01 — Exploratory Data Analysis (EDA)

Local data source: `/data/interim/10kDiabetes.csv`

Executive Summary

This notebook performs an initial sweep of the Diabetes Readmission dataset.

Findings:

- The dataset is highly imbalanced, with far fewer readmissions than non-readmissions. This makes ROC-AUC less informative and increases the importance of PR-AUC.
- Many features are categorical (e.g., admission source/type, discharge disposition, race, gender), requiring one-hot encoding for classical ML models.
- Several numerical features (e.g., number of inpatient visits, emergency visits, diagnoses) show long-tailed distributions and strong predictive potential.
- ICD-9 diagnostic codes are messy and high-cardinality; each patient has three diagnosis fields, and codes range from broad categories to highly granular subcodes. This leads to a very sparse and wide feature space if one-hot encoded directly. I explore this more in [03_ICD9_feature_engineering_prototype] and [04_Model-v2.ipynb].
- Missingness varies substantially by field; some categorical features (e.g., medical specialty) contain large proportions of 'Unknown' or 'Missing' values.
- Preliminary relationships (e.g., higher inpatient/emergency visit counts) suggest clinically plausible drivers of readmission that will be explored further in [02_Model.ipynb].

1. Imports and Project Setup

In [1]:
```python
import sys
import os

project_root = os.path.abspath("..") # Add project root to Python path so we can import data_loader etc etc
if project_root not in sys.path:
    sys.path.append(project_root)

project_root
```

Out[1]:
```
'C:\\work\\git\\diabetes-readmission-ml'
```

In [66]:
```python
import warnings
with warnings.catch_warnings():
    warnings.filterwarnings("ignore") # Not too bothered about message "Pyarrow will become a required dependency of pandas"
    import pandas as pd
    from IPython.core.display import display, HTML

import numpy as np
import missingno as msno
import re
import itertools

import matplotlib.pyplot as plt
import seaborn as sns
sns.set_theme(style="whitegrid", font_scale=1.4)  # try 1.3–1.6

from src.data_loader import load_diabetes_csv, DIABETES_DATA_CSV

plt.style.use("seaborn-v0_8")
pd.set_option("display.max_columns", None)
```

In [3]:
```python
df = load_diabetes_csv(DIABETES_DATA_CSV,project_root)
df.shape
```

Out[3]:
```
(10000, 52)
```

In [4]:
```python
df.head()
```

Out[4]:

	rowID	race	gender	age	weight	admission_type_id	discharge_disposition_id	admission_source_id	time_in_hospital	payer_code	medical_specialty	num_lab_pro
0	1	Caucasian	Female	[50-60)	?	Elective	Discharged to home	Physician Referral	1	CP	Surgery-Neuro	
1	2	Caucasian	Female	[20-30)	[50-75)	Urgent	Discharged to home	Physician Referral	2	UN	?	
2	3	Caucasian	Male	[80-90)	?	Not Available	Discharged/transferred to home with home healt...	NaN	7	MC	Family/GeneralPractice	
3	4	AfricanAmerican	Female	[50-60)	?	Emergency	Discharged to home	Transfer from another health care facility	4	UN	?	
4	5	AfricanAmerican	Female	[50-60)	?	Emergency	Discharged to home	Emergency Room	5	?	Psychiatry	

In [5]:
```python
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 10000 entries, 0 to 9999
Data columns (total 52 columns):
 #   Column                    Non-Null Count  Dtype 
---  ------                    --------------  ----- 
 0   rowID                     10000 non-null  int64 
 1   race                      10000 non-null  object
 2   gender                    10000 non-null  object
 3   age                       10000 non-null  object
 4   weight                    10000 non-null  object
 5   admission_type_id         9279 non-null   object
 6   discharge_disposition_id  9531 non-null   object
 7   admission_source_id       9064 non-null   object
 8   time_in_hospital          10000 non-null  int64 
 9   payer_code                10000 non-null  object
 10  medical_specialty         10000 non-null  object
 11  num_lab_procedures        10000 non-null  int64 
 12  num_procedures            10000 non-null  int64 
 13  num_medications           10000 non-null  int64 
 14  number_outpatient         10000 non-null  int64 
 15  number_emergency          10000 non-null  int64 
 16  number_inpatient          10000 non-null  int64 
 17  diag_1                    10000 non-null  object
 18  diag_2                    10000 non-null  object
 19  diag_3                    10000 non-null  object
 20  number_diagnoses          10000 non-null  int64 
 21  max_glu_serum             664 non-null    object
 22  A1Cresult                 1621 non-null   object
 23  metformin                 10000 non-null  object
 24  repaglinide               10000 non-null  object
 25  nateglinide               10000 non-null  object
 26  chlorpropamide            10000 non-null  object
 27  glimepiride               10000 non-null  object
 28  acetohexamide             10000 non-null  object
 29  glipizide                 10000 non-null  object
 30  glyburide                 10000 non-null  object
 31  tolbutamide               10000 non-null  object
 32  pioglitazone              10000 non-null  object
 33  rosiglitazone             10000 non-null  object
 34  acarbose                  10000 non-null  object
 35  miglitol                  10000 non-null  object
 36  troglitazone              10000 non-null  object
 37  tolazamide                10000 non-null  object
 38  examide                   10000 non-null  object
 39  citoglipton               10000 non-null  object
 40  insulin                   10000 non-null  object
 41  glyburide.metformin       10000 non-null  object
 42  glipizide.metformin       10000 non-null  object
 43  glimepiride.pioglitazone  10000 non-null  object
 44  metformin.rosiglitazone   10000 non-null  object
 45  metformin.pioglitazone    10000 non-null  object
 46  change                    10000 non-null  object
 47  diabetesMed               10000 non-null  object
 48  readmitted                10000 non-null  bool  
 49  diag_1_desc               9998 non-null   object
 50  diag_2_desc               9941 non-null   object
 51  diag_3_desc               9792 non-null   object
dtypes: bool(1), int64(9), object(42)
memory usage: 3.9+ MB
```

This summary shows:

- column data types (yes there are 50 columns, plus a numerical index!)
- missingness structure
- categorical vs numerical balance

Which fields have missing values/NaNs?

In [6]:
```python
missing = df.isna().sum().sort_values(ascending=False)
missing[missing > 0]
missing_df = (
    missing.to_frame(name="num_missing")
        .assign(
            pct_missing=lambda x: (x["num_missing"] / len(df) * 100).round(2),
            pct_present=lambda x: 100 - x["pct_missing"]
        )
)
print(f"\nNumber of rows: {df.shape[0]}")
missing_df
```

```
Number of rows: 10000
```

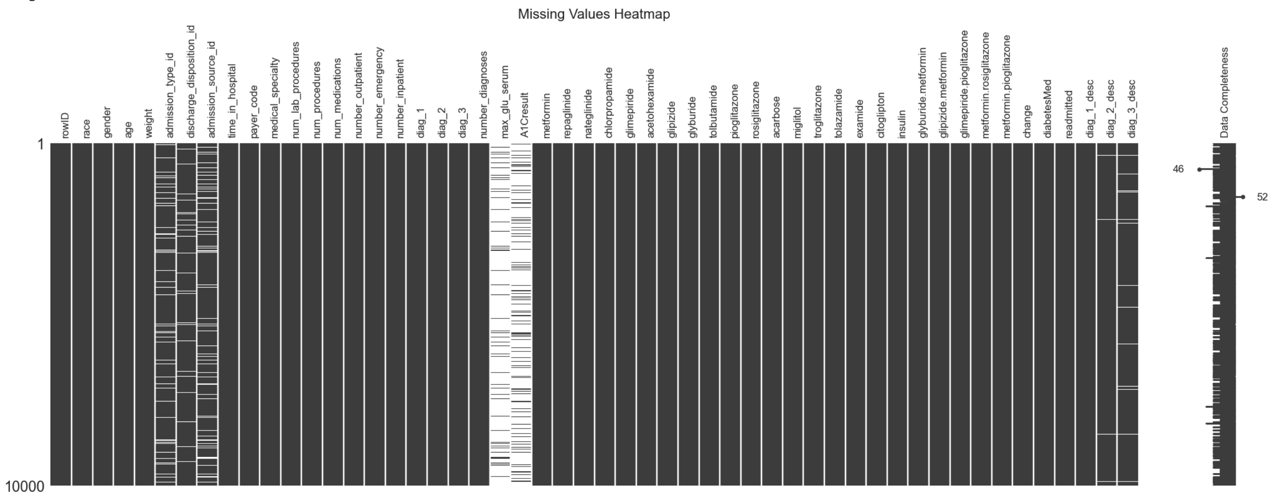
Out[6]:

	num_missing	pct_missing	pct_present
max_glu_serum	9336	93.36	6.64
A1Cresult	8379	83.79	16.21
admission_source_id	936	9.36	90.64
admission_type_id	721	7.21	92.79
discharge_disposition_id	469	4.69	95.31
diag_3_desc	208	2.08	97.92
diag_2_desc	59	0.59	99.41
diag_1_desc	2	0.02	99.98
examide	0	0.00	100.00
tolbutamide	0	0.00	100.00
pioglitazone	0	0.00	100.00
rosiglitazone	0	0.00	100.00
acarbose	0	0.00	100.00
miglitol	0	0.00	100.00
troglitazone	0	0.00	100.00
tolazamide	0	0.00	100.00
glyburide.metformin	0	0.00	100.00
citoglipton	0	0.00	100.00
insulin	0	0.00	100.00
glipizide	0	0.00	100.00
glipizide.metformin	0	0.00	100.00
glimepiride.pioglitazone	0	0.00	100.00
metformin.rosiglitazone	0	0.00	100.00
metformin.pioglitazone	0	0.00	100.00
change	0	0.00	100.00
diabetesMed	0	0.00	100.00
readmitted	0	0.00	100.00
glyburide	0	0.00	100.00
rowID	0	0.00	100.00
acetohexamide	0	0.00	100.00
number_outpatient	0	0.00	100.00
gender	0	0.00	100.00
age	0	0.00	100.00
weight	0	0.00	100.00
time_in_hospital	0	0.00	100.00
payer_code	0	0.00	100.00
medical_specialty	0	0.00	100.00
num_lab_procedures	0	0.00	100.00
num_procedures	0	0.00	100.00
num_medications	0	0.00	100.00
number_emergency	0	0.00	100.00
glimepiride	0	0.00	100.00
number_inpatient	0	0.00	100.00
diag_1	0	0.00	100.00
diag_2	0	0.00	100.00
diag_3	0	0.00	100.00
number_diagnoses	0	0.00	100.00
metformin	0	0.00	100.00
repaglinide	0	0.00	100.00
nateglinide	0	0.00	100.00
race	0	0.00	100.00
chlorpropamide	0	0.00	100.00

Heatmap of missing values

In [7]:
```
plt.figure(figsize=(16, 16))

ax = msno.matrix(  # Missingness matrix
    df,
    labels=True,
    fontsize=14,
)

fig = plt.gcf()
fig.canvas.draw()

for artist in fig.findobj(match=plt.Text):
    if artist.get_text() == "Data Completeness":
        artist.set_rotation(90)
        artist.set_fontsize(12)
        artist.set_horizontalalignment('left')
        artist.set_verticalalignment('bottom')

plt.xticks(rotation=90, fontsize=12)
plt.title("Missing Values Heatmap", fontsize=16)
plt.subplots_adjust(bottom=0.35, top=0.90)
plt.show()
```

```
<Figure size 1600x1600 with 0 Axes>
```



Data completeness is actually pretty good, with the notable exception of fields **max_glu_serum** and **A1Cresult**.

There appears to be no particular clustering when it comes to missing data attributes.

Given the low overall missingness, I am pretty confident in using simple imputation -- nothing complex needed here!

Target Distribution (Binary Readmission Flag)

Check the Boolean variable we're trying to predict for how well it is balanced across the dataset

In [8]:
```
target_col = "readmitted"
pct = df[target_col].value_counts(normalize=True).mul(100).round(2)
pct_df = pct.rename("pct").astype(str) + '%'
pct_df.to_frame()
```

Out[8]:

	pct
readmitted	
False	60.35%
True	39.65%

N.B. 60/40 is not too much of an imbalance. But we will go carefully, being mindful of Type I/Type II statistical errors.

We should be particularly cautious about false negatives, which have both clinical and operational implications: if a patient is at risk of readmission, we don't want the model to miss them - we have a **duty of care** to patients.

Investigate numerical features

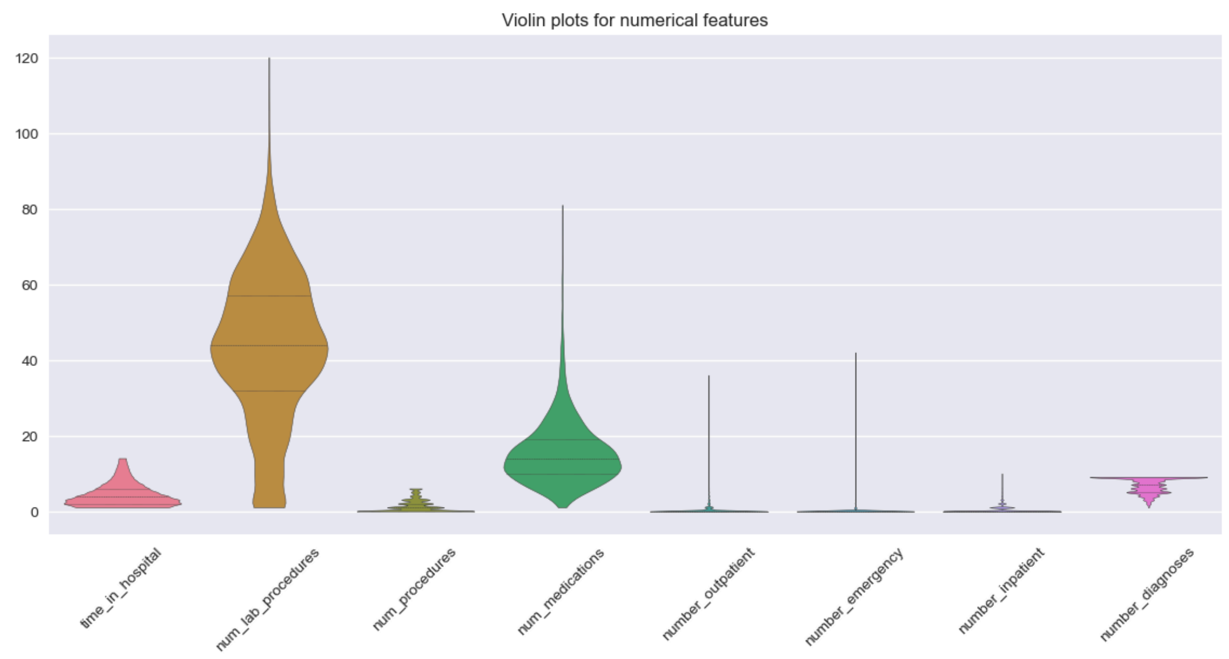
In [9]:
```
numeric_cols = df.select_dtypes(include=['int64', 'float64']).columns.tolist()
if "rowID" in numeric_cols:
    numeric_cols.remove("rowID")

df_numeric = df[numeric_cols]
df_numeric.describe().T
```

Out[9]:

	count	mean	std	min	25%	50%	75%	max
time_in_hospital	10000.0	4.4347	3.021597	1.0	2.0	4.0	6.0	14.0
num_lab_procedures	10000.0	43.0786	19.453315	1.0	32.0	44.0	57.0	120.0
num_procedures	10000.0	1.3992	1.706438	0.0	0.0	1.0	2.0	6.0
num_medications	10000.0	15.5638	8.391613	1.0	10.0	14.0	19.0	81.0
number_outpatient	10000.0	0.2817	1.119406	0.0	0.0	0.0	0.0	36.0
number_emergency	10000.0	0.1150	0.649475	0.0	0.0	0.0	0.0	42.0
number_inpatient	10000.0	0.3873	0.854267	0.0	0.0	0.0	0.0	10.0
number_diagnoses	10000.0	7.0253	2.020957	1.0	5.0	7.0	9.0	9.0

No missing values. I can use this.

