Clinical Data Extraction and Analysis

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Contents

1 Introduction

This project focuses on extracting, cleaning, and integrating data from multiple datasets, each with a different format. The first step involves extracting the data from each source and merging them into a unified structure. Given the diversity of formats, harmonization techniques will be applied to ensure consistency and compatibility across the datasets.

Once merged, the data will undergo a thorough cleaning process to address issues such as missing values, duplicates, and outliers. Following this, feature engineering and selection techniques will be applied to retain the most relevant attributes for model training, ensuring efficiency and performance.

The project will also explore various machine learning algorithms, selecting the most appropriate models based on the task's objectives. The ultimate goal is to develop a robust predictive model that can provide actionable insights and drive data-driven decisions.

2 Data Exploration and Initial Function Implementation

2.1 Data Exploration

To begin, I carefully examined the content of each dataset to understand its structure and identify potential challenges. For this, I developed a function that reads datasets in CSV format, checks for columns matching specific keywords, and provides an overview of their structure.

Overview of GSE6008_metadata.csv:

```
Found the following matching columns:
['characteristics_ch1.0.tumor_type', 'characteristics_ch1.1.stage',
 'characteristics_ch1.12.cel_file_name', 'contact_name', 'type',
 'source_name_ch1', 'characteristics_ch1.2.grade']
```

This function enabled me to quickly assess the dataset's structure and identify key columns that needed further attention or standardization. It also helped me spot any inconsistencies in column names or identify areas that required harmonization.
To further refine the dataset, I developed an additional function called `see_value`. This function displays the unique values in a specified column of a DataFrame, which is helpful for detecting patterns, categories, or inconsistencies that need to be addressed during the data cleaning process.
This function aids in exploratory data analysis by providing insights into the variations present in the dataset, ensuring that all necessary transformations or standardizations are applied before merging and harmonizing the datasets.

2.2 Functions for Data Standardization

To efficiently extract critical information from the datasets, I implemented a combination of string operations and **regular expressions** (regex). This method proved particularly effective in handling data inconsistencies and the varying formats across the datasets. Given that key information such as age, sex, stage, grade, cancer type, sample type, and

tumor subtype were not consistently located in the same columns or presented in a uniform format, I developed specialized functions tailored for extracting each specific type of data.
The use of **regular expressions** allowed for the identification and extraction of relevant patterns within the textual data. This approach ensured that even when information was stored in different formats or spread across multiple columns, it could still be systematically retrieved. For instance, age and sex were extracted through regex patterns that matched numerical values or specific keywords, while stage and grade were identified through pattern matching within descriptive text.
By creating dedicated functions for each type of data (age, sex, stage, grade, cancer type, sample type, and tumor subtype), I ensured that each piece of information was processed independently but consistently. These functions were tailored to accommodate the unique structure and irregularities of the datasets, making the extraction process both *flexible* and *adaptable*.

```
def standardize_age(df, input_column_name):
    df['Age'] = df[input_column_name].apply(
        lambda text: re.search(r'(\d+(\.\d+)?)', str(text)).group(1)
        if re.search(r'(\d+(\.\d+)?)', str(text)) else 'NA')
    return df

def standardize_cancer_type(df, input_column_name):
    df['Cancer Type'] = df[input_column_name].apply(
        lambda text: 'Ovarian Cancer' if 'ovarian' in str(text).lower()
        else 'Breast Cancer' if 'breast' in str(text).lower()
        else 'NA')
    return df
```

Listing 1: Examples of Data Standardization Functions

This modular approach ensures that:

- Functions can be reused across multiple datasets.
- Consistent outputs are generated regardless of the input format.
- Data is preprocessed systematically for further analysis.

3 Extraction and Merging

3.1 Extraction

After identifying relevant columns in the datasets, I applied the standardization functions to extract and harmonize the data. Below is an example of how these functions were applied to the first dataset:

```
df1 = standardize_cancer_type(df1, 'source_name_ch1')
df1 = standardize_tumour_subtype(df1, 'description')
df1 = standardize_stage(df1, 'characteristics_ch1.1.stage')
df1 = standardize_sample_type(df1, 'description')
df1 = standardize_grade(df1, 'characteristics_ch1.2.grade')

df1 = df1[['Cancer Type', 'Tumour Subtype', 'Stage', 'Sample Type', '
    Grade']]
```

Listing 2: Example of Data Standardization

This results in a DataFrame containing the relevant features needed for further analysis. This process is repeated for each dataset.

