BREAST CANCER

WISCONSIN (DIAGNOSTIC) DATASET

Supervised Analysis for Malignancy Detection

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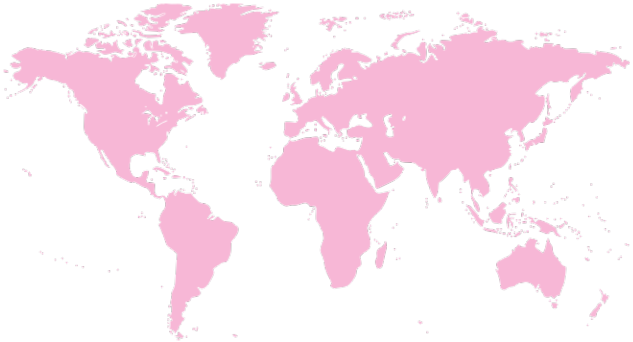
1. PRESENTATION OF THE PROBLEM

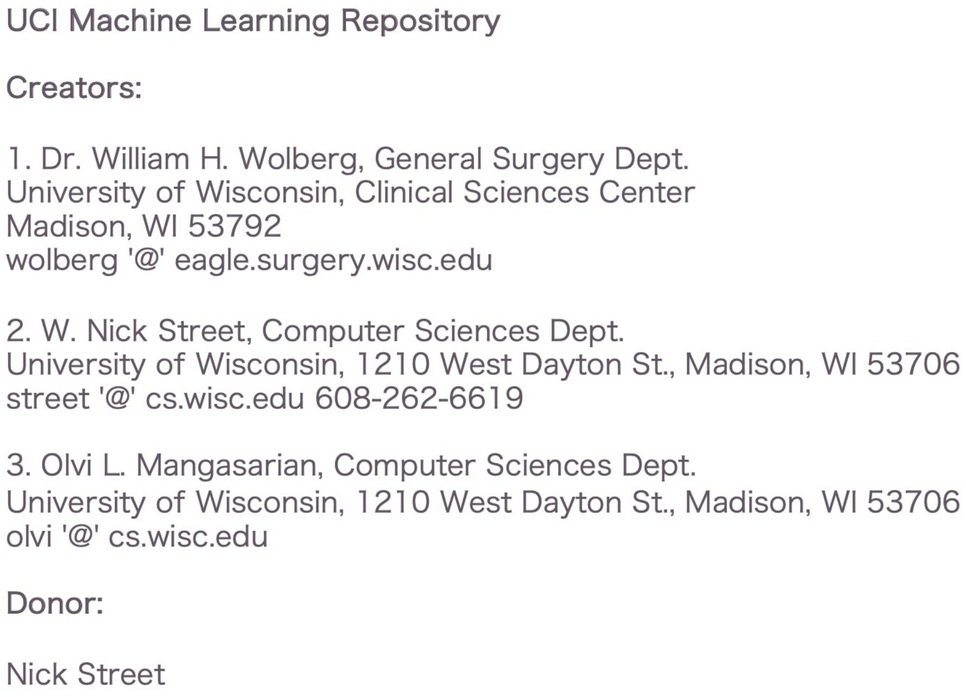


- Breast Cancer is the **most common type of cancer** among women across the world.
- **Leading cause of death from cancer in women**.

- **Biopsy is essential to distinguish between malignant and benignant tissue** but it requires **expensive** and **bulky equipment**, and **highly trained professionals**.
- **Digitalization** of pathology slides and **application of AI** can make diagnosis faster, cheaper, and provides a useful tool for phathologists.
- **Inferential analysis** can help statistically determine **differences between malignant and benignant populations**. It can also help determining **important features** for further AI modelling.

