



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

COMING SUMMER 2025

Module “1.3.4: Missing Data and Sampling Weights” will be posted prior to the In-Person Workshops in Summer 2025.

Session Objectives

1. Identify and summarize missing data.
2. Learn methods to handle missing data according to variable type.
3. Use a survey sampling weight to generate more representative descriptive and inferential statistical values (brief intro)
4. Discuss potential bias when removing missing observations without careful examination.

[to be removed.....]

Key points:

1. R packages that support missing data examination
2. Mean/median imputation for continuous variables
3. What to do with missing observations for categorical variables
4. Ways to examine potential differences between complete and missing observations in association between certain independent and dependent variables
 - What to do if such association significantly differs between complete and missing observations
5. R packages for complex survey data (e.g., survey package)
 - R codes to generate weighted descriptive statistics and contingency tables, as well as to develop weighted linear models



0. Pework - Before You Begin

Install Packages

Before you begin, please go ahead and install the following packages - these are all on CRAN, so you can install them using the RStudio Menu “Tools/Install” Packages interface:

- [VIM on CRAN](#) and [VIM package website](#)
- [skimr on CRAN](#) and [skimr website](#) - OPTIONAL
- [modelsummary on CRAN](#) and [modelsummary website](#) - OPTIONAL
- [tinytable on CRAN](#) and [tinytable website](#) - OPTIONAL
- [summarytools on CRAN](#) and [summarytools on Github](#) - OPTIONAL
- mice
- mi
-
-
- [palmerpenguins on CRAN](#)

See [Module 1.3.1 on Installing Packages](#)

See additional resources below...

add to prework?

Begin with a NEW RStudio Project

Let's begin with a new RStudio Project.



1. Identify and summarize 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

Showing 44 to 62 of 62 entries, 10 total columns

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)m 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.

i Rmarkdown for `modelsummary` package

The `tinytable` package is also used below with the `modelsummary` output to better control the placement of the resulting table when “knitting” to PDF.

```
library(modelsummary)
library(tinytable)
datasummary_skim(sleep) %>%
  theme_tt("placement", latex_float = "H")
```

	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)
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💡 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 - Too Many Variables