3.2 Merging

After processing all datasets, they were merged into a single DataFrame using the `pd.concat` function from the `pandas` library. The following code demonstrates how we merge the datasets: .

```
merged_df = pd.concat([df1, df2, df3, df4, df5, df6, df7, df8],
    ignore_index=True, sort=False)
```

Listing 3: Merging Process

Additionally, we create a new column `Patient ID` that uniquely identifies each row in the merged DataFrame. The `Patient ID` is generated using a simple formatting approach to ensure consistent numbering:

```
merged_df['Patient ID']=[f"{i:03}" for i in range(1, len(merged_df)+1)]
```

4 Standardization

4.1 Methodology for Column Standardization

The aim of using functions for column standardization is to transform raw data into a consistent format that is suitable for data analysis and machine learning. Each function is designed to apply specific transformations tailored to each column's content, ensuring uniformity and proper handling of missing or inconsistent values. By standardizing the data, we make it more reliable and comparable, thus enabling more accurate analysis and modeling.
Here an example of one of the functions :

```
def standardize_stage_grade(df, column):
    standard_map = {
        '1': 'I', '2': 'II', '3': 'III', '4': 'IV',
        'I': 'I', 'II': 'II', 'III': 'III', 'IV': 'IV',
        'early': 'I', 'advanced': 'IV', 'high': 'IV',
        'benign': 'NA', 'borderline': 'NA', 'microinvasion': 'NA',
        'NA': 'NA'
    }
    df[column] = df[column].replace(standard_map)
    df[column] = df[column].where(df[column].isin(['I', 'II', 'III', 'IV
        ', 'NA']), 'NA')
    return df
```

4.2 Key Points of the Method

Use of Functions:
To standardize the columns, we use dedicated functions, each designed to address specific

challenges presented by the dataset. These functions systematically clean, format, and structure the data, as described below:

- **Modularity:** Each function operates independently, ensuring that changes to one function do not impact others. This modular approach provides flexibility for maintenance and improvement.
- **Reusability:** The same functions can be applied across multiple datasets with similar structure, promoting consistency and reducing the need for redundant code.
- **Reliability:** The functions are designed to handle edge cases and errors, such as missing values or inconsistencies in the raw data. By systematically cleaning the data, we reduce the risk of errors in the analysis or modeling steps.

Benefits Using dedicated functions for column standardization offers several key benefits:

- **Data Consistency:** Standardization ensures that all data across different datasets is aligned in terms of format and structure, making it easier to compare and analyze.
- **Improved Data Quality:** By addressing missing or inconsistent data, we enhance the quality of the dataset. This improves the robustness of any subsequent analysis or predictive modeling.
- **Preparedness for Analysis and Modeling:** Once standardized, the data is ready for advanced processing, including machine learning and statistical analysis. Well-structured data enables more effective use of analytical tools and algorithms.

To give you a quick look at the first few rows of the dataset, here is an image showing the head of the dataset:

	Patient ID	Age	Sex	Stage	Grade	Cancer Type	Sample Type	Tumour Subtype
0	001	NA	NA	III	III	Ovarian cancer	NA	clear cell
1	002	NA	NA	IV	III	Ovarian cancer	NA	clear cell
2	003	NA	NA	I	III	Ovarian cancer	NA	clear cell
3	004	NA	NA	I	NA	Ovarian cancer	NA	clear cell
4	005	NA	NA	II	NA	Ovarian cancer	NA	clear cell
5	006	NA	NA	I	NA	Ovarian cancer	NA	clear cell
6	007	NA	NA	I	NA	Ovarian cancer	NA	clear cell
7	008	NA	NA	I	NA	Ovarian cancer	NA	clear cell
8	009	NA	NA	IV	III	Ovarian cancer	NA	endometrioid
9	010	NA	NA	I	I	Ovarian cancer	NA	endometrioid

Figure 1: Head of the dataset showing the first few rows.

5 Data Processing

The data processing phase is critical to ensuring that the dataset is in the best possible shape for machine learning model training. This involves a combination of statistical methods, rule-based approaches, and exploratory data analysis (EDA) techniques to clean and preprocess the data. The ultimate goal is to improve the dataset's quality and completeness, facilitating accurate and reliable model building.The iterative nature of this process ensures that each step builds upon the previous one, leading to a robust final dataset ready for advanced modeling and analysis.

5.1 Inspecting the Data

Before initiating the cleaning process, it is essential to thoroughly examine the dataset to verify its structure, consistency, and quality. Specifically, the following tasks were performed:

- Checking for mislabeled data or feature-column misalignments.
- Identifying columns with missing values or inconsistent formats.
- Identifying rows with many missing values or inconsistent formats.

