University of the Philippines Manila College of Arts and Sciences Department of Physical Sciences and Mathematics

CHITS DIABETES DATA WAREHOUSE WITH BIG DATA ANALYTICS

A special problem in partial fulfillment of the requirements for the degree of Bachelor of Science in Computer Science

Submitted by:

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ACCEPTANCE SHEET

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Abstract

Electronic medical records have made data collection efficient allowing health professionals and researchers to analyze patient records faster. CHITS, the first EMR in the Philippines has collected millions of data across different areas in Luzon however, CHITS does not contain any data analysis module. This project aims to make use of the large amount of data available in CHITS by developing a diabetes recommender system with big data analytics. The system recommends treatments by finding similar patients by analyzing patient profiles through the use of a similarity metric called Cosine Similarity.

Keywords: Recommender System, Big Data Analytics, Cosine Similarity

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I. Introduction

Diabetes is a chronic disease caused by the deficiency in production of insulin by the pancreas, or by the ineffectiveness of the insulin produced. Deficiency of insulin results in increased concentrations of glucose in the blood, which in turn damage many of the bodys systems particularly the blood vessels and nerves. [1]

There are two major types of diabetes, type 1 and type 2 diabetes. Type 1 diabetes occurs when the immune system attacks and destroys the insulin. Type 2 diabetes, the most common form of diabetes is caused by several factors such as lifestyle and genes. [2] Individuals with diabetes frequently experience symptoms such as frequent urination, blurry vision, increased hunger, extreme unexplained fatigue, frequent skin, bladder or gum infections and many more. Diabetes can be acquired through heredity. People who have close relatives who have history with diabetes are more likely to develop as well. Obese/Not physically active individuals are also likely to develop type 2 diabetes. Extra weight sometimes causes insulin resistance and is common in people with type 2 diabetes. [3]

Diabetes caused 57,000 deaths annually therefore ranked 4th most deadly disease in the Philippines. Health professionals predicted that globally, the number of people with diabetes would reach 320 million by 2025, however it has already been recorded that the number has reached over 400 million. According to the International Diabetes Federation, there were 3.5 million cases of diabetes in the Philippines in 2015 excluding the estimated 1.84 million cases that are presumed to be undiagnosed. [4] Last year, it was recorded that there are at least 6 million Filipinos diagnosed to have diabetes. According to Dr. Augusto Litonjua, President of the Philippine Center for Diabetes Education Foundation, this record could double or grow even further by 2040 because of undiagnosed diabetes cases. [5] Due to the increasing number of diabetes cases, Philippines is now being seen as as a diabetes hot spot by the Philippine Society of Endocrinology, Diabetes, and Metabolism (PSEDM). The cause of the growing number of diabetes cases were due to lifestyle among Filipinos. [6]

The number of diabetes cases increases due to the unhealthy lifestyle of many Filipinos particularly unhealthy eating patterns. Filipinos consume mainly rice, bread and other foods with high level of sugar content. [7] Filipinos are also fond of consuming calorie-dense food from fast food chains which may lead to obesity and a higher risk for diabetes.[5]

Reports show that undiagnosed cases are due to the following reasons: Education, Economic Standing, Cultural Issues, Folk Medicine Belief.

Due to lack of education, diabetes symptoms and treatment are not well taught in many countries (including Philippines). Filipinos lack awareness of what causes diabetes. Some may have financial issues that they are unable to visit or consult their doctor on a regular basis to see if they are diagnosed properly. Some may also resort to Folk Medicine Belief as it is cheaper but, it doesn't properly manage the diagnosis. [8]

The cost of medical treatments also keeps on increasing. One of the responsibilities of our government is to provide an effective healthcare system that should improve the healthcare management in the Philippines. One of the existing healthcare systems in the Philippines is an electronic medical record System called Community Health information Tracking System or CHITS. It was developed by the National Telehealth Center to further improve health information management at the rural health unit level. CHITS allows health personnel to be able to gather data and generate reports as needed for further analysis. 142 barangays were the first to use CHITS. The said system is also a platform for the health workers by allowing them to explore eHealth applications such a telemedicine and eLearning. [9, 10]

The eHealth program is not only limited to the health workers but to also researchers as the eLearning program is a training for anyone who is interested in doing research on eHealth. Rural Communities have difficulties in gaining access of health professional care. eMedicine allows patients to services from specialized doctors stationed in cities by allowing them to be referred directly to the clinical

specialist or to the Philippine General Hospital(PGH). As an eRecord, CHITS can easily work with other information system that would allow better information sharing to other platforms that would need for heatth information records that can be used for further analysis. Monitoring of health performance is done through the eSurveillance program by using mobile technology and web-based system allowing them to achieve goals of the DOH priority programs. The program gives guidance to the community on social protection, basic education, civil registration and disaster management through mReports. [9]

Healthcare data generated everyday from various sources grows exponentially. Application of Big Data Analytics allows us to make use of the vast amount of data by analyzing large and complex healthcare data. Healthcare quality is further improved when researchers are able to generate insights that could help explain relationships in the given data. Examples of how big data analytics is applied in healthcare are predicting diseases when they will be likely to occur or providing a patient centric treatment which means that the medication is calibrated and focus on the patient's conditions. [11, 12]

Health Recommendation Systems(HRS) is a specialization of a recommender system driven by individualized health data such as a personal health record. The main goal of an HRS is to supply the user with medical information which is meant to be highly relevant to the medical development of the patient. [13]

Recommender System are powered by an algorithm called Collaborative Filtering. This type of algorithm takes into account the user's preferences and recommends items that are similar to the user's interest. [11] The idea behind collaborative filtering is combining the users preference and item ratings which are critical factors in providing the best recommendations to the user. some of these examples are tv shows (Netflix) which sees what genre the user is interested in and recommends movies/tv shows that are highly rated and with the same genre.

In the context of health recommender systems, item ratings do not exist however, another way to provide a recommendation based upon a health record of a patient is through the use of a similarity score. The idea of this type of algorithm is to compare the new user to existing users in the database and find which user is the most similar and the system recommends treatments(diet plans, exercise regimen, etc) to the new user. [14]

A Statement of the Problem

Large volumes of multi-structured healthcare data are difficult to store, manage, and becomes useless when data is not analyzed. Healthcare data comes from many different sources such as physician notes, medical history, electronic health record and many more. It is important to properly organize these data for more efficient analysis and to generate accurate medical recommendations.

CHITS contains large amounts of patient data however, the system does not contain a data analytics module that will allow healthcare professionals/providers to have a decision support tool provides information about non medical aspects such as diet plans, exercise regimen or even for diabetes management.

To address these problems, it is essential to use Big Data Analytics to be able to process large amounts of data and gain insights from the analysis. Through data mining, the system can provide recommendations that are calibrated to the patients attributes therefore providing the best recommended treatment. This will also allow healthcare professionals to gain insight which will help them in understanding the relationships between factors concerning the increase of diabetes cases allowing them to provide an holistic assessment of the patient.

B Objectives of the Study

This research will create a Diabetes Recommender System in CHITS with the following functionalities:

- 1. Allows local physician/researcher to
 - (a) Input Patient Case information

- (b) View Recommendation output
- (c) Be able to do advance search queries
- (d) View medical record of patients
- (e) View statistical trends/dashboard
- (f) View Information regarding Diabetes
- (g) Allow extraction of patient record for anonymized data using SQL commands

C Significance of the Project

Big Data analytics is essential in improving quality of healthcare. Patient data contains vast information that when analyzed properly, may give valuable insights that helps in maintaining diabetic patients. The recommender system will be useful to as a guide to decision making process of a physician and helpful to improving diabetes research.

The system will allow CHITS to have a proper data warehouse and a data analytics component for Diabetes. The system will provide the health professional a guide/recommendation on how to treat the patient based on the data provided. This will allow a faster and better judgment for the professional as the system gives a guidance based on previous cases that are similar to the current case. The system minimizes cost as it makes information-retrieval faster compared to the traditional paper method. Researchers/Health professionals would be able to run analytic queries and view important relationships and trends on the increase of diabetes cases. Effective analysis lessens the frequency of the patient visiting the health professional therefore saving time and money.

D Scope and Limitations

- 1. The recommendation model will be based on the CHITS dataset locally.
- 2. The system provides recommendation treatments to Diabetes cases only

3. The basis for comparison will be based on the following features (a) Weight (b) Height (c) Waist Circumference (d) Hip Circumference (e) Age (f) Gender (g) Hba1C result (h) FBS result 4. The recommendations given by the system are based on the treatments provided by a doctor that is recorded in CHITS 5. The system will not save patient consultation in this module but rather in the original CHITS module 6. extraction of anonymized data is limited to deletion of name 7. The type of recommender system is limited to collaborative filtering by using similarity metrics. 8. The type of parameter to be measured is limited to similarity score as it is applicable to health care data 9. The system is to be deployed upon seperate workstation 10. Efficiency of data mining is dependent on machine workstation locally in-

stalled.

II. Review of Related Literature

There has been a lot of health recommender system that has been developed by using Big Data Analytics. Most recommender systems uses a technique called Collaborative Filtering. Collaborative Filtering is a data mining technique to predict a user's opinion about an item or a service based on the known preferences of a large group of users.[14] Systems that utilizes big data analytics must also use frameworks such as Apache Spark or Apache Mahout to be able to process large amounts of data in a short amount of time. Most of the systems have a similar flow on how they develop the recommender engine. The following systems share a common goal: to improve quality and efficiency to healthcare.

