Cardiovascular Disease Prediction System

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ABSTRACT

The aid domain is one of the distinguished analysis fields within the current situation with the fast improvement of technology and knowledge. it's troublesome to handle the massive quantity of information of the patients. it is easier to handle this knowledge through huge knowledge Analytics. There square measure tons of procedures for the treatment of multiple diseases across the planet. Machine Learning is Associate in Nursing rising approach that helps within the prediction and designation of a unwellness. This paper depicts the prediction of unwellness supported symptoms victimisation machine learning. Machine Learning algorithms like Naive Thomas Bayes, call Tree and Random Forest square measure utilized on the provided dataset and predict the unwellness. Its implementation is finished through the python programing language. The analysis demonstrates the most effective formula supported their accuracy. The accuracy of Associate in Nursing formula is decided by the performance of the given dataset.

KEYWORDS: knowledge Analytics, Machine Learning, Naïve Thomas Bayes, call Trees, Datasets, Prediction.

I. INTRODUCTION

At present, once one suffers from a specific unwellness, then the person should visit a doctor that is long and expensive too. Also, if the user is out of reach of doctors and hospitals it should be troublesome for the user because the unwellness cannotbe known. So, if the higher than method will be completed victimisation an automatic program which will save time furthermore as cash, it may well be easier for the patient which might create the method easier. There square measure different Hearts connected unwellness Prediction Systems victimisation data processing techniques that analyse the chance level of the patient. A heart diseasePredictor could be a web-based application that predicts the centre disease of the user with relevance the symptoms given by the user. the centre unwellness Prediction system has knowledge sets collected from totally different health-related sites. With the assistance of the centre unwellness Predictor, the user are going to be ready to understand the likelihood of the unwellness with the given symptoms. because the use of the web is growing daily, folks square measure invariably curious to understand totally different new things. folks invariably attempt to talk over with the web if any downside arises. folks have access to the web quite hospitals and doctors. folks don't have a direct choice once they suffer from a specific unwellness. So, this method will be useful to the folks as they need access to the web twenty-four hours.

II. LITERATURE SURVEY

1)   Design And Implementing Heart Disease Prediction Using Naïve Bayesian.
Author: Anjan Nikhil Repaka, Sai Deepak Ravikanti.
Abstract:— Data mining, a great developing technique that revolves around exploring and digging out significant information from a massive collection of data which can be further beneficial in examining and drawing out patterns for making business-related decisions. Talking about the Medical domain, implementation of data mining in

this field can yield in discovering and withdrawing valuable patterns and information which can prove beneficial in performing clinical diagnoses. The research focuses on heart disease diagnosis by considering previous data and information. To achieve this SHDP (Smart Heart Disease Prediction) is built via Navies Bayesian in order to predict risk factors concerning heart disease. The speedy advancement of technology has led to the remarkable rise in mobile health technology that is one of the web applications. The required data is assembled in a standardized form. For predicting the chances of heart disease in a patient, the following attributes are being fetched from the medical profiles, these includeage, BP, cholesterol, sex, blood, sugar etc. The collected attributes act as input for the Navies Bayesian classification for predicting heart disease. The dataset utilized is split into two sections, 80% dataset is utilized for training and the rest 20% is utilized for testing. The proposed approach includes the following stages: dataset collection, user registration and login (Application-based), classification via Navies Bayesian, prediction and secure data transfer by employing AES (Advanced Encryption Standard). Thereafter result is produced. The research elaborates and presents multiple knowledge abstraction techniques by making use of data mining methods that are adopted for heart disease prediction. The output reveals that the established diagnostic system effectively assists in predicting risk factors concerning heart diseases.

2)   Application of Machine Learning in Disease Prediction.
Author: Rahul Preet Singh Kohli, Shariya Arora.
Abstract: The application of machine learning in the field of medical diagnosis is increasing gradually. This can be contributed primarily to the improvement in the classification and recognition systems used in disease diagnosis which can provide data that aids medical experts in the early detection of fatal diseases and therefore, increase the survival rate of patients significantly. In this paper, we apply different classification algorithms, each with its own advantage to three separate databases of disease (Heart, Breast cancer, Diabetes) available in the UCI repository for disease prediction. The feature selection for each dataset was accomplished by backward modelling using the p-value test. The results of the study strengthen the idea of the application of machine learning in the early detection of diseases.

