PHP 2550: Worksheet 4

Due: September 27th at 11:59pm

Reading Recap

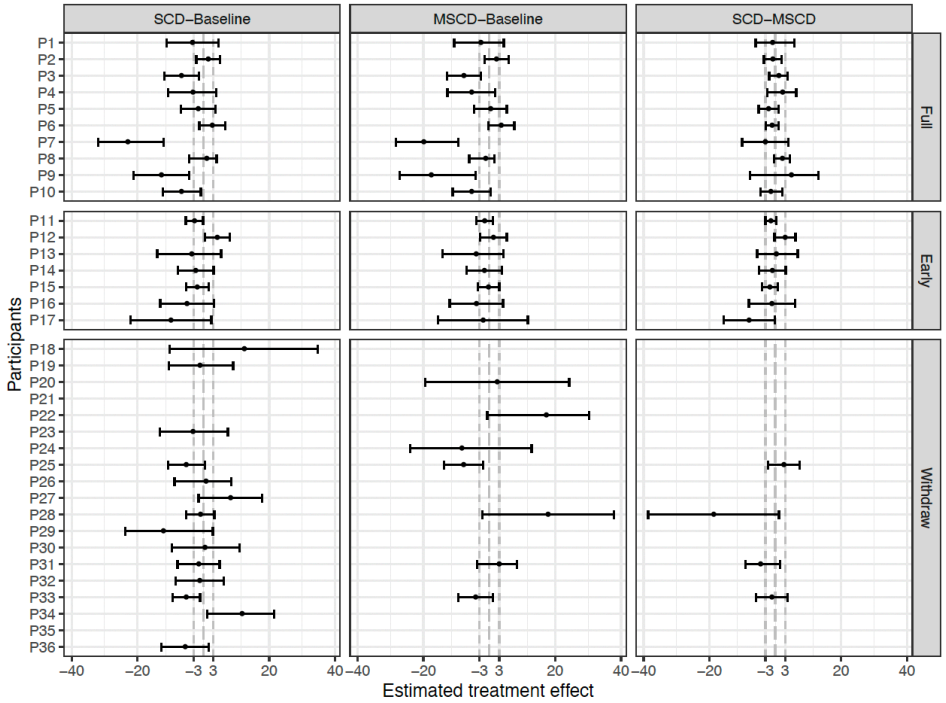
1. Recap Chapters 3-6 of the "The 9 Pitfalls of Data Science" in three points and choose your favorite example. Each point could be summarizing a key takeaway, something that surprised you, or something that you want to remember.

    - In pitfall 4, worshiping computer, the example of "Seeing the World Through Pixels" surprises me a lot. This example talks about how differently computers and human "see" an object. When a picture of school bus was shown, the DNN (deep neural network) identified it as an airplane instead of a school bus. This occurs since, unlike humans, computers would not understand the picture but analyzes the pixel patterns. Human always identify the object by understanding the context and meaning, even the picture is blocked or unclear, we rely on our experiences to identify it. I choose this example since it helped me understand something I had been confused about. When trying to log in to some websites, I have encountered tasks asking me to recognize traffic lights, buses, or taxis and they said this task can prevent computer from logging in. I used to believe this should be a easy task for "smart computers", but after reading this example, I understand the reason for that and I realize how important and sophisticated human perception really is. In addition, I would like to remember this tip and avoid overly trust computers.
    - In pitfall 5, Torturing Data, the example of "Aspartame doesn't cause cancer" does catch my attention. I usually drink diet coke to avoid suger intake and I was concerned about this topic previously when there are people saying that Aspartame could cause cancer. A lot of studies have shown that aspartame does not cause cancer, and this result is confirmed by both the FDA and European Food Safety Authority. However, because of fears inflamed by hoax emails, people continued to test it. Because of over-testing, there a few occasional anomal cases popped up, suggesting possible links between brain tumors and aspartame. This p-hacking case shows that over-testing or over-analyzing is a way to torturing data and this would increase the probability of finding meaningless patterns which are not the result we would like to have. This is also a tip I would like to remind myself.

- In pitall 6, fooling yourself, the example of "Wishful Thinking" attracts my attention since I also have experiences of overestimating my math test scores during high school and this scenario is common in our class. This example talks about how people can overestimate their ability that the 100 high school students predicted a score of 75 for a math test on average while their mean score is actually 60. This discrepancy occurs due to bias of optimism or an underestimation of the math test's difficulty, leading to wrong decision making or conclusion. Our human nature can lead us to be overly optimistic which is a way of fooling ourselves, letting our subjective biases and desires influence our judgement. This is also a tip I would remind myself in the future.

2. The questions below relate to the article Personalized Research on Diet in Ulcerative Colitis and Crohn's Disease: A Series of N-of-1 Diet Trials.

   - Summarize the paper in 1-2 paragraphs using your own words (a good way to help this is to not look at the paper when writing your response). Use the six questions from last week to help guide your summary
     - What do the author(s) want to know (motivation)?
     - What did they do (approach/methods)?
     - Why was it done that way (context within the field)?
     - What do the results show (figures and data tables)?
     - How did the author(s) interpret the results (interpretation/discussion)?
     - What should be done next (discussion/own reflection)?
   - Reflecting on the replication crisis and documentation discussion from class, how easy would it be to try to replicate this study? Explain your response.
   - How was the data presented in the paper? What parts of an exploratory analysis were included?
   - Take a look at the visual below that did not make into the paper and was replaced with Figure 1 in the paper. How is the data presented in each visual? Why do you think the authors went with Figure 1?



prob, less CI, dominance color better diet, extra info: split people into disease groups vs. descriptive stat / uncertainty / CI include 0

3. The following questions relate to the reading "An Introduction to Modern Missing Data Analyses".

   - Explain the three missing data mechanisms introduced Missing Completely at Random (MCAR), Missing at Random (MAR), and Missing Not at Random (MNAR) and give an example of each. Describe a setting in which it would be difficult to tell which setting is appropriate for our data.

   1. MCAR: MCAR, missing completely at random, is when the missing is completely random and it does not depend on any variables in the data. This means that the probability of missing data on a variable is unrelated to any observed or unobserved data. An example for MCAR is in a heart disease study, the technician accidently loses some lab samples of some participants. Here, the missingness is not related to any participants' health related or other observed and unobserved variables, making it completely random.

   2. MAR: MAR, missing at random, is when the missingness is related to observed variables, but not on the missing variable itself. In this situation, the missingness

can be explained by other observed variables, but not the missing variable itself. An example of MAR is, in a study of depression, male participants are less likely to complete the survey questions asking about depression severity compared to the female participants, leading to missingness. This missingness is not related to the severity of participants' severity of depression, but is related to their gender which is observed.

3. MNAR: MNAR, missing not at random, is when the probability of missing data is related to the incompleted variables itself. An example for MNAR is that people with higher incomes may be more likely to leave the income question blank due to privacy concerns in a survey. Here, the missing of income response is related to participants' income level but not related to other observed variables.