1. PRESENTATION OF THE PROBLEM

1.1 Source of the Database



UCI Machine Learning Repository

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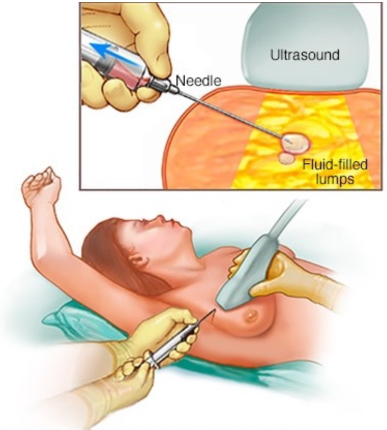
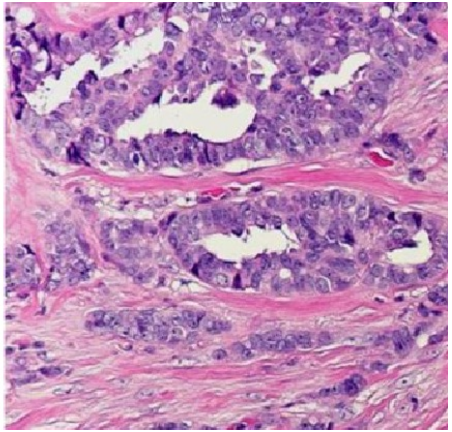
Is there any difference between benignant and malignant populations for each feature?

In other words, which features could significantly help determining diagnosis of each sample?

2. MATERIALS

2.2 Dataset Information: acquisition of the data





1. Tissue sample from Breast Tumor by Fine-Needle Aspiration (FNA)

569 tissue samples

2. Hystopathological analysis of 10 characteristics for each nucleus:

- **Radius** (mean of distances from the center to points on the perimeter)
- **Texture** (std of gry-scale values)
- **Perimeter**
- **Area**
- **Smoothness** (local variation in radius lentghs)
- **Compactness** ($perimeter^2/area - 1$)
- **Concavity** (severity of concave portions of the contour)
- **Concave points** (number of concave portions of the contour)
- **Simmetry**
- **Fractal Dimension** (“coastline approximation”-1)

**** No units were provided***

3. Mean, Ste and Worst Values of all nuclei characteristics in each sample

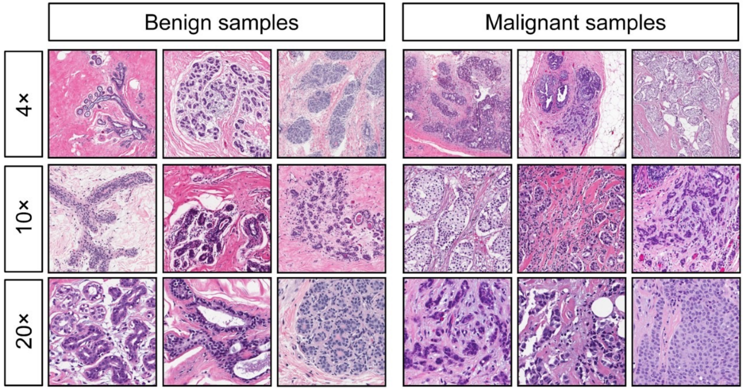
30 features

2. MATERIALS

2.2 Dataset Information: predictors and target variable

For each nucleus in each simple:

1. **Radius** (mean of distances from the center to points on the perimeter)
2. **Texture** (std of gry-scale values)
3. **Perimeter**
4. **Area**
5. **Smoothness** (local variation in radius lentghs)
6. **Compactness** ($perimeter^2/area - 1$)
7. **Concavity** (severity of concave portions of the contour)
8. **Concave points** (number of concave portions of the contour)
9. **Simmetry**
10. **Fractal Dimension** (“coastline approximation”-1)



Mean, Ste and Worst Values of nuclei characteristics in each sample

Diagnosis:

1. **Benignant (B)**
2. **Malignant (M)**

30 features + 1 Target Variable

3. EXPLORATORY DATA ANALYSIS

3.1 Data Types

Identifier

ID — Numerical and Discrete

Drop Column

Target Variable

Diagnosis — Categorical and Nominal

Transform to numerical discrete

Numerical and Continuous

Predictors

Mean, Std and Worst

Radius	Area	Concavity	Fractal dimension
Texture	Smoothness	Concave points	
Perimeter	Compactness	Simmetry	

Empty Column — Numerical, 0

Drop Column

3. EXPLORATORY DATA ANALYSIS

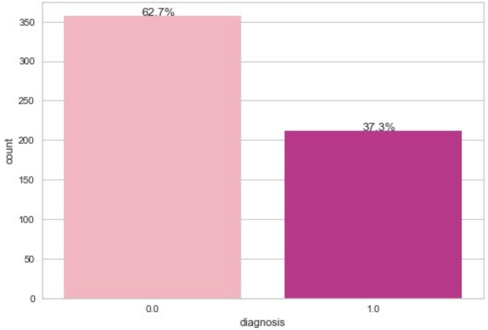
3.2 Descriptive statistics of the dataset

In order to summarize the main and most basic statistical characteristics of the dataset, we will use the method **describe:**

No abnormal values for max/min values were initially identified(e.g 0 values or max/min values highly above/below the mean).

