

Detection and Analysis of


Polycystic Ovary Syndrome


Data Science Boot Camp


Ethan Bootehsaz, Kaiyuan Ma, Joy Wang, Aaron Yang


04/02/2024


Created a Repository


**Analysis-and-Detection-of-PCOS** Public


 Unpin


 Unwatch 1


 Fork 0


 Star 0



 main

 3 Branches


 0 Tags














 Add file

 Code

**ebootehsaz** update readme 


055be89 · 9 minutes ago


 21 Commits


 .github/workflows	Modded tests	8 hours ago
 Kaggle_Data	Original data	4 days ago
 data	First clean processed data	4 days ago
 logs	Changed data flow structure	8 hours ago
 src	Changed data flow structure	8 hours ago
 .gitignore	modded .gitignore	8 hours ago
 LICENSE	Initial commit	4 days ago
 Makefile	Changed data flow structure	8 hours ago
 PCOS dataset info.docx	First commit	4 days ago
 PCOSData.ipynb	First commit	4 days ago
 README.md	update readme	9 minutes ago
 requirements.txt	Changed data flow structure	8 hours ago
 start.sh	precedent for logging	4 days ago


About


Our goal is to develop a predictive model for the early detection of Polycystic ovary syndrome (PCOS) and infertility-related issues. We will evaluate the model's performance using standard metrics.


 Readme

 MIT license

 Activity

 0 stars

 1 watching

 0 forks

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Contributors

 2

Analysis-and-Detection-of-PCOS

Our goal is to develop a predictive model for the early detection of Polycystic ovary syndrome (PCOS) and infertility-related issues. PCOS is a complex hormonal disorder, and early diagnosis is crucial for effective management.

We will analyze the dataset to identify patterns and trends. We will develop a model that can predict the likelihood of PCOS and infertility-related issues. We will evaluate the model's performance using various metrics. We will present the results in a clear and concise manner.

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Presentation 1 (Progress Report)

- Explore the PCOS dataset to understand its structure and features.
- Identify missing values, outliers, and patterns in the data.
- Select relevant physical and clinical parameters for PCOS and infertility detection.
 - Assessment of Ovarian Reserve: AMH (Anti-Müllerian Hormone) levels give insight into the ovarian reserve, which is crucial for fertility.
 - Women with PCOS often have higher than normal AMH levels. This is because AMH is produced by the granulosa cells of ovarian follicles, and women with PCOS tend to have a higher number of small follicles in their ovaries.
- Perform any necessary preprocessing steps, such as handling missing values or encoding categorical variables.
- Choose appropriate machine learning models for binary classification (e.g., Logistic Regression)
- Formulate hypotheses related to PCOS and infertility based on the dataset.
- Create visualizations to support your findings.
- Generate tables/graphs to show the distribution of the target variable and key features.

Created a Project Board

The screenshot displays a Jira Project Board for the project '@Analysis and Detection of PCOS Board'. The interface includes a top navigation bar with the user 'eboothsaz', project name, and search functionality. Below this, the project name is repeated, followed by a tabbed interface showing different views: Backlog, Priority board, Team items, Roadmap, In review, My items, and a New view button. A filter bar allows searching by keyword or field, with a Discard button. The main area is divided into five columns representing the project workflow: Backlog, Ready, In progress, In review, and Done. Each column has a header with a status icon, count, and estimate, and a description. The Backlog column shows 'This item hasn't been started'. The Ready column shows 'This is ready to be picked up' and contains a draft item: 'Choose appropriate machine learning models for binary classification (e.g., Logistic Regression)'. The In progress column shows 'This is actively being worked on' and contains a draft item: 'Generate tables/graphs to show the distribution of the target variable and key features.' The In review column shows 'This item is in review' and contains two draft items: 'group columns that correlate with each other' and 'Select relevant physical and clinical parameters for PCOS and infertility detection.' The Done column shows 'This has been completed' and contains two draft items: 'Identify missing values, outliers, and patterns in the data.' and 'Perform any necessary preprocessing steps, such as handling missing values or encoding categorical variables.' Each column has a '+ Add Item' button at the bottom.

Navigation: eboothsaz / Projects / @Analysis and Detection of PCOS Board

Search: Type to search

Project: @Analysis and Detection of PCOS Board


Views: Backlog, Priority board, Team items, Roadmap, In review, My items, New view

Filter: Filter by keyword or by field

Columns:

- Backlog** (0/5, Estimate: 0): This item hasn't been started. + Add Item
- Ready** (1, Estimate: 0): This is ready to be picked up. + Add Item
 - Draft: Choose appropriate machine learning models for binary classification (e.g., Logistic Regression)
- In progress** (1/3, Estimate: 0): This is actively being worked on. + Add Item
 - Draft: Generate tables/graphs to show the distribution of the target variable and key features.
- In review** (2/5, Estimate: 0): This item is in review. + Add Item
 - Draft: group columns that correlate with each other
 - Draft: Select relevant physical and clinical parameters for PCOS and infertility detection.
- Done** (2, Estimate: 0): This has been completed. + Add Item
 - Draft: Identify missing values, outliers, and patterns in the data.
 - Draft: Perform any necessary preprocessing steps, such as handling missing values or encoding categorical variables.

Script to help get started

Analysis-and-Detection-of-PCOS / start.sh 



ebootehsaz precedent for logging

Code

Blame

Executable File · 15 lines (12 loc) · 453 Bytes

```
1  #!/bin/bash
2
3  # Check if the virtual environment already exists
4  if [ ! -d "dsbootcamp" ]; then
5      # Create a virtual environment named dsbootcamp if it doesn't exist
6      python3 -m venv dsbootcamp
7  fi
8
9  # Activate the virtual environment and install the required packages
10 source dsbootcamp/bin/activate
11 pip install -r requirements.txt >> logs/requirements.log 2>&1
12
13 # Pull updates from Git repository
14 echo "Pulling updates from Git repository..."
15 git pull
```

Files

main

Go to file

.github/workflows

Kaggle_Data

PCOS_data_without_infertility.xlsx

PCOS_infertility.csv

data

PCOS_infertility_processed.csv

PCOS_merged_processed.csv

PCOS_woinf_processed.csv

logs

src

__pycache__

constants.py

process_kaggle_data.py

utils.py

visualize_data.py

.gitignore

LICENSE

Makefile

PCOS dataset info.docx

PCOSData.ipynb

README.md

requirements.txt

start.sh

Analysis-and-Detection-of-PCOS / src / utils.py



ebootehsaz Changed data flow structure

Code

Blame

88 lines (77 loc) · 2.89 KB

```
1 import re
2 import pandas as pd
3 import os
4 from pandas import DataFrame
5
6 # This program defines utility functions to load, merge, and save data.
7
8 from constants import PCOS_woinf_filepath_page
9
10 def load_data(filepath: str) -> DataFrame:
11     """
12     Load data from a file path into a DataFrame.
13     Args:
14         filepath: str - file path to the data
15     Returns:
16         df - data loaded into a DataFrame
17     """
18     # Check if the file path exists
19     if not os.path.exists(filepath):
20         # remove ../ from the start of filepath
21         filepath = re.sub(r'\.\./', '', filepath)
22         if not os.path.exists(filepath):
23             raise FileNotFoundError(f"File path {filepath} does not exist.")
24
25
26 # They data is either in csv or excel format
27 if filepath.endswith('.csv'):
28     df = pd.read_csv(filepath)
29     df.attrs['file_path'] = filepath # Storing file path as an attribute
30 elif filepath.endswith('.xlsx'):
31     sheet_name = PCOS_woinf_filepath_page
32     df = pd.read_excel(filepath, sheet_name)
33     df.attrs['file_path'] = filepath # Storing file path as an attribute
34 else:
35     raise ValueError(f"File path {filepath} is not a csv or excel file.")
36
37 return df
38
```

Files

main

Go to file

- github/workflows
- Kaggle_Data
 - PCOS_data_without_infertility.xlsx
 - PCOS_infertility.csv
- data
 - PCOS_infertility_processed.csv
 - PCOS_merged_processed.csv
 - PCOS_woinf_processed.csv
- logs
- src
- __pycache__
 - constants.py
 - process_kaggle_data.py
 - utils.py
 - visualize_data.py
- .gitignore
- LICENSE
- Makefile
- PCOS dataset info.docx
- PCOSData.ipynb
- README.md
- requirements.txt
- start.sh

Code

Blame 69 lines (49 loc) · 2.38 KB

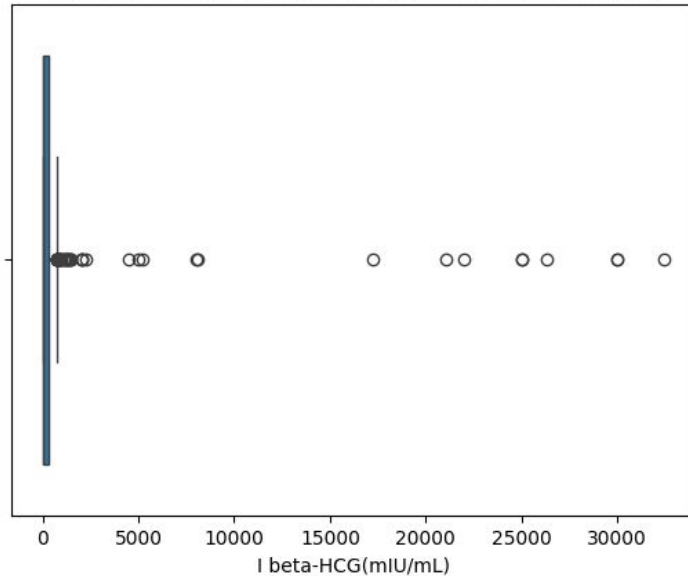
```
1 import re
2 from pandas import DataFrame
3
4 from constants import PCOS_inf_filepath, PCOS_woinf_filepath, \
5 PCOS_inf_processed_filepath, PCOS_woinf_processed_filepath, PCOS_merged_processed_filepath
6
7 from utils import load_data, merge_data, save_data_csv
8
9 # This program defines utility functions to process and clean data.
10
11 def process_data(df: DataFrame) -> DataFrame:
12     # Checking column names, missing values, duplicates
13     print(f'Columns in {df.attrs["file_path"]}:', df.columns)
14     print(f'Missing values in {df.attrs["file_path"]}: {df.isnull().sum()}')
15     print(f'Duplicates in {df.attrs["file_path"]}: {df.duplicated().sum()}')
16
17     # Dropping repeated/unnecessary columns
18     df = df.drop(['Unnamed: 44', 'Sl. No_wo', 'PCOS (Y/N)_wo', ' I beta-HCG(mIU/mL)_wo', 'II beta-HCG(mIU/mL)_wo', 'AMH(ng/mL)_wo'], axis=1, errors='ignore')
19
20     # Renaming column due to misspelling in original df
21     df.rename(columns={'Marraige Status (Yrs)': 'Marriage Status (Yrs)'}, inplace=True, errors='ignore')
22
23     # Fix column names - optional
24     df.columns = df.columns.str.strip() # .str.replace(' ', '_').str.lower()
25     df.columns = [re.sub(r'\s+', ' ', col).strip() for col in df.columns]
26
27     # Fix missing values
28     # Print out the first 5 missing rows for each column with missing values
29     # Find rows with missing data across any column
30     rows_with_missing_data = df[df.isnull().any(axis=1)]
31
32     # Display the rows with missing data if any
33     if not rows_with_missing_data.empty:
34         print("Rows with missing data:")
35         print(rows_with_missing_data)
36     else:
37         print("No missing data in any row.")
38
39     df = df.fillna('None')
40
41     # Drop duplicates
42     df = df.drop_duplicates()
43
44     # Take a random sample of the data
45     print(f'Sample of the data in {df.attrs["file_path"]}:', df.sample(5))
46
47     return df
48
```


Sample of data

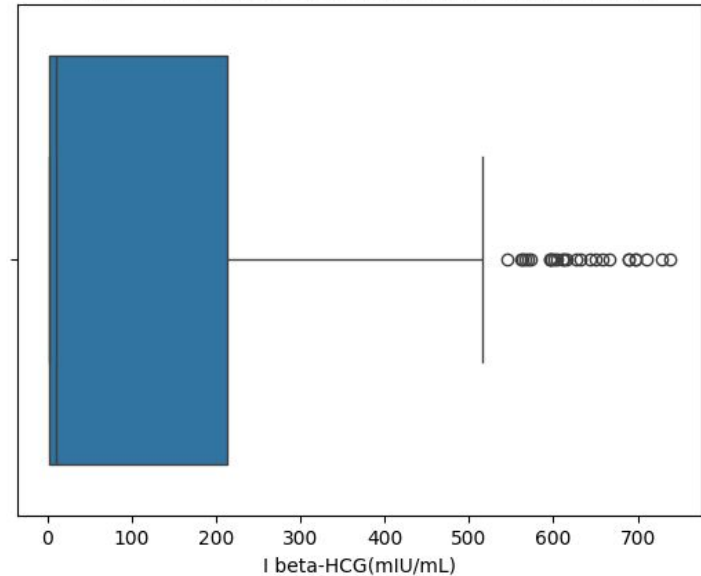
[illegible]

Boxplot of I beta-HCG (mIU/mL)

Boxplot of I beta-HCG(mIU/mL) before outlier removal

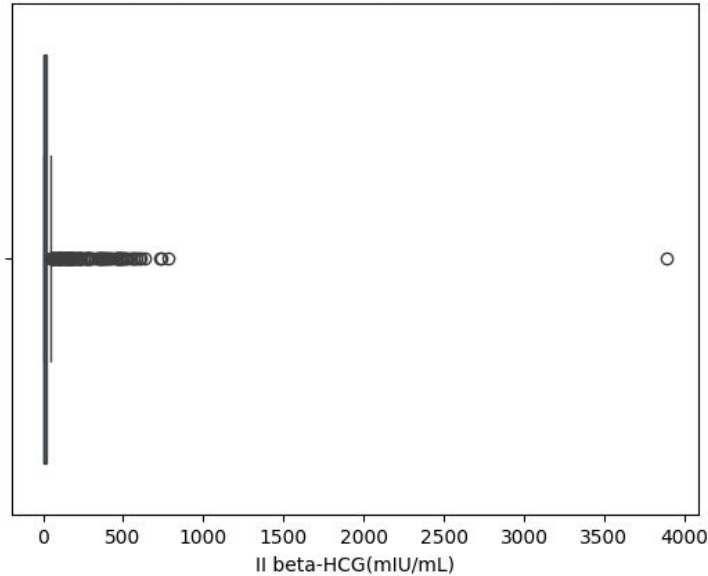


Boxplot of I beta-HCG(mIU/mL) after outlier removal

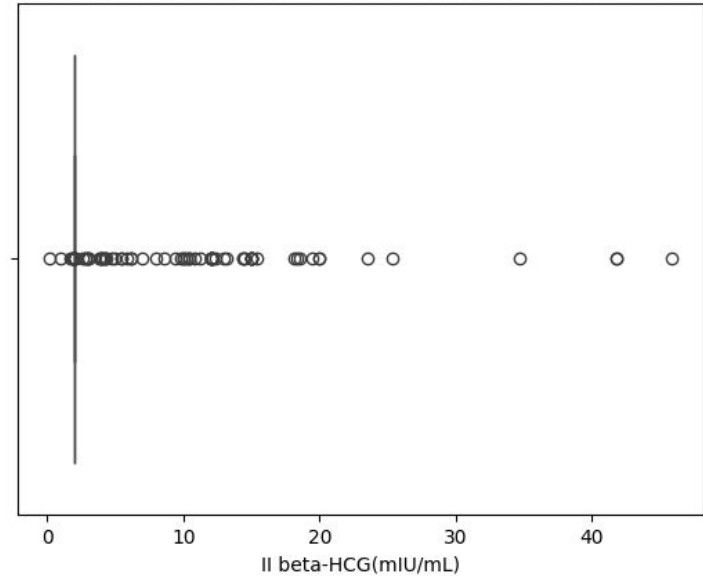


Boxplot II beta-HCG (mIU/mL)

Boxplot of II beta-HCG(mIU/mL) before outlier removal

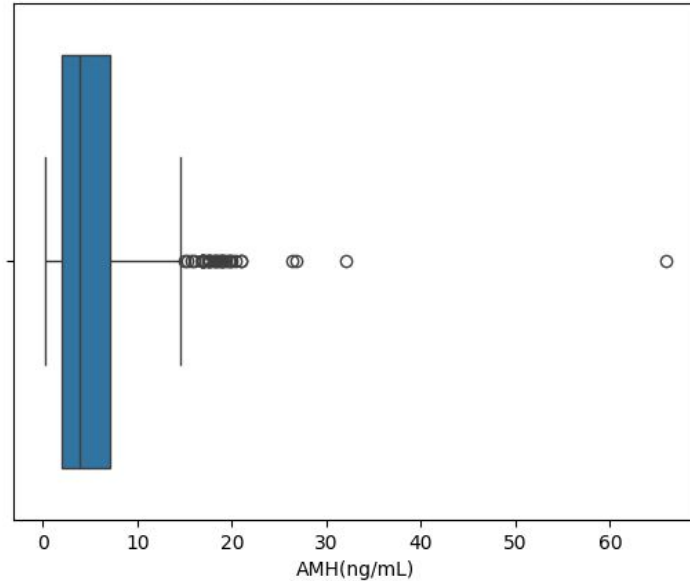


Boxplot of II beta-HCG(mIU/mL) after outlier removal

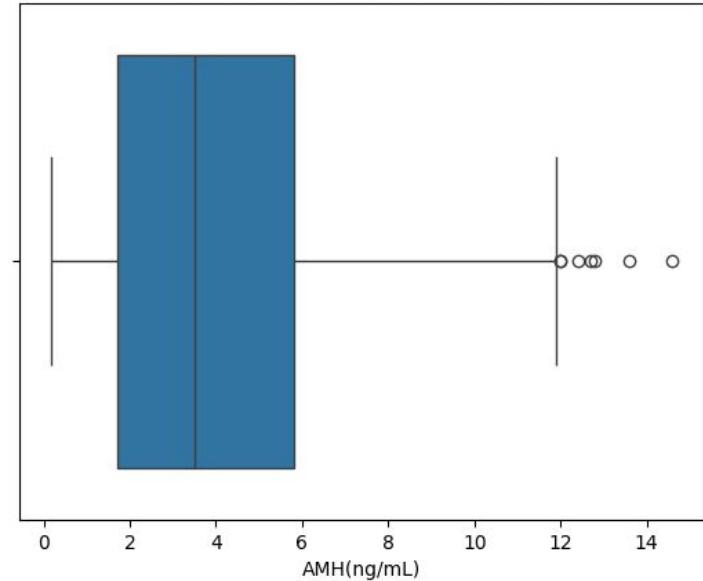


Boxplot of AMH (ng/mL)

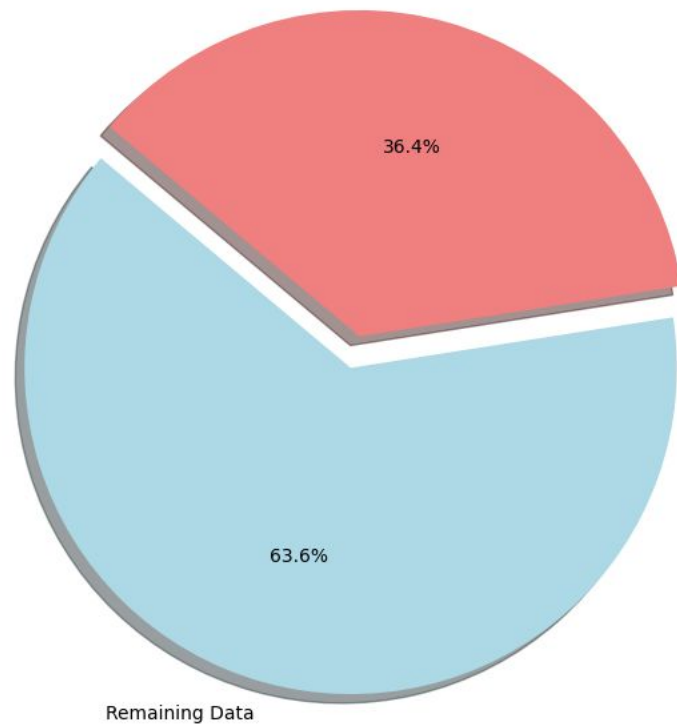
Boxplot of AMH(ng/mL) before outlier removal



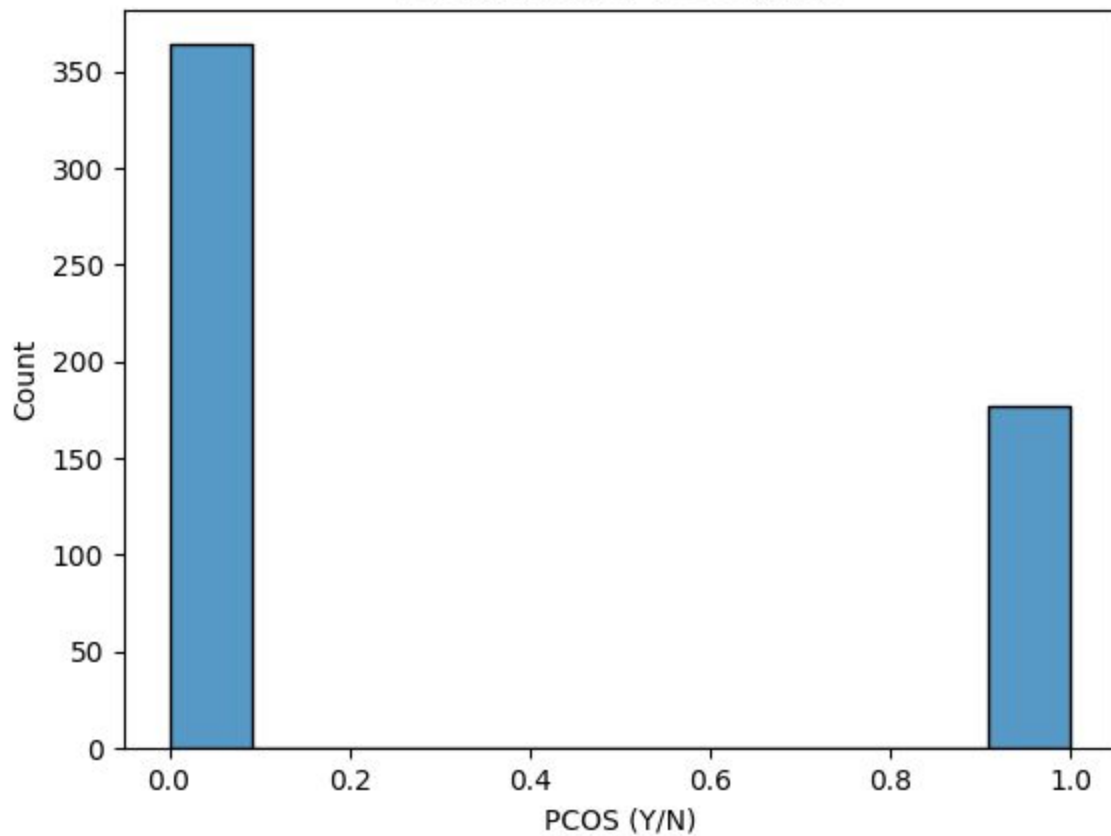
Boxplot of AMH(ng/mL) after outlier removal



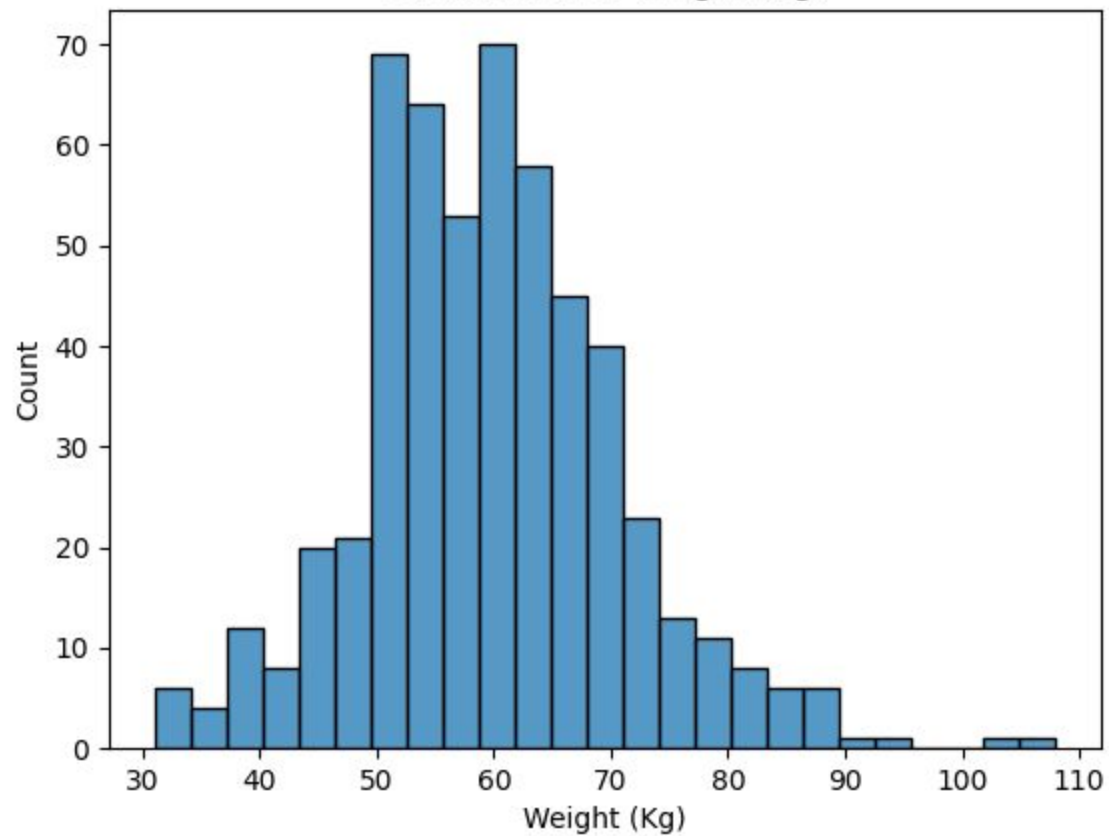
Percentage of Data Remaining vs. Removed Due to Outliers in Merged Dataset



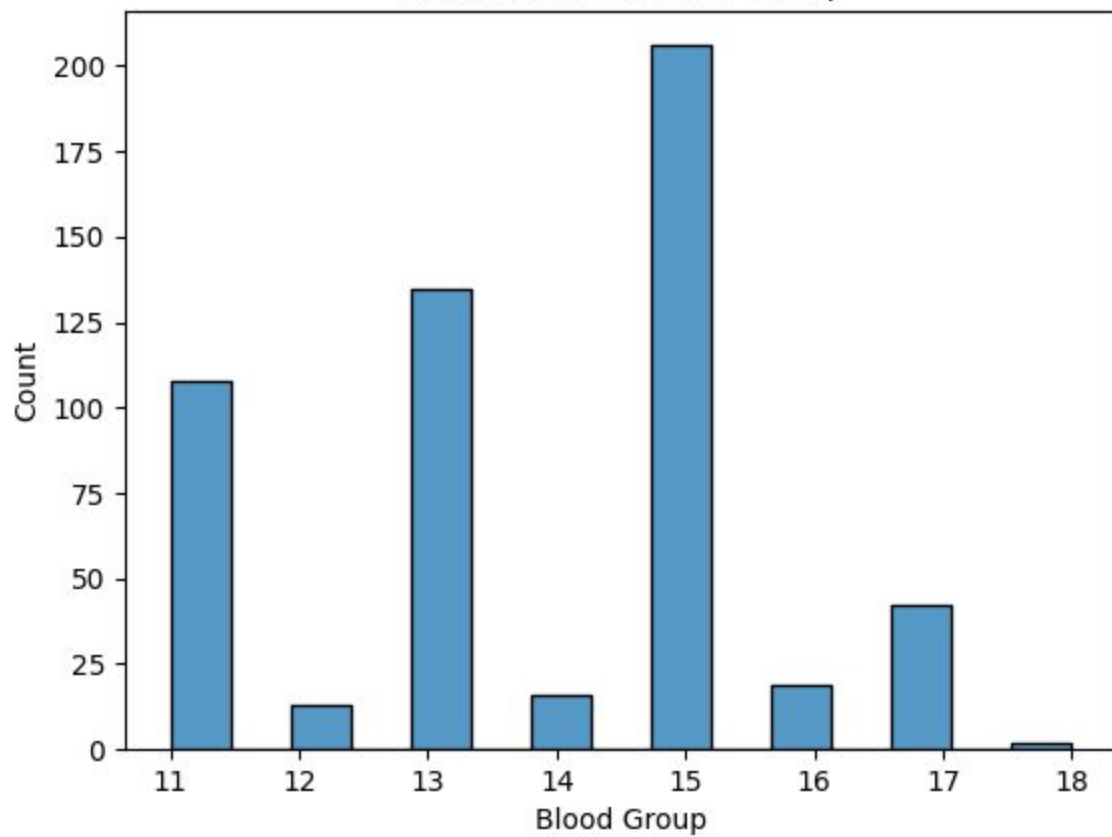
Distribution of PCOS (Y/N)

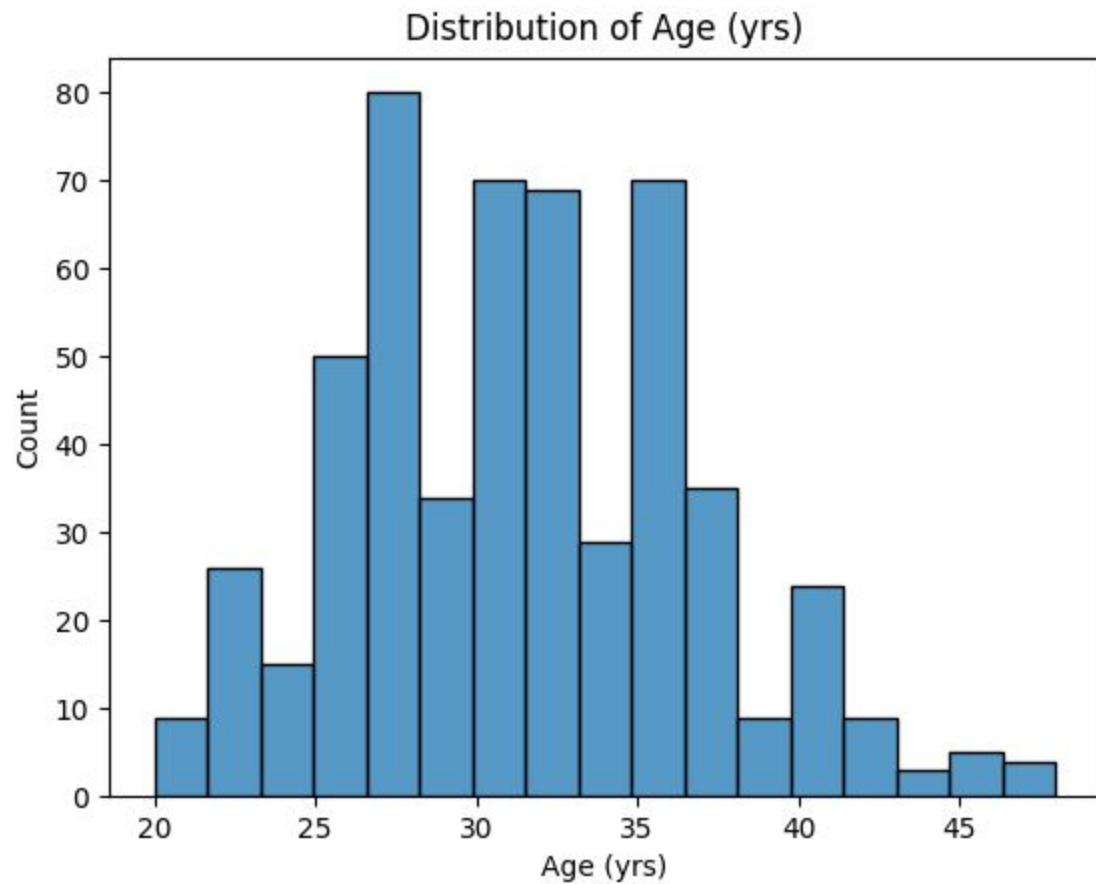


Distribution of Weight (Kg)

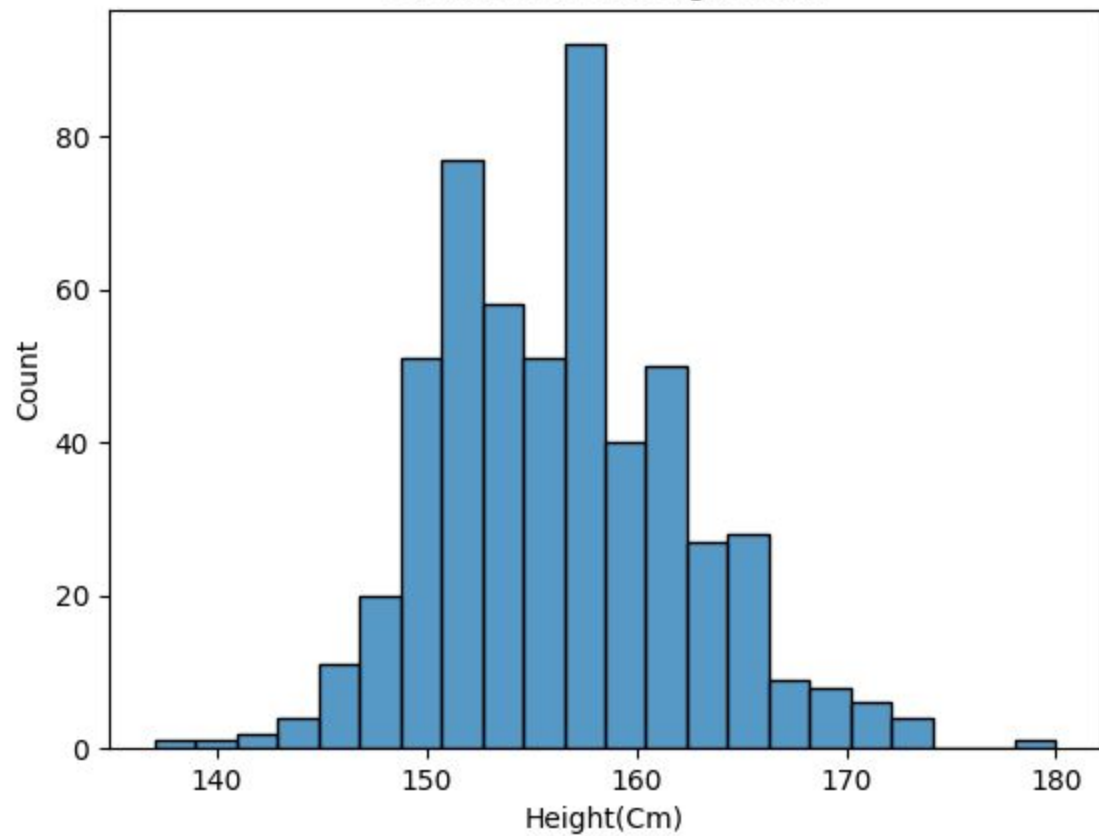


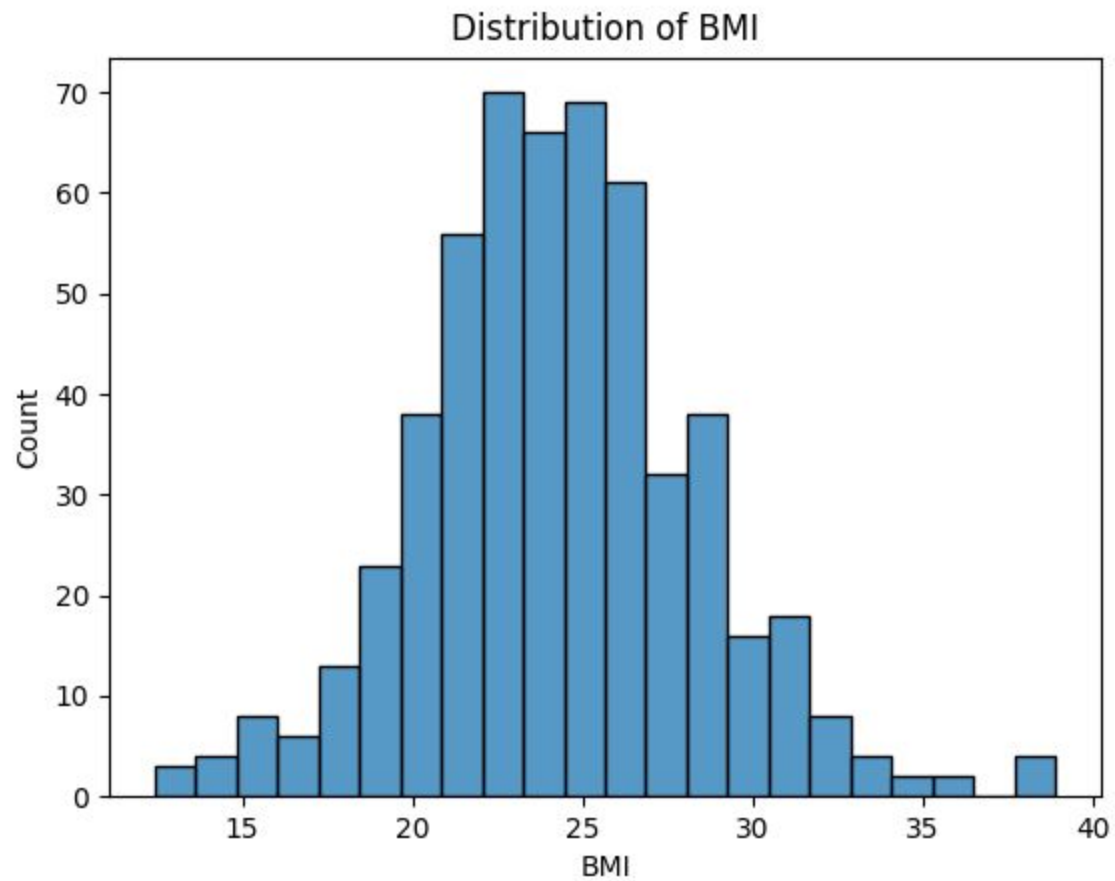
Distribution of Blood Group





Distribution of Height(Cm)





PCOS (Y/N)	1.000000
Follicle No. (R)	0.648327
Follicle No. (L)	0.603346
Skin darkening (Y/N)	0.475733
hair growth(Y/N)	0.464667
Weight gain(Y/N)	0.441047
Cycle(R/I)	0.401644
Fast food (Y/N)	0.376183
Pimples(Y/N)	0.286077
AMH(ng/mL)	0.264141
Weight (Kg)	0.211938
BMI	0.199534
Hair loss(Y/N)	0.172879
Waist(inch)	0.164598
Hip(inch)	0.162297
Avg. F size (L) (mm)	0.132992
Endometrium (mm)	0.106648
Avg. F size (R) (mm)	0.097690

Height(Cm)	0.068254
Reg.Exercise(Y/N)	0.065337
LH(mIU/mL)	0.063879
RBS(mg/dl)	0.048922
BP _Diastolic (mmHg)	0.038032
RR (breaths/min)	0.036928
Blood Group	0.036433
II beta-HCG(mIU/mL)	0.012760
Waist:Hip Ratio	0.012386
BP _Systolic (mmHg)	0.007942
PRL(ng/mL)	0.005143
TSH (mIU/L)	-0.010140
FSH/LH	-0.018336
Pregnant(Y/N)	-0.027565
I beta-HCG(mIU/mL)	-0.027617
FSH(mIU/mL)	-0.030319
PRG(ng/mL)	-0.043834
No. of abortions	-0.057158
Marraige Status (Yrs)	-0.113056
Age (yrs)	-0.168513
Cycle length(days)	-0.178480

Assumptions

We first want to focus on the first three feature that is present on both data set which were 'I beta-HCG(mIU/mL)', 'II beta-HCG(mIU/mL)', 'AMH(ng/mL)' as features to train our dataset.

And our target variable will be PCOS positive/negative rate

Future Goals

- Develop a predictive model for the early detection of PCOS and infertility-related issues.
- Analyze the dataset to identify patterns and trends.
- Develop a model that can predict the likelihood of PCOS and infertility-related issues.
- Evaluate the model's performance using various metrics.
- Present the results in a clear and concise manner.

Feedback 4/2 12pm

- Take good traceability of every decision point where the experiment changed / was done / for what reason – Dani
- Oh that's all
- Need more stats stuff