	NA's	:4	NA's	:4		
Exp		Danger					
Min.	:1.000	Min.	:1.000				
1st Qu.:	1.000	1st Qu.:	1.000				
Median :	2.000	Median :	2.000				
Mean :	2.419	Mean :	2.613				
3rd Qu.:	4.000	3rd Qu.:	4.000				
Max.	:5.000	Max.	:5.000				

**skimr package**

Another helpful package is the **skimr** package which has the **skim()** function which provides a count of the amount of missing data and the proportion of complete data for that variable.

**i** Rmarkdown for **skimr** package

When “knitting” to HTML the code below creates the summary table with the miniture histograms. However, when “knitting” to PDF (using the default portrait layout) the histograms get cutoff on the page. Additional LaTeX customization is needed to change the layout to landscape to be able to see the histograms.

```
library(skimr)
skim(sleep)
```

Table 1: Data summary

Name	sleep
Number of rows	62
Number of columns	10
Column type frequency:	
numeric	10
Group variables	None

**Variable type: numeric**

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
BodyWgt	0	1.00	198.79	899.16	0.00	0.60	3.34	48.20	6654.0	
BrainWgt	0	1.00	283.13	930.28	0.14	4.25	17.25	166.00	5712.0	
NonD	14	0.77	8.67	3.67	2.10	6.25	8.35	11.00	17.9	
Dream	12	0.81	1.97	1.44	0.00	0.90	1.80	2.55	6.6	
Sleep	4	0.94	10.53	4.61	2.60	8.05	10.45	13.20	19.9	
Span	4	0.94	19.88	18.21	2.00	6.62	15.10	27.75	100.0	
Gest	4	0.94	142.35	146.81	12.00	35.75	79.00	207.50	645.0	
Pred	0	1.00	2.87	1.48	1.00	2.00	3.00	4.00	5.0	
Exp	0	1.00	2.42	1.60	1.00	1.00	2.00	4.00	5.0	
Danger	0	1.00	2.61	1.44	1.00	1.00	2.00	4.00	5.0	

**modelsummary package**

Another helpful package is the `modelsummary` package which has the `datasummary_skim()` function which is a slightly better version built off the `skimr::skim()` package and function.

```
library(modelsummary)
datasummary_skim(sleep)
```

	Unique	Missing Pct.	Mean	SD	Min	Median	Max	Histogram
BodyWgt	60	0	198.8	899.2	0.0	3.3	6654.0	
BrainWgt	59	0	283.1	930.3	0.1	17.2	5712.0	
NonD	40	23	8.7	3.7	2.1	8.4	17.9	
Dream	31	19	2.0	1.4	0.0	1.8	6.6	
Sleep	45	6	10.5	4.6	2.6	10.4	19.9	
Span	48	6	19.9	18.2	2.0	15.1	100.0	
Gest	50	6	142.4	146.8	12.0	79.0	645.0	
Pred	5	0	2.9	1.5	1.0	3.0	5.0	
Exp	5	0	2.4	1.6	1.0	2.0	5.0	
Danger	5	0	2.6	1.4	1.0	2.0	5.0	

**summarytools package**

Another package that also provides a nice summary of the variables in the dataset, is the `dfSummary()` from the `summarytools` dataset.

*NOTE: Learn more about how to use `summarytools::dfSummary()` in an Rmarkdown document at <https://cran.r-project.org/web/packages/summarytools/vignettes/rmarkdown.html>.*

```
library(summarytools)
view(dfSummary(sleep))
```





## Data Frame Summary

## sleep

Dimensions: 62 x 10

Duplicates: 0

No	Variable	Stats / Values	Freqs (% of Valid)	Graph	Valid	Missing
1	BodyWgt [numeric]	Mean (sd) : 198.8 (899.2) min ≤ med ≤ max: 0 ≤ 3.3 ≤ 6654 IQR (CV) : 47.6 (4.5)	60 distinct values		62 (100.0%)	0 (0.0%)
2	BrainWgt [numeric]	Mean (sd) : 283.1 (930.3) min ≤ med ≤ max: 0.1 ≤ 17.2 ≤ 5712 IQR (CV) : 161.8 (3.3)	59 distinct values		62 (100.0%)	0 (0.0%)
3	NonD [numeric]	Mean (sd) : 8.7 (3.7) min ≤ med ≤ max: 2.1 ≤ 8.4 ≤ 17.9 IQR (CV) : 4.8 (0.4)	39 distinct values		48 (77.4%)	14 (22.6%)
4	Dream [numeric]	Mean (sd) : 2 (1.4) min ≤ med ≤ max: 0 ≤ 1.8 ≤ 6.6 IQR (CV) : 1.7 (0.7)	30 distinct values		50 (80.6%)	12 (19.4%)
5	Sleep [numeric]	Mean (sd) : 10.5 (4.6) min ≤ med ≤ max: 2.6 ≤ 10.4 ≤ 19.9 IQR (CV) : 5.1 (0.4)	44 distinct values		58 (93.5%)	4 (6.5%)
6	Span [numeric]	Mean (sd) : 19.9 (18.2) min ≤ med ≤ max: 2 ≤ 15.1 ≤ 100 IQR (CV) : 21.1 (0.9)	47 distinct values		58 (93.5%)	4 (6.5%)
7	Gest [numeric]	Mean (sd) : 142.4 (146.8) min ≤ med ≤ max: 12 ≤ 79 ≤ 645 IQR (CV) : 171.8 (1)	49 distinct values		58 (93.5%)	4 (6.5%)
8	Pred [integer]	Mean (sd) : 2.9 (1.5) min ≤ med ≤ max: 1 ≤ 3 ≤ 5 IQR (CV) : 2 (0.5)	1 : 14 (22.6%) 2 : 15 (24.2%) 3 : 12 (19.4%) 4 : 7 (11.3%) 5 : 14 (22.6%)		62 (100.0%)	0 (0.0%)
9	Exp [integer]	Mean (sd) : 2.4 (1.6) min ≤ med ≤ max: 1 ≤ 2 ≤ 5 IQR (CV) : 3 (0.7)	1 : 27 (43.5%) 2 : 13 (21.0%) 3 : 4 ( 6.5%) 4 : 5 ( 8.1%) 5 : 13 (21.0%)		62 (100.0%)	0 (0.0%)
10	Danger [integer]	Mean (sd) : 2.6 (1.4) min ≤ med ≤ max: 1 ≤ 2 ≤ 5 IQR (CV) : 3 (0.6)	1 : 19 (30.6%) 2 : 14 (22.6%) 3 : 10 (16.1%) 4 : 10 (16.1%) 5 : 9 (14.5%)		62 (100.0%)	0 (0.0%)

Generated by [summarytools](#) 1.1.4 (R version 4.5.1)