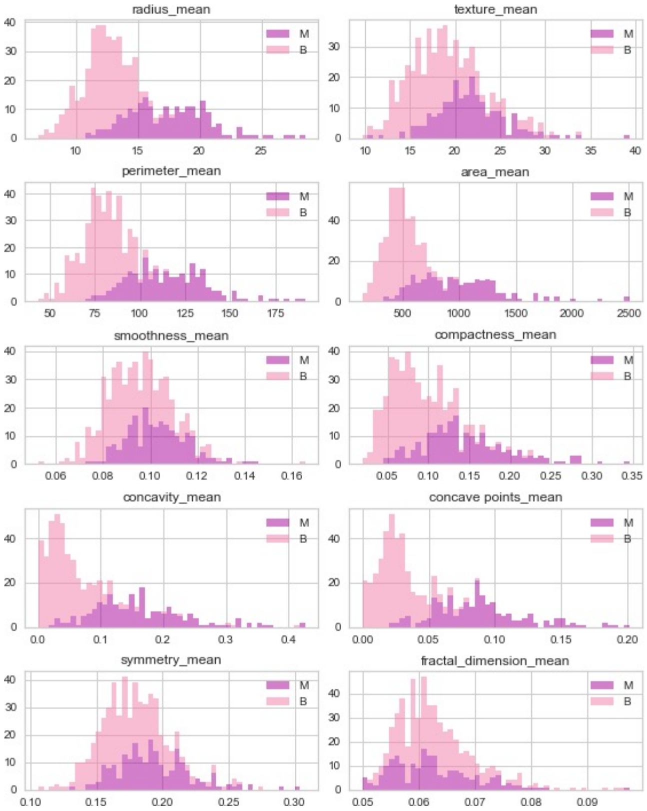
By plotting count of samples for each class we find that:

Class imbalance (62.7 %(B, majority class)/ 37.3% (M, minority class): moderate



3. EXPLORATORY DATA ANALYSIS

3.3 Univariate Analysis: Graphical



1. **Mean values** for radius, texture, perimeter, area, compactness, concavity and concave points **seem to be larger in malignant tissue.**

2. Features (distinguishing between malignant/benignant) follow, approximately, a **normal distribution.**

3. EXPLORATORY DATA ANALYSIS

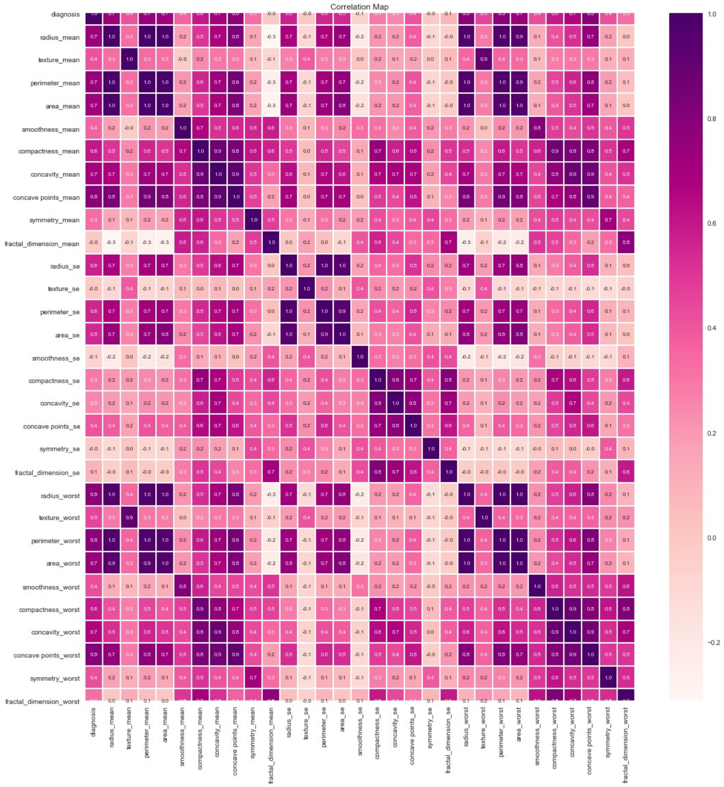
3.4 Multivariate Analysis: Correlation

1. **Strong** positive relationship between target variable and mean and worst values for **radius, area, perimeter, concavity and concave points (P. Correlation coefficient >0.7).**

2. **Strongest** relationship with **worst value for concave points**.