For the columns :

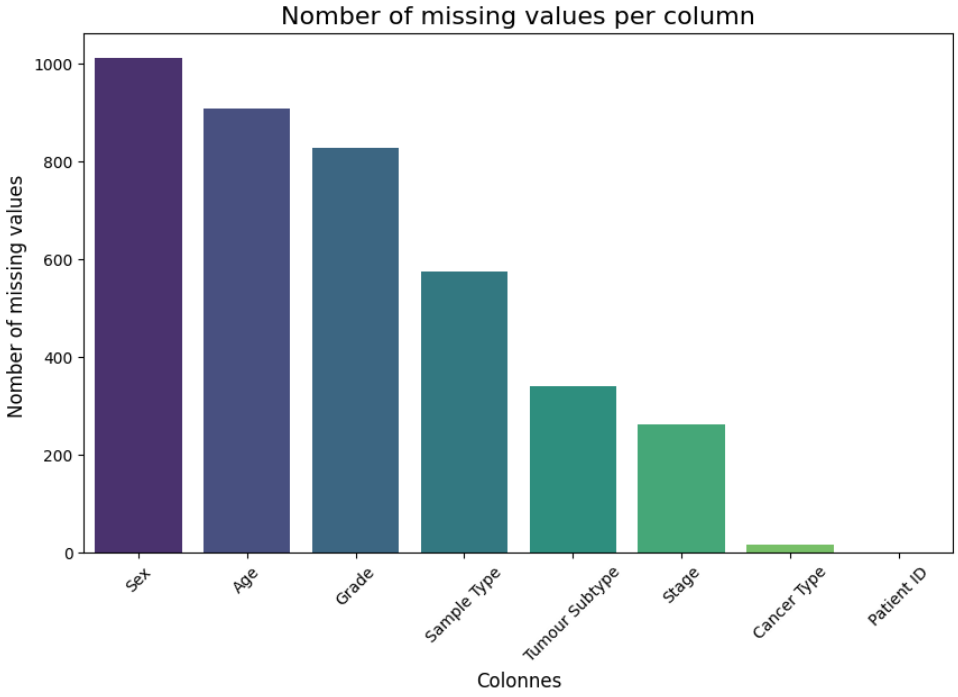


Figure 2: Number of missing values per column in the dataset.

5.2 Handling Missing Values

Dealing with missing values is a crucial step to ensure the dataset's completeness. Two main strategies were employed based on the extent and nature of missingness:

- **Imputation:** Missing values were filled using statistically methods, such as:
  - Mean or median imputation for numerical columns.
  - Mode imputation for categorical features.
- **Removal:** Rows with excessive missing data (e.g., more than 60%) were dropped to avoid introducing noise into the analysis.

```
data['missing_count'] = (data == 'NA').sum(axis=1)
rows_with_many_na = data[data['missing_count'] > 5]
data= data[data['missing_count'] <= 6]
data=data.drop(columns=["missing_count"])
```

Listing 4: Counting and removing missing values

	Patient ID	Age	Sex	Stage	Grade	Cancer Type	Sample Type	Tumour Subtype	missing_count
99	100	NA	NA	NA	NA	NA	normal	NA	6
100	101	NA	NA	NA	NA	NA	normal	NA	6
101	102	NA	NA	NA	NA	NA	normal	NA	6
102	103	NA	NA	NA	NA	NA	normal	NA	6
600	601	NA	NA	NA	NA	NA	NA	NA	7
601	602	NA	NA	NA	NA	NA	NA	NA	7
602	603	NA	NA	NA	NA	NA	NA	NA	7

Figure 3: Rows with many missing values.

5.3 Column-Specific Imputation Strategies

Gender (`Sex`)

- Missing values in the `Sex` column were filled with "Female" for rows where `Cancer Type` was "Ovarian Cancer," as this cancer exclusively affects women, we can see that out of 1012 'NA' values, it has been reduced to 590.
- For remaining rows with missing values, "Female" was also inferred since the dataset contains no records of male patients and that breast cancer can occur in men about 1% of cases so we can almost **certainly** deduce that the presence of male patients is **negligible** for our analysis.

Age

- A median-based imputation was performed, grouping patients by `Cancer Type` and `Stage`. This approach ensures that the imputation is contextually relevant, reflecting both the cancer type and the stage of the disease. By grouping the data in this way, we capture the nuances specific to each cancer classification, which leads to more accurate and realistic imputations compared to global methods like the overall median. This method was selected after testing several combinations, and it provided the best results in maintaining the integrity of the data for further analysis.

- The number of missing values for age has been reduced to 804, but it's still quite high, so I decided to use **the median** for the rest of the missing values. I chose the median because it is less affected by extreme values (**outliers**) in the dataset compared to the mean. For instance, there are patients with very high ages (e.g., 89), the median would still more accurately reflect the central tendency of the data than the mean.

And this is the result **(it is not the final version, as after handling all the other columns, we will redo it and notice a significant improvement.)**:

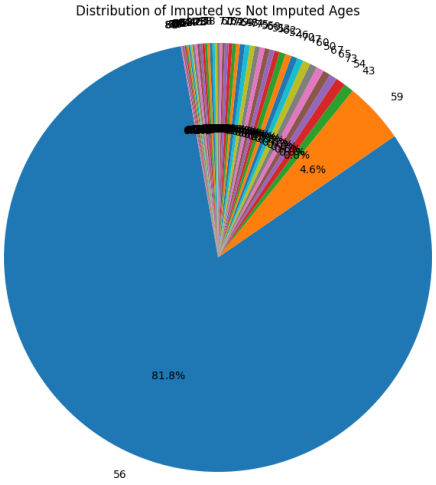


Figure 4: The age after the imputation

Cancer Type

This column has the fewest missing values (14). Below is a review of the rows with missing values.