2025-06-20



## 💡 Try It On Your Own

Try running `summary()` or `skim()` on the `penguins` dataset from the `palmerpenguins` package. Notice the summaries for the numeric and the factor type variables.

```
library(palmerpenguins)
summary(penguins)
```

```

      species      island bill_length_mm bill_depth_mm
Adelie   :152  Biscoe   :168   Min.    :32.10   Min.    :13.10
Chinstrap: 68  Dream    :124   1st Qu.:39.23   1st Qu.:15.60
Gentoo   :124  Torgersen: 52   Median :44.45   Median :17.30
                                Mean     :43.92   Mean   :17.15
                                3rd Qu.:48.50   3rd Qu.:18.70
                                Max.     :59.60   Max.   :21.50
                                NA's    :2      NA's   :2

flipper_length_mm  body_mass_g      sex      year
Min.    :172.0     Min.    :2700   female:165   Min.    :2007
1st Qu.:190.0     1st Qu.:3550   male  :168   1st Qu.:2007
Median :197.0     Median :4050   NA's  : 11   Median :2008
Mean    :200.9     Mean    :4202                   Mean    :2008
3rd Qu.:213.0     3rd Qu.:4750                   3rd Qu.:2009
Max.    :231.0     Max.    :6300                   Max.    :2009
NA's    :2        NA's    :2

```

`skim(penguins)`

Table 3: Data summary

Name	penguins
Number of rows	344
Number of columns	8
Column type frequency:	
factor	3
numeric	5
Group variables	None

**Variable type: factor**

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
species	0	1.00	FALSE	3	Ade: 152, Gen: 124, Chi: 68
island	0	1.00	FALSE	3	Bis: 168, Dre: 124, Tor: 52
sex	11	0.97	FALSE	2	mal: 168, fem: 165

**Variable type: numeric**

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
bill_length_mm	2	0.99	43.92	5.46	32.1	39.23	44.45	48.5	59.6	
bill_depth_mm	2	0.99	17.15	1.97	13.1	15.60	17.30	18.7	21.5	
flipper_length_mm	2	0.99	200.92	14.06	172.0	190.00	197.00	213.0	231.0	
body_mass_g	2	0.99	4201.75	801.95	2700.0	3550.00	4050.00	4750.0	6300.0	
year	0	1.00	2008.03	0.82	2007.0	2007.00	2008.00	2009.0	2009.0	



## Visualize Missing Data.

### Making plots with VIM package

The VIM package has an “aggregate” function `aggr()` which counts up the amounts of missing data for each variable and combinations of variables. The `sleep` dataset only has 10 variables.

#### ⚠ WARNING - Beware of Using Too Many Variables at Once

Before using the `aggr()` function, limit the number of variables. FIRST create a dataset with only the variables you are interested in BEFORE running the function - otherwise you may lock up your computer if you feed it too many variables at once.

```
# get the amount of missing data in the sleep dataset
a <- aggr(sleep, plot = FALSE)
a
```

Missings in variables:

Variable	Count
NonD	14
Dream	12
Sleep	4
Span	4
Gest	4

The default output from above only lists the variables that have one or more rows with missing data. However, you can get a list of all of the variables with this code:

```
a$missings
```

	Variable	Count
BodyWgt	BodyWgt	0
BrainWgt	BrainWgt	0
NonD	NonD	14
Dream	Dream	12
Sleep	Sleep	4
Span	Span	4
Gest	Gest	4
Pred	Pred	0
Exp	Exp	0
Danger	Danger	0



Next, let's get some plots of the missing data in the `sleep` dataset.

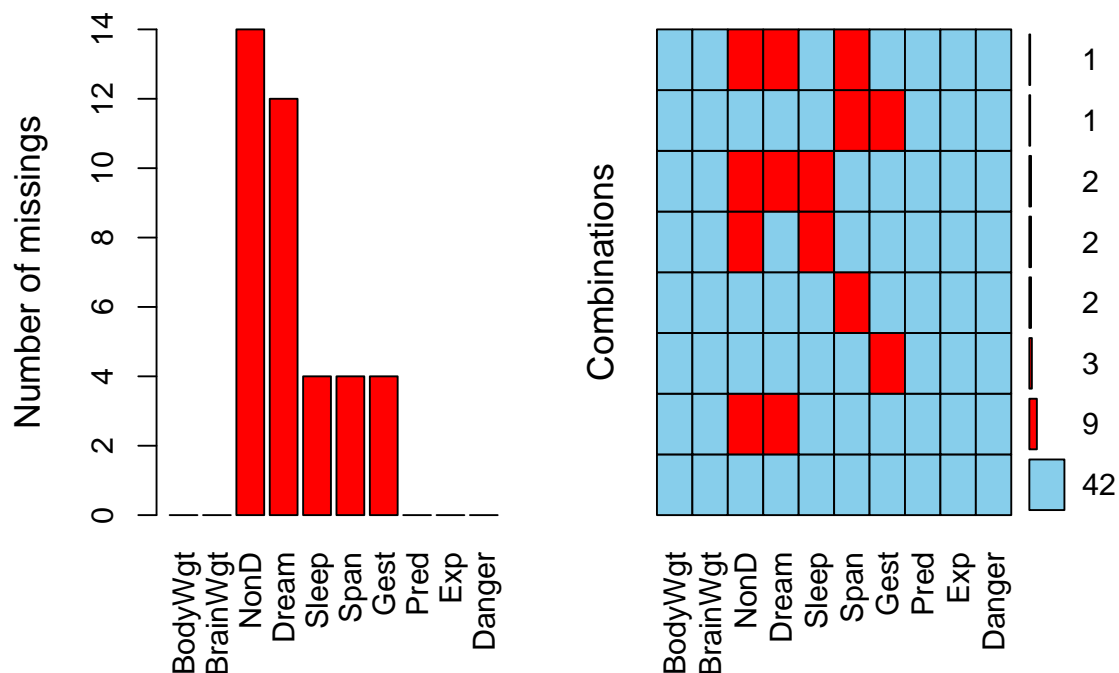
The plot on the LEFT below is a simple bar plot showing the missing counts for each variable in the dataset. Notice that there are only 5 variables with one or more missing values:

```
* `NonD`
* `Dream`
* `Sleep`
* `Span`
* `Gest`
```

The plot on the RIGHT however, shows the amounts of missing data for the various patterns of missing data for the 10 variables in the `sleep` dataset. For example, notice that of the 62 rows of data in the `sleep` dataset:

- there are only 42 rows with complete data with no missing data on all 10 variables (*i.e.*,  $42/62 = 67.7\%$  of the data is complete for all 10 variables);
- the next largest “pattern” of missing data is 9 rows that have both `NonD` and `Dream` variables with missing values; and
- there are 3 rows of data with the `gest` variable having missing data.

```
# make plots of the amounts and patterns of missing data
plot(a, numbers = TRUE, prop = FALSE)
```





