## **Data Cleaning Pipeline 1: Data Diagnostics**

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#### 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 diagnose dataset issues that warrant data cleaning through functions such as:

```
visdat::vis_dat()inspectdf::inspect_cat()inspectdf::inspect_num()gtsummary::tbl_summary()
```

## **Packages**

The packages loaded below will be required for this lesson:

#### **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</pre>
```

```
## # A tibble: 5 × 15
     patient_id District `Health unit` Sex
##
                                            Age 35
##
                  <dbl> <dbl> <chr> <dbl> <chr> <
          <dbl>
## 1
          10037
                                    1 Male over 35
## 2
         10537
                      1
                                    1 F
                                            over 35
                      2
                                    3 F
                                            Under 35
## 3
          5489
## 4
          5523
                      2
                                    3 Male Under 35
                      2
## 5
          4942
                                    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()

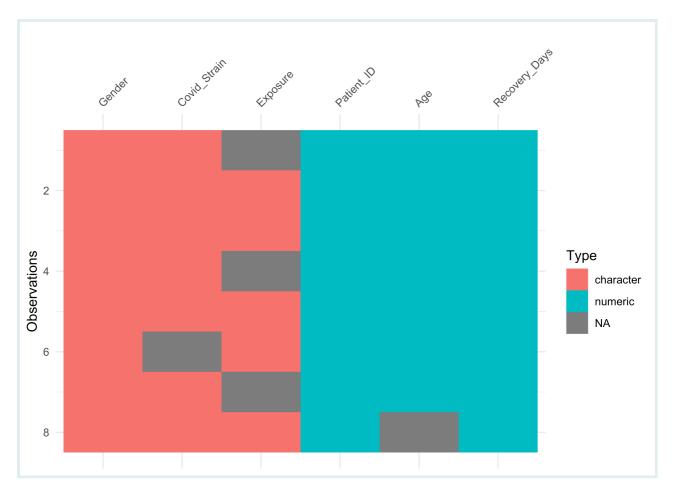
The vis\_dat() function from the visdat package is a wonderful way to quickly visualize data types and missing values in a dataset. It creates a plot that shows a "zoomed out" spreadsheet view of your data frame: each row in the dataframe is represented by a single line on the plot.

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

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

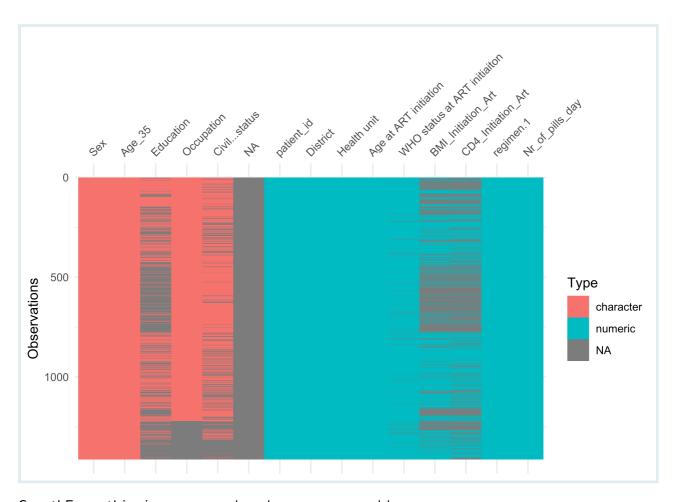
#### vis\_dat(covid\_pat)



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!

#### Spotting data issues with vis\_dat()

(NOTE: Answers are at the bottom of the page. Try to answer the questions yourself before checking.)