3)   Disease phenotype similarity improves the prediction of novel disease-associated microRNAs.
Author: Duc-Hau Le
Description: —Many studies have shown the roles of miRNAs (microRNAs) on human disease and a number of computational methods have been proposed to predict such associations by ranking candidate microRNAs according to their relevance to disease. Among them, network-based methods are becoming dominant since they well exploit the "disease module" principle in miRNA functional similarity networks. Of which, Random Walk with Restart (RWR) algorithm-based method on a miRNA functional similarity network, namely RWRMDA, is a state-of-threat one. The use of this algorithm was inspired by its success in predicting disease genes because the "disease module" principle also exists in protein interaction networks. Besides, many other algorithms were also designed for the prediction of disease genes. However, they have not yet been utilized for disease microRNA prediction. In this study, we proposed a method, namely RWRHMDA, for the prediction of disease-associated miRNAs. This method was based on the RWRH algorithm, which was successfully proposed for disease gene prediction on a heterogeneous network of genes and disease phenotypes. In particular, we used this algorithm to rank disease candidate miRNAs on a heterogeneous network of phenotypes and miRNAs, which was constructed by integrating a shared target gene-based microRNA functional similarity network and a disease phenotype similarity network. Comparing the prediction performance of RWRHMDA with that of RWRMDA on a set of 35 disease phenotypes, we found that RWRHMDA significantly outperformed RWRMDA irrespective of parameter settings since it better exploited the "disease module" principle. In addition, using the RWRHMDA method, we identified eight novels Alzheimer's disease-associated miRNAs.

4)   Efficient Heart Disease Prediction System using Decision Tree.
Author: - Purushottam, Prof. (Dr.) Kanak Saxena, Richa Sharma.
Description: - cardiovascular disease (CVD) is a big reason for morbidity and mortality in the current living style. Identification of Cardiovascular disease is an important but complex task that needs to be performed very minutely, efficiently and the correct automation would be very desirable. Every human being can not be equally skillful and so as doctors. All doctors cannot be equally skilled in every sub-specialty and at many places, we don't have skilled and specialist

doctors available easily. An automated system in medical diagnosis would enhance medical care and it can also reduce costs. In this study, we have designed a system that can efficiently discover the rules to predict the risk level of patients based on the given parameter about their health. The rules can be prioritized based on the user's requirement. The performance of the system is evaluated in terms of classification accuracy and the results show that the system has great potential in predicting the heart disease risk level more accurately.

5)   Diabetes Disease Prediction Using Data Mining
Author: - Dheeraj Shetty, Kishor Rit, Sohaila Shaikh.
Abstract: Data mining is a subfield in the subject of software engineering. It is the methodical procedure of finding examples in huge data sets including techniques at the crossing point of manufactured intelligence, machine learning, insights, and database systems. The goal of the data mining methodology is to think of data from a data set and change it into a reasonable structure for further use. Our examination concentrates on this part of medical conclusion learning design through the gathered data of diabetes and to create a smart therapeutic choice emotionally supportive network to help the physicians. The primary target of this examination is to assemble an Intelligent Diabetes Disease Prediction System that gives an analysis of diabetes malady utilizing a diabetes patient's databases. In this system, we propose the use of algorithms like Bayesian and KNN (K-Nearest Neighbour) to apply on diabetes patient's database and analyse them by taking various attributes of diabetes for the prediction of diabetes disease.

6)   Prediction Of Disease Infection Of Welsh Onions By Rust Fungus Based On Temperature And Wetness Duration
Author: - Hiroyuki Takahashi, HiromitsuFuruya and Seiji Cheonan
Abstract: - The style of agriculture practiced in Japan and other countries in Asia is small scale compared to that in North America. While systematic production and management systems have been maintained in Europe and America, Japanese agricultural style tends to depend on past experiences, and the application of agricultural chemicals is guided by the calendar and past experiences. Japan is also advanced in the field of plant disease prediction. This paper focuses on a prediction model of disease infection for a foliar parasite on Welsh onions. Rust fungus disease is the most typical disease on Welsh onions, and the

Weibull probability density function is appropriate for approximating the infection rate of the disease. The model utilizes temperature and wetness duration to predict the infection of Welsh onions by rust fungus. Producers, then, can use the model to determine the day on which the infection rate will rapidly increase, then carry out appropriate countermeasures to the disease. The proposed prediction method is applicable to several infections found throughoutAsia.