A health recommender system developed by the authors in [11] focuses on diabetes. The data analysis was done by utilizing Spark framework. The system used Naive Bayes algorithm to classify the patients by Pre-diabetic, Diabetes, and no Diabetes. To develop the hybrid recommender system, they used Content filtering, Rule and Case based filtering. Rule based filtering is used to filter profiles based on user queries. Case based filtering is used to extract similar profiles based on patient health history. To further improve the case filtering approach, they used the K-Nearest Neighbor Algorithm. The process is done by comparing the score of the new case and existing cases and nearest score will be given as the suggestion. The study presented on how the recommender system can be trusted by building recommender systems that suggests treatments from reliable sources(ex. Health on Net authority).

A study was done by Chaitanya and Ashmin Kaul and Saurav Verma on healthcare prediction systems using big data. Their study discusses three algorithms:(1) Collaborative and Recommendation Engine(CARE); (2) Collaborative Health Care System Model (COHESY) and (3) Hiearchical Association Rule Mining Model (HARM). CARE utilized collaborative filtering for analysis predictions of the disease. The process begins by selecting a patient to be tested. A cluster based on matching of diseases was also formed and collaborative filtering process

was applied to predict the patient's next visit. COHESY is based on a collaborative filtering mechanism for analyzing and recommending exercises that can improve a person's health. the algorithm suggests activities by modifying the value of any heath parameter to which the algorithm is being tested. HARM, on the other hand is based on the concept of associative mining through which the patient's future symptoms can be predicted against the current or the past symptoms. The study claims that these algorithms can be used more efficiently and generate more promising results with larger datasets.[15]

The system built by [16] was to predict the personalized mortality prediction by comparing the present case patient and a past patient recorded in an EMR by using a patient similarity metric. They hypothesize that analyzing similar patients can give a personalized and precise prediction. Idea of their hypothesis was the amount of predictive utility contributed by a past patient should be directly proportional to the degree of similarity between the past and index patient. To compare similar patients, they utilize a patient similarity metric called cosine similarity which calculates the dot product between the two patients which gives an cosine of the angle as the result. The result of this algorithm ranges from 1 to 1 which signifies minimum and maximum similarity respectively. They used this algorithm to separate the dataset to the most similar patients to train the dataset using predictive models namely death counting, logistic regression and decision tree. The idea behind using cosine similarity first to find similar patients was to improve mortality prediction rather than train the dataset with the whole population. [16]

The aim of this recommender system was to build a friend recommendation system by using lifestyle of users to suggest friend as required and system should be used for health application. The system was divided into 5 modules. (1) Data Collection, (2) Data Analysis, (3) Indexing, (4) Friend-Matching Module and (5) Recommendation Module. The method to build the recommendation was to use the knowledge of probability distribution and calculate lifestyle vectors, find similar users to user I by applying cosine similarity then sort the results. The

proposed method added a feature which applies by recommending based on blood group which can be used in healthcare applications.[17]

A data-driven recommender system was built by state author that is used for therapy decision support to assist physicians or other health professionals during clinical decision making. Their approach was to apply methods from data mining and machine learning to extract knowledge from the data to achieve more individual recommendations, learn from experience and reveal unknown patters in the dataset. They also describe the use of similarity metrics for rating prediction and recommendation computation which are capable of processing sparse and inhomogeneous data vectors as to compared to the use of collaborative filtering or hybrid approaches. [18]

The system built by author is an ICF based automated system that stores and monitors health status of patient with spinal cord injuries in order to recommend rehabilitation methods for patients based on his/her status. The system uses similarity measures to implement the recommender system namely cosine, correlation, spearman, hamming, and jaccard. The system consists of three phases (1) preprocessing phase in which the medical description of each patient status is converted into its equivalent ICF code. (2) Similarity phase which aims to get the similarity between two vectors by applying the similarity measures then getting the top score for the (3) recommend phase which gets the data of the patient with the highest score and the data returned to the system will be the recommended rehabilitation method for the current patient. The results of this study shoes that the cosine similarity measure gives the most accurate result. [19]

A recommender system was built for health personnel by recommending courses that would further stimulate their education. The goal was to recommend courses based the users course registration history and users interesting area. The steps to build the recommendation system was divided into three steps. (1) To select and to provide the correct data information source as input to the recommender system. Next, was to build the recommendations. And last (3) was to persist the

recommendations in an appropriate data collection. To calculate similar users, they implemented the cosine-similarity measures which calculates the distance between two points(vector). to implement the algorithm, they used Python, Pandas which is an open-source library which provides easy-to-use data structures and data analysis tools in Python and SciPy which is a scientific computing tool for Python. The similarity of the current course to any other course is stored in a similarity matrix which contains the ID of the course and the similarity score. The output of the system was a list of users and their five recommended courses.[20]

The purpose of this study is to survey the existing patient centric social networks and its functions, recommendation techniques and evaluation methods used. A health recommender system is described as a special type of recommender system that enables patients to find other patients similar to them and connects them by how social network connects people and share information such as experiences or treatments or may recommend caregivers to patients. The techniques applied in a health recommendation system uses the following. (1) Patient Data Similarity which is based on the distance among continuous data items found in the patient profile by suitable weighting. (2) Patient Similarity using Conditions and Treatments which finds similarity based on terms of patient conditions and treatments. (3) Content Matching which is based on the content of the users on similar topics then they might be interested in getting to know each other. This is computed using the cosine similarity measure. This type of system can be used to help patients find a solution same to their condition or symptoms. [21]

The CARE system by Nitesh V. Chawla, PhD and Darcy A. Davis, PhD was to serve as a data-driven computational aid for physician assessing the disease risks facing their patients. In their study, healthcare has transformed from a disease-centered model towards a patient-centered model. The difference between the two model is in the disease-model, the health professional decision making in centered around clinical expertise and data from medical evidence and tests while the patient-centered model, patients actively participate on their own care and re-

ceive services focused on individual needs and preferences, informed by advice and oversight from their healthcare providers. They also utilized collaborative filtering specifically using inverse frequency and vector similarity. They also explained the challenge involved using collaborative filtering as diseases do not have a rating system as to what books or movies have. the turn-around for this problem is that to compare similar cases between patients.[14]

The android application made by the authors in [22] used a different algorithm called Pearson Correlation for matching patient with similarities with other patients in the database. The algorithm compares the patients and rating them of values raging from -1 to 1 with a score of 1 means that the two patients are perfectly correlated. The closest patient is the one which has the score that is closest to 1. Once the closest patient is found, the system then recommends the same treatment(diet,exercise,medication) to the new user. The overall system includes a management module and reminding function which are also essential components to improve healthcare. The application can also be extended to other diseases to provide other kinds of healthcare guidelines recommendations.

III. Theoretical Framework

A Diabetes

Diabetes is a metabolic disease in which patients have abnormally high blood glucose(BG).[23] This condition influences the human body by diminishing the insulin which conveys glucose into the platelets. This expands the sugar level in the body causing difficulties like stroke, heart disease, blindness, kidney failure and death.[24]

1. Types

There are two main types of Diabetes:

- (a) Type 1 a disease in which the pancreas produces little or no insulin.

 This results into glucose building up in the blood instead of being used for energy. Individuals with Type1 Diabetes need to inject insulin as prescribed.[23]
- (b) Type 2 a disease in which the pancreas does not produce enough insulin, or the human body does not properly use the insulin it makes. [23]
- (c) Gestational Diabetes is a type of diabetes that occurs in pregnant women.[24, 25]

2. Symptoms: [26]

- (a) Loss of weight
- (b) Obscured vision
- (c) Skin Infections
- (d) Frequent urination
- (e) Fatigue
- (f) Increased Thirst and Hunger
- (g) Blurred Visions

- (h) Nausea
- (i) Irritability

3. Factors:[27]

- (a) Type 1
 - i. Family History
 - ii. Diseases of the Pancreas
 - iii. Infection/Illness
- (b) Type 2
 - i. Obesity
 - ii. Impaired Glucose Tolerance
 - iii. Insulin Resistance
 - iv. Ethnic Background
 - v. Gestational Diabetes
 - vi. Sedentary Lifestyle
 - vii. Family History
 - viii. Polycystic ovary Syndrome
 - ix. Age
- (c) Gestational
 - i. Obesity
 - ii. Glucose Intolerance
 - iii. Family History
 - iv. Age
 - v. Ethnic Background

4. Diagnosis

There are different medical test to identify and diagnose diabetes:[24]

(a) Fasting Blood Glucose Test (FBS)

- (b) Post Prandial Blood Sugar Test(PPBS)
- (c) Random Blood Sugar Level (RBS)
- (d) Oral Sugar Tolerance Test
- (e) Glycosylated hemoglobin(HbAlc)
- (f) Urine Test
- (g) There is also a protocol for type-2 diabetes called Self-Monitoring of Blood Glucose (SMBG) that is advised by healthcare providers to help the patient achieve proper blood glucose targets.[23] blood glucose is affected by many different factors, including diet, starting blood glucose level, physical activity, mental stress, illness, sleep patterns and many more. These factors has a different impact on a person's blood glucose. SMBG requires T2D patients to control these factors regularly and accurately especially diet.[23]

(h) Diet Management

The purpose of a diet plan for diabetes patients is to control the blood sugar, manage weight and control risk factors for heart disease.

