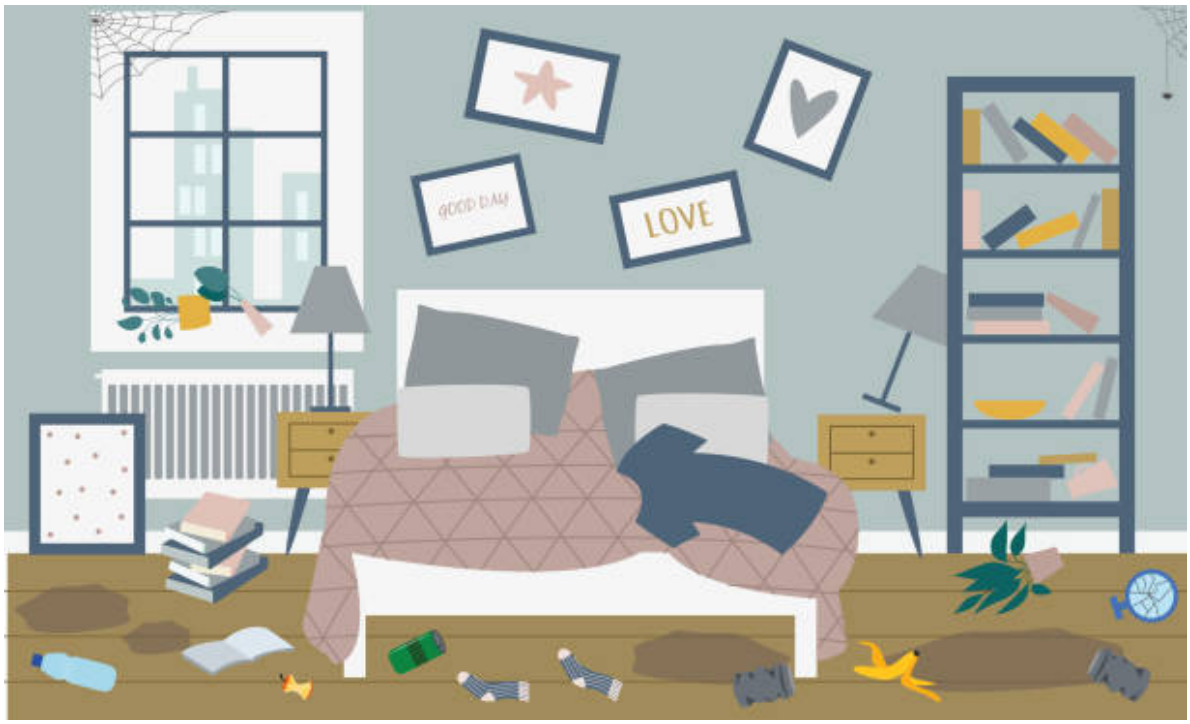
Data Cleaning

Data cleaning is the process of fixing or removing incorrect, corrupted, incorrectly formatted, duplicate, or incomplete data within a dataset.



Types of Unclean Data

There are 2 kinds of unclean data

1. Dirty Data (Data with Quality issues):

Dirty data, also known as low quality data. Low quality data has content issues.

- Duplicated data
- Missing Data
- Corrupt Data
- Inaccurate Data

2. Messy Data (Data with tidiness (neatness) issues):

Messy data, also known as untidy data. Untidy data has structural issues.Tidy data has the following properties:

- Each variable forms a column
- Each observation forms a row
- Each observational unit forms a table

country	year	rate
Afghanistan	1999	**745** / 19987071
Afghanistan	2000	**2666** / 20595360
Brazil	1999	**37737** / 172006362
Brazil	2000	**80488** / 174504898
China	1999	**212258** / 1272915272
China	2000	**213766** / 1280428583

table3

country	year	cases	population
Afghanistan	1999	**745**	19987071
Afghanistan	2000	**2666**	20595360
Brazil	1999	**37737**	172006362
Brazil	2000	**80488**	174504898
China	1999	**212258**	1272915272
China	2000	**213766**	1280428583

In [1]:
```
import pandas as pd
import numpy as np
```

In [2]:
```
patients = pd.read_csv("patients.csv")
treatments = pd.read_csv("treatments.csv")
adverse_reactions = pd.read_csv("adverse_reactions.csv")
treatments_cut = pd.read_csv("treatments_cut.csv")
```

In [3]:
```
# view datasets
patients.head(2)
```

Out[3]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	co
0	1	female	Zoe	Wellish	576 Brown Bear Drive	Rancho California	California	92390.0	U S
1	2	female	Pamela	Hill	2370 University Hill Road	Armstrong	Illinois	61812.0	U S

In [4]:
```
treatments.head(2)
```

Out[4]:

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
0	veronika	jindrová	41u - 48u	-	7.63	7.20	NaN
1	elliot	richardson	-	40u - 45u	7.56	7.09	0.97

In [5]:
```
treatments_cut.head(2)
```

Out[5]:

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
0	jožka	resanovič	22u - 30u	-	7.56	7.22	0.34
1	inunnguaq	heilmann	57u - 67u	-	7.85	7.45	NaN

In [6]:
```
adverse_reactions.head(2)
```

Out[6]:

	given_name	surname	adverse_reaction
0	berta	napolitani	injection site discomfort
1	lena	baer	hypoglycemia

1. Write a summary for your data

This is a dataset about 500 patients of which 350 patients participated in a clinical trial. None of the patients were using Novodra (a popular injectable insulin) or Auralin (the oral insulin being researched) as their primary source of insulin before. All were experiencing elevated HbA1c levels.

All 350 patients were treated with Novodra to establish a baseline HbA1c level and insulin dose. After 4 weeks, which isn't enough time to capture all the change in HbA1c that can be attributed by the switch to Auralin or Novodra:

- 175 patients switched to Auralin for 24 weeks
- 175 patients continued using Novodra for 24 weeks

Data about patients feeling some adverse effects is also recorded.