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 a quick count of the amount of missing
# data in the sleep dataset for each variable
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 complete list with:

```
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.

The plot on the LEFT below is a simple bar plot showing the missing counts for each variable in the dataset.

- Also notice that there are only 5 variables with one or more missing values:
 - NonD
 - Dream
 - Sleep
 - Span
 - Gest

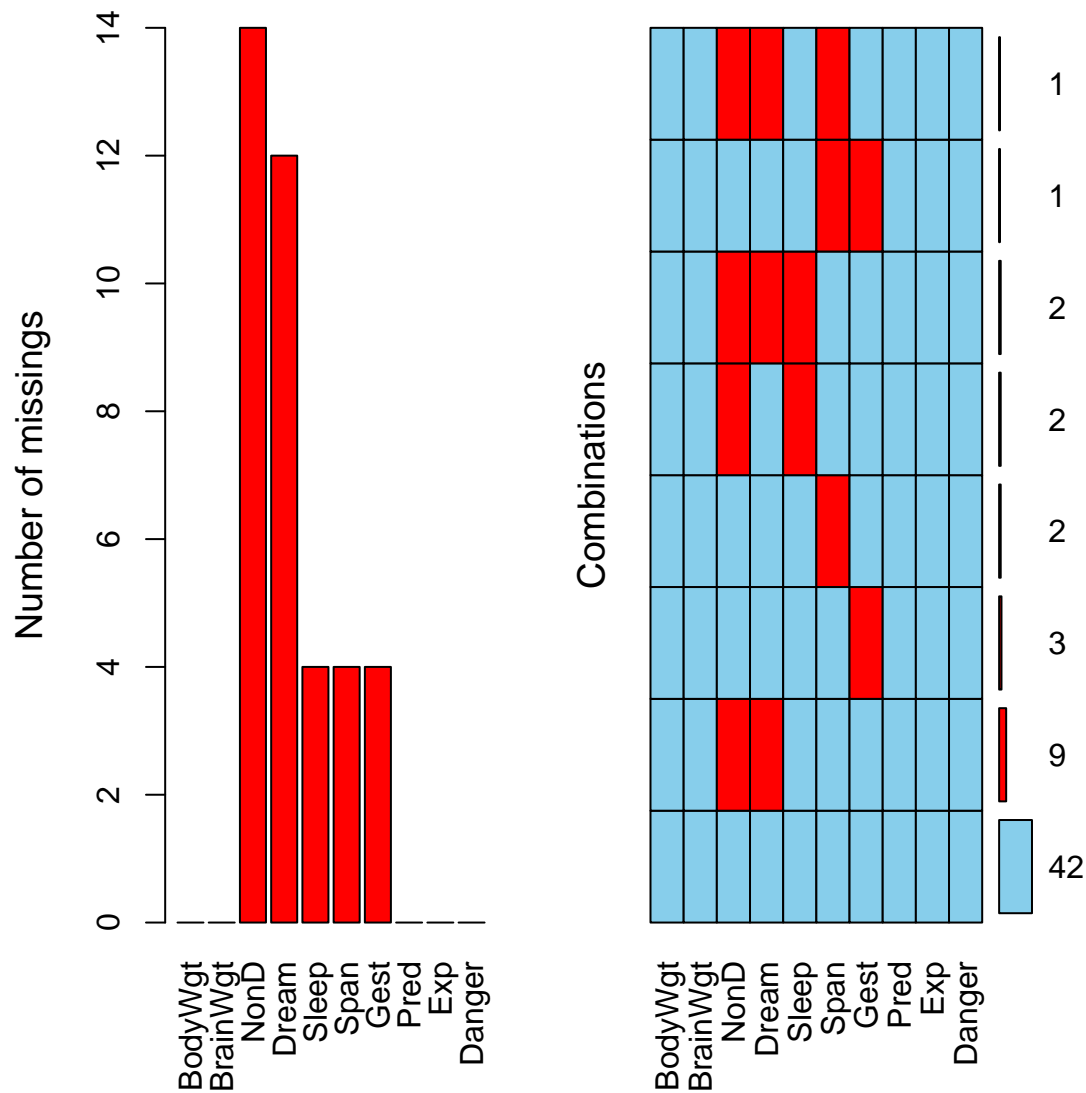
The plot on the RIGHT however, shows the amounts of missing data for the various patterns of missing data for the 10 variables in the `sleep` dataset.