	Patient ID	Age	Sex	Stage	Grade	Cancer Type	Sample Type	Tumour Subtype
99	100	56	Female	NA	NA	NA	normal	NA
100	101	56	Female	NA	NA	NA	normal	NA
101	102	56	Female	NA	NA	NA	normal	NA
102	103	56	Female	NA	NA	NA	normal	NA
231	232	56	Female	NA	NA	NA	normal	NA
232	233	56	Female	NA	NA	NA	normal	NA
233	234	56	Female	NA	NA	NA	normal	NA
234	235	56	Female	NA	NA	NA	normal	NA
235	236	56	Female	NA	NA	NA	normal	NA
236	237	56	Female	NA	NA	NA	normal	NA
237	238	56	Female	NA	NA	NA	normal	NA
238	239	56	Female	NA	NA	NA	normal	NA
239	240	56	Female	NA	NA	NA	normal	NA
240	241	56	Female	NA	NA	NA	normal	NA

Figure 5: The rows where the cancer type is missing

- Given the data, where the “Cancer Type” is missing and the “Sample Type” is "normal", these samples are from non-cancerous tissue. This suggests that the “Cancer Type” for these rows might not be directly relevant because the samples are not from tumor tissue. I’m going to classify these samples under a general category such as “Non-Cancerous” for this column. This would help in distinguishing these samples from those that are cancerous.

- It is reasonable to leave the Grade and Stage columns as NA because these values are typically associated with tumor characteristics, which are not applicable to normal tissue samples. However, for the Tumour Subtype column, it would not be appropriate to fill in values such as “serous”, “endometrioid”, “mucinous”, “clear cell”, “ductal”, “lobular”, or “apocrine” because these subtypes are specific to tumor tissues.

Sample Type

The method I used to impute missing values in the Sample Type column leverages existing data patterns and relationships in other columns such as Tumour Subtype, Cancer Type, Stage, and Grade. It’s a rule-based method (it can be wrong, but I created a function to easily change the rules later; in this case, I deduced them through web research, such as this article: [1].
Here’s the function I used :

```
def impute_sample_type(row):
    if row['Sample Type']=='NA':
        # Impute based on Tumour Subtype
        if row['Tumour Subtype'] in ['clear cell', 'serous', '
           endometrioid', 'ductal', 'lobular', 'apocrine']:
            return 'primary tumour'

        # Imputation based on Cancer Type, Stage, and Grade
        if row['Cancer Type'] == 'Breast cancer' or row['Cancer Type']
           == 'Ovarian cancer' :
            if row['Stage'] in ['III', 'IV'] or row['Grade'] == 'III':
                return 'primary tumour'
            elif row['Stage'] == 'I' and row['Grade'] == 'I':
                return 'normal'
        return row['Sample Type']
    return row['Sample Type']

data['Sample Type'] = data.apply(impute_sample_type, axis=1)
```

Explanation:

- Imputation Based on Tumour Subtype: Tumour subtypes often provide direct insight into whether the sample is from a primary tumour or normal tissue. Given that subtypes like clear cell, serous, and others are typically associated with tumour samples, imputing Sample Type as primary tumour for these subtypes is logical and contextually appropriate.

- Imputation Based on Cancer Type, Stage, and Grade: Both Stage and Grade are critical factors in determining the progression of cancer. Advanced stages (III and IV) and high Grades (like Grade III) are generally associated with more aggressive forms of cancer, which are usually represented by primary tumour samples.

Conversely, early-stage and low-grade cancers often correlate with normal tissue or benign states. This distinction is important in ensuring that the imputation reflects the biological reality of the cancer's progression.

5.3.1 Stage

I have developed a rule-based approach also to predict the stage of cancer using the "Sample Type" and "Tumour Subtype" columns. This method is based on general biological insights related to tumor characteristics and can be adapted and improved through expert feedback.
- **Sample Type:** Information such as "normal" or "primary tumour" can provide clues about the stage. For example, "normal" samples are often associated with "NA" (not applicable) stages, whereas "primary tumour" samples may correspond to stages I to IV.
- **Tumour Subtype:** Subtypes like "serous" or "clear cell" might indicate advanced stages (e.g., III or IV), while subtypes like "mucinous" might be associated with early stages (e.g., I or II).
This method provides an approximation and should be validated by medical professionals to ensure its accuracy. While I am not an expert in oncology, I am open to modifying these rules based on input from specialists and additional data. For more information on the relationships between sample types, tumor subtypes, and cancer staging, I referred to [2] , [3] and [4].