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.

```
## Rows: 201 Columns: 16
## — Column specification

## Delimiter: ","

## chr (11): sex, clage, origine, adquired, chronic, acute, latepresent,
reasonsdx, testlocal, consultcat, c...

## dbl (4): cd4, cd4_category, numberconsult, missed_ops

## igl (1): NaN.

##

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

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

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

## Visualizing variable distributions with functions from inspectdf

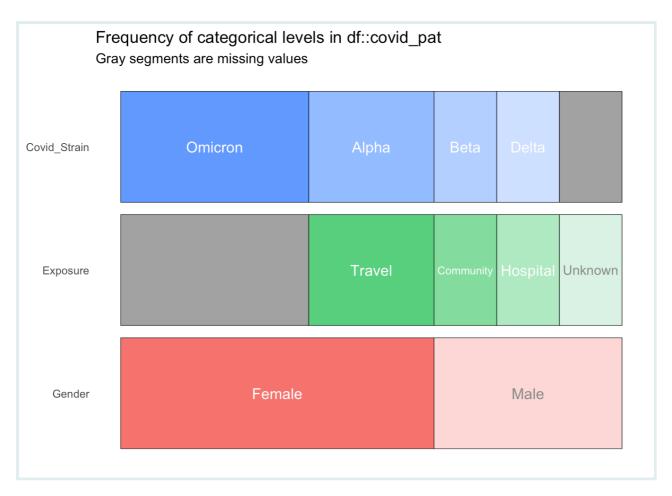
You may sometimes want to generate quick graphical summaries of your variable distributions. For this, the functions inspectdf::inspect\_cat() and inspectdf::inspect\_num() can be used.

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():

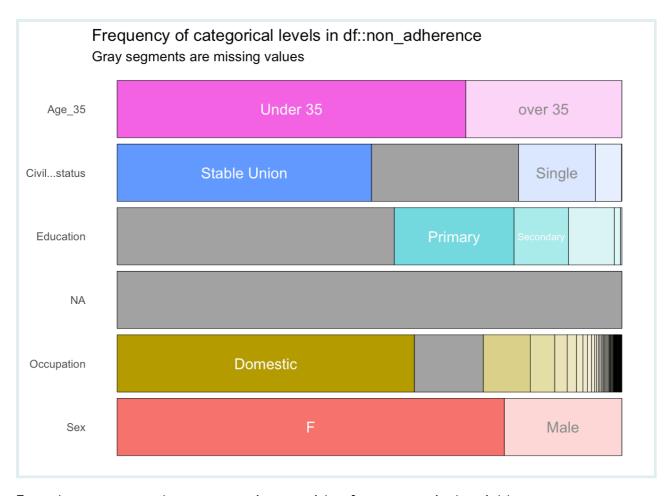
```
inspect_cat(covid_pat) %>%
  show_plot()
```



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

#### Spotting data issues with inspect\_cat()

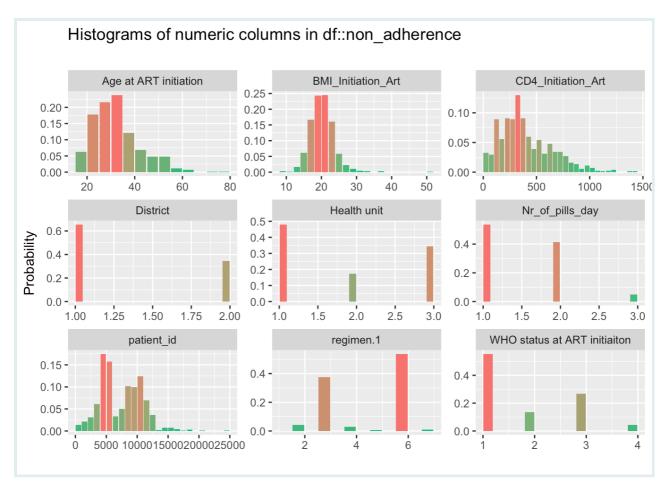
Complete the following code to obtain a visual summary of the categorical variables in the missed\_op dataset.

```
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!

#### Variable types with inspect\_num()

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.