2. Write Column descriptions

Table -> `patients` :

- `patient_id` : the unique identifier for each patient in the Master Patient Index (i.e. patient database) of the pharmaceutical company that is producing Auralin
- `assigned_sex` : the assigned sex of each patient at birth (male or female)
- `given_name` : the given name (i.e. first name) of each patient
- `surname` : the surname (i.e. last name) of each patient
- `address` : the main address for each patient
- `city` : the corresponding city for the main address of each patient
- `state` : the corresponding state for the main address of each patient
- `zip_code` : the corresponding zip code for the main address of each patient
- `country` : the corresponding country for the main address of each patient (all United states for this clinical trial)
- `contact` : phone number and email information for each patient

- `birthdate` : the date of birth of each patient (month/day/year). The inclusion criteria for this clinical trial is age >= 18 (there is no maximum age because diabetes is a growing problem among the elderly population)
- `weight` : the weight of each patient in pounds (lbs)
- `height` : the height of each patient in inches (in)
- `bmi` : the Body Mass Index (BMI) of each patient. BMI is a simple calculation using a person's height and weight. The formula is BMI = kg/m2 where kg is a person's weight in kilograms and m2 is their height in metres squared. A BMI of 25.0 or more is overweight, while the healthy range is 18.5 to 24.9. The inclusion criteria for this clinical trial is 16 >= BMI >= 38.

Table -> `adverse_reactions`

- `given_name` : the given name of each patient in the Master Patient Index that took part in the clinical trial and had an adverse reaction (includes both patients treated Auralin and Novodra)
- `surname` : the surname of each patient in the Master Patient Index that took part in the clinical trial and had an adverse reaction (includes both patients treated Auralin and Novodra)
- `adverse_reaction` : the adverse reaction reported by the patient

3. Add any additional information

Additional useful information:

- Insulin resistance varies person to person, which is why both starting median daily dose and ending median daily dose are required, i.e., to calculate change in dose.
- It is important to test drugs and medical products in the people they are meant to help. People of different age, race, sex, and ethnic group must be included in clinical trials. This diversity is reflected in the patients table.

Types of Assessment

There are 2 types of assessment styles

- `Manual` - Looking through the data manually in google sheets
- `Programmatic` - By using pandas functions such as info(), describe() or sample()

Steps in Assessment

There are 2 steps involved in Assessment

- Discover
- Documentation

In [7]:
```
# export data for manual assessment

with pd.ExcelWriter('clinical_trials.xlsx') as writer:
  patients.to_excel(writer,sheet_name='patients')
  treatments.to_excel(writer,sheet_name='treatments')
  treatments_cut.to_excel(writer,sheet_name='treatment_cut')
  adverse_reactions.to_excel(writer,sheet_name='adverse_reactions')
```

Issues with the dataset

1. Dirty Data (Quality Related)

Table - `Patients`

- **patient_id = 9 has misspelled name 'Dsvid' instead of David** `accuracy`

8	9 male	Dsvid	Gustafsson	1790 Nutter Street	Kansas City	MO
9	10 female	Sophie	Cabrera	3303 Anmoore Road	New York	New York

- **state col sometimes contain full name and some times abbrivietation** `consistency`

state
California
Illinois
Nebraska
NJ
AL
Florida
NV
CA
MO

  - **zip code col has entries with 4 digit** `validity`

zip_code
92390
61812
68467
7095
36303
32114
84728

- **data missing for 12 patients in address,city, state,zip_code ,country, contact** `completion`

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	country	contact	birthdate
209	210	female	Lalita	Eldarkhan	Nan	Nan	Nan	Nan	Nan	Nan	8/14/195
219	220	male	Mỹ	Quynh	Nan	Nan	Nan	Nan	Nan	Nan	4/9/1978
230	231	female	Elisabeth	Knudsen	Nan	Nan	Nan	Nan	Nan	Nan	9/23/197
234	235	female	Martina	Tománkov	Nan	Nan	Nan	Nan	Nan	Nan	4/7/1936
242	243	male	John	O'Brian	Nan	Nan	Nan	Nan	Nan	Nan	2/25/195
249	250	male	Benjamin	Mehler	Nan	Nan	Nan	Nan	Nan	Nan	10/30/19
257	258	male	Jin	Kung	Nan	Nan	Nan	Nan	Nan	Nan	5/17/199
264	265	female	Wafiyyah	Asfour	Nan	Nan	Nan	Nan	Nan	Nan	11/3/198
269	270	female	Flavia	Fiorentino	Nan	Nan	Nan	Nan	Nan	Nan	10/9/193
278	279	female	Generosa	Cabán	Nan	Nan	Nan	Nan	Nan	Nan	12/16/19
286	287	male	Lewis	Webb	Nan	Nan	Nan	Nan	Nan	Nan	4/1/1979
296	297	female	Chỉ	Lâm	Nan	Nan	Nan	Nan	Nan	Nan	5/14/199

- **incorrect data type assigned to sex, zip code, birthdate** `validity`

```
patient_id    503 non-null    int64
assigned_sex  503 non-null    object
given_name    503 non-null    object
surname       503 non-null    object
address       491 non-null    object
city          491 non-null    object
state         491 non-null    object
zip_code      491 non-null    float64
country       491 non-null    object
contact       491 non-null    object
birthdate     503 non-null    object
weight        503 non-null    float64
height        503 non-null    int64
bmi           503 non-null    float64
```

- **duplicate entries by the name of John Doe** `accuracy`

	patient_id	assigned_sex	given_name	surname	address	city	state
229	230	male	John	Doe	123 Main Street	New York	NY
237	238	male	John	Doe	123 Main Street	New York	NY
244	245	male	John	Doe	123 Main Street	New York	NY
251	252	male	John	Doe	123 Main Street	New York	NY
277	278	male	John	Doe	123 Main Street	New York	NY

- **one patient has weight = 48 pounds** `accuracy`

city	state	zip_code	country	contact	birthdate	weight	height	bmi
ster	OH	44691.0	United States	330-202-2145CamillaZaitseva@superrito.com	11/26/1938	48.8	63	19.1

