

# **MACHINE LEARNING FOR PREDICTING DIABETES MELLITUS**

A project report submitted in partial fulfilment of the  
requirement for the degree of

**Bachelor in Science**

**In**

**Computer Science**

by

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under the supervision of

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& SCIENCE AUTONOMOUS**

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### **Declaration by Candidate**

I declare that this project report has been prepared by me and to the best of my knowledge, it has not previously formed the basis for the award of any diploma or degree by any other University.

CERTIFICATE BY SUPERVISOR Certified that the Project Report is a record of work done by the candidate himself/herself/themselves under my guidance during the period of study and that to the best of my knowledge, it has not previously formed the basis of the award of any degree or diploma of any other University.

Ashweta Fondekar

Project Supervisor

## Work Record

# 1 Acknowledgements

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## 2 Introduction

In recent days, there has been a sharp increase in the cases of diabetes mellitus. Diabetes mellitus is on the rise amongst many people and the rate of contracting this lifestyle disease could be reduced significantly if proper measures and precautions were to be instilled amongst people the number of people can be reduced.

Machine learning is a growing field in computer science. With the development and introduction of many algorithms the prediction and accuracy of the predictions itself has improved substantially. Machine learning and healthcare systems are also becoming increasingly popular in the healthcare sector.

The project encompasses the qualities of Remote Patient Monitoring (RPM) and Clinical Decision Support (CDS). RPM provides medical facilities that have the ability to transmit patient data to healthcare professionals who might very well be halfway around the world. RPM can monitor blood glucose levels and blood pressure. It is particularly helpful for patients with chronic conditions such as type 2 diabetes, hypertension, or cardiac disease. Data collected and transmitted via PRM can be used by a healthcare professional or a healthcare team to detect medical events such as stroke or heart attack that require immediate and aggressive medical intervention. Data collected may be used as part of a research project or health study. RPM is a life-saving system for patients in remote areas who cannot access face-to-face health care. CDS analyzes data from clinical and administrative systems. The aim is to assist healthcare providers in making informed clinical decisions. Data available can provide information to medical professions who are preparing diagnoses or predicting medical conditions like drug interactions and reactions. CDS tools filter information to assist healthcare professionals in caring for individual clients.

The objective of this project is to create a system that is able to use the machine learning algorithms and predict the outcome of the parameters entered into the algorithm and help the patient draw a conclusion whether or not he/she has the same traits exhibited by similar patients that have diabetes. Also the system should have a UI that is capable of displaying the data of the patients to the doctor and to the patients themselves for further interpretation.

## **3 Software Requirements**

The main function of this project is to enable the doctors to advise their patients with the help of the prediction software. The system should be accessible to the patient as well as the doctor, therefore it should have a web interface for the two parties to interact with.

### **3.1 Functionalities for Doctors**

As an owner of a doctors account a doctor should be able to:

- Add new observations for the machine learning algorithm to predict.
- Analyse the patients previous records.

### **3.2 Functionalities for Patients**

As the patient, one should be able to:

- Should be able to see the predicted risk of developing diabetes.
- Should be able to view historic data.

### **3.3 Functionalities for Master Nodes**

As the master nodes:

- Control chunk size.
- Remotely update the slave nodes.
- Check the availability of nodes.
- Control the SQL database.

### **3.4 Functionalities for Slave Nodes**

- should have the machine learning algorithm with can be updated.
- Remote access should be possible.

## 4 Hardware Requirements

### 4.1 Raspberry Pi

According to [raspberrypi.org](http://raspberrypi.org), the Raspberry Pi 3 Model B is the earliest model of the third-generation Raspberry Pi. It replaced the Raspberry Pi 2 Model B in February 2016. Some of the key features of this single board computer or SBC are:

- Quad Core 1.2GHz Broadcom BCM2837 64bit CPU.
- 1GB RAM.
- BCM43438 wireless LAN and Bluetooth Low Energy (BLE) on board.
- 100 Base Ethernet.
- 40-pin extended GPIO.
- 4 USB 2 ports.
- Full size HDMI.
- Micro SD port for loading the operating system and storing data.

In this project I will be using 3 Raspberry Pi's to implement a cluster and deploy the machine learning algorithm on.

### 4.2 Switch

A network switch was used in the project to make up for the lack of ethernet ports available on the router. The dumb network switch was able to connect up-to 3 Raspberry Pi and one cable back to the network router itself to connect the switch to the main network.

### 4.3 Router

A router is required to assign internet protocol addresses to the nodes using dynamic host control protocol (DHCP). The router also is responsible for displaying the nodes connected to the network thereby displaying host names and making it more easier to capture the addresses of each node.

## **4.4 Master Node**

The master node is assigned the task of managing the the slave nodes connected to the network. The master node and the slave nodes should be connected to the same database to run and execute queries. The master node shall also be assigned with the task of killing a particular process or shutting down a particular node if required.

## **4.5 Slave Node**

The slave nodes are to be configured with the selected algorithm and are the most vital part of the structure. The slave nodes will be responsible for receiving instructions from the master node and will be responsible for learning from the dataset and then can generate predicted outcomes for the patient records received from the master.

## **4.6 Database**

The database will store all the records for the patients and doctors. The database is a SQL database that will not be subjected to a change in the database schema structure for consistency.

## **4.7 Web Server**

The web server provides an interface for the doctor and the patients to read the predictions and legacy data of the patient from the website.

## 5 Technology Stack

### 5.1 Python

#### 5.1.1 Pandas

Pandas, is a library that is required for loading the comma separated value file into python. Pandas is a package for data manipulation and analysis. In particular, it offers data structures and operations for manipulating numerical tables and time series.

#### 5.1.2 Sklearn

Scikit-learn is a free software machine learning library for the Python programming language. It features various classification, regression and clustering algorithms including support vector machines, random forests, gradient boosting, k-means and DBSCAN, and is designed to inter-operate with the Python numerical and scientific libraries NumPy and SciPy.

#### 5.1.3 Numpy

NumPy is a library for the Python programming language, adding support for large, multi-dimensional arrays and matrices, along with a large collection of high-level mathematical functions to operate on these arrays. The ancestor of NumPy, Numeric, was originally created by Jim Hugunin with contributions from several other developers. In 2005, Travis Oliphant created NumPy by incorporating features of the competing Numarray into Numeric, with extensive modifications. NumPy is open-source software and has many contributors.

#### 5.1.4 Itertools

The module standardizes a core set of fast, memory efficient tools that are useful by themselves or in combination. Together, they form an “iterator algebra” making it possible to construct specialized tools succinctly and efficiently in pure Python.

### 5.2 MYSQL

MySQL is an open-source relational database management system (RDBMS). Its name is a combination of “My”, the name of co-founder Michael Widenius’s daughter, and “SQL”, the abbreviation for Structured Query Language.

MySQL is free and open-source software under the terms of the GNU General Public License, and is also available under a variety of proprietary licenses. MySQL was owned and sponsored by the Swedish company MySQL AB, which was bought

by Sun Microsystems (now Oracle Corporation). In 2010, when Oracle acquired Sun, Widenius forked the open-source MySQL project to create MariaDB.

MySQL is a component of the LAMP web application software stack (and others), which is an acronym for Linux, Apache, MySQL, Perl/PHP/Python. MySQL is used by many database-driven web applications, including Drupal, Joomla, phpBB, and WordPress. MySQL is also used by many popular websites, including Facebook, Flickr, MediaWiki, Twitter and YouTube.

### **5.3 Apache Web Server**

The Apache HTTP Server, colloquially called Apache, is free and open-source cross-platform web server software, released under the terms of Apache License 2.0. Apache is developed and maintained by an open community of developers under the auspices of the Apache Software Foundation.

The vast majority of Apache HTTP Server instances run on a Linux distribution, but current versions also run on Microsoft Windows and a wide variety of Unix-like systems. Past versions also ran on OpenVMS, NetWare, OS/2 and other operating systems, including ports to mainframes.

### **5.4 PHP**

PHP is a general-purpose programming language originally designed for web development. PHP originally stood for Personal Home Page, but it now stands for the recursive initialism PHP: Hypertext Preprocessor.

PHP code may be executed with a command line interface (CLI), embedded into HTML code, or used in combination with various web template systems, web content management systems, and web frameworks. PHP code is usually processed by a PHP interpreter implemented as a module in a web server or as a Common Gateway Interface (CGI) executable. The web server outputs the results of the interpreted and executed PHP code, which may be any type of data, such as generated HTML code or binary image data. PHP can be used for many programming tasks outside of the web context, such as standalone graphical applications and robotic drone control.

### **5.5 AJAX**

Ajax is a set of web development techniques using many web technologies on the client side to create asynchronous web applications. With Ajax, web applications can send and retrieve data from a server asynchronously (in the background) without interfering with the display and behavior of the existing page. By decoupling the data interchange layer from the presentation layer, Ajax allows web pages and, by extension,



web applications, to change content dynamically without the need to reload the entire page.[3] In practice, modern implementations commonly utilize JSON instead of XML.

Ajax is not a single technology, but rather a group of technologies. HTML and CSS can be used in combination to mark up and style information. The webpage can then be modified by JavaScript to dynamically display—and allow the user to interact with—the new information. The built-in XMLHttpRequest object, or since 2017 the new "fetch()" function within JavaScript, is commonly used to execute Ajax on web pages allowing websites to load content onto the screen without refreshing the page. Ajax is not a new technology, or different language, just existing technologies used in new ways.

## **5.6 GitHub**

GitHub is a global company that provides hosting for software development version control using Git. It offers all of the distributed version control and source code management (SCM) functionality of Git as well as adding its own features. It provides access control and several collaboration features such as bug tracking, feature requests, task management, and wikis for every project.

## **5.7 SSH**

Secure Shell is a cryptography network protocol for operating network services securely over an unsecured network. Typical applications include remote command-line, login, and remote command execution, but any network service can be secured with SSH. The SSH is used to communicate between the master and slave nodes.

## 6 Selecting an Algorithm

The dataset used for this project is from the UCI Machine learning repository and can be found at their website. Table 2 is an outcome of the accuracy of the algorithms subjected to train and predict the outcomes for given sets of patients.

## 7 The Multi Layered Perceptron

### 7.1 Introduction

The multi layer perceptron (MLP) is the one of the most commonly used artificial neural networks. A multilayer perceptron is not a single perceptron with multiple layers, but rather multiple layers of artificial neurons that can be perceptrons. The layers of the MLP form a directed, acyclic graph. Generally, each layer is fully connected to the subsequent layer; the output of each artificial neuron in a layer is an input to every artificial neuron in the next layer towards the output. MLPs have three or more layers of artificial neurons.

## 8 Coding Process

The concept of the system remains simple. The system can be described using the following diagrams.

### 8.1 Designing the System

- The system firstly reads the records from the database that are not classified as 0 or 1. The master node then converts all the results obtained from the database into chunks as specified by the code.

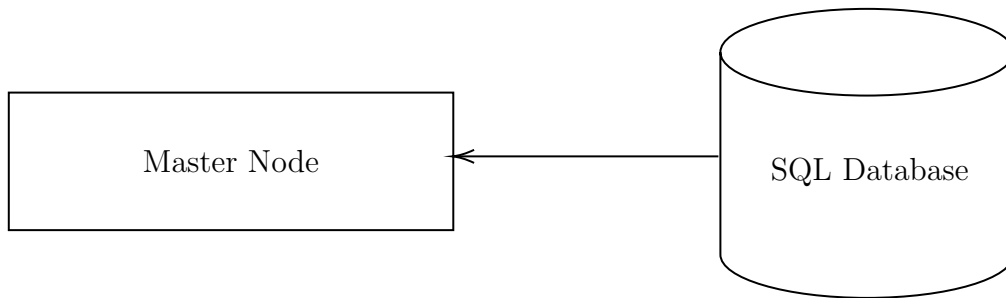
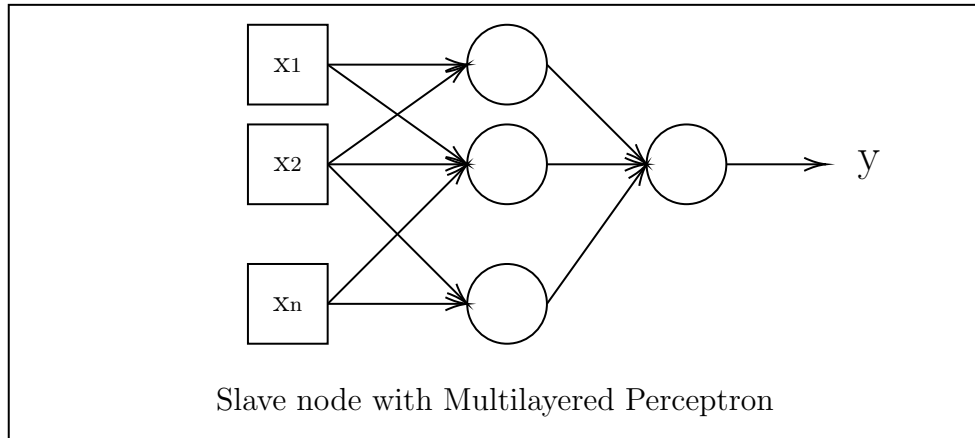
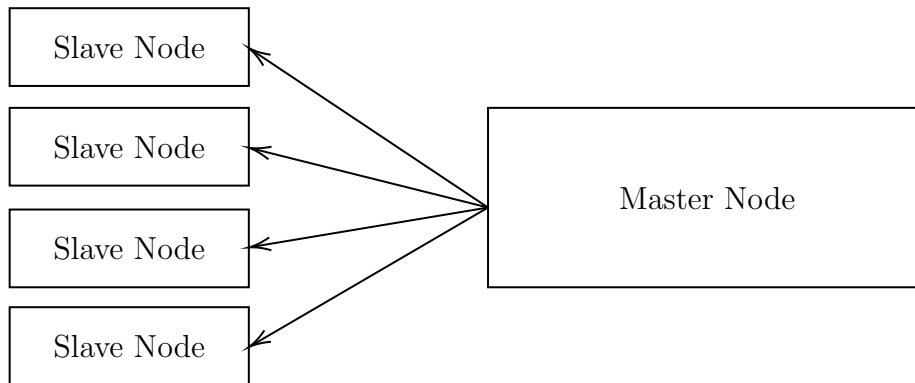


Figure 1: Master Node reading data from the SQL Database.

- odei



- The chunks containing the data of the queries that were left unpredicted via the cluster are sent to the cluster in a round robin fashion. The method of sending the queries can be set to either round robin fashion or all at once. The



## 9 Deploying to Cluster

A cluster is a group of two or more servers connected to each other in such a way that they behave like a single server. Each machine in the cluster is called a node. Because each machine in the cluster runs the same services as other machines in the cluster, any machine can stand in for any other machine in the cluster. This becomes important when one machine goes down or must be taken out of service for a time. The remaining machines in the cluster can seamlessly take over the work of the downed machine, providing users with uninterrupted access to services and data.

### 9.1 Benefits of Clustering

- **Increased resource availability:** If one Intelligence Server in a cluster fails, the other Intelligence Servers in the cluster can pick up the workload. This prevents the loss of valuable time and information if a server fails. **Strategic resource usage:** You can distribute projects across nodes in whatever configuration you prefer. This reduces overhead because not all machines need to be running all projects, and allows you to use your resources flexibly.

- **Increased performance:** Multiple machines provide greater processing power.
- **Greater scalability:** As your user base grows and report complexity increases, your resources can grow.
- **Simplified management:** Clustering simplifies the management of large or rapidly growing systems.
- **Fail-over support** ensures that a business intelligence system remains available for use if an application or hardware failure occurs. Clustering provides failover support in two ways:

**Load redistribution:** When a node fails, the work for which it is responsible is directed to another node or set of nodes. **Request recovery:** When a node fails, the system attempts to reconnect MicroStrategy Web users with queued or processing requests to another node. Users must log in again to be authenticated on the new node. The user is prompted to resubmit job requests.

**Load Balancing** Load balancing is a strategy aimed at achieving even distribution of user sessions across Intelligence Servers, so that no single machine is overwhelmed. This strategy is especially valuable when it is difficult to predict the number of requests a server will receive. MicroStrategy achieves four-tier load balancing by incorporating load balancers into the MicroStrategy Web and Web products.

Load is calculated as the number of user sessions connected to a node. The load balancers collect information on the number of user sessions each node is carrying. Using this information at the time a user logs in to a project, MicroStrategy Web connects them to the Intelligence Server node that is carrying the lightest session load. All requests by that user are routed to the node to which they are connected until the user disconnects from the MicroStrategy Web product.

**Project Distribution and Project Fail over** When you set up several server machines in a cluster, you can distribute projects across those clustered machines or nodes in any configuration, in both Windows and Linux environments. All servers in a cluster do not need to be running all projects. Each node in the cluster can host a different set of projects, which means only a subset of projects need to be loaded on a specific Intelligence Server machine. This feature provides you with flexibility in using your resources, and it provides better scalability and performance because of less overhead on each Intelligence Server machine.

Distributing projects across nodes also provides project fail-over support. For example, one server is hosting project A and another server is hosting projects B and C. If the first server fails, the other server can host all three projects to ensure project availability.

Project creation, duplication, and deletion in a three-tier, or server, connection are automatically broadcast to all nodes during run-time to ensure synchronization across the cluster.

**Work Fencing** User fences and workload fences allow you to reserve nodes of a cluster for either users or a project subscriptions.

## 10 Future Scope



## 11 Tables

| Column Name                | Description   |
|----------------------------|---|
| Pregnancies                | Number of times pregnant.   |
| Glucose                    | Plasma glucose concentration a 2 hours in an oral glucose tolerance test. |
| Blood Pressure             | Diastolic blood pressure (mm Hg)  |
| Skin Thickness             | Triceps skin fold thickness (mm)  |
| Insulin                    | 2-Hour serum insulin ( $\mu\text{U}/\text{ml}$ )                          |
| Body Mass Index            | Body mass index ( $\text{weight in kg}/(\text{height in m})^2$ )          |
| Diabetes Pedigree Function | Diabetes pedigree function  |
| Age                        | Age (years)   |
| Outcome                    | Class variable (0 or 1) 268 of 768 are 1, the others are 0                |

Table 1: Pima Indians dataset header.

| Algorithm              | Additional Parameters                              | Train Set Accuracy | Test Set Accuracy |
|------------------------|--|--------------------|-------------------|
| K Nearest Neighbour    | -  | 0.79               | 0.78              |
| Logistic Regression    | $C = 1$  | 0.781              | 0.771             |
| Logistic Regression    | $C = 0.01$   | 0.700              | 0.703             |
| Logistic Regression    | $C = 100$  | 0.785              | 0.766             |
| Decision Tree          | -  | 1.00               | 0.714             |
| Decision Tree          | Max Depth = 3                                      | 0.773              | 0.740             |
| Random Forest          | Estimators = 100                                   | 1.000              | 0.786             |
| Random Forest          | Estimators = 100; Max Depth = 3                    | 0.800              | 0.755             |
| Gradient Boosting      | -  | 0.917              | 0.792             |
| Gradient Boosting      | Max Depth = 1                                      | 0.804              | 0.781             |
| Gradient Boosting      | Learning Rate = 0.01                               | 0.802              | 0.776             |
| Support Vector Machine | -  | 1.00               | 0.65              |
| Support Vector Machine | Train and Test set scaled using MinMaxScaler       | 0.77               | 0.77              |
| Support Vector Machine | $C = 1000$   | 0.790              | 0.797             |
| MLP Classifier         | Random State = 42                                  | 0.73               | 0.72              |
| MLP Classifier         | Random State = 0                                   | 0.823              | 0.802             |
| MLP Classifier         | Max Iterations = 1000                              | 0.908              | 0.792             |
| MLP Classifier         | Max Iterations = 1000; Alpha = 1; Random State = 0 | 0.806              | 0.797             |

Table 2: Test and Train accuracy's using various machine learning algorithms with various parameters.