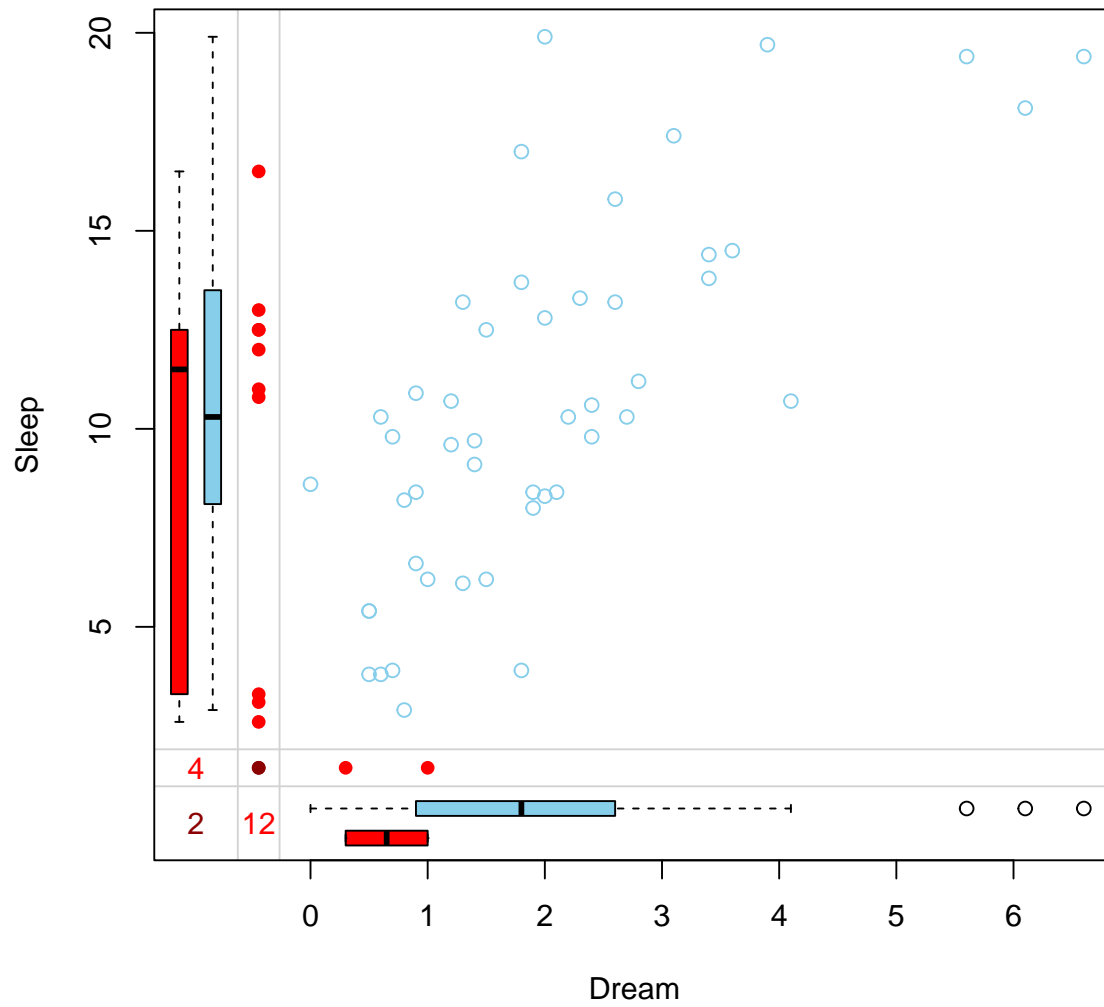
Exploring patterns of missingness can be informative to better understand why the data might be missing and possibly provide insights into the underlying mechanisms causing or leading to the missing data.

**Marginplots - see how missingness varies with other measures**

In addition to a usual scatterplot, the `marginplot()` function in the VIM package, also shows information about missing values in the plot margins.

The red boxplot on the left shows the distribution of all values of **Sleep** where **Dream** contains a missing value. The blue boxplot on the left shows the distribution of the values of **Sleep** where **Dream** is observed.

```
x <- sleep[, c("Dream", "Sleep")]  
marginplot(x)
```







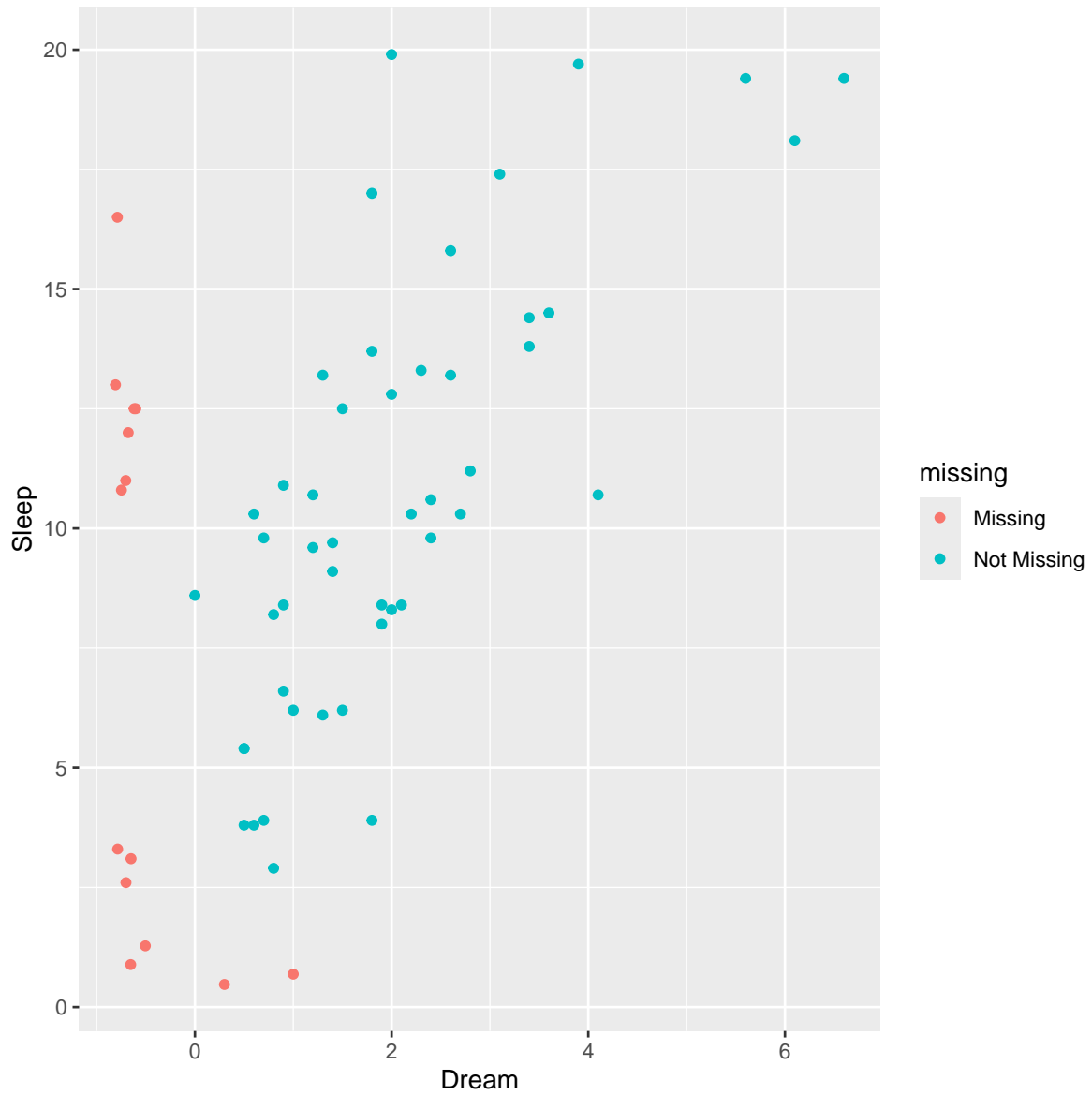
## Visualize Missing Data with the `naniar` package