A diabetes diet is based on eating three meals a day at regular times. This allows the body to make use of the insulin it produces or get through a medication. Sometimes, a doctor may recommend a registered dietitian to further improved the diet plan. Dietitians may talk the patient into improving eating habits by chooising the right portion size that suit the needs of the patient's size(by means of height and weight) and level of activity. [28]

Recommended diet:

- i. Healthy carbohydrates Focus on healthy carbohydrates such as fruits, vegetables, whole grains, legumes and low-fat dairy products
- Fiber-rich foods Fiber moderates how your body digests and helps control blood sugar levels.

- iii. Heart-healthy fish. Eat heart-healthy fish at least twice a week
 Fish can be a goold alternative to high-fat meat. Fish such as salmon, tuna are rich in omega-3 fatty acids that promote hearth health by lowering blood fats called triglycerides.
- iv. Good fats Foods containing monounsaturated and polyunsaturated fats can help lower your cholesterol levels.

Foods to avoid:

- i. Saturated fats High-fat dairy products and animal proteins.
- ii. Trans fats- Types of fats are found in processed snacks, baked goods, shortening and stick margarines.
- iii. Cholesterol include high-fat dairy products and high-fat animal proteins. Aim for no more than 200 mg of cholesterol a day. -
- iv. Sodium Aim for less than 2,300 mg of sodium a day. For patients with hypertension, aim for less than 1,500 mg a day.

(i) Exericse Management

Diabetes prevention is crucial to maintaining health and prevent complications. Exercise is one proven way to help manage diabetes.

According to The American College of Sports Medicine and the American Diabetes Association, exercise

- i. plays a vital role in preventing and controlling blood sugar levels
- ii. can prevent/delay type 2 diabetes
- iii. can prevent diabetes during pregnancy.

Exercise is essential because it improves insulin sensitivity by helping the cells of the body use available insulin. It also stimulates a separate mechanism to allow the cells to use glucose for energy thus allowing regulation of blood glucose levels.

i. Aerobic Exercise:

helps the body use insulin more effectively. Examples include:

- A. Swimming
- B. Rowing
- C. Cycling
- D. Basketball
- E. Dancing
- F. Skating
- G. Hiking and many more.

The amount of time recommended (ages 18-64) for aerobic activity is

- A. 30 minutes of daily moderate physical aerobic activity.
- B. at least 5 times a week.

ii. Strength Training:

helps lower blood sugar levels and increase insulin sensitivity. Examples include:

- A. weight machines
- B. Lifting free weights
- C. Resistance bands
- D. Exercises that use body weight such as sit-ups, squats, planks, and push-ups and many more.

The amount of time recommended for strength training is

A. at least twice a week, in addition to the recommended amount of aerobic activity.

iii. Monitoring blood glucose levels when exercising

Monitoring blood glucose levels before and after exercise is essential. This indicates how well the body is responding to the exercise regimen and may help avoid blood sugar fluctuations which can be dangerous.

Testing of blood sugar should be done 30 minutes before exercise. If they are:

- A. Lower than 100 milligrams per deciliter (mg/dL) blood sugar may be too low to exercise. Low blood sugar is known as hypoglycemia.
- B. Between 100 and 250 mg/dL this is the optimal range which is safe for most people to begin exercising.
- C. 250 mg/dL or higher blood sugar may be too high to exercise.
 Carry out a urine test for ketones (which indicate more insulin is needed to control blood sugar)

During exercise, blood sugar should be tested every 30 minutes. Exercise should be stopped if the patient is experiencing blood sugar falls below 70mg/dl, weakness, tingling, and confision.

Rechecking of blood sugar should be done several times. Physical activity can lower blood glucose for up to 24 hours.[29]

B CHITS

Community Health Information Tracking System(CHITS) is the first electronic medical record system in the Philippines. It was developed to improve health information management at the RHU level by enabling users to to gather data and generate reports needed for decision making. There are currently a total of 169 health stations across the Philippines using CHITS. For NCR, 63 health centers in Quezon City, 9 in Navotas, 29 in Taguig and 10 in Pasay City

CHITS started as a research on computer-based information system by the University of the Philippines Manila in 2004 and was taken over by UP Manila National Telehealth Center for its development and implementation in 2006.

CHITS is a capacity-building program which instils relevant health information systems components among health workers. CHITS runs on free and open source software. As of 2011, the second version of CHITS uses the Open Medical Record

System as a platform. It allowed the developers/organizations to modify or adopt the code without developing the system from scratch. This also allows CHITS software developers can study and modify the CHITS-openMRS freely.[30, 9]

Key Features of CHITS as an EMR:

- 1. user friendly interface which presents to the health worker a signified view of the various DOH program data fields.
- 2. codifies their patient's clinical conditions and the care the health workers provided
- 3. tracks patient health status
- 4. remind them of services of patients seeking or needing follow up care

C Big Data

Big Data is defined as the exponential growth and availability of huge amount of data. It is believed and proven that with bigger data, leads to better and more accurate analysis and could lead to confident decision making which allows better judgment which results to higher operation efficiency, reduced risk and cost reduction.[31]

There are seven properties that makes Big Data different from other data.[32, 31, 33]

- 1. Volume Large quantity of data (in terms of petabytes or more). Storing of data was an issue prior to advance and affordable storage devices.
- 2. Velocity The pace at which the volume of data grows. It poses a problem with respect to time and efficiency therefore, there is a need to deal with the huge amount of data in real time
- 3. Variety Data is growing in variety of formats. Examples would include structured, instructed, relational, non-relational, and different data sources such as videos, images, reports, etc.

- 4. Variability Data is constantly changing.
- 5. Visualization using graphs/charts that is more effective in conveying meaning/information compared to a spreadsheet.
- 6. Veracity represents both the credibility of the data source and the suitability of the data for the target audience.
- 7. Value after addressing the issues of the different properties mentioned above, an organization must gain some value from the data (insights, predictions etc).

D Recommender System

Recommender Systems in general suggest items to purchase that takes into consideration the user's preferences. The system takes into account items similar to your past purchases or videos watched by other similar users. The prediction for which item to suggest is based upon similarity measures. Many techniques are used for recommendation task such as collaborative recommender systems, content-based recommender systems, knowledge-based recommender systems and various other techniques. [22]

E Collaborative Filtering

Collaborative Filtering is the most common technique used in most recommender systems. The technique works by suggesting products/items to the user basing on user or item similarity.[11]

The method considers the ratings of other users in the system to make personalized predictions on an active user's preferences. The computation for rating prediction and generating recommendations are based on the similarity metrics which are capable of processing sparse and inhomogeneous data vectors.[34]

As mentioned in [14]. Healthcare data do not have ratings systems. The alternative to this solution is to utilize similarity metrics. To give a recommendation

to a patient, the system must compare similar cases between patients.

The following algorithm is used to compute for similarity:

1. Cosine Similarity

Formula:
$$cos(\theta) = \frac{AB}{||A||^2||B||^2} = \sum_{i=1}^{n} \frac{A_i B_i}{\sqrt{\sum_{i=1}^{n} A_i^2 \sum_{i=1}^{n} B_i^2}}$$

The algorithm returns the output similarity of numerical vectors A and B which ranges from 0 - 1 in which a value close to 0 indicates no correlation and a value close to 1 indicates the two items/person are similar.[20]

F Python

Python is an interpreted, object-oriented, high-level Programming language used in many different applications such as data analysis, machine learning, web development and many more. [35]

Python includes libraries to help in data analysis:

- Pandas An open source, BSD licesend libraty providing high performance, easy-to-use data structures and data analysis for Python [36]
- sckikit-learn a Python library for machine learning with simple and efficient tools of data mining and analysis which is built on Numpy, SciPy and matplotlib. [37]

G Finnish Diabetes Risk Score

The Finnish Diabetes Risk Score is a questionnaire for assessing risk for type 2 Diabetes. The questionnaire consist of 8 questions and each question has a corresponding criteria that a person should encircle. Each answer corresponds to a number of points and is totalled after the person answers all the questions. the total points is matched to a particular risk assessment. For example, having a total score of below 7 states that the person has a low risk while a score higher than 20 implies a very high risk of type 2 diabetes.[38]

IV. Design and Implementation

1. The diagram below shows the interaction between the CHITS personel and the recommender system. The user inputs the patient case information by using the web application then the web app sends the data to a web server where the server feeds the data to the recommender model which will send back to recommendation back to the web server and back to the web application and be presented to the user through the user interface of the web application.

The system will be developed using Python. The recommender model and analytics will be implemented using Pandas and scikit-learn. The web application will be developed using Flask, a python web framework.

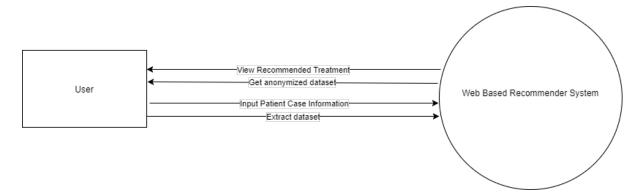


Figure 1: Context Diagram

2. The figure below shows the overall view of the system functionalities which focuses on the CHITS personnel. They can input patient case information to the system and view the recommendation output through the system's user interface. The system also allows the user to do search queries for specific information and be able to analyze statistical trends on diabetes through a dashboard.



