# Lesson Notes | Data Cleaning Pipeline 1: Exploratory Data Analysis

## Introduction

Data cleaning is the process of transforming raw, "messy" data into reliable data that can be properly analyzed. This entails identifying **inaccurate**, **incomplete**, or **improbable** data points and resolving data inconsistencies or errors, as well as renaming variable names to make them more clear and simple to manipulate.

Data cleaning tasks can often be tedious and time-consuming. A common joke among data analysts goes "80% of data science is cleaning the data and the remaining 20% is complaining about cleaning the data." But data cleaning is an essential step of the data analysis process. A little bit of cleaning at the start of the data analysis process will go a long way to improving the quality of your analyses and the ease with which these analyses can be done. And a range of packages and functions in R can significantly simplify the data cleaning process.

In this lesson, we will begin to look at a typical data cleaning pipeline in R. The cleaning steps covered here are unlikely to be exactly what is needed for your own datasets, but they will certainly be a good starting point.

Let's get started!

## Learning objectives

- You can list typical operations involved in data cleaning process
- You can diagnose dataset issues that warrant data cleaning through functions such as:
    - `visdat::vis_dat()`
    - `skimr::skim()`
    - `inspectdf::inspect_cat()`
    - `inspectdf::inspect_num()`
    - `gtsummary::tbl_summary()`
    - `DataExplorer::create_report()`

---

## Packages

The packages loaded below will be required for this lesson:

```
if(!require("pacman")) install.packages("pacman")
pacman::p_load(visdat,
               skimr,
               inspectdf,
               gtsummary,
               DataExplorer,
               tidyverse)
```

---

## Dataset

The primary dataset we will use in this lesson is from a study conducted in three healthcare centres in Zambezia, Mozambique. The study investigated individual factors associated with time to non-adherence to HIV care and treatment services. For the sake of this lesson, we will only be looking at a modified subset of the full dataset.

The full dataset can be obtained from Zenodo, and the paper can be viewed here.

Let's take a look at this dataset:

```
non_adherence <- read_csv(here("data/non_adherence_moz.csv"))
```

```
non_adherence
```

```
## # A tibble: 5 × 15
##   patient_id District `Health unit` Sex   Age_35
##        <dbl>    <dbl>         <dbl> <chr> <chr>
## 1      10037        1             1 Male  over 35
## 2      10537        1             1 F     over 35
## 3       5489        2             3 F     Under 35
## 4       5523        2             3 Male  Under 35
## 5       4942        2             3 F     over 35
## # ℹ 10 more variables: `Age at ART initiation` <dbl>,
## #   Education <chr>, Occupation <chr>, …
```

The first step of data cleaning will be to explore this dataset in order to identify potential issues that warrant cleaning. This preliminary step is sometimes called "exploratory data analysis" or EDA.

Let's take a look at a few simple EDA commands in R that will help you identify possible data errors and inconsistencies.