The `naniar` package “provides principled, tidy ways to summarise, visualise, and manipulate missing data with minimal deviations from the workflows in `ggplot2` and tidy data.” See [naniar website](#).

For example, let’s make a similar to plot to what we did above to visualize the scatterplot between `Dream` and `Sleep` but also consider the amounts of missing data of one variable relative to the other variable in the plot. We can do this using the `geom_miss_point()` function provided in the `naniar` package which works with `ggplot2`.

```
library(naniar)
library(ggplot2)

ggplot(sleep,
       aes(x = Dream,
           y = Sleep)) +
  geom_miss_point()
```





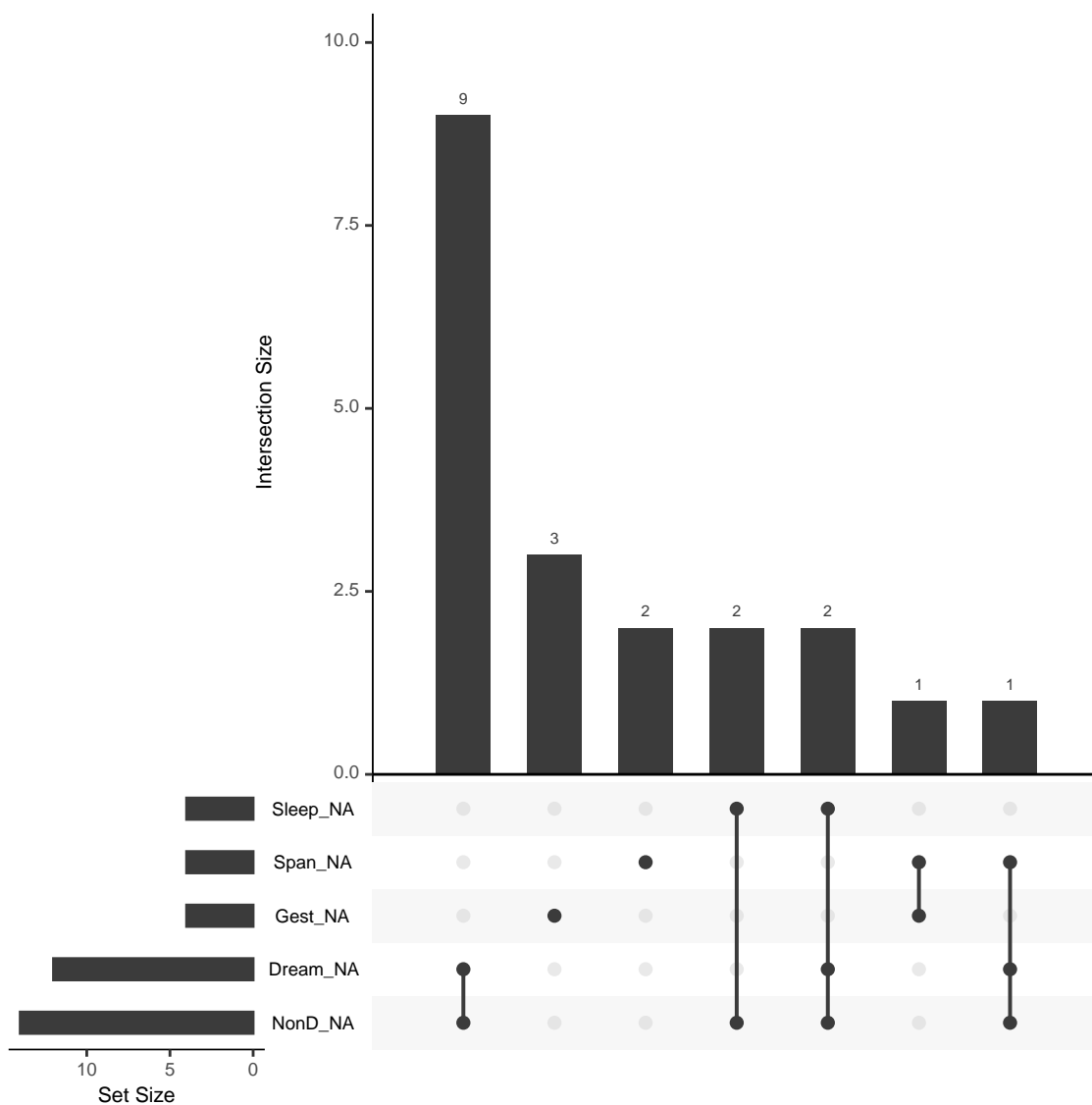
We can also create an **UpSet plot** which is useful for visualizing intersections between sets. In the case of missing data, we are interested in visualizing how the missing data for each variable overlaps with each other (i.e., the missing data patterns).

To create an UpSet plot for the missing data patterns for the 10 variables in the **sleep** dataset, we can use the `gg_miss_upset()` function. The plot produced is similar to the plot above from the **VIM** package.

Notice that the plot **ONLY** shows patterns for the 20 of 62 rows and for the 5 of 10 variables with any missing data. The plot shows that:

- 9 rows have missing data for both the **Dream** and **NonD** variables
- 3 rows have missing data for the **Gest** variable
- 2 rows have missing data for the **Span** variable
- 2 rows have missing data for both **Sleep** and **NonD**
- 2 rows have missing data for **Sleep**, **Dream** and **NonD** variables
- 1 row has missing data for both **Span** and **Gest**
- 1 row has missing data for **Span**, **Dream** and **NonD** variables

```
gg_miss_upset(sleep)
```





## 2. Missing Data Mechanisms (bias mechanisms or models)

### Why should we worry about missing data?

Setting aside bias concerns for the moment, missing data logistically causes issues with code - especially in R. At first glance this seems to be a huge pain since we get errors or nonsensical output. But these issues force us to deal with the missing data and provide explicit instructions to the computer code on how we want to address the missing data. *Learn more in the [Flexible Imputation of Missing Data BOOK](#).*

### Impact of missing data for descriptive stats like the mean

For example, let's find the mean of the `Dream` variable in the `sleep` dataset.

```
mean(sleep$Dream)
```

```
[1] NA
```

We get NA since there is missing data for the `Dream` variable, thus the mean of all rows is “not available”. So, we need to tell R to first remove the missing values (the NAs) prior to computing the mean.

```
mean(sleep$Dream, na.rm = TRUE)
```

```
[1] 1.972
```



## Impact of missing data for summary statistics

We did do a deep dive above and we know that there are 12 rows with missing values for the Dream variable. But if we had run the `mean()` function with `na.rm = TRUE`, we might not have known just how much data was missing. So, it is always a good idea to make sure to check for missing data and assess how much you have PRIOR to conducting any analyses.