- **one patient has height = 27 inches** `accuracy`

dress	city	state	zip_code	country	contact	birthdate	weight	height	bmi
1428 urkey Pen Lane	Dothan	AL	36303.0	United States	334-515-7487TimNeudorf@cuvox.de	2/18/1928	192.3	27	26.1

Table - `Treatments` & `Treatments_cut`

- **given_name and surname col is is all lower case** `consistency`

given_name	surname
veronika	jindrová
elliot	richardson
yukitaka	takenaka

- **remove u from Auralin and Novadra cols** `validity`

auralin	novodra
41u - 48u	-
-	40u - 45u
-	39u - 36u
33u - 36u	-
-	33u - 29u

- **'-' in novadra and Auralin col treated as nan** `validity`

auralin	novodra
41u - 48u	-
-	40u - 45u
-	39u - 36u
33u - 36u	-

- **missing values in hba1c_change col** `completion`

hba1c_change
0.97
0.35
0.32
0.38
0.38
0.34

- 1 duplicate entry by the name Joseph day `accuracy`

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
136	joseph	day	29u - 36u	-	7.7	7.19	NaN

- **in hba1c_change 9 instead of 4** `accuracy`

7.99	7.51	0.48	0.98
7.88	7.40		0.98
7.95	7.46		0.99
7.61	7.12		0.99
7.87	7.38		0.99

Table - `Adverse_reactions`

- **given_name and surname are all in lower case `consistency`**

given_name	surname
berta	napolitani
lena	baer
joseph	day

2. Messy Data (Structural Related)

Table - `Patients`

- **contact col contains both phone and email**

contact
951-719-9170ZoeWellish@superrito.com
PamelaSHill@cuvox.de+1 (217) 569-3204
402-363-6804JaeMDebord@gustr.com
PhanBaLiem@jourrapide.com+1 (732) 636-8246
334-515-7487TimNeudorf@cuvox.de
386-334-5237RafaelCardosoCosta@gustr.com

Table - `Treatments` & `Treatments_cut`

- **Auralin and Novadra col should be split into 2 cols start and end dose merge both the tables**

auralin	novodra
41u - 48u	-
-	40u - 45u

Automatic Assessment

- head and tail
- sample
- info
- isnull
- duplicated
- describe

In [8]:
```
# head
patients.head(1)
```

Out[8]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	cour
0	1	female	Zoe	Wellish	576 Brown Bear Drive	Rancho California	California	92390.0	Un Sta

In [9]:
```
# tail

patients.tail(1)
```

Out[9]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	countr
502	503	male	Pat	Gersten	2778 North Avenue	Burr	Nebraska	68324.0	Unite State

In [10]:
```
# sample

treatments.sample()
```

Out[10]:

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
263	rebecca	jephcott	53u - 63u	-	7.96	7.57	0.39

In [11]:
```
# info

patients.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 503 entries, 0 to 502
Data columns (total 14 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   patient_id    503 non-null    int64
 1   assigned_sex  503 non-null    object
 2   given_name    503 non-null    object
 3   surname       503 non-null    object
 4   address       491 non-null    object
 5   city          491 non-null    object
 6   state         491 non-null    object
 7   zip_code      491 non-null    float64
 8   country       491 non-null    object
 9   contact       491 non-null    object
 10  birthdate     503 non-null    object
 11  weight        503 non-null    float64
 12  height        503 non-null    int64
 13  bmi           503 non-null    float64
dtypes: float64(3), int64(2), object(9)
memory usage: 55.1+ KB
```

In [12]:
```
# Patients data 'Address' column as 12 Null values

patients[patients['address'].isnull()]
```

Out[12]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	country
209	210	female	Lalita	Eldarkhanov	NaN	NaN	NaN	NaN	NaN
219	220	male	Mỹ	Quynh	NaN	NaN	NaN	NaN	NaN
230	231	female	Elisabeth	Knudsen	NaN	NaN	NaN	NaN	NaN
234	235	female	Martina	Tománková	NaN	NaN	NaN	NaN	NaN
242	243	male	John	O'Brian	NaN	NaN	NaN	NaN	NaN
249	250	male	Benjamin	Mehler	NaN	NaN	NaN	NaN	NaN
257	258	male	Jin	Kung	NaN	NaN	NaN	NaN	NaN
264	265	female	Wafiyyah	Asfour	NaN	NaN	NaN	NaN	NaN
269	270	female	Flavia	Fiorentino	NaN	NaN	NaN	NaN	NaN
278	279	female	Generosa	Cabán	NaN	NaN	NaN	NaN	NaN
286	287	male	Lewis	Webb	NaN	NaN	NaN	NaN	NaN
296	297	female	Chỉ	Lâm	NaN	NaN	NaN	NaN	NaN

In [13]:
```
# Table 2

treatments.info() # missing values in hb1ac
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 280 entries, 0 to 279
Data columns (total 7 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   given_name    280 non-null    object
 1   surname       280 non-null    object
 2   auralin       280 non-null    object
 3   novodra       280 non-null    object
 4   hba1c_start   280 non-null    float64
 5   hba1c_end     280 non-null    float64
 6   hba1c_change  171 non-null    float64
dtypes: float64(3), object(4)
memory usage: 15.4+ KB
```

In [14]:
```
# Table 3

treatments_cut.info() # missing values in hba1c
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 70 entries, 0 to 69
Data columns (total 7 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   given_name    70 non-null     object
 1   surname       70 non-null     object
 2   auralin       70 non-null     object
 3   novodra       70 non-null     object
 4   hba1c_start   70 non-null     float64
 5   hba1c_end     70 non-null     float64
 6   hba1c_change  42 non-null     float64
dtypes: float64(3), object(4)
memory usage: 4.0+ KB
```