---

## Visualizing missing data with `visdat::vis_dat()`

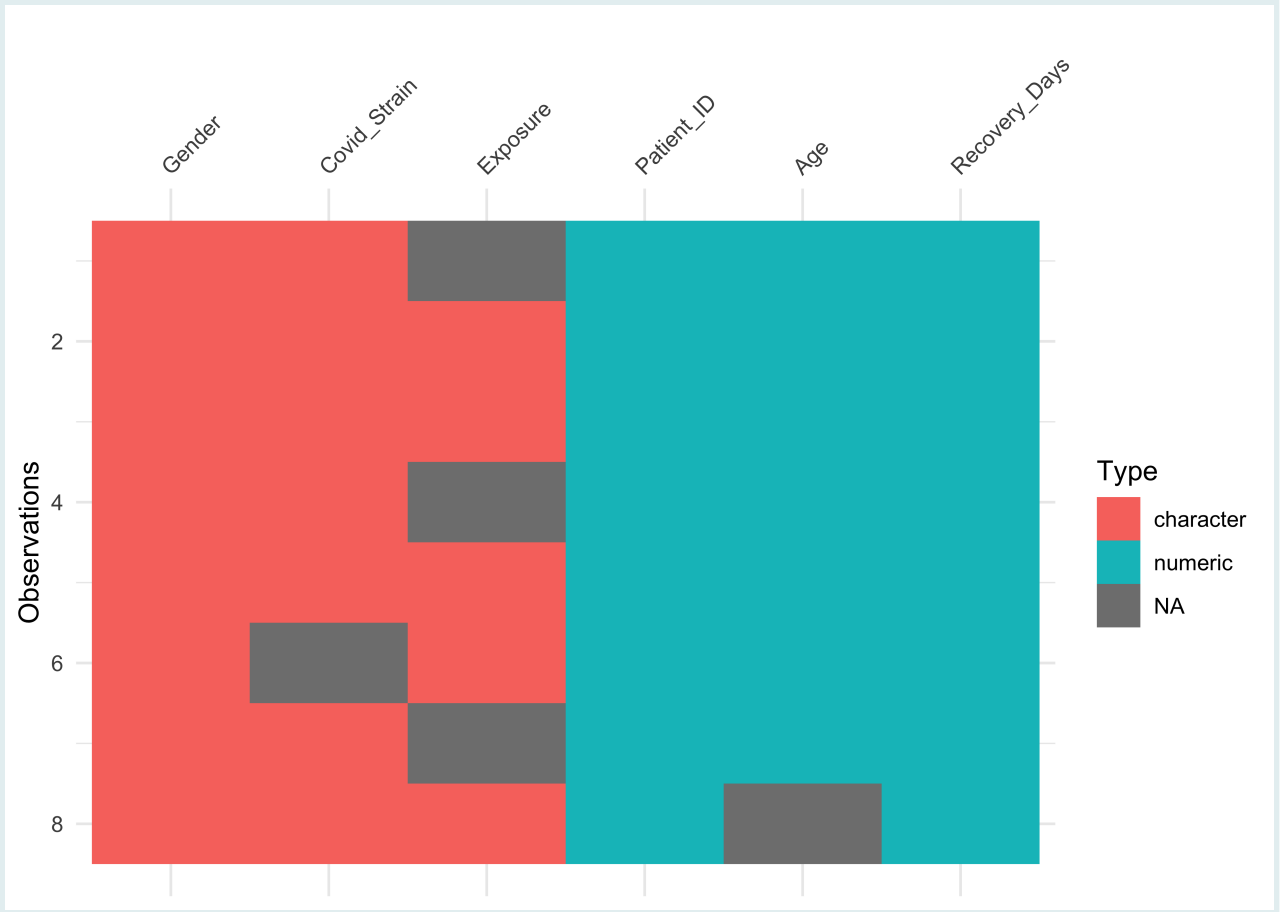
The `vis_dat()` function from the `visdat` package is a wonderful way to quickly visualize data types and missing values in a dataset. It creates a plot that shows a "zoomed out" spreadsheet view of your data frame: each row in the dataframe is represented by a single line on the plot.

Let's try it out with small mock dataset first to get an idea of how it works. Copy the following code to create a dataframe of 8 patients and their COVID-19 diagnosis and recovery information. As you can see below, some patients have missing information, represented as NA.

```
        covid_pat <- tribble(
          ~Patient_ID, ~Age, ~Gender,  ~Covid_Strain, ~Exposure,
~Recovery_Days,
           1,           25,   "Male",   "Alpha",        NA,          10,
           2,           32,   "Female", "Delta",       "Hospital",  15,
           3,           45,   "Male",   "Beta",        "Travel",     7,
           4,           19,   "Female", "Omicron",      NA,          21,
           5,           38,   "Male",   "Alpha",       "Unknown",   14,
           6,           55,   "Female",  NA,           "Community", 19,
           7,           28,   "Female", "Omicron",      NA,           8,
           8,           NA,   "Female", "Omicron",     "Travel",     26
        )
        covid_pat
```

Now, let's use the function `vis_dat()` on our dataframe to get visual representation of the data types and missing values.