## 12 Appendices

### 12.1 K Nearest Neighbours

#### 12.1.1 Function Syntax

```
1 class sklearn.neighbors.KNeighborsClassifier(n_neighbors=5, weights='uniform', algorithm='auto', leaf_size=30, p=2, metric='minkowski', metric_params=None, n_jobs=None, **kwargs)
```

#### 12.1.2 Parameters

- `n_neighbors` Number of neighbors to use by default for kneighbors queries.
- `weights` weight function used in prediction. Possible values:
  - `uniform` All points in each neighborhood are weighted equally.
  - `distance` weight points by the inverse of their distance.
- `algorithm` Algorithm used to compute the nearest neighbors:
  - `ball_tree` will use BallTree
  - `kd_tree` will use KDTree
  - `brute` will use a brute-force search.
- `leaf_size` int, optional (default = 30) Leaf size passed to BallTree or KDTree. This can affect the speed of the construction and query, as well as the memory required to store the tree. The optimal value depends on the nature of the problem.
- `p` integer, optional (default = 2) Power parameter for the Minkowski metric. When  $p = 1$ , this is equivalent to using `manhattan_distance` (11), and `euclidean_distance` (12) for  $p = 2$ . For arbitrary  $p$ , `minkowski_distance (l_p)` is used.
- `metric` string or callable, default 'minkowski' the distance metric to use for the tree. The default metric is `minkowski`, and with  $p=2$  is equivalent to the standard Euclidean metric. See the documentation of the `DistanceMetric` class for a list of available metrics. If `metric` is "precomputed", `X` is assumed to be a distance matrix and must be square during fit. `X` may be a `Glossary`, in which case only "nonzero" elements may be considered neighbors.
- `metric_params` dict, optional (default = None) Additional keyword arguments for the metric function.

- `n_jobs` or `None`, optional (default=`None`) The number of parallel jobs to run for neighbors search. `None` means 1 unless in a `joblib.parallel_backend` context. `-1` means using all processors. See Glossary for more details. Doesn't affect fit method.

### 12.1.3 Logistic Regression

```
1 class sklearn.linear_model.LogisticRegression(penalty='l2', dual=False
    , tol=0.0001, C=1.0, fit_intercept=True, intercept_scaling=1,
    class_weight=None, random_state=None, solver='lbfgs', max_iter
    =100, multi_class='auto', verbose=0, warm_start=False, n_jobs=None
    , l1_ratio=None)
```

- `penalty`['l1', 'l2', 'elasticnet', 'none', default='l2'] Used to specify the norm used in the penalization. The 'newton-cg', 'sag' and 'lbfgs' solvers support only l2 penalties. 'elasticnet' is only supported by the 'saga' solver. If 'none' (not supported by the liblinear solver), no regularization is applied.
- `dual`bool, default=False Dual or primal formulation. Dual formulation is only implemented for l2 penalty with liblinear solver. Prefer dual=False when `n_samples` > `n_features`.
- `tol`float, default=1e-4 Tolerance for stopping criteria.
- `C`float, default=1.0 Inverse of regularization strength; must be a positive float. Like in support vector machines, smaller values specify stronger regularization.
- `fit_intercept`bool, default=True Specifies if a constant (a.k.a. bias or intercept) should be added to the decision function.
- `intercept_scaling`float, default=1 Useful only when the solver 'liblinear' is used and `self.fit_intercept` is set to True. In this case, `x` becomes `[x, self.intercept_scaling]`, i.e. a "synthetic" feature with constant value equal to `intercept_scaling` is appended to the instance vector. The intercept becomes `intercept_scaling * synthetic_feature_weight`.
- `class_weight`dict or 'balanced', default=None Weights associated with classes in the form `class.label: weight`. If not given, all classes are supposed to have weight one.
- The "balanced" mode uses the values of `y` to automatically adjust weights inversely proportional to class frequencies in the input data as `n_samples / (n_classes * np.bincount(y))`.
- `random_state`int, RandomState instance, default=None The seed of the pseudo random number generator to use when shuffling the data. If int, `random_state` is the seed used by the random number generator; If RandomState instance, `random_state` is the random number generator; If None, the random number generator is the RandomState instance used by `np.random`. Used when `solver` == 'sag' or 'liblinear'.

- `solver`['newton-cg', 'lbfgs', 'liblinear', 'sag', 'saga', default='lbfgs'] Algorithm to use in the optimization problem.

For small datasets, 'liblinear' is a good choice, whereas 'sag' and 'saga' are faster for large ones.

For multiclass problems, only 'newton-cg', 'sag', 'saga' and 'lbfgs' handle multinomial loss; 'liblinear' is limited to one-versus-rest schemes.

'newton-cg', 'lbfgs', 'sag' and 'saga' handle L2 or no penalty

'liblinear' and 'saga' also handle L1 penalty

'saga' also supports 'elasticnet' penalty

'liblinear' does not support setting `penalty='none'`

- `max_iterint`, default=100 Maximum number of iterations taken for the solvers to converge.
- `multi_class`['auto', 'ovr', 'multinomial', default='auto'] If the option chosen is 'ovr', then a binary problem is fit for each label. For 'multinomial' the loss minimised is the multinomial loss fit across the entire probability distribution, even when the data is binary. 'multinomial' is unavailable when `solver='liblinear'`. 'auto' selects 'ovr' if the data is binary, or if `solver='liblinear'`, and otherwise selects 'multinomial'.
- `verboseint`, default=0 For the liblinear and lbfgs solvers set verbose to any positive number for verbosity.
- `warm_startbool`, default=False When set to True, reuse the solution of the previous call to fit as initialization, otherwise, just erase the previous solution. Useless for liblinear solver. See the Glossary.
- `n_jobsint`, default=None Number of CPU cores used when parallelizing over classes if `multi_class='ovr'`". This parameter is ignored when the solver is set to 'liblinear' regardless of whether 'multi\_class' is specified or not. None means 1 unless in a `joblib.parallel_backend` context. -1 means using all processors. See Glossary for more details.
- `l1_ratio`float, default=None The Elastic-Net mixing parameter, with  $0 \leq \text{l1\_ratio} \leq 1$ . Only used if `penalty='elasticnet'`. Setting "l1\_ratio=0 is equivalent to using `penalty='l2'`", while setting `l1_ratio=1` is equivalent to using `penalty='l1'`. For  $0 < \text{l1\_ratio} < 1$ , the penalty is a combination of L1 and L2.

### 12.1.4 Decision Tree

```
1 class sklearn.tree.DecisionTreeClassifier(criterion='gini', splitter='best', max_depth=None, min_samples_split=2, min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features=None, random_state=None, max_leaf_nodes=None, min_impurity_decrease=0.0, min_impurity_split=None, class_weight=None, presort='deprecated', ccp_alpha=0.0)
```

- `criterion` “gini”, “entropy”, default=“gini” The function to measure the quality of a split. Supported criteria are “gini” for the Gini impurity and “entropy” for the information gain.
- `splitter` “best”, “random”, default=“best” The strategy used to choose the split at each node. Supported strategies are “best” to choose the best split and “random” to choose the best random split.
- `max_depth` int, default=None The maximum depth of the tree. If None, then nodes are expanded until all leaves are pure or until all leaves contain less than `min_samples_split` samples.
- `min_samples_split` int or float, default=2 The minimum number of samples required to split an internal node:  
If int, then consider `min_samples_split` as the minimum number.  
If float, then `min_samples_split` is a fraction and  $\text{ceil}(\text{min\_samples\_split} * \text{n\_samples})$  are the minimum number of samples for each split.
- `min_samples_leaf` int or float, default=1 The minimum number of samples required to be at a leaf node. A split point at any depth will only be considered if it leaves at least `min_samples_leaf` training samples in each of the left and right branches. This may have the effect of smoothing the model, especially in regression.  
If int, then consider `min_samples_leaf` as the minimum number.  
If float, then `min_samples_leaf` is a fraction and  $\text{ceil}(\text{min\_samples\_leaf} * \text{n\_samples})$  are the minimum number of samples for each node.
- `min_weight_fraction_leaf` float, default=0.0 The minimum weighted fraction of the sum total of weights (of all the input samples) required to be at a leaf node. Samples have equal weight when `sample_weight` is not provided.  
`max_features` int, float or “auto”, “sqrt”, “log2”, default=None The number of features to consider when looking for the best split:  
If int, then consider `max_features` features at each split.



If float, then `max_features` is a fraction and `int(max_features * n_features)` features are considered at each split.

If “auto”, then `max_features=sqrt(n_features)`.

If “sqrt”, then `max_features=sqrt(n_features)`.

If “log2”, then `max_features=log2(n_features)`.

If None, then `max_features=n_features`.

Note: the search for a split does not stop until at least one valid partition of the node samples is found, even if it requires to effectively inspect more than `max_features` features.

- `random_state`int or RandomState, default=None If int, `random_state` is the seed used by the random number generator; If RandomState instance, `random_state` is the random number generator; If None, the random number generator is the RandomState instance used by `np.random`.
- `max_leaf_nodes`int, default=None Grow a tree with `max_leaf_nodes` in best-first fashion. Best nodes are defined as relative reduction in impurity. If None then unlimited number of leaf nodes.
- `min_impurity_decrease`float, default=0.0 A node will be split if this split induces a decrease of the impurity greater than or equal to this value.
- `ccp_alpha`non-negative float, default=0.0 Complexity parameter used for Minimal Cost-Complexity Pruning. The subtree with the largest cost complexity that is smaller than `ccp_alpha` will be chosen. By default, no pruning is performed. See Minimal Cost-Complexity Pruning for details.

### 12.1.5 Random Forest Classifier

```
1 class sklearn.ensemble.RandomForestClassifier(n_estimators=100,  
        criterion='gini', max_depth=None, min_samples_split=2,  
        min_samples_leaf=1, min_weight_fraction_leaf=0.0, max_features='  
        auto', max_leaf_nodes=None, min_impurity_decrease=0.0,  
        min_impurity_split=None, bootstrap=True, oob_score=False, n_jobs=  
        None, random_state=None, verbose=0, warm_start=False, class_weight  
        =None, ccp_alpha=0.0, max_samples=None)
```

- `n_estimators` integer, optional (default=100) The number of trees in the forest.
- `criterion` string, optional (default="gini") The function to measure the quality of a split. Supported criteria are "gini" for the Gini impurity and "entropy" for the information gain. Note: this parameter is tree-specific.
- `max_depth` integer or None, optional (default=None) The maximum depth of the tree. If None, then nodes are expanded until all leaves are pure or until all leaves contain less than `min_samples_split` samples.
- `min_samples_split` int, float, optional (default=2) The minimum number of samples required to split an internal node:  
  
If int, then consider `min_samples_split` as the minimum number.  
  
If float, then `min_samples_split` is a fraction and `ceil(min_samples_split * n_samples)` are the minimum number of samples for each split.
- `min_samples_leaf` int, float, optional (default=1) The minimum number of samples required to be at a leaf node. A split point at any depth will only be considered if it leaves at least `min_samples_leaf` training samples in each of the left and right branches. This may have the effect of smoothing the model, especially in regression.  
  
If int, then consider `min_samples_leaf` as the minimum number.  
  
If float, then `min_samples_leaf` is a fraction and `ceil(min_samples_leaf * n_samples)` are the minimum number of samples for each node.  
  
Changed in version 0.18: Added float values for fractions.
- `min_weight_fraction_leaf` float, optional (default=0.) The minimum weighted fraction of the sum total of weights (of all the input samples) required to be at a leaf node. Samples have equal weight when `sample_weight` is not provided.
- `max_features` int, float, string or None, optional (default="auto") The number of features to consider when looking for the best split:

If int, then consider `max_features` features at each split.

If float, then `max_features` is a fraction and `int(max_features * n_features)` features are considered at each split.

If “auto”, then `max_features=sqrt(n_features)`.

If “sqrt”, then `max_features=sqrt(n_features)` (same as “auto”).

If “log2”, then `max_features=log2(n_features)`.

If None, then `max_features=n_features`.

Note: the search for a split does not stop until at least one valid partition of the node samples is found, even if it requires to effectively inspect more than `max_features` features.

- `max_leaf_nodes`int or None, optional (default=None) Grow trees with `max_leaf_nodes` in best-first fashion. Best nodes are defined as relative reduction in impurity. If None then unlimited number of leaf nodes.
- `min_impurity_decrease`float, optional (default=0.) A node will be split if this split induces a decrease of the impurity greater than or equal to this value.
- `min_impurity_split`float, (default=1e-7) Threshold for early stopping in tree growth. A node will split if its impurity is above the threshold, otherwise it is a leaf.
- `oob_score`bool (default=False) Whether to use out-of-bag samples to estimate the generalization accuracy.
- `n_jobs`int or None, optional (default=None) The number of jobs to run in parallel. fit, predict, decision\_path and apply are all parallelized over the trees. None means 1 unless in a joblib.parallel\_backend context. -1 means using all processors. See Glossary for more details.
- `random_state`int, RandomState instance or None, optional (default=None) Controls both the randomness of the bootstrapping of the samples used when building trees (if `bootstrap=True`) and the sampling of the features to consider when looking for the best split at each node (if `max_features < n_features`). See Glossary for details.
- `verbose`int, optional (default=0) Controls the verbosity when fitting and predicting.
- `warm_start`bool, optional (default=False) When set to True, reuse the solution of the previous call to fit and add more estimators to the ensemble, otherwise, just fit a whole new forest. See the Glossary.

- `class_weightdict`, list of dicts, “balanced”, “balanced\_subsample” or None, optional (default=None) Weights associated with classes in the form `class_label: weight`. If not given, all classes are supposed to have weight one. For multi-output problems, a list of dicts can be provided in the same order as the columns of `y`.
- `ccp_alpha` non-negative float, optional (default=0.0) Complexity parameter used for Minimal Cost-Complexity Pruning. The subtree with the largest cost complexity that is smaller than `ccp_alpha` will be chosen. By default, no pruning is performed. See Minimal Cost-Complexity Pruning for details.
- `max_samples` int or float, default=None If bootstrap is True, the number of samples to draw from `X` to train each base estimator.

If None (default), then draw `X.shape[0]` samples.

If int, then draw `max_samples` samples.

If float, then draw `max_samples * X.shape[0]` samples. Thus, `max_samples` should be in the interval  $(0, 1)$ .

### 12.1.6 Gradient Boosting

```
1 class sklearn.ensemble.GradientBoostingClassifier(loss='deviance',  
    learning_rate=0.1, n_estimators=100, subsample=1.0, criterion='  
    friedman_mse', min_samples_split=2, min_samples_leaf=1,  
    min_weight_fraction_leaf=0.0, max_depth=3, min_impurity_decrease  
    =0.0, min_impurity_split=None, init=None, random_state=None,  
    max_features=None, verbose=0, max_leaf_nodes=None, warm_start=  
    False, presort='deprecated', validation_fraction=0.1,  
    n_iter_no_change=None, tol=0.0001, ccp_alpha=0.0)
```

- `loss` 'deviance', 'exponential', optional (default='deviance') loss function to be optimized. 'deviance' refers to deviance (= logistic regression) for classification with probabilistic outputs. For loss 'exponential' gradient boosting recovers the AdaBoost algorithm.

`learning_rate` float, optional (default=0.1) learning rate shrinks the contribution of each tree by `learning_rate`. There is a trade-off between `learning_rate` and `n_estimators`.

`n_estimators` int (default=100) The number of boosting stages to perform. Gradient boosting is fairly robust to over-fitting so a large number usually results in better performance.

`subsample` float, optional (default=1.0) The fraction of samples to be used for fitting the individual base learners. If smaller than 1.0 this results in Stochastic Gradient Boosting. `subsample` interacts with the parameter `n_estimators`. Choosing `subsample` < 1.0 leads to a reduction of variance and an increase in bias.

`criterion` string, optional (default="friedman\_mse") The function to measure the quality of a split. Supported criteria are "friedman\_mse" for the mean squared error with improvement score by Friedman, "mse" for mean squared error, and "mae" for the mean absolute error. The default value of "friedman\_mse" is generally the best as it can provide a better approximation in some cases.

New in version 0.18.

`min_samples_split` int, float, optional (default=2) The minimum number of samples required to split an internal node:

If int, then consider `min_samples_split` as the minimum number.

If float, then `min_samples_split` is a fraction and `ceil(min_samples_split * n_samples)` are the minimum number of samples for each split.

Changed in version 0.18: Added float values for fractions.

`min_samples_leaf` int, float, optional (default=1) The minimum number of samples required to be at a leaf node. A split point at any depth will only be considered

if it leaves at least `min_samples_leaf` training samples in each of the left and right branches. This may have the effect of smoothing the model, especially in regression.

If int, then consider `min_samples_leaf` as the minimum number.

If float, then `min_samples_leaf` is a fraction and  $\text{ceil}(\text{min\_samples\_leaf} * \text{n\_samples})$  are the minimum number of samples for each node.

Changed in version 0.18: Added float values for fractions.

`min_weight_fraction_leaf`float, optional (default=0.) The minimum weighted fraction of the sum total of weights (of all the input samples) required to be at a leaf node. Samples have equal weight when `sample_weight` is not provided.

`max_depth`integer, optional (default=3) maximum depth of the individual regression estimators. The maximum depth limits the number of nodes in the tree. Tune this parameter for best performance; the best value depends on the interaction of the input variables.

`min_impurity_decrease`float, optional (default=0.) A node will be split if this split induces a decrease of the impurity greater than or equal to this value.