7)   Neurodegenerative disease prediction based on gait analysis signals acquired with force-sensitive
Author: -RozgerSelzler 1, James R. Green 1, Rafik Goubran.
Abstract: - neurodegenerative diseases such as Parkinson's Disease (PD), Huntington Disease (HD), and Amyotrophic Lateral Sclerosis (ALS) affect the lives of thousands of people around the world. One of the consequences of such diseases occurs in the motor neurons of the patients, resulting in problems in movement, causing a change in gait pattern. Force-sensitive resistors can be used to measure the force/pressure between the shoe and the patient's foot, providing information about the gait dynamics when the patient walks. This project uses signals from the Gait Dynamics in Neuro-Degenerative Disease database to extract features for the classification of neurodegenerative diseases (NDD). Manually labelled features from the database are used for comparison with previous studies. Time series signals are also used, where algorithms for signal reliability, feature extraction and feature selection are implemented, allowing real-time signal processing and classification. Multiple feature sets are used for classification with algorithms such as K-nearest neighbour, Support Vector Machines, and Decision Trees, and the performance of these algorithms are then reported. This study presents a real-time system with accuracy exceeding 82% for the aforementioned diseases. Finally, a discussion about possible improvements for future studies are presented.

8)   Chatbot for Disease Prediction and Treatment Recommendation using Machine Learning.
Author: - Rohit Binu Mathew, Sandra Varghese, Sera Elsa Joy, Santhanam Susan Alex.
Abstract: - Hospitals are the most widely used means by which a sick person gets medical check-ups, disease diagnosis and treatment recommendation. This has been a practice by almost all the people over the world. People

consider it as the most reliable means to check their health status. The proposed system is to create an alternative to this conventional method of visiting a hospital and making an appointment with a doctor to get diagnosis. This research intends to apply the concepts of natural language processing and machine learning to create a chatbot application. People can interact with the chatbot just like they do with another human and through a series of queries, a chatbot will identify the symptoms of the user and thereby, predicts the disease and recommends treatment. This system can be of great use to people in conducting daily check-ups, makes people aware of their health status and encourages people to take proper measures to remain healthy. According to this research, such a system is not widely used and people are less aware of it. Executing this proposed framework can help people avoid the time-consuming method of visiting hospitals by using this free-of-cost application, wherever they are.

III. PROJECT REQUIREMENT
● **External Interface Requirement**
1. User Interface
Application Based Heart Disease Prediction

2. Hardware Interface
RAM: 8 GB
As we are using Machine Learning Algorithm and Various High-Level Libraries Laptop
RAM minimum required is 8 GB.
Hard Disk: 40 GB
Data Set of CT Scan images is to be used hence minimum 40 GB of Hard Disk memory is required.
Processor: Intel i5 Processor
PyCharm IDE that Integrated Development Environment is to be used and data loading should be fast hence Fast Processor is required
IDE: PyCharm
Best Integrated Development Environment as it gives possible suggestions at the time of typing code snippets that make typing feasible and fast.
Coding Language: Python Version 3.5
Highly specified Programming Language for Machine Learning because of availability of High-Performance Libraries.
Operating System: Windows 10
Latest Operating System that supports all types of installation and development
Environment

3. Software Interfaces
Operating System: Windows 10
IDE: Spyder
Programming Language: Python

● **Non-Functional Requirement**
I. Performance Requirement
The performance of the functions and every module must be well. The overall performance of the software will enable the users to work efficiently. The Performance of encryption of data should be fast. Performance of the providing virtual environment should be fast Safety Requirement.
The application is designed in modules where errors can be detected and easily.
This makes it easier to install and update new functionality if required.

II. Safety Requirement
The application is designed in modules where errors can be detected and fixed easily. This makes it easier to install and update new functionality if required.

III. Software Quality Attributes
Our software has many quality attribute that are given below:
Adaptability: This software is adaptable by all users.
Availability: This software is freely available to all users. The availability of the software is easy for everyone.

Maintainability: After the deployment of the project if any error occurs then it can be easily maintained by the software developer.
Reliability: The performance of the software is better which will increase the reliability of the Software.
User Friendliness: Since, the software is a GUI application; the output generated is much user friendly in its behaviour.
Integrity: Integrity refers to the extent to which access to software or data by unauthorized persons can be controlled.
Security: Users are authenticated using many security phases so reliable security is provided.
Testability: The software will be tested considering all the aspects.