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;
- the next largest “pattern” of missing data is 9 rows that are missing both `NonD` and `Dream` variables.; and
- there are 3 rows of data with the `gest` variable with missing data.



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



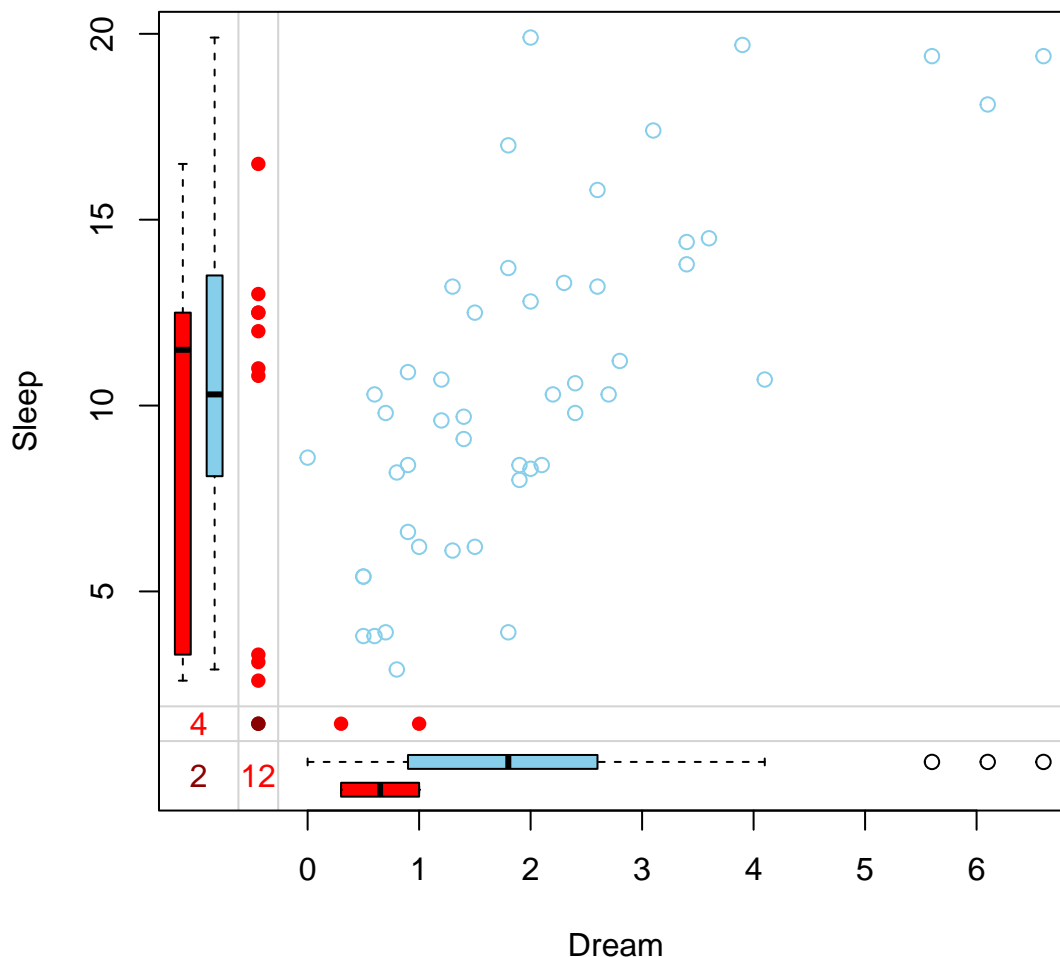
Marginplots - see how missingness varies with other measures

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](#).

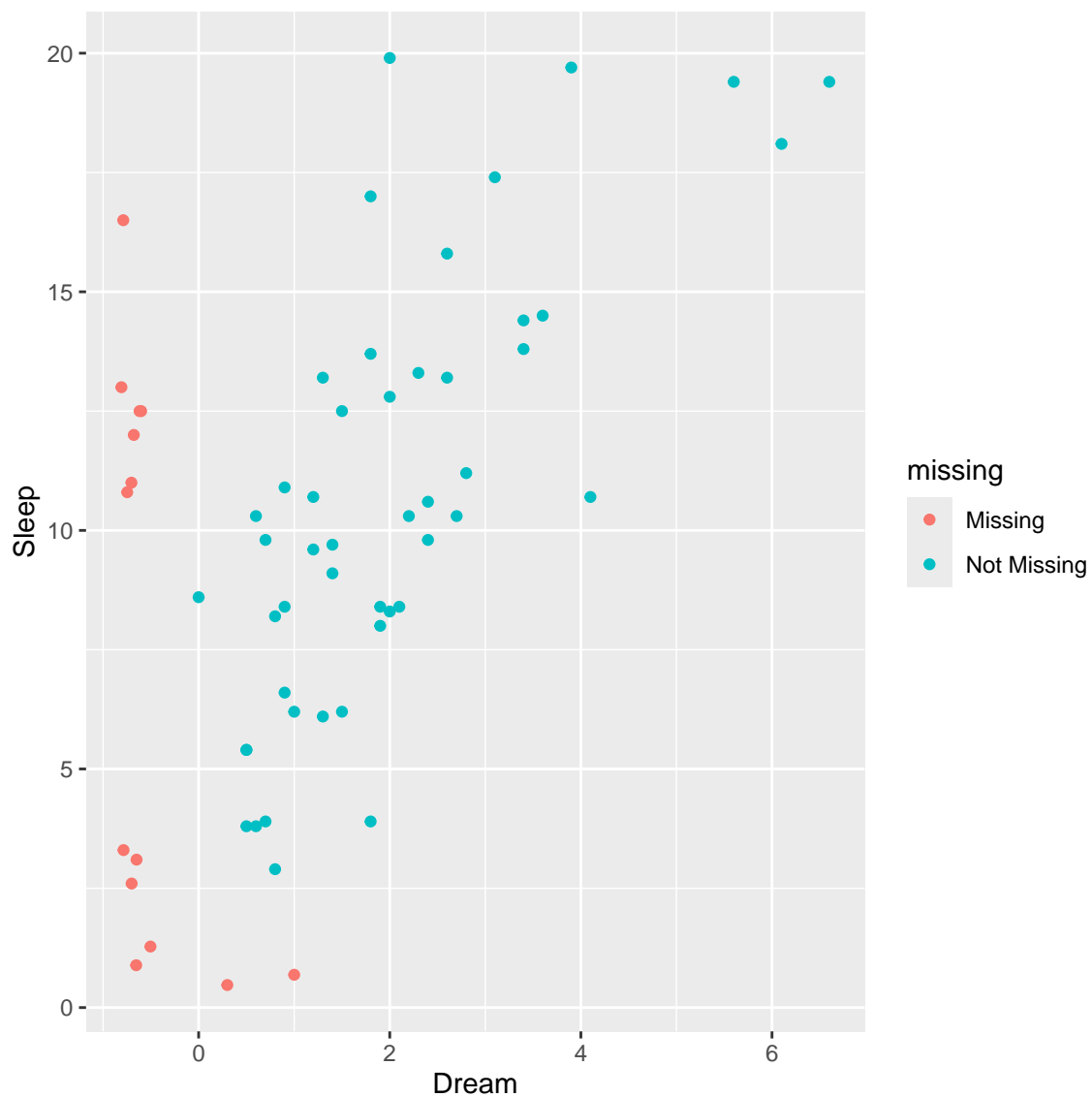
For example, let’s make a similar to plot to what we did above to visualize the scatterplot between `Dream` and `Sleep` but also consider the amounts of missing data of one variable



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()
```