5.3.2 Grade

Tumour subtypes are classifications based on specific biological features of the tumour cells. Certain subtypes are generally associated with particular grades. For instance:

- **Serous Tumours:** In ovarian cancer, high-grade serous carcinomas are the most common and are typically associated with Grade III due to their aggressive nature. In breast cancer, serous carcinomas are rare but also tend to be high-grade.
- **Endometrioid Tumours:** These can vary in grade. In ovarian cancer, endometrioid tumours are often found in lower grades (Grade I or II) but can also present as high-grade.
- **Clear Cell Tumours:** These are generally high-grade and aggressive in both ovarian and breast cancers, often associated with Grade III due to their poor prognosis.

Some tumour subtypes are more aggressive and thus may be associated with Grade III, while others may be more indolent and associated with Grade I or II.

5.3.3 Bonus

I noticed that in some DataFrames, there was a description related to the aggressiveness of a condition, which could help in filling out the grade column. I extracted this information from the initial notebook during data extraction and set it aside. Then, I placed this extracted information into a new DataFrame and used it to fill in the missing grade values. Finally, I replaced the modified rows in my main DataFrame using the Patient ID as a reference.
The new column, **description**, contains two values: "low malignant potential" and "invasive". These values can be used to infer the grade:

- **Low malignant potential:** Typically associated with lower grades (Grade I or II).
- **Invasive:** Generally associated with higher grades (Grade III).

We can observe that the number of missing values has decreased from 828 to 691, which is a significant improvement.

5.3.4 Tumour Subtype

The **Tumour Subtype** was predicted using a rule-based method, leveraging known associations between **Cancer Type**, **Stage**, **Grade**, and **Sample Type**. Here's the reasoning behind the rules applied:

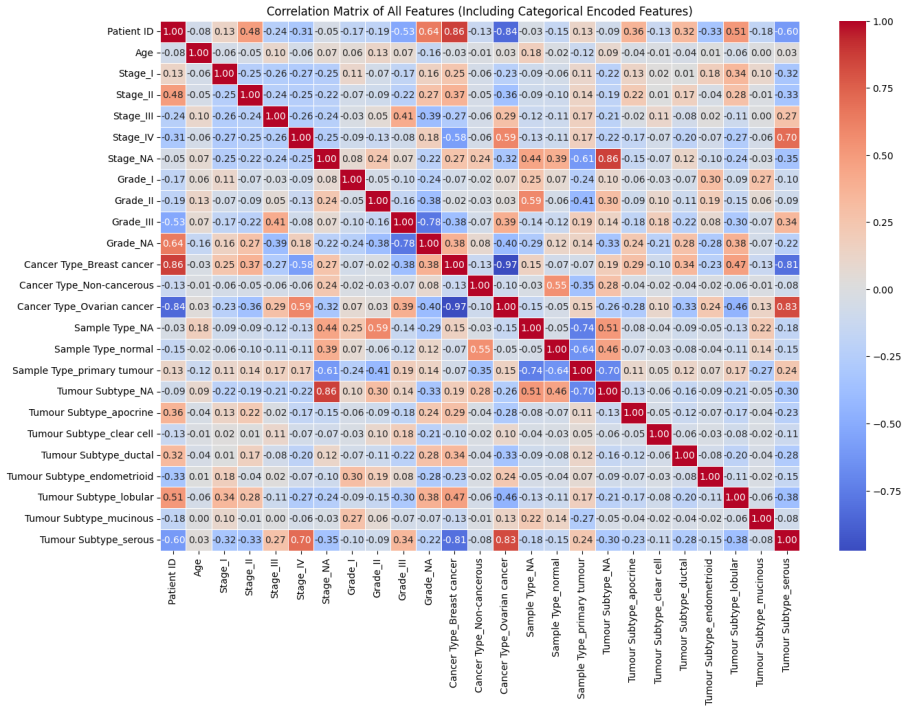
- **Cancer Type:** Specific cancers are associated with certain subtypes. For example:
  - **Ovarian Cancer** is commonly linked with subtypes like **serous**, **endometrioid**, and **clear cell**.
  - **Breast Cancer** is usually associated with **ductal** and **lobular** subtypes.
- **Stage:** The stage of cancer often indicates its aggressiveness. Late-stage cancers (Stage III or IV) are typically more aggressive and may correspond to specific subtypes like **serous** or **mucinous**.
- **Grade:** High-grade tumours are often more aggressive and can be linked to subtypes like **serous** or **clear cell**.

By following these steps, I ensure that the dataset is clean, consistent, and ready for analysis. The handling of missing data is an essential part of the data preprocessing pipeline, and by systematically applying the appropriate methods, I can ensure that the dataset is suitable for building reliable and accurate machine learning models.