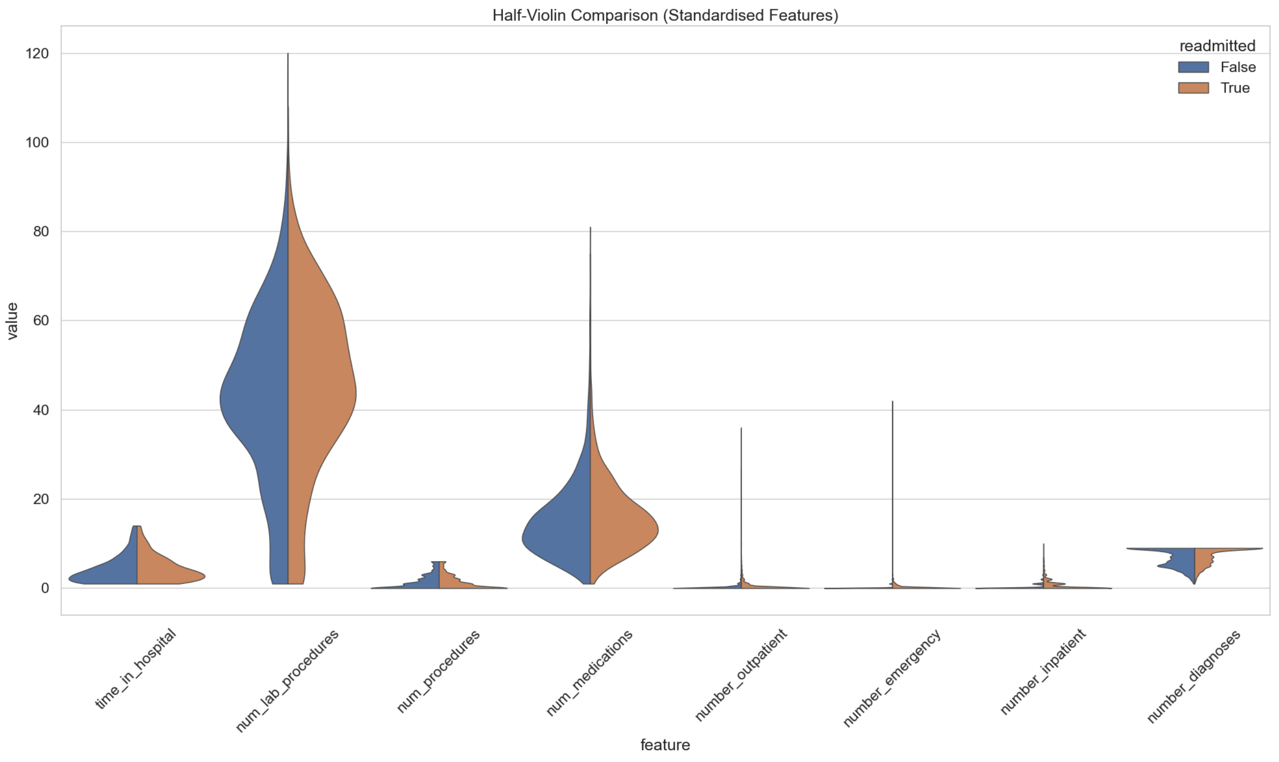
In [10]:
```
import seaborn as sns
import matplotlib.pyplot as plt

plt.figure(figsize=(14, 6))
sns.violinplot(data=df_numeric, inner='quartile', cut=0)
plt.title("Violin plots for numerical features")
plt.xticks(rotation=45)
plt.show()
```



Let's see the distributions separately for (i) patients who were readmitted, and (b) patients who weren't.

In [11]:
```python
numeric_cols = df.select_dtypes(include=['int64', 'float64']).columns.tolist()
numeric_cols = [c for c in numeric_cols if c != "rowID"]

df_long = df.melt(
    id_vars="readmitted",
    value_vars=numeric_cols,
    var_name="feature",
    value_name="value"
)
```

In [12]:
```python
from sklearn.preprocessing import MinMaxScaler

numeric_cols = df.select_dtypes(include=['int64','float64']).columns.tolist()
numeric_cols = [c for c in numeric_cols if c != "rowID"]

scaler = MinMaxScaler()
df_scaled = df.copy()
df_scaled[numeric_cols] = scaler.fit_transform(df[numeric_cols])

df_long_scaled = df_scaled.melt(
    id_vars="readmitted",
    value_vars=numeric_cols,
    var_name="feature",
    value_name="value"
)

sns.set_theme(style="whitegrid", font_scale=1.5)
plt.figure(figsize=(20, 12))

sns.violinplot(
    data=df_long,
    x="feature",
    y="value",
    hue="readmitted",
    split=True,
    inner=None,
    cut=0,
    width=0.9,        # <-- MUCH WIDER VIOLINS
    density_norm="count",    # <-- Uses sample size to expand violins
    bw_adjust=1.2,    # <-- optional smoothing
    linewidth=1.0,
)

plt.title("Half-Violin Comparison (Standardised Features)")
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```



Patients who are readmitted tend to have more lab procedures, medication counts skewed slightly highly, and slightly longer hospital stays.

This early stage view suggests that the greater interaction with hospital procedures, *possibly* the higher the risk of readmission.

In [13]:
```
cols = ['readmitted', 'time_in_hospital', 'num_lab_procedures', 'num_medications']
df_sub = df[cols]

summary = (
    df_sub
    .groupby('readmitted')
    .agg(['mean', 'median', 'std', 'min', 'max']).T
)
summary
```

Out[13]:

	readmitted	False	True
time_in_hospital	mean	4.308534	4.626734
	median	4.000000	4.000000
	std	3.027208	3.003260
	min	1.000000	1.000000
	max	14.000000	14.000000
num_lab_procedures	mean	41.791218	45.038083
	median	43.000000	46.000000
	std	19.244476	19.607779
	min	1.000000	1.000000
	max	120.000000	108.000000
num_medications	mean	15.261475	16.023960
	median	14.000000	15.000000
	std	8.650100	7.961194
	min	1.000000	1.000000
	max	75.000000	81.000000

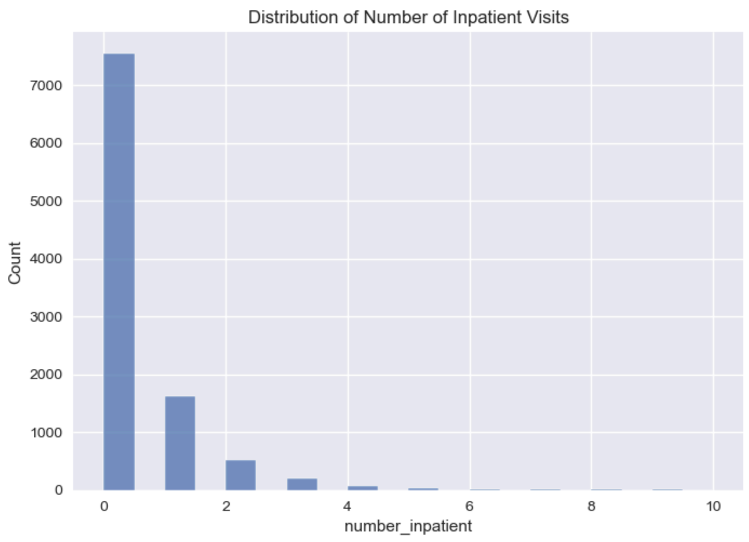
In [14]:
```
summary2 = (
    df_sub
    .groupby('readmitted')
    .agg(['mean', 'median', 'std']).T
)
summary2.columns = ['Not_readmitted', 'Readmitted']
summary2['% Difference'] = (
    (summary2["Readmitted"] / summary2["Not_readmitted"] - 1) * 100
).round(1)