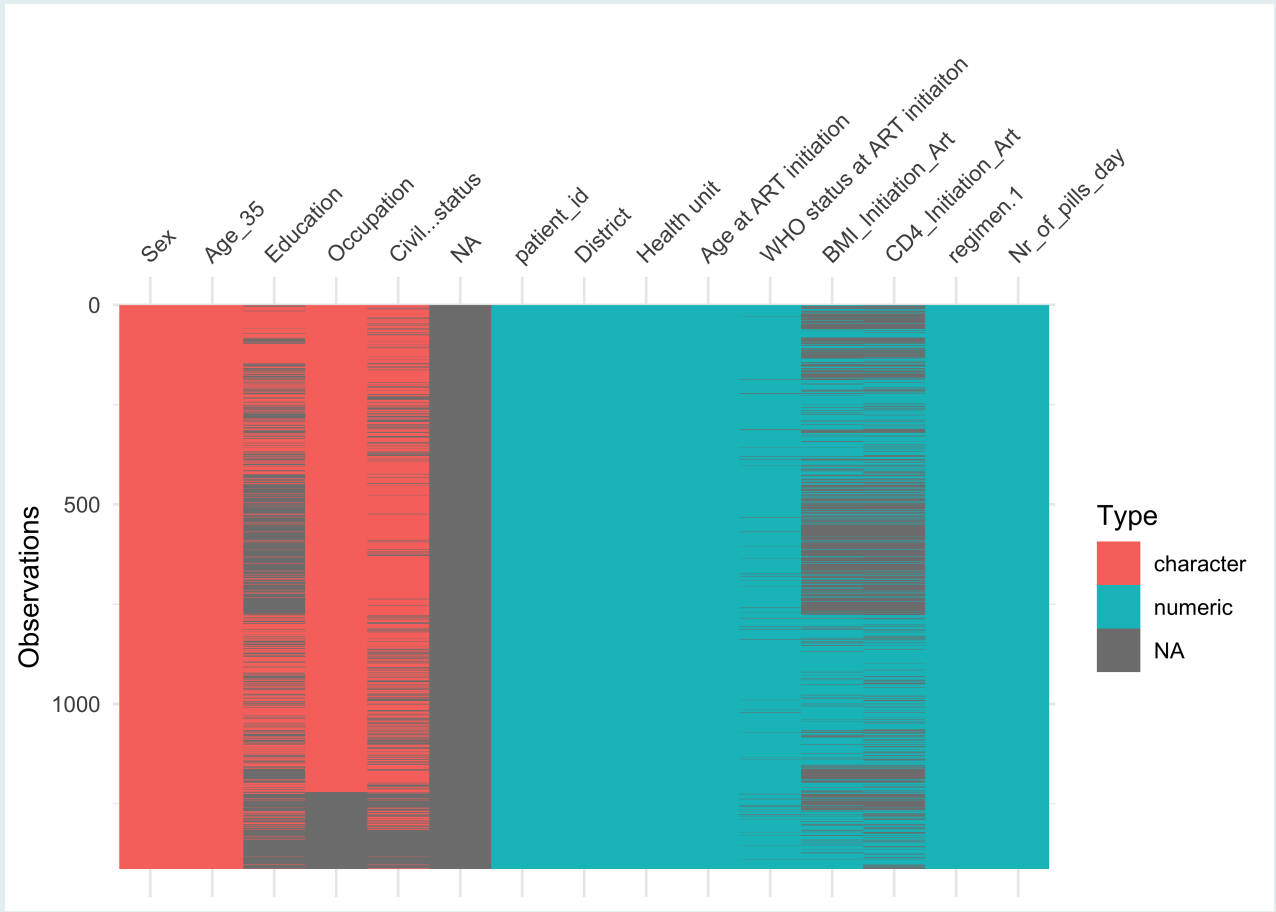
```
        vis_dat(covid_pat)
```




That looks great! Each row in our dataframe is represented by a single line in the plot and different colours are used to illustrate the character (pink) and numeric (blue) variables, as well as missing values (grey). From this plot, we can tell that quite a few patients in our dataset are missing data for the `Exposure` variable.

Now let's turn back to our real-world dataset which is much larger and messier. Large real-world datasets may exhibit intricate patterns in the data that are difficult to spot without visualization, so using functions such as `vis_dat()` can be particularly useful. Let's try it out now!

```
vis_dat(non_adherence)
```




Great! From this view we can already see some problems:

- there seems to be a completely empty column in the data (the column `NA` which is fully gray)
- several variables have a lot of missing values (such as `Education`, `BMI_Initation_Art`, and `CD4_Initation_ART`)
- the names of some variables are unclear/unclean (e.g., `Age at ART initation` and `WHO status at ART initiaion` have whitespaces in their names and `Civil...status` and `regimen.1` have special characters, `.`)

In the next lesson, we will try to remedy these and other issues as best as possible during the data cleaning process. But for now, the goal is that we understand the functions used to identify them. So now that we have a solid grasp on how to visualize missing data with `vis_dat()`, let's take a look at another package and function that can help us generate summary statistics of our variables!

The following dataset was adapted from a study that investigated missed opportunities for HIV testing among patients newly presenting for HIV care at a Swiss university hospital. The full dataset can be found here.

```
missed_ops <- read_csv(here("data/HIV_missed_ops.csv"))
```

Use the `vis_dat()` function to get a visual representation of the data. What potential issues can you spot based on the output?