As we saw in [Module 1.3.2, section 5](#) we can use the `gtsummary` package with the `tbl_summary()` function to get better summary statistics including a list of the amount of unknown (missing) rows. Let's get the means (and standard deviations) for 3 of the variables in the `sleep` dataset. Notice that there are no “unknowns” for `BrainWgt` since it has no missing values.

### 💡 Customizing `gtsummary::tbl_summary()`

Learn more at [Multiline Summaries Using `tbl\_summary\(\)`](#) on how I customized this table to include the count (N) of non-missing rows, mean and standard deviation along with the counts for the unknowns.

```
library(dplyr)
library(gtsummary)

sleep %>%
  select(Dream, Gest, BrainWgt) %>%
  tbl_summary(
    type = all_continuous() ~ "continuous2",
    statistic = all_continuous() ~ c(
      "{N_nonmiss}",
      "{mean} ({sd})"
    )
  )
```



Characteristic	N = 62
Dream	
N Non-missing	50
Mean (SD)	1.97 (1.44)
Unknown	12
Gest	
N Non-missing	58
Mean (SD)	142 (147)
Unknown	4
BrainWgt	
N Non-missing	62
Mean (SD)	283 (930)

### Impact of missing data for regression models

When running a model, like a regression model between **Dream** and **Sleep**, let's look at the summary output from fitting a linear model using the built-in `lm()` function:

```
summary(lm(Sleep ~ Dream, data = sleep))
```

Call:

```
lm(formula = Sleep ~ Dream, data = sleep)
```

Residuals:

```
      Min       1Q   Median       3Q      Max
-6.2765 -2.0384 -0.1096  2.1599  9.2624
```

Coefficients:

```
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   6.0273     0.7960   7.572 1.27e-09 ***
Dream         2.3051     0.3209   7.183 4.85e-09 ***
```

---

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Residual standard error: 3.178 on 46 degrees of freedom

(14 observations deleted due to missingness)

Multiple R-squared: 0.5287, Adjusted R-squared: 0.5184

F-statistic: 51.59 on 1 and 46 DF, p-value: 4.849e-09

Notice the output tells us that (14 observations deleted due to missingness). So this



model was fit with only  $62 - 14 = 48$  rows (77.4%) of the original 62 rows of data. The model was fit using only the complete dataset based on the 2 variables in the model: **Dream** and **Sleep**, where

- there are 10 rows missing data for only the **Dream** variable,
- 2 rows missing data for both **Dream** and **Sleep** variables,
- and 2 rows missing data for only the **Sleep** variable.

Keep in mind, when you are fitting any model (linear or logistic regression, analysis of variance, etc), the default is (almost) always to use a LISTWISE deletion, which removes ALL rows with any missing data on any of the variables considered in the model - including predictors, covariates, and outcome(s).





## Impact of missing data for correlation matrix - cor() function

Let's also look at a small correlation matrix considering PAIRWISE versus LISTWISE deletion of missing data for 3 variables from the `sleep` dataset. Notice that the correlation between `BrainWgt` and `Dream` and `Sleep` are slightly different between LISTWISE and PAIRWISE approaches. These are all `pearson` correlations by default.

### LISTWISE deletion

```
# LISTWISE deletion, use = "complete.obs"
sleep %>%
  select(BrainWgt, Dream, Sleep) %>%
  cor(use = "complete.obs")
```

	BrainWgt	Dream	Sleep
BrainWgt	1.00000000	-0.08437367	-0.3221748
Dream	-0.08437367	1.00000000	0.7270870
Sleep	-0.32217479	0.72708696	1.0000000

### PAIRWISE deletion

```
# PAIRWISE deletion, use = "pairwise.complete.obs"
sleep %>%
  select(BrainWgt, Dream, Sleep) %>%
  cor(use = "pairwise.complete.obs")
```

	BrainWgt	Dream	Sleep
BrainWgt	1.0000000	-0.1051388	-0.358102
Dream	-0.1051388	1.0000000	0.727087
Sleep	-0.3581020	0.7270870	1.000000

**Impact of missing data for correlation matrix - Hmisc package**

There is also a helpful correlation function `rcorr()` in the `Hmisc` package. From this function we can save the output and get the n's and p-values in addition to the (Pearson) correlations. These numeric data have to be converted to a numeric matrix prior to inputting them to the `rcorr()` function, which is why `as.matrix()` is used in the code chunk below.

**NOTE:** PAIRWISE deletion is the default setting for `Hmisc::rcorr()`.

```
library(Hmisc)
c1 <- sleep %>%
  select(BrainWgt, Dream, Sleep) %>%
  as.matrix() %>%
  rcorr()
```

Show the correlations:

```
c1$r
```

	BrainWgt	Dream	Sleep
BrainWgt	1.0000000	-0.1051388	-0.358102
Dream	-0.1051388	1.0000000	0.727087
Sleep	-0.3581020	0.7270870	1.000000

Get the sample sizes for each correlation in the matrix:

```
c1$n
```

	BrainWgt	Dream	Sleep
BrainWgt	62	50	58
Dream	50	50	48
Sleep	58	48	58

Get each individual p-value for each correlation:

```
c1$P
```

	BrainWgt	Dream	Sleep
BrainWgt	NA	4.674359e-01	5.779531e-03
Dream	0.467435869	NA	4.849120e-09
Sleep	0.005779531	4.849120e-09	NA

**i** Getting complete data

Note: The `rcorr()` function uses a PAIRWISE missing values deletion approach. If we want the LISTWISE correlations, we have to get complete data first. Use `complete.cases()` from the built-in `stats` package with `dplyr::filter()` to pull out only the 48 rows in the `sleep` dataset with complete cases on these 3 variables.

```
c2 <- sleep %>%
  select(BrainWgt, Dream, Sleep) %>%
  filter(complete.cases(.)) %>%
  as.matrix() %>%
  rcorr()
```

Show the correlations:

```
c2$r
```

	BrainWgt	Dream	Sleep
BrainWgt	1.00000000	-0.08437367	-0.3221748
Dream	-0.08437367	1.00000000	0.7270870
Sleep	-0.32217479	0.72708696	1.0000000

Get the sample sizes for each correlation in the matrix:

```
c2$n
```

	BrainWgt	Dream	Sleep
BrainWgt	48	48	48
Dream	48	48	48
Sleep	48	48	48

Get each individual p-value for each correlation:

```
c2$P
```

	BrainWgt	Dream	Sleep
BrainWgt	NA	5.685642e-01	2.553771e-02
Dream	0.56856416	NA	4.849120e-09
Sleep	0.02553771	4.849120e-09	NA



## Missing Data Mechanisms

There are entire books and entire courses dedicated to understanding and dealing with missing data mechanisms, which we will not have time to go into depth in this TIDAL course.