summary2['% Difference'] = summary2['% Difference'].astype(str) + '%' # Convert to string with % symbol
summary2
```

Out[14]:

		Not_readmitted	Readmitted	% Difference
time_in_hospital	**mean**	4.308534	4.626734	7.4%
	median	4.000000	4.000000	0.0%
	std	3.027208	3.003260	-0.8%
num_lab_procedures	**mean**	41.791218	45.038083	7.8%
	median	43.000000	46.000000	7.0%
	std	19.244476	19.607779	1.9%
num_medications	**mean**	15.261475	16.023960	5.0%
	median	14.000000	15.000000	7.1%
	std	8.650100	7.961194	-8.0%

Number of Inpatient Visits

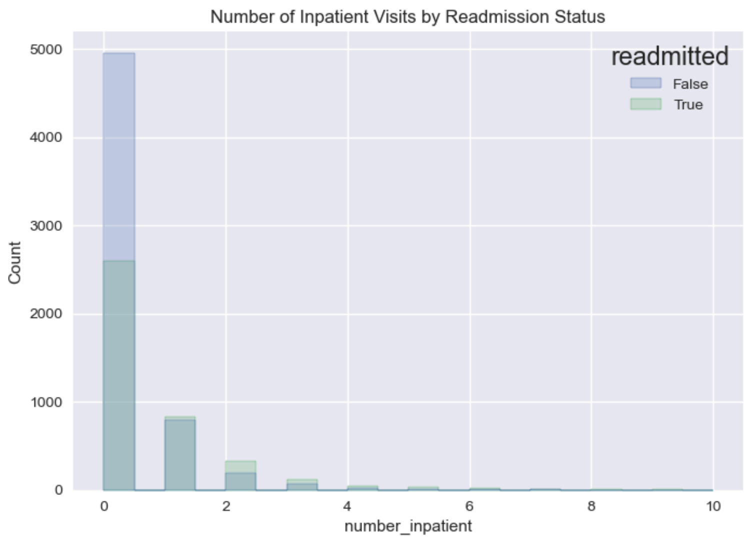
In [76]:
```
sns.histplot(df['number_inpatient'], bins=20)
plt.title("Distribution of Number of Inpatient Visits")
plt.show()
```



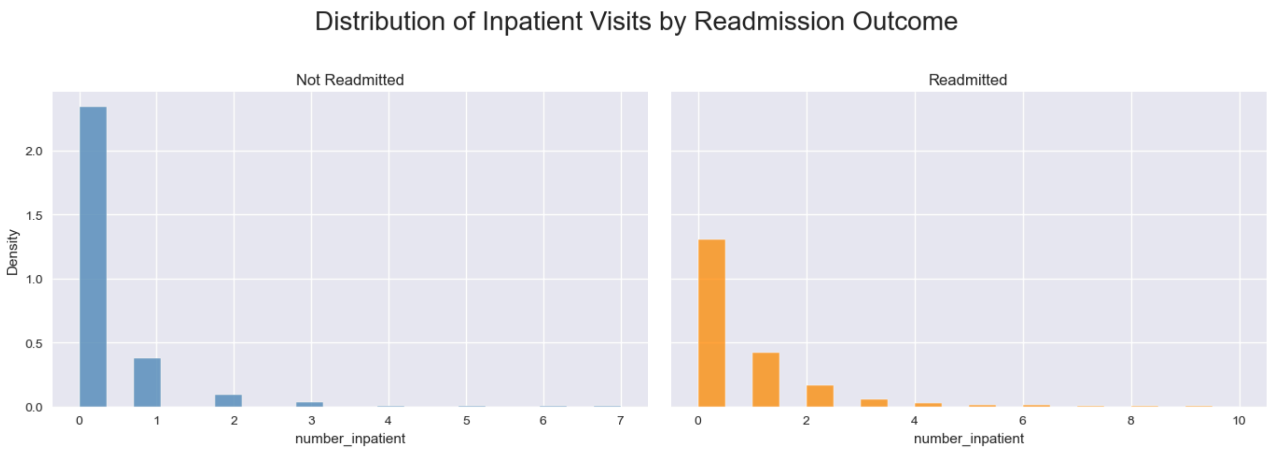
Most patients have zero or one inpatient visit, while a smaler minority have repeated admissions, as one would expect.

Note that there appears to be some dependency structure between this and hospital readmission.

In [82]:
```
sns.histplot(
    data=df,
    x='number_inpatient',
    hue='readmitted',
    bins=20,
    stat='count',
    common_norm=False,   # prevents normalization across groups
    element='step'       # optional: cleaner overlapping lines
)

plt.title("Number of Inpatient Visits by Readmission Status")
plt.show()
```



In [99]:
```
fig, axes = plt.subplots(1, 2, figsize=(14, 5), sharey=True)

sns.histplot(
    df[df['readmitted'] == 0]['number_inpatient'],
    bins=20,
    ax=axes[0],
    stat='density',
    color='steelblue'
)
axes[0].set_title("Not Readmitted")
axes[0].set_xlabel("number_inpatient")

sns.histplot(
    df[df['readmitted'] == 1]['number_inpatient'],
    bins=20,
    ax=axes[1],
    stat='density',
    color='darkorange'
)
axes[1].set_title("Readmitted")
axes[1].set_xlabel("number_inpatient")

plt.suptitle("Distribution of Inpatient Visits by Readmission Outcome")
plt.tight_layout()
plt.show()
```



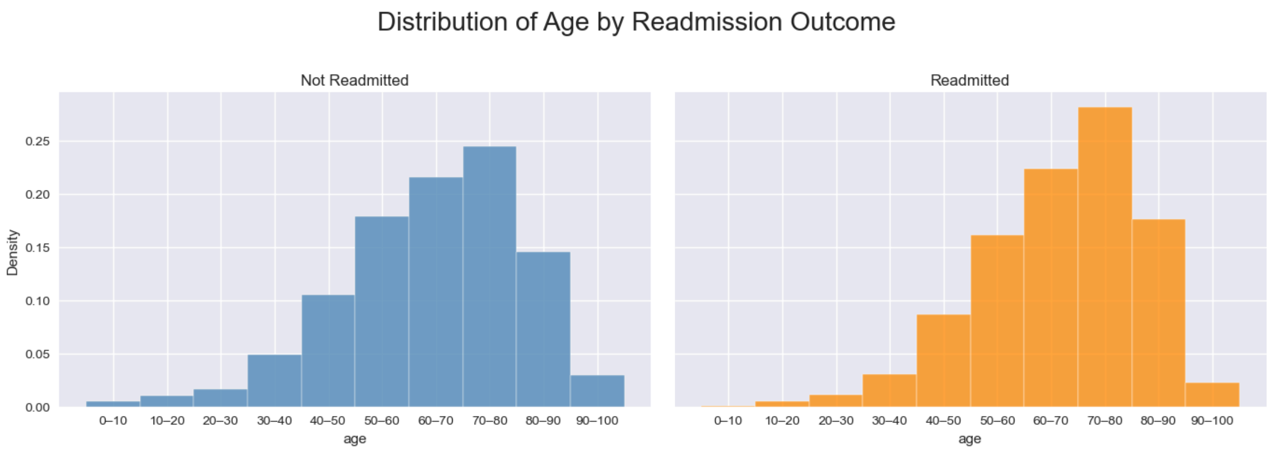
While most patients have zero or one inpatient visit, the readmitted group shows a visibly higher frequency of repeated visits (≥2).

Repeated prior inpatient admittance appears predictive of readmission risk.

Distribution of Age

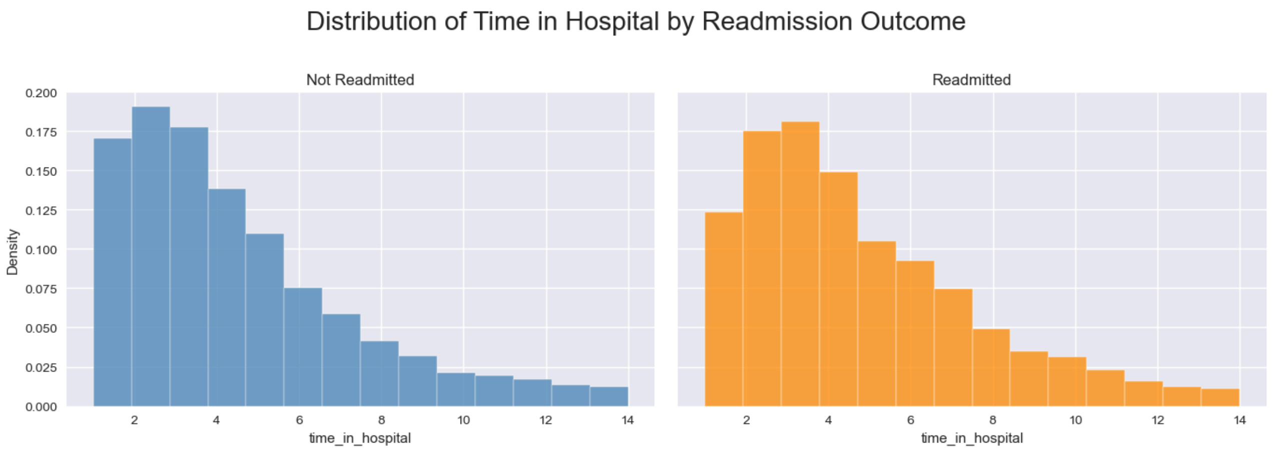
In [105…