The weighted impurity decrease equation is the following:

$$N_t / N * (\text{impurity} - N_{t\_R} / N_t * \text{right\_impurity} - N_{t\_L} / N_t * \text{left\_impurity})$$
where  $N$  is the total number of samples,  $N_t$  is the number of samples at the current node,  $N_{t\_L}$  is the number of samples in the left child, and  $N_{t\_R}$  is the number of samples in the right child.

$N$ ,  $N_t$ ,  $N_{t\_R}$  and  $N_{t\_L}$  all refer to the weighted sum, if `sample_weight` is passed.

New in version 0.19.

`min_impurity_split`float, (default=1e-7) Threshold for early stopping in tree growth. A node will split if its impurity is above the threshold, otherwise it is a leaf.

Deprecated since version 0.19: `min_impurity_split` has been deprecated in favor of `min_impurity_decrease` in 0.19. The default value of `min_impurity_split` will change from 1e-7 to 0 in 0.23 and it will be removed in 0.25. Use `min_impurity_decrease` instead. `init_estimator` or 'zero', optional (default=None) An estimator object that is used to compute the initial predictions. `init` has to provide `fit` and `predict_proba`. If 'zero', the initial raw predictions are set to zero. By default, a `DummyEstimator` predicting the classes priors is used.

`random_state`int, `RandomState` instance or None, optional (default=None) If int, `random_state` is the seed used by the random number generator; If `RandomState` instance, `random_state` is the random number generator; If None, the random number generator is the `RandomState` instance used by `np.random`.

`max_features`int, float, string or None, optional (default=None) The number of features to consider when looking for the best split:

If int, then consider `max_features` features at each split.

If float, then `max_features` is a fraction and `int(max_features * n_features)` features are considered at each split.

If “auto”, then `max_features=sqrt(n_features)`.

If “sqrt”, then `max_features=sqrt(n_features)`.

If “log2”, then `max_features=log2(n_features)`.

If None, then `max_features=n_features`.

Choosing `max_features < n_features` leads to a reduction of variance and an increase in bias.

Note: the search for a split does not stop until at least one valid partition of the node samples is found, even if it requires to effectively inspect more than `max_features` features.

`verbose`int, default: 0 Enable verbose output. If 1 then it prints progress and performance once in a while (the more trees the lower the frequency). If greater than 1 then it prints progress and performance for every tree.

`max_leaf_nodes`int or None, optional (default=None) Grow trees with `max_leaf_nodes` in best-first fashion. Best nodes are defined as relative reduction in impurity. If None then unlimited number of leaf nodes.

`warm_start`bool, default: False When set to True, reuse the solution of the previous call to fit and add more estimators to the ensemble, otherwise, just erase the previous solution. See the Glossary.

`presort`deprecated, default='deprecated' This parameter is deprecated and will be removed in v0.24.

Deprecated since version 0.22. `validation_fraction`float, optional, default 0.1 The proportion of training data to set aside as validation set for early stopping. Must be between 0 and 1. Only used if `n_iter_no_change` is set to an integer.

New in version 0.20.

`n_iter_no_change`int, default None `n_iter_no_change` is used to decide if early stopping will be used to terminate training when validation score is not improving. By default it is set to None to disable early stopping. If set to a number, it will set aside `validation_fraction` size of the training data as validation and terminate training when validation score is not improving in all of the previous `n_iter_no_change` numbers of iterations. The split is stratified.

New in version 0.20.

tolfloat, optional, default 1e-4 Tolerance for the early stopping. When the loss is not improving by at least tol for n\_iter\_no\_change iterations (if set to a number), the training stops.

New in version 0.20.

ccp\_alpha non-negative float, optional (default=0.0) Complexity parameter used for Minimal Cost-Complexity Pruning. The subtree with the largest cost complexity that is smaller than ccp\_alpha will be chosen. By default, no pruning is performed. See Minimal Cost-Complexity Pruning for details.

New in version 0.22.



## 12.1.7 Multi Layered Perceptron

```
1 class sklearn.neural_network.MLPClassifier(hidden_layer_sizes=(100, ),
      activation='relu', solver='adam', alpha=0.0001, batch_size='auto',
      learning_rate='constant', learning_rate_init=0.001, power_t
      =0.5, max_iter=200, shuffle=True, random_state=None, tol=0.0001,
      verbose=False, warm_start=False, momentum=0.9, nesterovs_momentum=
      True, early_stopping=False, validation_fraction=0.1, beta_1=0.9,
      beta_2=0.999, epsilon=1e-08, n_iter_no_change=10, max_fun=15000)
```

`hidden_layer_sizes` tuple, length = `n_layers - 2`, default=(100,)

The *i*th element represents the number of neurons in the *i*th hidden layer.

`activation`{'identity', 'logistic', 'tanh', 'relu'}, default='relu'

Activation function for the hidden layer.

'identity', no-op activation, useful to implement linear bottleneck, returns  $f(x) = x$

'logistic', the logistic sigmoid function, returns  $f(x) = 1 / (1 + \exp(-x))$ .

'tanh', the hyperbolic tan function, returns  $f(x) = \tanh(x)$ .

'relu', the rectified linear unit function, returns  $f(x) = \max(0, x)$

`solver`{'lbfgs', 'sgd', 'adam'}, default='adam'

The solver for weight optimization.

'lbfgs' is an optimizer in the family of quasi-Newton methods.

'sgd' refers to stochastic gradient descent.

'adam' refers to a stochastic gradient-based optimizer proposed by Kingma, Diederik, and Ba.

Note: The default solver 'adam' works pretty well on relatively large datasets (with thousands of features).

`alpha` float, default=0.0001

L2 penalty (regularization term) parameter.

`batch_size` int, default='auto'

Size of minibatches for stochastic optimizers. If the solver is 'lbfgs', the classification

`learning_rate`{'constant', 'invscaling', 'adaptive'}, default='constant'  
Learning rate schedule for weight updates.

'constant' is a constant learning rate given by 'learning\_rate\_init'.

'invscaling' gradually decreases the learning rate at each time step 't' using an inverse

'adaptive' keeps the learning rate constant to 'learning\_rate\_init' as long as training

Only used when solver='sgd'.

`learning_rate_init`double, default=0.001

The initial learning rate used. It controls the step-size in updating the weights. Only

`power_t`double, default=0.5

The exponent for inverse scaling learning rate. It is used in updating effective learning

`max_iter`int, default=200

Maximum number of iterations. The solver iterates until convergence (determined by 'tol')

`shuffle`bool, default=True

Whether to shuffle samples in each iteration. Only used when solver='sgd' or 'adam'.

`random_state`int, RandomState instance or None, default=None

If int, random\_state is the seed used by the random number generator; If RandomState

`tol`float, default=1e-4

Tolerance for the optimization. When the loss or score is not improving by at least tol

`verbose`bool, default=False

Whether to print progress messages to stdout.

`warm_start`bool, default=False

When set to True, reuse the solution of the previous call to fit as initialization, o

`momentum`float, default=0.9

Momentum for gradient descent update. Should be between 0 and 1. Only used when solver

`nesterovs_momentum`boolean, default=True

Whether to use Nesterov's momentum. Only used when solver='sgd' and momentum > 0.

early\_stoppingbool, default=False

Whether to use early stopping to terminate training when validation score is not improved.

validation\_fractionfloat, default=0.1

The proportion of training data to set aside as validation set for early stopping. Must be in [0, 1].

beta\_1float, default=0.9

Exponential decay rate for estimates of first moment vector in adam, should be in [0, 1].

beta\_2float, default=0.999

Exponential decay rate for estimates of second moment vector in adam, should be in [0, 1].

epsilonfloat, default=1e-8

Value for numerical stability in adam. Only used when solver='adam'

n\_iter\_no\_changeint, default=10

Maximum number of epochs to not meet tol improvement. Only effective when solver='sgd'

New in version 0.20.

max\_funint, default=15000

Only used when solver='lbfgs'. Maximum number of loss function calls. The solver iterates until the maximum number of calls is reached or the tolerance is met.

New in version 0.22.

## 12.2 SVM

```
1 class sklearn.svm.SVC(C=1.0, kernel='rbf', degree=3, gamma='scale',
    coef0=0.0, shrinking=True, probability=False, tol=0.001,
    cache_size=200, class_weight=None, verbose=False, max_iter=-1,
    decision_function_shape='ovr', break_ties=False, random_state=None
    )
```

Cfloat, optional (default=1.0)

Regularization parameter. The strength of the regularization is inversely proportional to C.

kernelstring, optional (default='rbf')

Specifies the kernel type to be used in the algorithm. It must be one of 'linear', 'poly', 'rbf', 'sigmoid', 'precomputed' or 'kernel

degreeint, optional (default=3)

Degree of the polynomial kernel function ('poly'). Ignored by all other kernels.

gamma{'scale', 'auto'} or float, optional (default='scale')

Kernel coefficient for 'rbf', 'poly' and 'sigmoid'.

if gamma='scale' (default) is passed then it uses  $1 / (n\_features * X.var())$  as value

if 'auto', uses  $1 / n\_features$ .

Changed in version 0.22: The default value of gamma changed from 'auto' to 'scale'.

coef0float, optional (default=0.0)

Independent term in kernel function. It is only significant in 'poly' and 'sigmoid'.

shrinkingboolean, optional (default=True)

Whether to use the shrinking heuristic.

probabilityboolean, optional (default=False)

Whether to enable probability estimates. This must be enabled prior to calling fit, with

tolfloat, optional (default=1e-3)

Tolerance for stopping criterion.

cache\_sizefloat, optional

Specify the size of the kernel cache (in MB).

`class_weight`{dict, 'balanced'}, optional

Set the parameter  $C$  of class  $i$  to `class_weight[i]*C` for SVC. If not given, all classes

`verbose`bool, default: False

Enable verbose output. Note that this setting takes advantage of a per-process runtime

`max_iter`int, optional (default=-1)

Hard limit on iterations within solver, or -1 for no limit.

`decision_function_shape`'ovo', 'ovr', default='ovr'

Whether to return a one-vs-rest ('ovr') decision function of shape (n\_samples, n\_class)

Changed in version 0.19: `decision_function_shape` is 'ovr' by default.

New in version 0.17: `decision_function_shape='ovr'` is recommended.

Changed in version 0.17: Deprecated `decision_function_shape='ovo'` and None.

`break_ties`bool, optional (default=False)

If true, `decision_function_shape='ovr'`, and number of classes > 2, predict will break

New in version 0.22.

`random_state`int, RandomState instance or None, optional (default=None)

The seed of the pseudo random number generator used when shuffling the data for probab

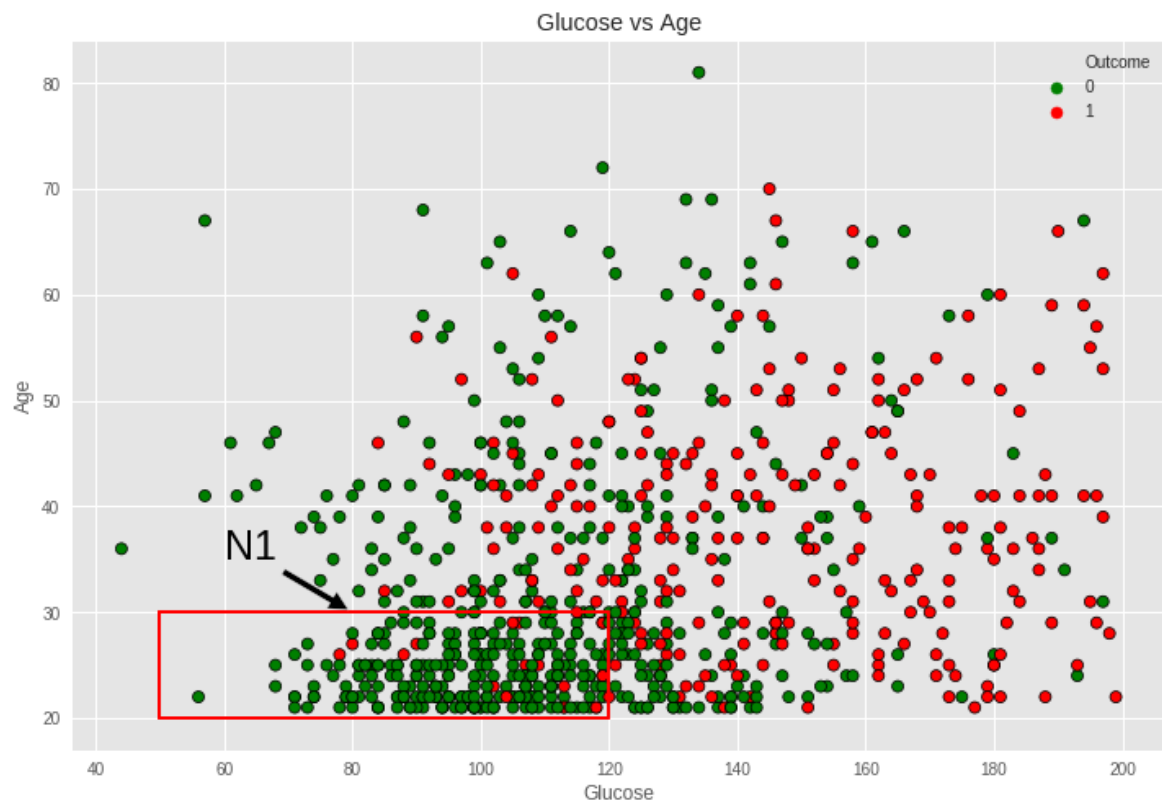


Figure 2: Master Node reading data from the SQL Database.

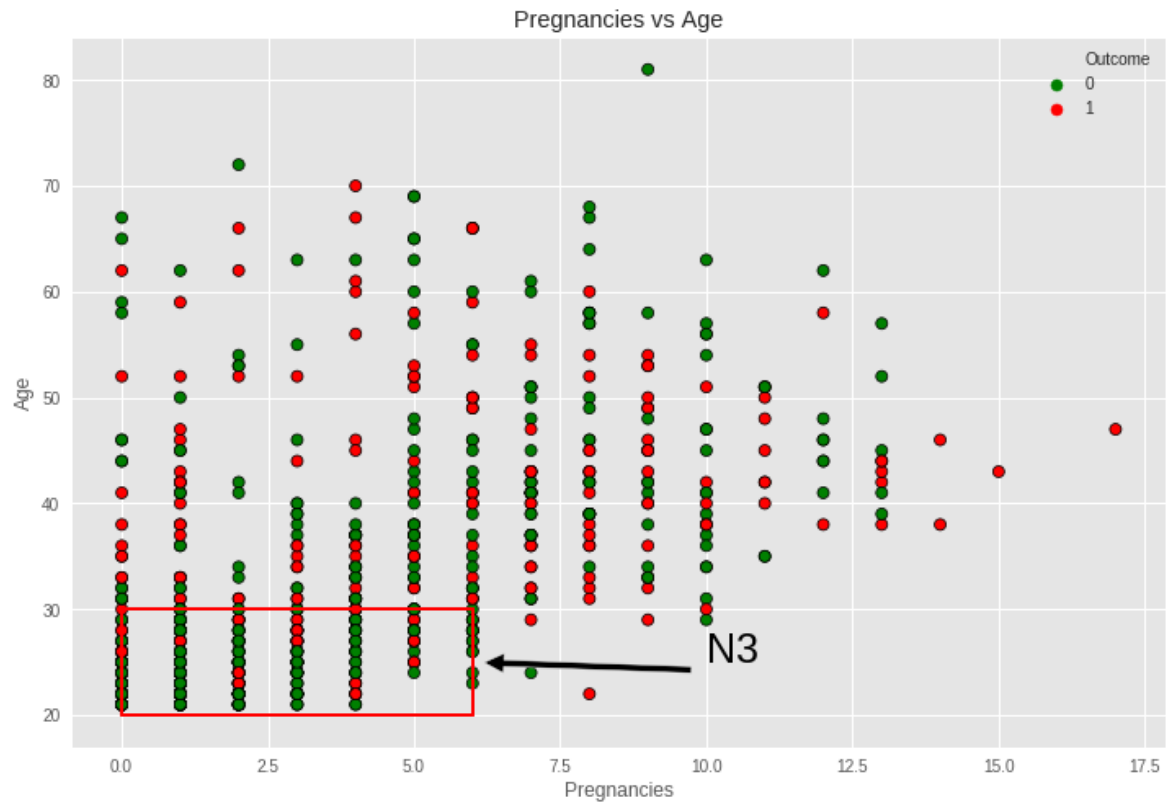


Figure 3: Master Node reading data from the SQL Database.

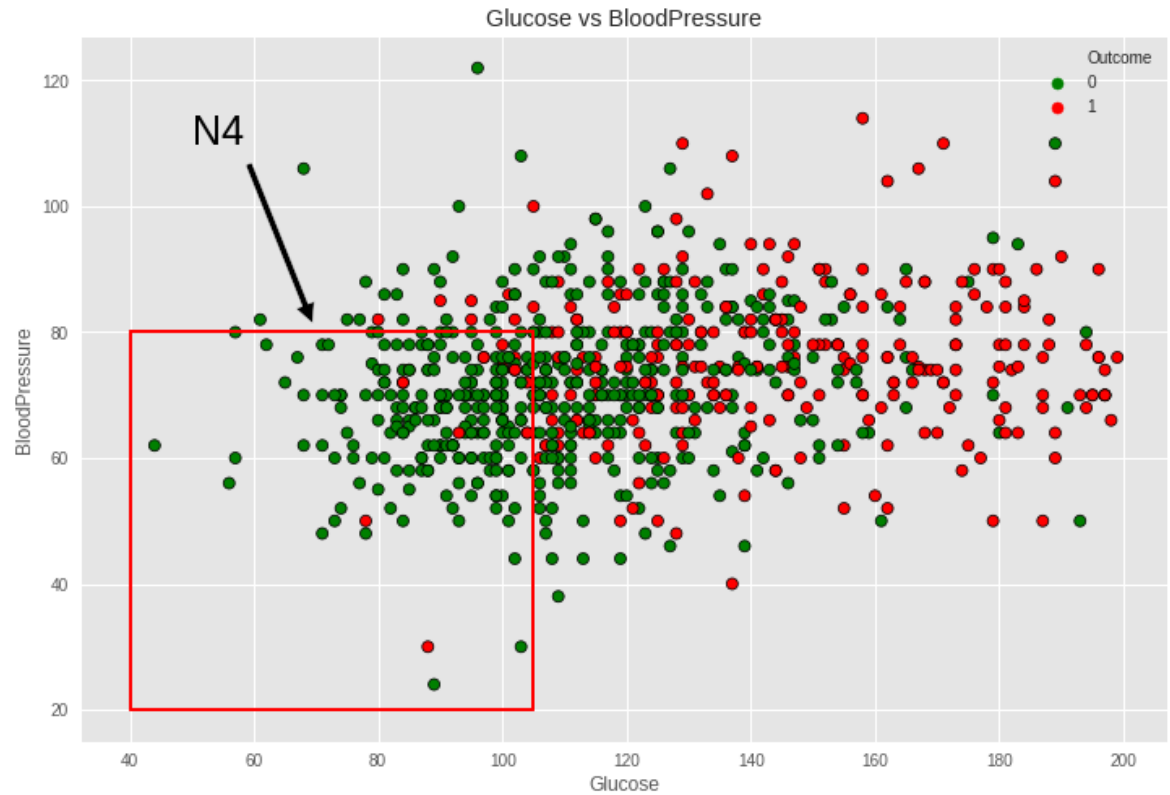


Figure 4: Master Node reading data from the SQL Database.