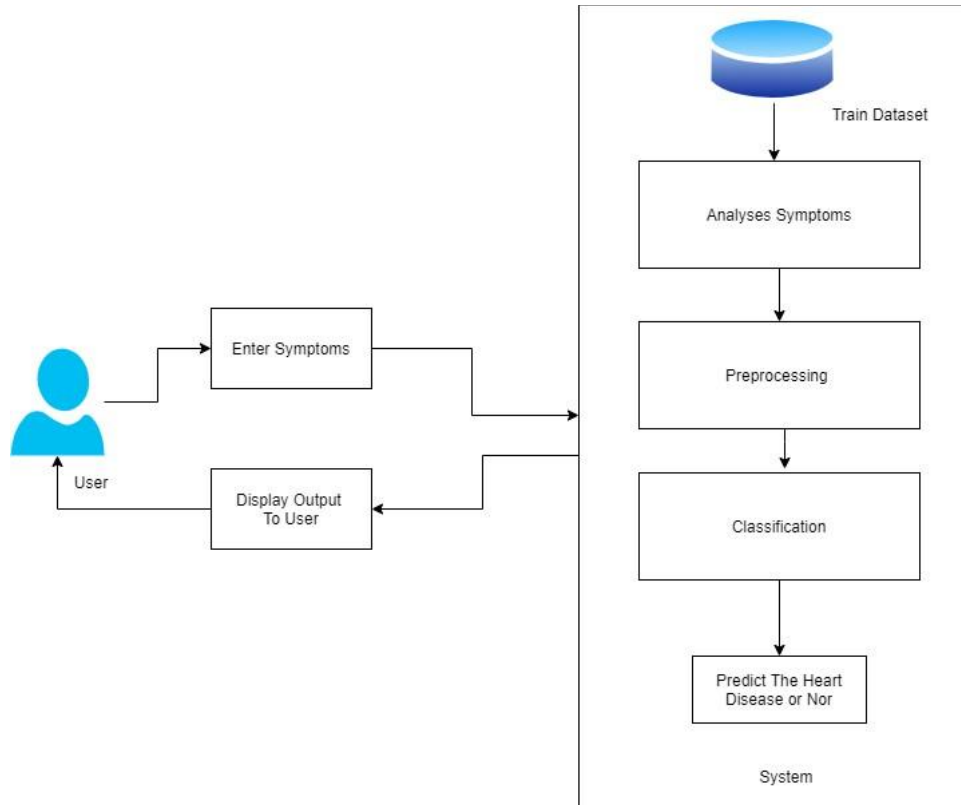# IV. SYSTEM ANALYSIS

a) **System Architecture**

Figure : System Architecture

b) **Module**
- Pre-processing
- Analyses Symptoms
- Classification

c) **Data Flow Diagram**

In Data Flow Diagram, we Show the flow of data in our system in DFD0 we show the base DFD in which the rectangle presents input as well as output and circle shows our system, In DFD1 we show the actual input and the actual output of system input of our system is text or image and output is rumour detected likewise in DFD 2 we present operation of a user as well as admin.
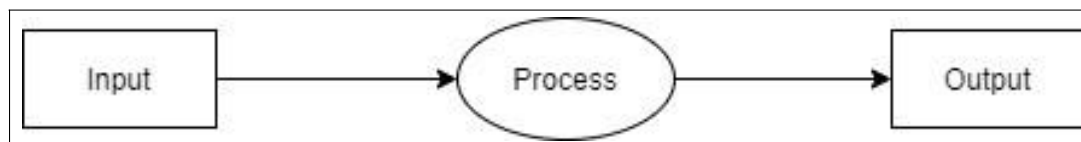