2. Learn methods to handle missing data according to variable type.

discuss pairwise versus listwise and discuss impacts on modeling especially for stepwise variable selection - always check the final N for each model

show correlations pairwise and listwise

add details on modeling adjustments - covariate predicted missingness

options on imputation - brief intro

```
sleep$NonD_missing <-
  as.numeric(is.na(sleep$NonD))

correlation::correlation(sleep)
```

Correlation Matrix (pearson-method)

Parameter1	Parameter2	r	95% CI	t	df	p
BodyWgt	BrainWgt	0.93	[0.89, 0.96]	20.28	60	< .001***
BodyWgt	NonD	-0.38	[-0.60, -0.10]	-2.75	46	0.211
BodyWgt	Dream	-0.11	[-0.38, 0.17]	-0.76	48	> .999
BodyWgt	Sleep	-0.31	[-0.52, -0.05]	-2.42	56	0.418
BodyWgt	Span	0.30	[0.05, 0.52]	2.37	56	0.441
BodyWgt	Gest	0.65	[0.47, 0.78]	6.42	56	< .001***
BodyWgt	Pred	0.06	[-0.19, 0.30]	0.46	60	> .999
BodyWgt	Exp	0.34	[0.10, 0.54]	2.78	60	0.186
BodyWgt	Danger	0.13	[-0.12, 0.37]	1.04	60	> .999
BodyWgt	NonD_missing	0.23	[-0.02, 0.45]	1.80	60	> .999
BrainWgt	NonD	-0.37	[-0.59, -0.10]	-2.69	46	0.226
BrainWgt	Dream	-0.11	[-0.37, 0.18]	-0.73	48	> .999
BrainWgt	Sleep	-0.36	[-0.56, -0.11]	-2.87	56	0.156
BrainWgt	Span	0.51	[0.29, 0.68]	4.43	56	0.002**
BrainWgt	Gest	0.75	[0.61, 0.84]	8.41	56	< .001***
BrainWgt	Pred	0.03	[-0.22, 0.28]	0.26	60	> .999
BrainWgt	Exp	0.37	[0.13, 0.57]	3.06	60	0.098
BrainWgt	Danger	0.15	[-0.11, 0.38]	1.14	60	> .999
BrainWgt	NonD_missing	0.18	[-0.07, 0.41]	1.41	60	> .999
NonD	Dream	0.51	[0.27, 0.70]	4.07	46	0.007**
NonD	Sleep	0.96	[0.93, 0.98]	24.14	46	< .001***
NonD	Span	-0.38	[-0.61, -0.10]	-2.73	43	0.219
NonD	Gest	-0.59	[-0.76, -0.36]	-4.79	42	< .001***