In [15]:
```
# table 4
adverse_reactions.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 34 entries, 0 to 33
Data columns (total 3 columns):
 #   Column            Non-Null Count  Dtype
---  ------            --------------  -----
 0   given_name        34 non-null     object
 1   surname           34 non-null     object
 2   adverse_reaction  34 non-null     object
dtypes: object(3)
memory usage: 944.0+ bytes
```

duplicated

In [16]:
```
# table 1
patients.duplicated().sum()
```

Out[16]: 0

In [17]:
```
patients.duplicated(subset=['given_name','surname']).sum()
```

Out[17]: 5

In [18]:
```
patients[patients.duplicated(subset=['given_name','surname'])]
```

Out[18]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	country	
229	230	male	John	Doe	123 Main Street	New York	NY	12345.0	United States	j
237	238	male	John	Doe	123 Main Street	New York	NY	12345.0	United States	j
244	245	male	John	Doe	123 Main Street	New York	NY	12345.0	United States	j
251	252	male	John	Doe	123 Main Street	New York	NY	12345.0	United States	j
277	278	male	John	Doe	123 Main Street	New York	NY	12345.0	United States	j

In [19]:
```
# table 2

treatments[treatments.duplicated()]
```

Out[19]:

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
136	joseph	day	29u - 36u	-	7.7	7.19	NaN

In [20]:
```
treatments[treatments.duplicated(subset=['given_name','surname'])]
```

Out[20]:

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
136	joseph	day	29u - 36u	-	7.7	7.19	NaN

In [21]:
```
# table 3

treatments_cut[treatments_cut.duplicated()]
```

Out[21]:

given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change

In [22]:
```
treatments_cut[treatments_cut.duplicated(subset=['given_name','surname'])]
```

Out[22]:

given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change

In [23]:
```
# Table 4

adverse_reactions.duplicated().sum()
```

Out[23]: 0

describe

In [24]:
```
patients.describe()
```

Out[24]:

	patient_id	zip_code	weight	height	bmi
count	503.000000	491.000000	503.000000	503.000000	503.000000
mean	252.000000	49084.118126	173.434990	66.634195	27.483897
std	145.347859	30265.807442	33.916741	4.411297	5.276438
min	1.000000	1002.000000	48.800000	27.000000	17.100000
25%	126.500000	21920.500000	149.300000	63.000000	23.300000
50%	252.000000	48057.000000	175.300000	67.000000	27.200000
75%	377.500000	75679.000000	199.500000	70.000000	31.750000
max	503.000000	99701.000000	255.900000	79.000000	37.700000

In [25]:
```
patients[patients['weight']== 48.8]
```

Out[25]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	country
210	211	female	Camilla	Zaitseva	4689 Briarhill Lane	Wooster	OH	44691.0	United States

In [26]:
```
patients[patients['height']== 27]
```

Out[26]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	country
4	5	male	Tim	Neudorf	1428 Turkey Pen Lane	Dothan	AL	36303.0	United States

In [27]:
```
# table 2
treatments.describe()
```

Out[27]:

	hba1c_start	hba1c_end	hba1c_change
count	280.000000	280.000000	171.000000
mean	7.985929	7.589286	0.546023
std	0.568638	0.569672	0.279555
min	7.500000	7.010000	0.200000
25%	7.660000	7.270000	0.340000
50%	7.800000	7.420000	0.380000
75%	7.970000	7.570000	0.920000
max	9.950000	9.580000	0.990000

In [28]:
```
treatments.sort_values('hba1c_start') # max
```

Out[28]:

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
270	mika	martinsson	34u - 43u	-	7.50	7.17	0.33
113	kari	laatikainen	39u - 43u	-	7.50	7.11	NaN
126	jowita	wiśniewska	-	22u - 23u	7.50	7.08	0.92
53	nasser	mansour	-	33u - 31u	7.51	7.06	0.95
105	finlay	sheppard	-	31u - 30u	7.51	7.17	0.34
...	...	...	...	...	...	...	...
25	benoît	bonami	-	44u - 43u	9.82	9.40	0.92
171	justyna	kowalczyk	24u - 34u	-	9.84	9.44	NaN
81	robert	wagner	43u - 49u	-	9.84	9.52	0.32
75	mackenzie	mckay	-	44u - 43u	9.87	9.48	0.39
166	annie	allen	36u - 42u	-	9.95	9.58	0.37

280 rows × 7 columns

In [29]:
```
treatments.sort_values('hba1c_change',na_position='first')
```

Out[29]:

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
0	veronika	jindrová	41u - 48u	-	7.63	7.20	NaN
2	yukitaka	takenaka	-	39u - 36u	7.68	7.25	NaN
8	saber	ménard	-	54u - 54u	8.08	7.70	NaN
9	asia	woźniak	30u - 36u	-	7.76	7.37	NaN
10	joseph	day	29u - 36u	-	7.70	7.19	NaN
...	...	...	...	...	...	...	...
49	jackson	addison	-	42u - 42u	7.99	7.51	0.98
17	gina	cain	-	36u - 36u	7.88	7.40	0.98
32	laura	ehrlichmann	-	43u - 40u	7.95	7.46	0.99
245	wu	sung	-	47u - 48u	7.61	7.12	0.99
138	giovana	rocha	-	23u - 21u	7.87	7.38	0.99

280 rows × 7 columns

In [30]:
```
# table 3

treatments_cut.describe() # same prblem as treatments table
```

Out[30]:

	hba1c_start	hba1c_end	hba1c_change
count	70.000000	70.000000	42.000000
mean	7.838000	7.443143	0.518810
std	0.423007	0.418706	0.270719
min	7.510000	7.020000	0.280000
25%	7.640000	7.232500	0.340000
50%	7.730000	7.345000	0.370000
75%	7.860000	7.467500	0.907500
max	9.910000	9.460000	0.970000

Note - Assessing Data is an Iterative Process

Data Quality Dimensions

- Completeness -> is data missing?
- Validity -> is data invalid -> negative height -> duplicate patient id
- Accuracy -> data is valid but not accurate -> weight -> 1kg
- Consistency -> both valid and accurate but written differently -> New Youk and NY

- labelling is only for Dirty data

Order of severity

Completeness <- Validity <- Accuracy <- Consistency

Data Cleaning Order

1. Quality (Dirty data)-> Completeness (Missing values)
2. Tidiness (Messy data)
3. Quality -> Validity
4. Quality -> Accuracy
5. Quality -> Consistency