---

## Generating summary statistics with `skimr::skim()`

The `skim()` function from the `skimr` package provides a console-based overview of the data frame and a summary of every column (by class/type). Let's try it on our `covid_pat` mock data first to get an idea of how it works. First, as a reminder, here is our `covid_pat` dataframe:

```
covid_pat
```

Great, now let's run the `skim()` function!

```
skimr::skim(covid_pat)
```

Table 1: Data summary

| | |
|---|---|
| Name | covid_pat |
| Number of rows | 8 |
| Number of columns | 6 |
| _____ | |
| Column type frequency: | |
| character | 3 |
| numeric | 3 |
| _____ | |
| Group variables | None |

**Variable type: character**

| skim_variable | n_missing | complete_rate | min | max | empty | n_unique | whitespace |
|---|---|---|---|---|---|---|---|
| Gender | 0 | 1.00 | 4 | 6 | 0 | 2 | 0 |
| Covid_Strain | 1 | 0.88 | 4 | 7 | 0 | 4 | 0 |
| Exposure | 3 | 0.62 | 6 | 9 | 0 | 4 | 0 |

**Variable type: numeric**

| skim_variable | n_missing | complete_rate | mean | sd | p0 | p25 | p50 | p75 | p100 | hist |
|---|---|---|---|---|---|---|---|---|---|---|
| Patient_ID | 0 | 1.00 | 4.50 | 2.45 | 1 | 2.75 | 4.5 | 6.25 | 8 | ▇▃▇▃▇ |
| Age | 1 | 0.88 | 34.57 | 12.39 | 19 | 26.50 | 32.0 | 41.50 | 55 | ▇▇▃▂▂ |
| Recovery_Days | 0 | 1.00 | 15.00 | 6.68 | 7 | 9.50 | 14.5 | 19.50 | 26 | ▇▂▂▃▂ |

Amazing! As we can see, this function provides:

- An overview of the rows and columns of the dataframe
- The data type for each variable
- `n_missing`, the number of missing values for each variable
- `complete_rate`, the completeness rate for each variable
- A set of summary statistics: the mean, standard deviation and quartiles for numerical variables; and the frequency and proportions for categorical variables
- Spark histograms for the numerical variables

Now we can tell why this is so valuable with large dataframes! Let's return to our `non-adherence` dataset and run the `skim()` function on it.

```
non_adherence
```

```
skimr::skim(non_adherence)
```

Table 2: Data summary

| | |
|---|---|
| Name | non_adherence |
| Number of rows | 1413 |
| Number of columns | 15 |
| _____ | |
| Column type frequency: | |
| character | 5 |
| logical | 1 |
| numeric | 9 |
| _____ | |
| Group variables | None |

**Variable type: character**

| skim_variable | n_missing | complete_rate | min | max | empty | n_unique | whitespace |
|---|---|---|---|---|---|---|---|
| Sex | 0 | 1.00 | 1 | 4 | 0 | 2 | 0 |
| Age_35 | 0 | 1.00 | 7 | 8 | 0 | 2 | 0 |
| Education | 776 | 0.45 | 4 | 10 | 0 | 5 | 0 |
| Occupation | 193 | 0.86 | 4 | 22 | 0 | 50 | 0 |
| Civil…status | 412 | 0.71 | 6 | 12 | 0 | 4 | 0 |

**Variable type: logical**

| skim_variable | n_missing | complete_rate | mean | count |
|---|---|---|---|---|
| NA | 1413 | 0 | NaN | : |

**Variable type: numeric**

| skim_variable | n_missing | complete_rate | mean | sd | p0 | p25 | p50 | p75 | p100 |
|---|---|---|---|---|---|---|---|---|---|
| patient_id | 0 | 1.00 | 7364.75 | 3312.95 | 147.0 | 4705.00 | 7355.0 | 10098.0 | 24377.0 |
| District | 0 | 1.00 | 1.35 | 0.48 | 1.0 | 1.00 | 1.0 | 2.0 | 2.0 |
| Health unit | 0 | 1.00 | 1.87 | 0.90 | 1.0 | 1.00 | 2.0 | 3.0 | 3.0 |
| Age at ART initiation | 0 | 1.00 | 32.07 | 9.51 | 15.1 | 25.20 | 30.4 | 36.8 | 75.3 |
| WHO status at ART initiaiton | 45 | 0.97 | 1.80 | 0.98 | 1.0 | 1.00 | 1.0 | 3.0 | 4.0 |
| BMI_Initiation_Art | 588 | 0.58 | 20.37 | 3.54 | 9.0 | 18.12 | 20.1 | 22.2 | 52.0 |
| CD4_Initiation_Art | 674 | 0.52 | 398.19 | 243.64 | 3.0 | 233.00 | 343.0 | 538.0 | 1401.0 |
| regimen.1 | 0 | 1.00 | 4.64 | 1.54 | 1.0 | 3.00 | 6.0 | 6.0 | 7.0 |
| Nr_of_pills_day | 0 | 1.00 | 1.51 | 0.59 | 1.0 | 1.00 | 1.0 | 2.0 | 3.0 |

From this output, we can identify some potential issues with our data:

- we can confirm that the column NA, which you saw from the `vis_dat()` output, is indeed completely empty: it has a `complete_rate` of 0
- the distribution for `Age at ART initation` is skewed

Use `skim()` to obtain a detailed overview of the `missed_ops` dataset.