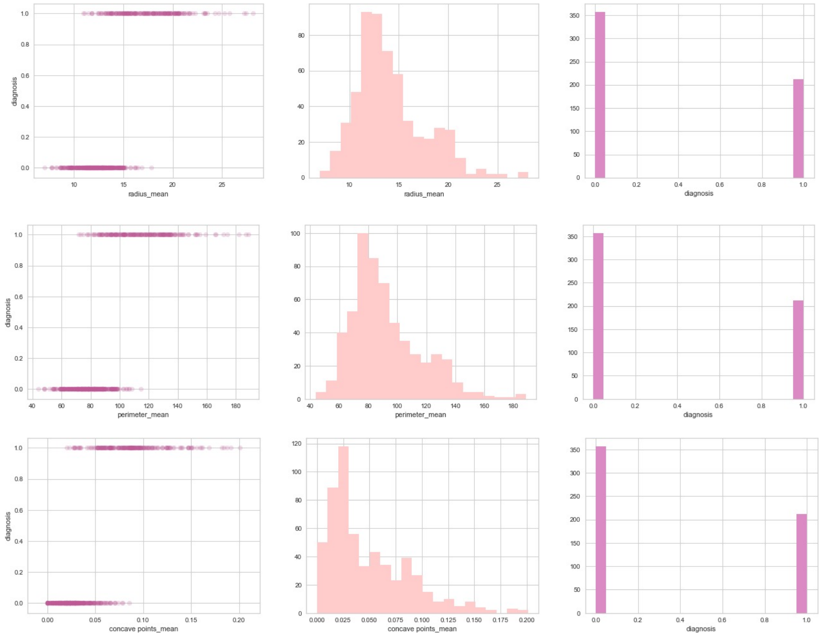
3. **Strong correlation between radius, perimeter and area.**