Steps involved in Data cleaning

- Define
- Code
- Test

```
Always make sure to create a copy of your pandas dataframe before you start
the cleaning process
```

In [31]:
```
# Making the copies

patients_df = patients.copy()
treatments_df =treatments.copy()
treatments_cut_df =treatments_cut.copy()
adverse_reactions_df = adverse_reactions.copy()
```

In [32]:
```
patients.head(1) # original
```

Out[32]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	cour
0	1	female	Zoe	Wellish	576 Brown Bear Drive	Rancho California	California	92390.0	Un Sta

In [33]:
```
patients_df.head(1) # copy
```

Out[33]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	cour
0	1	female	Zoe	Wellish	576 Brown Bear Drive	Rancho California	California	92390.0	Un Sta

Define

- replace all missing values of patients df with no data
- sub hba1c_start from hba1c_end to get all the change values
- in patients table we will use regex to separate email and phone

In [34]:
```
patients_df[patients_df['address'].isnull()]
```

Out[34]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	country
209	210	female	Lalita	Eldarkhanov	NaN	NaN	NaN	NaN	NaN
219	220	male	Mỹ	Quynh	NaN	NaN	NaN	NaN	NaN
230	231	female	Elisabeth	Knudsen	NaN	NaN	NaN	NaN	NaN
234	235	female	Martina	Tománková	NaN	NaN	NaN	NaN	NaN
242	243	male	John	O'Brian	NaN	NaN	NaN	NaN	NaN
249	250	male	Benjamin	Mehler	NaN	NaN	NaN	NaN	NaN
257	258	male	Jin	Kung	NaN	NaN	NaN	NaN	NaN
264	265	female	Wafiyyah	Asfour	NaN	NaN	NaN	NaN	NaN
269	270	female	Flavia	Fiorentino	NaN	NaN	NaN	NaN	NaN
278	279	female	Generosa	Cabán	NaN	NaN	NaN	NaN	NaN
286	287	male	Lewis	Webb	NaN	NaN	NaN	NaN	NaN
296	297	female	Chỉ	Lâm	NaN	NaN	NaN	NaN	NaN

In [35]:
```
# code

patients_df.fillna('No data',inplace=True)
```

In [36]:
```
# test

patients_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 503 entries, 0 to 502
Data columns (total 14 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   patient_id    503 non-null    int64
 1   assigned_sex  503 non-null    object
 2   given_name    503 non-null    object
 3   surname       503 non-null    object
 4   address       503 non-null    object
 5   city          503 non-null    object
 6   state         503 non-null    object
 7   zip_code      503 non-null    object
 8   country       503 non-null    object
 9   contact       503 non-null    object
 10  birthdate     503 non-null    object
 11  weight        503 non-null    float64
 12  height        503 non-null    int64
 13  bmi           503 non-null    float64
dtypes: float64(2), int64(2), object(10)
memory usage: 55.1+ KB
```

In [37]:
```
# table 2

treatments_df.head(2)
```

Out[37]:

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
0	veronika	jindrová	41u - 48u	-	7.63	7.20	NaN
1	elliot	richardson	-	40u - 45u	7.56	7.09	0.97

In [38]:
```

treatments_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 280 entries, 0 to 279
Data columns (total 7 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   given_name    280 non-null    object
 1   surname       280 non-null    object
 2   auralin       280 non-null    object
 3   novodra       280 non-null    object
 4   hba1c_start   280 non-null    float64
 5   hba1c_end     280 non-null    float64
 6   hba1c_change  171 non-null    float64
dtypes: float64(3), object(4)
memory usage: 15.4+ KB
```

In [39]:
```
# code

treatments_df['hba1c_change']= treatments_df['hba1c_start'] - treatments_df['h
```

In [40]:
```
#test

treatments_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 280 entries, 0 to 279
Data columns (total 7 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   given_name    280 non-null    object
 1   surname       280 non-null    object
 2   auralin       280 non-null    object
 3   novodra       280 non-null    object
 4   hba1c_start   280 non-null    float64
 5   hba1c_end     280 non-null    float64
 6   hba1c_change  280 non-null    float64
dtypes: float64(3), object(4)
memory usage: 15.4+ KB
```

In [41]:
```
# table 3
treatments_cut_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 70 entries, 0 to 69
Data columns (total 7 columns):
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   given_name    70 non-null     object
 1   surname       70 non-null     object
 2   auralin       70 non-null     object
 3   novodra       70 non-null     object
 4   hba1c_start   70 non-null     float64
 5   hba1c_end     70 non-null     float64
 6   hba1c_change  42 non-null     float64
dtypes: float64(3), object(4)
memory usage: 4.0+ KB
```

In [42]:
```
treatments_cut_df['hba1c_change']= treatments_cut_df['hba1c_start'] - treatmen
```

In [43]:
```
treatments_cut_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 70 entries, 0 to 69
Data columns (total 7 columns):
 #   Column        Non-Null Count  Dtype  
---  ------        --------------  -----  
 0   given_name    70 non-null     object 
 1   surname       70 non-null     object 
 2   auralin       70 non-null     object 
 3   novodra       70 non-null     object 
 4   hba1c_start   70 non-null     float64
 5   hba1c_end     70 non-null     float64
 6   hba1c_change  70 non-null     float64
dtypes: float64(3), object(4)
memory usage: 4.0+ KB
```

In [44]:
```
# tiddyness

patients_df.head() # contact
```

Out[44]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	c
0	1	female	Zoe	Wellish	576 Brown Bear Drive	Rancho California	California	92390.0	
1	2	female	Pamela	Hill	2370 University Hill Road	Armstrong	Illinois	61812.0	
2	3	male	Jae	Debord	1493 Poling Farm Road	York	Nebraska	68467.0	
3	4	male	Liêm	Phan	2335 Webster Street	Woodbridge	NJ	7095.0	
4	5	male	Tim	Neudorf	1428 Turkey Pen Lane	Dothan	AL	36303.0	