6 Feature Selection

6.1 Correlation Matrix Analysis

To assess the relationships between all features in the dataset, we compute the correlation matrix. The process followed is outlined below:
First, since the correlation matrix only works with numeric values, we convert all categorical features into binary variables using **one-hot encoding**. This technique creates a new column for each unique value in a categorical feature, where the column contains 1 for the presence of the value and 0 for its absence. This allows us to include categorical features in the correlation analysis.
Once all the features are numeric (either from the original numerical columns or the newly created binary columns for categorical data), we calculate the correlation matrix.



Strong Relationships with Cancer Type:

- **Cancer Type_Breast cancer and Cancer Type_Ovarian cancer**: Strong negative correlation (-0.97), reflecting the exclusivity between these two cancer types.
- **Cancer Type_Breast cancer and Age**: Moderately positive correlation (0.66), suggesting that patients with breast cancer in this dataset tend to be older, on average.

Relationships with Cancer Stages:

- **Stage_I and Stage_IV**: Moderately negative correlation (-0.37), indicating a low overlap between patients diagnosed at these extreme stages.
- **Stage_I and Cancer Type_Ovarian cancer**: Negative correlation (-0.36), suggesting that ovarian cancer cases are more likely to be diagnosed at an advanced stage.

Relationships between Tumour Subtypes:

- **Tumour Subtype_ductal and Tumour Subtype_mucinous**: Negative correlation (-0.33), suggesting that these subtypes rarely occur together.
- **Tumour Subtype_serous and Cancer Type_Ovarian cancer**: Strong positive correlation (0.80), which is consistent, as the serous subtype is often associated with ovarian cancer.

Relationships between Cancer Grades:

- **Grade_III and Grade_I**: Moderately negative correlation (-0.22), indicating that extreme grades rarely appear together in the same patient.

- **Grade_III and Age**: Moderately positive correlation (0.30), suggesting that higher grades are more common in older patients.

Other Notable Relationships:

- **Sample Type_normal and Sample Type_primary tumour**: Strong negative correlation (-0.74), as a sample cannot be both normal and tumour tissue for the same patient.
- **Sample Type_primary tumour and Tumour Subtype_serous**: Moderately positive correlation (0.35), indicating that primary tumour samples are more often associated with the serous subtype.

The correlation matrix provides an overview of the relationships between the dataset's features. While some correlations are intuitive, they also offer valuable analytical insights for exploring associations between cancer types, tumour subtypes, and other demographic factors. Further analyses, such as statistical models and dimensionality reduction techniques, could be employed to examine these relationships in greater detail.

7 Model Selection

After performing imputation to handle the missing values in the dataset, we proceed to build machine learning models to predict these missing values. As shown in the analysis, the **Grade** and **Stage** columns have the highest number of missing entries, making them the primary focus for imputation through predictive modeling [5].

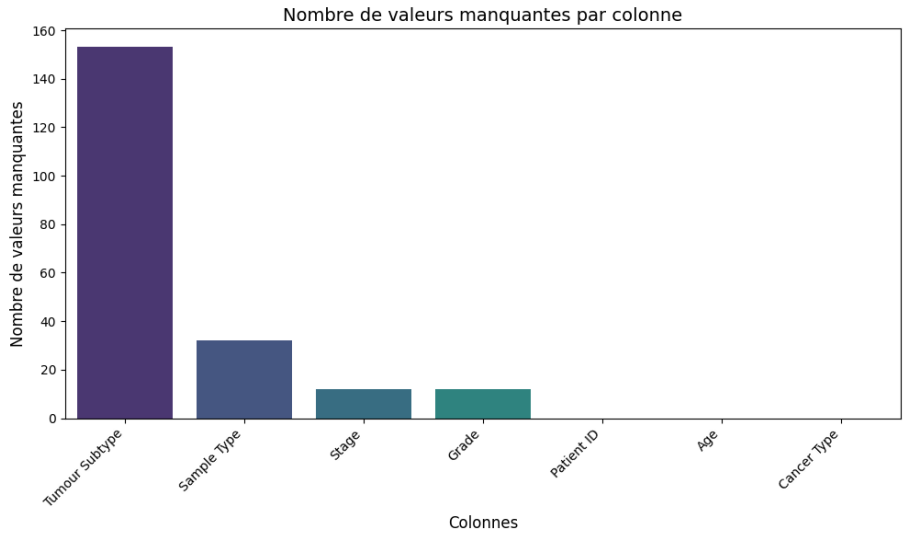


Figure 6: Missing values after imputation

For each of these columns, the following approach will be taken:

7.0.1 Target Variable Identification:

First, we identify the missing target variables, which in this case are the **Grade** , **Tumour Subtype** and **Stage** columns. These columns represent critical features in understanding the cancer progression and are thus essential for accurate model training and prediction.

