UNIVERSITÄT LEIPZIG

Medizinische Fakultät

Universitätsklinikum Leipzig

Medizin ist unsere Berufung.

Data Handling and Preprocessing for Medical Data

Data Science and AI for Medicine - Training School 2025

MDS
Medical Data Science

Why Preprocessing Matters

- **Raw data** from hospitals, laboratories, or electronic health records (EHRs) often contains:
  - **Errors** - impossible values (e.g., age = 150 years)
  - **Inconsistencies** - same variable stored differently (e.g., “male”, “M”, “m”)
  - **Missing values** - follow-up information not recorded
  - **Outliers** - extremely high or low lab values

→ Problems distort research results and bias AI models

→ Clean data = more reliable analyses and safer medical decision-making

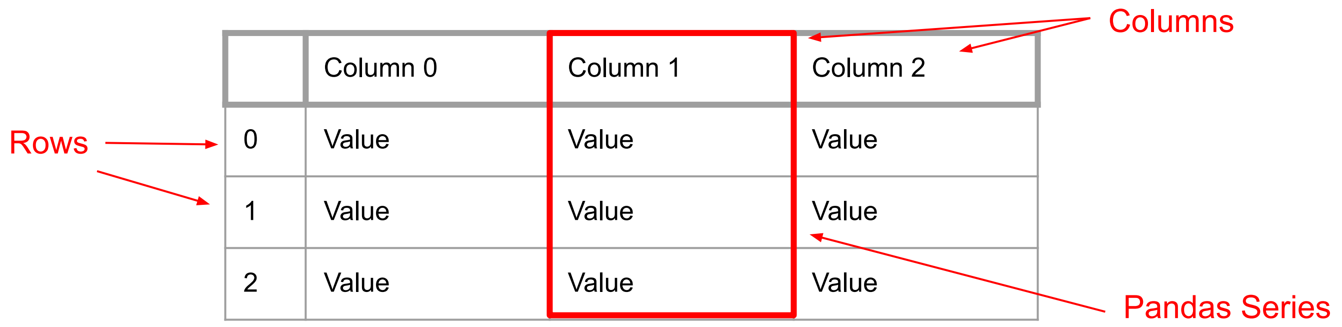
https://www.pexels.com/de-de/foto/marketing-angebot-mann-hande-5816299/

What is *pandas*?

- *pandas* is a Python library for data handling and analysis
  - https://pandas.pydata.org/
- It works especially well with tabular data (similar to Excel tables)
- Built on NumPy, with seamless integration into the Python data ecosystem
- *pandas* is the de facto standard for working with tabular data in Python

Core *pandas* Structures

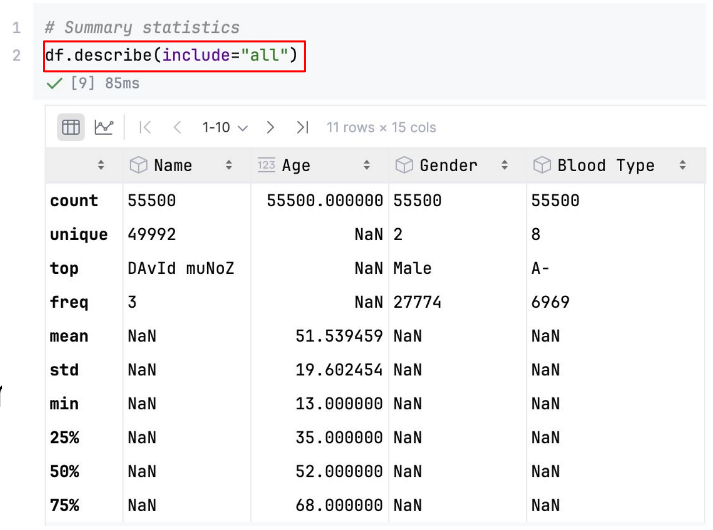
- Series:
  - One-dimensional labeled array (like a single column)
- DataFrame:
  - Two-dimensional table with rows and columns
  - Each row = one patient record
  - Each column = one variable (e.g., patient ID, gender, admission date)
- pandas makes it easy to filter, merge, and summarize datasets



	Column 0	Column 1	Column 2
0	Value	Value	Value
1	Value	Value	Value
2	Value	Value	Value

Exploring DataFrames

- Always start with a data overview:
  - `df.head()` → first few rows
  - `df.info()` → datatypes, missing values, number of rows
  - `df.describe()` → summary stats (mean, mi max, outliers)
- To check completeness, detect errors early, understand dataset scope