Figure : Data Flow Diagram

d) **UML Diagrams**

Unified Modelling Language is a standard language for writing software blueprints. The UML may be used to visualize, specify, construct and document the artifacts of a software-intensive system. UML is process independent, although optimally it should be used in a process that is use case driven, architecture-centric, iterative, and incremental. The Number of UML Diagram is available.
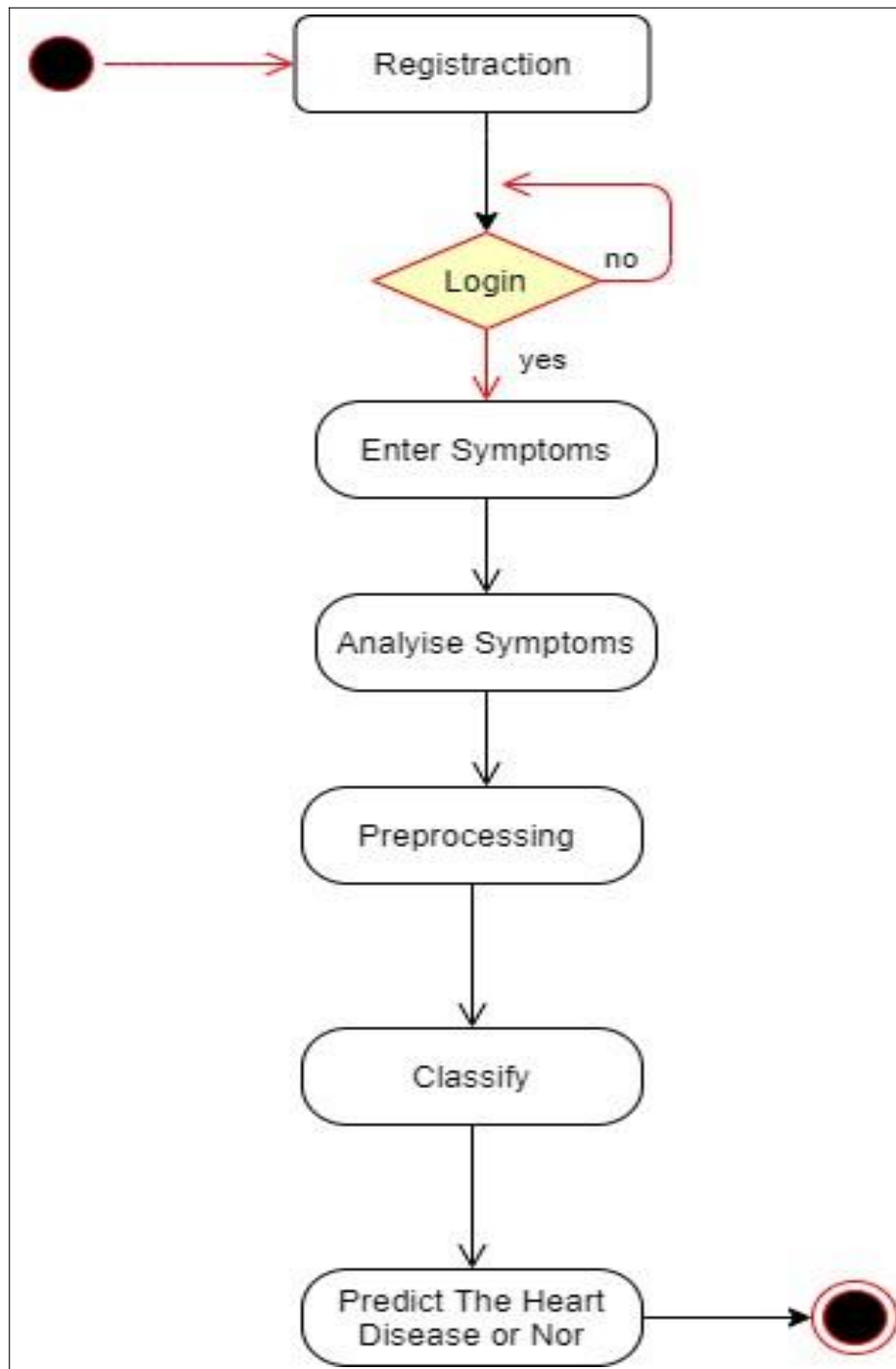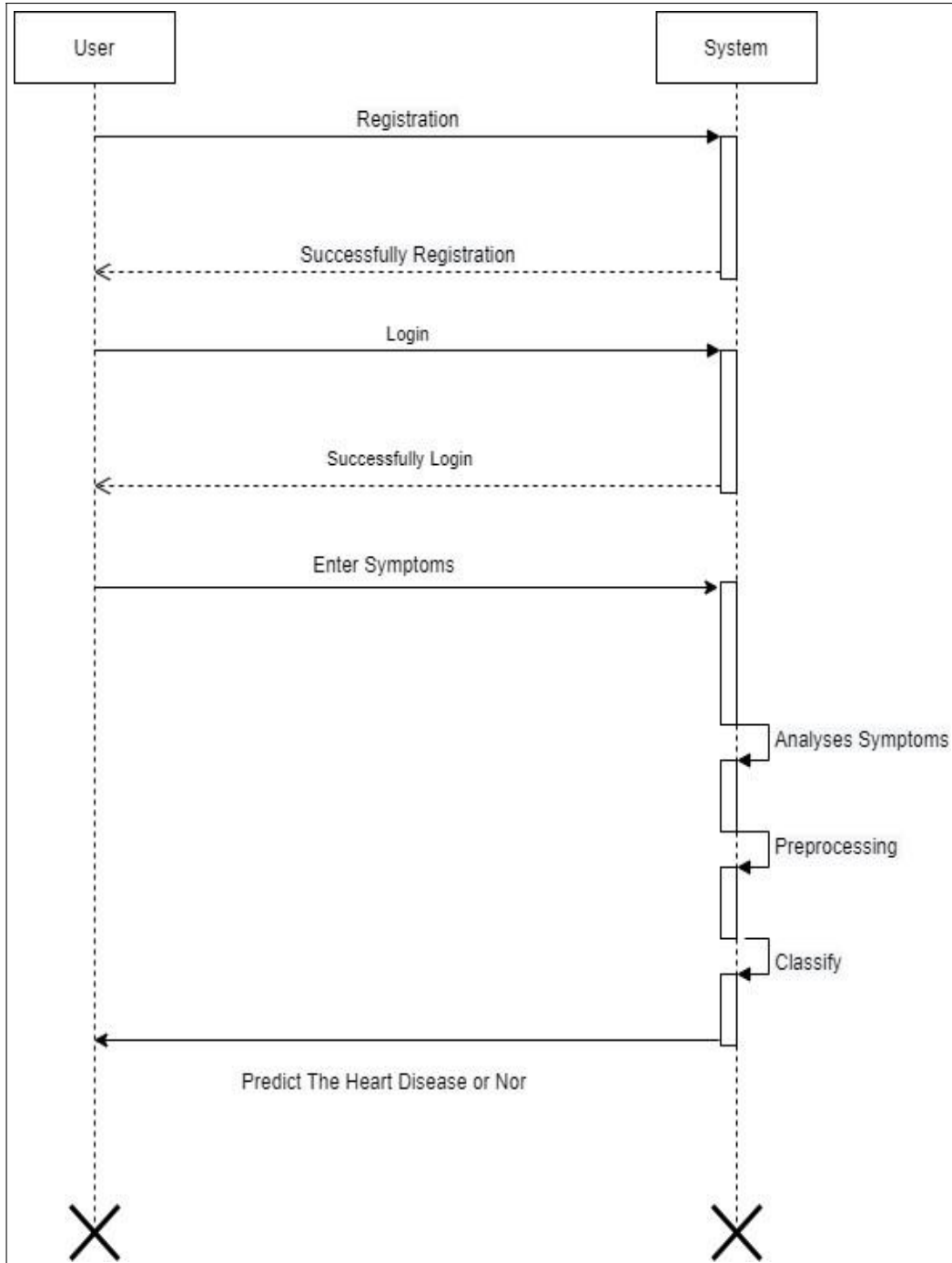
- Use Case Diagram
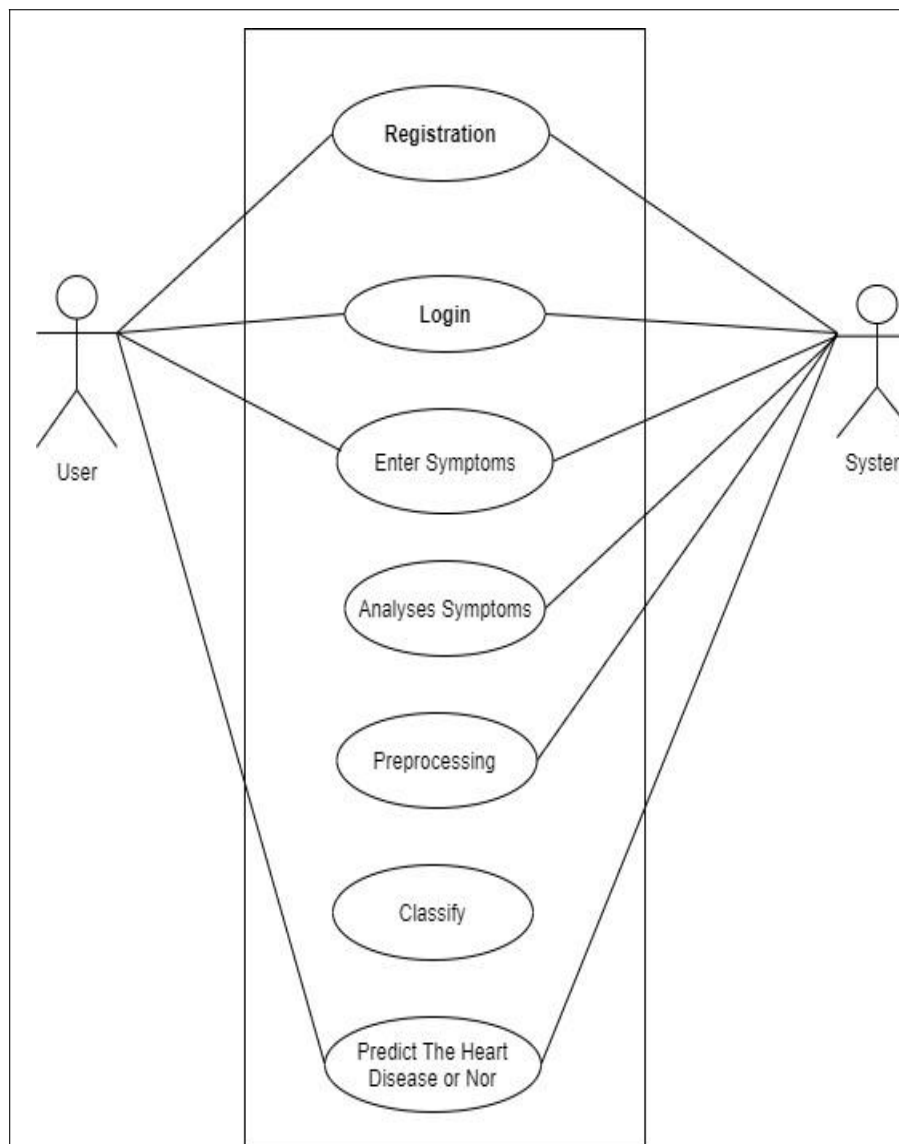
- Activity Diagram