   In a longitudinal depression study, people complete surveys regularly through time and some participants might drop out from the study. This missingness might have various causes which might be difficult to distinguish among these three types. For example, if the participants move to other places where the reason for the moving is not related to any variables in our studies, this missingness is random and it should be MCAR. Or, if the participants are too old to make regular appointment and complete the survey, the missing data is related to their age, but not related to their severity of depression. This case is MAR. Or, if the participants' depression severity becomes much worse and they drop out since they are not willing to share their worse conditions, this missingness is MNAR where it is related to the missing variable itself. In this case, it would be difficult to tell which setting is appropriate for our data because in reality, researchers might not have clear information about the drop our reason and drop out might occur due to mix of reasons mentioned earlier.

- In this class, we will focus on exploring missing data, thinking through what could have contributed to missing data, and introduce using multiple imputation as a possible tool to use. Write a 3-5 sentence explanation of multiple imputation and then describe settings when multiple imputation might not be appropriate to use.

  Multiple imputation is a modern statistical technique to handle missing data. The basic procedure for multiple imputation includes three steps: the imputation phase, the analysis phase, and the pooling phase. In the imputation phase, we generate a specified number of datasets with different estimates of missing values. Then, we perform analyses separately using the same methods and steps (with no change due to missingness) on each dataset generated during the imputation phase, yielding multiple sets of estimates of each parameter and standard error. Last, in the pooling phase, we combine these multiple sets of results from each dataset's analysis into a single set of results.

  Multiple imputation might not be appropriate to use when MNAR occurs, that is, when the missingness is related to the missing variable itself. This is because mul-

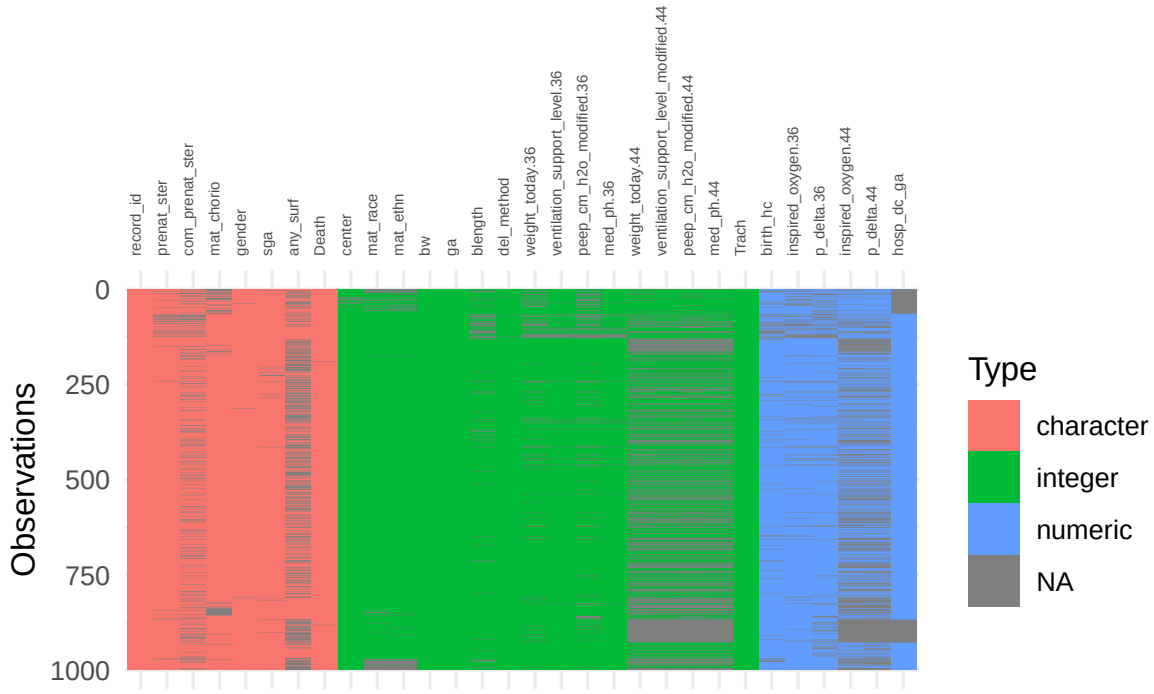
tiple imputation assumes the missingness in the data can be explained by observed data. The implementation of multiple imputation on MNAR data would lead to biases. Or, if our data has small sample size, it would be challenged to do reliable imputation using limited observations. Moreover, if the proportion of missingness is extremely high, our imputation might also be unreliable due to lack of information which would introduce uncertainty.

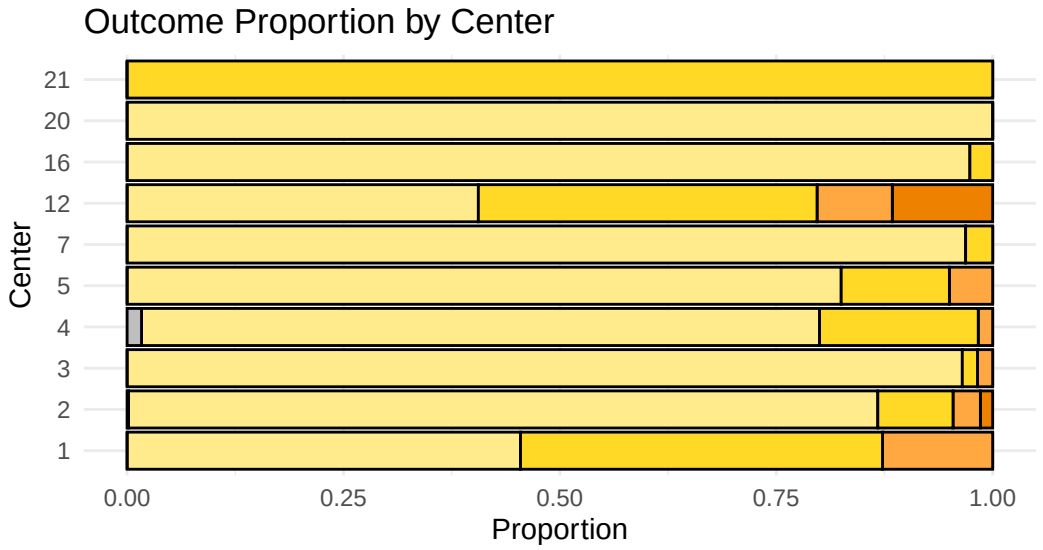
Data Exploration and Visualization

The data (schmid_data.csv and schmid_codebook.xslx) in this question comes from a previous PhD qualifying exam. The data is a national data set of demographic, diagnostic, and respiratory parameters of infants with severe bronchopulmonary dysplasia (sBPD) admitted to collaborative NICUs and with known respiratory support parameters at 36 weeks postmenstrual age (PMA). This data was used to develop a regression model to predict the composite outcome of tracheostomy/death to guide the indication criteria and timing of tracheostomy placement. For our purposes, we will focus on exploratory analysis of this data and you do not need to do any modeling.