4. **Strong correlation between concave points, concavity and compactness.**

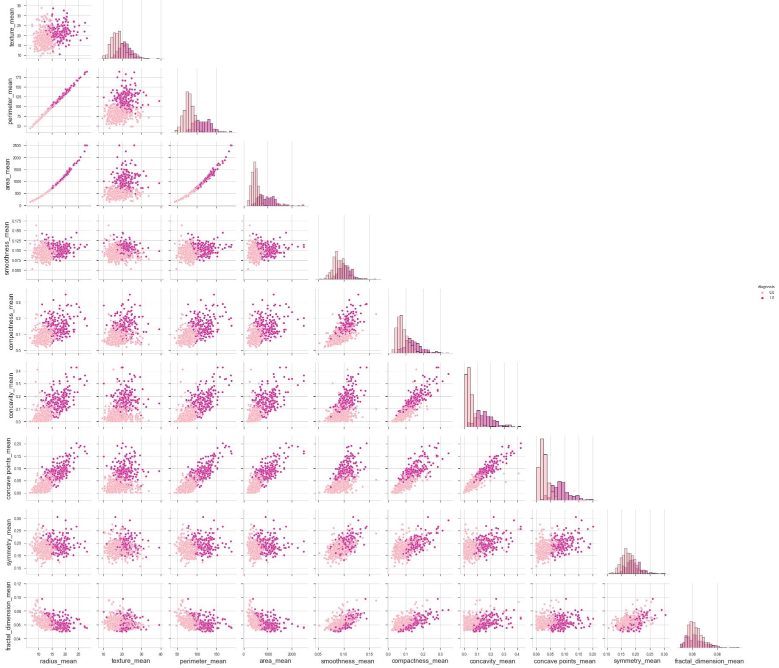


3. EXPLORATORY DATA ANALYSIS

3.5 Multivariate Analysis: Scatter Plots (Diagnosis vs each feature/ Feature vs Feature)



Only 1 feature suitable for Logistic Regression



Only 2 features suitable for models such as KNN

3. EXPLORATORY DATA ANALYSIS

3.6 Test for Normality

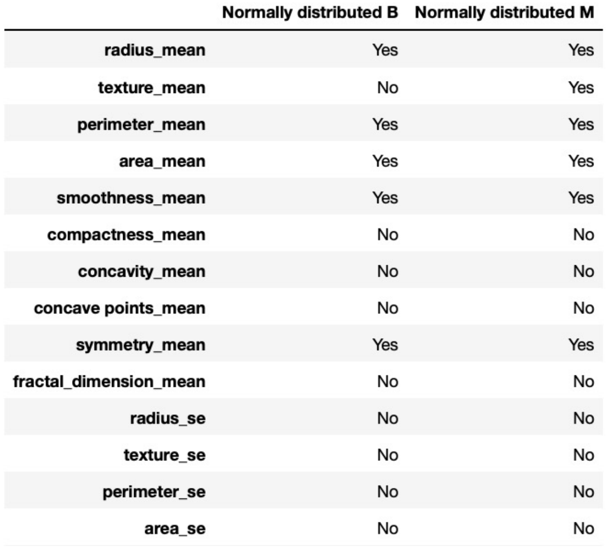
Kolmogorov-Smirnov (KS) test for normality (n > 50) for each population (malignant/benignant), for each feature:

H_0: The sample data are not significantly different than a normal population.

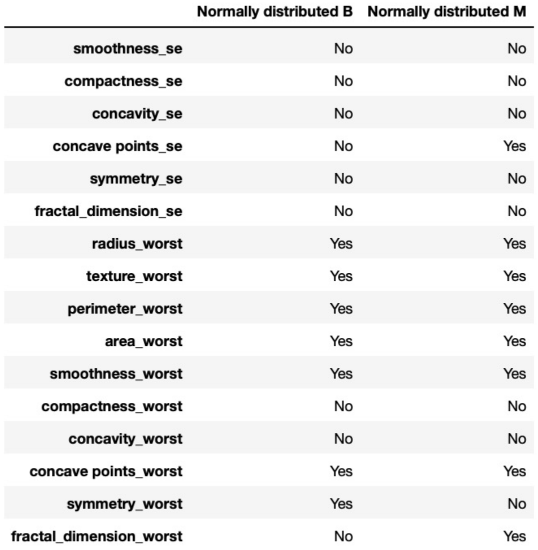
H_1: The sample data are significantly different than a normal population.

In general, normally/non-normally distribution between malignant and benignant populations for one feature.

Non-parametric methods should be used for hypothesis testing.



	Normally distributed B	Normally distributed M
radius_mean	Yes	Yes
texture_mean	No	Yes
perimeter_mean	Yes	Yes
area_mean	Yes	Yes
smoothness_mean	Yes	Yes
compactness_mean	No	No
concavity_mean	No	No
concave points_mean	No	No
symmetry_mean	Yes	Yes
fractal_dimension_mean	No	No
radius_se	No	No
texture_se	No	No
perimeter_se	No	No
area_se	No	No



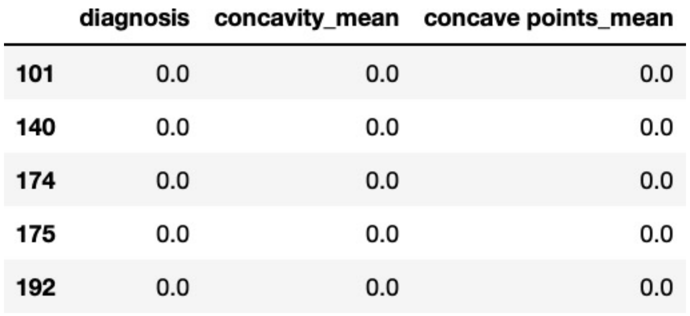
	Normally distributed B	Normally distributed M
smoothness_se	No	No
compactness_se	No	No
concavity_se	No	No
concave points_se	No	Yes
symmetry_se	No	No
fractal_dimension_se	No	No
radius_worst	Yes	Yes
texture_worst	Yes	Yes
perimeter_worst	Yes	Yes
area_worst	Yes	Yes
smoothness_worst	Yes	Yes
compactness_worst	No	No
concavity_worst	No	No
concave points_worst	Yes	Yes
symmetry_worst	Yes	No
fractal_dimension_worst	No	Yes