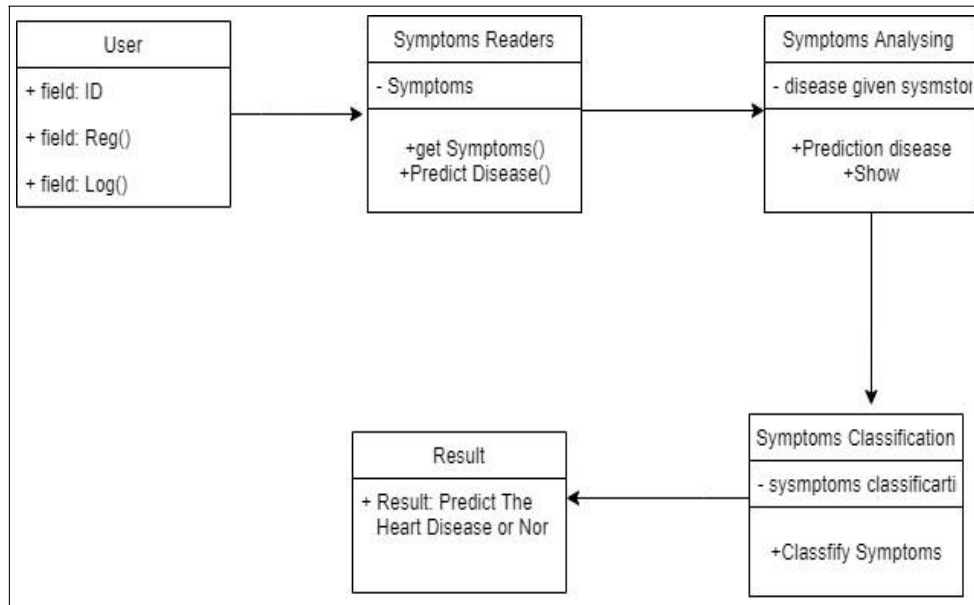Figure: Activity Diagram

- Sequence Diagram

- Class Diagram

Figure : Class Diagram

V. SOFTWARE INFORMATION

Python is an interpreted, high-level and general-purpose programming language. Created by Guido van Rossum and first released in 1991, Python's design philosophy emphasizes code readability with its notable use of significant whitespace. Its language constructs and object-oriented approach aim to help programmers write clear, logical code for small and large-scale projects.

Python is dynamically typed and garbage-collected. It supports multiple programming paradigms, including structured (particularly, procedural), object-oriented, and functional programming. Python is often described as a" batteries included" language due to its comprehensive standard library.

Python was created in the late 1980s as a successor to the ABC language. Python 2.0, released in 2000, introduced features like list comprehensions and a garbage collection system with reference counting.

Python 3.0, released in 2008, was a major revision of the language that is not completely backward-compatible, and much Python 2 code does not run unmodified on Python 3.

The Python 2 language was officially discontinued in 2020 (first planned for 2015), and" Python 2.7.18 is the last Python 2.7 release and therefore the last Python 2 release." No more

security patches or other improvements will be released for it. With Python 2's end-of-life, only Python 3.6.x and later are supported.

Python interpreters are available for many operating systems. A global community of programmers develops and maintains Python, a free and open-source reference implementation. A non-profit organization, the Python Software Foundation, manages and directs resources for Python and Python development.

Python was conceived in the late 1980s by Guido van Rossum at Centrum Wickenden Informatica (CWI) in the Netherlands as a successor to the ABC language (itself inspired by SETL), capable of exception handling and interfacing with the Amoeba operating system. Its implementation began in December 1989. Van Rossum shouldered sole responsibility for the project, as the lead developer, until 12 July 2018, when he announced his" permanent vacation" from his responsibilities as Python's Benevolent Dictator for Life, a title the Python community bestowed upon him to reflect his long-term commitment as the project's chief decision-maker. He now shares his leadership as a member of a five-person steering council. In January 2019, active Python core developers elected Brett Cannon, Nick Coghlan, Barry Warsaw, Carol Willing and Van Rossum to a five-member" Steering Council" to lead the project.