Great! Now that we know how to generate a short report of summary statistics for our variables. In the next section, we'll learn about a couple useful functions from the `inspectdf` package that allows us to visualize different summary stats.

---

## Visualizing summary statistics with functions from `inspectdf`

While the `skimr::skim()` function gives you variable summaries in the console, you may sometimes want variables summaries in richer graphical form instead. For this, the functions `inspectdf::inspect_cat()` and `inspectdf::inspect_num()` can be used.

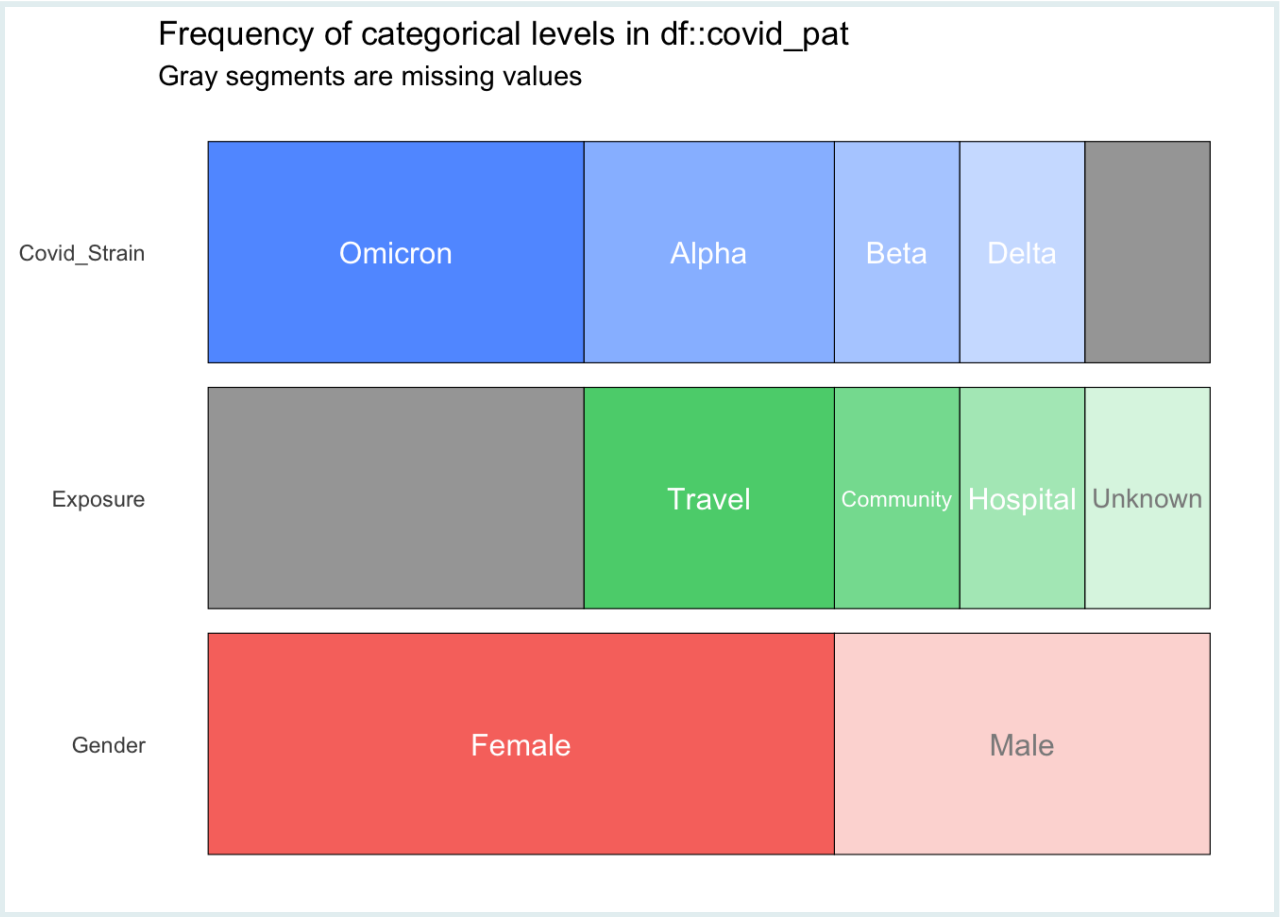
If you run `inspect_cat()` on a data object, you get a tabular summary of the categorical variables in the dataset (the important information is hidden in the `levels` column). Let's try it out on the `covid_pat` dataset first. As a reminder, here is our dataset:

```
covid_pat
```

```
inspect_cat(covid_pat)
```