4. PRE- PROCESSING OF THE DATASET

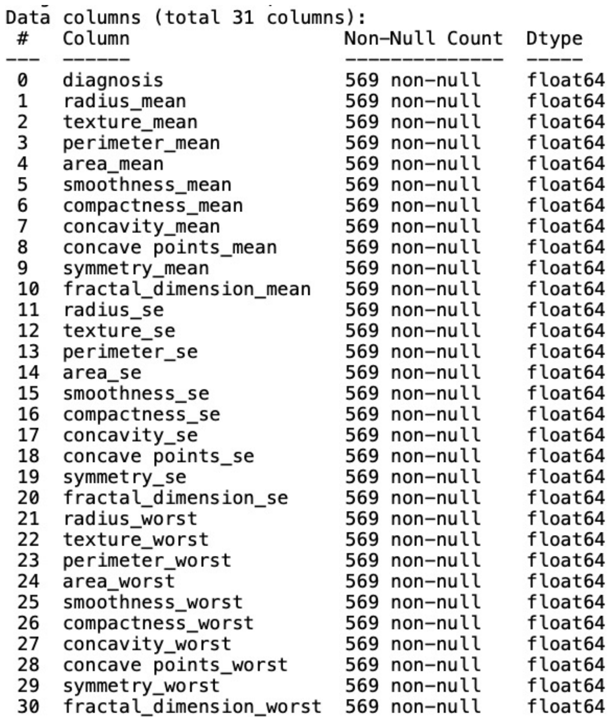
4.1Missing Values

1. **No missing values**, neither explicit (NaN values) nor implicit (e.g. repeated 0 values for an instance for different features).

2. Samples with 0 values show the same behavior, all associated with diagnosis=B and same zero features, which may imply that these values are indeed correct.



	diagnosis	concavity_mean	concave points_mean
101	0.0	0.0	0.0
140	0.0	0.0	0.0
174	0.0	0.0	0.0
175	0.0	0.0	0.0
192	0.0	0.0	0.0



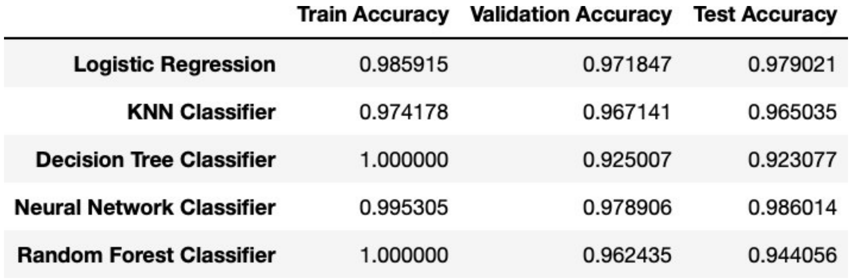
```
Data columns (total 31 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   diagnosis                569 non-null    float64
 1   radius_mean              569 non-null    float64
 2   texture_mean             569 non-null    float64
 3   perimeter_mean           569 non-null    float64
 4   area_mean                569 non-null    float64
 5   smoothness_mean          569 non-null    float64
 6   compactness_mean         569 non-null    float64
 7   concavity_mean           569 non-null    float64
 8   concave points_mean      569 non-null    float64
 9   symmetry_mean            569 non-null    float64
 10  fractal_dimension_mean   569 non-null    float64
 11  radius_se                569 non-null    float64
 12  texture_se               569 non-null    float64
 13  perimeter_se             569 non-null    float64
 14  area_se                  569 non-null    float64
 15  smoothness_se            569 non-null    float64
 16  compactness_se           569 non-null    float64
 17  concavity_se             569 non-null    float64
 18  concave points_se        569 non-null    float64
 19  symmetry_se              569 non-null    float64
 20  fractal_dimension_se     569 non-null    float64
 21  radius_worst             569 non-null    float64
 22  texture_worst            569 non-null    float64
 23  perimeter_worst          569 non-null    float64
 24  area_worst               569 non-null    float64
 25  smoothness_worst         569 non-null    float64
 26  compactness_worst        569 non-null    float64
 27  concavity_worst          569 non-null    float64
 28  concave points_worst     569 non-null    float64
 29  symmetry_worst           569 non-null    float64
 30  fractal_dimension_worst  569 non-null    float64
```