Conduct an exploratory analysis of this data (3-5 pages). To guide yourself, think of at least three questions you want to answer using your EDA. You should also look at patterns of missing data. As part of your analysis, create a summary table and include at least two visualizations. When creating your visuals, you should think about what you want the reader to learn from your visual, making your visual clear and effective, and the data-to-ink ratio (i.e. how much information your visual contains and whether the visual is more effective than putting the same information in text). Your writing accompanying your analysis can be short and informal.

codebook - structure: longitudinal (36/44) correlation; missing ate over time (a lot 44 wk are missing, healthier babies are more likely to lose data at 44 wk); explain missing: due to the center clinical setting: multiple centers: clustering, difference between centers; race: data quality issue (unable to answer); missing / center / relationship outcome

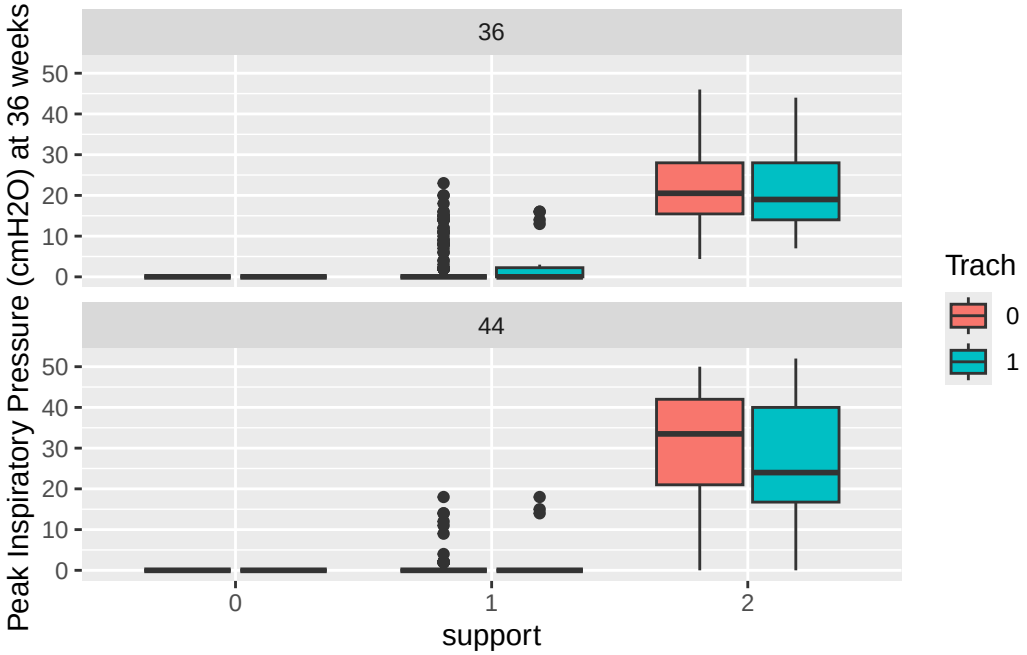




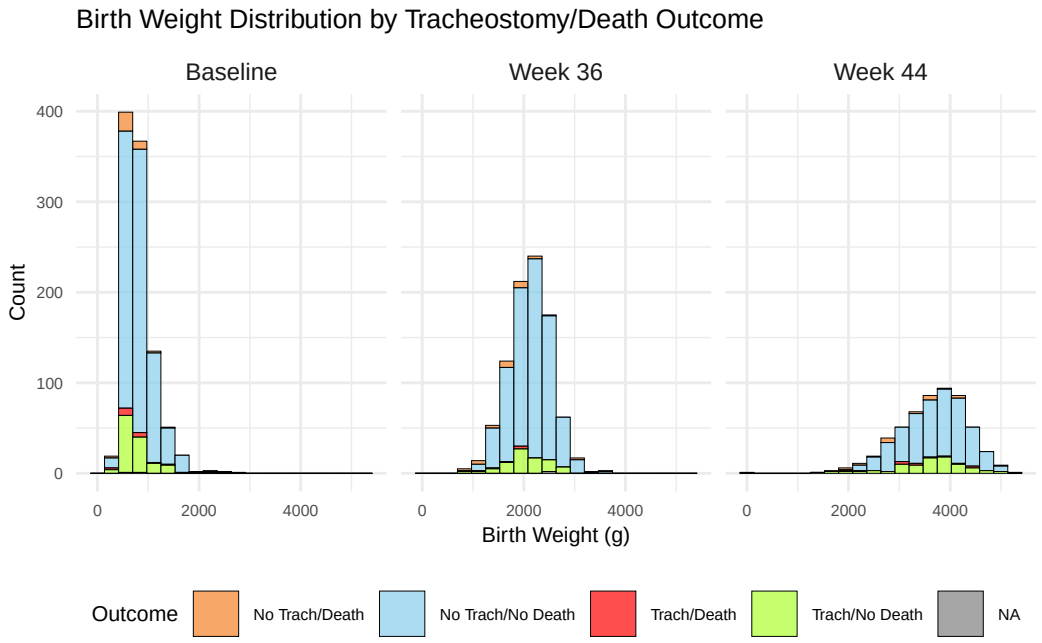
	Trachoestomy	Death

Characteristic	**No**, N = 853[1]	**Yes**, N = 146[1]	**No**, N = 943[1]	**Yes**, N = 54[1]
Gender				
Female	348 (41%)	60 (41%)	390 (41%)	17 (31%)
Male	501 (59%)	86 (59%)	549 (58%)	37 (69%)
Missing	4 (0.5%)	0 (0%)	4 (0.4%)	0 (0%)
Race				
0	477 (59%)	64 (47%)	519 (58%)	20 (40%)
1	243 (30%)	47 (35%)	272 (31%)	18 (36%)
2	87 (11%)	25 (18%)	100 (11%)	12 (24%)
Unknown	46	10	52	4
Ethnicity				
Hispanic or Latino	66 (7.7%)	8 (5.5%)	71 (7.5%)	3 (5.6%)
Not Hispanic or Latino	740 (87%)	128 (88%)	818 (87%)	48 (89%)
Missing	47 (5.5%)	10 (6.8%)	54 (5.7%)	3 (5.6%)
Birth Weight	814 (295)	761 (303)	811 (288)	721 (406)
Gestational Age	26 (2)	26 (2)	26 (2)	26 (2)
Birth Length	33 (4)	32 (4)	33 (4)	30 (4)
Unknown	48	30	71	7
Birth Head Circumference	23.22 (2.71)	22.99 (3.07)	23.24 (2.70)	22.34 (3.54)
Unknown	46	31	72	5
Delivery Method				
Vaginal delivery	254 (30%)	31 (21%)	274 (29%)	10 (19%)
Cesarean section	597 (70%)	114 (78%)	666 (71%)	44 (81%)
Missing	2 (0.2%)	1 (0.7%)	3 (0.3%)	0 (0%)
Prenatal Corticosteroids				
Yes	715 (84%)	123 (84%)	792 (84%)	44 (81%)
No	118 (14%)	8 (5.5%)	121 (13%)	5 (9.3%)
Missing	20 (2.3%)	15 (10%)	30 (3.2%)	5 (9.3%)
Small for gestational age				
SGA	161 (19%)	42 (29%)	177 (19%)	26 (48%)
Not SGA	681 (80%)	100 (68%)	751 (80%)	28 (52%)
Missing	11 (1.3%)	4 (2.7%)	15 (1.6%)	0 (0%)
Complete Prenatal Steroids				
Yes	527 (62%)	86 (59%)	577 (61%)	34 (63%)
No	166 (19%)	27 (18%)	184 (20%)	9 (17%)
Missing	160 (19%)	33 (23%)	182 (19%)	11 (20%)
Maternal Chorioamnionitis				
Yes	138 (16%)	22 (15%)	153 (16%)	7 (13%)
No	665 (78%)	112 (77%)	732 (78%)	43 (80%)
Missing	50 (5.9%)	12 (8.2%)	58 (6.2%)	4 (7.4%)

[1]Mean (SD) for continuous; n (%) for categorical



Lower Birth Weights: Infants who required a tracheostomy (green and red bars) or those who died (orange and red bars) tend to have lower birth weights across all time points. Survivors without Tracheostomy: The light blue section (No Trach/No Death) is consistently the largest, indicating that infants who did not require a tracheostomy and survived generally had higher weights at all time points.