The magic happens when you run `show_plot()` on the result from `inspect_cat()`:

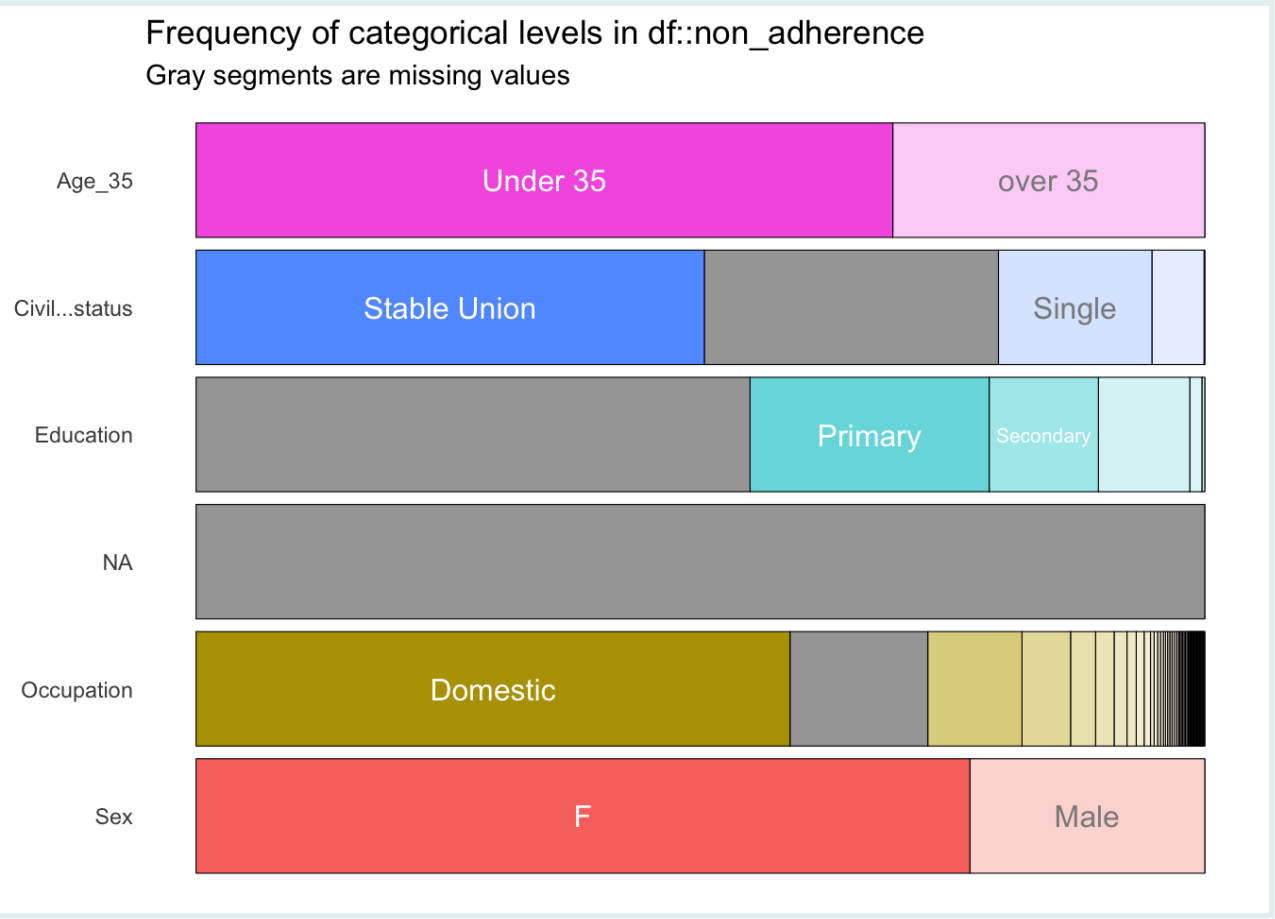
```
inspect_cat(covid_pat) %>%
  show_plot()
```




That looks great! You get a nice summary figure showing the distribution of categorical variables! Variable levels are also nicely labelled (if there is sufficient space to show a label).