In [45]:
```
import re
```

In [46]:
```
# re - Regualar expression

def find_contact_details(text: str) -> tuple:
    # it the value is NaN, then return it
    if pd.isna(text):
        return np.nan

    # create the phone number pattern
    phone_number_pattern = re.compile(r"(\+[\d]{1,3}\s)?(\(?[\d]{3}\)?\s?-?[\d
    # find the phone number from the value/text, as a result we will get a lis
    phone_number  = re.findall(phone_number_pattern, text)

    # if length is 0, then the regex can't find any ph number, then define wit
    if len(phone_number) <= 0:
        phone_number = np.nan
    # if the country code is attached with the ph number, for that case, the f
    # element will be the country code and the 2nd element will be the actual
    # number. So, get that ph number
    elif len(phone_number) >= 2:
        phone_number = phone_number[1]
    # else, we will get the ph number. Grab it.
    else:
        phone_number = phone_number[0]

    # if we found the ph number (with/without country code), then remove that
    # after removing the ph number, the remaining string might be the email ad
    possible_email_add = re.sub(phone_number_pattern, "", text).strip()

    # then return the ph number and the email address
    return phone_number, possible_email_add
```

In [ ]:

In [47]:
```
patients_df['phone'] = patients_df["contact"].apply(lambda x: find_contact_det
patients_df['email'] = patients_df["contact"].apply(lambda x: find_contact_det
```

In [48]:
```
patients_df.head(2)
```

Out[48]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	co
0	1	female	Zoe	Wellish	576 Brown Bear Drive	Rancho California	California	92390.0	U S
1	2	female	Pamela	Hill	2370 University Hill Road	Armstrong	Illinois	61812.0	U S

In [49]:
```
patients_df.drop(columns='contact',inplace=True)
```

In [50]:
```
patients_df.head(2)
```

Out[50]:

	patient_id	assigned_sex	given_name	surname	address	city	state	zip_code	co
0	1	female	Zoe	Wellish	576 Brown Bear Drive	Rancho California	California	92390.0	U S
1	2	female	Pamela	Hill	2370 University Hill Road	Armstrong	Illinois	61812.0	U S

In [51]:
```
# merging two tables

treatments_df = pd.concat([treatments_df,treatments_cut_df])
```

In [52]:
```
treatments_df
```

Out[52]:

	given_name	surname	auralin	novodra	hba1c_start	hba1c_end	hba1c_change
0	veronika	jindrová	41u - 48u	-	7.63	7.20	0.43
1	elliot	richardson	-	40u - 45u	7.56	7.09	0.47
2	yukitaka	takenaka	-	39u - 36u	7.68	7.25	0.43
3	skye	gormanston	33u - 36u	-	7.97	7.62	0.35
4	alissa	montez	-	33u - 29u	7.78	7.46	0.32
...	...	...	...	...	...	...	...
65	rovzan	kishiev	32u - 37u	-	7.75	7.41	0.34
66	jakob	jakobsen	-	28u - 26u	7.96	7.51	0.45
67	bernd	schneider	48u - 56u	-	7.74	7.44	0.30
68	berta	napolitani	-	42u - 44u	7.68	7.21	0.47
69	armina	sauvé	36u - 46u	-	7.86	7.40	0.46

350 rows × 7 columns

In [54]:
```
# Use melt function

treatments_df = treatments_df.melt(id_vars=['given_name',
                                            'surname' ,'hba1c_start',
                                            'hba1c_end','hba1c_change'],
                                   var_name='type',
                                   value_name='dosage_range')
```

In [55]:
```
treatments_df # here we have variable and value columns
```

Out[55]:

	given_name	surname	hba1c_start	hba1c_end	hba1c_change	type	dosage_range
0	veronika	jindrová	7.63	7.20	0.43	auralin	41u - 48u
1	elliot	richardson	7.56	7.09	0.47	auralin	-
2	yukitaka	takenaka	7.68	7.25	0.43	auralin	-
3	skye	gormanston	7.97	7.62	0.35	auralin	33u - 36u
4	alissa	montez	7.78	7.46	0.32	auralin	-
...	...	...	...	...	...	...	...
695	rovzan	kishiev	7.75	7.41	0.34	novodra	-
696	jakob	jakobsen	7.96	7.51	0.45	novodra	28u - 26u
697	bernd	schneider	7.74	7.44	0.30	novodra	-
698	berta	napolitani	7.68	7.21	0.47	novodra	42u - 44u
699	armina	sauvé	7.86	7.40	0.46	novodra	-

700 rows × 7 columns

In [56]:
```
# remove "-" from dose range , it givs 350 rows

treatments_df = treatments_df[treatments_df['dosage_range']!='-']
```

In [57]:
```
treatments_df
```

Out[57]:

	given_name	surname	hba1c_start	hba1c_end	hba1c_change	type	dosage_range
0	veronika	jindrová	7.63	7.20	0.43	auralin	41u - 48u
3	skye	gormanston	7.97	7.62	0.35	auralin	33u - 36u
6	sophia	haugen	7.65	7.27	0.38	auralin	37u - 42u
7	eddie	archer	7.89	7.55	0.34	auralin	31u - 38u
9	asia	woźniak	7.76	7.37	0.39	auralin	30u - 36u
...	...	...	...	...	...	...	...
688	christopher	woodward	7.51	7.06	0.45	novodra	55u - 51u
690	maret	sultygov	7.67	7.30	0.37	novodra	26u - 23u
694	lixue	hsueh	9.21	8.80	0.41	novodra	22u - 23u
696	jakob	jakobsen	7.96	7.51	0.45	novodra	28u - 26u
698	berta	napolitani	7.68	7.21	0.47	novodra	42u - 44u

350 rows × 7 columns

In [58]:
```
treatments_df['dosage_range'].str.split('-') # split data into two columns
```

Out[58]:
```
0      [41u ,  48u]
3      [33u ,  36u]
6      [37u ,  42u]
7      [31u ,  38u]
9      [30u ,  36u]
           ...
688    [55u ,  51u]
690    [26u ,  23u]
694    [22u ,  23u]
696    [28u ,  26u]
698    [42u ,  44u]
Name: dosage_range, Length: 350, dtype: object
```