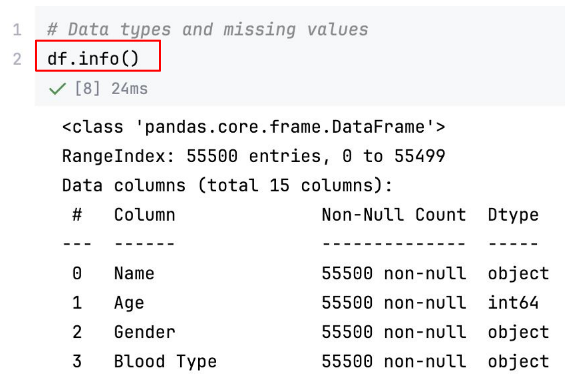


```
# Summary statistics
df.describe(include="all")
```

✓ [9] 85ms

1-10 | 11 rows × 15 cols

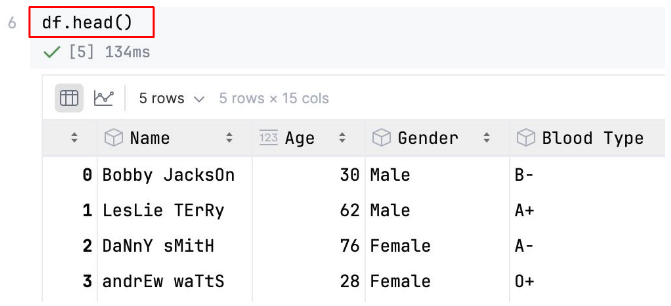
	Name	Age	Gender	Blood Type
count	55500	55500.000000	55500	55500
unique	49992	NaN	2	8
top	DAvId muNoZ	NaN	Male	A-
freq	3	NaN	27774	6969
mean	NaN	51.539459	NaN	NaN
std	NaN	19.602454	NaN	NaN
min	NaN	13.000000	NaN	NaN
25%	NaN	35.000000	NaN	NaN
50%	NaN	52.000000	NaN	NaN
75%	NaN	68.000000	NaN	NaN



```
# Data types and missing values
df.info()
```

✓ [8] 24ms

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 55500 entries, 0 to 55499
Data columns (total 15 columns):
 #   Column              Non-Null Count  Dtype
---  ------              --------------  -----
 0   Name                55500 non-null  object
 1   Age                 55500 non-null  int64
 2   Gender              55500 non-null  object
 3   Blood Type          55500 non-null  object
```



```
df.head()
```

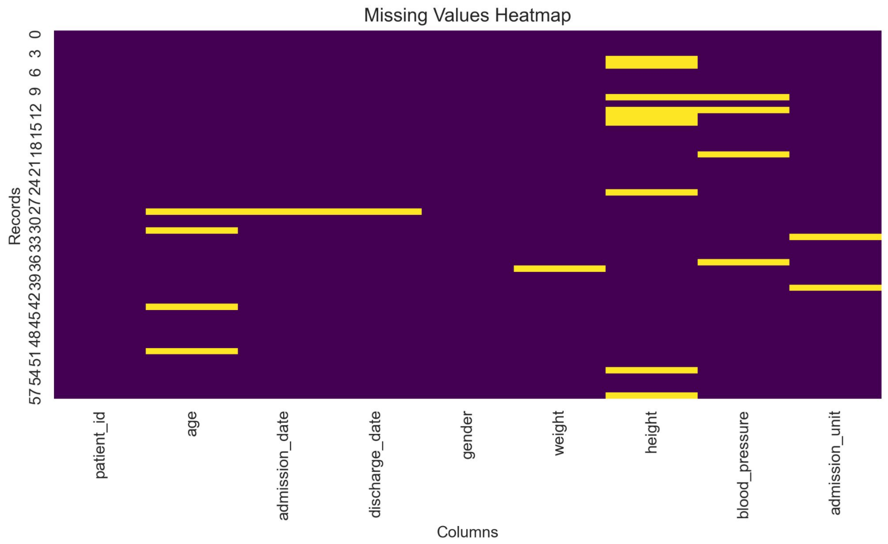
✓ [5] 134ms

5 rows | 5 rows × 15 cols

	Name	Age	Gender	Blood Type
0	Bobby JacksOn	30	Male	B-
1	LesLie TErRy	62	Male	A+
2	DaNnY sMitH	76	Female	A-
3	andrEw waTtS	28	Female	O+

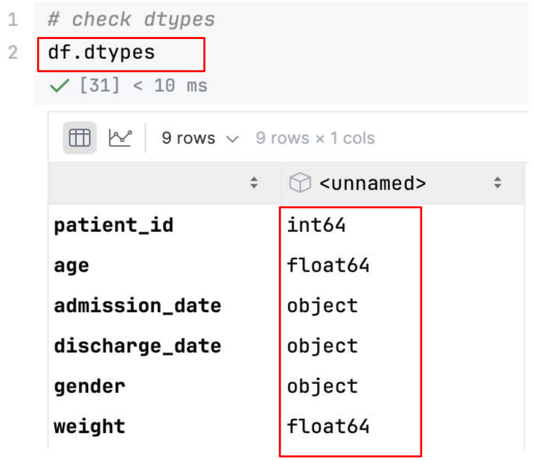
Visual Exploration

- Before and after cleaning, always explore your data visually
  - **Histograms** show distribution of numeric variables
  - **Boxplots** reveal outliers
  - **Missing value heatmaps** highlight gaps
- Visualizations make patterns and errors obvious, validate preprocessing decisions and detect mistakes



Step 1 - Data Cleaning: Handling Data Types

- Wrong data types lead to wrong results (e.g., dates or numbers stored as strings)
- Check data types
  - `df.dtypes`