Now, let's try it out on our `non_adherence` dataset:

```
inspect_cat(non_adherence) %>%
  show_plot()
```




From here you can observe some issues with a few categorical variables:

- The variable level `Under 35` is capitalized, whereas `over 35` is not. It could be worth standardizing this.
- The variable sex has the levels `F` and `Male`. This too could be worth standardizing.
- As we have previously seen, `NA` is completely empty

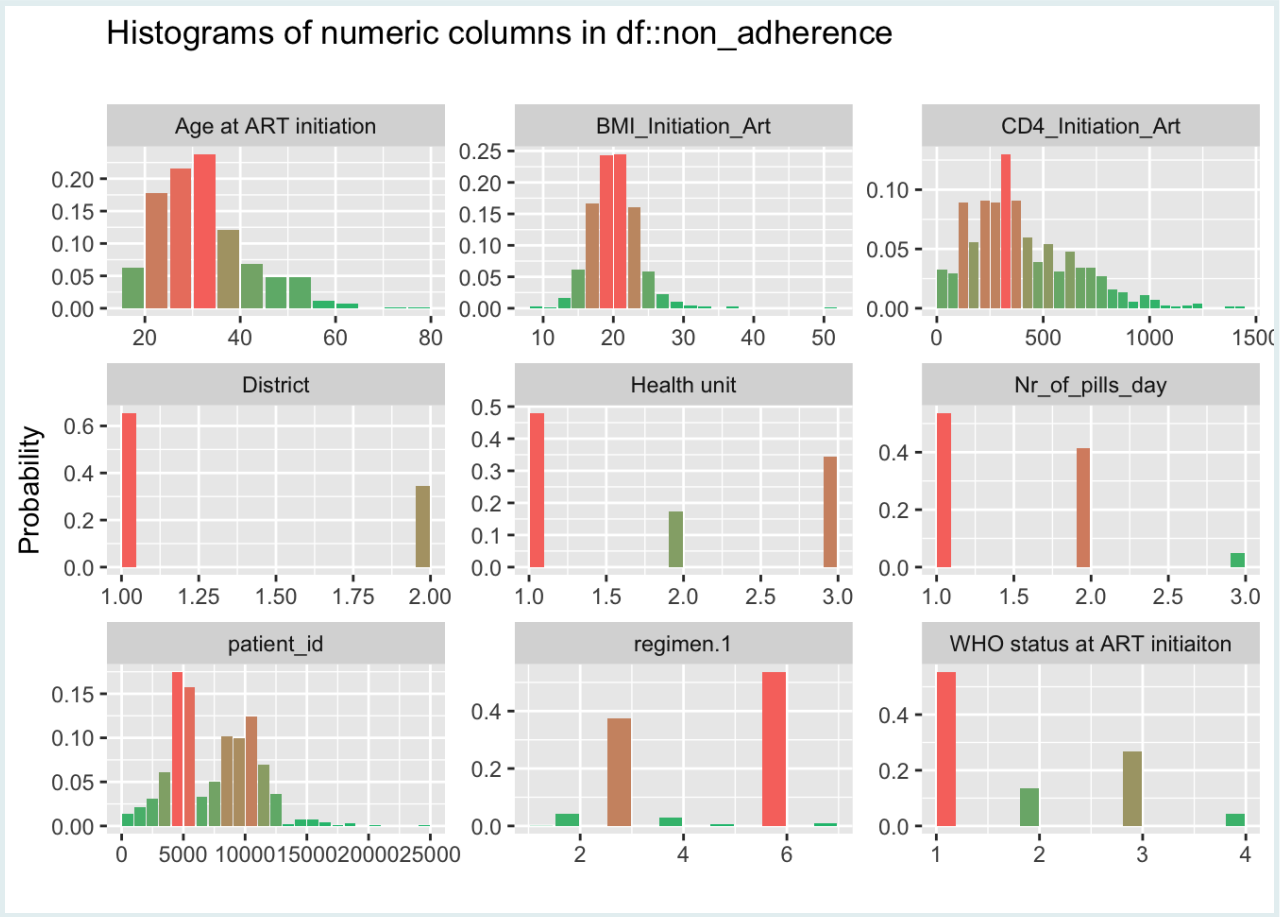
Complete the following code to obtain a visual summary of the categorical variables in the `missed_op` dataset.

```
inspect___() %>%
  _________
```

How many potential data issues can you spot?

Similarly, you can obtain a summary plot for the numerical variables in the dataset with `inspect_num()`. Let's run this on our `non_adherence` dataset:

```
inspect_num(non_adherence) %>%
  show_plot()
```




From this output, you can notice that many variables which should be factor variables are coded as numeric. In fact, the only true numeric variables are `Age at ART initiation`, `BMI_Initiation_ART`, `CD4_Initation_ART`, and `Nr_of_pills_day`. We will fix these issues in the next lesson when we move on to data cleaning. For now though, let's take a look at our another function that's particularly helpful for categorical varibales!