NonD	Pred	-0.32	[-0.55, -0.04]	-2.28	46	0.551
NonD	Exp	-0.54	[-0.72, -0.31]	-4.39	46	0.002**
NonD	Danger	-0.48	[-0.68, -0.23]	-3.75	46	0.017*
NonD	NonD_missing				46	
Dream	Sleep	0.73	[0.56, 0.84]	7.18	46	< .001***
Dream	Span	-0.30	[-0.54, -0.01]	-2.08	45	0.828
Dream	Gest	-0.45	[-0.66, -0.18]	-3.35	44	0.055
Dream	Pred	-0.45	[-0.65, -0.19]	-3.47	48	0.038*
Dream	Exp	-0.54	[-0.71, -0.30]	-4.41	48	0.002**
Dream	Danger	-0.58	[-0.74, -0.36]	-4.92	48	< .001***
Dream	NonD_missing	-0.19	[-0.44, 0.09]	-1.33	48	> .999
Sleep	Span	-0.41	[-0.61, -0.16]	-3.24	52	0.066
Sleep	Gest	-0.63	[-0.77, -0.44]	-5.87	52	< .001***
Sleep	Pred	-0.40	[-0.59, -0.15]	-3.23	56	0.066
Sleep	Exp	-0.64	[-0.77, -0.46]	-6.27	56	< .001***
Sleep	Danger	-0.59	[-0.73, -0.39]	-5.44	56	< .001***
Sleep	NonD_missing	-0.08	[-0.33, 0.18]	-0.60	56	> .999
Span	Gest	0.61	[0.42, 0.76]	5.68	53	< .001***
Span	Pred	-0.10	[-0.35, 0.16]	-0.77	56	> .999
Span	Exp	0.36	[0.11, 0.57]	2.89	56	0.153
Span	Danger	0.06	[-0.20, 0.32]	0.46	56	> .999
Span	NonD_missing	0.08	[-0.18, 0.33]	0.63	56	> .999
Gest	Pred	0.20	[-0.06, 0.44]	1.53	56	> .999
Gest	Exp	0.64	[0.45, 0.77]	6.20	56	< .001***
Gest	Danger	0.38	[0.13, 0.58]	3.06	56	0.098
Gest	NonD_missing	0.20	[-0.06, 0.44]	1.55	56	> .999
Pred	Exp	0.62	[0.44, 0.75]	6.09	60	< .001***
Pred	Danger	0.92	[0.86, 0.95]	17.69	60	< .001***
Pred	NonD_missing	0.05	[-0.20, 0.29]	0.37	60	> .999
Exp	Danger	0.79	[0.67, 0.87]	9.89	60	< .001***
Exp	NonD_missing	0.25	[0.00, 0.47]	1.96	60	0.981
Danger	NonD_missing	0.07	[-0.19, 0.31]	0.51	60	> .999

p-value adjustment method: Holm (1979)