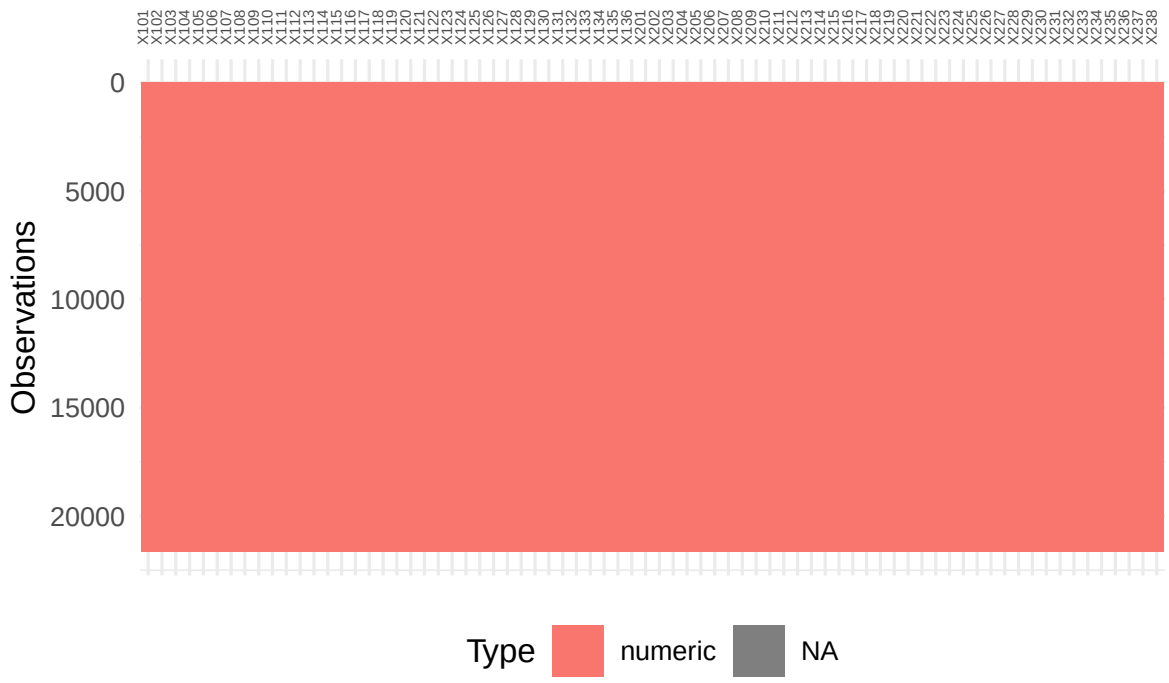
Missing Data and Imputation with MICE

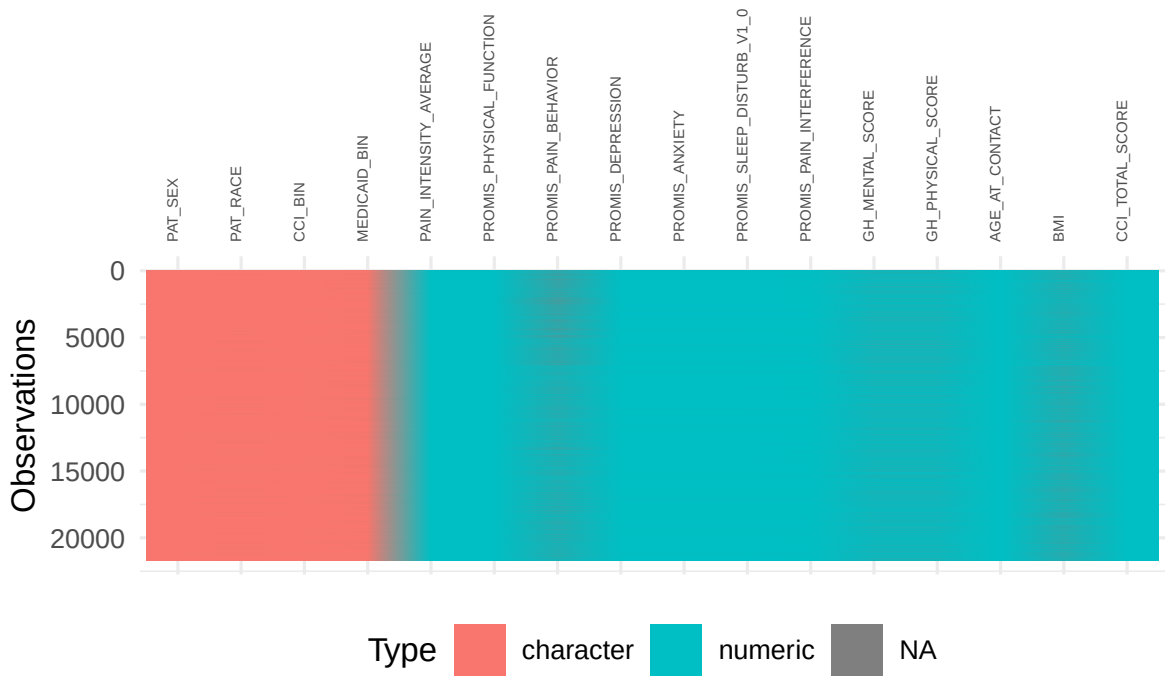
Load in the data called `pain` from the `HDSinRdata` package and read the documentation. The data contains information from patient-reported pain assessments at baseline and at a 3-month follow-up.

1. First, describe the patterns of missing data observed in the data set overall. How would you present this information in an exploratory analysis?

   I would present the missing data pattern using heat map. Base on the data structure, I plot three separate heat maps focusing on the body region variables, baseline characteristics, and the follow-up variable, respectively.

   In the heat map of the body region variables, we see that most variables have nearly complete data since there is no visible grey area on the plot, indicating minimal or no missing values. Our baseline characteristics, including both continuous and categorical, exhibits some missingness among certain columns. Categorical variables, such as `PAT_RACE` and `MEDICAID_BIN`, having small portion of missing data, while continuous variables like `BMI` and `GH_PHYSICAL_SCORE` have larger proportion of missingness. To be noticed, the follow-up variable in the third heat map exhibits a significantly large portion of missingness, with over 50% of value missing, which might be a crucial issue.