Use `inspect_num` to create a histograms of your numeric variables in the `missed_op` dataset. Are the numeric variable types correct?

---

## Exploring categorical variable levels with `gtsummary::tbl_summary()`

While the `inspect_cat()` function is useful for a graphical overview of categorical variables, it doesn't provide frequency counts or percentages for the various levels. For this, the `tbl_summary()` from the `gtsummary` package is particularly helpful! The output is particularly long so we'll look at the tibble form and show a photo of the important part for our dataset. You can explore the whole output as you code along at home.

```
        gtsummary::tbl_summary(non_adherence) %>%
          as_tibble()
```

```
## # A tibble: 104 × 2
##    `**Characteristic**` `**N = 1,413**`
##    <chr>                <chr>
##  1 patient_id           7,355 (4,705, 10,098)
##  2 District             <NA>
##  3 1                    925 (65%)
##  4 2                    488 (35%)
##  5 Health unit          <NA>
##  6 1                    678 (48%)
##  7 2                    247 (17%)
##  8 3                    488 (35%)
##  9 Sex                  <NA>
## 10 F                    1,084 (77%)
## # ℹ 94 more rows
```

That looks great! As we can see it outputs a summary of the frequency and percentages for categorical variables and the median and IQR for numeric variables.

Below is a photo of part of the output where we can see additional issues with our data that wasn't clear using the `inspect_cat()` function. Some values from our `Occupation` variable are capitalized, whereas others are all in lower case.

| | |
|---|---|
| Office worker | 1 (<0.1%) |
| Police | 3 (0.2%) |
| professor | 11 (0.9%) |
| Professor | 35 (2.9%) |
| Receptionist | 1 (<0.1%) |
| Retired | 2 (0.2%) |
| rock cutter | 9 (0.7%) |

This means that R doesn't recognize them as being the same value which would be problematic during analysis. We'll fix these errors in the next lesson, for now though let's move on to our last function for exploratory data analysis!


The `tbl_summary()` function is not appropriate for checking variable names. As you may have noticed, all whitespaces were replaced by a period. For example, `Age at ART initation` becomes `Age.at.ART.initation`.

Use `tbl_summary()` to output a summary of your `missed_ops` dataset. Can you identify any additional data issues?

---

## Creating data reports with `DataExplorer::create_report()`

Finally, the `create_report()` function from the `DataExplorer` package creates a full data profile of a provided data frame: an HTML file with basic statistics and distribution visualizations.

Let's run this function on the `non_adherence` dataframe and observe its output. Note that it may take a while to run. If it takes too long, you can run it on a dataset sample, rather than the entire dataset.

```
        create_report(non_adherence)
```

As you can see, the report is quite extensive. We won't go over all of the outputs from this data report because many of the graphical outputs are the same as those we have seen with previous functions! However, some new outputs include:

- QQ plot to assess the normality of numeric variables
- Correlation analysis (when there are sufficient complete rows)
- Principal component analysis (when there are sufficient complete rows)

Feel free to explore the package documentation on your own time.

Create a data report for your `missed_ops` data using the `create_report()` function!

---

## Wrapping up

By familiarizing ourselves with the data, we have been able to identify some potential problems that may need to be addressed before the data are used in an analysis.

And as you have seen, the actual code needed to do this data exploration is very little; other R developers have done the difficult work for us by building amazing packages to quickly scan datasets and identify issues.

From the next lesson, we will begin to take on these identified issues one by one, starting with the problem of inconsistent, messy variable names.

See you in the next lesson!

---

## Contributors

The following team members contributed to this lesson:


### LAURE VANCAUWENBERGHE

Data analyst, the GRAPH Network
A firm believer in science for good, striving to ally programming, health and education

### KENE DAVID NWOSU

Data analyst, the GRAPH Network
Passionate about world improvement

### AMANDA MCKINLEY

R Developer and Instructor, the GRAPH Network


## References

Some material in this lesson was adapted from the following sources:


- Batra, Neale, et al. The Epidemiologist R Handbook. 2021. *Cleaning data and core functions*. https://epirhandbook.com/en/cleaning-data-and-core-functions.html#cleaning-data-and-core-functions
- Waring E, Quinn M, McNamara A, Arino de la Rubia E, Zhu H, Ellis S (2022). skimr: Compact and Flexible Summaries of Data. https://docs.ropensci.org/skimr/ (website), https://github.com/ropensci/skimr/.