Figure 2: Use Case Diagram for Health Professional/Researcher

3. Building the Recommendation Model

- (a) Select Diabetes cases from CHITS dataset
- (b) Get all records(family history, social history, treatment, medication, lab reports, etc) of the patients identified as diabetic patients.
- (c) Save data to Diabetes to Diabetes Health Recommender System Database as a CSV file.
- (d) Load CSV to Pandas and load the data as a dataframe. This will allow to insert the vectors into the cosine similarity algorithm easier.
- (e) Make a new dataframe by dropping the following columns: person_id, weight, height, encounter_id, birthdate, CN, HN, DN, DIAG_DM, DIAG_NONDM, TPN, and gender as these parameters are not needed for computation
- (f) Make a seperate dataframe using the values inputted from the system.

 The system automatically computes the BMI of the inputted data then uses it as a parameter in the seperate dataframe as BMI is needed for the Finnish Risk Score Assessment.
 - Both the recommender and the seperate dataframe (inputted data) must contain data for waist circumference, hip circumference, age, gender, Hba1c result, fbs result, and BMI.
- (g) Apply Finnish Risk Score Assessment as weights to newly created dataframe and recommender dataframe. The scores can be found in [38]
- (h) Append recommender dataframe with the newly created dataframe
- (i) Normalize Dataframe by using the pre-processing package found in sklearn library.
 - i. Get all the values from the newly created dataframe and store it inside a list variable
 - ii. get a min-max object from pre-processing package using MinMaxS-calar() function.

- iii. use the function of the min-max object, fit_transform(values) to normalize the values
- iv. create a new recommender dataframe with the normalized values
- (j) Get last row of the recommender dataframe and remove last row from the recommender dataframe
- (k) Compute for each row of the recommender dataframe the Cosine Similarity(from sklearn.metrics.pairwise) with the acquired dataframe.

The computation for cosine similarity is as follows

- i. Cosine Similarity takes two numerical vectors A and B. Each vector containing data for Waist Circumference, Hip Circumference, Age, Gender, Hba1c Result, FBS result and BMI
- ii. Vector A contains the data of each parameter for one record in the dataset. Vector B contains the inputted data from the system. Both vectors must contain the same number of parameters, otherwise the algorithm wont work.
- iii. the algorithm computes the angle between these two vectors by computing the dot product of the vectors divided by the magnitude of these two vectors
- (1) Store each result in a 2 dimension List in a format of [index,result]
- (m) Sort the List according to result
- (n) Return the top 5 results of the list

- 4. Minimum System Architecture:
 - (a) at least 4 GB RAM
 - (b) AMD A10/Intel I3 or better
 - ${\rm (c)\ Windows/Linux/MacOS}$
 - (d) Python 2.7

V. Results

Below is the user interface of the Diabetes Recommender System which includes the home page, treatment page, search page, and dashboard page.

The main functionality of the system is the treatment page where the health professional can input the patient profile and get the recommended treatment in the results page.

Researchers can also search for patient profiles in the search component of the system.

The data analytics component of the system is presented through a dashboard and shown using graphs.

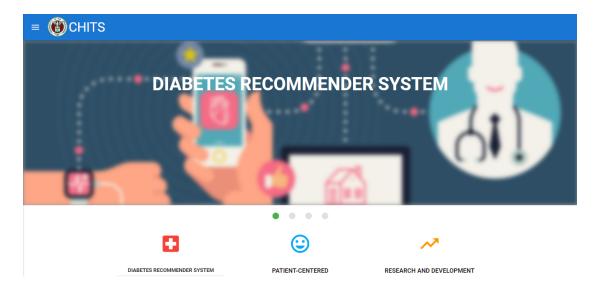


Figure 3: Homepage of the System

This is the homepage of the system which includes what the system is all about and includes facts about diabetes in the Philippines.

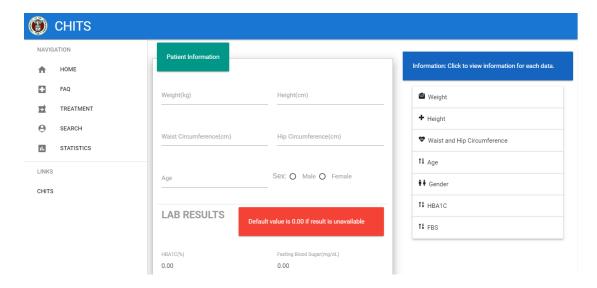


Figure 4: Patient Profile Form

fig 4 is the form in which the health professional must input the patient's profile then clicking the submit button in order to get the recommended treatments. The page also includes facts about each parameter and explains how it contributes as a diabetes factor.

The parameters included in the form are

- 1. Weight
- 2. Height
- 3. Waist Circumference
- 4. Hip Circumference
- 5. Age
- 6. Gender
- 7. Hba1C Lab Result
- 8. FBS lab Result

To find similar patients, the system compares patient profiles using the Cosine Similarity algorithm. The system also uses the Finnish Risk Score Assessment to add weights to the parameters before being computed.

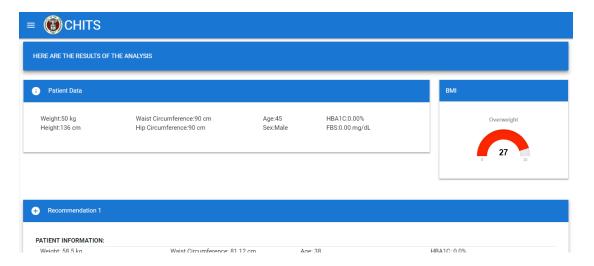


Figure 5: Recommender System Results

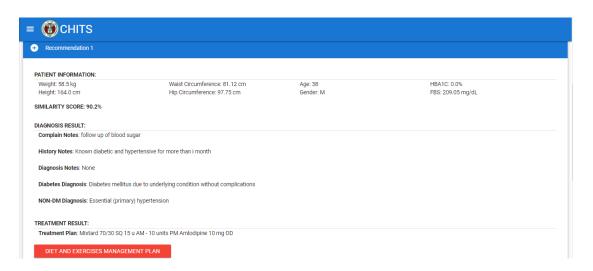


Figure 6: Recommender System Results

fig 5 and fig 6 shows the recommended treatment after the system finds the similar patients to the new patient. The page includes the information inputted by the health professional as well as the gauge of the body mass index of the patient. The system shows the top 5 recommendation and displays all information of that patient including profile, diagnosis notes, and treatments.



Figure 7: Top 5 Recommendations

The other recommendations can be clicked upon by the user (same as the first recommendation) to view other patient profiles and treatments.

```
[[12L, 0.90203316396071287], [11L, 0.89806068455933663], [24L, 0.84186288906977413], [23L, 0.84122979764288697], [22L, 0.84025797787098711]]
127.0.0.1 - - [25/May/2018 01:11:25] "POST /recommender HTTP/1.1" 200 -
```

Figure 8: Score Results

fig 8 show the following score results from the algorithm. The scores shown in the command prompt are the top five similar patients. the results show which row the patient record is in the dataset followed by the similarity score

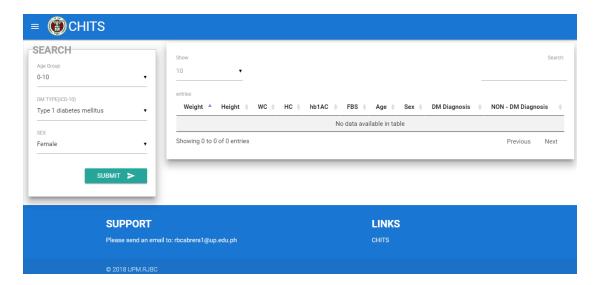


Figure 9: Search page with Datatable

Users can search for patient profiles here by querying their sex, DM type(based on ICD10) and age group. A datatable is included to enable users to sort any parameter or search any text query. Users may also limit the search results by the select field on the upper left side of the data table

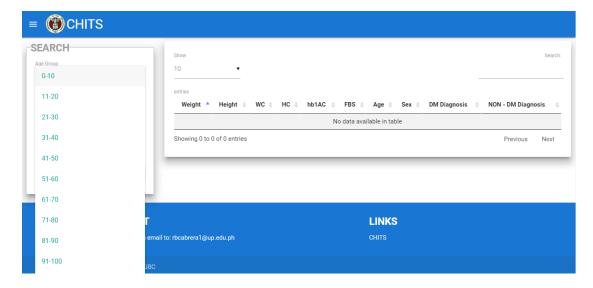


Figure 10: Select Field: Age Group

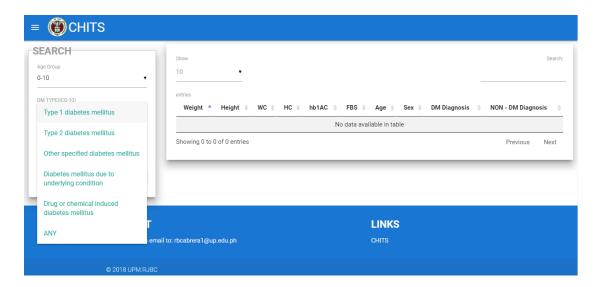


Figure 11: Select Field: DM Type

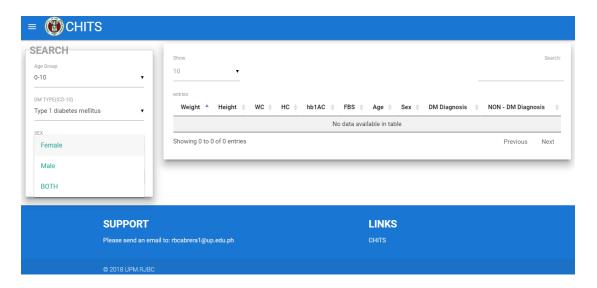


Figure 12: Select Field: Sex

In fig 10, 11 and 12, the user can choose wit parameters he/she is interested in. After selecting which options in the parameters to search, clicking the submit button will show the search results in the datatable.