Learn more at:

- <https://stefvanbuuren.name/fimd/sec-MCAR.html>
- [BOOK: Statistical Analysis with Missing Data, Third Edition, by Roderick Little, Donald Rubin](#)

The 3 missing data mechanisms to know are:

- MCAR = “missing completely at random”
  - This assumes that the missingness is not related to the data at all.
  - If the probability of being missing is the same for all cases, then the data are said to be missing completely at random (MCAR).
- MAR = “missing at random”
  - If the probability of being missing is the same only within groups defined by the observed data, then the data are missing at random (MAR).
  - For example, if people with higher levels of depression who were more likely to not answer a question or not complete the study, the the missingness is “dependent” upon depression levels measured in the study.
- MNAR (or NMAR) = “missing not at random (not missing at random)”
  - MNAR means that the probability of being missing varies for reasons that are unknown to us.
  - An example of MNAR in public opinion research occurs if those with weaker opinions respond less often (e.g., non-response bias).

There is a nice summary of different approaches and assumptions and the effects to the models and statistical estimates, see [FIMD Book, Section 1.3.8 Summary](#). This table illustrates that many “ad hoc” missing imputation approaches can result in standard errors that are too large or too small leading to incorrect calculations for p-values and confidence intervals.



### Compare rows with and without missing data

Let's take a look at the `BodyWgt` and `BrainWgt` variables and compare the values for rows with and without missing data for the `Dream` variable. Here are the steps involved:

1. Create an indicator variable where 0=not missing and 1=missing for the `Dream` variable.
2. Run comparisons for the rows (subjects) with and without missing `Dream` data.
3. Potentially make plots to compare the rows with and without missing values for `Dream`.

Note: Both `BodyWgt` and `BrainWgt` are highly right skewed, so I did a log transform of both. Notice that the p-values for the non-parametric independent group test (Mann Whitney/Wilcoxon Rank Sum test) are the same, since the tests are based on ranks.

```
# make small dataset
s1 <- sleep %>%
  select(BodyWgt, BrainWgt, Dream)

# add missing indicator
s1$Dream_missing <- as.numeric(is.na(s1$Dream))

# both BodyWgt and BrainWgt are highly right skewed
# do a log transform of both
s1 <- s1 %>%
  mutate(log_BodyWgt = log(BodyWgt),
         log_BrainWgt = log(BrainWgt))
```

Table comparing `BodyWgt` and `BrainWgt` for rows with and without missing `Dream` data. Both are statistically significant - the animals with missing `Dream` values are larger (bigger body and brain weights).

```
s1 %>%
  tbl_summary(
    by = Dream_missing,
    include = c(BodyWgt, log_BodyWgt,
                BrainWgt, log_BrainWgt)
  ) %>%
  add_p()
```

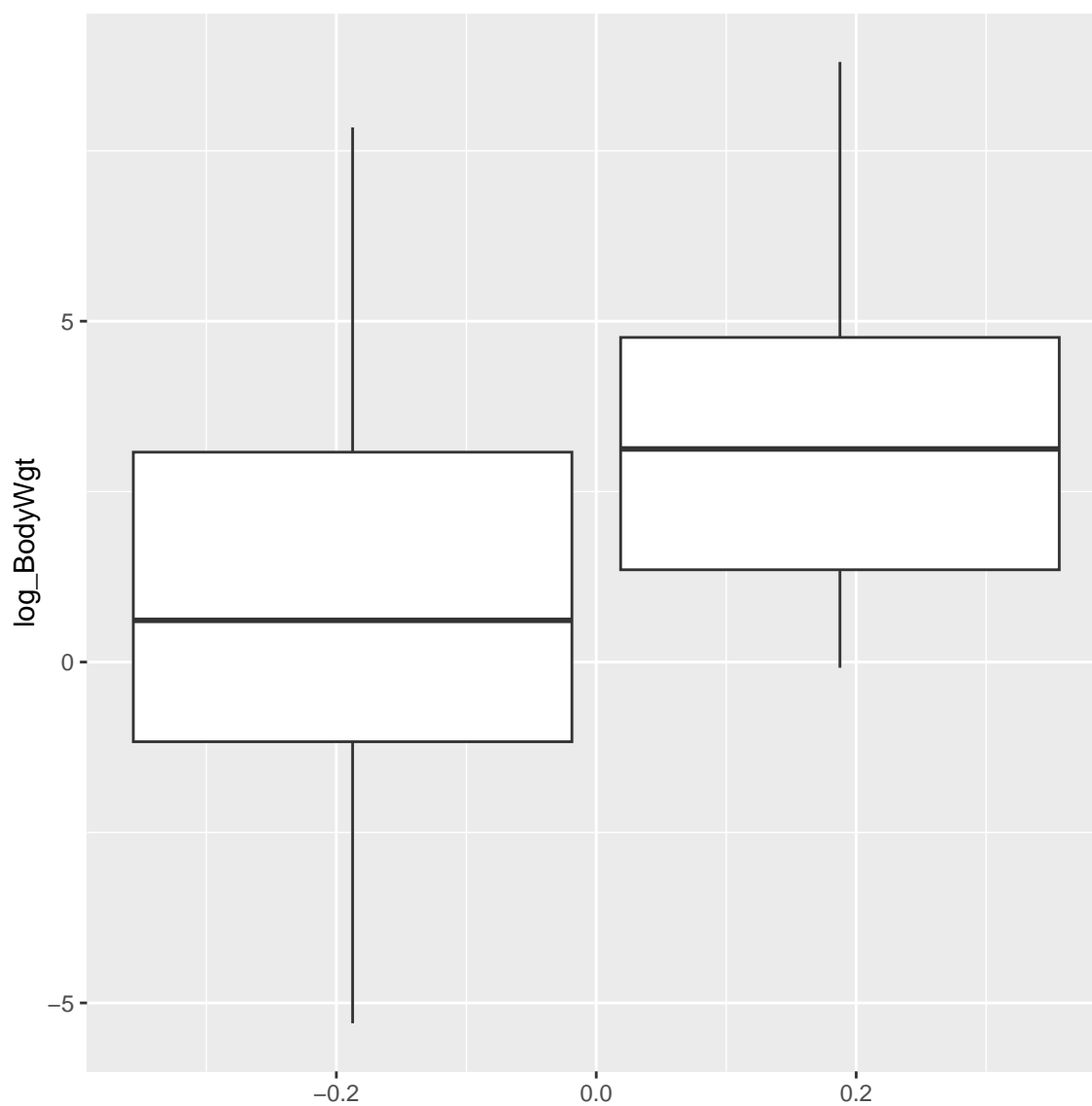


Characteristic	0 N = 50 <sup>1</sup>	1 N = 12 <sup>1</sup>	p-value <sup>2</sup>
BodyWgt	2 (0, 28)	25 (4, 144)	0.020
log_BodyWgt	0.61 (-1.27, 3.32)	3.13 (1.31, 4.92)	0.020
BrainWgt	12 (3, 169)	77 (28, 282)	0.041
log_BrainWgt	2.50 (1.10, 5.13)	4.31 (3.25, 5.53)	0.041