```
fig, axes = plt.subplots(1, 2, figsize=(14, 5), sharey=True)

age_order = [ '[0-10)', '[10-20)', '[20-30)', '[30-40)', '[40-50)', '[50-60)', '[60-70)', '[70-80)', '[80-90)', '[90-100)' ]

clean_labels = ["0-10", "10-20", "20-30", "30-40", "40-50", "50-60", "60-70", "70-80", "80-90", "90-100"]

# Convert to ordered categorical
df['age'] = pd.Categorical(df['age'], categories=age_order, ordered=True)

sns.histplot(
    df[df['readmitted'] == 0]['age'],
    bins=20,
    ax=axes[0],
    stat='density',
    color='steelblue'
)
axes[0].set_title("Not Readmitted")
axes[0].set_xlabel("age")

sns.histplot(
    df[df['readmitted'] == 1]['age'],
    bins=20,
    ax=axes[1],
    stat='density',
    color='darkorange'
)
axes[1].set_title("Readmitted")
axes[1].set_xlabel("age")

positions = range(len(clean_labels))

axes[0].set_xticks(positions)
axes[0].set_xticklabels(clean_labels)

axes[1].set_xticks(positions)
axes[1].set_xticklabels(clean_labels)

plt.suptitle("Distribution of Age by Readmission Outcome")
plt.tight_layout()
plt.show()
```



Distribution of Length of Stay

In [98]:
```python
fig, axes = plt.subplots(1, 2, figsize=(14, 5), sharey=True)

sns.histplot(
    df[df['readmitted'] == 0]['time_in_hospital'],
    ax=axes[0],
    bins=14,
    stat='density',
    color='steelblue'
)
axes[0].set_title("Not Readmitted")
axes[0].set_xlabel("time_in_hospital")

sns.histplot(
    df[df['readmitted'] == 1]['time_in_hospital'],
    ax=axes[1],
    bins=14,
    stat='density',
    color='darkorange'
)
axes[1].set_title("Readmitted")
axes[1].set_xlabel("time_in_hospital")

plt.suptitle("Distribution of Time in Hospital by Readmission Outcome")
plt.tight_layout()
plt.show()
```



Categorical Cardinality

In [15]:
```python
cat_cols = df.select_dtypes(include='object').columns          # Identify categorical columns (object dtype)
cardinality = (
    df[cat_cols]
    .nunique()
    .sort_values(ascending=False)
    .to_frame("unique_values")
)
cardinality.style.background_gradient(cmap="Blues")
```

Out[15]:

	unique_values
diag_3	461
diag_3_desc	460
diag_1	458
diag_1_desc	457
diag_2	430
diag_2_desc	429
medical_specialty	53
discharge_disposition_id	21
payer_code	16
age	10
admission_source_id	10
weight	8
race	6
admission_type_id	6
glyburide	4
miglitol	4
repaglinide	4
nateglinide	4
glimepiride	4
glipizide	4
glyburide.metformin	4
insulin	4
pioglitazone	4
rosiglitazone	4
metformin	4
max_glu_serum	3
A1Cresult	3
acarbose	3
chlorpropamide	3
tolazamide	2
tolbutamide	2
gender	2
glipizide.metformin	2
change	2
diabetesMed	2
examide	1
citoglipton	1
glimepiride.pioglitazone	1
metformin.rosiglitazone	1
metformin.pioglitazone	1
acetohexamide	1
troglitazone	1

The cardinality of the diagnostic codes is going to need some attention.

Everything else looks very manageable.

Let's look at some of the categorical fields with mid-range cardinality.

In [16]:
```
df['medical_specialty'].unique().tolist()
```

```
Out[16]: ['Surgery-Neuro',
          '?',
          'Family/GeneralPractice',
          'Psychiatry',
          'Cardiology',
          'InternalMedicine',
          'Surgery-Cardiovascular/Thoracic',
          'Nephrology',
          'Emergency/Trauma',
          'Gastroenterology',
          'Orthopedics',
          'Cardiology-Pediatric',
          'PhysicalMedicineandRehabilitation',
          'Gynecology',
          'Pulmonology',
          'Surgery-General',
          'Pediatrics',
          'Orthopedics-Reconstructive',
          'Surgery-Pediatric',
          'Otolaryngology',
          'Pediatrics-CriticalCare',
          'Hematology/Oncology',
          'ObstetricsandGynecology',
          'Pediatrics-Endocrinology',
          'Surgery-Vascular',
          'Urology',
          'Neurology',
          'Radiologist',
          'Osteopath',
          'Surgery-Cardiovascular',
          'Psychology',
          'Oncology',
          'Endocrinology',
          'OutreachServices',
          'Podiatry',
          'Ophthalmology',
          'Hospitalist',
          'Radiology',
          'Obsterics&Gynecology-GynecologicOnco',
          'Surgery-Thoracic',
          'Surgeon',
          'Pathology',
          'Surgery-Plastic',
          'InfectiousDiseases',
          'Anesthesiology-Pediatric',
          'Pediatrics-Pulmonology',
          'Pediatrics-Hematology-Oncology',
          'Hematology',
          'Surgery-Colon&Rectal',
          'Surgery-PlasticwithinHeadandNeck',
          'Pediatrics-EmergencyMedicine',
          'Obstetrics',
          'PhysicianNotFound']
```