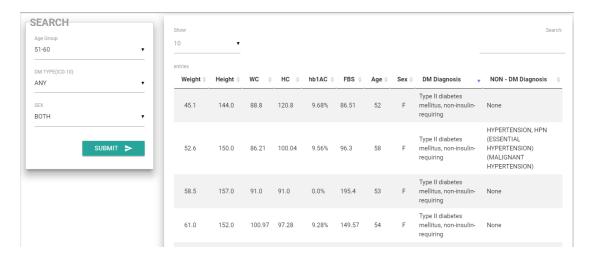


Figure 13: Datatable Results

The datatable shows the result of the queries. The data can be sorted by clicking on the column header. This can be sorted in descending or ascending order.



Figure 14: Datatable Results when using search

The datatable automatically limits the results while the user types on the search field.

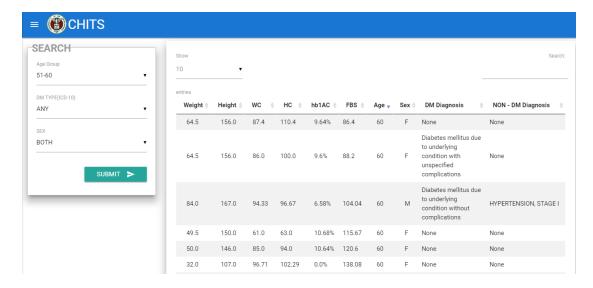


Figure 15: Datatable Results with pagination

The datatable automatically adds a pagination when the results of the search query exceeds the number of results to be shown on the table.

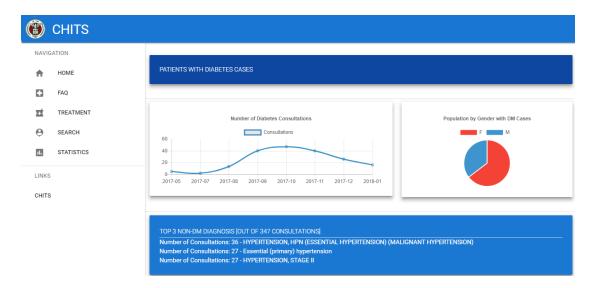


Figure 16: Dasboard Results

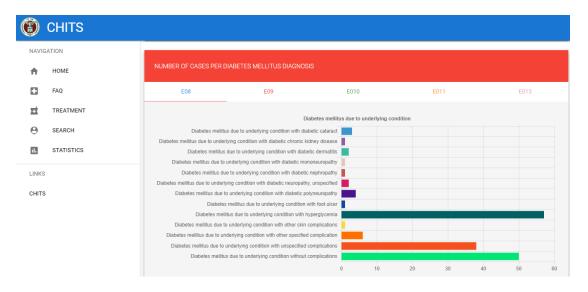


Figure 17: Dasboard Results



Figure 18: Dasboard Results

The dashboard shows different statistics on the diabetes data. Some graphs show the number of cases per diagnosis, top recorded FBS result, specific age groups of patients, the number of cases per month, the number of patients with past history or family history.

VI. Discussions

The Diabetes Recommendation System is an web application that gives treatment recommendations to the diabetes cases. The system includes a recommedation component and a data analytics component through the use of a dashboard and a data table.

The advantages of the system is it gives out complete information (except for patient's sensitive data) that maybe useful to the health professional such as the patient profile and history. This gives the health professional the complete idea of why a certain treatment is given as compared by just giving the diabetes diagnosis and treatment. This is due to some diseases being related to diabetes.

The system also views the patient profile in the search component and it allows the users to sort the data which is a great component for data analysis as it allows the user to understand the patient profile easily.

Another advantage of the system is that the system utilizes the data collection module of CHITS by presenting charts that tell the conditions of the patients which will allow health organizations or health care stations to further improve their health care modules/systems.

The disadvantages of the system is that it may give out results that are not the best treatment in some cases. This is due because some patients are not diagnosed with diabetes during that encounter period therefore, some treatments may include also non diabetes treatments. There are also some cases in which the better treatment(by a health professional) is not the first recommendation by the system. This is because the similarity is based on the patient profile and the treatment is not included in the similarity computation. There are also cases wherein the diabetes diagnosis is not indicated but a treatment for diabetes is included. This is due to a data entry problem involved in CHITS.

In comparison to other recommendation system, the system uses cosine similarity to find similar patients while other recommendation systems used other sim-

ilarity metrics such as Pearson Correlation. Most of the data needed for the similarity computation requires numerical variables while other systems used mostly categorical variables.

A lot of problems were encountered during the development of the system. The first problem I encountered was the system's core functionality was supposed to be built using a big data framework, Apache Spark but issues came up when building the python script as I was unable to run it as a python script but was able to successfully run the code in a Jupyter notebook. There is an instruction on how to run the code as a python script but was still unable to successfully run it.

While testing the algorithm, some potential problems can be noticed. These are the following:

- 1. The algorithm computes similar columns therefore requiring the dataset to be transposed first.
- 2. the dataset must be transformed into a Coordinate Matrix to be transposed which leads to more confusion if it actually returns the right result when DIMSUM is applied.
- 3. The algorithm computes all similarities between columns which is not needed for the system therefore wasting computational time and effort.

The solution to this problem was to use a python library called scikit-learn which contains an implementation of cosine similarity which is also the basis of DIMSUM. the function also solves the problem presented with DIMSUM as it enables the computation to be done by row, data was not needed to be transformed into another object, and reducing the time and effort for computing the needed result from the dataset.

Another problem encountered in developing the system was the data extraction from CHITS. Studying the system was not an easy task as it was designed in a different way. CHITS was designed to present their records by column which means for example, I have two rows with a record of the same person, same encounter id but different concept id with means that I have to build the dataset to present the records by row. The main obstacle in data extraction was a data entry problem as the fields needed for the system is either null or not formatted in a proper way. Examples are some patient entry does not have a record of the height or weight, most patient do not have any past or family history recorded, food intake and physical activity was not recorded, lab results such as FBS was not recorded in the proper field but rather was saved in a different field. Another problem was finding the diabetic patient themselves since the dataset is dependent on their records.

To strategy to build the recommender system data set was to find the treatments that are specifically for diabetes such as Metformin. Finding the diagnosis is not that helpful since not all diagnosis was given a treatment therefore will become useless for the recommendation system. After finding the those treatments, you get the patient profile needed(weight, height, waist circumference,gender,etc) and save it as a CSV file. I also saved a another csv file which contains the distinct encounter id and person id of that record which will be used later for pre-processing. This process is done to different health stations to obtain the different datasets which will become combined as a single recommender data set.

To build per health station dataset, a python script was built to make a dataframe which would present the data by row as mentioned before. The strategy here was by using pandas library, loading the two datasets gathered from one health stations and using the distinct encounter id and person id with the dataset containing their information and looping to properly place the data in their respective columns to that specific person during that encounter.

Once the different datasets was built, another python script was built to append all the datasets into one csv file. I tested the datasets for potential errors and the results were not very convincing since almost all patients were similar with the minimum result 0.7 which means they are likely similar but with not convincing explanation. the problem was due to the high value of the weight and height parameters were covering the other parameters needed so the algorithm was mostly relying on those two parameters for the result and was "disregarding" the others. To solve this issue, normalizing the dataset before it was being used in the system which will level all the parameters equally. This was done using sklearn preprocessing. The values of the data was ranging from 0 - 1 therefore allowing the algorithm to function properly and including the other parameters.

as mentioned before, data entry was the main obstacle to the recommender as the system relies on the dataset that it uses as basis. the solution was to apply linear interpolation to fill up the null values of numeric parameters. Pandas as a function to apply it a dataframe and it was able to at least fill up most of the null values with estimated values in order to make the system more functional.

Despite the problems stated above, the system was successfully built and is able to give out recommendations that are properly computed and presented by giving out the top 5 recommendations.

VII. Conclusions

The Diabetes Recommendation System is a web application that allows health professionals to get treatment recommendations which could be a useful tool to help the doctor analyze the profile of the patient and help in deciding the proper treatment to improve the patient's condition. A successful treatment does not only take care of the patient's well being but also reducing additional costs to both the patient and the hospital.

Researchers can also use the system for data analysis that enables to learn more about the condition of diabetic Filipinos and the current trends in diabetes cases. This will allow them to improve their health programs that they provide therefore also improving the heatlhcare quality of the patients.

The system was developed by gathering data from CHITS, creating python scripts to build the dataset, building the user-interface of the system, pre-processing the data for the system, and implementing the cosine similarity algorithm and other processes of the system.

To gather data from CHITS, studying the how CHITS works was the first step then after understanding the core of the CHITS system, different data mining techniques were applied. Text mining was applied to get lab results and treatments needed for the system. A python script was also built that made creating the dataset faster.

Building the user-interface of the system, The Materializecss framework made it as user-friendly and as responsive as possible. The charts are properly organized to properly tell the story of data, what it means and how valuable it could be to a researcher. Doctors can also input data using the forms provided by the system and view the top 5 recommendations containing the information of the patient profile including history notes, non-diabetes diagnosis, diabetes diagnosis and the provided treatment.