X101 X102 X103 X104 X105 X106 X107 X108 X109 X110 X111 X112 X113 X114 X115 X116 X117 X118 X119 X120 X121 X122 X123 X124 X125 X126 X127 X128 X129 X130 X131 X132 X133 X134 X135 X136 X201 X202 X203 X204 X205 X206 X207 X208 X209 X210 X211 X212 X213 X214 X215 X216 X217 X218 X219 X220 X221 X222 X223 X224 X225 X226 X227 X228 X229 X230 X231 X232 X233 X234 X235 X236 X237 X238
Observations
0
5000
10000
15000
20000
Type
numeric
NA


PAT_SEX
PAT_RACE
CCI_BIN
MEDICAID_BIN
PAIN_INTENSITY_AVERAGE
PROMIS_PHYSICAL_FUNCTION
PROMIS_PAIN_BEHAVIOR
PROMIS_DEPRESSION
PROMIS_ANXIETY
PROMIS_SLEEP_DISTURB_V1_0
PROMIS_PAIN_INTERFERENCE
GH_MENTAL_SCORE
GH_PHYSICAL_SCORE
AGE_AT_CONTACT
BMI
CCI_TOTAL_SCORE
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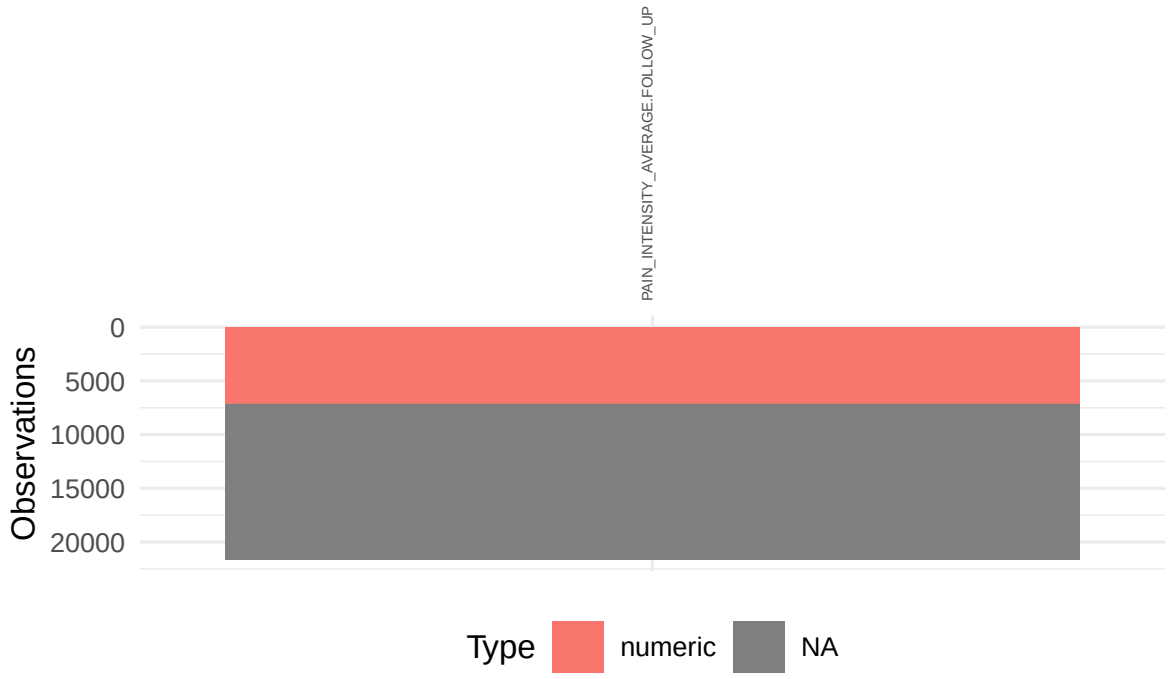


2. If we were interested in analyzing the change in pain over time, it would be important to think about the missing data due to loss to follow-up. Compare the baseline characteristics between those with and without follow-up information. Comment on your results and discuss whether you think the data is MCAR, MAR, or MNAR.

Characteristic	**Follow-up**, N = 7,138	**No Follow-up**, N = 14,521	**p-value**
PAIN_INTENSITY_AVERAGE	6.00 (5.00, 8.00)	7.00 (5.00, 8.00)	<0.001
PROMIS_PHYSICAL_FUNCTION	35 (31, 39)	35 (30, 39)	0.045
PROMIS_PAIN_BEHAVIOR	61.6 (59.0, 63.4)	61.7 (59.5, 63.4)	<0.001
PROMIS_DEPRESSION	55 (48, 62)	55 (48, 62)	0.009
PROMIS_ANXIETY	56 (49, 63)	58 (50, 63)	<0.001
PROMIS_SLEEP_DISTURB	59 (54, 65)	60 (54, 65)	<0.001
PROMIS_PAIN_INTERFERENCE	67 (62, 70)	67 (63, 72)	<0.001
GH_MENTAL_SCORE	44 (36, 51)	44 (36, 51)	0.5
GH_PHYSICAL_SCORE	35 (30, 40)	35 (30, 40)	0.028
AGE_AT_CONTACT	58 (48, 67)	57 (45, 68)	0.001
BMI	30 (25, 35)	29 (25, 34)	<0.001
CCI_TOTAL_SCORE			0.6
0	6,405 (90%)	13,119 (90%)	

Characteristic	**Follow-up**, N = 7,138	**No Follow-up**, N = 14,521	**p-value**
1	606 (8.5%)	1,149 (7.9%)	
2	104 (1.5%)	196 (1.3%)	
3	19 (0.3%)	45 (0.3%)	
4	4 (<0.1%)	10 (<0.1%)	
5	0 (0%)	1 (<0.1%)	
PAT_SEX			<0.001
female	4,431 (62%)	8,671 (60%)	
male	2,707 (38%)	5,849 (40%)	
PAT_RACE			<0.001
ALASKA NATIVE	1 (<0.1%)	1 (<0.1%)	
AMERICAN INDIAN	29 (0.4%)	29 (0.2%)	
BLACK	934 (13%)	2,295 (16%)	
CHINESE	4 (<0.1%)	17 (0.1%)	
DECLINED	28 (0.4%)	93 (0.6%)	
FILIPINO	3 (<0.1%)	3 (<0.1%)	
GUAM/CHAMORRO	0 (0%)	1 (<0.1%)	
HAWAIIAN	1 (<0.1%)	0 (0%)	
INDIAN (ASIAN)	13 (0.2%)	36 (0.2%)	
JAPANESE	1 (<0.1%)	8 (<0.1%)	
KOREAN	3 (<0.1%)	7 (<0.1%)	
NOT SPECIFIED	2 (<0.1%)	2 (<0.1%)	
OTHER	0 (0%)	1 (<0.1%)	
OTHER ASIAN	8 (0.1%)	39 (0.3%)	
OTHER PACIFIC ISLANDER	1 (<0.1%)	11 (<0.1%)	
VIETNAMESE	3 (<0.1%)	3 (<0.1%)	
WHITE	6,080 (86%)	11,860 (82%)	
CCI_BIN			0.2
Any comorbidity	733 (10%)	1,401 (9.6%)	
No comorbidity	6,405 (90%)	13,119 (90%)	
MEDICAID_BIN	1,338 (19%)	3,263 (23%)	<0.001