<sup>1</sup>Median (Q1, Q3)<sup>2</sup>Wilcoxon rank sum test

Side-by-side boxplots for the (log) of `BodyWgt` for rows with missing `Dream` data and without.

```
ggplot(s1, aes(group = Dream_missing,
               y = log_BodyWgt)) +
  geom_boxplot()
```





### 3. Missing Data Handling and Imputation Methods (brief intro)

#### Imputation - Mean Substitution

There are many ideas and options for creating data to “fill-in” or “impute” the spots for the missing values. Keep in mind that these methods are “making up” new (unobserved) data. Ideally, the missing imputation methods should be as unbiased as possible and should not increase or decrease the variability of the data. As good as some methods may be, always keep in mind that we will never know for sure if these new imputed data are “correct” or if they are the best they can be.

A simple example, suppose we have a variable with 5 numbers. Let’s compute the mean and standard deviation of these numbers.

```
x <- c(2, 4, 3, 5, 10)
mean(x, na.rm = TRUE)
```

```
[1] 4.8
```

```
sd(x, na.rm = TRUE)
```

```
[1] 3.114482
```

Now let’s set the 1st value to missing - replace the 2 with NA. Notice that the mean increases and the standard deviation decreased slightly from 3.114 to 3.109.

```
xna <- c(NA, 4, 3, 5, 10)
mean(xna, na.rm = TRUE)
```

```
[1] 5.5
```

```
sd(xna, na.rm = TRUE)
```

```
[1] 3.109126
```





Now, let's take the mean we just computed from the 4 non-missing values which was 5.5 and substitute it in for the missing value and recompute the new mean and standard deviation.

```
xsub <- c(5.5, 4, 3, 5, 10)
mean(xsub, na.rm = TRUE)
```

```
[1] 5.5
```

```
sd(xsub, na.rm = TRUE)
```

```
[1] 2.692582
```

**IMPORTANT** The new mean of `xsub` is the same = 5.5 as the mean for `xna`, but the standard deviation for this new list of 5 numbers is much smaller = 2.693 down from 3.109. And this “shrinking” of the standard deviation is even more pronounced from the original 5 numbers which was 3.114 for `x`. And the mean of the original numbers was 4.8 which is smaller than the mean-substituted list for `xsub`.

This is a simple example and illustrates why we don't want to use mean-substitution for missing data. It also highlights that the goals of missing data imputation ideally shouldn't cause bias for estimating statistics like the mean and shouldn't increase or decrease the underlying variance of the original variables. And in theory the new variable with imputed data also shouldn't change the correlations (relationships) between the variables in the dataset. As you can see this can get complex rapidly and no imputation method is perfect. Often multiple missing imputation methods should be explored and some methods may work better for different models and statistical tests than others.

#### **i** Commonly accepted use of mean-substitution

The one place where I see mean substitution used often is for survey instruments. For example the [CESD \(Center for Epidemiological Studies-Depression\)](#) which has 20 items with a 4-point Likert-scaled response coded 0, 1, 2, 3.

For this instrument you can compute a valid score from only 16 of the 20 items by taking the mean of these 16 items. This is equivalent to using mean-substitution for the 4 missing responses (e.g. CESD allows up to 20% missing items within a given subject, within a given row of data). But this is ROWWISE mean substitution. The example above is illustrating COLUMNWISE mean substitution.

To avoid mean-substitution bias even for ROWWISE substitution, you ideally want to use this on less than 5%-10% of your sample. If more than 5%-10% of your sample is not completing the survey, there may still be underlying response bias issues that need to be addressed.



### Example of k-nearest neighbor (kNN) missing imputation method

Instead of using mean substitution, let's look at another method - k-nearest neighbor, which is a “donor-based” method. Learn more at:

- [VIM Vignette on “Donor based Imputation Methods”](#)
- [Datacamp Course on Imputation](#)

Let's take the little dataset `x` which is a subset of the `sleep` dataset which has all 62 rows but only the `Dream` and `Sleep` variables. For these 2 variables, let's see what the `kNN()` (k-nearest neighbor) function in the `VIM` package does.

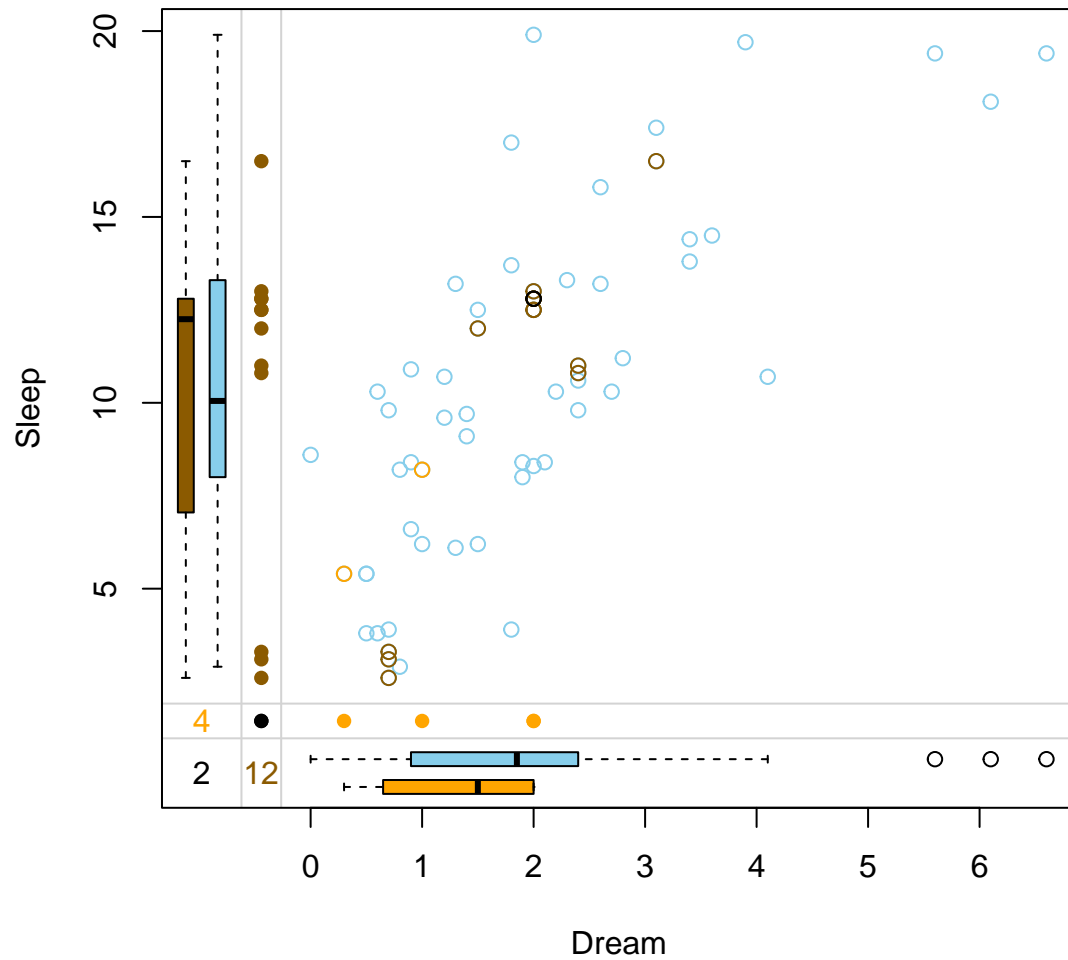
```
x <- sleep[, c("Dream", "Sleep")]
x_imputed <- kNN(x)
```