7.0.2 Separation of Data:

The dataset was split into two subsets:

-DataWithoutGrade(e.g stage,Tumour Subtype): Contains rows where the **Grade** column has missing values.
-DataWithGrade(e.g stage,Tumour Subtype): Contains rows where the **Grade** column has valid values.

7.0.3 Feature Engineering:

After separating the data, we prepared the features for the model:
-**Feature Selection**: The dataset was split into features (X) and target variable (y) for rows with valid **Grade** values. The **Patient ID** and **Sex** column was excluded as it is not relevant for predictive modeling.
-**One-Hot Encoding**: Categorical variables such as **Stage**, **Cancer Type**, **Sample Type**, and **Tumour Subtype** were encoded using `OneHotEncoder`. This technique converts categorical features into binary columns, ensuring that the machine learning models can handle them effectively.

7.0.4 Model Selection and Evaluation:

We explore several machine learning algorithms to predict the missing values in these two columns, including:

- **Random Forests:** A powerful ensemble learning method that can model complex, non-linear relationships in the data. Random forests are particularly useful for handling both numerical and categorical variables and are known for their robustness in predicting missing values.
- **Gradient Boosting Machines (GBM):** A high-performance machine learning technique that builds models sequentially to correct the errors of previous models. GBMs, including **XGBoost** and **LightGBM**, are effective in capturing intricate patterns and are highly scalable.
- **Support Vector Machines (SVM):** SVM is a classification technique that finds the hyperplane which best separates the data into different classes.
- **K-Nearest Neighbors (KNN):** A non-parametric method that makes predictions based on the similarity between data points. KNN is straightforward and interpretable, often used when the relationship between features is not well-defined.
- **Decision Tree Classifier:** A decision tree builds a model by recursively splitting the data based on feature values. It is intuitive and provides clear decision rules.

After training the machine learning models, their performance was evaluated using the accuracy metric. The steps for model evaluation are outlined below:

1. **Training the Model:** Each model was trained on the training dataset ($X_{\text{train}}, y_{\text{train}}$) using the `fit` method, which allows the model to learn the underlying patterns from the features and the target variable (i.e., the **Grade** column).

2. **Prediction:** After training, the models were used to predict the target variable (**Grade**) on the test set (X_{test}) using the `predict` method. The predicted values (y_{pred}) were compared to the true values in the test set.

3. **Accuracy Calculation:** The performance of each model was assessed using the accuracy score, which measures the proportion of correct predictions made by the model. The accuracy score was calculated using the `accuracy_score` function from the `sklearn.metrics` module.

4. **Model Comparison:** For each model, the accuracy score was printed, and the model that achieved the highest accuracy was selected as the best-performing model. If the accuracy of a new model was higher than the current best, it replaced the previous model as the top performer.

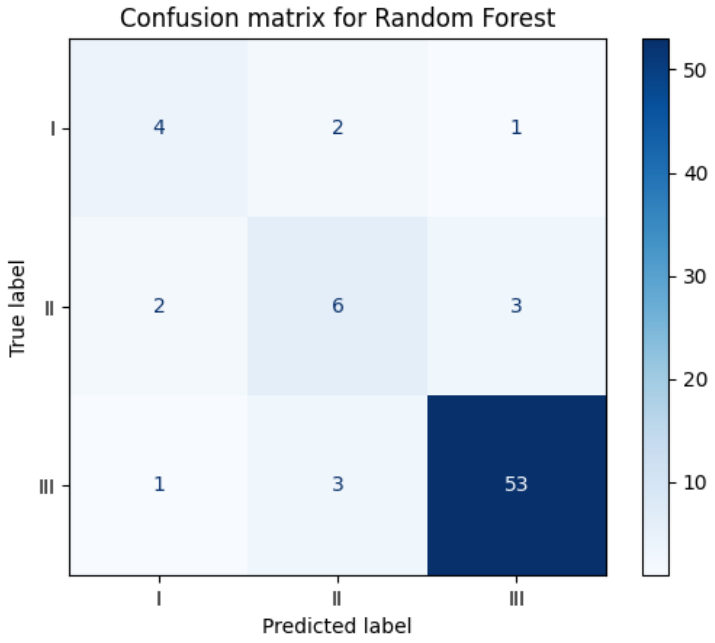
5. **Best Model Selection:** After evaluating all models, the one with the highest accuracy was chosen as the final model for imputing missing values in the **Grade** column.

The final outcome of this evaluation :
-Grade: The best model is: Random Forest with an accuracy of 0.84.