3. Now suppose we are interested in mental and physical function at baseline and how that is associated with pain intensity. We will use the `mice` package to perform multiple imputation on this data. First, drop the variable `PAIN_INTENSITY_AVERAGE.FOLLOW_UP` and the body map variables `X101:X238`.

```
pain_mod <- pain[, -c(1:75)] %>%
  select(-PAIN_INTENSITY_AVERAGE.FOLLOW_UP)
```

```
pain_mod$PAT_SEX <- as.factor(pain_mod$PAT_SEX)
pain_mod$PAT_RACE <- as.factor(pain_mod$PAT_RACE)
pain_mod$CCI_BIN <- as.factor(pain_mod$CCI_BIN)
pain_mod$MEDICAID_BIN <- as.factor(pain_mod$MEDICAID_BIN)
```

4. Use the `mice()` function to perform multiple imputation to create five imputed data sets and save the result as `pain_mice`. You should read the documentation on this function to understand how it is implementing this and what arguments you might want to set. What is the structure of the returned object?

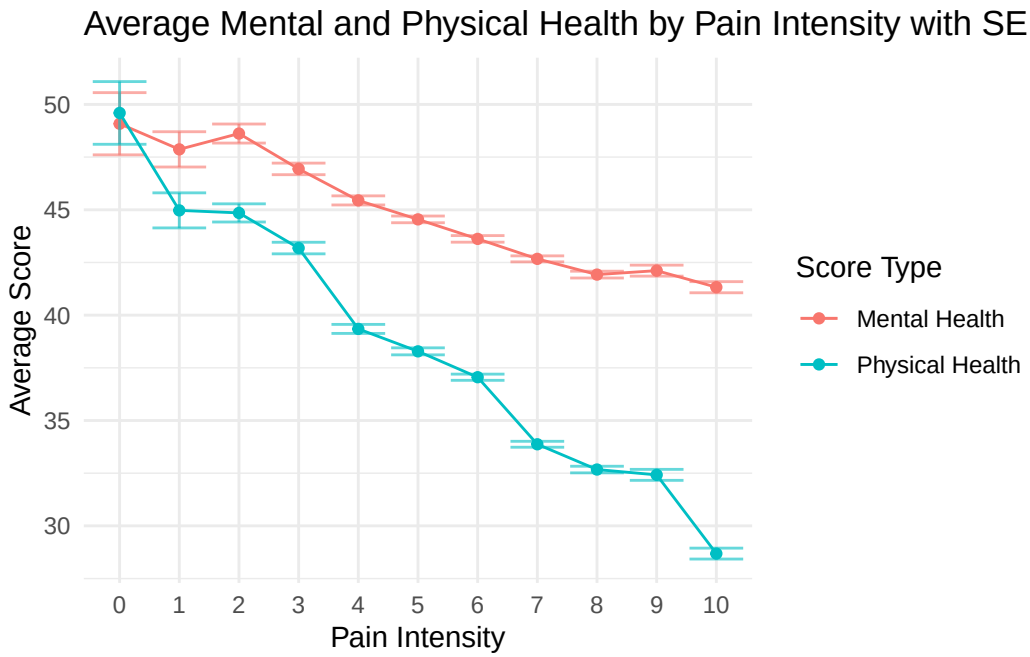
```
# pain_mice <- mice(pain_mod, maxit = 5, seed = (2550))
# saveRDS(pain_mice, file = "mice_result.rds")
pain_mice <- readRDS("mice_result.rds")
```

5. For one imputed data set, find the average mental and physical health score for each possible pain intensity level (0-10). To access the first imputed data set you can use the code below.
   `mice::complete(pain_mice,1)`

Table 3: Average Summary of Pain Intensity Score

PAIN_INTENSITY_AVERAGE	avg_mental_health	avg_physical_health
0	49.12553	49.43191
1	47.97703	45.07432
2	48.68802	44.81221
3	46.97733	43.19800
4	45.47257	39.30918
5	44.58407	38.27742
6	43.67522	37.04332
7	42.71223	33.86519
8	41.94154	32.67854
9	42.12265	32.38978
10	41.34510	28.63168

6. Repeat this for the other four data sets and then use Rubin's rules to plot the results. https://bookdown.org/mwheymans/bookmi/rubins-rules.html