4. PRE-PROCESSING OF THE DATASET

4.2 Outliers

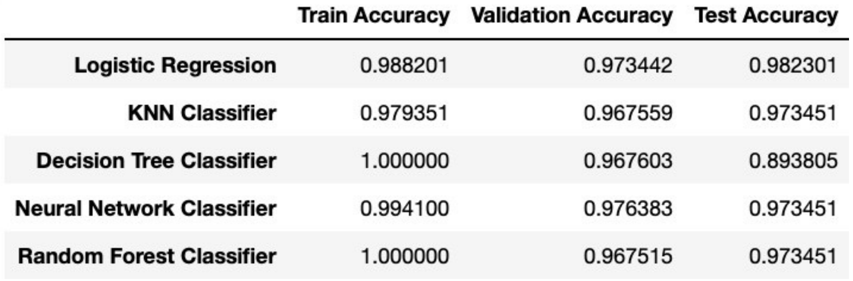
1. Outlier detection **independently for Benignant/Malignant samples**, as they showed different distributions.
2. For detection, **considered as outliers those values with abs(z-score) >= 2.5**.
3. **Very low percentage of outliers per feature (0.3-2%)**.
4. 20.5% (117 instances) of rows with, at least, one outlier. **We shouldn't consider dropping this quantity of data.**
5. Since variables are highly correlated, random/mean/median imputation methods can introduce bias in the analysis → **Tailored Imputation Method** → Computationally expensive
6. ***From previous work with AI methods: Performance metrics after dropping outliers are not improved. They are similar → Outliers may not be deleted incorrect values, just values far from the population.***
7. We **decide to maintain these values.**

Original dataset



	Train Accuracy	Validation Accuracy	Test Accuracy
Logistic Regression	0.985915	0.971847	0.979021
KNN Classifier	0.974178	0.967141	0.965035
Decision Tree Classifier	1.000000	0.925007	0.923077
Neural Network Classifier	0.995305	0.978906	0.986014
Random Forest Classifier	1.000000	0.962435	0.944056

Dataset without outliers (deletion)



	Train Accuracy	Validation Accuracy	Test Accuracy
Logistic Regression	0.988201	0.973442	0.982301
KNN Classifier	0.979351	0.967559	0.973451
Decision Tree Classifier	1.000000	0.967603	0.893805
Neural Network Classifier	0.994100	0.976383	0.973451
Random Forest Classifier	1.000000	0.967515	0.973451

5. HYPOTHESIS TESTING

Two populations for each feature: **malignant and benignant.**

H_0: Mean values for malignant and benignant populations are the same.

H_1: Mean values for malignant are higher than those for benignant.

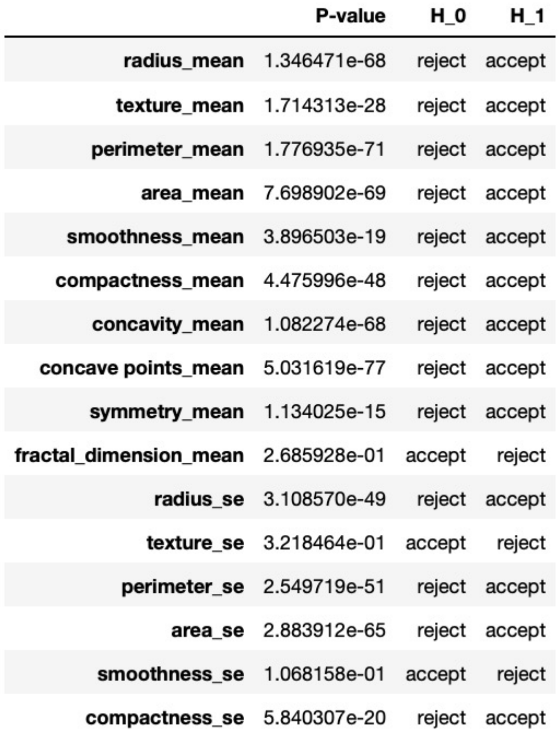
Two independent samples, two-sided hypothesis testing problem**.**

Non-parametric methods preferred.