Model	**Accuracy**
Random Forest	0.84
Gradient Boosting	0.81
Logistic Regression	0.83
Support Vector Machine	0.76
K-Nearest Neighbors	0.77
Decision Tree	0.83

Table 1: Model Accuracy Comparison for the Grade

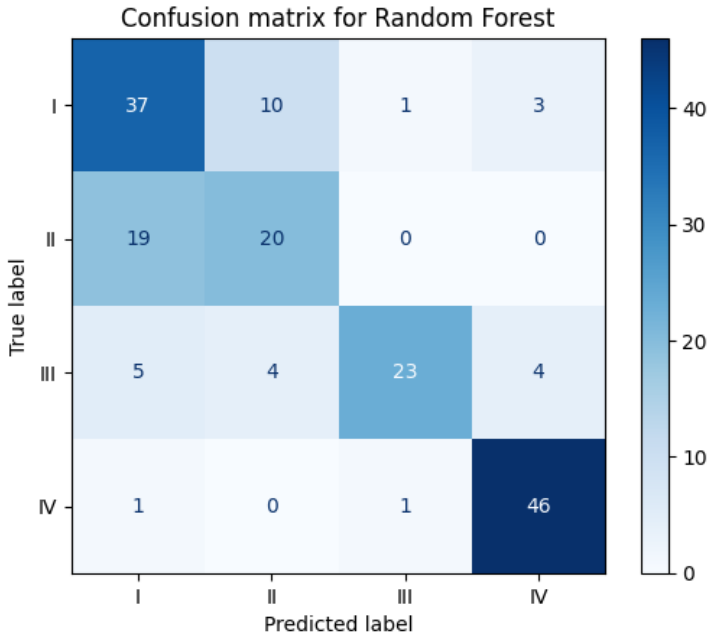
Here's its **Confusion Matrix** :



Model	Accuracy
Random Forest	0.72
Gradient Boosting	0.72
Support Vector Machine	0.29
K-Nearest Neighbors	0.67
Decision Tree	0.72

Table 2: Model Accuracy Comparison (Second Set)

-Stage: The best model is: Random Forest with an accuracy of 0.72.
Here's its **Confusion Matrix** :

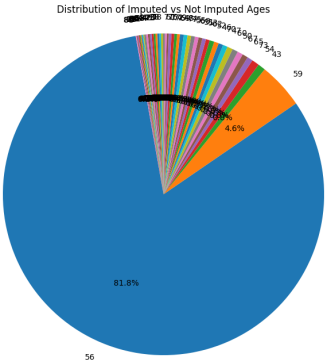


By implementing these machine learning models, we aim to predict the missing values in the **Grade** and **Stage** columns effectively, ensuring the dataset is complete and ready for downstream analysis.

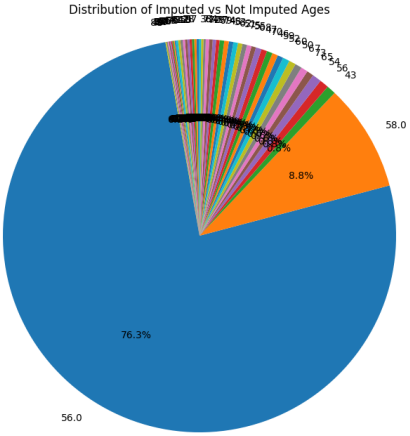
8 Enhancing Our Data

When working with the `Age` variable, we initially handled missing values by imputing them based on the `Cancer Type` and `Stage`. This initial method provided a basic approach to fill in the missing values. However, it was clear that this approach needed further refinement to ensure more precise and robust results for subsequent analyses. To better handle missing data and improve the overall model performance, we decided to refine our imputation strategy. We will now redo the imputation with a more sophisticated approach, leveraging additional insights from the new dataset.

We can observe that the percentage for 56 has decreased, while the percentage for 58 has increased.



[nitial Imputation]



[Improved imputation with refined dataset]

Figure 7: Comparison of imputation methods for the Age variable. On the left, the initial imputation. On the right, the improved imputation strategy using a more refined dataset.

9 Conclusion

In this analysis, we explored various approaches to data imputation, harmonization, and predictive modeling applied to clinical data from breast and ovarian cancer studies. By leveraging advanced machine learning techniques, including Random Forests, Gradient Boosting, and Logistic Regression, we aimed to uncover valuable insights.

Throughout the process, we observed how different models perform in terms of predictive accuracy, highlighting the importance of carefully selecting and fine-tuning algorithms to best suit the complexity of clinical datasets. The methods used for handling missing data, such as imputation based on patient characteristics and cancer subtypes, proved essential in improving the quality and robustness of our predictions.

Our analysis underscores the need for continuous innovation in data science, particularly in the healthcare sector, where the potential for predictive models to influence clinical decisions is immense. Moving forward, further enhancements in data processing techniques, as well as the incorporation of additional features like genetic markers and treatment responses, could further improve model accuracy and applicability in real-world scenarios.

In conclusion, this work not only contributes to our understanding of cancer prediction models but also emphasizes the importance of data quality and methodological rigor in achieving reliable, actionable insights in clinical research.

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