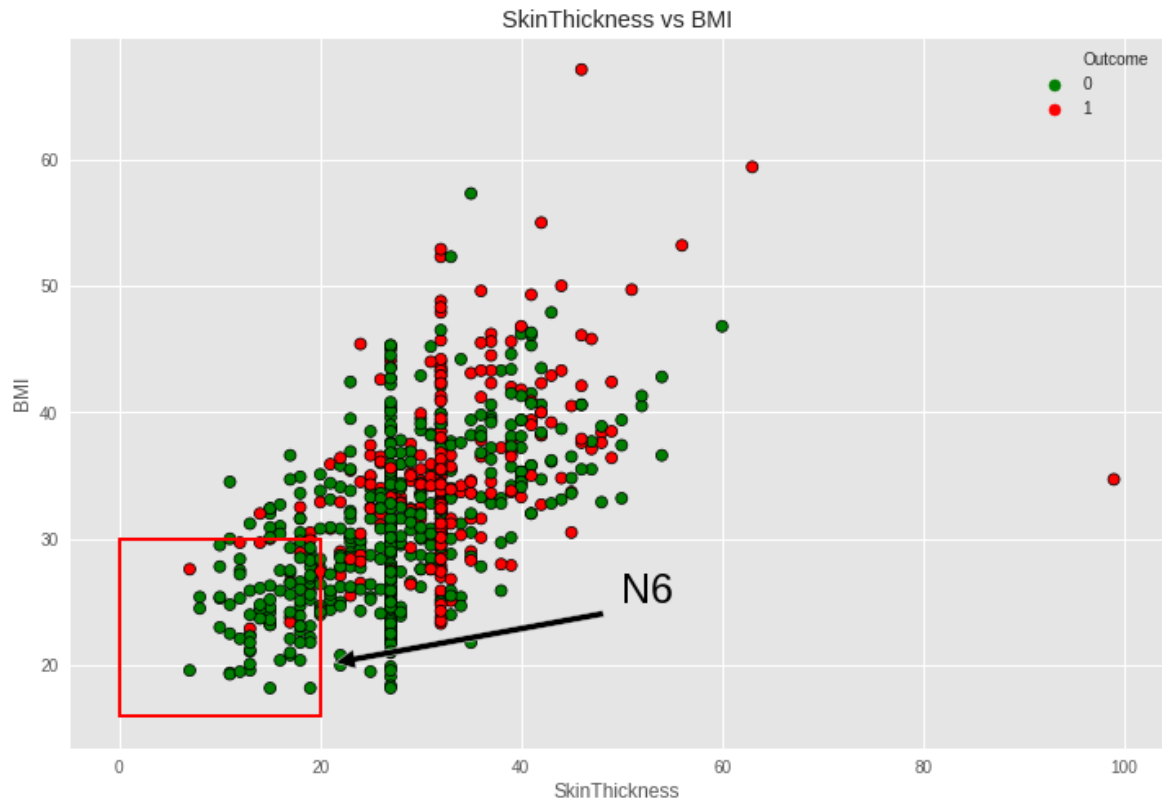


Figure 5: Master Node reading data from the SQL Database.

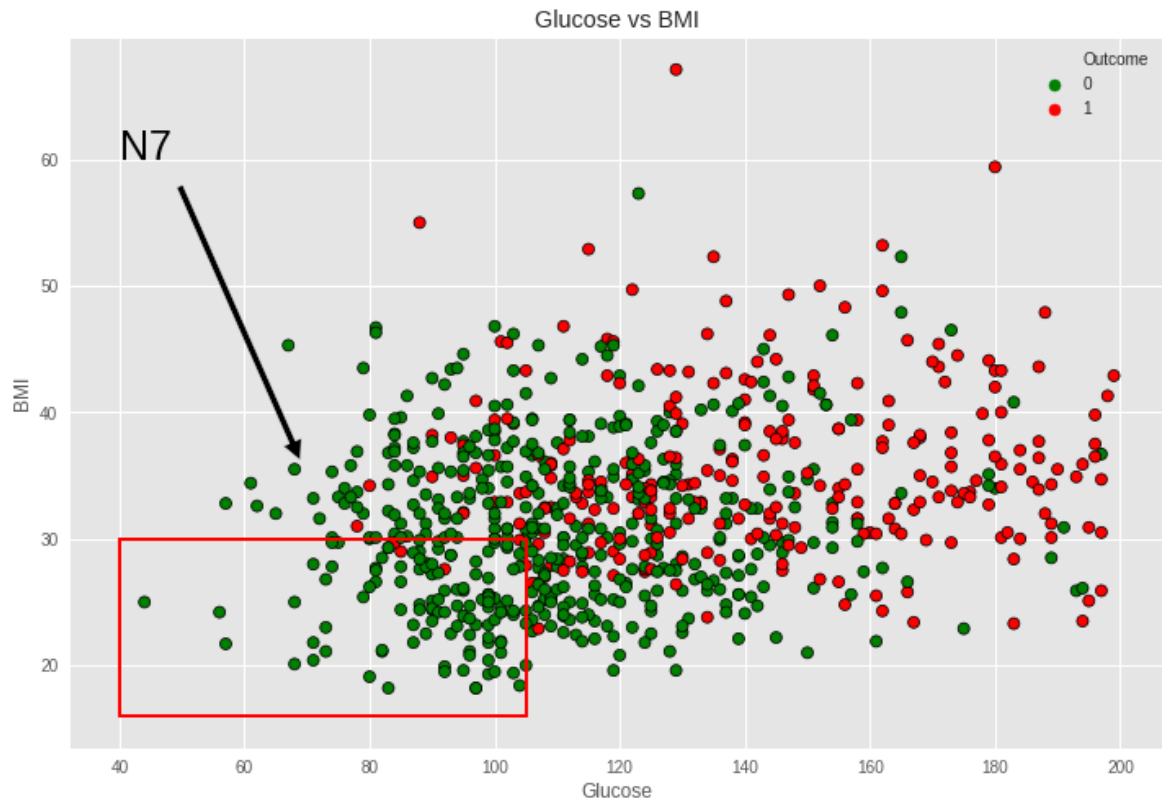


Figure 6: Master Node reading data from the SQL Database.



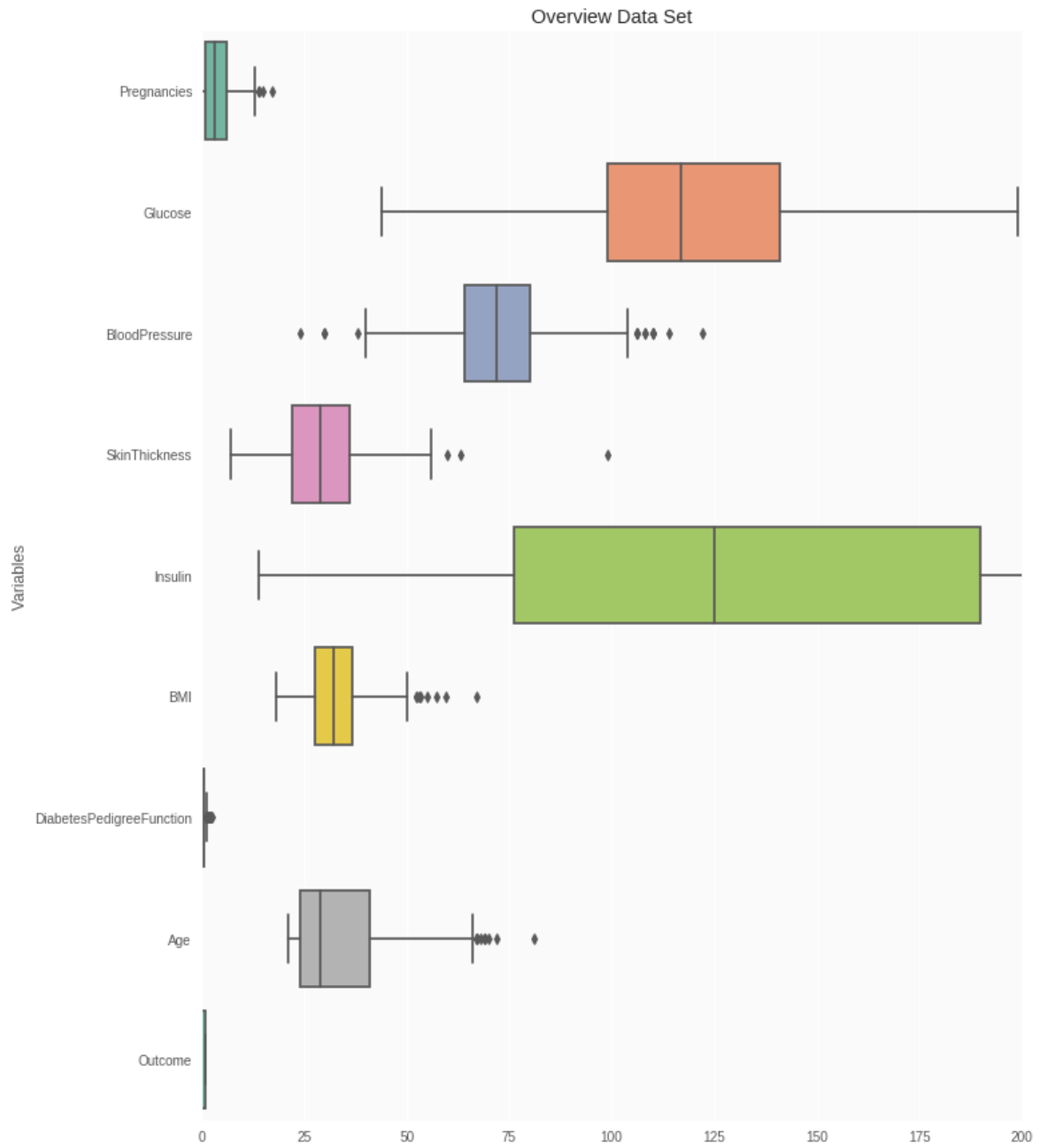


Figure 7: Master Node reading data from the SQL Database.

## Pregnancies

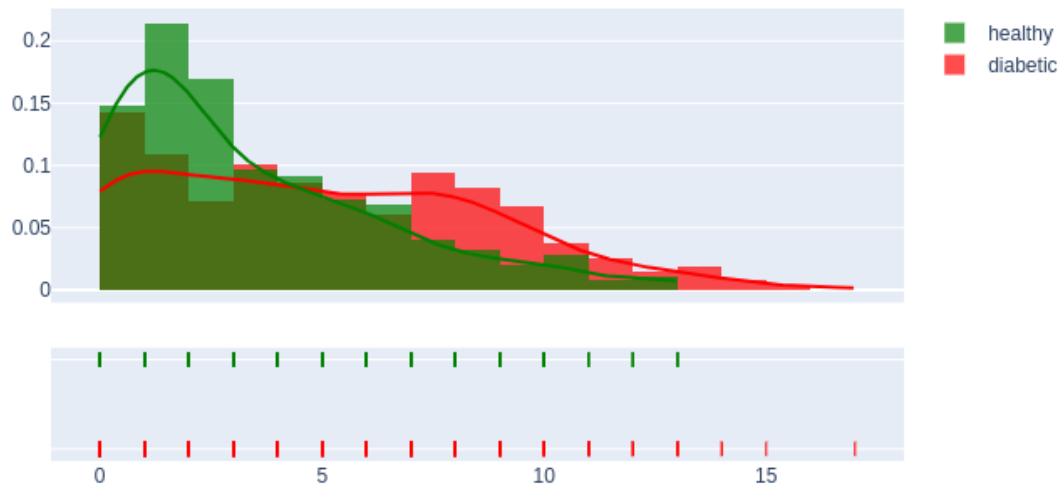


Figure 8: Master Node reading data from the SQL Database.

## DiabetesPedigreeFunction

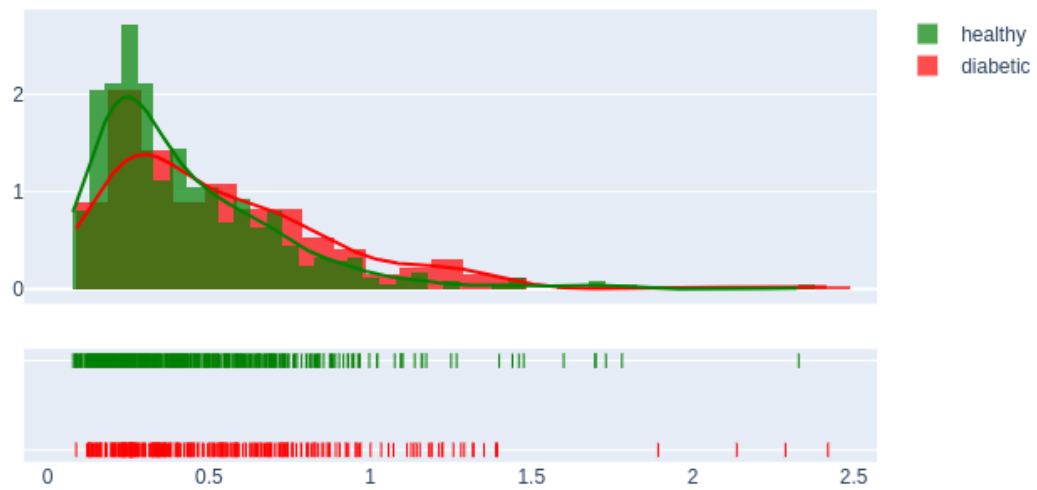


Figure 9: Master Node reading data from the SQL Database.

Glucose vs Age

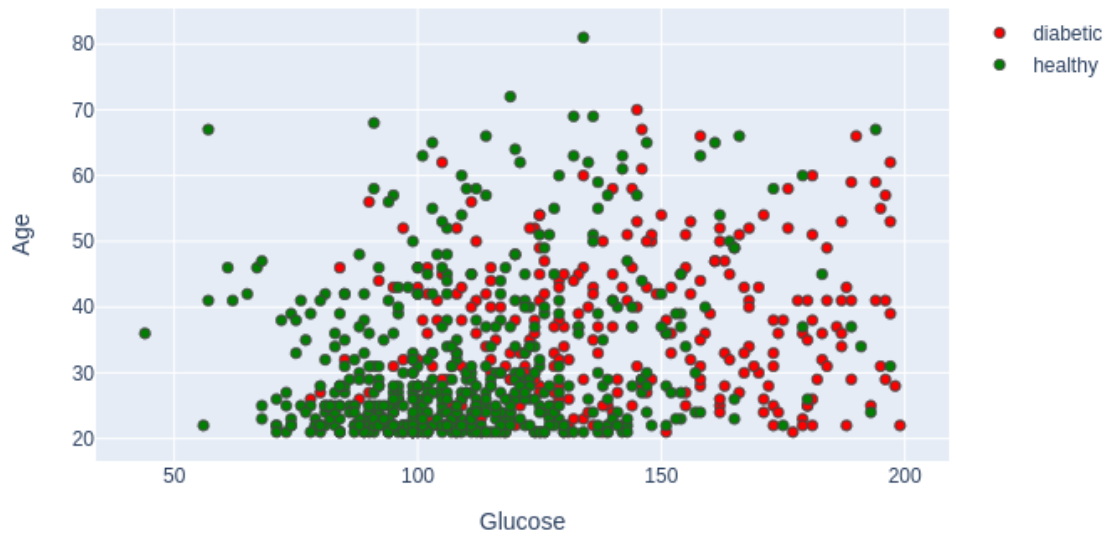


Figure 10: Master Node reading data from the SQL Database.

N1 :Glucose <= 120 and Age <= 30

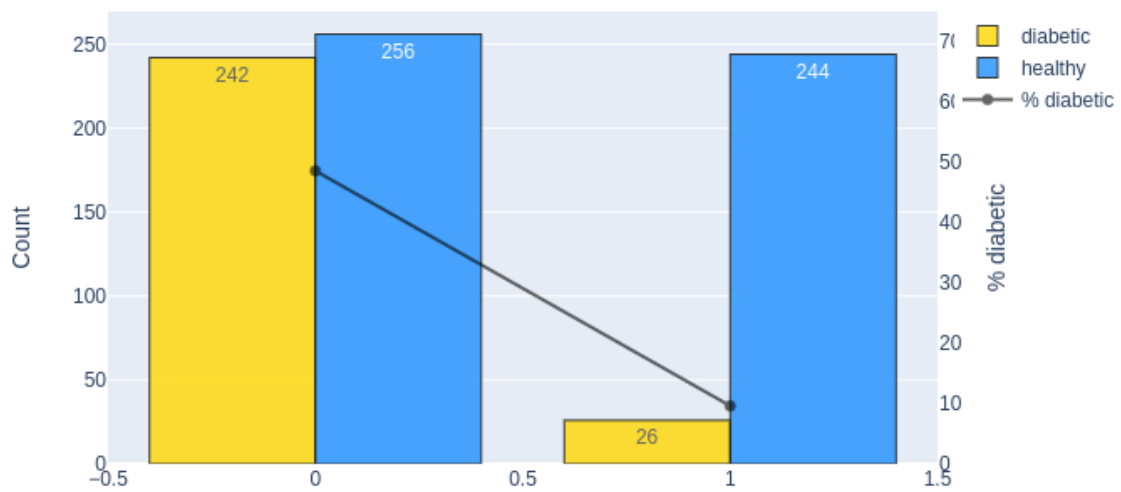


Figure 11: Master Node reading data from the SQL Database.