```
In [17]: df['discharge_disposition_id'].unique().tolist()
```

```
Out[17]: ['Discharged to home',
          'Discharged/transferred to home with home health service',
          'Expired',
          'Discharged/transferred to a long term care hospital.',
          'Discharged/transferred to SNF',
          'Discharged/transferred to another  type of inpatient care institution',
          'Not Mapped',
          'Discharged/transferred to another short term hospital',
          nan,
          'Left AMA',
          'Discharged/transferred to another rehab fac including rehab units of a hospital.',
          'Hospice / medical facility',
          'Hospice / home',
          'Discharged/transferred/referred to a psychiatric hospital of a psychiatric distinct part unit of a hospital',
          'Discharged/transferred to ICF',
          'Discharged/transferred to home under care of Home IV provider',
          'Admitted as an inpatient to this hospital',
          'Discharged/transferred/referred another institution for outpatient services',
          'Discharged/transferred to a federal health care facility.',
          'Discharged/transferred within this institution to Medicare approved swing bed',
          'Discharged/transferred/referred to this institution for outpatient services',
          'Discharged/transferred to a nursing facility certified under Medicaid but not certified under Medicare']
```

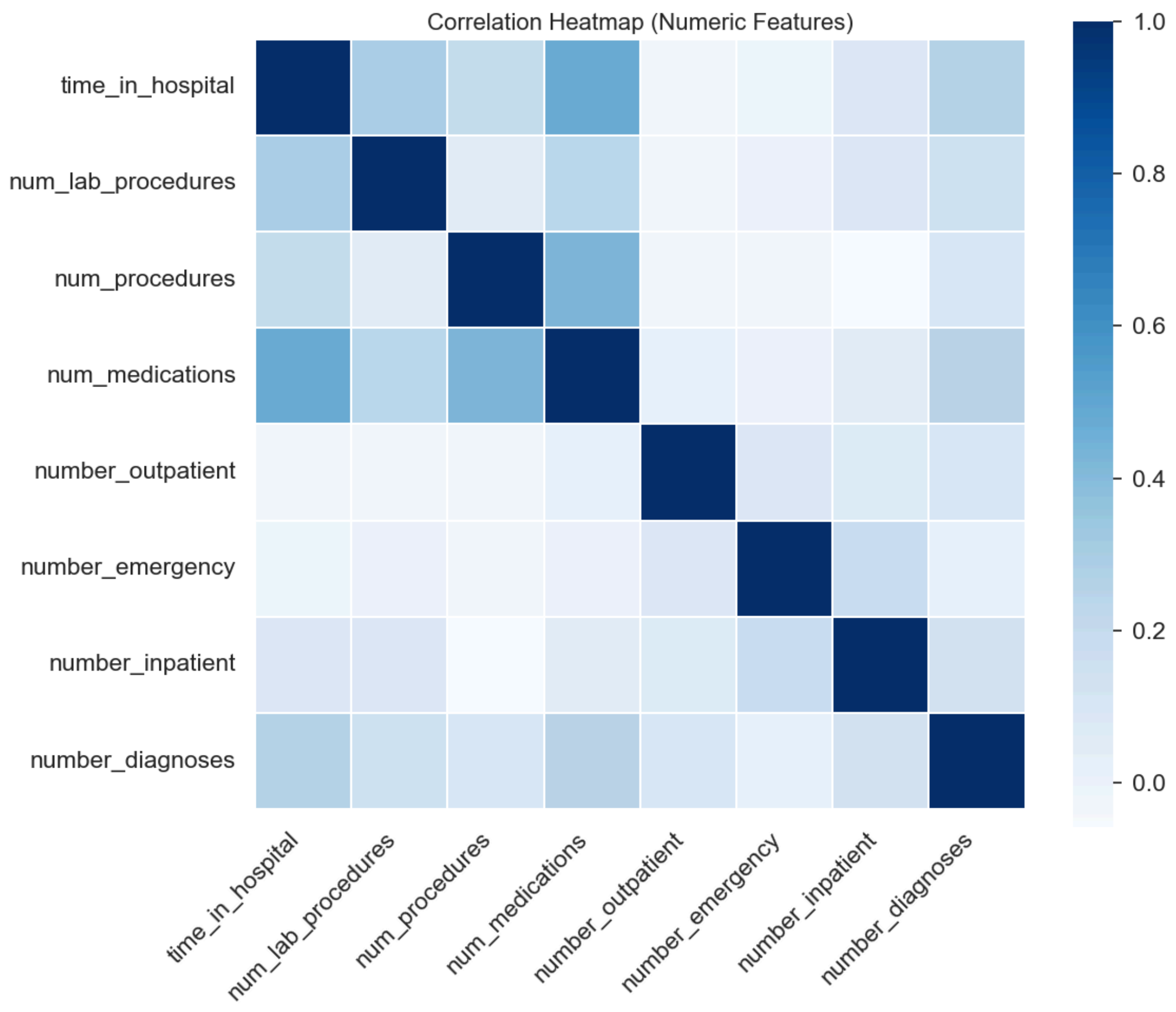
```
In [18]: str(df['payer_code'].unique().tolist())
```

```
Out[18]: "['CP', 'UN', 'MC', '?', 'HM', 'SP', 'CM', 'BC', 'MD', 'WC', 'OG', 'PO', 'DM', 'SI', 'OT', 'CH']"
```

`medical_specialty` is the only attribute with any real semantic complexity, but it's still small enough for encoding.

High level correlation overview ✈️

```
In [19]: numeric_cols = list(df.select_dtypes(include=['int64', 'float64']).columns)
numeric_cols.remove('rowID')
corr = df[numeric_cols].corr()

plt.figure(figsize=(12, 10))
sns.heatmap(
    corr,
    cmap="Blues",
    annot=False,
    cbar=True,
    square=True,
    linewidths=0.3,
)

plt.title("Correlation Heatmap (Numeric Features)", fontsize=16)
plt.xticks(rotation=45, ha='right')
plt.yticks(rotation=0)
plt.tight_layout()
plt.show()
```



No notable off-diagonal correlation structure noted

```
In [20]: corr = df[numeric_cols].corr().round(3)
         corr
```

Out[20]:

	time_in_hospital	num_lab_procedures	num_procedures	num_medications	number_outpatient	number_emergency	number_inpatient	number_diagnoses
time_in_hospital	1.000	0.292	0.202	0.475	-0.033	-0.007	0.081	0.259
num_lab_procedures	0.292	1.000	0.054	0.236	-0.029	-0.001	0.087	0.152
num_procedures	0.202	0.054	1.000	0.424	-0.021	-0.026	-0.058	0.101
num_medications	0.475	0.236	0.424	1.000	0.026	0.007	0.044	0.251
number_outpatient	-0.033	-0.029	-0.021	0.026	1.000	0.083	0.076	0.095
number_emergency	-0.007	-0.001	-0.026	0.007	0.083	1.000	0.187	0.033
number_inpatient	0.081	0.087	-0.058	0.044	0.076	0.187	1.000	0.125
number_diagnoses	0.259	0.152	0.101	0.251	0.095	0.033	0.125	1.000

Examine the diagnostic codes

```
In [21]: str(df['diag_1'].unique().tolist()[:20])

Out[21]: "['723', '664', '481', '682', '296', '428', '434', '558', '440', '997', '250.8', '250.7', '584', '414', '250.82', '415', '432', '786', '410', '276']"

In [22]: str(df['diag_2'].unique().tolist()[:20])

Out[22]: "['723', '648', '428', '41', '250.01', '427', '345', '562', '425', '998', '799', '440', '453', '486', '411', '707', '414', '581', '300', '157']"

In [23]: str(df['diag_3'].unique().tolist()[:20])

Out[23]: "['719', '285', '276', '250', '298', '414', '584', '455', '70', '998', '511', '401', '707', '426', '496', '427', '731', '425', 'V45', '585']"

In [24]: df['diag_1_desc'].unique()[:10].tolist()

Out[24]: ['Spinal stenosis in cervical region',
          'First-degree perineal laceration, unspecified as to episode of care or not applicable',
          'Pneumococcal pneumonia [Streptococcus pneumoniae pneumonia]',
          'Cellulitis and abscess of face',
          'Bipolar I disorder, single manic episode, unspecified',
          'Congestive heart failure, unspecified',
          'Cerebral thrombosis without mention of cerebral infarction',
          'Other and unspecified noninfectious gastroenteritis and colitis',
          'Atherosclerosis of aorta',
          'Nervous system complication, unspecified']