Observations: 44-62

```
t.test(BodyWgt ~ NonD_missing,
       data = sleep)
```

Welch Two Sample t-test



```
data: BodyWgt by NonD_missing
t = -1.0239, df = 13.351, p-value = 0.3241
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to
95 percent confidence interval:
 -1502.0470  534.3593
sample estimates:
mean in group 0 mean in group 1
   89.53492      573.37879
```

```
t.test(BrainWgt ~ NonD_missing,
       data = sleep)
```

Welch Two Sample t-test

```
data: BrainWgt by NonD_missing
t = -0.96511, df = 14.651, p-value = 0.3502
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to
95 percent confidence interval:
 -1272.563  480.454
sample estimates:
mean in group 0 mean in group 1
   193.7025      589.7571
```

```
t.test(Sleep ~ NonD_missing,
       data = sleep)
```

Welch Two Sample t-test

```
data: Sleep by NonD_missing
t = 0.57598, df = 12.498, p-value = 0.5749
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to
95 percent confidence interval:
 -2.683161  4.623161
sample estimates:
mean in group 0 mean in group 1
    10.70         9.73
```



```
t.test(Span ~ NonD_missing,  
       data = sleep)
```

Welch Two Sample t-test

```
data: Span by NonD_missing  
t = -0.86773, df = 38.531, p-value = 0.3909  
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to  
95 percent confidence interval:  
 -12.021726  4.805658  
sample estimates:  
mean in group 0 mean in group 1  
    19.06889      22.67692
```

```
t.test(Gest ~ NonD_missing,  
       data = sleep)
```

Welch Two Sample t-test

```
data: Gest by NonD_missing  
t = -1.2435, df = 16.636, p-value = 0.2309  
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to  
95 percent confidence interval:  
 -185.81590  48.15032  
sample estimates:  
mean in group 0 mean in group 1  
    125.7386      194.5714
```

```
t.test(Pred ~ NonD_missing,  
       data = sleep)
```

Welch Two Sample t-test

```
data: Pred by NonD_missing  
t = -0.33283, df = 18.543, p-value = 0.743  
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to  
95 percent confidence interval:
```



```
-1.2165041  0.8831708
sample estimates:
mean in group 0 mean in group 1
      2.833333      3.000000
```

```
t.test(Exp ~ NonD_missing,
       data = sleep)
```

Welch Two Sample t-test

```
data:  Exp by NonD_missing
t = -1.7467, df = 18.278, p-value = 0.09747
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to
95 percent confidence interval:
 -2.0573419  0.1882943
sample estimates:
mean in group 0 mean in group 1
      2.208333      3.142857
```

```
t.test(Danger ~ NonD_missing,
       data = sleep)
```

Welch Two Sample t-test

```
data:  Danger by NonD_missing
t = -0.44672, df = 18.075, p-value = 0.6604
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to
95 percent confidence interval:
 -1.2726861  0.8262576
sample estimates:
mean in group 0 mean in group 1
      2.562500      2.785714
```

Marginplot of Imputed Values - Example

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.

There are a few built-in imputation functions in `VIM`. Let's see what the `kNN()` (k-nearest neighbor) function does.