N1 distribution by target  
(Glucose  $\leq 120$  and Age  $\leq 30$ )

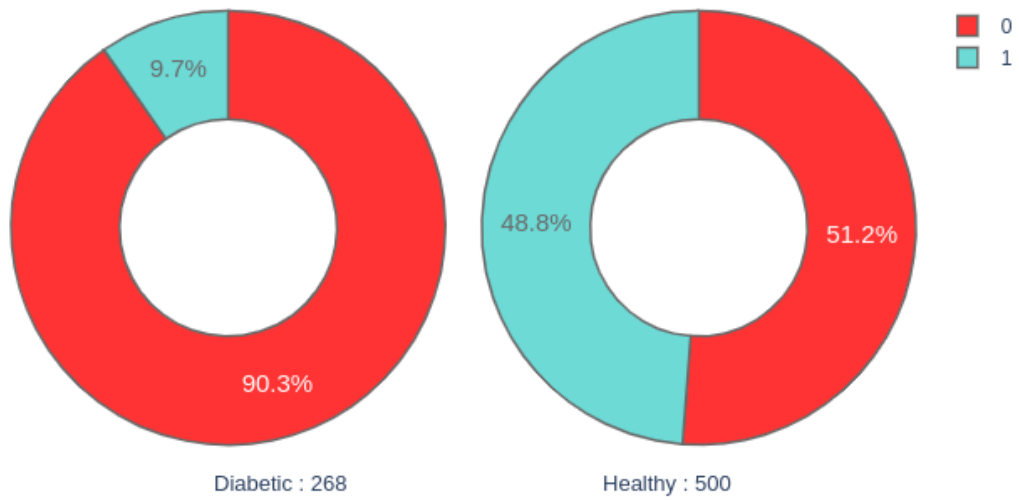


Figure 12: Master Node reading data from the SQL Database.

N2 : BMI  $\leq 30$

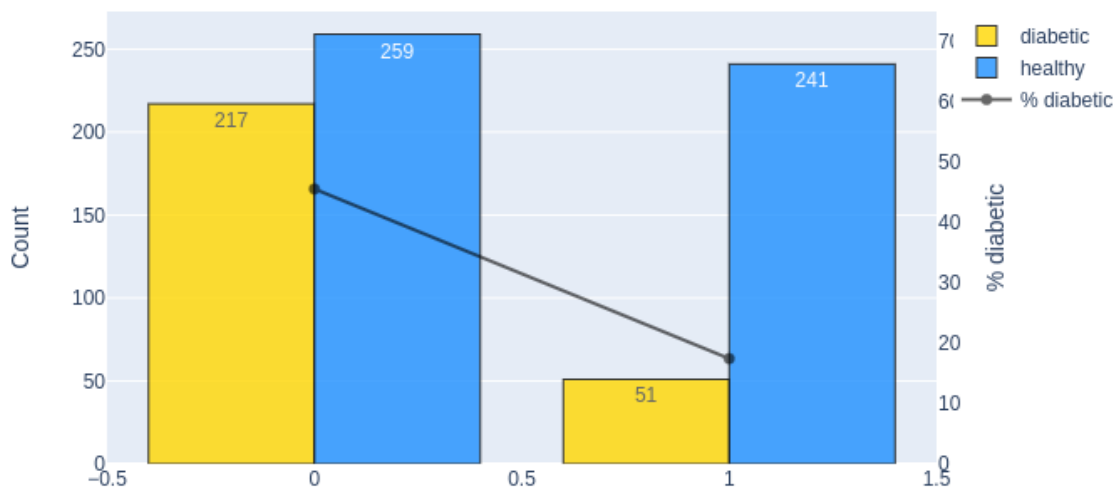


Figure 13: Master Node reading data from the SQL Database.

N2 distribution by target  
BMI <= 30

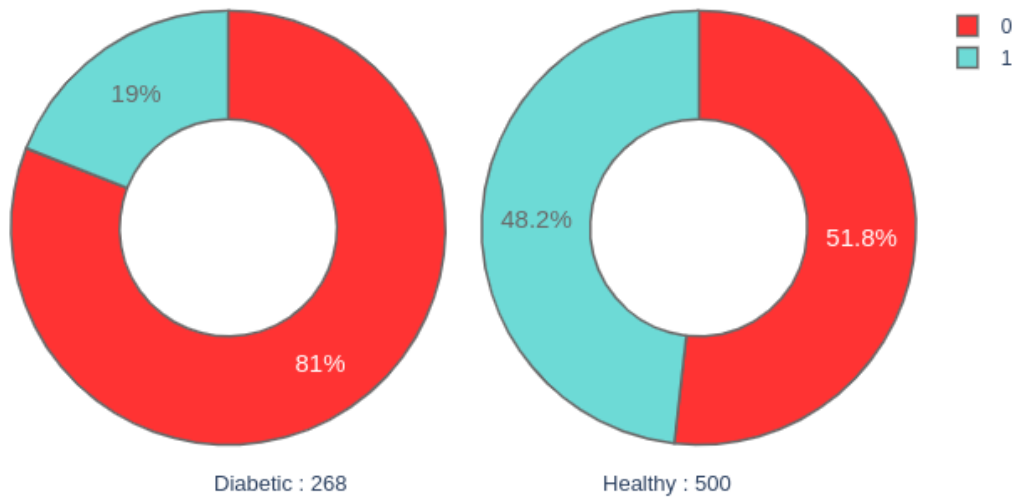


Figure 14: Master Node reading data from the SQL Database.

Pregnancies vs Age

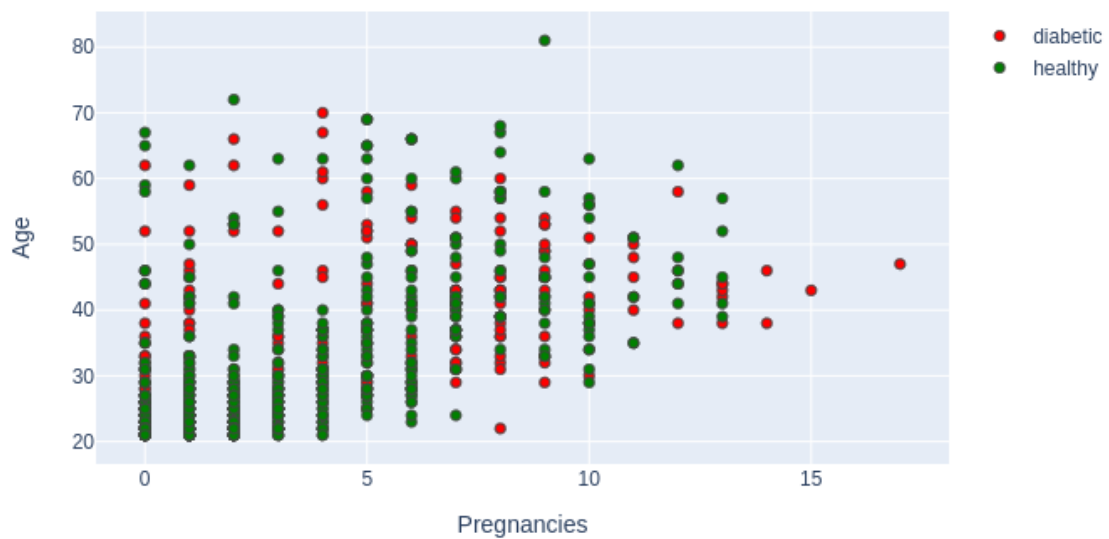


Figure 15: Master Node reading data from the SQL Database.

N3 : Age <= 30 and Pregnancies <= 6

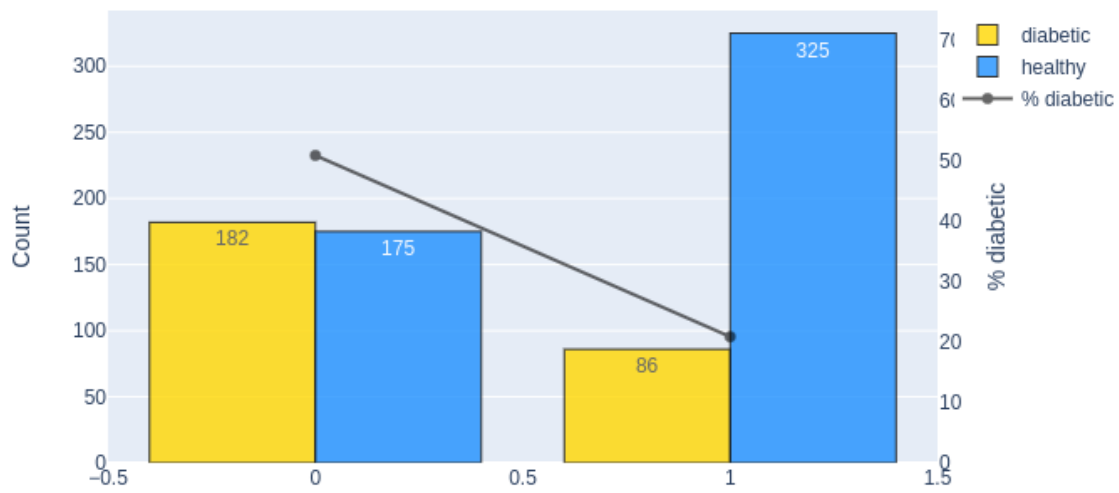


Figure 16: Master Node reading data from the SQL Database.

N3 distribution by target  
Age <= 30 and Pregnancies <= 6

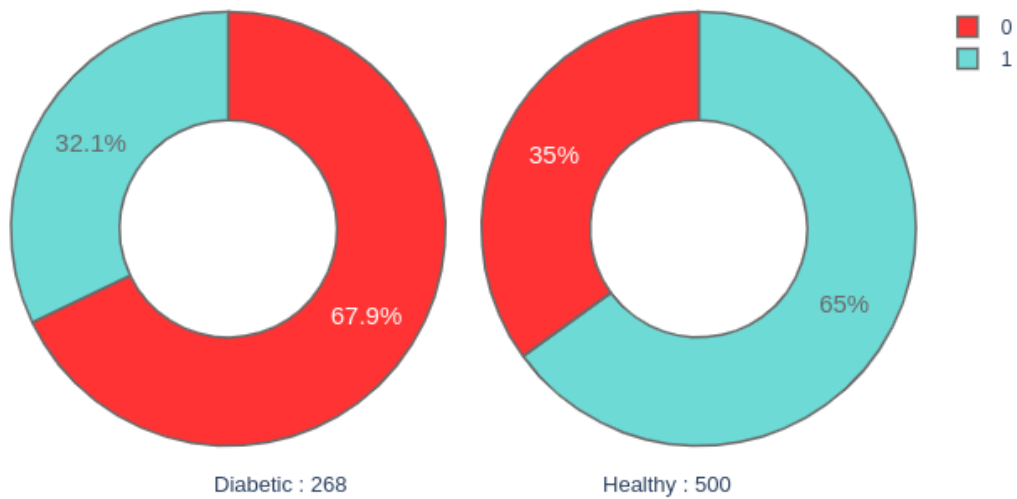


Figure 17: Master Node reading data from the SQL Database.

### Distribution of Outcome variable

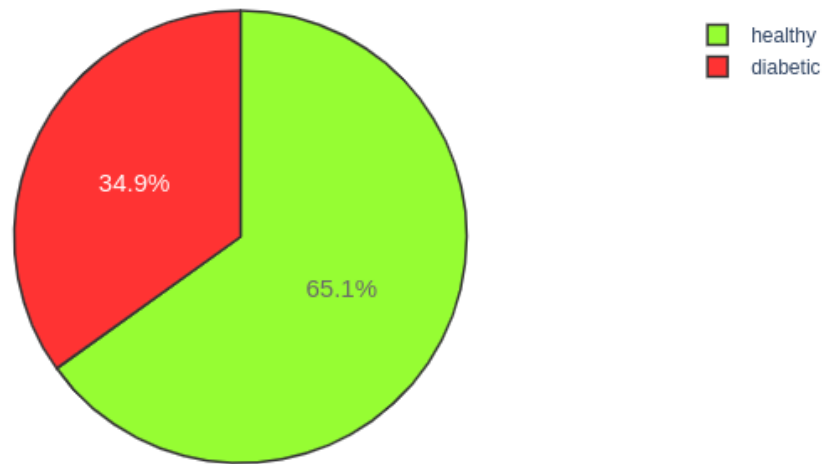


Figure 18: Master Node reading data from the SQL Database.

### Glucose vs BloodPressure

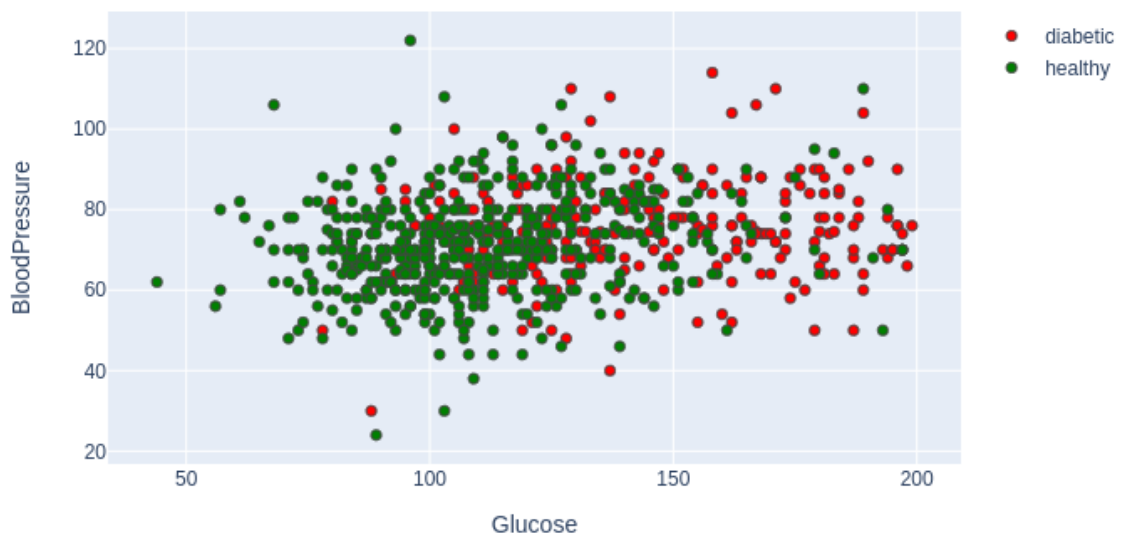


Figure 19: Master Node reading data from the SQL Database.

N4 : Glucose  $\leq$  105 and BloodPressure  $\leq$  80

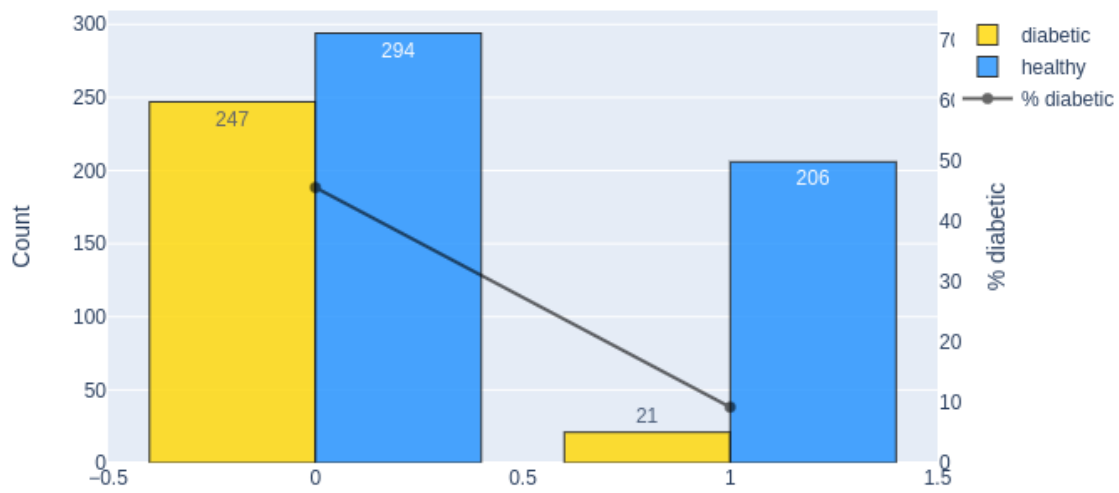


Figure 20: Master Node reading data from the SQL Database.

N4 distribution by target  
Glucose  $\leq$  105 and BloodPressure  $\leq$  80

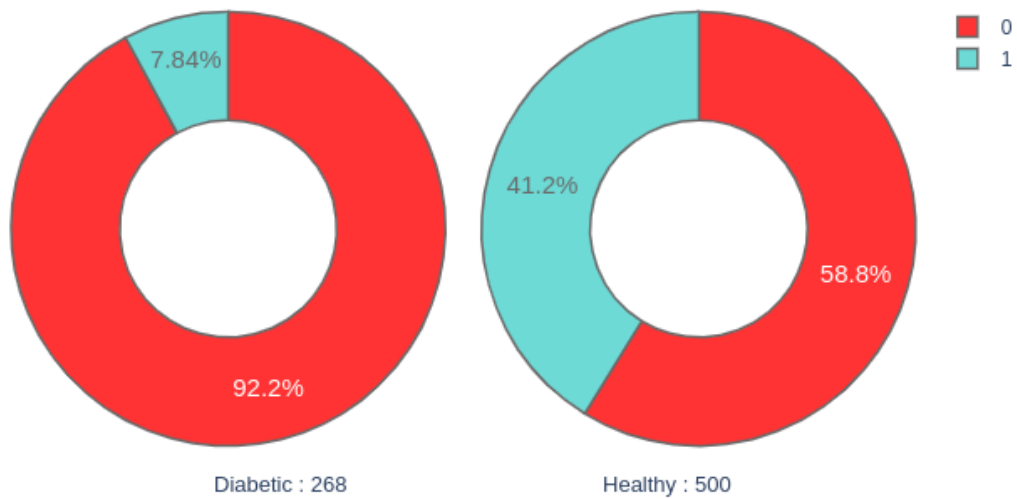


Figure 21: Master Node reading data from the SQL Database.



N5 :SkinThickness <= 20

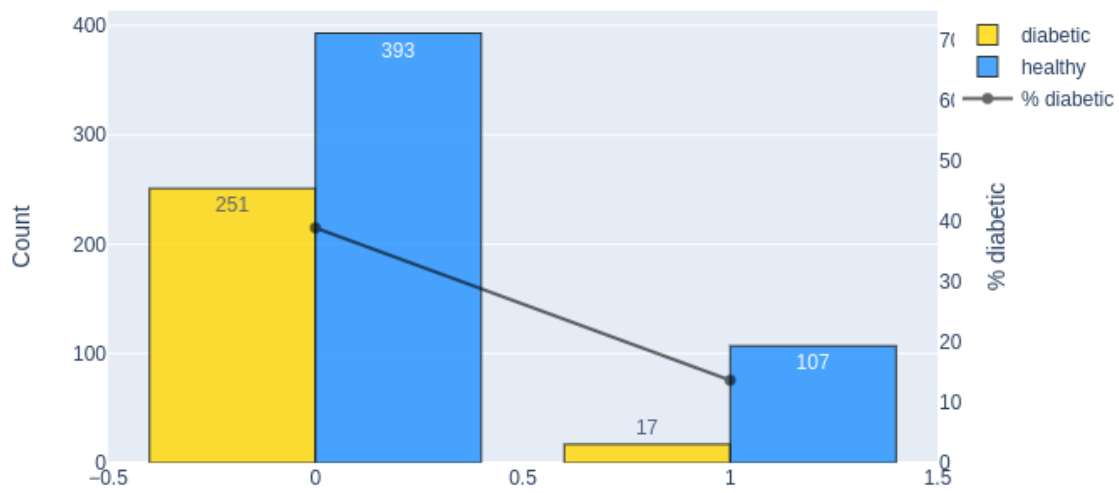


Figure 22: Master Node reading data from the SQL Database.