Pre-processing the data allows the system to calculate how similar the patients

are which is the most crucial component of the system as it is depend on the result of the similarity metric to give out the recommendation.

With the potential of CHITS as an electronic medical record system, the Diabetes Recommendation System, can be a potential healthcare application that will allow improving quality heath care in the Philippines through data analytics and treatment recommendations.

VIII. Recommendations

1. Dataset

To improve the performance of the system, it is important to continue adding more data to the data set by collecting more datasets from different health centers that uses CHITS as the recommendations is dependent on how many records exist the data set. The recommendations stated below are further notes on how make the dataset more useful for the system.

Currently, the data set contains only 7 parameters to be used by the algorithm as the some factors related to diabetes cannot be mined. A possible way to improve the system is to provide more parameters that the can be implemented in the algorithm. Categorical variables such as physical activity or alcohol drinking frequency. Numerical variables such as lab results could further improve finding similar patients.

The data set was also interpolated due to many null values in important fields for computation. To further improve the calculation for similarity, the data as much as possible must not contain null values for fields which are required by the algorithm.

The data set only contains medical treatments mined from CHITS, to further improve the recommendation the system provides, the data set must also contain non-medical treatments such as diet plans or exercise regimens provided by a health professional

A crucial part of how to improve the dataset is to have a health professional review the dataset or better, review the patient's history to show that the treatment provided by the previous doctor is a good treatment therefore eliminating any treatment that are not suitable by an expert's judgment. In this manner, the system will be more reliable.

To enhance the performance of finding similar patients, other similarity metrics could be implemented in the system.

2. Web Application

If the system can be hosted in a server hosted through HTTPS, it can be used as a desktop or mobile application by implementing a service worker to transform the web application to a progressive web application. This allows the user to install the application in their device(mobile,tablet,desktop) instead of accessing the system through a browser.

The data table in the search component of the system could not be properly viewed in a mobile platform. Some tweaks are required in order to arrange the way it presents data without losing it's functionality

The data analysis component of the system could also be improved by adding more statistical information that can be found in the dataset such as correlation of diabetes with non-diabetes diagnosis(ex. Hypertension).

The system could also improve the recommendation quality if it includes a data collection component that allows the doctor to confirm if the recommended treatment improved the condition of the patient. This allows removing treatments that are not effective. The system can be greatly improved and more reliable if this step is followed.

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X. Appendix

A Source Code

```
app.pv
                                                                                                                 return render_template('search.html', s_form = s_form,
from flask import Flask, render_template , request, flash
                                                                                                                                               search_df)
from forms import CaseForm
from search_forms import SearchForm
                                                                                                               return render_template('search.html', s_form = s_form)
# how to import external .py file
from diagnosis.dashboard import get_ICD10.list,
get_dmcases_counts_mmyy, get_dmcasesbygender_count,
                                                                                                              @app.route('/ statistics ')
                                                                                                              def dashboard ():
          get_dmcases_counts, get_age_group, get_dm_cases_average_age_gender,\
                                                                                                               #send value to template
cases_gender = get_dmcasesbygender_count()
dm_cases_count = get_dmcases_counts()
dm_cases_year_month = get_dmcases_counts_mmyy()
 get_age_group_past_tam_history,
get_count_ph_fh_by_gender,\
get_ICD10_type2_get_ICD10_type1,
get_ICD10_dm_underlying_cond,get_ICD10_otherDM,
get_ICD10_Drug_chemical_induced,\
get_ICD10_type2_withgender, get_ICD10_type1_withgender,
get_ICD10_dm_underlying_cond_withgender,
get_ICD10_otherDM_withgender,
                                                                                                               # print cases_gender
                                                                                                               dm_cases_ave_age = get_dm_cases_average_age_gender() dm_cases_age_grp = get_age_group()
                                                                                                               dm\_cases\_specific\_count = get\_ICD10\_list()
                                                                                                               {\tt dm\_history\_gender} = {\tt get\_history\_cases} {\tt bygender\_count}()
                                                                                                               dm_history_gender_age_ave = get_average_age_gender()
            get_ICD10_Drug_chemical_induced_withgender
                                                                                                               {\rm dm\_history\_gender\_age\_grp} \ \ = \ {\rm get\_age\_group\_past\_fam\_history}
                                                                                                               dm_history_gender_count_by_gender =
# from cs_pandas import calculate_CS,get_data,get_treatments
                                                                                                                         get_count_ph_fh_by_gender()
from recommend import calculate_CS,get_data,
get_max_FBS_value,get_max_HBA1C_value.
                                                                                                               fbs_max_value = get_max_FBS_value()
          get_nonDM_count,get_bmi_label,get_data_df_count,
get_max_fbs_value_column, get_max_hbalc_value_column
                                                                                                               HBA1C_max_value = get_max_HBA1C_value()
non_dm_max_value = get_nonDM_count()
from query import get_search_data
                                                                                                               ICD10_type2 = get_ICD10_type2()
ICD10_type1 = get_ICD10_type1()
ICD10_underlying_cond = get_ICD10_dm_underlying_cond()
ICD10_otherDM = get_ICD10_otherDM()
ICD10_Drug_Chemical_induced =
app = Flask(__name__)
app.config['SECRET_KEY'] = 'reuben158'
                                                                                                                         get_ICD10_Drug_chemical_induced()
@app.route('/')
def index():
  return render_template('index.html')
                                                                                                               ICD10_type2_withgender = get_ICD10_type2_withgender()
ICD10_type1_withgender = get_ICD10_type1_withgender()
ICD10_dm_underlying_cond_withgender =
get_ICD10_dm_underlying_cond_withgender()
ICD10_th_cond_withgender()
@app.route('/faq')
def faq():
return render_template('faq.html')
                                                                                                               ICD10_otherDM_withgender = get_ICD10_otherDM_withgender()
                                                                                                                \begin{split} ICD10\_Drug\_chemical\_induced\_withgender = \\ get\_ICD10\_Drug\_chemical\_induced\_withgender() \end{split} 
@app.route('/recommender',methods = ['POST', 'GET'])
def recommender():
 form = CaseForm()
                                                                                                               dataset_count = get_data_df_count()
highest_fbs_profile = get_max_fbs_value_column()
highest_hba1c_profile = get_max_hba1c_value_column()
 if form.validate_on_submit():
bmi = (form.weight.data/ (form.height.data/100) **2)
bmi = str(round(bmi, 2))
                                                                                                               return render_template('dashboard.html',
   bmi_res = get_bmi_label(bmi)
                                                                                                                  dm_cases_specific_count = dm_cases_specific_count, dm_cases_year_month = dm_cases_year_month,
                                                                                                                  cases_gender = cases_gender,
dm_cases_count = dm_cases_count,
   #res = calculate_CS(form.weight.data, form.height.data,
             form.wc.data, form.hc.data, form.sex.data, form.age data, form.hbalc.data, form.fbs.data)
                                                                                                                  dm_cases_ave_age = dm_cases_ave_age, dm_cases_age_grp = dm_cases_age_grp,
          = calculate_CS(bmi, form.wc.data, form.hc.data, form. sex.data, form.age.data, form.hbalc.data, form.fbs.
                                                                                                                  \begin{array}{l} dm\_history\_gender = dm\_history\_gender, \\ dm\_history\_gender\_age\_ave = dm\_history\_gender\_age\_ave, \end{array}
             data)
                                                                                                                  dm_history_gender_age_grp = dm_history_gender_age_grp, dm_history_gender_count_by_gender =
   print res
    list\_treatments = get\_data(i[0] for i in res)
                                                                                                                  dm.history.gender.count.by.gender =
dm.history.gender.count.by.gender,
fbs.max.value = fbs.max.value,
HBA1C.max.value = HBA1C.max.value,
non.dm.max.value = non.dm.max.value,
ICD10.type2 = ICD10.type2,
ICD10.type1 = ICD10.type1,
ICD10.underlying.cond = ICD10.underlying.cond,
ICD10.prug.Chemical.induced =
ICD10.Drug.Chemical.induced.
   for i in res:
     i \, [1] \, = \, round(i \, [1], \, \, 4) \, \, * \, 100
   if form.sex.data == '2':
     sex_label = 'Female'
   else ·
     sex_label = 'Male'
                                                                                                                  ICD10_Drug_Chemical_induced,
ICD10_type2_withgender = ICD10_type2_withgender,
ICD10_type1_withgender = ICD10_type1_withgender,
ICD10_dm_underlying_cond_withgender =
   \label{eq:continuous_result} return \ render\_template(`result .html', \ list\_treatments = \\ list\_treatments \, , \ form = form, sex\_label = sex\_label , \\
             bmi = bmi,bmi_res= bmi_res, res = res)
                                                                                                                   ICD10_dm_underlying_cond_withgender,
ICD10_otherDM_withgender = ICD10_otherDM_withgender,
 return render_template('recommender.html',form = form)
                                                                                                                  ICD10_Drug_chemical_induced_withgender = ICD10_Drug_chemical_induced_withgender,
@app.route('/search',methods = ['POST', 'GET'])
def search():
                                                                                                                  dataset_count = dataset_count,
highest_fbs_profile = highest_fbs_profile,
highest_hbalc_profile = highest_hbalc_profile)
 s_form = SearchForm()
                                                                                                              if __name__ == '__main__':
  if s_form.validate_on_submit():
                                                                                                               app.run(debug=True)
   search\_df = get\_search\_data(s\_form.search\_sex.data,s\_form.
```