```
# check dtypes
df.dtypes
✓ [31] < 10 ms
```

9 rows   9 rows × 1 cols

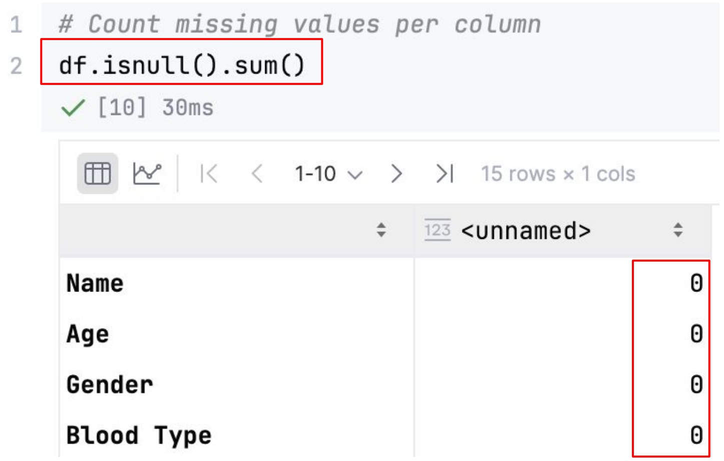
	<unnamed>
patient_id	int64
age	float64
admission_date	object
discharge_date	object
gender	object
weight	float64

- Convert types
  - Dates: `df['admission_date'] = pd.to_datetime(df['admission_date'])`
  - Numbers: `pd.to_numeric(df['age'], errors='coerce')`
- Medical example
  - Length of stay = discharge date – admission date → only works if dates are datetime

Handling Missing Data

- Why it matters in clinical data
  - Missingness is extremely common (e.g., missing labs, unrecorded weight)
  - Ignoring missing data can bias results

- How to detect missing values
  - `df.isnull().sum()` → count missing values per column



```
# Count missing values per column
df.isnull().sum()
```

✓ [10] 30ms

1-10 15 rows × 1 cols