In [60]:
```
treatments_df['dosage_range'].str.split('-').str.get(0) # startig range
```

Out[60]:
```
0      41u
3      33u
6      37u
7      31u
9      30u
       ...
688    55u
690    26u
694    22u
696    28u
698    42u
Name: dosage_range, Length: 350, dtype: object
```

In [61]:
```
treatments_df['dosage_range'].str.split('-').str.get(1) # ending range
```

Out[61]:
```
0       48u
3       36u
6       42u
7       38u
9       36u
       ...
688     51u
690     23u
694     23u
696     26u
698     44u
Name: dosage_range, Length: 350, dtype: object
```

In [62]:
```
treatments_df['dosage_start'] = treatments_df['dosage_range'].str.split('-').s
treatments_df['dosage_end'] = treatments_df['dosage_range'].str.split('-').str
```

```
C:\Users\user\AppData\Local\Temp/ipykernel_10564/2612136710.py:1: SettingWith
CopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/s
table/user_guide/indexing.html#returning-a-view-versus-a-copy (https://panda
s.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-ver
sus-a-copy)
  treatments_df['dosage_start'] = treatments_df['dosage_range'].str.split('-
').str.get(0) # starting range
C:\Users\user\AppData\Local\Temp/ipykernel_10564/2612136710.py:2: SettingWith
CopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/s
table/user_guide/indexing.html#returning-a-view-versus-a-copy (https://panda
s.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-ver
sus-a-copy)
  treatments_df['dosage_end'] = treatments_df['dosage_range'].str.split('-').
str.get(1) # ending range
```

In [63]:
```
treatments_df
```

Out[63]:

	given_name	surname	hba1c_start	hba1c_end	hba1c_change	type	dosage_range	d
0	veronika	jindrová	7.63	7.20	0.43	auralin	41u - 48u	
3	skye	gormanston	7.97	7.62	0.35	auralin	33u - 36u	
6	sophia	haugen	7.65	7.27	0.38	auralin	37u - 42u	
7	eddie	archer	7.89	7.55	0.34	auralin	31u - 38u	
9	asia	woźniak	7.76	7.37	0.39	auralin	30u - 36u	
...	...	...	...	...	...	...	...	
688	christopher	woodward	7.51	7.06	0.45	novodra	55u - 51u	
690	maret	sultygov	7.67	7.30	0.37	novodra	26u - 23u	
694	lixue	hsueh	9.21	8.80	0.41	novodra	22u - 23u	
696	jakob	jakobsen	7.96	7.51	0.45	novodra	28u - 26u	
698	berta	napolitani	7.68	7.21	0.47	novodra	42u - 44u	

350 rows × 9 columns

In [65]:
```
treatments_df.drop(columns='dosage_range', inplace=True)
```

```
C:\Users\user\anaconda3\lib\site-packages\pandas\core\frame.py:4906: SettingW
ithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/s
table/user_guide/indexing.html#returning-a-view-versus-a-copy (https://panda
s.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-ver
sus-a-copy)
  return super().drop(
```

In [66]:
```
treatments_df
```

Out[66]:

	given_name	surname	hba1c_start	hba1c_end	hba1c_change	type	dosage_start	do
0	veronika	jindrová	7.63	7.20	0.43	auralin	41u	
3	skye	gormanston	7.97	7.62	0.35	auralin	33u	
6	sophia	haugen	7.65	7.27	0.38	auralin	37u	
7	eddie	archer	7.89	7.55	0.34	auralin	31u	
9	asia	woźniak	7.76	7.37	0.39	auralin	30u	
...	...	...	...	...	...	...	...	
688	christopher	woodward	7.51	7.06	0.45	novodra	55u	
690	maret	sultygov	7.67	7.30	0.37	novodra	26u	
694	lixue	hsueh	9.21	8.80	0.41	novodra	22u	
696	jakob	jakobsen	7.96	7.51	0.45	novodra	28u	
698	berta	napolitani	7.68	7.21	0.47	novodra	42u	

350 rows × 8 columns

In [67]:
```
# remove 'U' in dosage

treatments_df['dosage_start'].str.replace('u','')
```

Out[67]:
```
0      41
3      33
6      37
7      31
9      30
      ...
688    55
690    26
694    22
696    28
698    42
Name: dosage_start, Length: 350, dtype: object
```

In [68]:
```
treatments_df['dosage_start'] = treatments_df['dosage_start'].str.replace('u',
treatments_df['dosage_end'] = treatments_df['dosage_end'].str.replace('u','')
```

```
C:\Users\user\AppData\Local\Temp/ipykernel_10564/3184756727.py:1: SettingWith
CopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/s
table/user_guide/indexing.html#returning-a-view-versus-a-copy (https://panda
s.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-ver
sus-a-copy)
  treatments_df['dosage_start'] = treatments_df['dosage_start'].str.replace
('u','')
C:\Users\user\AppData\Local\Temp/ipykernel_10564/3184756727.py:2: SettingWith
CopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/s
table/user_guide/indexing.html#returning-a-view-versus-a-copy (https://panda
s.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-ver
sus-a-copy)
  treatments_df['dosage_end'] = treatments_df['dosage_end'].str.replace
('u','')
```

In [69]:
```
treatments_df # removed 'u from dosage'
```

Out[69]:

	given_name	surname	hba1c_start	hba1c_end	hba1c_change	type	dosage_start	dc
0	veronika	jindrová	7.63	7.20	0.43	auralin	41	
3	skye	gormanston	7.97	7.62	0.35	auralin	33	
6	sophia	haugen	7.65	7.27	0.38	auralin	37	
7	eddie	archer	7.89	7.55	0.34	auralin	31	
9	asia	woźniak	7.76	7.37	0.39	auralin	30	
...	...	...	...	...	...	...	...	
688	christopher	woodward	7.51	7.06	0.45	novodra	55	
690	maret	sultygov	7.67	7.30	0.37	novodra	26	
694	lixue	hsueh	9.21	8.80	0.41	novodra	22	
696	jakob	jakobsen	7.96	7.51	0.45	novodra	28	
698	berta	napolitani	7.68	7.21	0.47	novodra	42	