N5 distribution by target  
SkinThickness <= 20

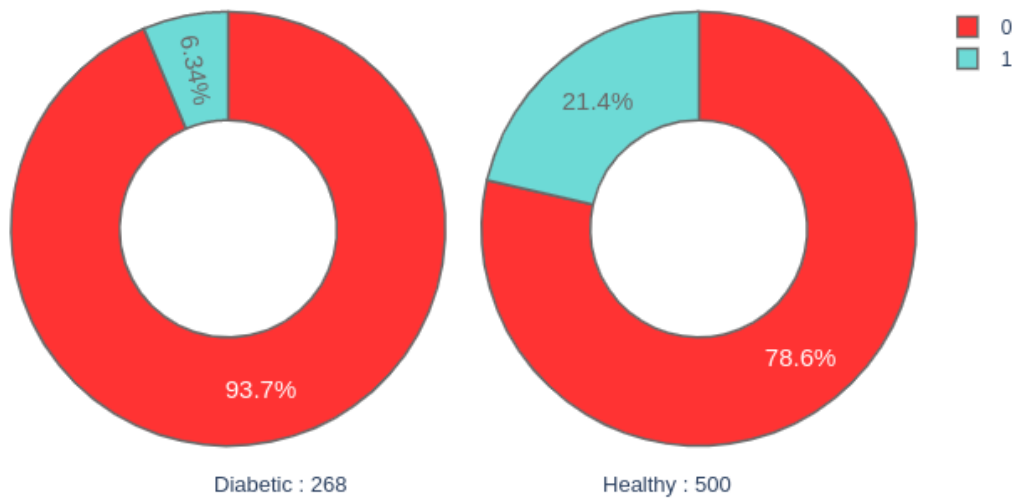


Figure 23: Master Node reading data from the SQL Database.

SkinThickness vs BMI

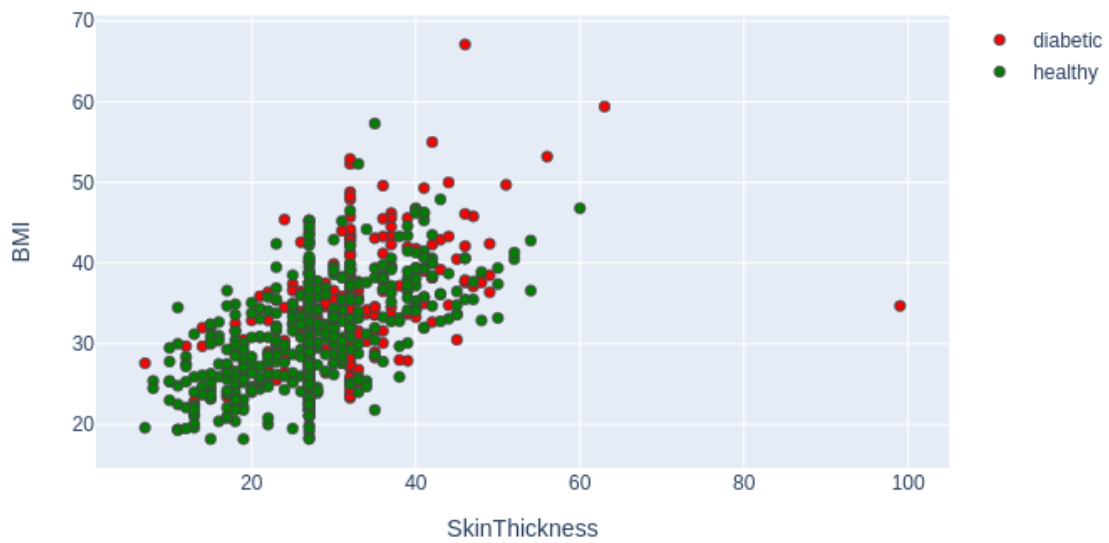


Figure 24: Master Node reading data from the SQL Database.

N6 : BMI < 30 and SkinThickness <= 20

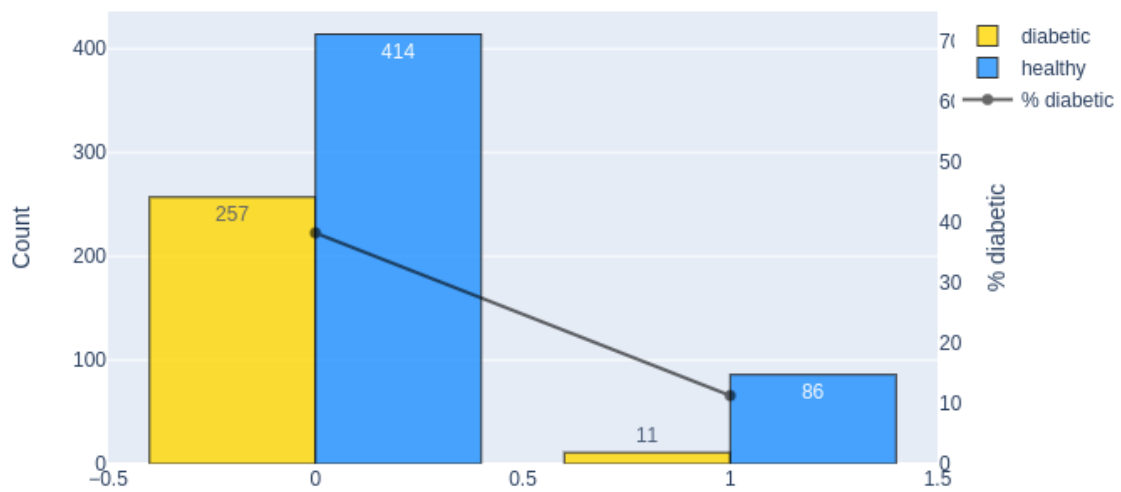


Figure 25: Master Node reading data from the SQL Database.

N6 distribution by target  
BMI < 30 and SkinThickness <= 20

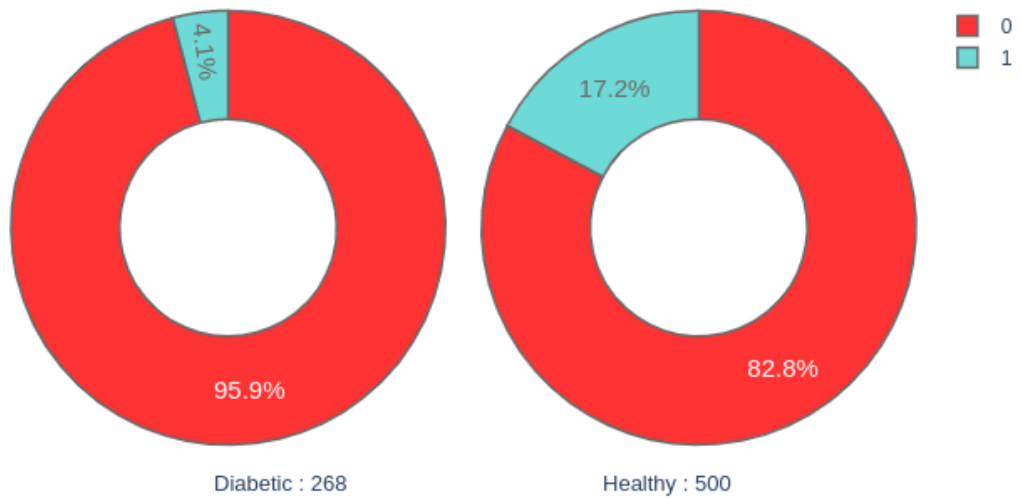


Figure 26: Master Node reading data from the SQL Database.

Glucose vs BMI

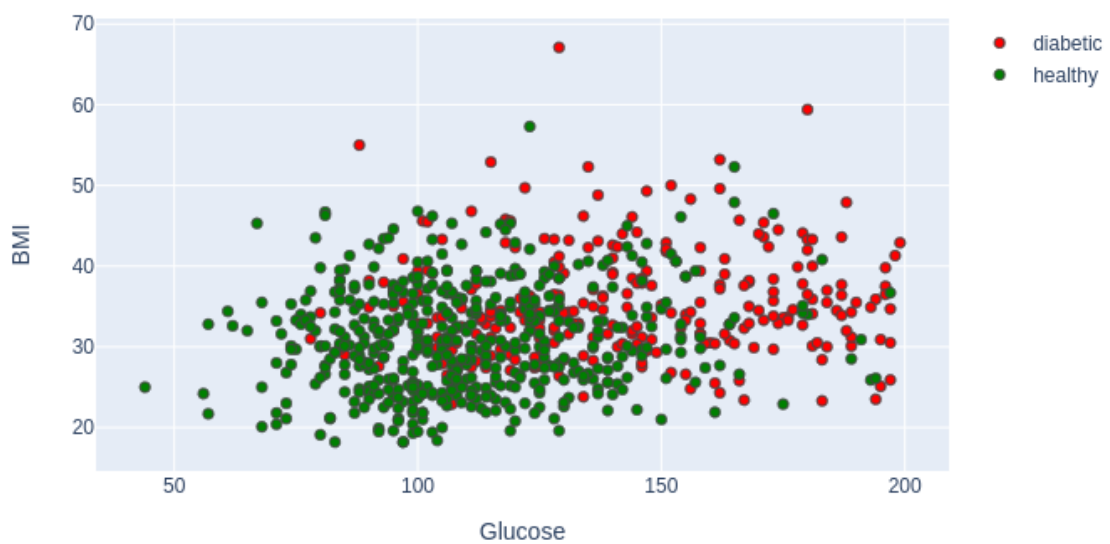


Figure 27: Master Node reading data from the SQL Database.

N7 : Glucose  $\leq$  105 and BMI  $\leq$  30

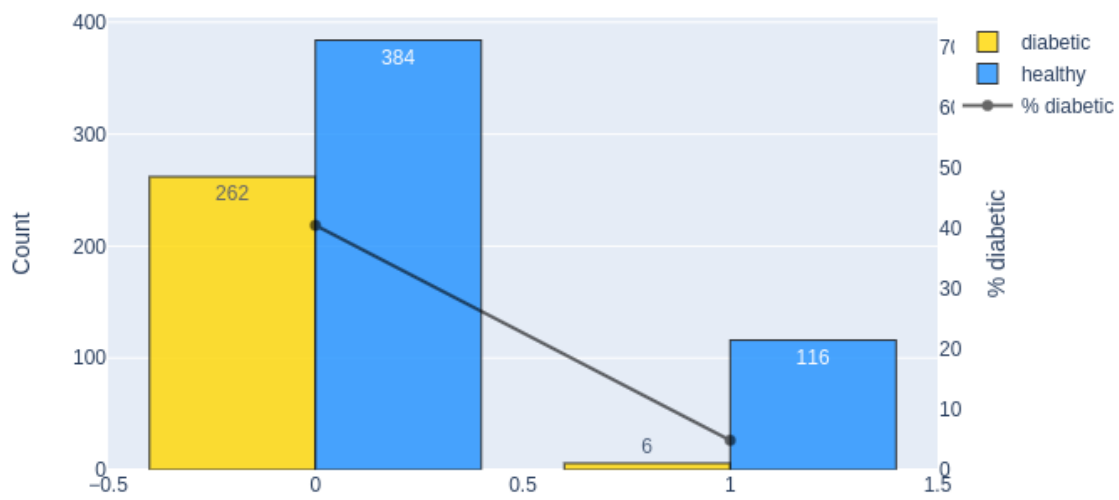


Figure 28: Master Node reading data from the SQL Database.

Missing Values (count & %)

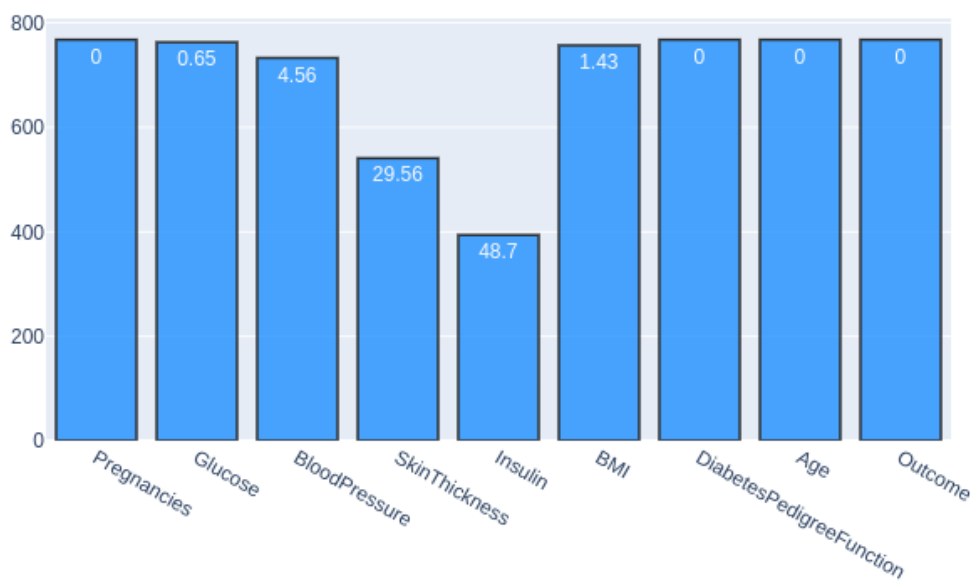


Figure 29: Master Node reading data from the SQL Database.

N7 distribution by target

Glucose  $\leq 105$  and BMI  $\leq 30$

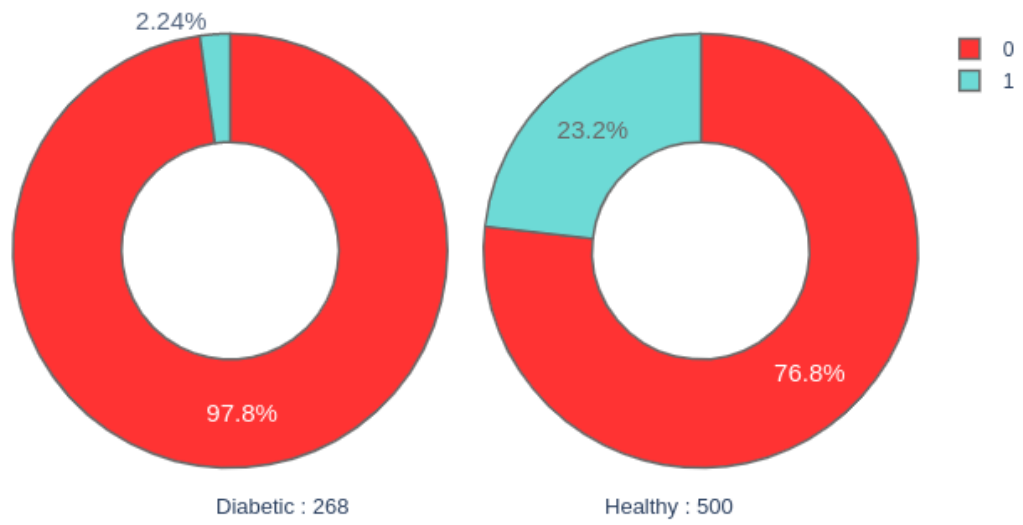


Figure 30: Master Node reading data from the SQL Database.

Insulin

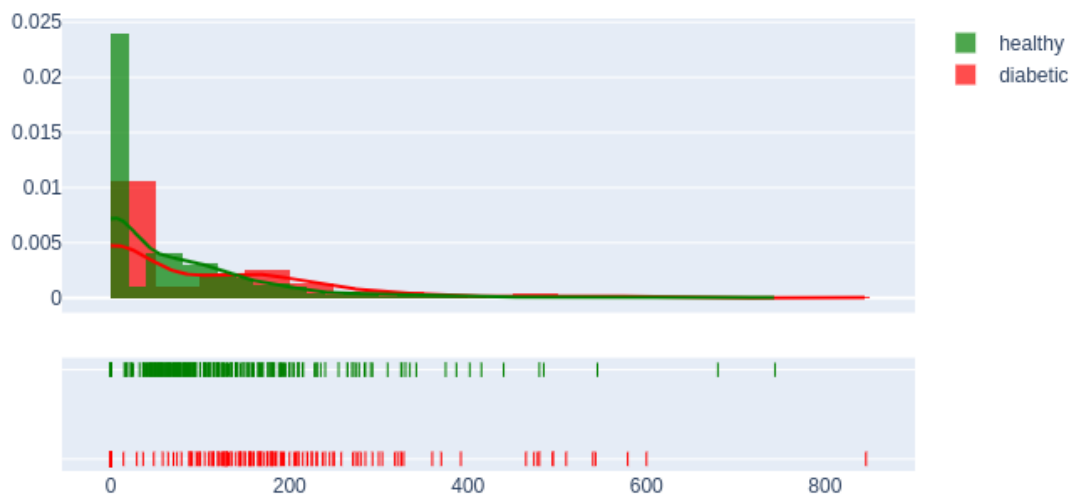


Figure 31: Master Node reading data from the SQL Database.

N9 : Insulin < 200

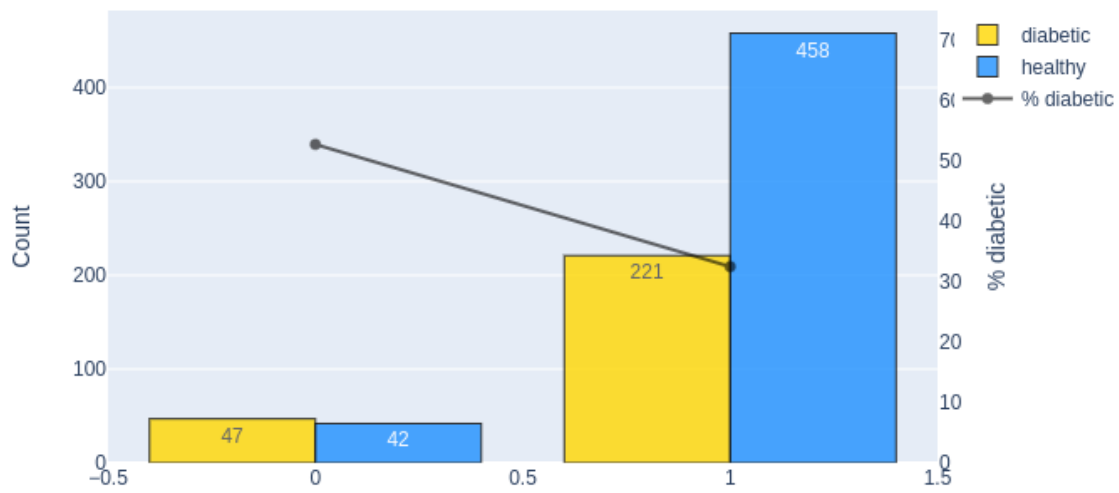


Figure 32: Master Node reading data from the SQL Database.