Appendix

```
library(tidyverse)
library(ggplot2)
library(visdat)
schmid_data <- read.csv("schmid_data.csv")
vis_dat(schmid_data) +
theme(axis.text.x = element_text(angle = 90, size = 5))
schmid_data <- schmid_data %>%
  mutate(Outcome = case_when(Trach == 1 & Death == "Yes" ~ "Trach/Death",
                             Trach == 1 & Death == "No" ~ "Trach/No Death",
                             Trach == 0 & Death == "Yes" ~ "No Trach/Death",
                             Trach == 0 & Death == "No" ~ "No Trach/No Death"))
schmid_count <- schmid_data %>%
  filter(!is.na(center)) %>%
  group_by(center) %>%
  count(Outcome) %>%
  spread(Outcome, n, fill = 0)
 schmid_count <-  schmid_count %>%
   gather(`Trach/Death`,`No Trach/Death`,`No Trach/No Death`,`Trach/No Death`,`<NA>`,
          key = "Outcomes", value = "Count") %>%
```

```
    mutate(Outcomes = factor(Outcomes,
                             levels = c("Trach/Death", "No Trach/Death", "Trach/No Death",
                                        "No Trach/No Death", "<NA>"))) %>%
    group_by(center) %>%
    mutate(Proportion = Count/sum(Count))

ggplot(schmid_count, aes(x = Proportion, y = factor(center), fill = Outcomes)) +
  geom_bar(stat = "identity", position = "stack", color = "black") +
  labs(title = "Outcome Proportion by Center", x = "Proportion", y = "Center") +
  theme_minimal() +
  theme(legend.position = "bottom") +
  scale_fill_manual(values = c("Trach/Death" = "#EF8100",
                               "No Trach/Death" = "#FFA842",
                               "Trach/No Death" = "#FFD925",
                               "No Trach/No Death" = "#FFEB8C",
                               "<NA>" = "gray"))
library(tidyr)
library(gtsummary)
library(ggpubr)

schmid_trach <- schmid_data %>%
  select(gender, mat_race, mat_ethn, bw, ga, blength, birth_hc, del_method,
         prenat_ster, sga, com_prenat_ster,mat_chorio,Trach) %>%
  mutate(Trach = recode(Trach, `0` = "No", `1` ="Yes")) %>%
  mutate(
    # mat_race = case_when(mat_race == 1 ~ "American Indian or Alaskan Native",
    #                      mat_race == 2 ~ "Asian",
    #                      mat_race == 3 ~ "Black or African American",
    #                      mat_race == 4 ~ "Native Hawaiian or Other Pacific Islande",
    #                      mat_race == 5 ~ "White",
    #                      mat_race == 6 ~ "Other",
    #                      TRUE  ~ "Missing")
    gender = case_when(gender == "Female" ~  "Female",
                       gender == "Male" ~  "Male",
                      TRUE ~ "Missing"),
    mat_ethn = case_when(mat_ethn == 1 ~ "Hispanic or Latino",
                         mat_ethn == 2 ~ "Not Hispanic or Latino",
                         TRUE ~ "Missing"),
    del_method = case_when(del_method==1 ~ 'Vaginal delivery',
                           del_method==2 ~ 'Cesarean section',
                           TRUE ~ "Missing"),
```

```
  sga = case_when(sga=="SGA" ~ "SGA",
                  sga=="Not SGA" ~ "Not SGA",
                  TRUE ~ "Missing"),
  prenat_ster = case_when(prenat_ster == "Yes" ~ "Yes",
                          prenat_ster == "No" ~ "No",
                          TRUE ~ "Missing"),
  com_prenat_ster = case_when(com_prenat_ster == "Yes" ~ "Yes",
                          com_prenat_ster == "No" ~ "No",
                          TRUE ~ "Missing"),
  mat_chorio = case_when(mat_chorio == "Yes" ~ "Yes",
                          mat_chorio == "No" ~ "No",
                          TRUE ~ "Missing")) %>%
mutate(mat_ethn = factor(mat_ethn, levels = c('Hispanic or Latino',
                                              'Not Hispanic or Latino', 'Missing')),
       del_method = factor(del_method,
                           levels = c('Vaginal delivery',
                                      'Cesarean section', 'Missing')),
       sga = factor(sga, levels = c('SGA', 'Not SGA', 'Missing')),
       prenat_ster = factor(prenat_ster, levels = c('Yes', 'No', 'Missing')),
       com_prenat_ster = factor(com_prenat_ster, levels = c('Yes', 'No', 'Missing')),
       mat_chorio = factor(mat_chorio, levels = c('Yes', 'No', 'Missing'))) %>%
tbl_summary(by=Trach,
            label = list(gender ~ "Gender",
                         mat_race ~ "Race",
                         mat_ethn ~ "Ethnicity",
                         bw ~ "Birth Weight",
                         ga ~ " Gestational Age",
                         blength ~ "Birth Length",
                         birth_hc ~ "Birth Head Circumference",
                         del_method ~ "Delivery Method",
                         prenat_ster ~ "Prenatal Corticosteroids",
                         sga ~ "Small for gestational age",
                         com_prenat_ster ~ "Complete Prenatal Steroids",
                         mat_chorio ~ "Maternal Chorioamnionitis"
                         ),
            statistic = all_continuous() ~ "{mean} ({sd})") %>%
modify_spanning_header(update =  all_stat_cols() ~  "**Trachoestomy**") %>%
modify_footnote(update = all_stat_cols() ~ "Mean (SD) for continuous; n (%) for categori
bold_labels()
```

```r
schmid_death <- schmid_data %>%
  select(gender, mat_race, mat_ethn, bw, ga, blength, birth_hc, del_method,
         prenat_ster, sga, com_prenat_ster,mat_chorio,Death) %>%
  mutate(Death = recode(Death, `0` = "No", `1` ="Yes")) %>%
  mutate(
    # mat_race = case_when(mat_race == 1 ~ "American Indian or Alaskan Native",
    #                      mat_race == 2 ~ "Asian",
    #                      mat_race == 3 ~ "Black or African American",
    #                      mat_race == 4 ~ "Native Hawaiian or Other Pacific Islande",
    #                      mat_race == 5 ~ "White",
    #                      mat_race == 6 ~ "Other",
    #                      TRUE  ~ "Missing")
    gender = case_when(gender == "Female" ~  "Female",
                       gender == "Male" ~  "Male",
                      TRUE ~ "Missing"),
    mat_ethn = case_when(mat_ethn == 1 ~ "Hispanic or Latino",
                         mat_ethn == 2 ~ "Not Hispanic or Latino",
                         TRUE ~ "Missing"),
    del_method = case_when(del_method==1 ~ 'Vaginal delivery',
                           del_method==2 ~ 'Cesarean section',
                           TRUE ~ "Missing"),
    sga = case_when(sga=="SGA" ~ "SGA",
                    sga=="Not SGA" ~ "Not SGA",
                    TRUE ~ "Missing"),
    prenat_ster = case_when(prenat_ster == "Yes" ~ "Yes",
                            prenat_ster == "No" ~ "No",
                            TRUE ~ "Missing"),
    com_prenat_ster = case_when(com_prenat_ster == "Yes" ~ "Yes",
                            com_prenat_ster == "No" ~ "No",
                            TRUE ~ "Missing"),
    mat_chorio = case_when(mat_chorio == "Yes" ~ "Yes",
                            mat_chorio == "No" ~ "No",
                            TRUE ~ "Missing")) %>%
  mutate(mat_ethn = factor(mat_ethn, levels = c('Hispanic or Latino',
                                                'Not Hispanic or Latino', 'Missing')),
         del_method = factor(del_method, levels = c('Vaginal delivery', 'Cesarean section'
                                                    'Missing')),
         sga = factor(sga, levels = c('SGA', 'Not SGA', 'Missing')),
         prenat_ster = factor(prenat_ster, levels = c('Yes', 'No', 'Missing')),
         com_prenat_ster = factor(com_prenat_ster, levels = c('Yes', 'No', 'Missing')),
