



Data Collection and Preprocessing Phase

Date	09 July 2024
Team ID	740024
Project Title	Evolving efficient classification patterns in Lymphography
Maximum Marks	6 Marks

Data Exploration and Preprocessing Template

Dataset variables will be statistically analyzed to identify patterns and outliers, with Python employed for preprocessing tasks like normalization and feature engineering. Data cleaning will address missing values and outliers, ensuring quality for subsequent analysis and modeling, and forming a strong foundation for insights and predictions.





Section	Description





```
Attribute information:
 --- NOTE: All attribute values in the database have been entered as
            numeric values corresponding to their index in the list
            of attribute values for that attribute domain as given below.

    class: normal find, metastases, malign lymph, fibrosis
    lymphatics: normal, arched, deformed, displaced

 3. block of affere: no, yes
 4. bl. of lymph. c: no, yes
 5. bl. of lymph. s: no, yes
 6. by pass: no, yes
 B, regeneration of: no, yes
9. early uptake in: no, yes
10. lym.nodes dimin: 0-3
11. lym.nodes enlar: 1-4
12. changes in lym.: bean, oval, round
13. defect in node: no, lacunar, lac. marginal, lac. central

    changes in node: no, lacunar, lac. margin, lac. central
    changes in stru: no, grainy, drop-like, coarse, diluted, reticular,
stripped, faint,

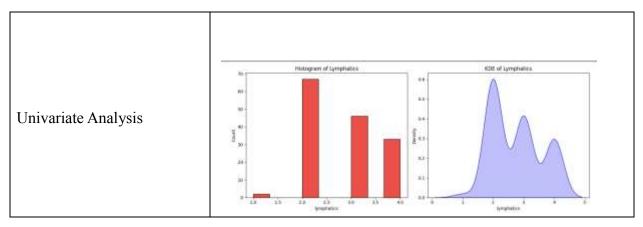
16. special forms: no, chalices, vesicles
17. dislocation of: no, yes
18. exclusion of no: no, yes
19. no. of nodes in: 0-9, 10-19, 20-29, 30-39, 40-49, 50-59, 60-69, >=70
Missing Attribute Values: None
Class Distribution:
                Number of Instances:
Class:
 normal find: 2
 malign lymph: 61
 fibrosis:
```

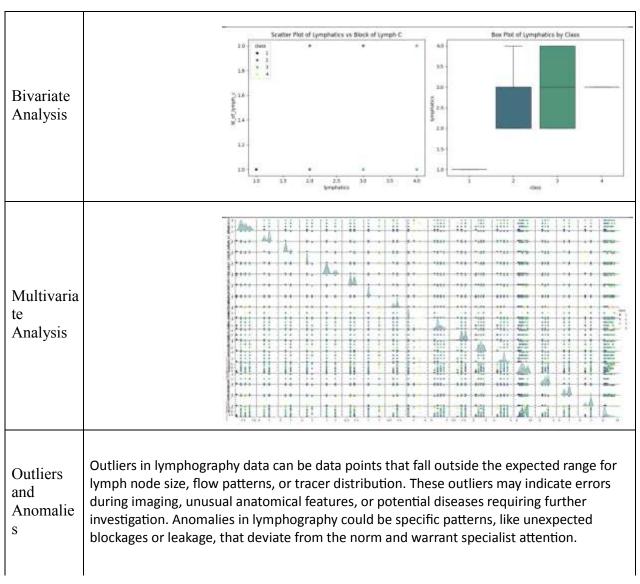
Data Overview

Dimension: 614 rows × 13 columns Descriptive statistics













Data Preprocessing Code Screenshots df = pd.read_csv("https://archive.ics.uci.edu/nl/machine-learning-databases/lymphography/lymphography.data",names= Loading Data df.head()

Handling Missing	No missing attributes
Data	

Data Transformation	<pre>column_names = ["class", "lymphatics", "block of affere", 'bl of lymph c", "bl of lymph s", 'by pass", "extravasates", regeneration of", 'early uptake io", "lym nudes dimin", 'lym nodes enlar", 'changes in lym , "defect in mode", 'changes in mode", 'changes in stru", "special forms', "dislocation of", "exclusion of no", 'no of nodes in'] data.columns = column_names</pre>
Feature Engineering	Attached the codes in final submission.
Save Processed Data	Done