Let's try it out on our non\_adherence dataset:

```
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>
                           925 (65%)
## 3 1
                           488 (35%)
## 4 2
## 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.

#### Spotting data issues with tbl\_summary()

Use tbl\_summary() to output a summary of your missed\_ops dataset. Can you identify any additional data issues?

## Wrap 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.

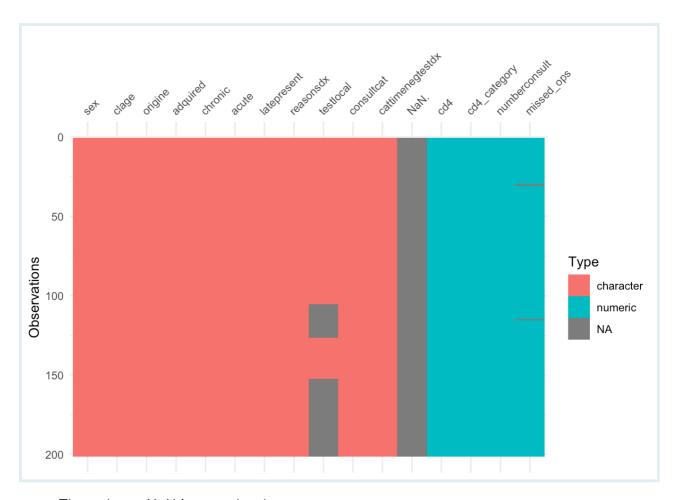
From the next lesson, we will begin to take on these identified issues one by one, starting with the problem of inconsistent, messy variable names.

See you in the next lesson!

## **Answer Key**

Q: Spotting data issues with vis\_dat()

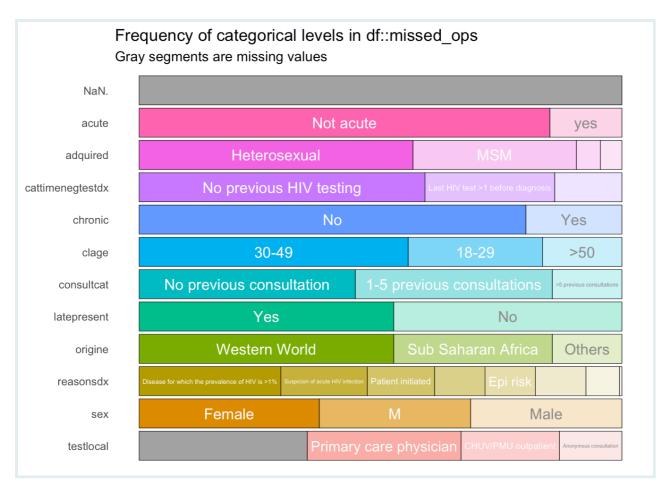
vis\_dat(missed\_ops)



• The column NaN is completely empty

#### Q: Spotting data issues with inspect\_cat()

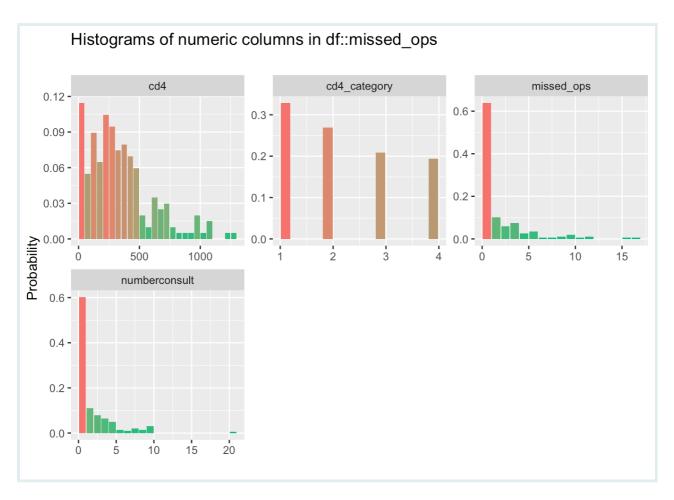
```
inspect_cat(missed_ops) %>%
  show_plot()
```



- The variable acute has 2 levels: Not acute and yes. This should be standardized.
- The varibale sex has 3 levels: Female, Male, and M. The M should be changed to Male.

#### Q: Variable types with inspect\_num()

```
inspect_num(missed_ops) %>%
  show_plot()
```



• The variable cd4category should be a factor variabale

Q: Spotting data issues with tbl\_summary()

tbl\_summary(missed\_ops)

Characteristic	$N = 201^{1}$
sex	
Female	75 (37%)
М	63 (31%)
Male	63 (31%)
clage	
>50	33 (16%)
18-29	56 (28%)
30-49	112 (56%)
origine	
Others	29 (14%)
Sub Saharan Africa	66 (33%)
Western World	106 (53%)
adquired	
Heterosexual	114 (57%)
IV drug use	9 (4.5%)
MSM	68 (34%)
Other	10 (5.0%)
chronic	40 (20%)
cd4	293 (147, 452)
cd4_category	
1	66 (33%)
2	54 (27%)
3	42 (21%)
4	39 (19%)

Characteristic	N = 201 <sup>1</sup>
Not acute	171 (85%)
yes	30 (15%)
latepresent	106 (53%)
reasonsdx	
AIDS defining illness	21 (10%)
Disease for which the prevalence of HIV is >1%	59 (29%)
Epi risk	21 (10%)
Epidemiological risk	21 (10%)
Introduction of immunosuppressive treatment	1 (0.5%)
Patient initiated	28 (14%)
Pregnancy	14 (7.0%)
Suspicion of acute HIV infection	36 (18%)
testlocal	
Anonymous consultation	26 (20%)
CHUV/PMU outpatient	41 (31%)
Primary care physician	64 (49%)
Unknown	70
numberconsult	1.00 (0.00, 3.00)
consultcat	
>5 previous consultations	29 (14%)
1-5 previous consultations	82 (41%)
No previous consultation	90 (45%)
cattimenegtestdx	
HIV testing the previous year	28 (14%)
Last HIV test >1 before diagnosis	54 (27%)
No previous HIV testing	119 (59%)
missed_ops	0.00 (0.00, 3.00)
Unknown	2
NaN.	0 (NA%)
Unknown	201
<sup>1</sup> n (%); Median (IQR)	

• For the variable reasonsdx, there are the categories Epidemiological risk and Epi risk which should be a single category

#### 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/.

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