         mat_chorio = factor(mat_chorio, levels = c('Yes', 'No', 'Missing'))) %>%
```

```
  tbl_summary(by=Death,
              label = list(gender ~ "Gender",
                           mat_race ~ "Race",
                           mat_ethn ~ "Ethnicity",
                           bw ~ "Birth Weight",
                           ga ~ " Gestational Age",
                           blength ~ "Birth Length",
                           birth_hc ~ "Birth Head Circumference",
                           del_method ~ "Delivery Method",
                           prenat_ster ~ "Prenatal Corticosteroids",
                           sga ~ "Small for gestational age",
                           com_prenat_ster ~ "Complete Prenatal Steroids",
                           mat_chorio ~ "Maternal Chorioamnionitis"
                           ),
              statistic = all_continuous() ~ "{mean} ({sd})") %>%
  modify_spanning_header(update =  all_stat_cols() ~  "**Death**") %>%
  modify_footnote(update = all_stat_cols() ~ "Mean (SD) for continuous; n (%) for categori

schimd_tbl <- tbl_merge(list(schmid_trach, schmid_death),
                        tab_spanner = c("**Trachoestomy**", "**Death**"))

schimd_tbl %>%
  as_gt()
schmid_data$ventilation_support_level.36 <-
  as.factor(schmid_data$ventilation_support_level.36)
schmid_data$ventilation_support_level_modified.44 <-
  as.factor(schmid_data$ventilation_support_level_modified.44)

schmid_data$Trach <- as.factor(schmid_data$Trach)
schmid_data$Death <- as.factor(schmid_data$Death)

schmid_long <- schmid_data %>%
  rename(ventilation_support_level.44 = 'ventilation_support_level_modified.44') %>%
  pivot_longer(cols = c('ventilation_support_level.36',
                        'ventilation_support_level.44',
                        'p_delta.36',
                        'p_delta.44'),
               names_to = c(".value", "time"),
               names_pattern = "(ventilation_support_level|p_delta).(\\d+)")
schmid_long$time <- as.factor(schmid_long$time)
schmid_long$Trach <- as.factor(schmid_long$Trach)
```

```r
schmid_long$ventilation_support_level <- as.factor(schmid_long$ventilation_support_level)

schmid_pressure <- schmid_long %>%
  filter(!is.na(ventilation_support_level) & !is.na(p_delta) & !is.na(Trach)) %>%
  group_by(time) %>%
  ggplot(aes(y = p_delta, x = ventilation_support_level, fill =  Trach)) +
  geom_boxplot() +
  labs(y = "Peak Inspiratory Pressure (cmH2O) at 36 weeks", x = "support", fill = "Trach") +
  facet_wrap(~time, nrow = 2)

schmid_pressure
weight_df <- schmid_data %>%
  pivot_longer(cols = c("bw", "weight_today.36", "weight_today.44"),
               names_to = "Time",
               values_to = "Weight")

weight_df <- weight_df %>%
  mutate(Time = case_when(Time == "bw" ~ "Baseline",
                          Time == "weight_today.36" ~ "Week 36",
                          Time == "weight_today.44" ~ "Week 44",
                          TRUE ~ NA))
options(repr.plot.width = 10, repr.plot.height = 10)

weight_df %>%
  group_by(Time) %>%
  ggplot(aes(x = Weight, fill = Outcome)) +
  geom_histogram(bins = 20, position = "stack", color = "black", alpha = 0.7, size = 0.1) +
  labs(title = "Birth Weight Distribution by Tracheostomy/Death Outcome",
       x = "Birth Weight (g)", y = "Count") +
  facet_wrap(~Time, ncol = 3) +
  theme_minimal() +
  theme(legend.position = "bottom") +
  scale_fill_manual(values = c("#F48126", "skyblue", "red", "greenyellow")) +
  theme(legend.text = element_text(size = 6), # Adjust the size of legend text
        legend.title = element_text(size = 8),
        axis.text = element_text(size = 6),
        plot.title = element_text(size = 10),
        axis.title = element_text(size = 8)
        )

library(HDSinRdata)
```

```r
library(mice)
library(dplyr)
library(ggplot2)
library(kableExtra)
library(visdat)
library(gtsummary)
data(pain)

vis_dat(pain[, 2:75], warn_large_data = FALSE) +
  theme(axis.text.x = element_text(angle = 90, size = 5)) +
  theme(legend.position = "bottom")

vis_dat(pain[, c(76:87, 89:92)]) +
  theme(axis.text.x = element_text(angle = 90, size = 5)) +
  theme(legend.position = "bottom")

vis_dat(pain[, 88]) +
  theme(axis.text.x = element_text(angle = 90, size = 5)) +
  theme(legend.position = "bottom")
pain_followup <- pain %>%
  mutate(follow_up_status = ifelse(is.na(PAIN_INTENSITY_AVERAGE.FOLLOW_UP),
                                   "No Follow-up", "Follow-up"))

tbl <- pain_followup %>%
  select(follow_up_status, colnames(pain)[c(76:87, 89:92)]) %>%
  tbl_summary(
    by = follow_up_status,
    missing = "no"
  ) %>%
  add_p(
    test = list(
      all_categorical() ~ "fisher.test",
      all_continuous() ~ "t.test"
    ),
    test.args = list(
      all_categorical() ~ list(simulate.p.value = TRUE)
    )
  )

tbl
pain_mod <- pain[, -c(1:75)] %>%
```

```r
  select(-PAIN_INTENSITY_AVERAGE.FOLLOW_UP)

pain_mod$PAT_SEX <- as.factor(pain_mod$PAT_SEX)
pain_mod$PAT_RACE <- as.factor(pain_mod$PAT_RACE)
pain_mod$CCI_BIN <- as.factor(pain_mod$CCI_BIN)
pain_mod$MEDICAID_BIN <- as.factor(pain_mod$MEDICAID_BIN)
# pain_mice <- mice(pain_mod, maxit = 5, seed = (2550))
# saveRDS(pain_mice, file = "mice_result.rds")
pain_mice <- readRDS("mice_result.rds")
score_list <- list()

for (i in 1:5) {
  mice_imp <- mice::complete(pain_mice, i)

  score <- mice_imp %>%
  group_by(PAIN_INTENSITY_AVERAGE) %>%
  summarize(
    avg_mental_health = mean(GH_MENTAL_SCORE),
    se_mental_health = sd(GH_MENTAL_SCORE)/sqrt(n()),
    avg_physical_health = mean(GH_PHYSICAL_SCORE),
    se_physical_health = sd(GH_PHYSICAL_SCORE)/sqrt(n())
  )

  score_list[[i]] <-  score
}

score1_avg <- score_list[[1]][, c("PAIN_INTENSITY_AVERAGE", "avg_mental_health",
                                  "avg_physical_health")]
knitr::kable(score1_avg,
             caption = "Average Summary of Pain Intensity Score") %>%
  kable_styling(latex_options = "HOLD_position")
mice_pool <- do.call(rbind, score_list)

score_pool <- mice_pool %>%
  group_by(PAIN_INTENSITY_AVERAGE) %>%
  summarize(
    avg_mental_health_pool = mean(avg_mental_health),

    se_mental_health_pool = sqrt(mean(se_mental_health^2)
    + (sum((avg_mental_health - mean(avg_mental_health))^2))/4
    + (sum((avg_mental_health - mean(avg_mental_health))^2))/20),
```

```
    avg_physical_health_pool = mean(avg_physical_health),

    se_physical_health_pool = sqrt(mean(se_mental_health^2)
    + (sum((avg_physical_health - mean(avg_physical_health))^2))/4
    + (sum((avg_physical_health - mean(avg_physical_health))^2))/20)
    )

ggplot(score_pool, aes(x = factor(PAIN_INTENSITY_AVERAGE))) +
  geom_point(aes(y = avg_mental_health_pool, color = "Mental Health")) +
  geom_line(aes(y = avg_mental_health_pool, color = "Mental Health"), group = 1) +
  geom_errorbar(aes(ymin = avg_mental_health_pool - se_mental_health_pool,
                    ymax = avg_mental_health_pool + se_mental_health_pool,
                    color = "Mental Health",), alpha = 0.6) +
  geom_point(aes(y = avg_physical_health_pool, color = "Physical Health")) +
  geom_line(aes(y = avg_physical_health_pool, color = "Physical Health"), group = 1) +
  geom_errorbar(aes(ymin = avg_physical_health_pool - se_physical_health_pool,
                    ymax = avg_physical_health_pool + se_physical_health_pool,
                    color = "Physical Health"), alpha = 0.6) +
  labs(x = "Pain Intensity", y = "Average Score",
       title = "Average Mental and Physical Health by Pain Intensity with SE",
       color = "Score Type") +
  theme_minimal()
```