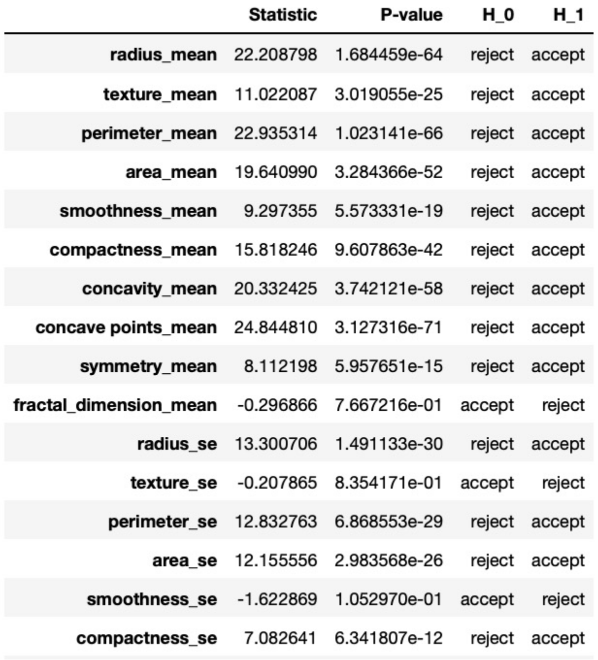
Both **parametric and non-parametric (Mann-Whitney-Wilcoxon)** methods will be compared for learning purposes

5. HYPOTHESIS TESTING

E.g. : Non-parametric vs Parametric (just some features)



	P-value	H_0	H_1
radius_mean	1.346471e-68	reject	accept
texture_mean	1.714313e-28	reject	accept
perimeter_mean	1.776935e-71	reject	accept
area_mean	7.698902e-69	reject	accept
smoothness_mean	3.896503e-19	reject	accept
compactness_mean	4.475996e-48	reject	accept
concavity_mean	1.082274e-68	reject	accept
concave points_mean	5.031619e-77	reject	accept
symmetry_mean	1.134025e-15	reject	accept
fractal_dimension_mean	2.685928e-01	accept	reject
radius_se	3.108570e-49	reject	accept
texture_se	3.218464e-01	accept	reject
perimeter_se	2.549719e-51	reject	accept
area_se	2.883912e-65	reject	accept
smoothness_se	1.068158e-01	accept	reject
compactness_se	5.840307e-20	reject	accept



	Statistic	P-value	H_0	H_1
radius_mean	22.208798	1.684459e-64	reject	accept
texture_mean	11.022087	3.019055e-25	reject	accept
perimeter_mean	22.935314	1.023141e-66	reject	accept
area_mean	19.640990	3.284366e-52	reject	accept
smoothness_mean	9.297355	5.573331e-19	reject	accept
compactness_mean	15.818246	9.607863e-42	reject	accept
concavity_mean	20.332425	3.742121e-58	reject	accept
concave points_mean	24.844810	3.127316e-71	reject	accept
symmetry_mean	8.112198	5.957651e-15	reject	accept
fractal_dimension_mean	-0.296866	7.667216e-01	accept	reject
radius_se	13.300706	1.491133e-30	reject	accept
texture_se	-0.207865	8.354171e-01	accept	reject
perimeter_se	12.832763	6.868553e-29	reject	accept
area_se	12.155556	2.983568e-26	reject	accept
smoothness_se	-1.622869	1.052970e-01	accept	reject
compactness_se	7.082641	6.341807e-12	reject	accept

Taking into account results from non-parametric method, mean values are different between benignant and beningant samples for every feature but for **"fractal_dimension_mean", "texture_se", and "smoothness_se".**

6. CONCLUSION

Dataset **with excellent quality** for its purpose:

1. Simple data visualization allows to get a great insight into data distribution.

    We saw behavior of malignant nuclei just by scatter plotting B vs M for each feature. **Malignant samples tend to have greater values than benignant. It was statistically determined that malignant mean values were different from those of benignant samples.**

    Statistically concluded that nuclei characteristics vary depending on malignancy/benignancy of the sample. Along with AI models, inferential analysis can help determining decision boundaries and translate them to clinical practice.

2. Exhaustive and complicated pre-processing is not needed to perform inferential analysis and draw relevant conclusions.
3. Results show that some features are more relevant than others when determining the diagnosis, which is relevant for feature selection ➔ discard "fractal_dimension_mean", "texture_se", and "smoothness_se".
4. Feature selection can improve the efficiency of the histopathological analysis by discarding non-relevant features.