search_dm_type.data,s_form.search_age_group.data)

```
diagnosis_dashboard.py
                                                                                                                                                def get_ICD10_Drug_chemical_induced():
                                                                                                                                                  return frame[frame['value_text'].str.match('Drug or chemical induced diabetes mellitus')].groupby('
  import pandas as pd
                                                                                                                                                               value_text') [' value_text']. count()
  import glob
  import datetime as dt
                                                                                                                                                def get_dmcases_counts_mmyy():
 def create_dataframe(path_name):
    path =r'DS/'+path_name # use your path
    allFiles = glob.glob(path + "/*.csv")
    frame = pd.DataFrame()
    list_ = []
    for file_ in allFiles:
        df = pd.read_csv(file_,index_col=None, header=0)
                                                                                                                                                  v = frame['date_created'].value_counts().sort_index()
v_2017 = v[v.index.str [:4].astype(int) >= 2017]
                                                                                                                                                  return v 2017
    list_ .append(df)
frame = pd.concat(list_)
    return frame
                                                                                                                                                \begin{array}{ll} \mbox{def get\_dmcases\_counts():} \\ \mbox{return frame.groupby(['value\_text ']) ['value\_text ']. count().} \\ \mbox{sort\_values (ascending = False)} \end{array} 
  frame = create_dataframe('Diabetes_Cases')
                                                                                                                                               def get_dmcasesbygender_count():
  return frame.groupby(('gender')) ['gender'].count()
  def change_time_format(df):
         \begin{array}{ll} df \ ['date\_created \ '] &= pd.to\_datetime (df ['date\_created \ ']) \ .dt \\ &. \ strftime ("\%Y-\%m") \end{array}
                                                                                                                                                def get_dm_cases_average_age_gender():
                                                                                                                                                  return frame.groupby(['gender'])['age'].mean().round()

def get_age(df):

    df ['birthdate'] = pd.to_datetime(df['birthdate'])

now = dt.date.today()

df ['age'] = ((now - df['birthdate'])/365).dt.days
                                                                                                                                                def get_age_group():
                                                                                                                                                  return age_grp
                                                                                                                                               def get_ICD10_type2_withgender():
    return frame[frame['value_text ']. str.match('Type 2') |
        frame['value_text ']. str.match('Type II diabetes')]\
        .groupby(['value_text ',' gender']) [' value_text ']. count()\
  change\_time\_format(frame)
                                                                                                                                                    unstack(). fillna (0).stack()
  get_age(frame)
                                                                                                                                                def get_ICD10_type1_withgender():
    return frame[frame['value_text ']. str.match('Type 1') |
        frame['value_text ']. str.match('Type I diabetes')]\
        .groupby(['value_text ', gender']) [' value_text ']. count()\
        .unstack(). fillna (0) .stack()
  #calculate age group https://stackoverflow.com/questions
 #calculate age group https://stackoverflow.com/question/35550486/data-grouping-in-pandas frame['count'] = 1 frame['age.group'] = pd.cut(frame.age, [0,10,20,30,40,50,60,70,80,90,100]) age_grp = frame.pivot.table('count', index='age_group', columns='gender', aggfunc='sum').fillna(0)
                                                                                                                                                def get_ICD10_dm_underlying_cond_withgender():
    return frame[frame['value_text'].str.match('Diabetes
                                                                                                                                                   mellitus')]\\
.groupby(['value_text ',' gender']) [' value_text ']. count()\\
.unstack(). fillna (0).stack()
#shape[0] = row count ICD10_count.list = []
ICD10_count.list = []
ICD10_count.list.append(['Type 2 diabetes mellitus',frame[
frame['value_text ']. str.match('Type 2') | frame['
value_text ']. str.match('Type II diabetes')][' value_text ']. str.match('Type II diabetes') | ['
ICD10_count.list.append(['Type 1 diabetes mellitus',frame[
frame['value_text ']. str.match('Type I') | frame['
value_text ']. str.match('Type I diabetes') | ['
value_text ']. shape[0]])
ICD10_count.list.append(['Diabetes mellitus due to underlying condition',frame[frame['value_text ']. str.match('
Diabetes mellitus')]['value_text ']. str.match('
Diabetes mellitus') | ['value_text ']. str.match('Other specified diabetes mellitus'),frame[frame['value_text ']. str.match('Other specified diabetes mellitus'),frame[frame['value_text ']. str.match('Drug or chemical induced diabetes mellitus',frame[frame['value_text ']. str.match('Drug or chemical induced diabetes mellitus')] | ['value_text ']. str.match('Drug or chemical induced diabetes mellitus')] | ['value_text ']. shape [0]])
   #shape[0] = row count
                                                                                                                                                def get_ICD10_Drug_chemical_induced_withgender():
                                                                                                                                                  return frame[frame[value.text ']. str.match('Drug or chemical induced diabetes mellitus')]\
.groupby(['value_text ',' gender']) ['value_text ']. count()\
                                                                                                                                                   .unstack().fillna(0).stack()
                                                                                                                                                 #get data from past and family history dataset
                                                                                                                                                 past_fam_history_df = create_dataframe('DM_PH_FH_2')
                                                                                                                                               \label{lem:change_time_format} $$\# change\_time\_format(past\_fam\_history\_df)$ $$ get\_age(past\_fam\_history\_df)$
               shape [0]])
                                                                                                                                                \begin{array}{l} past\_fam\_history\_df \ ['count'] = 1 \\ past\_fam\_history\_df \ ['age\_group'] = pd.cut(past\_fam\_history\_df \\ .age, \quad [0,10,20,30,40,50,60,70,80,90,100]) \end{array}
  #get Functions here
def get_ICD10_list():
                                                                                                                                                past_fam_history_age_grp = past_fam_history_df.pivot_table ('
count', index='age_group', columns='gender', aggfunc
='sum').fillna(0)
    return ICD10_count_list
  def get_ICD10_type2():
    frame['rame[rame[tax] : str.match('Type 2') | frame['value.text']. str.match('Type II diabetes')].
groupby('value.text') ['value.text']. count()
                                                                                                                                                def get_history_casesbygender_count():
                                                                                                                                                  return past_fam_history_df.groupby(['gender']) ['gender'].
count()
  def get_ICD10_type1():
    return frame['rane['value_text']. str.match('Type 1') |
frame['value_text']. str.match('Type I diabetes')].
groupby('value_text') [' value_text']. count()
                                                                                                                                                def get_average_age_gender():
                                                                                                                                                  return past_fam_history_df.groupby(['gender']) ['age'].mean ().round(decimals=2)
  def get_ICD10_dm_underlying_cond():
    return frame[frame['value_text ']. str.match('Diabetes
        mellitus')].groupby('value_text')[' value_text '].count()
                                                                                                                                                 #dataframe
                                                                                                                                                def get_age_group_past_fam_history():
                                                                                                                                                  return past_fam_history_age_grp
 def get_count_ph_fh_by_gender():
    return past_fam_history_df.groupby(['gender','value_coded'])
                                                                                                                                                                ['gender'].count()
```

```
forms.py
                                                                                                                                                                   '), NumberRange(min=0, max=200)])
                                                                                                                                                      wc = DecimalField('First Name', places=2, rounding=
                                                                                                                                                                    None, validators=[InputRequired('Waist Circumference is required'), NumberRange(min=0,
from flask_wtf import FlaskForm
                                                                                                                                                                    \max = 200)])
                                                                                                                                                              = DecimalField('HipCircum.(cm)', places=2, rounding
                                                                                                                                                                    =None, validators=[InputRequired('Hip Circumference is required'), NumberRange(min=0,
from\ wtforms\ import\ StringField,\ IntegerField,\ TextAreaField,
SubmitField,\ RadioField,\ SelectField,\ DecimalField \\ from\ wtforms.fields.html5\ import\ TelField
                                                                                                                                                                    \max = 200)
                                                                                                                                                     \begin{array}{ll} \mbox{hba1c} &= \mbox{DecimalField('HBA1C', places=2,default=0.0, \\ \mbox{rounding=None, validators=[InputRequired('HBA1C', places=2,default=0.0, \\ \mbox{rounding=None, validators=[InputRequired('HB
from wtforms.validators import InputRequired, Length, AnyOf
                                                                                                                                                                    Result is required'), NumberRange(min=0, max
                                                                                                                                                                -100]]/
= DecimalField('fbs', places=2, default=0.0,rounding
=None, validators=[InputRequired('FBS Result is
required'), NumberRange(min=0, max=500)])
class CaseForm(FlaskForm):
      \begin{array}{l} {\rm age = IntegerField('Age', \ validators = [InputRequired('age \ is \ required'), \ NumberRange(min=0, \ max=100)])} \end{array}
                                                                                                                                                      sex = RadioField('Sex', choices = [('1',' Male') ,('2','
      height = DecimalField('Height(cm)', places=2, rounding=
None, validators=[InputRequired('height is required')
, NumberRange(min=0, max=200)])
                                                                                                                                                     submit = SubmitField("Send")
                   , Number (Lange (limit—V, intal 2007))

t = DecimalField ('Weight (kg)', places=2, rounding=

None, validators=[InputRequired('weight is required
                                                                                                                                                    return '(gender == "F" or gender == "M")'
           query.py
                                                                                                                                               def get_age_group_data(grp_value):
import pandas as pd
import numpy as np
                                                                                                                                                  if grp_value == "0":
                                                                                                                                                   \begin{array}{l} \mathrm{query1} = \mathrm{`age}{>}{=}0 \ \mathrm{'} \\ \mathrm{query2} = \mathrm{`age}{<}{=}10 \ \mathrm{'} \end{array}
from recommend import get_data_df
                                                                                                                                                   elif grp_value == "1":
                                                                                                                                                   query1 = 'age>=11'
query2 = 'age<=20'
search_df = get_data_df()
                                                                                                                                                   elif grp_value == "2":
def get_search_data(sex,dm_type,age_group):
  print sex,dm_type,age_group
df = get_dm_type_data(dm_type)
                                                                                                                                                   query1 = 'age>=21',
query2 = 'age<=30',
                                                                                                                                                   elif grp_value == "3":
    \label{eq:sex_data} \begin{split} & sex\_query = get\_sex\_data(sex) \\ & age\_group\_query = get\_age\_group\_data(age\_group) \\ & return \ df.query(sex\_query + " \ and " + age\_group\_query) \end{split}
                                                                                                                                                   query1 = 'age>=31'
query2 = 'age<=40'
                                                                                                                                                  elif grp_value == "4":
query1 = 'age>=41'
query2 = 'age<=50'
{\tt def \ get\_dm\_type\_data(dm\_type\_value):}
  if dm.type_value == '1':
return search_df [search_df ['DIAG_DM'].str.match('Type 1')
| search_df ['DIAG_DM'].str.match('Type I diabetes')
                                                                                                                                                  elif grp_value == "5":
query1 = 'age>=51'
query2 = 'age<=60'
    elif dm_type_value == '2':
    return search_df [search_df ['DIAG_DM'].str.match('Type 2')
| search_df ['DIAG_DM'].str.match('Type II diabetes')
                                                                                                                                                  elif grp_value == "6":
query1 = 'age>=61'
query2 = 'age<=70'
    elif dm_type_value == '3':
    return search_df [search_df ['DIAG_DM'].str.match('Diabetes mellitus')]
                                                                                                                                                  elif grp_value == "7":

query1 = 'age>=71'

query2 = 'age<=80'
   elif dm_type_value == '4':
return search_df[search_df['DIAG_DM'].str.match('Other
   specified diabetes mellitus')]
elif dm_type_value == '5':
                                                                                                                                                   elif grp_value == "8":
                                                                                                                                                   query1 = 'age>=81'
query2 = 'age<=90'
    elif dm.type_value == '5':
return search_df[search_df['DIAG_DM'].str.match('Drug or
chemical induced diabetes mellitus')]
                                                                                                                                                   elif grp_value == "9":
    return search_df
                                                                                                                                                   query1 = 'age>=91'
query2 = 'age<=100'
                                                                                                                                                   elif grp_value == "ANY":
def get_sex_data(sex_value):
                                                                                                                                                   query1 = 'age>=0 '
query2 = 'age<=100'
  if sex_value == "1":
return 'gender == "F"'
elif sex_value == "2":
return 'gender == "M"'
                                                                                                                                                 return query1 + " and " +query2
            recommend.pv
                                                                                                                                                  if sex == '2':
                                                                                                                                                    df-flask = pd.DataFrame([[wc,hc,0,1,hba1c,fbs,age,bmi]],
columns=['wc','hc','isMale',' isFemale',' HBA1C','FBS
import numpy as np; import pandas as pd from sklearn.metrics.pairwise import cosine_similarity
                                                                                                                                                    ','age','BMI'])
# df_flask = pd.DataFrame([[weight,height,wc,hc,0,1,hba1c,
from sklearn import preprocessing
                                                                                                                                                                 fbs,age]], columns=['weight','height',' wc','hc',' isMale',' isFemale',' HBA1C','FBS','age'])
                                                                                                                                                  #male
def get_data_df():
                                                                                                                                                   {\tt def \ get\_data\_df\_count():}
  return len(df)
                                                                                                                                                                 fbs,age]],columns=['weight','height','wc','hc',' isMale',' isFemale',' HBA1C','FBS','age'])
 #def calculate_CS(weight,height,wc,hc,sex,age,hba1c,fbs):
def calculate_CS(bmi,wc,hc,sex,age,hba1c,fbs):
```