```
             <unnamed>
Name                 0
Age                  0
Gender               0
Blood Type           0
```

Handling Missing Data

- How to handle them
  - Remove incomplete rows

    `df.dropna(subset=['admission_date'])`
  - Impute missing values
    - Median age for missing age values

      `df['age'].fillna(df['age'].median(), inplace=True)`
    - Forward-fill for longitudinal time series data

      `df.fillna(method='ffill')`

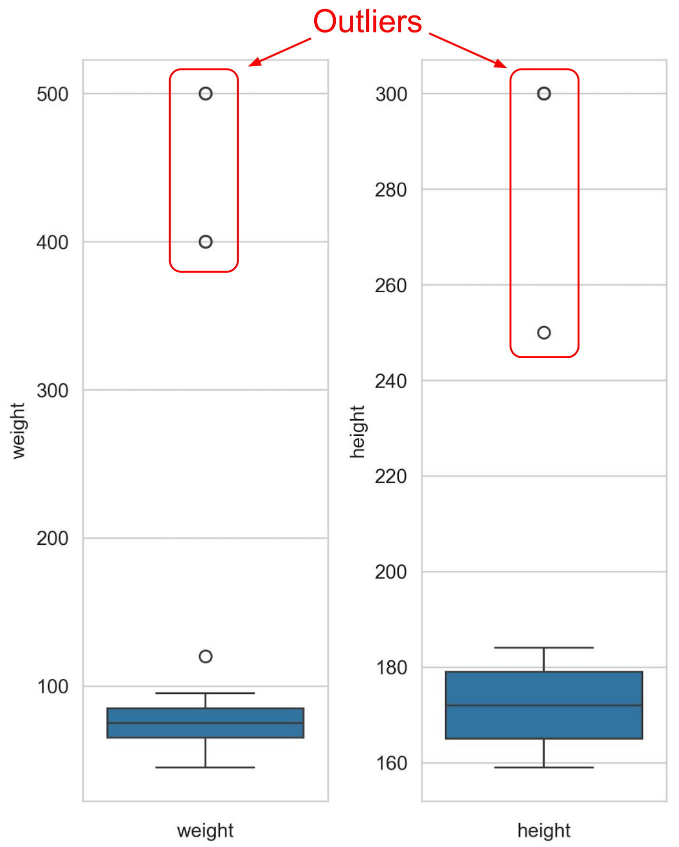
➔ **Strategy depends on clinical context (don't blindly fill!)**

Types of Missing Data

- **MCAR** (Missing Completely At Random):
  - No relationship to other data
  - **Example**: a lab machine randomly fails for some patients
- **MAR** (Missing At Random):
  - Related to other variables
  - **Example**: cholesterol missing more often in younger patients
- **MNAR** (Missing Not At Random):
  - Depends on the unobserved value itself
  - **Example**: patients with very high BMI avoid reporting weight
- Visualization helps to detect patterns of missingness help distinguish between MCAR, MAR, and MNAR

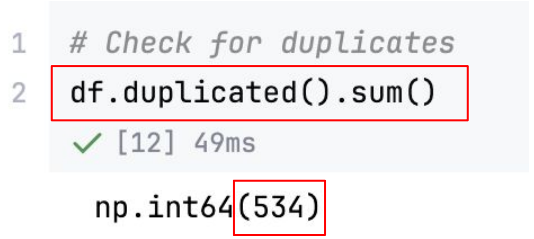
Handling Outliers

- Outliers may represent errors (e.g., weight = 500 kg), or real but rare events (e.g., extremely high BP in ICU)
- Detect with pandas
  - `df['weight'].describe()` → min, max, quartiles
- Visualization: `sns.boxplot(x=df['weight'])`
- Possible strategies
  - Exclude implausible values (clear errors)
  - Cap extreme but possible values
  - Keep rare but clinically valid cases (flag them for review)



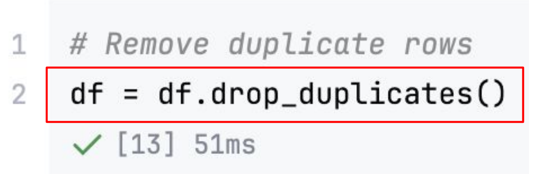
Handling Duplicates

- Why it matters in medicine
  - Duplicate patient records can lead to double-counting
  - Example: a patient transferred between units may appear multiple times
- Detect duplicates
  - `df.duplicated().sum()` → count duplicates
- Remove duplicates
  - `df.drop_duplicates(inplace=True)`
- Decision needed
  - sometimes duplicates are real (e.g., re-admissions) → check clinical logic