N9 distribution by target  
Insulin < 200



Figure 33: Master Node reading data from the SQL Database.

N10 : BloodPressure < 80

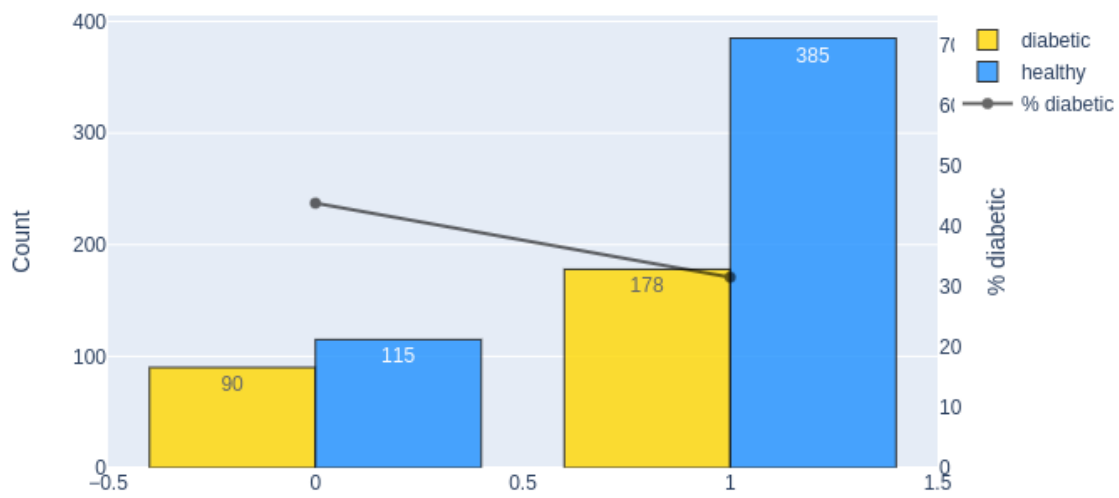


Figure 34: Master Node reading data from the SQL Database.

N10 distribution by target  
BloodPressure < 80

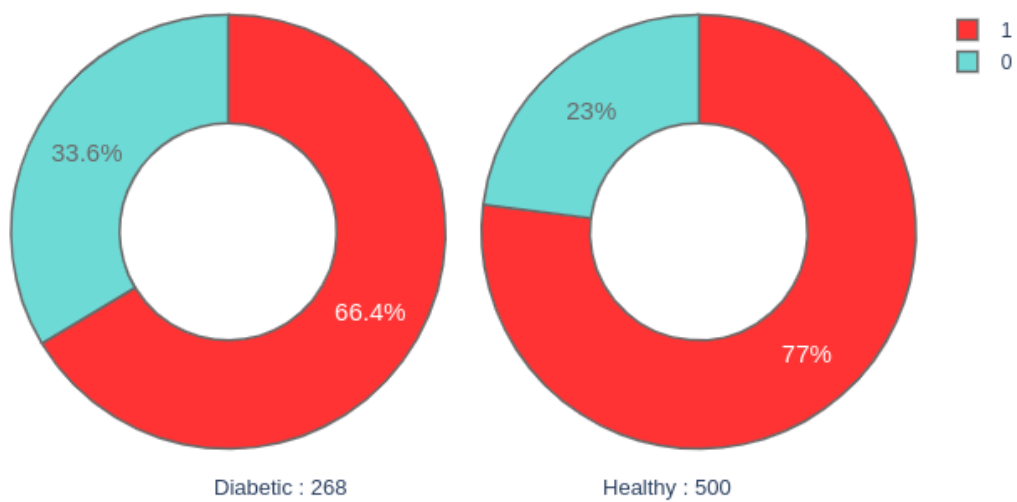


Figure 35: Master Node reading data from the SQL Database.

## Pregnancies

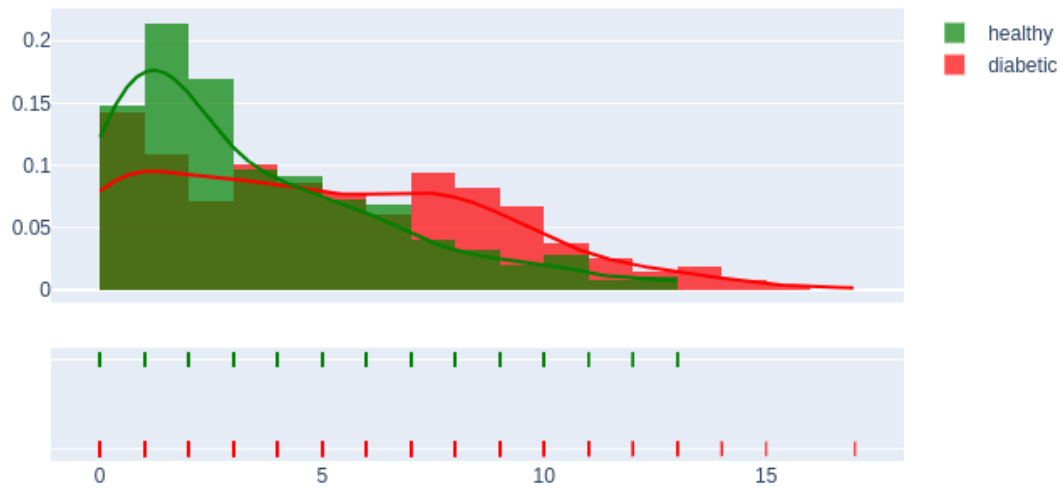


Figure 36: Master Node reading data from the SQL Database.

## N11 : Pregnancies > 0 and < 4

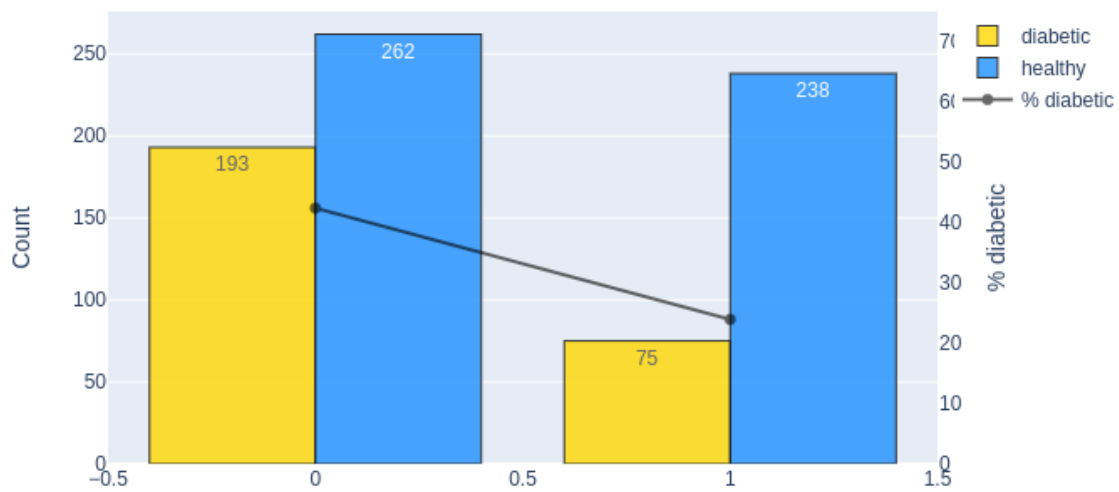


Figure 37: Master Node reading data from the SQL Database.



N11 distribution by target  
Pregnancies > 0 and < 4

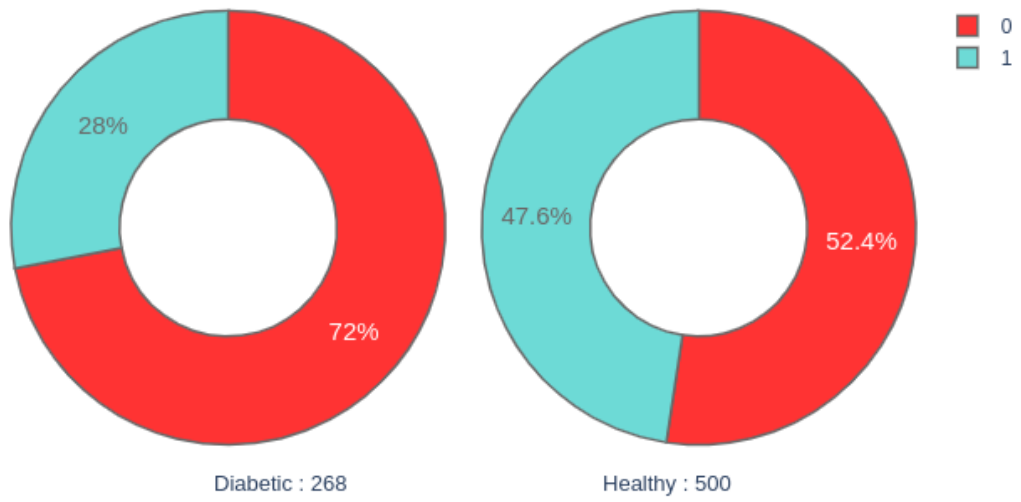


Figure 38: Master Node reading data from the SQL Database.

NO

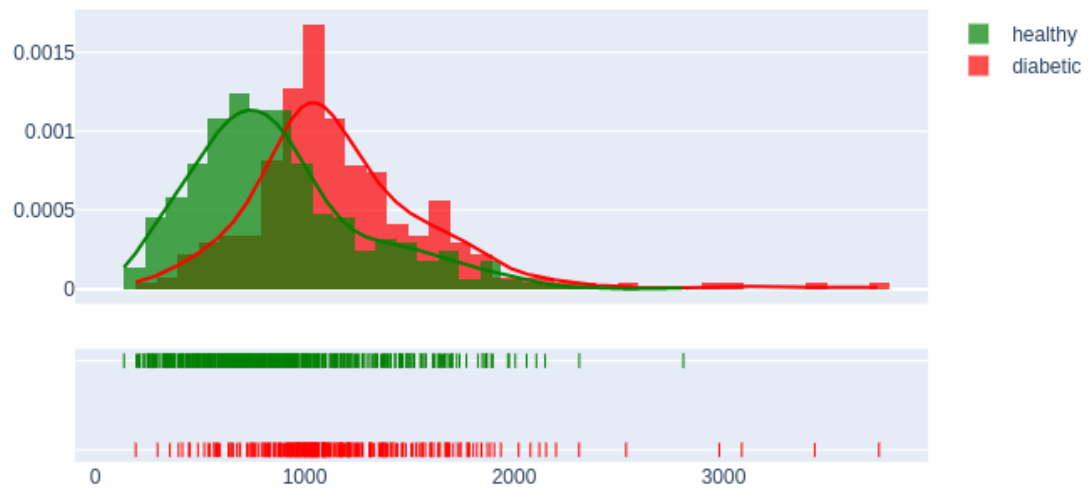


Figure 39: Master Node reading data from the SQL Database.

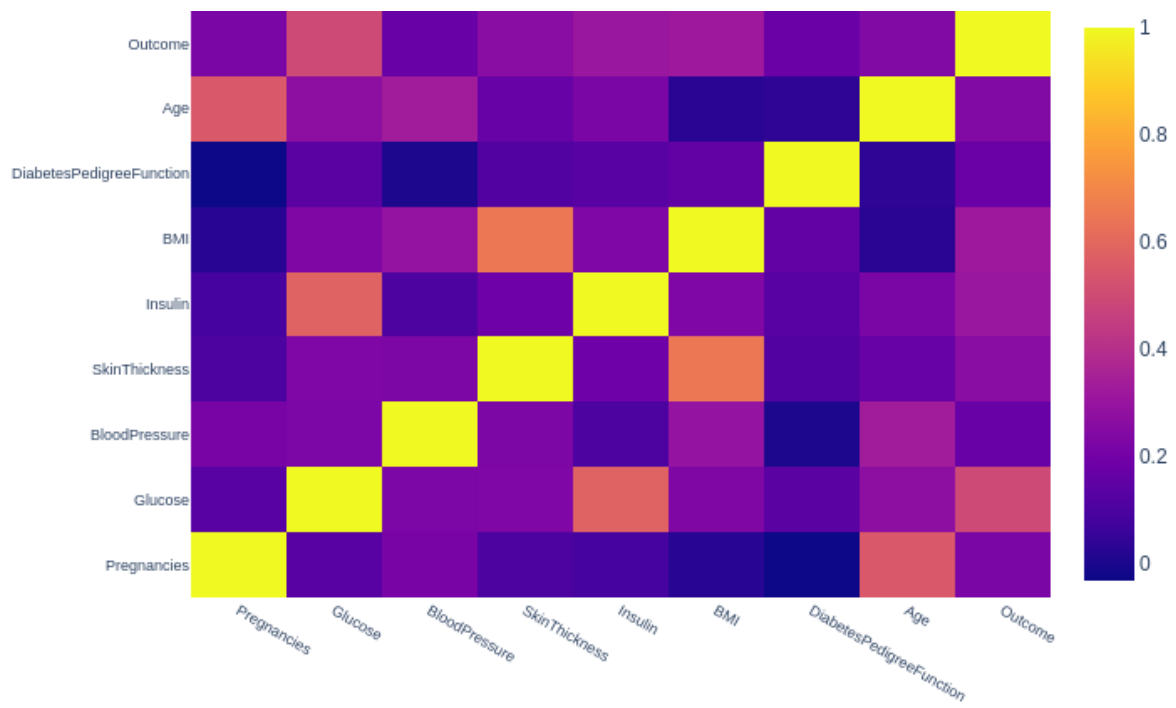


Figure 40: Master Node reading data from the SQL Database.

N15 : N0 < 1034

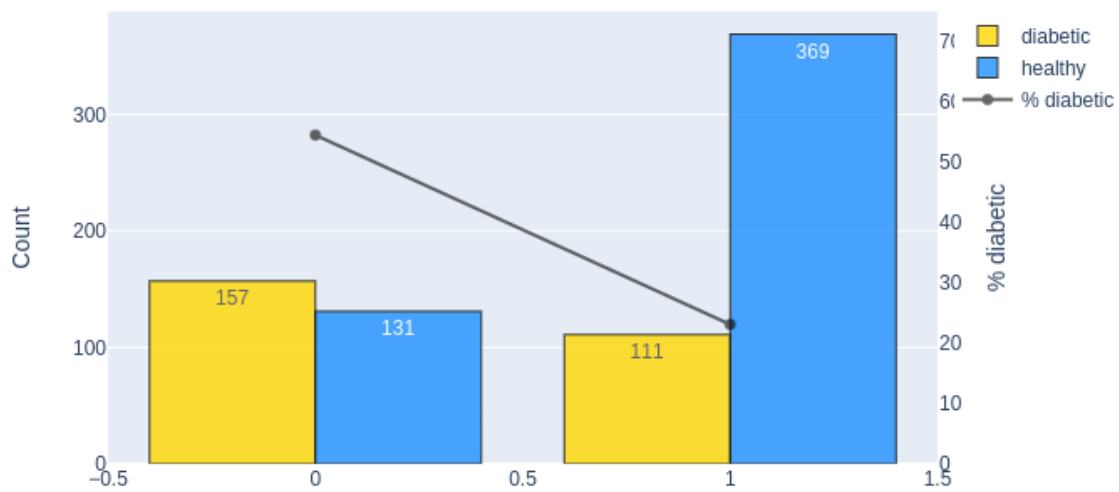


Figure 41: Master Node reading data from the SQL Database.

N15 distribution by target  
N0 < 1034

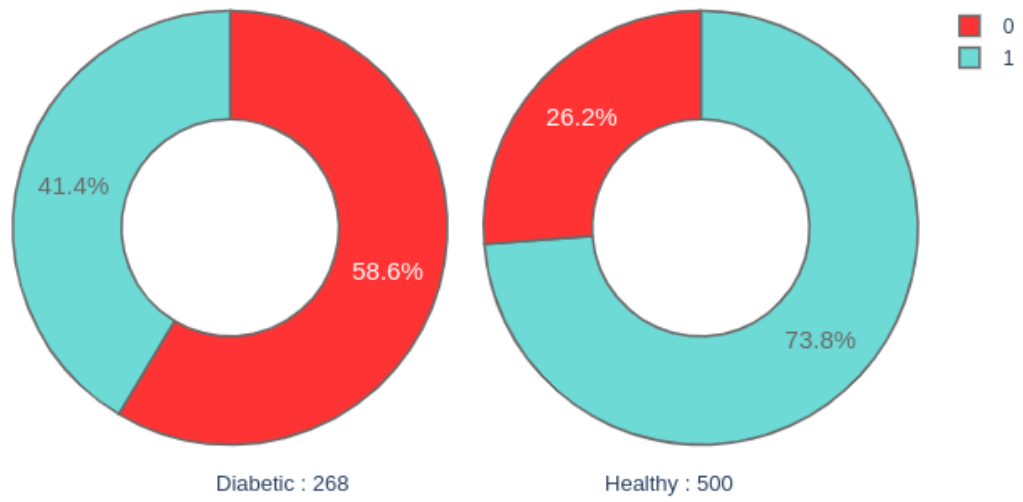


Figure 42: Master Node reading data from the SQL Database.