350 rows × 8 columns

In [71]:
```
treatments_df.info() # here dosage is in "object"
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 350 entries, 0 to 698
Data columns (total 8 columns):
 #   Column        Non-Null Count  Dtype  
---  ------        --------------  -----  
 0   given_name    350 non-null    object 
 1   surname       350 non-null    object 
 2   hba1c_start   350 non-null    float64
 3   hba1c_end     350 non-null    float64
 4   hba1c_change  350 non-null    float64
 5   type          350 non-null    object 
 6   dosage_start  350 non-null    object 
 7   dosage_end    350 non-null    object 
dtypes: float64(3), object(5)
memory usage: 32.7+ KB
```

In [72]:
```
# changing into 'int'

treatments_df['dosage_start'] = treatments_df['dosage_start'].astype('int')
treatments_df['dosage_end'] = treatments_df['dosage_end'].astype('int')
```

```
C:\Users\user\AppData\Local\Temp/ipykernel_10564/3541383869.py:3: SettingWith
CopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/s
table/user_guide/indexing.html#returning-a-view-versus-a-copy (https://panda
s.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-ver
sus-a-copy)
  treatments_df['dosage_start'] = treatments_df['dosage_start'].astype('int')
C:\Users\user\AppData\Local\Temp/ipykernel_10564/3541383869.py:4: SettingWith
CopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/s
table/user_guide/indexing.html#returning-a-view-versus-a-copy (https://panda
s.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-ver
sus-a-copy)
  treatments_df['dosage_end'] = treatments_df['dosage_end'].astype('int')
```

In [73]:
```
treatments_df.info() # changed object to int
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 350 entries, 0 to 698
Data columns (total 8 columns):
 #   Column        Non-Null Count  Dtype  
---  ------        --------------  -----  
 0   given_name    350 non-null    object 
 1   surname       350 non-null    object 
 2   hba1c_start   350 non-null    float64
 3   hba1c_end     350 non-null    float64
 4   hba1c_change  350 non-null    float64
 5   type          350 non-null    object 
 6   dosage_start  350 non-null    int32  
 7   dosage_end    350 non-null    int32  
dtypes: float64(3), int32(2), object(3)
memory usage: 30.0+ KB
```

In [74]:
```
treatments_df
```

Out[74]:

	given_name	surname	hba1c_start	hba1c_end	hba1c_change	type	dosage_start	dc
0	veronika	jindrová	7.63	7.20	0.43	auralin	41	
3	skye	gormanston	7.97	7.62	0.35	auralin	33	
6	sophia	haugen	7.65	7.27	0.38	auralin	37	
7	eddie	archer	7.89	7.55	0.34	auralin	31	
9	asia	woźniak	7.76	7.37	0.39	auralin	30	
...	...	...	...	...	...	...	...	
688	christopher	woodward	7.51	7.06	0.45	novodra	55	
690	maret	sultygov	7.67	7.30	0.37	novodra	26	
694	lixue	hsueh	9.21	8.80	0.41	novodra	22	
696	jakob	jakobsen	7.96	7.51	0.45	novodra	28	
698	berta	napolitani	7.68	7.21	0.47	novodra	42	

350 rows × 8 columns

In [75]:
```
adverse_reactions_df
```

Out[75]:

	given_name	surname	adverse_reaction
0	berta	napolitani	injection site discomfort
1	lena	baer	hypoglycemia
2	joseph	day	hypoglycemia
3	flavia	fiorentino	cough
4	manouck	wubbels	throat irritation
5	jasmine	sykes	hypoglycemia
6	louise	johnson	hypoglycemia
7	albinca	komavec	hypoglycemia
8	noe	aranda	hypoglycemia
9	sofia	hermansen	injection site discomfort
10	tegan	johnson	headache
11	abel	yonatan	cough
12	abdul-nur	isa	hypoglycemia
13	leon	scholz	injection site discomfort
14	gabriele	saenger	hypoglycemia
15	jia li	teng	nausea
16	jakob	jakobsen	hypoglycemia
17	christopher	woodward	nausea
18	ole	petersen	hypoglycemia
19	finley	chandler	headache
20	anenechi	chidi	hypoglycemia
21	miłosław	wiśniewski	injection site discomfort
22	lixue	hsueh	injection site discomfort
23	merci	leroux	hypoglycemia
24	kang	mai	injection site discomfort
25	elliot	richardson	hypoglycemia
26	clinton	miller	throat irritation
27	idalia	moore	hypoglycemia
28	xiuxiu	chang	hypoglycemia
29	alex	crawford	hypoglycemia
30	monika	lončar	hypoglycemia
31	steven	roy	headache
32	cecilie	nilsen	hypoglycemia
33	krisztina	magyar	hypoglycemia

In [76]:
```
# add extra column , which is adverse reaction table to treatments_df

treatments_df = treatments_df.merge(adverse_reactions_df, how ='left' , on =['
```

In [77]:
```
treatments_df
```

Out[77]:

	given_name	surname	hba1c_start	hba1c_end	hba1c_change	type	dosage_start	dc
0	veronika	jindrová	7.63	7.20	0.43	auralin	41	
1	skye	gormanston	7.97	7.62	0.35	auralin	33	
2	sophia	haugen	7.65	7.27	0.38	auralin	37	
3	eddie	archer	7.89	7.55	0.34	auralin	31	
4	asia	woźniak	7.76	7.37	0.39	auralin	30	
...	...	...	...	...	...	...	...	
345	christopher	woodward	7.51	7.06	0.45	novodra	55	
346	maret	sultygov	7.67	7.30	0.37	novodra	26	
347	lixue	hsueh	9.21	8.80	0.41	novodra	22	
348	jakob	jakobsen	7.96	7.51	0.45	novodra	28	
349	berta	napolitani	7.68	7.21	0.47	novodra	42	

350 rows × 9 columns

In [ ]:

In [ ]: