

Using Machine Learning Algorithms to Predict the likelihood of Polycystic Ovarian Syndrome based on Demographic, Clinical and Lifestyle Factors

CUNY SPS Data 698 - Analytics Masters Research Project

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Abstract:

Polycystic Ovarian Syndrome (PCOS) stands as a prevalent endocrine disorder affecting women of reproductive age worldwide, presenting a confluence of hormonal imbalances, reproductive irregularities, and potential metabolic complications. Characterized by irregular menstrual cycles, hyperandrogenism, and polycystic ovaries, PCOS poses multifaceted challenges that extend beyond reproductive health, encompassing metabolic disturbances and psychological implications. This multifaceted syndrome, influenced by intricate interactions among genetic predispositions, hormonal imbalances, and environmental elements, presents with diverse manifestations among those affected. The clinical landscape of PCOS often requires a comprehensive, multidisciplinary approach, incorporating lifestyle modifications, pharmacological interventions, and personalized treatments to address symptoms and reduce associated health risks. Despite ongoing research efforts, unraveling the exact cause and identifying the most effective management approaches for PCOS remains an evolving field of investigation within modern medicine. This research project aims to investigate the current studies on PCOS diagnosis, assessing the effectiveness of various machine learning algorithms including Decision Tree (rpart), Random Forest (randomForest), Gradient Boosting Machines (xgboost or gbm), Support Vector Machines (SVM; e1071), Neural Networks (neuralnet), and K-Nearest Neighbors (knn or class). From my analysis, it was concluded that the accuracies of Decision Tree 2, SVM 2, SVM 1, and Random Forest 2 performed relatively better in distinguishing between PCOS and non-PCOS cases in this dataset, while Gradient Boost Machines 1 and k-Nearest 2 demonstrated slightly reduced yet still sufficiently acceptable predictive accuracies.

Key words:

Polycystic Ovarian Syndrome, PCOS, Women's Health, Machine Learning Algorithms, Predictive Modeling

The Problem:

Polycystic Ovarian Syndrome (PCOS) is a hormonal imbalance disorder affecting women of reproductive age. Determining the precise global count of women affected by PCOS poses challenges due to many cases remaining undiagnosed. However, the World Health Organization (WHO) estimates that approximately 3.4% of women are affected [WHO, 2023]. While this percentage might seem relatively small, considering that women constitute 49.7% of today's population [Knoema, 2022], nearly 13% of them fall within the reproductive age bracket [MarchofDimes, 2022]. This data suggests that approximately 17.5 million women report suffering from PCOS. Beyond the physical and emotional toll PCOS exacts, it also disrupts ovarian function, leading to challenges in maintaining a healthy menstrual cycle and can result in the formation of cysts, ultimately impacting fertility. It's important to note that the prevalence of PCOS varies by region and ethnic groups, with some studies suggesting higher rates of PCOS in certain populations [Engmann, 2017]. Early identification of risk factors associated with PCOS can assist in timely interventions and lifestyle adjustments. Tailoring suggestions or treatments based on individualized risk profiles has the potential to enhance patient outcomes. Employing predictive models can play a pivotal role in increasing awareness regarding PCOS risk factors and preventive measures. However, limitations may exist in accessing comprehensive and varied datasets containing accurate demographic, clinical, and lifestyle data [Thakre, 2020]. Addressing these challenges involves the development of a robust predictive model using machine learning techniques. Such an endeavor holds the promise of significantly contributing to the identification of individuals at risk of PCOS, thereby enabling early interventions and guiding personalized healthcare strategies for improved management of the condition. This project will investigate publicly available datasets that will be used to develop machine learning models that predicts the probability or risk of an individual having or developing PCOS based on demographic information (age, ethnicity, geographical location), clinical data (hormonal levels, BMI, menstrual irregularities), and lifestyle factors (dietary habits, exercise routine, stress levels).

Objectives:

Construct predictive models using machine learning techniques that utilize a dataset comprising demographic, clinical, and lifestyle variables as features and PCOS diagnosis as the target variable. Machine learning algorithms have shown promise in advancing our understanding of the disease and improving its diagnosis and treatment.

I anticipate answering the following questions with my data:

1. Are there commonalities women with and without PCOS have that can be easily dismissed as normal?
2. Are there differences for women of different race/ethnic background when it comes to having PCOS? What about women without PCOS?
3. What is the likelihood of a woman developing PCOS based on her age, ethnicity, and BMI history?
4. Can we predict the risk of insulin resistance, diabetes, and cardiovascular disease in women with PCOS based on their medical history, hormone levels, and lifestyle factors?
5. Can we predict the likelihood of successful pregnancy outcomes in women with PCOS based on their age, weight, hormone levels, and treatment history?
6. Can we predict the long-term health outcomes and quality of life of women with PCOS based on their age, lifestyle factors, hormone levels, and treatment history?

Literature Review:

For this project, my emphasis was on discovering literature reviews that validate the relevance of the dataset utilized alongside the chosen machine learning algorithms. In pursuit of this goal, I've come across various articles that make reference to the dataset [Kottarakkathil, 2020]. These articles investigate studies associated with PCOS, presenting findings aimed at providing a deeper comprehension of the dataset I'm analyzing.

The literature reviews collectively delve into various aspects of Polycystic Ovarian Syndrome (PCOS), employing diverse methodologies and approaches for diagnosis, classification, understanding clinical manifestations, and proposing potential treatments. Researchers across these studies have primarily utilized data mining, machine learning, and clinical investigations to address the complexity of PCOS. Below are the key characteristics, achievements, advantages, and drawbacks across these reviews:

Common Focus Areas: Multiple studies emphasize the use of machine learning algorithms, such as Naïve Bayes, Decision Trees, Artificial Neural Networks, Support Vector Machines, and ensemble methods, for PCOS diagnosis. They explore the accuracy and predictive power of these models using diverse datasets, including clinical, lifestyle, and physiological parameters. Investigations into clinical parameters and anthropometric measures aim to identify potential predictors or indicators of PCOS, such as hormonal imbalances, insulin resistance, metabolic traits, obesity, and associated risks like infertility and cardiovascular issues. Studies examine the diverse clinical presentations and phenotypic variations within PCOS, shedding light on how different subgroups may manifest the syndrome and respond to various treatments.

Achievements: Machine learning models, particularly those utilizing Convolutional Neural Networks (CNNs) and ensemble methods, have shown high accuracy in diagnosing PCOS. The findings revealed that CNN models performed best, achieving accuracies ranging from 85% to 98.12% in different studies [Anda, 2022]. These models effectively utilize diverse datasets, ranging from ultrasound images to clinical parameters. Research has identified several potential predictive factors for PCOS, including hormonal markers, lifestyle attributes, and metabolic indicators, offering insights into early detection and tailored treatment strategies. The study done by Aggarwal, S., & Pandey, K. (2023) used supervised learning algorithms (like

random forest, gradient boosting) to assess performance metrics, indicating that these crucial features offer high accuracy in identifying PCOS. Unsupervised learning (K-means clustering) corroborates these findings, suggesting that these key features are pivotal for PCOS analysis. In another study, Tiwari (2022) uses machine learning to screen PCOS patients based on non-invasive parameters. It employed various algorithms like SVM, Decision Trees, Random Forest, etc., for classification, finding that Random Forest achieved the highest accuracy of 93.25%. Overall, studies evaluating PCOS awareness among women have highlighted the importance of education and awareness campaigns in enhancing understanding and facilitating early diagnosis.

Advantages: Machine learning algorithms offer promising accuracy rates, particularly CNNs and ensemble models, in diagnosing PCOS using various non-invasive parameters. Understanding phenotypic variations aids in tailoring treatments based on specific subgroups, potentially improving patient outcomes and management. Efforts toward identifying early markers or predictive factors can facilitate early intervention and lifestyle modifications, mitigating long-term health risks associated with PCOS.

Drawbacks and Recommendations: Some studies may suffer from limited sample sizes or datasets, impacting the generalizability of findings. Larger and more diverse datasets are recommended for robust model development and validation [Goodarzi, 2015]. While certain machine learning models showcase high accuracy, the variability in dataset characteristics and preprocessing methods could influence their effectiveness across different populations or settings [Tiwari, 2022]. The multifaceted nature of PCOS, influenced by both genetic and environmental factors, presents challenges in pinpointing a singular cause or standard diagnostic criteria.

The collective body of literature reviews signifies advancements in PCOS diagnosis, understanding clinical manifestations, and potential avenues for tailored treatments. The use of machine learning models, especially those employing CNNs and ensemble methods, showcases significant promise in accurate PCOS diagnosis based on non-invasive parameters. However, further research is necessary, emphasizing larger and more diverse datasets, refined models, and a multidisciplinary approach to fully comprehend the complexity of PCOS and enhance diagnostic and treatment strategies.

Dataset:

The Polycystic ovary syndrome (PCOS) dataset, available on Kaggle.com, is comprised of two csv files labeled `PCOS_data_without_infertility` and `PCOS_infertility`. In total, these files encompass 48 variables and 541 data entries all collected from 10 different hospitals across Kerala, India. The dataset contains all physical and clinical parameters to determine PCOS and infertility related issues.

Full description of the variables below:

- Units used range from imperial to metric system of measurement
- For Yes | No questions
 - Yes = 1
 - No = 0

Variables	Description
“Sl..No”	unique identification number assigned to each entry
“Patient.File.No.”	file number for each patient’s record.
“PCOS..Y.N.”	presence or absence of PCOS
“I...beta.HCG.mIU.mL”	pregnancy hormone case I measured in milli-international units per liter (mIU/L)

Variables	Description
“II....beta.HCG.mIU.mL.”	pregnancy hormone case II measured in milli-international units per liter (mIU/L)
“AMH.ng.mL.”	detects ovarian reserve (egg count)
“Age..yrs.”	age of patient in years
“Weight..Kg.”	weight of patient in kg
“Height.Cm.”	height of patient in cm
“BMI”	body mass index
“Blood.Group”	Blood Groups: A+ = 11, A- = 12, B+ = 13, B- = 14, O+ = 15, O- = 16, AB+ = 17, AB- = 18
“Pulse.rate.bpm.”	beats per minute
“RR..breaths.min.”	respiration rates per minute
“Hb.g.dL.”	hemoglobin concentration measured in grams per deciliter (g/dL).
“Cycle.R.I.”	cycle Regularity Index used to assess the regularity or irregularity of menstrual cycles in women: 4 indicates irregular menstrual cycle, 2 indicates a regular menstrual cycle
“Cycle.length.days.”	length of menstrual cycle
“Marraige.Status..Yrs.”	years married
“Pregnant.Y.N.”	pregnant yes or no
“No..of.abortions”	number of abortions
“FSH.mIU.mL.”	follicle stimulating hormone measured in milli-international units per liter (mIU/L)
“LH.mIU.mL.”	luteinizing hormone (increases during ovulation) measured in milli-international units per liter (mIU/L)
“FSH.LH”	ratio between Follicle-Stimulating Hormone (FSH) and Luteinizing Hormone (LH)
“Hip.inch.”	measurement of hips in inches
“Waist.inch.”	measurement of waist in inches
“Waist.Hip.Ratio”	ratio of measurement of waist and hip
“TSH..mIU.L.”	thyroid stimulating hormone measured in milli-international units per liter (mIU/L)
“AMH.ng.mL.”	Anti-Müllerian Hormone (AMH) measured in nanograms per milliliter (ng/mL); a marker used in reproductive medicine to assess ovarian reserve
“PRL.ng.mL.”	Prolactin measured in nanograms per milliliter (ng/mL); a hormone produced by the pituitary gland
“Vit.D3..ng.mL.”	Vitamin D3 measured in nanograms per milliliter (ng/mL); is essential for bone health, immune function, and various other bodily processes.
“PRG.ng.mL.”	Progesterone measured in nanograms per milliliter (ng/mL); a hormone involved in the menstrual cycle, pregnancy, and maintaining the uterine lining for a developing embryo.
“RBS.mg.dL.”	Random Blood Sugar measured in milligrams per deciliter (mg/dL); it represents the level of glucose (sugar) present in the blood at a random time, without fasting.
“Weight.gain.Y.N.”	weight gain yes or no
“hair.growth.Y.N.”	hair growth yes or no (hirsutism)
“Skin.darkening..Y.N.”	darkening of skin yes or no
“Hair.loss.Y.N.”	hair loss yes or no
“Pimples.Y.N.”	pimples (acne) yes or no

Variables	Description
“Fast.food..Y.N.”	consumption of fast food yes or no
“Reg.Exercise.Y.N.”	regularly exercise yes or no
“BP._Systolic..mmHg.”	systolic blood pressure measured in millimeters of mercury (mmHg)
“BP._Diastolic..mmHg.”	diastolic blood pressure measured in millimeters of mercury (mmHg)
“Follicle.No...L.”	number of follicles on left ovary
“Follicle.No...R.”	number of follicles in right ovary
“Avg..F.size..L...mm.”	average size of follicles in left ovary measured in millimeters (mm)
“Avg..F.size..R...mm.”	average size of follicles in right ovary measured in millimeters (mm)
“Endometrium..mm.”	size of the endometrial thickness in millimeters (mm)

Methodology:

Upon importing the data into R, I conducted an assessment to gain a comprehensive understanding of the dataset. The exploration revealed a necessity for substantial data preparation before commencing model construction. Utilizing the `skimr` library, I generated concise summaries for both datasets, which indicated the presence of character and numeric column types without any missing values. Employing the `Data Explorer` library, histograms were created to examine the distribution of variables in both datasets. However, these distributions did not display any discernible patterns or distinct shapes.

The data preparation phase involved standardizing the `pcos` and `pcos2` datasets as numeric due to variations in variable classes. While confirming the absence of missing data, it was identified that `pcos2` contained a few variables with missing values. Upon obtaining a comprehensive overview of both datasets, the procedure involved eliminating unnecessary columns, renaming columns for enhanced readability, and merging the datasets. Additionally, transformations were applied, converting `Height` from centimeters to meters, `Hip` and `Waist` from inches to centimeters. Subsequently, missing values in columns such as `BMI`, `Waist_Hip_Ratio`, and `FSH/LH` were computed and replaced. For `Married_yrs`, `AMH_ngmL`, and `Fast_food`, the missing values were substituted with the median values, as these replacements did not significantly impact the data distribution. Detecting outliers was crucial and accomplished through boxplots for visual representation. Despite their presence, I chose to retain these outliers, acknowledging their importance in representing natural variations within the population. Furthermore, additional visualizations were created to scrutinize trends within the refined `pcos_cleaned` dataset.

Building the models involved the development of six distinct machine learning algorithms: Decision Trees, Random Forest, Gradient Boost Machines, Support Vector Machines, Neural Networks, and k-Nearest Neighbor. We initiate by dividing the dataset into training and validation subsets tailored for machine learning models. The training subset is utilized for model training, while the validation subset assesses its performance. Employing a 75:25 ratio strikes a balance, ensuring adequate data for effective model training and a sizable validation set for robust evaluation.

For each algorithm, the following procedures were executed:

1. Establish a cross-validation configuration, employing the `PCOS` variable as the target against the entire dataset. The split data designated `train` and `valid` labeled the training and testing subsets, respectively. Additionally, another cross-validation setup centered on the `PCOS` target variable, utilizing pivotal contributing variables: `Follicle_NoL`, `Follicle_NoR`, `Hair_growth`, `Skin_darkening`, and `Weight_gain`.
2. After the model creation using the `train` dataset, predictions were generated for the model utilizing the `valid` data. The output encompassed a confusion matrix and associated statistics affirming the predictive output for the target variable (`PCOS`). Moreover, this included metrics providing insights into the model's efficacy in classifying positive and negative cases accurately in binary classification.
3. Evaluate the individual contributions of each variable within the model and, if necessary, visualize their significance.

4. Retrieve the accuracy metric for subsequent comparison with other models.

The procedure was replicated for all six algorithms on two occasions: first, using the complete dataset, and second, utilizing the reduced dataset containing the highest contributing variables. The culmination of the project involved aggregating all accuracies obtained from the models to compare the performance of each model in differentiating between PCOS and non-PCOS cases across the datasets.

Assumptions:

While there's limited information available in the medical field and even less data sets available to analyze, I have some concerns on being successful in predicting a PCOS diagnosis. Yet there are justifications exploring PCOS in depth:

- Identify diagnostic biomarkers that can distinguish PCOS patients from healthy individuals or those with other disorders. These biomarkers can aid in earlier diagnosis and better management of the disease.
- Predict the likelihood of disease progression and the risk of developing complications, such as diabetes and cardiovascular disease, in PCOS patients. This information can guide treatment decisions and improve patient outcomes.
- Develop personalized treatment plans for PCOS patients based on their individual characteristics and medical history. This approach can lead to more effective and targeted interventions.
- Integrate data from various sources, such as electronic health records, imaging studies, and genetic analyses, to provide a more comprehensive understanding of PCOS. This can help identify new pathways involved in the disease and potential targets for therapy.
- Aid in the design and analysis of clinical trials, leading to more efficient and informative studies. This can accelerate the development of new treatments for PCOS.

Early diagnosis and management of PCOS can lead to better health outcomes, improved quality of life, and reduced long-term health risks. Therefore, predicting PCOS diagnosis can have several societal benefits, including:

- Predicting PCOS diagnosis can help healthcare providers identify women at risk of developing PCOS and intervene early with appropriate treatment, such as lifestyle modifications and medication, to prevent or minimize the long-term health consequences of the disorder.
- Early diagnosis and treatment of PCOS can help manage symptoms such as irregular periods, infertility, acne, and excess hair growth, leading to improved physical and mental health outcomes for affected women.
- By predicting PCOS diagnosis and intervening early, healthcare providers can prevent or reduce the need for more expensive treatments or surgeries later in life, resulting in cost savings for individuals, healthcare systems, and society.
- Predicting PCOS diagnosis can increase awareness of the disorder among healthcare providers, patients, and the public, leading to more education, research, and advocacy efforts aimed at improving PCOS diagnosis, treatment, and management.
- Early intervention and management of PCOS can improve the quality of life for affected women, leading to increased productivity, better mental health, and greater overall well-being.

Overall, I'll be able to explore the insights into PCOS pathophysiology, diagnosis, and treatment. Their use in PCOS research can lead to more personalized and effective care for patients with this complex disorder.

Experimentation and Results:

Overall the top 5 models with the highest accuracies were: Decision Tree (second model), SVM (second and first model), Random Forest (second model), and Gradient Boost Machine (first model).

Both Decision Tree 2 and SVM 2 achieved similar high accuracies of approximately 91.85%. This implies that these models were quite successful in making accurate predictions for PCOS diagnosis based on the given data and features. SVM 1 achieved a slightly lower accuracy compared to Decision Tree 2 and SVM 2 but still performed reasonably well at approximately 91.11%. It remains effective in predicting PCOS diagnosis but might be slightly less accurate than the aforementioned models. The second Random Forest model achieved an accuracy of around 90.37%, indicating its capability to correctly classify PCOS and non-PCOS cases with slightly less accuracy than SVM 1 and Decision Tree 2. Both Gradient Boost Machines 1 and k-Nearest 2 models obtained accuracies around 88.15%, which, while lower than the previous models, still demonstrate a moderate ability to predict PCOS diagnosis based on the provided features.

Overall, these accuracies suggest that Decision Tree 2, SVM 2, SVM 1, and Random Forest 2 performed relatively better in distinguishing between PCOS and non-PCOS cases in this dataset, while Gradient Boost Machines 1 and k-Nearest 2 showed somewhat lower but still reasonably acceptable prediction accuracies.

Conclusion:

My initial assumption was that while there's limited information available in the medical field and even less data sets available to analyze, I have some concerns on being successful in predicting a PCOS diagnosis. I anticipated answering the following questions with my data:

1. Are there commonalities women with and without PCOS have that can be easily dismissed as normal?
 - Some shared patterns identified through analysis included Body Mass Index (BMI), vital signs, anthropometric measures, and specific hormone levels, yet within this dataset, insufficient evidence exists to conclusively dismiss these as unrelated to Polycystic Ovary Syndrome (PCOS).
2. Are there differences for women of different race/ethnic background when it comes to having PCOS? What about women without PCOS?
 - These accuracies don't directly address racial or ethnic differences. Further analysis involving feature exploration or specific subgroup analysis using demographic data might unveil associations or variations among different racial/ethnic groups in PCOS prevalence or features.
3. What is the likelihood of a woman developing PCOS based on her age, ethnicity, and BMI history?
 - The accuracies do not explicitly signify predictions regarding probability due to the lack of diverse ethnic backgrounds in the collected records. Moreover, age and BMI were not influential variables across most of the created models in this dataset.. Specific models with feature importance or coefficients might offer insights into how age, ethnicity, and BMI contribute to predicting PCOS likelihood.
4. Can we predict the risk of insulin resistance, diabetes, and cardiovascular disease in women with PCOS based on their medical history, hormone levels, and lifestyle factors?
 - Machine learning models could help predict the risk of insulin resistance, diabetes, and cardiovascular disease in women with PCOS based on available medical history, hormone levels, and lifestyle factors. For this a larger dataset would be needed in order to create specialized modeling to derive precise predictions.

5. Can we predict the likelihood of successful pregnancy outcomes in women with PCOS based on their age, weight, hormone levels, and treatment history?
 - Similar to the above, machine learning models can potentially predict the likelihood of successful pregnancy outcomes in women with PCOS based on various factors like age, weight, hormone levels, and treatment history. A larger dataset, specific models or analyses could provide more detailed predictive insights.
6. Can we predict the long-term health outcomes and quality of life of women with PCOS based on their age, lifestyle factors, hormone levels, and treatment history?
 - Machine learning models, when trained with extensive data including age, lifestyle factors, hormone levels, and treatment history, might offer predictive insights into long-term health outcomes and quality of life for women with PCOS. However, these models might need additional feature engineering and specialized analyses to offer accurate predictions.

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Appendices:

Appendix A - Figures:

Fig. 1 - Histogram of `pcos` data

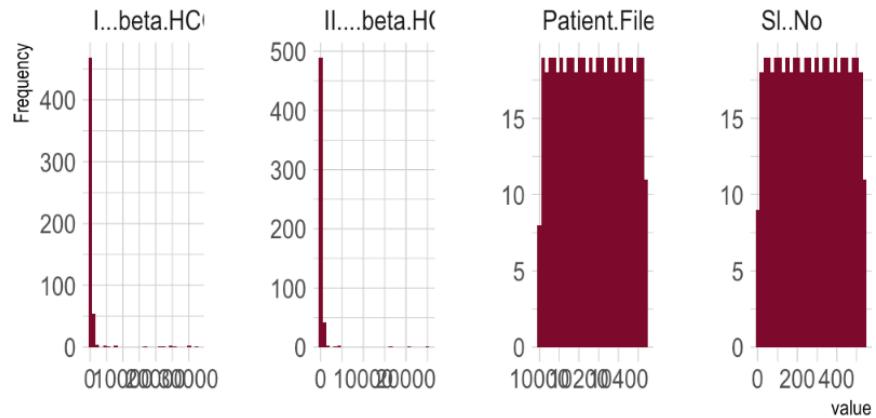


Fig. 2 - Histogram of `pcos2` data

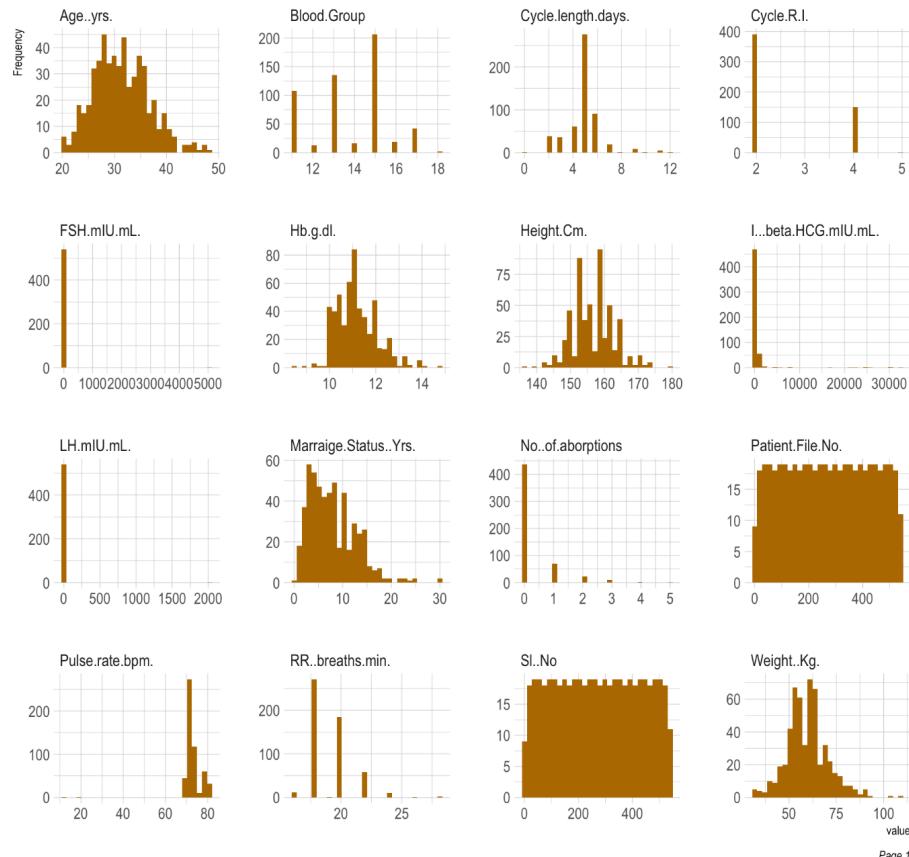
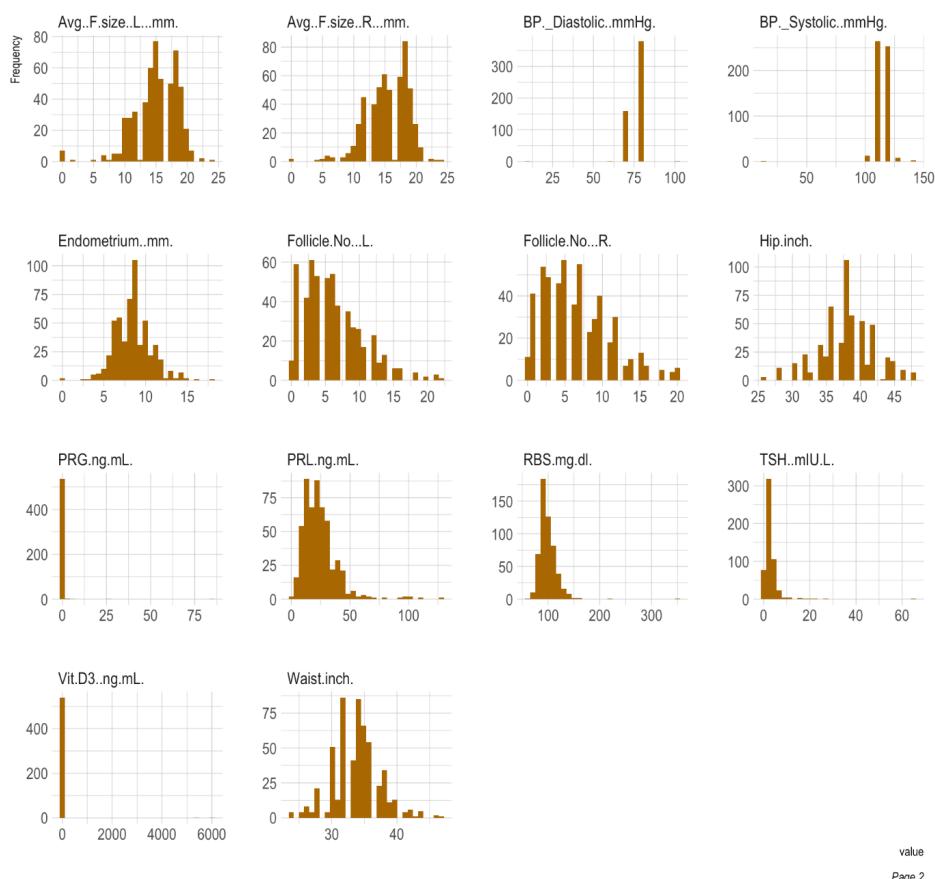


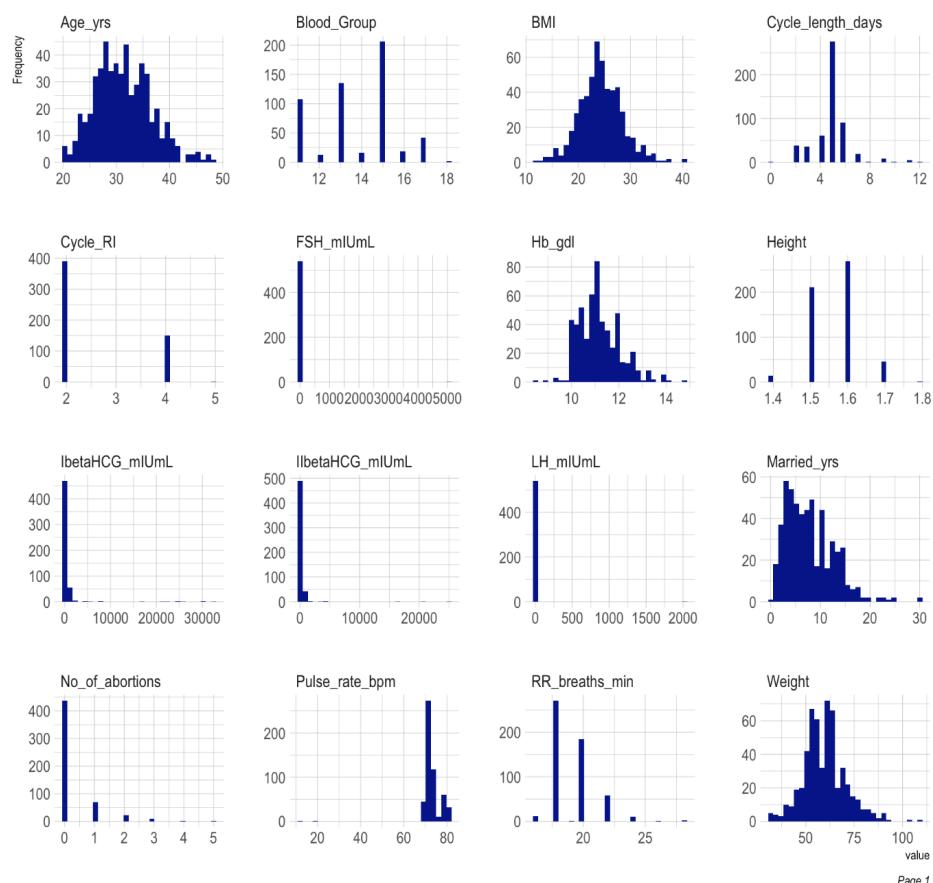
Fig. 2 - Histogram of 'pcos2' data



value

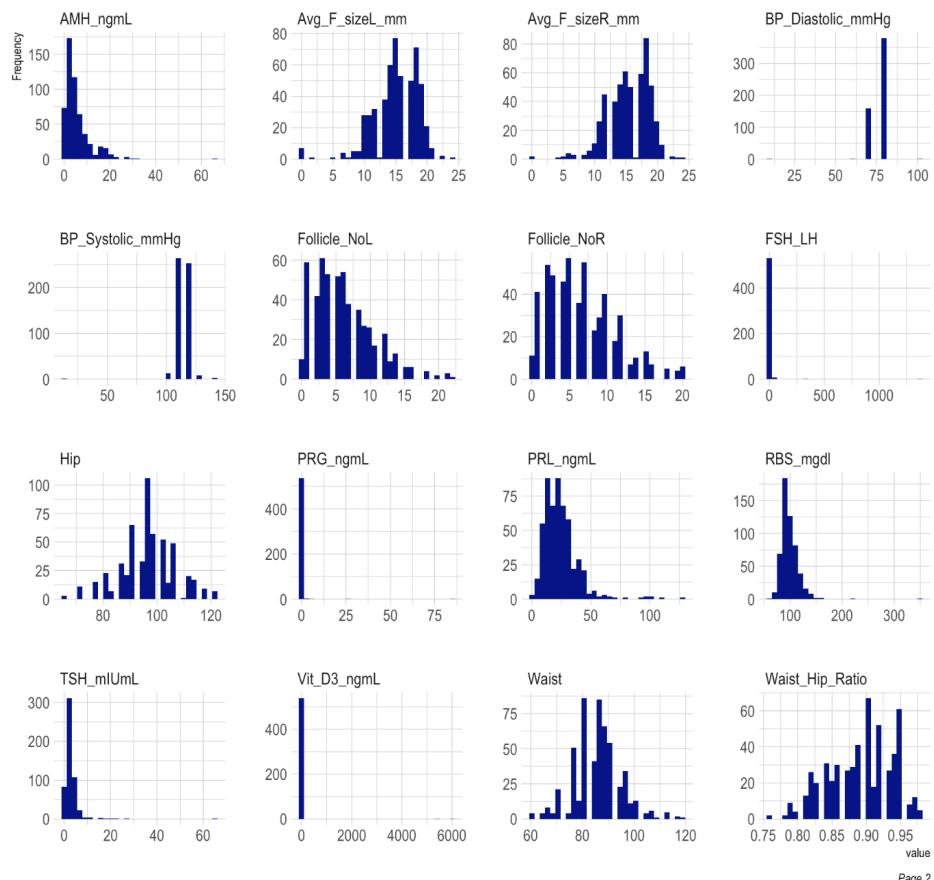
Page 2

Fig. 3 - Histogram of `pcos_cleaned` data



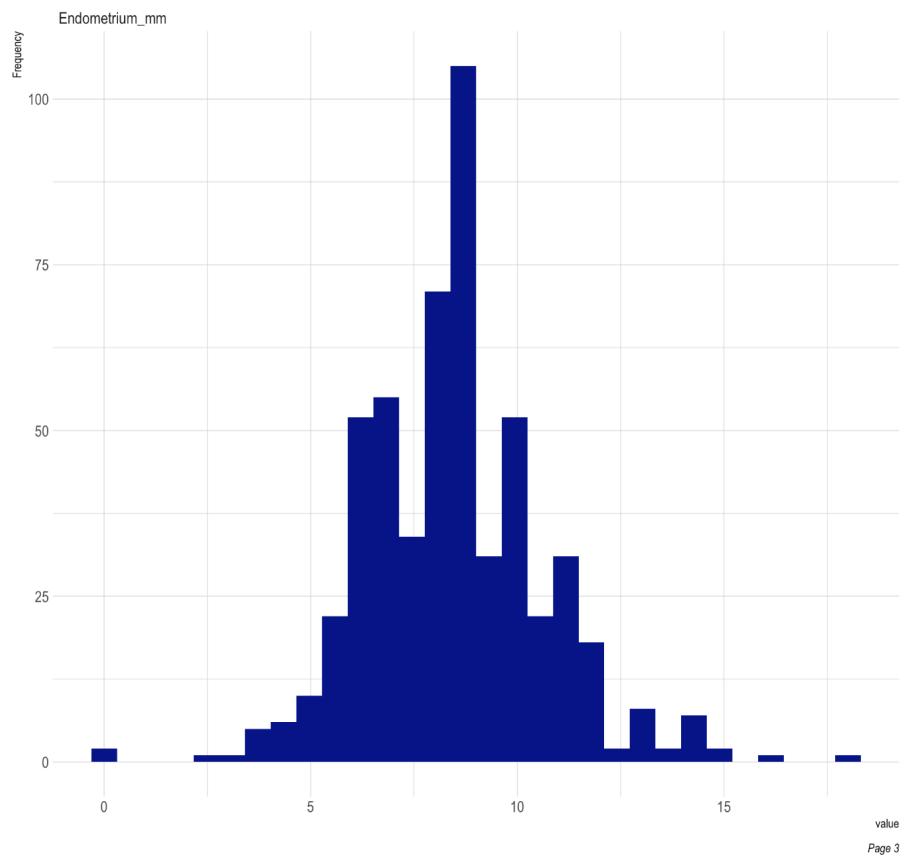
Page 1

Fig. 3 - Histogram of `pcos_cleaned` data



Page 2

Fig. 3 - Histogram of `pcos_cleaned` data



Page 3

Fig. 4 Correlation plot of `pcos_cleaned` data

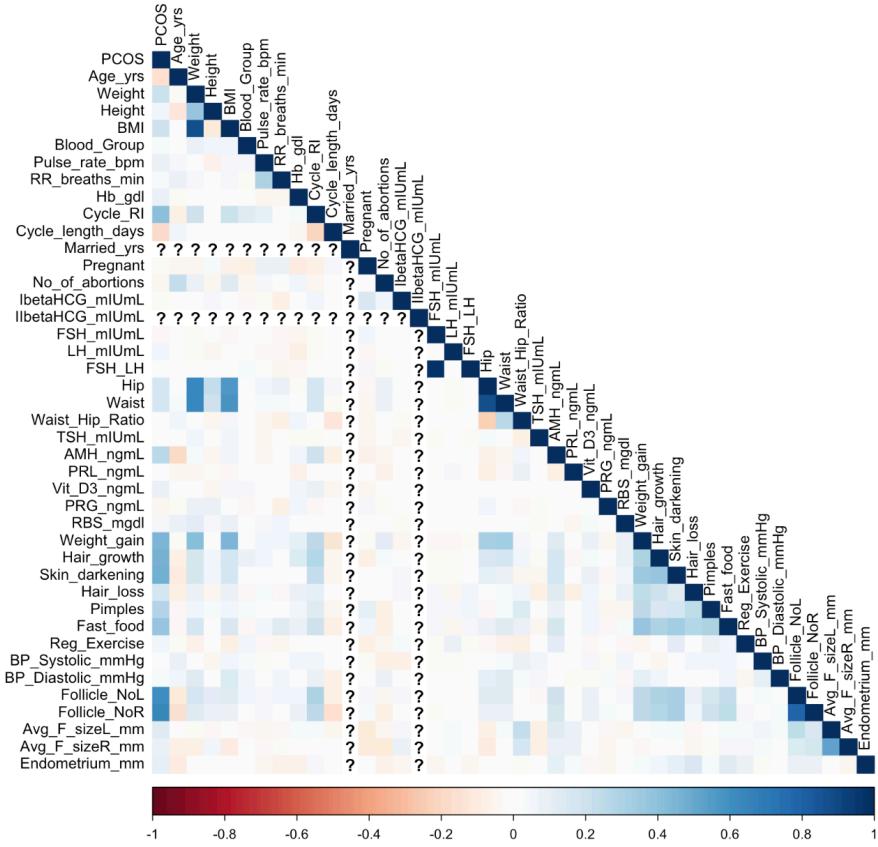


Fig. 5 - Boxplot outliers for 'pcos_cleaned' data

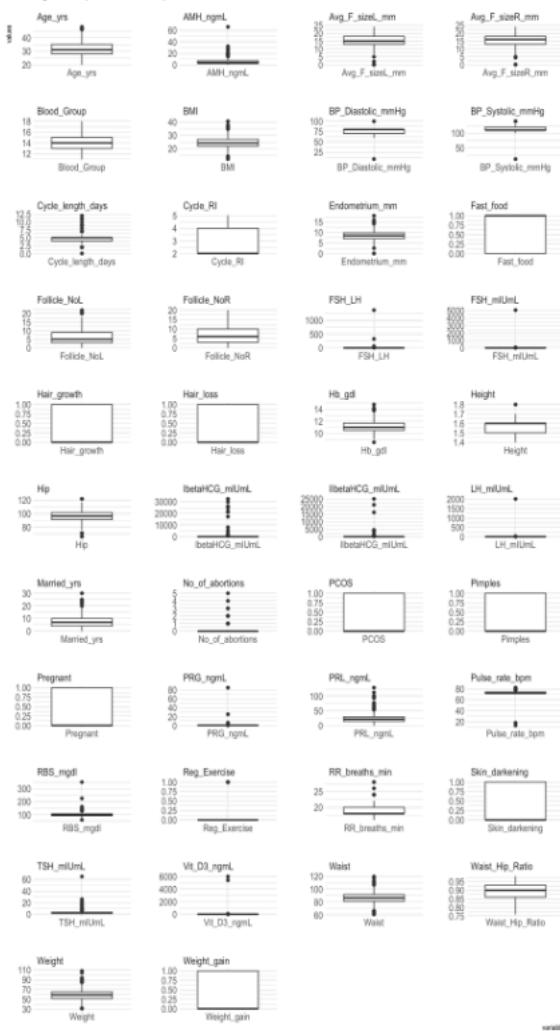


Fig. 6 - Scatterplot of Biometric measures Variables

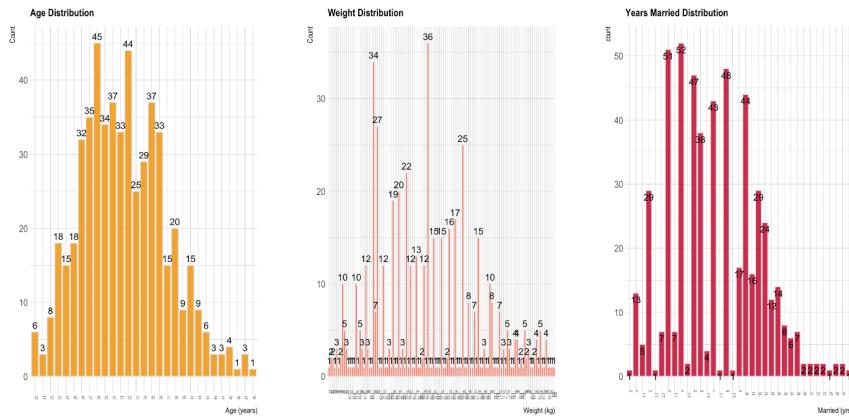


Fig. 7 - Scatterplot of variables with PCOS (Y/N) as factor

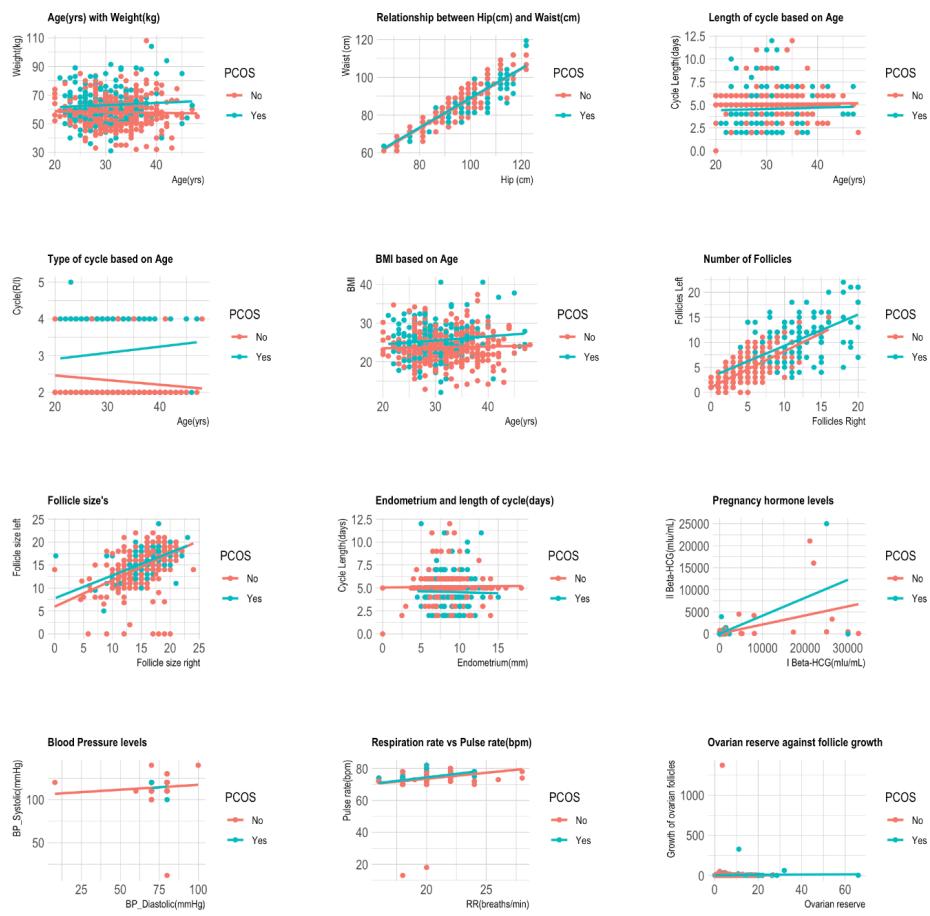


Fig. 8 - Bar charts of Bloodwork variables



Fig. 9 - Bar charts of yes or no variables



Fig. 10 - Bar charts of Biometrics Measures including PCOS (Y/N) as factor

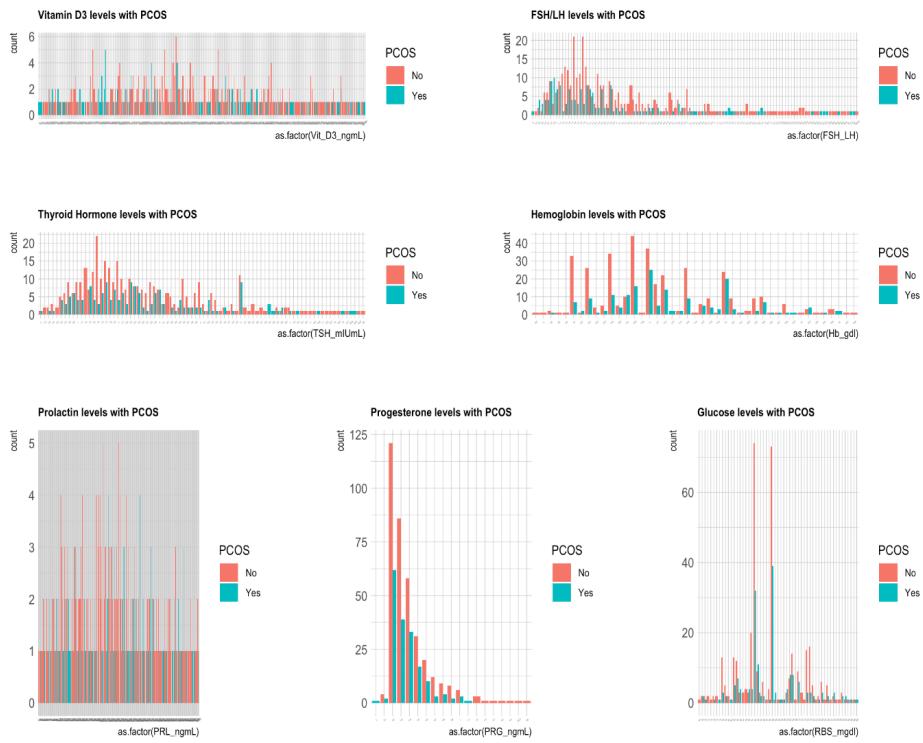


Fig. 11 - Decision Tree with entire dataset

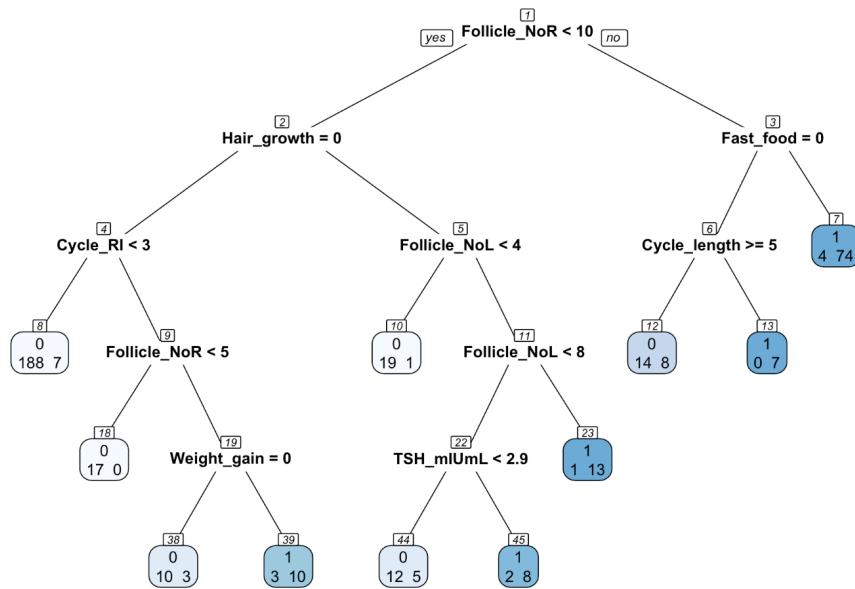


Fig. 12 - Second Decision Tree with 6 variables

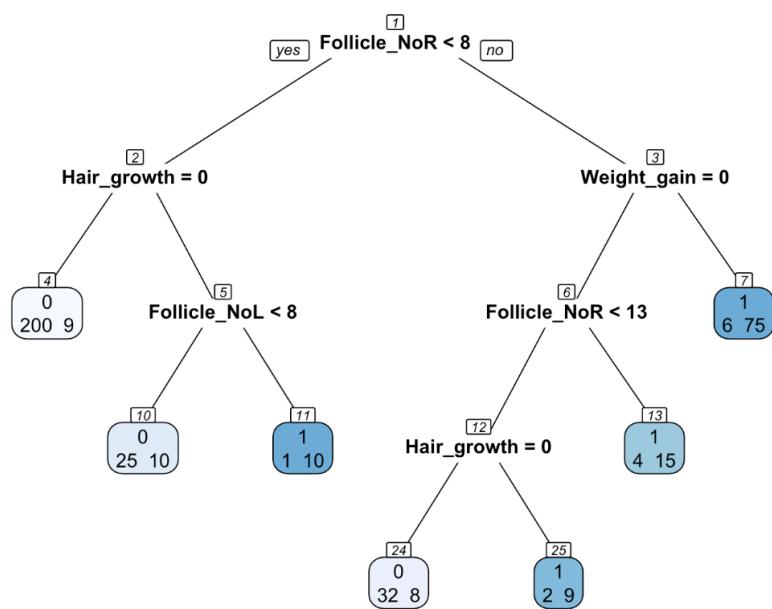


Fig. 13 - Feature importance of first random forest model

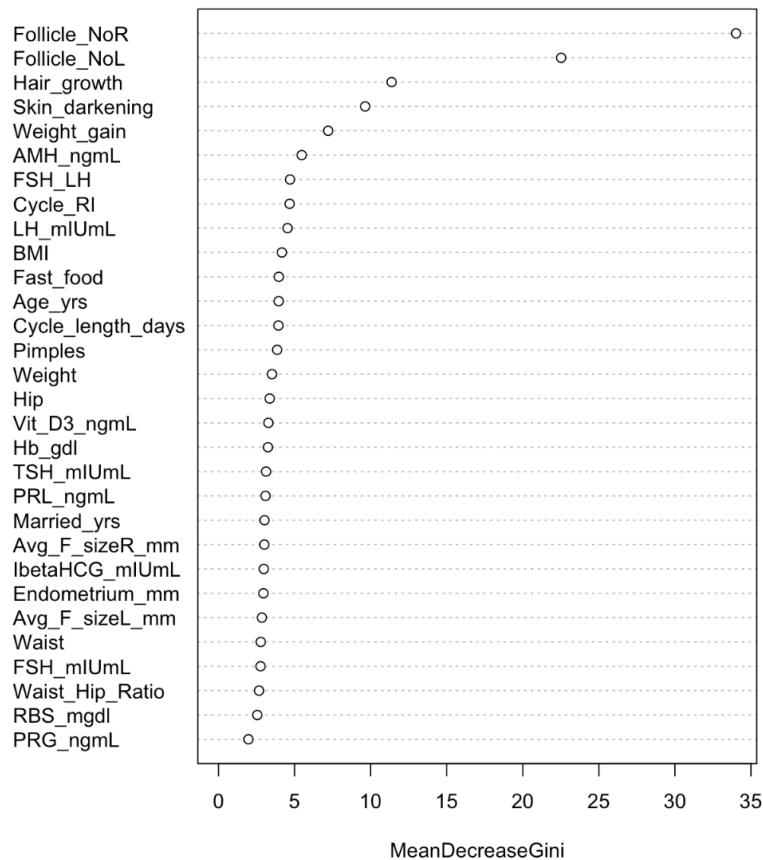
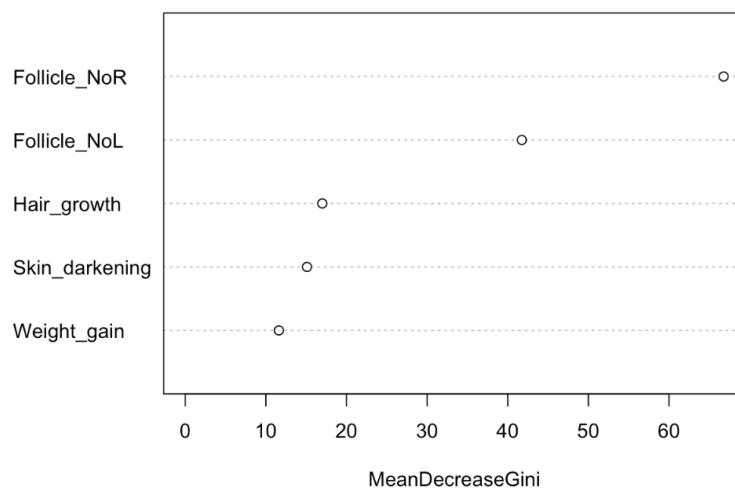
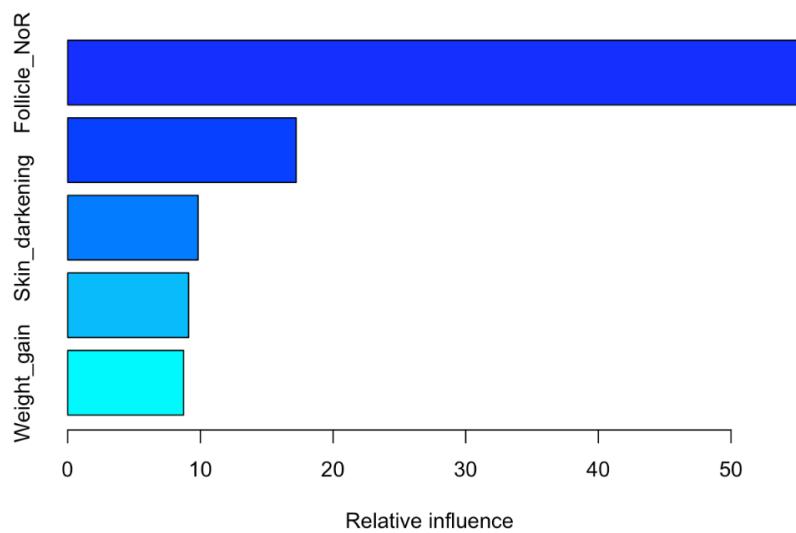
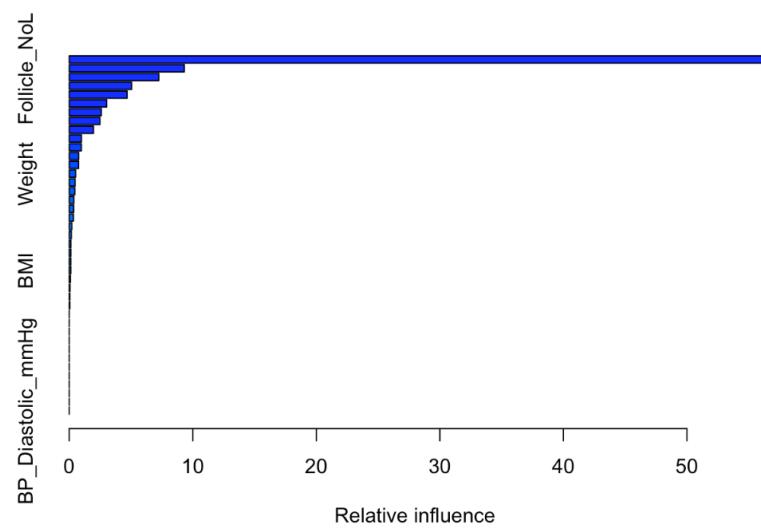
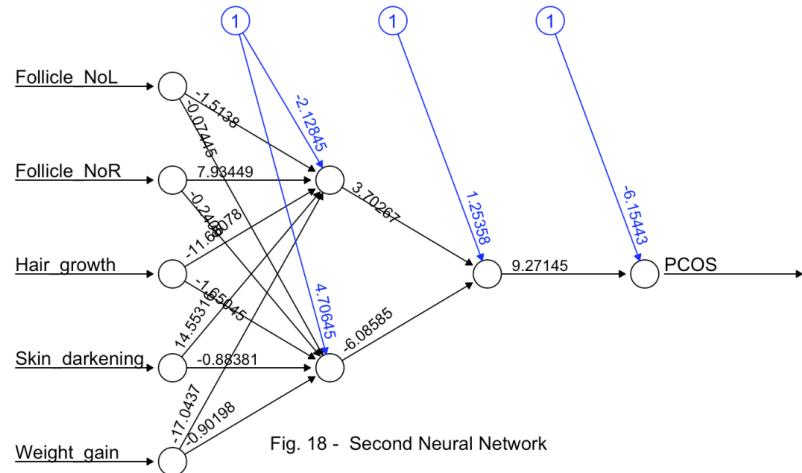
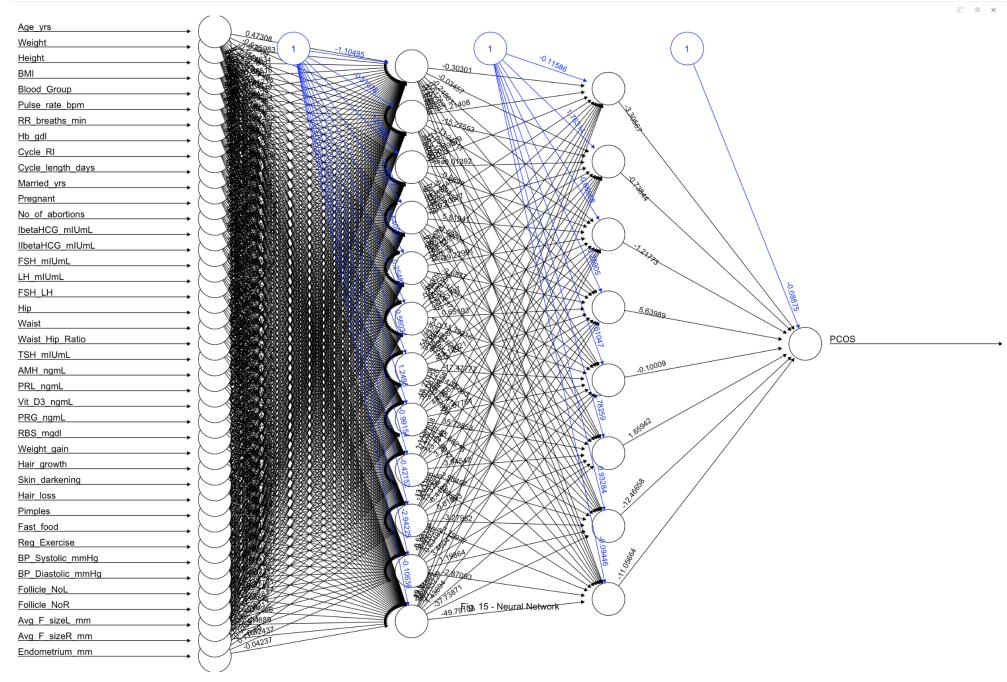


Fig. 14 - Feature importance of second random forest model







Error: 13.733636 Steps: 2518

Appendix B - Tables:

Table 1. pcos data					
Sl.No	Patient.File.No.	PCOS.Y.N.	I...beta.HCG.mIU.mL.	II....beta.HCG.mIU.mL.	AMH.ng.mL.
1	10001	0	1.990	1.990000e+00	2.07
2	10002	0	60.800	1.990000e+00	1.53
3	10003	1	494.080	4.940800e+02	6.63
4	10004	0	1.990	1.990000e+00	1.22
5	10005	0	801.450	8.014500e+02	2.26
6	10006	0	237.970	1.990000e+00	6.74
7	10007	0	1.990	1.990000e+00	3.05
8	10008	0	100.510	1.005100e+02	1.54
9	10009	0	1.990	1.990000e+00	1
10	10010	0	1.990	1.990000e+00	1.61
11	10011	0	158.510	1.585100e+02	4.47

Table 2. pcos2 data												
Sl.No	Patient.File.No.	PCOS.Y.N.	Age.yrs.	Weight.Kg.	Height.Cm.	BMI	Blood.Group	Pulse.rate.bpm.	RR..breaths.min.	Hb.g.dl.	Cycle.R.I.	Comments
1	1	0	28	44.6	152.000	19.3	15	78	22	10.48	2	
2	2	0	36	65.0	161.500	#NAME?	15	74	20	11.70	2	
3	3	1	33	68.8	165.000	#NAME?	11	72	18	11.80	2	
4	4	0	37	65.0	148.000	#NAME?	13	72	20	12.00	2	
5	5	0	25	52.0	161.000	#NAME?	11	72	18	10.00	2	
6	6	0	36	74.1	165.000	#NAME?	15	78	28	11.20	2	
7	7	0	34	64.0	156.000	#NAME?	11	72	18	10.90	2	
8	8	0	33	58.5	159.000	#NAME?	13	72	20	11.00	2	
9	9	0	32	40.0	158.000	#NAME?	11	72	18	11.80	2	
10	10	0	36	52.0	150.000	#NAME?	15	80	20	10.00	4	
11	11	0	20	71.0	163.000	#NAME?	15	80	20	10.00	2	

Table 3. pcos_data merged data													
Sl.No	PCOS	Age_yrs	Weight	Height	BMI	Blood_Group	Pulse_rate_bpm	RR_breaths_min	Hb_gdl	Cycle_RI	Cycle_length_days	Married_yrs	P
1	0	28	44.6	152.000	19.3	15	78	22	10.48	2	5	7.0	
2	0	36	65.0	161.500	NA	15	74	20	11.70	2	5	11.0	
3	1	33	68.8	165.000	NA	11	72	18	11.80	2	5	10.0	
4	0	37	65.0	148.000	NA	13	72	20	12.00	2	5	4.0	
5	0	25	52.0	161.000	NA	11	72	18	10.00	2	5	1.0	
6	0	36	74.1	165.000	NA	15	78	28	11.20	2	5	8.0	
7	0	34	64.0	156.000	NA	11	72	18	10.90	2	5	2.0	
8	0	33	58.5	159.000	NA	13	72	20	11.00	2	5	13.0	
9	0	32	40.0	158.000	NA	11	72	18	11.80	2	5	8.0	
10	0	36	52.0	150.000	NA	15	80	20	10.00	4	2	4.0	
11	0	20	71.0	163.000	NA	15	80	20	10.00	2	5	4.0	

Table 4. pcos_cleaned dataset

PCOS	Age_yrs	Weight	Height	BMI	Blood_Group	Pulse_rate_bpm	RR_breaths_min	Hb_gdl	Cycle_RI	Cycle_length_days	Married_yrs	Pregnant
0	28	44.6	1.5	19.8	15	78	22	10.5	2	5	7.0	0
0	36	65.0	1.6	25.4	15	74	20	11.7	2	5	11.0	1
1	33	68.8	1.7	23.8	11	72	18	11.8	2	5	10.0	1
0	37	65.0	1.5	28.9	13	72	20	12.0	2	5	4.0	0
0	25	52.0	1.6	20.3	11	72	18	10.0	2	5	1.0	1
0	36	74.1	1.7	25.6	15	78	28	11.2	2	5	8.0	1
0	34	64.0	1.6	25.0	11	72	18	10.9	2	5	2.0	0
0	33	58.5	1.6	22.9	13	72	20	11.0	2	5	13.0	1
0	32	40.0	1.6	15.6	11	72	18	11.8	2	5	8.0	0
0	36	52.0	1.5	23.1	15	80	20	10.0	4	2	4.0	0
0	20	71.0	1.6	27.7	15	80	20	10.0	2	5	4.0	1

Table 5. Model Comparison

Model	Accuracy
2 Decision Tree 2	0.9185185
8 SVM 2	0.9185185
7 SVM 1	0.9111111
4 Random Forest 2	0.9037037
5 Gradient Boost Machines 1	0.8814815
12 k-Nearest 2	0.8814815
1 Decision Tree 1	0.8592593
11 k-Nearest 1	0.7111111
6 Gradient Boost Machines 2	0.6222222
3 Random Forest 1	0.6148148
9 Neural Network 1	0.3037037

Appendix C - R Code:

```
# load libraries
library(tidyverse) # data prep
library(DataExplorer) # histograms for datasets
library(skimr) # data prep
library(rpart) # decision tree package
library(rpart.plot) # decision tree display package
library(kableExtra) # kable function for tables
library(knitr) # kable function for table
library(tidyr) # splitting data
library(ggplot2) # graphing
library(hrbrthemes) # chart customization
library(gridExtra) # layering charts
library(stringr) # data prep
library(tidymodels) # predictions
library(corrplot) # correlation plot
library(randomForest) # for the random forest
library(caret) # confusion matrix
```

```

library("e1071") #sum
library(formattable)
library(corrplot) # correlation plot
library(caret) # confusion matrix
library(neuralnet) # neural network
library(stats) # linear and logistic regression
library(gbm) # generalized boosted models
library(xgboost) # extreme gradient boosting
library(kknn) # weighted k-Nearest neighbors
library(jtools) # use of summ()
library(patchwork) # ggplot2 multiplot title
library(class) # knn function

# load the dataset from github
pcos <- read.csv("https://raw.githubusercontent.com/letisalba/Data-698/master/Data-Collection-and-Analy...
pcos2 <- read.csv("https://raw.githubusercontent.com/letisalba/Data-698/master/Data-Collection-and-Analy...

# display the `pcos` dataset
pcos %>%
  kable(caption = "<font color=#000000><b>Table 1.</b>`pcos` data </font>", format = "html", col.names = ...
  kable_styling(bootstrap_options = c("hover", "condensed"), font_size = 13) %>%
  kableExtra::scroll_box(width = "100%", height = "400px")

# display the `pcos2` dataset
pcos2 %>%
  kable(caption = "<font color=#000000><b>Table 2.</b>`pcos2` data </font>", format = "html", col.names = ...
  kable_styling(bootstrap_options = c("hover", "condensed"), font_size = 13) %>%
  kableExtra::scroll_box(width = "100%", height = "400px")

# summary of the pcos dataset
skim(pcos)

# summary of the pcos2 dataset
skim(pcos2)

DataExplorer::plot_histogram(
  geom_histogram_args = list(alpha = 1, fill = "#7e102c"),
  title = "Fig. 1 - Histogram of `pcos` data",
  data = pcos,
  ggtheme=theme_ipsum())

DataExplorer::plot_histogram(
  geom_histogram_args = list(alpha = 1, fill = "#a86800"),
  title = "Fig. 1 - Histogram of `pcos2` data",
  data = pcos2,
  ggtheme=theme_ipsum())

# change variables to numeric
pcos <- mutate_all(pcos, function(x) as.numeric(as.character(x)))
pcos2 <- mutate_all(pcos2, function(x) as.numeric(as.character(x)))

```

```

# missing data
colSums(is.na(pcos))

# missing data
colSums(is.na(pcos2))

# removing first two column for `pcos` data
pcos <- dplyr::select(pcos, -c(2:6))

# renaming columns for `pcos` data
pcos <- pcos %>%
  rename("Sl.No" = "Sl..No")

# removing columns not needed for `pcos_infertility` data
pcos2 <- dplyr::select(pcos2, -c(2, 45))

# renaming columns for `pcos_infertility` data
pcos2 <- pcos2 %>%
  rename("Sl.No" = "Sl..No",
        "PCOS" = "PCOS..Y.N.",
        "Age_yrs" = "Age..yrs.",
        "Weight" = "Weight..Kg.",
        "Height" = "Height.Cm.",
        "BMI" = "BMI",
        "Blood_Group" = "Blood.Group",
        "Pulse_rate_bpm" = "Pulse.rate.bpm.",
        "RR_breaths_min" = "RR..breaths.min.",
        "Hb_gdl" = "Hb.g.dl.",
        "Cycle_RI" = "Cycle.R.I.",
        "Cycle_length_days" = "Cycle.length.days.",
        "Married_yrs" = "Marraige.Status..Yrs.",
        "Pregnant" = "Pregnant.Y.N.",
        "No_of_abortions" = "No..of.aborptions",
        "IbetaHCG_mIUmL" = "I...beta.HCG.mIU.mL.",
        "IIbetaHCG_mIUmL" = "II...beta.HCG.mIU.mL.",
        "FSH_mIUmL" = "FSH.mIU.mL.",
        "LH_mIUmL" = "LH.mIU.mL.",
        "FSH_LH" = "FSH.LH",
        "Hip" = "Hip.inch.",
        "Waist" = "Waist.inch.",
        "Waist_Hip_Ratio" = "Waist.Hip.Ratio",
        "TSH_mIUmL" = "TSH..mIU.L.",
        "AMH_ngmL" = "AMH.ng.mL.",
        "PRL_ngmL" = "PRL.ng.mL.",
        "Vit_D3_ngmL" = "Vit.D3..ng.mL.",
        "PRG_ngmL" = "PRG.ng.mL.",
        "RBS_mgdL" = "RBS.mg.dL",
        "Weight_gain" = "Weight.gain.Y.N.",
        "Hair_growth" = "hair.growth.Y.N.",
        "Skin_darkening" = "Skin.darkening..Y.N.",
        "Hair_loss" = "Hair.loss.Y.N.",
        "Pimples" = "Pimples.Y.N.",
        "Fast_food" = "Fast.food..Y.N.",

```

```

"Reg_Exercise" = "Reg.Exercise.Y.N.",
"BP_Systolic_mmHg" = "BP._Systolic..mmHg.",
"BP_Diastolic_mmHg" = "BP._Diastolic..mmHg.",
"Follicle_NoL" = "Follicle.No...L.",
"Follicle_NoR" = "Follicle.No...R.",
"Avg_F_sizeL_mm" = "Avg..F.size..L...mm.",
"Avg_F_sizeR_mm" = "Avg..F.size..R...mm.",
"Endometrium_mm" = "Endometrium..mm.")

# merge data sets
pcos_data <- merge(pcos, pcos2, by=c("Sl.No"))
# display the merged dataset
pcos_data %>%
kable(caption = "<font color=#000000><b>Table 3.</b>`pcos_data` merged data </font>",
      format = "html", col.names = colnames(pcos_data)) %>%
kable_styling(bootstrap_options = c("hover", "condensed"), font_size = 13) %>%
kableExtra::scroll_box(width = "100%", height = "400px")

# convert Height from cm to
pcos_data$"Height" <- round((pcos_data$"Height" * 0.01),1)

# convert hip and waist from inches to cm
pcos_data$"Hip" <- round((pcos_data$"Hip" * 2.54),1)
pcos_data$"Waist" <- round((pcos_data$"Waist" * 2.54),1)

#calculate BMI
pcos_data$"BMI" <- round((pcos_data$"Weight" / pcos_data$"Height"^-2), 1)

# calculate waist-hip ratio
pcos_data$"Waist_Hip_Ratio" <- round((pcos_data$"Waist" / pcos_data$"Hip")),2)

# calculate FSH/LH
pcos_data$"FSH_LH" <- round((pcos_data$"FSH_mIUmL"/pcos_data$"LH_mIUmL"),2)

# calculate Married years
pcos_data$"Married(yrs)"[is.na(pcos_data$"Married(yrs)")] <- median(pcos_data$"Married(yrs)",
na.rm = T)

# calculate Fast food
pcos_data$"Fast_food"[is.na(pcos_data$"Fast_food")] <- median(pcos_data$"Fast_food",
na.rm = T)

# calculate
pcos_data$"AMH_ngmL"[is.na(pcos_data$"AMH_ngmL")] <- median(pcos_data$"AMH_ngmL",
na.rm = T)

# List of variables to round
vars_to_round <- c("Hb_gdl", "Married_yrs", "IbetaHCG_mIUmL", "IbetaHCG_mIUmL",
"FSH_mIUmL", "LH_mIUmL", "FSH_LH", "TSH_mIUmL", "AMH_ngmL", "PRL_ngmL",
"Vit_D3_ngmL", "PRG_ngmL", "Avg_F_sizeR_mm", "Endometrium_mm")

# Rounding the variables to 1 decimal places
pcos_data <- pcos_data %>%

```

```

mutate_at(vars(vars_to_round), ~ round(., digits = 1))

# remove 1st column
pcos_cleaned <- pcos_data[-1]

# display results of cleaned pcos
pcos_cleaned %>%
kable(caption = "<font color=#000000><b>Table 4.</b>`pcos_cleaned` dataset </font>",
      format = "html", col.names = colnames(pcos_cleaned)) %>%
  kable_styling(bootstrap_options = c("hover", "condensed"), font_size = 13) %>%
  kableExtra::scroll_box(width = "100%", height = "400px")

DataExplorer:::plot_histogram(
  geom_histogram_args = list(alpha = 1, fill = "dark blue"),
  title = "Fig. 3 - Histogram of `pcos_cleaned` data",
  data = pcos_cleaned,
  ggtheme=theme_ipsum())

# Selecting only the numerical variables for correlation
numerical_data <- pcos_cleaned[, sapply(pcos_cleaned, is.numeric)]

# Calculating the correlation matrix
cor_matrix <- cor(numerical_data)

# Print the correlation matrix
corrplot(cor_matrix, method = "color", type = "lower",
         tl.col = "black", tl.cex = 0.9, title = "Fig. 4 Correlation plot of `pcos_cleaned` data", mar=0)

# boxplot of the variables with the outlier parameters
pcos_df2 <- pcos_cleaned %>%
  gather(variable, values, 1:dim(pcos_cleaned)[2])
pcos_df2 %>%
  ggplot() +
  geom_boxplot(aes(x = variable, y = values)) +
  facet_wrap(~variable, ncol = 4, scales = "free") +
  ggtitle("Fig. 5 - Boxplot outliers for `pcos_cleaned` data") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=12)
  )

# Histogram of Age distribution
p1 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`Age_yrs`))) +
  geom_histogram(stat = "count", fill = "#F39C12", color = "#e9ecef", alpha = 0.9) +
  geom_text(stat = "count", aes(label = ..count..), position = position_dodge(width = 1), vjust = -0.5,
            labs(title = "Age Distribution", x = "Age (years)", y = "Count") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size = 10), axis.text.x = element_text(angle = 90, vjust = 1, hjust=2, size = 10)
  )

```

```

# Histogram of Weight distribution
p2 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`Weight`))) +
  geom_histogram(stat = "count", fill = "#FF5733", color = "#e9ecef", alpha = 0.9) +
  geom_text(stat = "count", aes(label = ..count..), position = position_dodge(width = 1), vjust = -0.5,
            labs(title="Weight Distribution", x ="Weight (kg)", y = "Count") +
            theme_ipsum() +
            theme(
              plot.title = element_text(size=12), axis.text.x = element_text(angle = 90, vjust = 1, hjust=2, vpad=5)
            )
  )

# Histogram of years married distribution
p3 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`Married_yrs`))) +
  geom_histogram(stat="count", show.legend = FALSE, fill = "#C70039", color = "#e9ecef", alpha=0.9) +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5,
            labs(title="Years Married Distribution", x ="Married (yrs)", y = "count") +
            theme_ipsum() +
            theme(
              plot.title = element_text(size=12), axis.text.x = element_text(angle = 90, vjust = 1, hjust=2, vpad=5)
            )
  )

# plot all histograms
ggp_all <- (p1 + p2 + p3) +      # Create grid of plots with title
  plot_annotation(title = "Fig. 6 - Scatterplot of Biometric measures Variables") &
  theme(plot.title = element_text(hjust = 0.5))
ggp_all

# Scatterplot of Age and Weight
p4 <- pcos_cleaned %>%
  ggplot(aes(x=`Age_yrs`, y=`Weight`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
                                           "Yes")) +
  labs(title="Age(yrs) with Weight(kg)",
       x = "Age(yrs)", y = "Weight(kg)") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot of Hip and Waist
p5 <- pcos_cleaned %>%
  ggplot(aes(x=`Hip`, y=`Waist`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
                                           "Yes")) +
  labs(title="Relationship between Hip(cm) and Waist(cm)",
       x = "Hip (cm)", y = "Waist (cm)") +
  theme_ipsum() +
  theme(

```

```

    plot.title = element_text(size=10)
  )

# Scatterplot of Length of Cycle and Age
p6 <- pcos_cleaned %>%
  ggplot(aes(x=`Age_yrs`, y=`Cycle_length_days`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
  "Yes")) +
  labs(title="Length of cycle based on Age",
       x ="Age(yrs)", y = "Cycle Length(days)") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot of Type of Cycle and Age
p7 <- pcos_cleaned %>%
  ggplot(aes(x=`Age_yrs`, y=`Cycle_RI`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
  "Yes")) +
  labs(title="Type of cycle based on Age",
       x ="Age(yrs)", y = "Cycle(R/I)") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot of BMI and Age
p8 <- pcos_cleaned %>%
  ggplot(aes(x=`Age_yrs`, y=BMI, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
  "Yes")) +
  labs(title="BMI based on Age",
       x ="Age(yrs)", y = "BMI") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot of number of follicles in left and right ovaries and PCOS
p9 <- pcos_cleaned %>%
  ggplot(aes(x=`Follicle_NoR`, y=`Follicle_NoL`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
  "Yes")) +
  labs(title="Number of Follicles",

```

```

      x ="Follicles Right", y = "Follicles Left") +
theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot of follicle size and PCOS
p10 <- pcos_cleaned %>%
ggplot(aes(x=`Avg_F_sizeR_mm`, y=`Avg_F_sizeL_mm`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
  "Yes")) +
  labs(title="Follicle size's",
       x ="Follicle size right", y = "Follicle size left") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot of Endometrium and Length of Cycles
p11 <- pcos_cleaned %>%
ggplot(aes(x=`Endometrium_mm`, y=`Cycle_length_days`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
  "Yes")) +
  labs(title="Endometrium and length of cycle(days)",
       x ="Endometrium(mm)", y = "Cycle Length(days)") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot of pregnancy hormone levels
p12 <- pcos_cleaned %>%
ggplot(aes(x=`IbetaHCG_mIUmL`, y=`IIbetaHCG_mIUmL`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
  "Yes")) +
  labs(title="Pregnancy hormone levels",
       x ="I Beta-HCG(mIU/mL)", y = "II Beta-HCG(mIU/mL)") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot of blood pressure levels against PCOS
p13 <- pcos_cleaned %>%
ggplot(aes(x=`BP_Diastolic_mmHg`, y=`BP_Systolic_mmHg`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +

```

```

    scale_colour_discrete("PCOS", labels = c("No",
    "Yes")) +
  labs(title="Blood Pressure levels",
      x ="BP_Diastolic(mmHg)", y = "BP_Systolic(mmHg)") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot of Respiration rate and Pulse rate against PCOS
p14 <- pcos_cleaned %>%
  ggplot(aes(x=`RR_breaths_min`, y=`Pulse_rate_bpm`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
    "Yes")) +
  labs(title="Respiration rate vs Pulse rate(bpm)",
      x ="RR(breaths/min)", y = "Pulse rate(bpm)") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# Scatterplot on Ovarian reserve against PCOS
p15 <- pcos_cleaned %>%
  ggplot(aes(x=`AMH_ngmL`, y=`FSH_LH`, color=as.factor(`PCOS`))) +
  geom_point() +
  geom_smooth(method="lm", se=FALSE) +
  scale_colour_discrete("PCOS", labels = c("No",
    "Yes")) +
  labs(title="Ovarian reserve against follicle growth",
      x ="Ovarian reserve", y = "Growth of ovarian follicles") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# plot all scatterplots
ggp_all2 <- (p4 + p5 + p6) / (p7 + p8 + p9) / (p10 + p11 + p12) / (p13 + p14 + p15) +
  plot_annotation(title = "Fig. 7 - Scatterplot of variables with PCOS yes or no as factor") &
  theme(plot.title = element_text(hjust = 0.5))
ggp_all2

# barchart of PCOS variable
p16 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`PCOS`), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  labs(title="PCOS", x ="PCOS(Yes or No)", y = "count") +
  theme_ipsum() +
  theme(

```

```

    plot.title = element_text(size=10)
  )

# barchart of Pregnant variable
p17 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Pregnant), fill = as.factor(Pregnant))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  scale_fill_discrete(name = "Pregnant", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  labs(title="Pregnant", x ="Pregnant(Yes or No)", y = "count") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# barchart of Weight gain variable
p18 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Weight_gain), fill = as.factor(Weight_gain))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  scale_fill_discrete(name = "Weight Gain", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  labs(title="Weight Gain", x ="Weight Gain (Yes or No)", y = "count") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# barchart of Hair growth variable
p19 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Hair_growth), fill = as.factor(Hair_growth))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  scale_fill_discrete(name = "Hair Growth", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  labs(title="Hair Growth", x ="Hair Growth(Yes or No)", y = "count") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# barchart of Skin darkening variable
p20 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Skin_darkening), fill = as.factor(Skin_darkening))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  scale_fill_discrete(name = "Skin Darkening", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  labs(title="Skin Darkening", x ="Skin Darkening (Yes or No)", y = "count") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

```

```

)

# barchart of Hair loss variable
p21 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Hair_loss), fill = as.factor(Hair_loss))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  scale_fill_discrete(name = "Hair Loss", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  labs(title="Hair Loss", x ="Hair Loss(Yes or No)", y = "count") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# barchart of Pimples variable
p22 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Pimples), fill = as.factor(Pimples))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  scale_fill_discrete(name = "Pimples", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  labs(title="Pimples", x ="Pimples(Yes or No)", y = "count") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# barchart of Fast food variable
p23 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Fast_food), fill = as.factor(Fast_food))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  scale_fill_discrete(name = "Fast Food", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  labs(title="Fast Food", x ="Fast Food(Yes or No)", y = "count") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

# barchart of Regularly Exercise variable
p24 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Reg_Exercise), fill = as.factor(Reg_Exercise))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  scale_fill_discrete(name = "Regular Exercise", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  labs(title="Regularly Exercise", x ="Regular Exercise(Yes or No)", y = "count") +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10)
  )

```

```

# plot all barcharts
ggp_all3 <- (p16 + p17 + p18) / (p19 + p20 + p21) / (p22 + p23 + p24) +
  plot_annotation(title = "Fig. 8 - Bar charts of Bloodwork variables") &
  theme(plot.title = element_text(hjust = 0.5))
ggp_all3

# barchart of Blood Group variable against PCOS
p25 <- pcos_cleaned %>%
  ggplot(aes(x = Blood_Group, fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggtitle("Blood Group with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# barchart of Pregnant variable against PCOS
p26 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Pregnant), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  ggtitle("Pregnant with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# barchart of Weight gain variable against PCOS
p27 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Weight_gain), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  ggtitle("Weight gain with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# barchart of Hair growth variable against PCOS
p28 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Hair_growth), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  ggtitle("Hair growth with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No', 'Yes')) +
  theme_ipsum() +
  theme(

```

```

    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# barchart of Skin darkening variable against PCOS
p29 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Skin_darkening), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  ggttitle("Skin darkening with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No','Yes')) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# barchart of Hair loss variable against PCOS
p30 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Hair_loss), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  ggttitle("Hair loss with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No','Yes')) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# barchart of Pimples variable against PCOS
p31 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Pimples), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  ggttitle("Pimples with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No','Yes')) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# barchart of Fast food variable against PCOS
p32 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Fast_food), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  ggttitle("Fast food consumption with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No','Yes')) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

```

```

)

# barchart of Reg. Exercise variable against PCOS
p33 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(Reg_Exercise), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  geom_text(aes(label = ..count..), position = position_dodge(width = 1), stat = "count", vjust = 1.5)
  ggttitle("Regularly exercises with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  scale_x_discrete(labels=c('No','Yes')) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# barchart of Length of Cycle variable against PCOS
p34 <- pcos_cleaned %>%
  ggplot(aes(x = `Cycle_length_days`, fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggttitle("Cycle length in days with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# barchart of Number of abortions variable against PCOS
p35 <- pcos_cleaned %>%
  ggplot(aes(x = No_of_abortions, fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggttitle("Number of abortions with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45)
  )

# plot all barcharts
ggp_all4 <- (p25 + p26 + p27) / (p28 + p29 + p30) / (p31 + p32 + p33) / (p34 + p35) +
  plot_annotation(title = "Fig. 9 - Bar charts of yes or no variables") &
  theme(plot.title = element_text(hjust = 0.5))
ggp_all4

# Barchart for Vitamin D3 levels with PCOS
p36 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`Vit_D3_ngmL`), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggttitle("Vitamin D3 levels with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45, size = 2)
  )

```

```

# Barchart for FSH/LH levels with PCOS
p37 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`FSH_LH`), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggtitle("FSH/LH levels with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45, size = 2)
  )

# Barchart for Thyroid Hormone levels with PCOS
p38 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`TSH_mIUmL`), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggtitle("Thyroid Hormone levels with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45, size = 2)
  )

# Barchart of hemoglobin levels with PCOS
p39 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`Hb_gdl`), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggtitle("Hemoglobin levels with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45, size = 2)
  )

# Barchart of Prolactin levels with PCOS
p40 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`PRL_ngmL`), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggtitle("Prolactin levels with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45, size = 2)
  )

# Barchart of Progesterone levels with PCOS
p41 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`PRG_ngmL`), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggtitle("Progesterone levels with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(

```

```

    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45, size = 2)
)

# Barchart of Glucose levels with PCOS
p42 <- pcos_cleaned %>%
  ggplot(aes(x = as.factor(`RBS_mgdl`), fill = as.factor(`PCOS`))) +
  geom_bar(position = "dodge") +
  ggtitle("Glucose levels with PCOS") +
  scale_fill_discrete(name = "PCOS", labels = c("No", "Yes")) +
  theme_ipsum() +
  theme(
    plot.title = element_text(size=10), axis.text.x = element_text(angle = 45, size = 2)
  )

# plot barcharts
ggp_all15 <- (p36 + p37 + p38 + p39) / (p40 + p41 + p42) +
  plot_annotation(title = "Fig. 10 - Bar charts of Yes or No variables") &
  theme(plot.title = element_text(hjust = 0.5))
ggp_all15

```



```

# DECISION TREE:

# create some random numbers for reproduction
set.seed(29)

# Cross Validation Set-up
inTrain <- createDataPartition(pcos_cleaned$`PCOS`, p=.75, list = F)
train <- pcos_cleaned[inTrain,]
valid <- pcos_cleaned[-inTrain,]

# create the decision tree
rpart_model <- rpart(`PCOS` ~ ., method = "class", data = train)

# display the decision tree
prp(rpart_model, main = "Fig. 12 - Decision Tree with entire dataset",
     extra=1, faclen=0, nn=T, box.palette="Blues")

# creating our prediction
rpart_result <- predict(rpart_model,
                         newdata = valid[, !colnames(valid) %in% "PCOS"],
                         type = 'class')

# confusion matrix
confusionMatrix(rpart_result, as.factor(valid$`PCOS`))

# contribution of variables
varImp(rpart_model) %>% kable()

# Extract accuracy from the confusion matrix
accuracy_rpart <- confusionMatrix(rpart_result, as.factor(valid$`PCOS`))$overall["Accuracy"]
kable(accuracy_rpart, align = "l")

```

```

# creating the second dataset from the original
pcos_cleaned2 <- pcos_cleaned %>%
  select(`PCOS`, `Follicle_NoR`, `Follicle_NoL`, `Weight_gain`,
         `Skin_darkening`, `Hair_growth`)

# create some random number for reproduction
set.seed(28)

# Second Cross Validation Set-up
inTrain2 <- createDataPartition(pcos_cleaned2$`PCOS`, p=.75, list = F)
train2 <- pcos_cleaned2[inTrain2,]
valid2 <- pcos_cleaned2[-inTrain2,]

# create the second decision tree
rpart_model2 <- rpart(`PCOS` ~ ., method = "class", data = train2)

# display the decision tree
prp(rpart_model2, main = "Fig. 13 - Second Decision Tree with 6 variables",
     extra=1, faclen=0, nn=T, box.palette="Blues")

# creating our prediction
rpart_result2 <- predict(rpart_model2,
                           newdata = valid2[, !colnames(valid2) %in% "PCOS"],
                           type = 'class')

# creating the second confusion matrix
confusionMatrix(rpart_result2, as.factor(valid2$`PCOS`))

# contribution of variables
varImp(rpart_model2) %>% kable()

# Extract accuracy from the confusion matrix
accuracy_rpart2 <- confusionMatrix(rpart_result2,
                                      as.factor(valid2$`PCOS`))$overall["Accuracy"]
kable(accuracy_rpart2, align = "l")

# RANDOM FOREST:

# create some random numbers for reproduction
set.seed(30)

# Cross Validation Set-up
rf_inTrain <- createDataPartition(pcos_cleaned$`PCOS`, p=.75, list = F)
rf_train <- pcos_cleaned[rf_inTrain,]
rf_valid <- pcos_cleaned[-rf_inTrain,]

# check the levels of PCOS using levels()
levels(rf_train$PCOS)
levels(rf_valid$PCOS)

# Convert PCOS to factor in rf_train
rf_train$PCOS <- factor(rf_train$PCOS)

```

```

# Convert PCOS to factor in rf_valid
rf_valid$PCOS <- factor(rf_valid$PCOS)

# rechecking levels again to ensure no NULL values
levels(rf_train$PCOS)
levels(rf_valid$PCOS)

# explicitly set the levels to match the levels in srf_train.
rf_valid$PCOS <- factor(rf_valid$PCOS, levels = levels(rf_train$PCOS))
levels(rf_valid$PCOS)

# # Check the length of rf_result and rf_valid$PCOS
# length_rf_result <- length(rf_result)
# length_rf_valid <- length(rf_valid$PCOS)
#
# # Print the lengths for comparison
# print(length_rf_result)
# print(length_rf_valid)

# create some random number for reproduction
set.seed(39)

# create random forest model using the training data
rf_model <- randomForest(PCOS~., rf_train)
rf_model

# prediction
rf_result <- predict(rf_model, newdata = valid[, !colnames(valid) %in% "PCOS"])

# Create a confusion matrix
confusionMatrix(data = rf_result, reference = rf_valid$PCOS)

# plot for rf_model
varImpPlot(rf_model)

# table for rf_model variable contribution
varImp(rf_model) %>% kable()

# Extract accuracy from the confusion matrix for the rf_model
accuracy_rf <- confusionMatrix(rf_result, valid$PCOS)$overall["Accuracy"]
accuracy_rf

# create some random numbers for reproduction
set.seed(78)

# Second RF Cross Validation Set-up
rf_inTrain2 <- createDataPartition(pcos_cleaned2$`PCOS`, p=.75, list = F)
rf_train2 <- pcos_cleaned2[rf_inTrain2,]
rf_valid2 <- pcos_cleaned2[-rf_inTrain2,]

# check the levels of PCOS using levels()
levels(rf_train2$PCOS)
levels(rf_valid2$PCOS)

```

```

# Convert PCOS to factor in rf_train
rf_train2$PCOS <- factor(rf_train2$PCOS)

# Convert PCOS to factor in rf_valid
rf_valid2$PCOS <- factor(rf_valid2$PCOS)

# rechecking levels again to ensure no NULL values
levels(rf_train2$PCOS)
levels(rf_valid2$PCOS)

# explicitly set the levels to match the levels in rf_train.
rf_valid2$PCOS <- factor(rf_valid2$PCOS, levels = levels(rf_train2$PCOS))
levels(rf_valid2$PCOS)

# # Check the length of rf_result and rf_valid$PCOS
# length_rf_result2 <- length(rf_result2)
# length_rf_valid2 <- length(rf_valid2$PCOS)
#
# # Print the lengths for comparison
# print(length_rf_result2)
# print(length_rf_valid2)

# create some random number for reproduction
set.seed(7)

# create the second random forest model using the training data from the third decision tree
rf_model2 <- randomForest(PCOS ~ Follicle_NoR + Follicle_NoL +
                           Weight_gain + Skin_darkening +
                           Hair_growth, data = rf_train2)
rf_model2

# creating the prediction for the third decision tree
rf_result2 <- predict(rf_model2, newdata = rf_valid2[, !colnames(rf_valid2) %in% "PCOS"])

# Convert PCOS column to factor in rf_train2 and rf_valid2
rf_train2$PCOS <- factor(rf_train2$PCOS)
rf_valid2$PCOS <- factor(rf_valid2$PCOS)

# # Check unique levels in rf_result2 and rf_valid2$PCOS
# unique_levels_result <- unique(rf_result2)
# unique_levels_valid <- unique(rf_valid2$PCOS)
#
# # Check if the levels match
# identical(unique_levels_result, unique_levels_valid)
#
# # If levels do not match, manually set levels in rf_result2 to match those in rf_valid2$PCOS
# levels(rf_result2) <- levels(rf_valid2$PCOS)
#
# Convert rf_result2 to factor and align levels with rf_valid2$PCOS
rf_result2_factor <- factor(rf_result2, levels = levels(rf_valid2$PCOS))

# Create a confusion matrix
confusionMatrix(data = rf_result2_factor, reference = rf_valid2$PCOS)

```

```

# plot for the second rf_model
varImpPlot(rf_model2)

# table for rf_model2 variable contribution
varImp(rf_model2) %>% kable()

# Extract accuracy from the confusion matrix for the rf_model2
accuracy_rf2 <- confusionMatrix(data = rf_result2_factor,
                                    reference = rf_valid2$PCOS)$overall["Accuracy"]
accuracy_rf2

# GRADIENT BOOSTING MACHINES:

# Set seed for reproducibility
set.seed(67)

# Train the GBM model
gbm_model <- gbm(`PCOS` ~ ., data = train,
                  distribution = "bernoulli", n.trees = 100,
                  interaction.depth = 4, shrinkage = 0.01,
                  bag.fraction = 0.5)

# Print the summary of the trained model
summary(gbm_model)

# Predict on the validation dataset (assuming 'valid' contains your validation dataset)
gbm_pred <- predict(gbm_model, newdata = valid, type = "response")

# Calculate predicted classes (0 or 1) based on the predicted probabilities
predicted_classes <- ifelse(gbm_pred > 0.5, 1, 0)

# Create confusion matrix
confusionMatrix(data = factor(predicted_classes), reference = factor(valid$`PCOS`))

# Calculate accuracy
gbm_accuracy <- sum(predicted_classes == valid$`PCOS`) / length(valid$`PCOS`)
cat("Accuracy:", gbm_accuracy)

# creating the second dataset from the original
pcos_cleaned3 <- pcos_cleaned %>%
  select(`PCOS`, `Follicle_NoR`, `Follicle_NoL`,
         `Weight_gain`, `Skin_darkening`, `Hair_growth`)

# Set seed for reproducibility
set.seed(68)

# Cross Validation Set-up
inTrain3 <- createDataPartition(pcos_cleaned3$`PCOS`, p=.75, list = F)
train3 <- pcos_cleaned3[inTrain3,]
valid3 <- pcos_cleaned3[-inTrain3,]

# Train the GBM model
gbm_model2 <- gbm(`PCOS` ~ ., data = train3,

```

```

        distribution = "bernoulli", n.trees = 100,
        interaction.depth = 4, shrinkage = 0.01,
        bag.fraction = 0.5)

# Print the summary of the trained model
summary(gbm_model2)

# Predict on the validation dataset (assuming 'valid' contains your validation dataset)
gbm_pred2 <- predict(gbm_model2, newdata = valid3, type = "response")

# Calculate predicted classes (0 or 1) based on the predicted probabilities
predicted_classes2 <- ifelse(gbm_pred2 > 0.5, 1, 0)

# Create confusion matrix
confusionMatrix(data = factor(predicted_classes2), reference = factor(valid3$`PCOS`))

# Calculate accuracy
gbm_accuracy2 <- sum(predicted_classes2 == valid3$`PCOS`) / length(valid3$`PCOS`)
cat("Accuracy:", gbm_accuracy2)

# SUPPORT VECTOR MACHINES:

# check the levels of PCOS using levels()
levels(train$PCOS)
levels(valid$PCOS)

# Convert PCOS to factor in sum_train
train$PCOS <- factor(train$PCOS)

# Convert PCOS to factor in sum_valid
valid$PCOS <- factor(valid$PCOS)

# rechecking levels again to ensure no NULL values
levels(train$PCOS)
levels(valid$PCOS)

# checking the structure of both valid and train datasets
str(valid)
str(train)

# explicitly set the levels to match the levels in sum_train.
valid$PCOS <- factor(valid$PCOS, levels = levels(train$PCOS))
levels(valid$PCOS)

# # Check the length of sum_result and sum_valid$PCOS
# length_sum_result <- length(sum_result)
# length_sum_valid <- length(sum_valid$PCOS)
#
# # Print the lengths for comparison
# print(length_sum_result)
# print(length_sum_valid)

#create some random numbers for reproduction

```

```

set.seed(31)

# SVM
svm_model <- svm(PCOS ~ ., train)

# create prediction
svm_result <- predict(svm_model, newdata = valid)

# confusion matrix for sum
confusionMatrix(svm_result, valid$PCOS)

# summary of sum_result
summary(svm_result)

#Extract accuracy from the confusion matrix
accuracy_svm <- confusionMatrix(svm_result, as.factor(valid$`PCOS`))$overall["Accuracy"]
accuracy_svm

# create some random numbers for reproduction
set.seed(8)

# Cross Validation Set-up
svm_inTrain2 <- createDataPartition(pcos_cleaned2$PCOS, p=.75, list = FALSE)
svm_train2 <- pcos_cleaned2[svm_inTrain2,]
svm_valid2 <- pcos_cleaned2[-svm_inTrain2,]

# check the levels of PCOS using levels()
levels(svm_train2$PCOS)
levels(svm_valid2$PCOS)

# Convert PCOS to factor in sum_train2
svm_train2$PCOS <- factor(svm_train2$PCOS)

# Convert PCOS to factor in sum_valid2
svm_valid2$PCOS <- factor(svm_valid2$PCOS)

# rechecking levels again to ensure no NULL values
levels(svm_train2$PCOS)
levels(svm_valid2$PCOS)

# explicitly set the levels to match the levels in sum_train2
valid$PCOS <- factor(svm_valid2$PCOS, levels = levels(svm_train2$PCOS))
levels(svm_valid2$PCOS)

## Check the length of sum_result and sum_valid$PCOS
# length_sum_result <- length(sum_result)
# length_sum_valid2 <- length(sum_valid2$PCOS)
#
## Print the lengths for comparison
# print(length_sum_result)
# print(length_sum_valid2)

```

```

# Second SVM
svm_model2 <- svm(PCOS ~ Follicle_NoR + Follicle_NoL +
                    Weight_gain + Skin_darkening +
                    Hair_growth, svm_train2)

# create prediction
svm_result2 <- predict(svm_model2, newdata = svm_valid2)

# confusion matrix for sum_valid2
confusionMatrix(svm_result2, svm_valid2$PCOS)

# summary
summary(svm_result2)

#Extract accuracy from the confusion matrix
accuracy_svm2 <- confusionMatrix(svm_result2, svm_valid2$`PCOS`)$overall["Accuracy"]
accuracy_svm2

# NEURAL NETWORKS:

# create some random numbers for reproduction
set.seed(67)

# Cross Validation Set-up
nn_inTrain <- createDataPartition(pcos_cleaned$PCOS, p=.75, list = F)
nn_train <- pcos_cleaned[nn_inTrain,]
nn_valid <- pcos_cleaned[-nn_inTrain,]

# set a seed for reproducibility purposes
set.seed(19)

# create the model
nn_model <- neuralnet(`PCOS`~.,
                        data = nn_train,
                        hidden = c(12, 8), # Specify the number of hidden layers and neurons
                        linear.output = FALSE,
                        stepmax = 20000 # Increase the maximum number of iterations
)

# create the plot based on the model above
#plot(nn_model, rep = "best", main="")
#grid::grid.text("Fig. 15 - Neural Network", x = 0.5, y = 0.1)

# make predictions on the test data using a previously trained model
pred <- predict(nn_model, valid)

# create a vector of labels for the two possible `PCOS(Y/N)` status in the dataset.
labels <- c("0", "1")

# creates a data frame with the column index of the maximum value in each row of the "pred" variable
prediction_label <- data.frame(max.col(pred)) %>%
# use the mutate function to add a new column to the data frame called "pred"

```

```

mutate(pred=labels[max.col.pred.]) %>%
select(2) %>%
# convert the data frame to a vector.
unlist()

# print the table
table(valid$`PCOS`, prediction_label)

#checking the accuracy
check <- as.numeric(valid$`PCOS`) == max.col(pred)
nn_accuracy <- (sum(check)/nrow(valid))
nn_accuracy

# set a seed for reproducibility purposes
set.seed(13)

# create the second model
nn_model2 <- neuralnet(`PCOS`~Follicle_NoL + Follicle_NoR +
                         Hair_growth + Skin_darkening + Weight_gain,
                         data=train2,
                         hidden=c(2,1),
                         linear.output = FALSE,
                         stepmax = 10000 # Increase the maximum number of iterations
)

# create the plot based on the model above
plot(nn_model2, rep = "best", main="")
grid::grid.text("Fig. 15 - Neural Network", x = .5, y = .2)

# make predictions on the test data using a previously trained model
pred2 <- predict(nn_model2, valid2)

# create a vector of labels for the two possible `PCOS` status in the dataset.
labels2 <- c("0", "1")

# creates a data frame with the column index of the maximum value in each row of the "pred" variable
prediction_label2 <- data.frame(max.col(pred2)) %>%
# use the mutate function to add a new column to the data frame called "pred"
mutate(pred=labels2[max.col.pred2.]) %>%
select(2) %>%
# convert the data frame to a vector.
unlist()

# print the table
table(valid2$`PCOS`, prediction_label2)

# checking the accuracy
check2 <- as.numeric(valid2$`PCOS`) == max.col(pred2)
nn_accuracy2 <- (sum(check2)/nrow(valid2))
nn_accuracy2

# Remove rows with missing values from train and valid datasets
train <- train[complete.cases(train), ]

```

```

valid <- valid[complete.cases(valid), ]

# set a seed for reproducibility purposes
set.seed(78)

# Set the value of k for kNN
k <- 5 # Change this value as needed

# Fit the kNN model using the training data
knn_model <- knn(train[, -which(names(train) == "PCOS")],
                  valid[, -which(names(valid) == "PCOS")],
                  train$`PCOS`,
                  k = k)

# Calculate accuracy
knn_accuracy <- mean(knn_model == valid$`PCOS`)
knn_accuracy

# Filter and select the desired columns for the new dataset
pcos_cleaned4 <- pcos_cleaned %>%
  select(`PCOS`, `Follicle_NoR`, `Follicle_NoL`, `Weight_gain`,
         `Skin_darkening`, `Hair_growth`)

# Split the data into training and validation sets (if needed)
set.seed(123) # Set seed for reproducibility
inTrain4 <- createDataPartition(pcos_cleaned4$`PCOS`, p = 0.75, list = FALSE)
train4 <- pcos_cleaned4[inTrain4, ]
valid4 <- pcos_cleaned4[-inTrain4, ]

# Check for missing values and remove them if present
train4 <- train4[complete.cases(train4), ]
valid4 <- valid4[complete.cases(valid4), ]

# Set the value of k for kNN
k <- 5 # Change this value as needed

# Fit the kNN model using the training data
knn_model2 <- knn(train4[, -which(names(train4) == "PCOS")],
                   valid4[, -which(names(valid4) == "PCOS")],
                   train4$`PCOS`,
                   k = k)

# Calculate accuracy for the new kNN model
knn_accuracy2 <- mean(knn_model2 == valid4$`PCOS`)
knn_accuracy2

# Compare models
model_names <- c("Decision Tree 1", "Decision Tree 2",
                 "Random Forest 1", "Random Forest 2",
                 "Gradient Boost Machines 1",
                 "Gradient Boost Machines 2",
                 "SVM 1", "SVM 2", "Neural Network 1",
                 "Neural Network 2", "k-Nearest 1", "k-Nearest 2")

```

```

accuracies <- c(0.8592593, 0.9185185, 0.6148148, 0.9037037,
               0.8814815, 0.6222222, 0.9111111, 0.9185185,
               0.3037037, 0.3037037, 0.7111111, 0.8814815)

# place accuracies in data frame
results <- data.frame(Model = model_names, Accuracy = accuracies)

# order in descending order
results <- results[order(results$Accuracy, decreasing = TRUE), ]

# Display the results
kable(results, caption = "<font color=#000000><b>Table 5.</b>Model Comparison </font>",
       format = "html") %>%
  kable_styling(bootstrap_options = c("hover", "condensed"), font_size = 13) %>%
  kableExtra::scroll_box(width = "100%", height = "400px")

```