```
# Check for duplicates
df.duplicated().sum()
✓ [12] 49ms

np.int64(534)
```



```
# Remove duplicate rows
df = df.drop_duplicates()
✓ [13] 51ms
```

Step 2 - Data Integration – Merging Data Sources

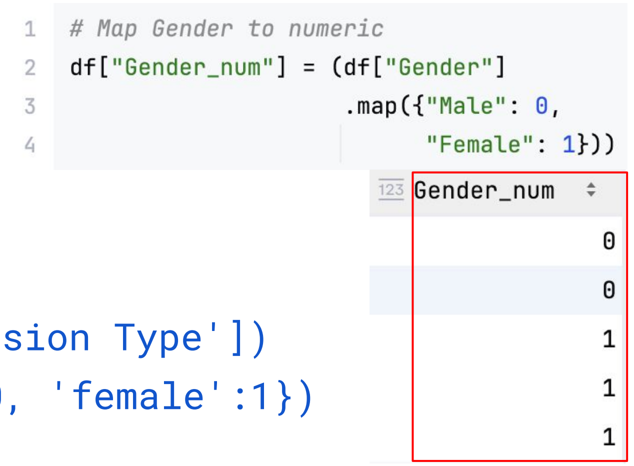
- Why it matters
  - Clinical data often comes from **multiple systems** (labs, ICU, billing)
  - Must be merged for meaningful analysis
- *pandas* merge
  - `df.merge(labs, on='patient_id', how='left')`
- Join types
  - Inner: only patients with labs
  - Left: keep all patients, add lab values if available
- **Challenges**
  - Different schemas (column names, formats)
  - Patient matching (IDs, pseudonyms)
  - Conflicts in values

Step 3 - Data Transformation - Feature Engineering

- Transform raw data into features that have (clinical) meaning
- Examples
    - New features: `df['BMI'] = df['weight'] / (df['height']/100)**2`
    - Group and summarize: `df.groupby('admission_unit')['age'].mean()`
    - Pivot tables: `df.pivot_table(index='admission_unit', values='albumin_g_dl', aggfunc='mean')`
- Why it matters
    - Provides variables clinicians understand (BMI instead of raw height & weight)
    - Can improve model accuracy by encoding medical knowledge
    - Enhances interpretability for clinical decision-making

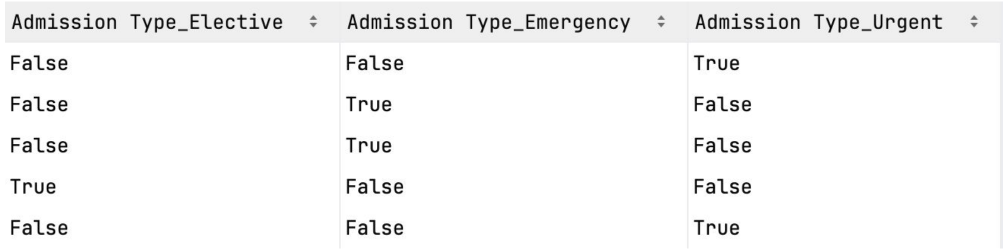
Encoding Categorical Data

- ML Algorithms require numbers, not text
- Check categories
  - `df['gender'].unique()`
- Encoding
  - One-hot encoding: `pd.get_dummies(df['Admission Type'])`
  - Binary mapping: `df['gender'].map({'male':0, 'female':1})`
  - Label encoding: `LabelEncoder().fit_transform(df['column_name'])`
- Medical examples
  - Admission type: elective, Emergency, urgent
  - → one-hot encoded for analysis



```
# Map Gender to numeric
df["Gender_num"] = (df["Gender"]
                    .map({"Male": 0,
                          "Female": 1}))
```

```
Gender_num
         0
         0
         1
         1
         1
```



Admission Type_Elective	Admission Type_Emergency	Admission Type_Urgent
False	False	True
False	True	False
False	True	False
True	False	False
False	False	True

Scaling & Standardization

- Why it matters
  - Lab values, vital signs, and scores are measured in different units
  - Scaling ensures comparability across features (e.g., blood pressure vs. albumin)
- Min-Max scaling → rescales values to [0, 1]

```
from sklearn.preprocessing import MinMaxScaler
df['bp_scaled'] = MinMaxScaler().fit_transform(df[['blood_pressure']])
```

- Standardization (Z-score) → mean = 0, std = 1

```
from sklearn.preprocessing import StandardScaler
df['age_scaled'] = StandardScaler().fit_transform(df[['age']])
```

Step 4 - Data Reduction - Filtering & Subsetting Data

- **Reducing features**
  - High-dimensional data → harder to analyze, risk of overfitting
  - Reduction strategies:
    - Drop irrelevant variables
    - Correlation analysis (drop highly correlated features)
    - Dimensionality reduction (PCA)
- **Subsetting**
  - Focus on relevant patient groups for analysis
  - Examples:
    - Patients with diabetes who attended follow-up
    - Patients above 65 years admitted in winter months
  - Enables targeted, clinically relevant analyses

Key Takeaways

- → **Preprocessing** is critical for reliable analysis and safe use of AI in medicine
- → **Visualization** is essential to detect hidden problems
- → **Missing data** handling must consider the clinical context
- → **Outliers** may be errors or clinically meaningful extremes — treat carefully
- → **Feature engineering, scaling,** and **encoding** prepare data for valid analysis
- → Always **document** your decisions to ensure **reproducibility** and **trustworthiness**