Now look at a scatterplot plot for these new `Dream` and `Sleep` variables with imputed values from the k-nearest neighbor approach. Notice the coloring of the points - the blue are the original values and the other colors represent the structure of missings.

- brown points represent values where `Dream` was missing initially
- beige points represent values where `Sleep` was missing initially
- black points represent values where both `Dream` and `Sleep` were missing initially

The `kNN()` method appears to preserve the correlation between `Dream` and `Sleep`.

```
marginplot(x_imputed, delimiter = "_imp")
```





### kNN imputed values - compare correlations before and after

Let's compare the results before and after the imputation for correlation and for a simple regression model. This is a “sensitivity” test of sorts. It is always a good idea to compare the results before and after applying any imputation method.

Correlation Original Data:

```
x %>%  
  as.matrix() %>%  
  Hmisc::rcorr()
```

```
      Dream Sleep  
Dream  1.00  0.73  
Sleep  0.73  1.00
```

```
n  
      Dream Sleep  
Dream    50    48  
Sleep    48    58
```

```
P  
      Dream Sleep  
Dream          0  
Sleep    0
```

Correlation kNN Imputed Data:

```
x_imputed %>%  
  select(Dream, Sleep) %>%  
  as.matrix() %>%  
  Hmisc::rcorr()
```

```
      Dream Sleep  
Dream  1.00  0.74  
Sleep  0.74  1.00
```

```
n= 62
```

```
P  
      Dream Sleep  
Dream          0  
Sleep    0
```

**kNN imputed values - compare regression before and after**

Simple Linear Regression Original Data:

```
summary(lm(Sleep ~ Dream, data = x))
```

Call:

```
lm(formula = Sleep ~ Dream, data = x)
```

Residuals:

Min	1Q	Median	3Q	Max
-6.2765	-2.0384	-0.1096	2.1599	9.2624

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	6.0273	0.7960	7.572	1.27e-09 ***
Dream	2.3051	0.3209	7.183	4.85e-09 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.178 on 46 degrees of freedom

(14 observations deleted due to missingness)

Multiple R-squared: 0.5287, Adjusted R-squared: 0.5184

F-statistic: 51.59 on 1 and 46 DF, p-value: 4.849e-09

Simple Linear Regression kNN Imputed Data:

```
summary(lm(Sleep ~ Dream, data = x_imputed))
```

Call:

```
lm(formula = Sleep ~ Dream, data = x_imputed)
```

Residuals:

Min	1Q	Median	3Q	Max
-6.241	-2.283	-0.221	2.157	9.257

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	5.6222	0.6920	8.125	3.00e-11 ***
Dream	2.5106	0.2949	8.512	6.58e-12 ***

---



```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 3.074 on 60 degrees of freedom
```

```
Multiple R-squared:  0.547, Adjusted R-squared:  0.5395
```

```
F-statistic: 72.46 on 1 and 60 DF,  p-value: 6.579e-12
```

Notice that the correlations were similar. The regression intercepts and slopes were slightly different and the “Std. Error” for the regression coefficients for the imputed model were smaller than for the original data.

**Example of multiple missing imputation method (using mice)**

Let's take a look at the `mice` (Multivariate Imputation by Chained Equations) package. The `mice` package provides for Multiple imputation using Fully Conditional Specification (FCS) implemented by the MICE algorithm as described in [Van Buuren and Groothuis-Oudshoorn \(2011\)](#).

Let's re-run the simple linear regression model above, but this time let's create 20 imputed datasets, run 20 regression models and then pool the results. See [FIMD Book Section 1.4](#)

Compare these regression results to the models above. Notice that the “std.error” for the regression coefficients are larger than they were for the kNN results and closer to fitting the model with the original data.

```
library(mice)
imp <- mice(x, seed = 1, m = 20, print = FALSE)
fit <- with(imp, lm(Sleep ~ Dream))
summary(pool(fit))
```

	term	estimate	std.error	statistic	df	p.value
1	(Intercept)	5.904120	0.7560889	7.808764	48.78611	3.858037e-10
2	Dream	2.326442	0.3216144	7.233638	45.29561	4.431364e-09

💡 Look at one of the regression models from the impute data

We can “peek under the hood” to look at one of the individual imputed datasets by running the following code. If you'd like to look at another model just change 1 to another number up to 20 (since there were 20 imputations performed).

```
# see simple output
fit[["analyses"]][[1]]

# get summary detailed output
summary(fit[["analyses"]][[1]])
```

Call:

```
lm(formula = Sleep ~ Dream)
```

Coefficients:

(Intercept)	Dream
6.090	2.216



```
Call:
lm(formula = Sleep ~ Dream)

Residuals:
    Min       1Q   Median       3Q      Max
-7.4782 -2.0541  0.0424  2.2630  9.3787

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   6.0897     0.7318   8.322 1.39e-11 ***
Dream         2.2158     0.2953   7.504 3.45e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.407 on 60 degrees of freedom
Multiple R-squared:  0.4841,    Adjusted R-squared:  0.4755
F-statistic: 56.31 on 1 and 60 DF,  p-value: 3.449e-10
```

---





#### 4. Impact of Sampling Weights for Survey Data (brief intro)

see [Missing Data in PRAMS module](#).

---



## R Code For This Module

- [module\\_134.R](#)

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## Other Helpful Resources

### Missing Data Resources

- [CRAN Task View for Missing Data](#)
- [R-miss-tastic Website](#)
- [Flexible Imputation of Missing Data](#) (online book for 2nd edition) by Stef van Buuren
- [Blog post on Missing Data Visualization in R using ggplot2](#)
- [Missing data R tutorial](#)
- [CRAN Task View on Missing Data](#)
- [A resource website on missing values](#)
- [Handling missing values with R - tutorial](#)
- [Blog post “My favourite R package for: summarising data”](#)

and

### Other Helpful Resources