Anaconda: Anaconda is a free and open-source distribution of the Python and R programming languages for scientific computing (data science, machine learning applications, large-scale data processing, predictive analytics, etc.), that aims to simplify package management and deployment. The distribution includes data-science packages suitable for Windows, Linux, and macOS. It is developed and maintained by Anaconda, Inc., which was founded by Peter Wang and Travis Oliphant in 2012. As an Anaconda, Inc. product, it is also known as Anaconda Distribution or Anaconda Individual Edition, while other products from the company are Anaconda Team Edition and Anaconda Enterprise Edition, both of which are not free.

Package versions in Anaconda are managed by the package management system conda. This package manager was spun out as a separate open-source package as it ended up being useful on its own and for other things than Python. There is also a small, bootstrap version of Anaconda called Miniconda, which includes only conda, Python, the packages they depend on, and a small number of other packages. Anaconda distribution comes with over 250 packages automatically installed, and over 7,500 additional open-source packages can be installed from PyPI as well as the conda package and virtual environment manager. It also includes a GUI, Anaconda Navigator, as a graphical alternative to the command-line interface (CLI).

The big difference between conda and the pip package manager is in how package dependencies are managed, which is a significant challenge for Python data science and the reason conda exists.

When pip installs a package, it automatically installs any dependent Python packages without checking if these conflict with previously installed packages [citation needed]. It will install a package and any of its dependencies regardless of the state of the existing installation [citation needed]. Because of this, a user with a working installation of, for example, Google TensorFlow, can find that it stops working having used pip to install a different package that requires a different version of the dependent NumPy library than the one used by TensorFlow. In some cases, the package may appear to work but produce different results in detail.

In contrast, conda analyses the current environment including everything currently installed, and, together with any version limitations specified (e.g., the user may wish to have TensorFlow version 2,0 or higher), works out how to install a compatible set of dependencies, and shows a warning if this cannot be done.

Open-source packages can be individually installed from the Anaconda repository, Anaconda Cloud (anaconda.org), or the user's own private repository or mirror, using the conda install command. Anaconda, Inc. compiles and builds the packages available in the Anaconda repository itself, and provides binaries for Windows 32/64 bit, Linux 64 bit and MacOS 64-bit. Anything available on PyPI may be installed into a conda environment using pip, and conda will keep track of what it has installed itself and what pip has installed.

Custom packages can be made using the conda build command, and can be shared with others by uploading them to Anaconda Cloud, PyPI or other repositories.

The default installation of Anaconda2 includes Python 2.7 and Anaconda3 includes Python 3.7. However, it is possible to create new environments that include any version of Python packaged with conda Spyder

Spyder is an open-source cross-platform integrated development environment (IDE) for scientific programming in the Python language. Spyder integrates with a number of prominent packages in the scientific Python stack, including NumPy, SciPy, Matplotlib, pandas, I Python, NumPy and python, as well as other open-source software. It is released under the MIT license.

Initially created and developed by Pierre Raybaut in 2009, since 2012 Spyder has been maintained and continuously improved by a team of scientific Python developers and the community.

Spyder is extensible with first-party and third-party plugins, includes support for interactive tools for data inspection and embeds Python-specific code quality assurance and introspection instruments, such as Pyflakes, Pylint and Rope. It is available cross-platform through Anaconda, on Windows, on macOS through MacPorts, and on major Linux distributions such as Arch Linux, Debian, Fedora, Gentoo Linux, openSUSE and Ubuntu.

Spyder uses Qt for its GUI and is designed to use either of the PyQt or PySide Python bindings. QtPy, a thin abstraction layer developed by the Spyder project and later adopted by multiple other packages, provides the flexibility to use either backend.

Features
- An Editor With Syntax Highlighting, Introspection, Code completion
- Support For Multiple Python Consoles
- The Ability To Explore and Edit Variables From a GUI

- A Help Pain Able To Retrieve and Render Rich Text Documentation On Functions, Classes And Methods Automatically Or On-demand
- A debugger linked to IP dB, for step-by-step execution Static code analysis, powered by Pylint
- A run-time Profiler, to benchmark code
- Project support, allowing work on multiple development efforts simultaneously
- A built-in file explorer, for interacting with the filesystem and managing projects
- A" Find in Files" feature, allowing full regular expression search over a specified scope
- An online help browser, allowing users to search and view Python and package documentation inside the IDE history log, recording every user command entered in each console
- An internal console, allowing for introspection and control over Spyder's own operation.

VI. CONCLUSION

This project aims to predict heart disease on the basis of the symptoms. The project is designed in such a way that the system takes symptoms from the user as input and produces output i.e., predicting heart disease. Average prediction accuracy probability of 55obtained. AHeart Disease Predictor was successfully implemented using the grails framework.

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