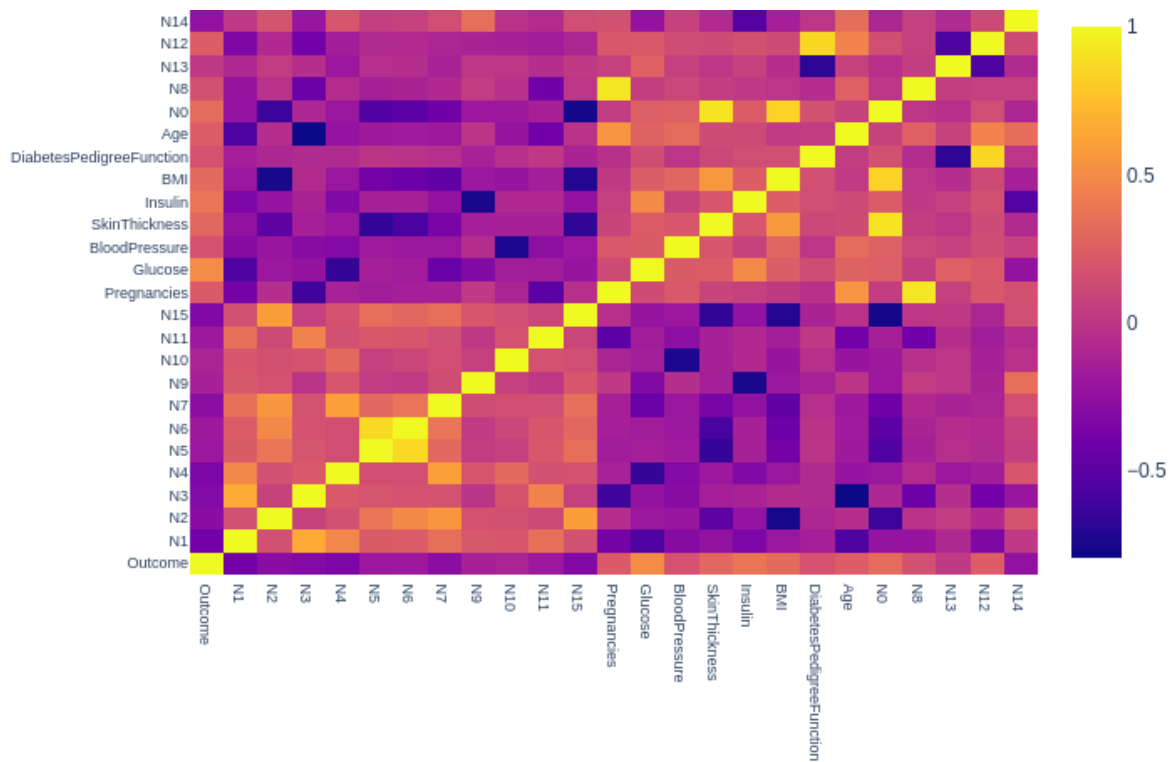


Figure 43: Master Node reading data from the SQL Database.

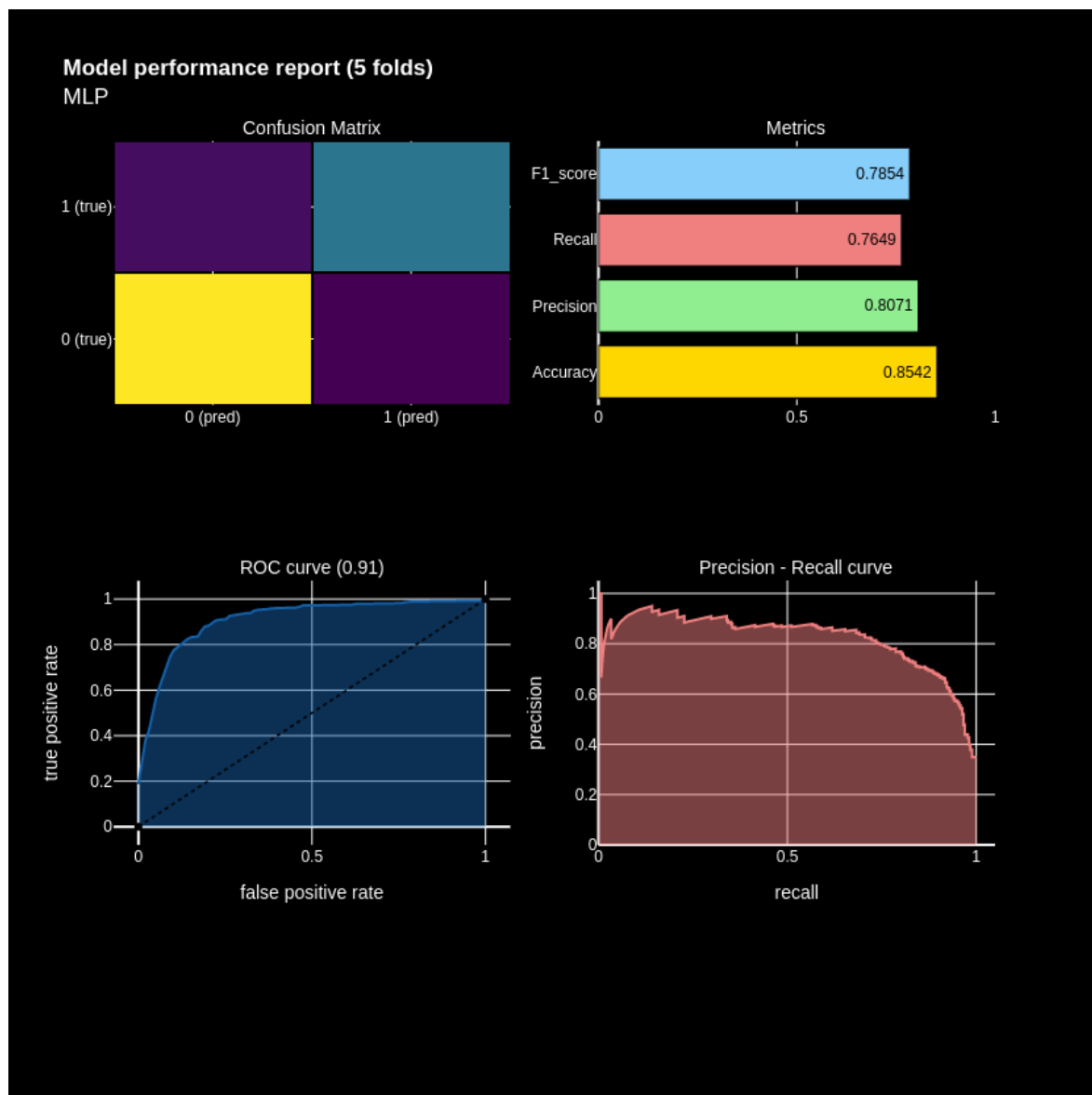


Figure 44: Master Node reading data from the SQL Database.

## Cross Validation - 5 folds

MLP

| Fold | Accuracy | Precision | Recall | F1 score | Roc auc |
|------|----------|-----------|--------|----------|---------|
| 1    | 0.864    | 0.811     | 0.796  | 0.804    | 0.908   |
| 2    | 0.825    | 0.787     | 0.685  | 0.733    | 0.896   |
| 3    | 0.844    | 0.841     | 0.685  | 0.755    | 0.902   |
| 4    | 0.863    | 0.82      | 0.774  | 0.796    | 0.92    |
| 5    | 0.876    | 0.783     | 0.887  | 0.832    | 0.933   |
| mean | 0.854    | 0.809     | 0.765  | 0.784    | 0.912   |
| std  | 0.018    | 0.021     | 0.076  | 0.035    | 0.013   |

Figure 45: Master Node reading data from the SQL Database.

Insulin

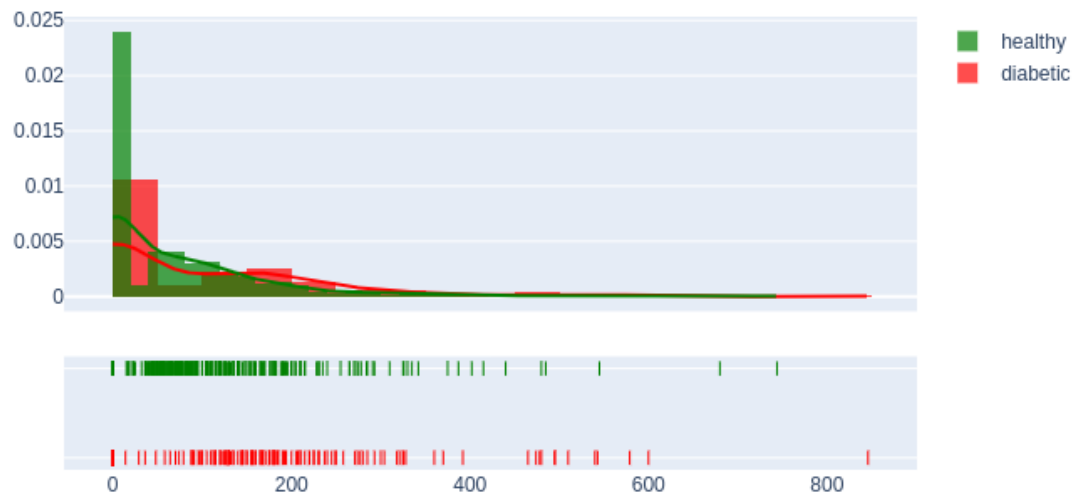


Figure 46: Master Node reading data from the SQL Database.

### Glucose

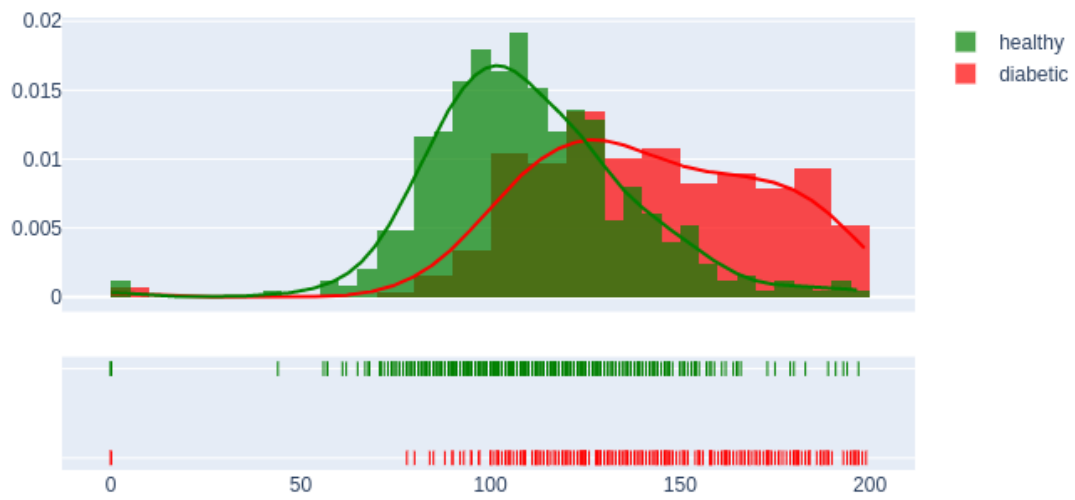


Figure 47: Master Node reading data from the SQL Database.

### SkinThickness

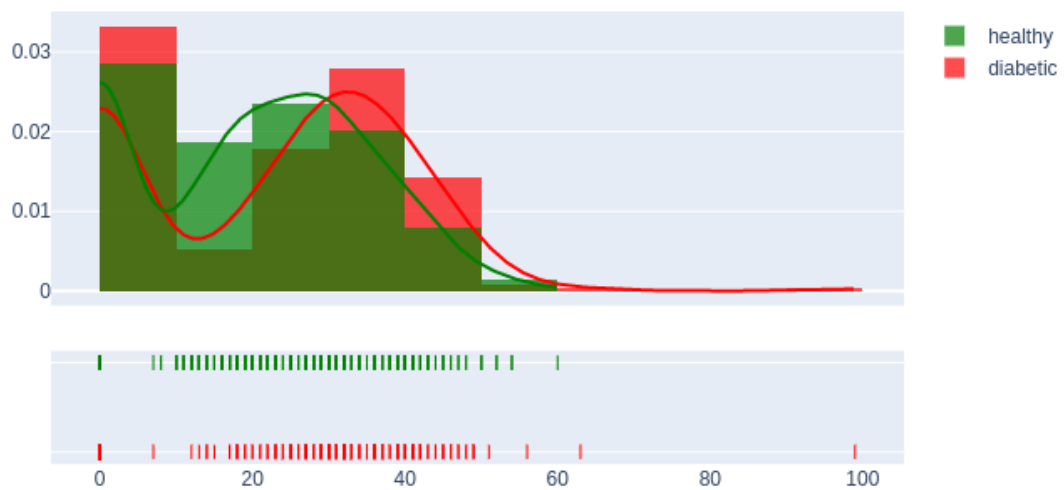


Figure 48: Master Node reading data from the SQL Database.

## BloodPressure

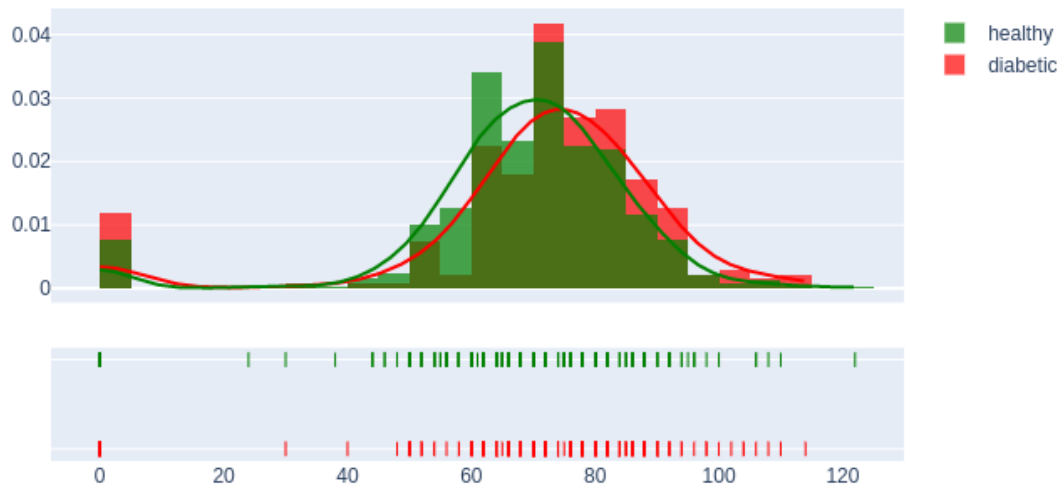


Figure 49: Master Node reading data from the SQL Database.

## BMI

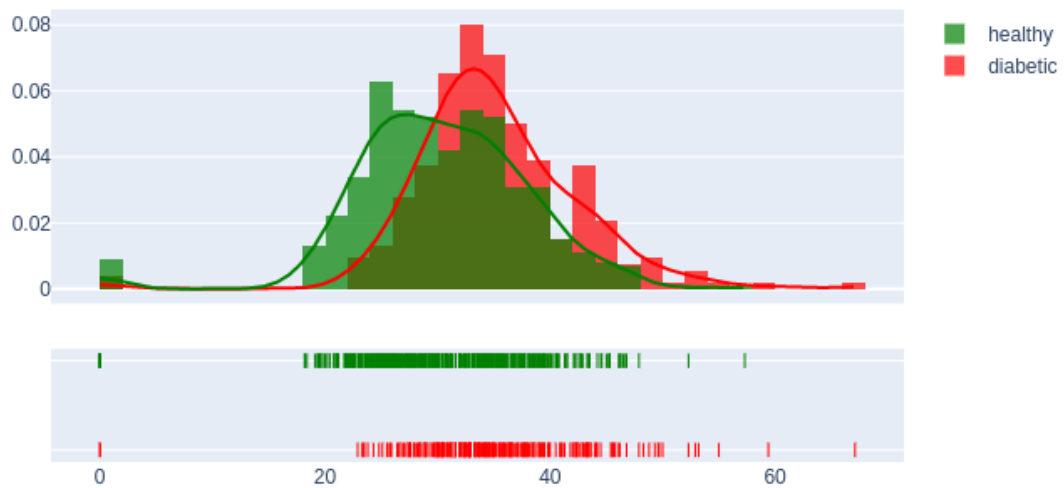


Figure 50: Master Node reading data from the SQL Database.

Age

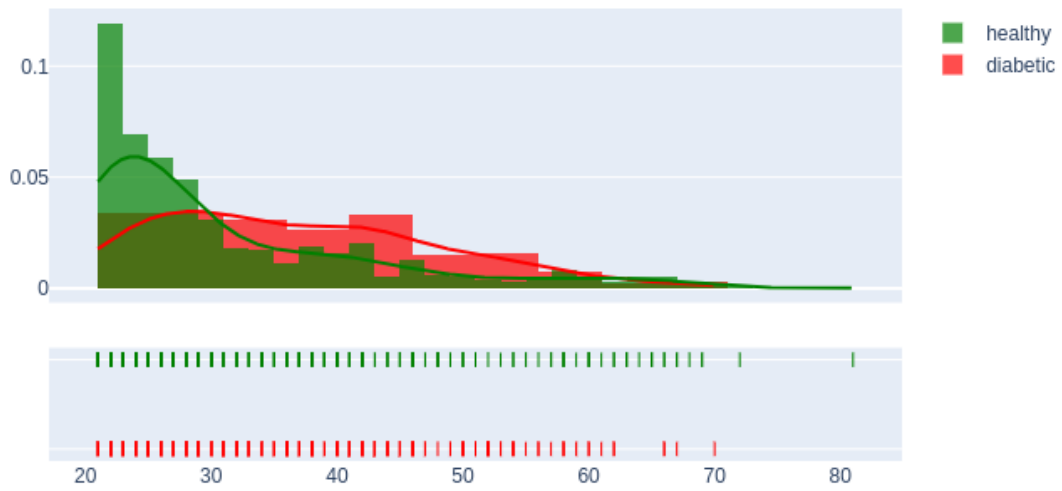


Figure 51: Master Node reading data from the SQL Database.

Count of Outcome variable

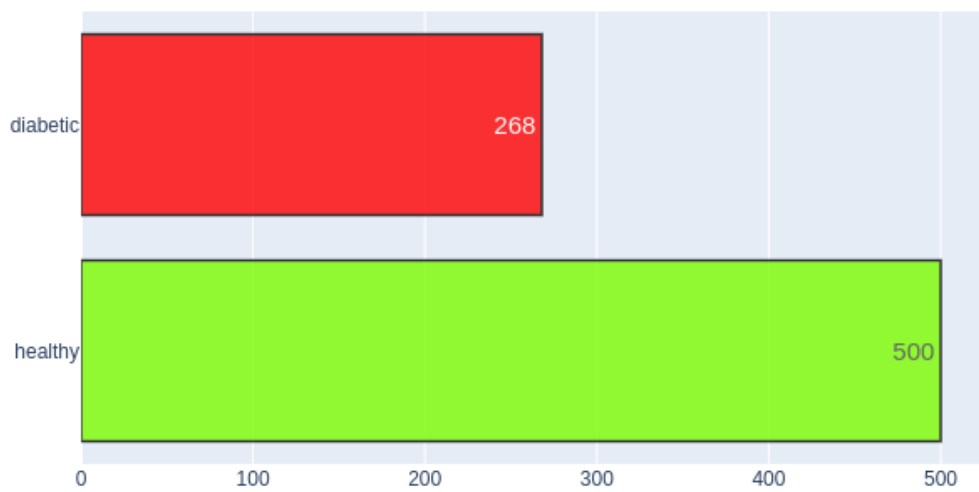


Figure 52: Master Node reading data from the SQL Database.



## 13 Conclusion

## References