In [25]: df['diag_2_desc'].unique()[:10].tolist()
```

Out[25]:
```
['Spinal stenosis in cervical region',
 'Diabetes mellitus of mother, complicating pregnancy, childbirth, or the puerperium, unspecified as to episode of care or not applicable',
 'Congestive heart failure, unspecified',
 'Streptococcus infection in conditions classified elsewhere and of unspecified site, streptococcus, unspecified',
 'Diabetes mellitus without mention of complication, type I [juvenile type], not stated as uncontrolled',
 'Paroxysmal supraventricular tachycardia',
 'Generalized nonconvulsive epilepsy, without mention of intractable epilepsy',
 'Diverticulosis of small intestine (without mention of hemorrhage)',
 'Endomyocardial fibrosis',
 'Postoperative shock, unspecified']
```

In [26]:
```python
df['diag_3_desc'].unique()[:10].tolist()
```

Out[26]:
```
['Effusion of joint, site unspecified',
 'Sideroblastic anemia',
 'Hyperosmolality and/or hypernatremia',
 'Diabetes mellitus without mention of complication, type II or unspecified type, not stated as uncontrolled',
 'Depressive type psychosis',
 'Coronary atherosclerosis of unspecified type of vessel, native or graft',
 'Acute kidney failure',
 'Internal hemorrhoids without mention of complication',
 'Viral hepatitis A with hepatic coma',
 'Postoperative shock, unspecified']
```

In [27]:
```python
mask = ( (df['diag_1'] == '723') | (df['diag_2'] == '723') | (df['diag_3'] == '723') )
df_723 = df[mask][['diag_1','diag_1_desc','diag_2','diag_2_desc','diag_3','diag_3_desc']]
df_723
```

Out[27]:

	diag_1	diag_1_desc	diag_2	diag_2_desc	diag_3	diag_3_desc
0	723	Spinal stenosis in cervical region	723	Spinal stenosis in cervical region	719	Effusion of joint, site unspecified
1043	723	Spinal stenosis in cervical region	710	Systemic lupus erythematosus	250	Diabetes mellitus without mention of complicat...
1378	434	Cerebral thrombosis without mention of cerebra...	723	Spinal stenosis in cervical region	401	Malignant essential hypertension
2385	723	Spinal stenosis in cervical region	V42	Kidney replaced by transplant	272	Pure hypercholesterolemia
2759	434	Cerebral thrombosis without mention of cerebra...	425	Endomyocardial fibrosis	723	Spinal stenosis in cervical region
4495	723	Spinal stenosis in cervical region	722	Displacement of cervical intervertebral disc w...	401	Malignant essential hypertension
4519	722	Displacement of cervical intervertebral disc w...	723	Spinal stenosis in cervical region	787	Nausea and vomiting
4615	723	Spinal stenosis in cervical region	401	Malignant essential hypertension	250	Diabetes mellitus without mention of complicat...
4697	723	Spinal stenosis in cervical region	723	Spinal stenosis in cervical region	733	Osteoporosis, unspecified
4967	723	Spinal stenosis in cervical region	786	Respiratory abnormality, unspecified	250	Diabetes mellitus without mention of complicat...
5059	786	Respiratory abnormality, unspecified	723	Spinal stenosis in cervical region	250	Diabetes mellitus without mention of complicat...
7545	723	Spinal stenosis in cervical region	401	Malignant essential hypertension	250	Diabetes mellitus without mention of complicat...
8036	V57	Care involving breathing exercises	723	Spinal stenosis in cervical region	721	Cervical spondylosis without myelopathy
8159	723	Spinal stenosis in cervical region	305	Alcohol abuse, unspecified	250	Diabetes mellitus without mention of complicat...
9730	250.11	Diabetes with ketoacidosis, type I [juvenile t...	723	Spinal stenosis in cervical region	276	Hyperosmolality and/or hypernatremia
9867	723	Spinal stenosis in cervical region	428	Congestive heart failure, unspecified	401	Malignant essential hypertension

It looks like there is a 1:1 relationship between the diagnostic codes and their descriptions. But we should check.

In [28]:
```python
pairs = pd.concat([
    df[['diag_1', 'diag_1_desc']].rename(columns={'diag_1':'code', 'diag_1_desc':'desc'}),
    df[['diag_2', 'diag_2_desc']].rename(columns={'diag_2':'code', 'diag_2_desc':'desc'}),
    df[['diag_3', 'diag_3_desc']].rename(columns={'diag_3':'code', 'diag_3_desc':'desc'})
], axis=0).dropna()
```

In [29]:
```python
pairs
```

Out[29]:

	code	desc
0	723	Spinal stenosis in cervical region
1	664	First-degree perineal laceration, unspecified ...
2	481	Pneumococcal pneumonia [Streptococcus pneumoni...
3	682	Cellulitis and abscess of face
4	296	Bipolar I disorder, single manic episode, unsp...
...	...	...
9995	272	Pure hypercholesterolemia
9996	V53	Fitting and adjustment of other device
9997	536	Achlorhydria
9998	599	Urinary tract infection, site not specified
9999	427	Paroxysmal supraventricular tachycardia

29731 rows × 2 columns

In [30]:
```python
desc_counts = pairs.groupby('code')['desc'].nunique()
desc_counts
```

Out[30]:
```
code
11     1
110    1
112    1
117    1
131    1
      ..
V66    1
V70    1
V71    1
V72    1
V85    1
Name: desc, Length: 643, dtype: int64
```

```
In [31]: (desc_counts.min(),desc_counts.max())
```

```
Out[31]: (1, 1)
```

This shows a **one-to-one correspondence** (mathematically, a bijection) between diagnosis codes and their textual descriptions

Let's build this as a map.

I performed a Google search on "786: Respiratory abnormality, unspecified"

https://www.aapc.com/codes/icd9-codes/786.00

Home> Codes > ICD-9 Codes > Symptoms, Signs, And Ill-defined Conditions > Symptoms> (786.00)

Respiratory abnormality, unspecified (786.00)

ICD-9 code 786.00 for Respiratory abnormality, unspecified is a medical classification as listed by WHO under the range -SYMPTOMS (780-789)

Build mappings from code to desc, and v.v.

```
In [32]: code_to_desc = pairs.drop_duplicates('code').set_index('code')['desc'].to_dict()

         desc_to_code = pairs.drop_duplicates('desc').set_index('desc')['code'].to_dict()
```

Check

```
In [33]: code_to_desc['786']
```

```
Out[33]: 'Respiratory abnormality, unspecified'
```

```
In [34]: desc_to_code['Respiratory abnormality, unspecified']
```

```
Out[34]: '786'
```

Can we get by with using numeric codes (not str) ?

```
In [35]: cols = ['diag_1', 'diag_2', 'diag_3']
         non_numeric=[]

         for col in cols:
             bad = pd.to_numeric(df[col], errors='coerce').isna() & df[col].notna()
             if bad.any():
                 print(f"{col} has non-numeric values:")
                 vals = list(df.loc[bad, col].unique())
                 non_numeric.append(vals)
                 print(vals, "\n")
             else:
                 print(f"{col} ✓ all values cast cleanly to float\n")

         non_numeric = list(set(x for sub in non_numeric for x in sub))
         print(f"Complete list of non-numeric ICD-9 codes:\n{non_numeric}")
```

```
diag_1 has non-numeric values:
['V57', 'V58', 'V55', 'V54', 'V56', 'V45', 'V71', 'V53', 'V25', 'V63', '?']

diag_2 has non-numeric values:
['V58', 'V45', 'E849', 'E942', '?', 'V43', 'E934', 'E885', 'V42', 'V64', 'V15', 'V54', 'E878', 'V10', 'V72', 'V65', 'E930', 'E888', 'V57', 'E947', 'V63', 'E932', 'E
858', 'V11', 'E928', 'E812', 'V12', 'E941', 'V85', 'V18', 'E927', 'E935', 'E854', 'E880', 'E879', 'V44', 'E944', 'E939', 'E915', 'V70', 'V16', 'V49', 'V08', 'E905']

diag_3 has non-numeric values:
['V45', '?', 'V43', 'E888', 'V12', 'V15', 'E878', 'V10', 'V58', 'E916', 'E937', 'V14', 'V54', 'E942', 'V17', 'E980', 'E879', 'V42', 'E849', 'E949', 'E816', 'V09',
'V46', 'V63', 'V65', 'E885', 'E932', 'V16', 'E933', 'V85', 'V72', 'E880', 'E917', 'E819', 'E884', 'E935', 'V64', 'E950', 'V18', 'E938', 'E905', 'E947', 'E887', 'V0
8', 'V44', 'E930', 'V27', 'E939', 'V49', 'E944', 'E815', 'E929', 'E943', 'V25', 'E822', 'E882', 'E812', 'V66', 'V62', 'V53']

Complete list of non-numeric ICD-9 codes:
['E939', 'E887', 'E822', 'E930', 'E942', 'V63', 'E927', 'E937', 'E947', 'V72', 'V09', 'V12', '?', 'V64', 'E888', 'E932', 'V11', 'V46', 'V17', 'V45', 'V55', 'V53',
'E885', 'V54', 'V43', 'E943', 'E941', 'V57', 'V85', 'E944', 'V14', 'E915', 'E916', 'V65', 'E935', 'E854', 'E879', 'V44', 'E816', 'E929', 'E917', 'E812', 'E858', 'E8
19', 'V16', 'V56', 'E980', 'E938', 'V27', 'E949', 'V66', 'E928', 'E933', 'E950', 'V15', 'V71', 'V62', 'V70', 'V25', 'V18', 'E934', 'E882', 'V58', 'V10', 'E905', 'E8
84', 'E880', 'E815', 'E878', 'E849', 'V49', 'V42', 'V08']
```

Let's try to work out how to handle these. Start with the "?" symbol.