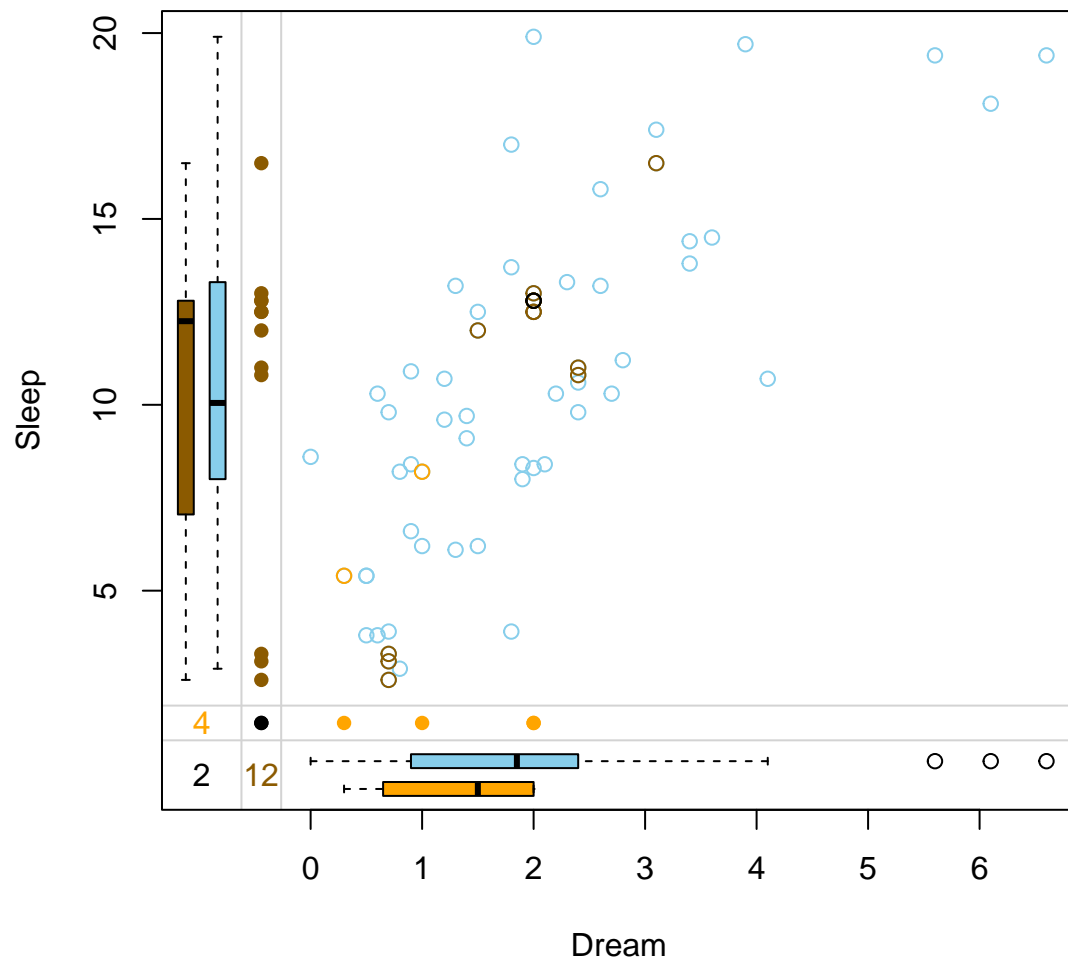
```
x_imputed <- kNN(x)
```

Now look at the plot again for these new **Dream** and **Sleep** variables for the k-nearest neighbor imputed variables. 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")
```





3. Use a survey sampling weight to generate more representative descriptive and inferential statistical values (brief intro)

introduction to survey weights

show how this impacts the amounts of missing data



4. Discuss potential bias when removing missing observations without careful examination.

talk about assumptions for missing data - MCAR, MAR and NMAR (or MNAR)

add more examples here

also for publication - running models for comparison - sensitivity tests - model for all complete data - models based on pairwise selections - n changes - models before and after covariate adjustments - models before and after imputation



R Code For This Module

- [module_134.R](#)

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Other Helpful Resources

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
- more ...
- <https://www.datawim.com/post/missing-data-visualization-in-r/>
- <https://libguides.princeton.edu/R-Missingdata>
- <https://cran.r-project.org/web/packages/mice/index.html>
- <https://cran.r-project.org/web/views/MissingData.html>
- <https://rmisstastic.netlify.app/>
- https://rmisstastic.netlify.app/tutorials/josse_tierney_bookdown_user2018tutorial_2018
- <https://modelssummary.com/vignettes/datasummary.html>
- <https://dabblingwithdata.amedcalf.com/2018/01/02/my-favourite-r-package-for-summarising-data/>
- <https://cran.r-project.org/web/packages/summarytools/vignettes/introduction.html>
- <https://cran.r-project.org/web/packages/skimr/vignettes/skimr.html>