```
In [36]: df[df['diag_1']=='?'][['diag_1','diag_1_desc']].drop_duplicates()
```

Out[36]:

	diag_1	diag_1_desc
9250	?	NaN

```
In [37]: df[df['diag_2']=='?'][['diag_2','diag_2_desc']].drop_duplicates()
```

Out[37]:

	diag_2	diag_2_desc
276	?	NaN

```
In [38]: df[df['diag_3']=='?'][['diag_3','diag_3_desc']].drop_duplicates()
```

Out[38]:

	diag_3	diag_3_desc
25	?	NaN

```
In [39]: known_non_numeric = [x for x in non_numeric if x !='?']
         (len(non_numeric), len(known_non_numeric))
```

```
Out[39]: (73, 72)
```

```
In [49]: # Wider notebook canvas
         display(HTML("<style>.container { width:100% !important; }</style>"))

         df_non_numeric_codes = pd.DataFrame([(x,code_to_desc[x]) for x in known_non_numeric],columns=['diag_code','diag_desc'])
         df_non_numeric_codes.set_index('diag_code', inplace=True)
         with pd.option_context('display.max_rows', None,
                                'display.max_columns', None,
                                'display.width', 2000,
                                'display.max_colwidth', None):
             display(df_non_numeric_codes.head(25))
```

diag_code	diag_desc
E939	Antidepressants causing adverse effects in therapeutic use
E887	Fracture, cause unspecified
E822	Other motor vehicle nontraffic accident involving collision with moving object injuring driver of motor vehicle other than motorcycle
E930	Penicillins causing adverse effects in therapeutic use
E942	Cardiac rhythm regulators causing adverse effects in therapeutic use
V63	Residence remote from hospital or other health care facility
E927	Overexertion from sudden strenuous movement
E937	Barbiturates causing adverse effects in therapeutic use
E947	Dietetics causing adverse effects in therapeutic use
V72	Examination of eyes and vision
V09	Infection with microorganisms resistant to penicillins
V12	Personal history of unspecified infectious and parasitic disease
V64	Vaccination not carried out, unspecified reason
E888	Fall resulting in striking against sharp object
E932	Adrenal cortical steroids causing adverse effects in therapeutic use
V11	Personal history of schizophrenia
V46	Dependence on aspirator
V17	Family history of psychiatric condition
V45	Unspecified cardiac device in situ
V55	Attention to tracheostomy
V53	Fitting and adjustment of other device
E885	Fall from (nonmotorized) scooter
V54	Other orthopedic aftercare
V43	Eye globe replaced by other means
E943	Antacids and antigastric secretion drugs causing adverse effects in therapeutic use

Having seen the non-numeric codes, now look at the numeric codes with a fractional component

In [64]:
```
diag_cols = ['diag_1', 'diag_2', 'diag_3']

fractional = pd.Series(dtype=str)

for col in diag_cols:
    fractional = pd.concat([
        fractional,
        df[col][df[col].astype(str).str.contains(r'^\d+\.\d+$', na=False)]
    ])

fractional_list = sorted(fractional.unique().astype(float).tolist())
print(fractional_list)
```

```
[250.01, 250.02, 250.03, 250.1, 250.11, 250.12, 250.13, 250.2, 250.21, 250.22, 250.23, 250.3, 250.31, 250.32, 250.33, 250.4, 250.41, 250.42, 250.43, 250.5, 250.51,
250.52, 250.53, 250.6, 250.7, 250.8, 250.81, 250.82, 250.83, 250.9, 250.91, 250.92, 250.93]
```

In [68]:
```
y = [[int(x)] + [x] for x in fractional.unique().astype(float)]
fractional_plus_parent = sorted(set(itertools.chain.from_iterable(y)))
print(fractional_plus_parent)
```

```
[250, 250.01, 250.02, 250.03, 250.1, 250.11, 250.12, 250.13, 250.2, 250.21, 250.22, 250.23, 250.3, 250.31, 250.32, 250.33, 250.4, 250.41, 250.42, 250.43, 250.5, 25
0.51, 250.52, 250.53, 250.6, 250.7, 250.8, 250.81, 250.82, 250.83, 250.9, 250.91, 250.92, 250.93]
```

In [106…
```
df_fractional_codes = pd.DataFrame([(x,code_to_desc[str(x)]) for x in fractional_plus_parent],columns=['diag_code','diag_desc'])
df_fractional_codes.set_index('diag_code', inplace=True)
with pd.option_context('display.max_rows', None,
                       'display.max_columns', None,
                       'display.width', 2000,
                       'display.max_colwidth', None):
    display(df_fractional_codes.head(90))
```

diag_code	diag_desc
250.00	Diabetes mellitus without mention of complication, type II or unspecified type, not stated as uncontrolled
250.01	Diabetes mellitus without mention of complication, type I [juvenile type], not stated as uncontrolled
250.02	Diabetes mellitus without mention of complication, type II or unspecified type, uncontrolled
250.03	Diabetes mellitus without mention of complication, type I [juvenile type], uncontrolled
250.10	Diabetes with ketoacidosis, type II or unspecified type, not stated as uncontrolled
250.11	Diabetes with ketoacidosis, type I [juvenile type], not stated as uncontrolled
250.12	Diabetes with ketoacidosis, type II or unspecified type, uncontrolled
250.13	Diabetes with ketoacidosis, type I [juvenile type], uncontrolled
250.20	Diabetes with hyperosmolarity, type II or unspecified type, not stated as uncontrolled
250.21	Diabetes with hyperosmolarity, type I [juvenile type], not stated as uncontrolled
250.22	Diabetes with hyperosmolarity, type II or unspecified type, uncontrolled
250.23	Diabetes with hyperosmolarity, type I [juvenile type], uncontrolled
250.30	Diabetes with other coma, type II or unspecified type, not stated as uncontrolled
250.31	Diabetes with other coma, type I [juvenile type], not stated as uncontrolled
250.32	Diabetes with other coma, type II or unspecified type, uncontrolled
250.33	Diabetes with other coma, type I [juvenile type], uncontrolled
250.40	Diabetes with renal manifestations, type II or unspecified type, not stated as uncontrolled
250.41	Diabetes with renal manifestations, type I [juvenile type], not stated as uncontrolled
250.42	Diabetes with renal manifestations, type II or unspecified type, uncontrolled
250.43	Diabetes with renal manifestations, type I [juvenile type], uncontrolled
250.50	Diabetes with ophthalmic manifestations, type II or unspecified type, not stated as uncontrolled
250.51	Diabetes with ophthalmic manifestations, type I [juvenile type], not stated as uncontrolled
250.52	Diabetes with ophthalmic manifestations, type II or unspecified type, uncontrolled
250.53	Diabetes with ophthalmic manifestations, type I [juvenile type], uncontrolled
250.60	Diabetes with neurological manifestations, type II or unspecified type, not stated as uncontrolled
250.70	Diabetes with peripheral circulatory disorders, type II or unspecified type, not stated as uncontrolled
250.80	Diabetes with other specified manifestations, type II or unspecified type, not stated as uncontrolled
250.81	Diabetes with other specified manifestations, type I [juvenile type], not stated as uncontrolled
250.82	Diabetes with other specified manifestations, type II or unspecified type, uncontrolled
250.83	Diabetes with other specified manifestations, type I [juvenile type], uncontrolled
250.90	Diabetes with unspecified complication, type II or unspecified type, not stated as uncontrolled
250.91	Diabetes with unspecified complication, type I [juvenile type], not stated as uncontrolled
250.92	Diabetes with unspecified complication, type II or unspecified type, uncontrolled
250.93	Diabetes with unspecified complication, type I [juvenile type], uncontrolled

Surely we can collapse these all into the parent code 250 without loss of predictive power?

```
In [ ]:
```