#female

```
df_flask ['FBS'] = df_flask .apply(apply_FRA_FBS,axis =
                                                                                                                          elif row['age'] >= 45 and row['age'] <= 54: return row['age'] * 2
  df_flask ['BMI'] = df_flask .apply(apply_FRA_BMI,axis =
             1)
                                                                                                                          elif row['age'] >= 55 and row['age'] <= 64:
                                                                                                                           return row['age'] * 3
                                                                                                                           return row['age'] * 4
  frames = [rec\_df, df\_flask]
  c_df = pd.concat(frames)
                                                                                                                        def apply_FRA_wc(row):
                                                                                                                         if row['sermle'] == 1:

if row['wc'] < 80:

return row['wc'] >= 80 and row['wc'] <=88:

return row['wc'] * 3

else:

return row['wc'] * 4
  #normalize values from 0 to 1
  df_{val} = c_{df.values}
 min.max_scaler = preprocessing.MinMaxScaler()
df_val_scaled = min_max_scaler.fit_transform(df_val)
df_scaled = pd.DataFrame(df_val_scaled)
                                                                                                                            return row['wc'] * 4
  #get last row.
   df\_input = df\_scaled.iloc [[df\_scaled.shape[0]-1]] 
                                                                                                                           else:
if row['wc'] < 94:
return row['wc'] * 0
elif row['wc'] >= 94 and row['wc'] <=102:
return row['wc'] * 3
  #drop last row
  df_sc = df_scaled.drop(df_scaled.index[df_scaled.shape[0]-1])
   \begin{array}{ll} {\rm for \ i\,, row\ in\ df\_sc\,. iterrows\,():} \\ {\rm result} \ = \ {\rm cosine\_similarity\,(df\_sc\,.\,iloc\,[[\,i\,\,]],\,df\_input)}\ [0][0] \end{array} 
                                                                                                                             return row['wc'] * 4
                                                                                                                       def apply_FRA_BMI(row):

if isinstance(row['BMI'], str):
    row['BMI'] = (float(row['BMI']))

if row['BMI'] < 25:
    return row['BMI'] * 0

elif row['BMI'] >= 25 and row['BMI'] <= 30:
    return row['BMI'] * 1

else:
    return row['BMI'] * 2
    #print result
   aList.append([i, result])
  aList = sorted(aList,key=lambda l:l[1], reverse=True)
 z = aList[0:5]
return z
  # return [i [0] for i in z]
                                                                                                                           return row['BMI'] * 3
                                                                                                                       def apply_FRA_FBS(row):

if row['FBS'] >= 126:

return row['FBS'] * 5

return row['FBS'] * 0
def get_data(row_num):
  # data_list = pd.Series()
data_list = []
  for i in row_num:
    #.squeze to convert dataframe to a pandas Series
                                                                                                                       def get_bmi_label(res):
res = (float(res))
if res < 18.5:
return 'Underweight'
    data_list .append(df.iloc[[ i ]]. squeeze())
  return data list
                                                                                                                          elif res>=18.5 and res <=24.9: return 'Normal'
                                                                                                                          elif res>=25 and res <=29.9:
return 'Overweight'
#for dashboard purpses
def get_max_FBS_value():
                                                                                                                         else:
 return rec_df ['FBS'].max()/5
                                                                                                                           return "Obesed"
def get_max_HBA1C_value():
return rec_df ['HBA1C'].max()
                                                                                                                       # df = pd.read_csv('DS/RS_DS/final_dataset_3.csv')
df = pd.read_csv('DS/RS_DS/interpolated_data_withBMI.csv')
rec_df = df.drop(['person_id',' weight',' height',' encounter_id
',' birthdate',' CN','HN','DN','DIAG_DM','
DIAG_NONDM','TPN','gender'], axis=1)
def get_nonDM_count():
 non_dm = df.groupby(['DIAG_NONDM'])['DIAG_NONDM'].
count().sort_values(ascending=False)
  return \ non\_dm.drop(non\_dm.index[0]).head(3)
                                                                                                                       # apply FINISH RISK ASSESMENT POINTS AS WEIGHTS.
rec.df ['age'] = rec.df.apply(apply_FRA_age,axis = 1)
rec.df ['wc'] = rec.df.apply(apply_FRA_wc,axis = 1)
rec.df ['FBS'] = rec.df.apply(apply_FRA_FBS,axis = 1)
rec.df ['BMI'] = rec.df.apply(apply_FRA_BMI,axis = 1)
def get_max_fbs_value_column():
 row = df['FBS'].idxmax()
  return df. iloc [[row]]
                                                                                                                        # print get_max_fbs_value_column()
# df_val = rec_df.values
{\tt def \ get\_max\_hba1c\_value\_column():}
 row = df['HBA1C'].idxmax()
return df.iloc [[row]]
                                                                                                                        # min.max.scaler = preprocessing.MinMaxScaler()
# df_val_scaled = min_max_scaler.fit_transform(df_val)
# df_scaled = pd.DataFrame(df_val_scaled)
                                                                                                                        # g = cosine_similarity(df_scaled)
                                                                                                                       # print pd.DataFrame(g)
# print rec.df.columns.values
# np.savetxt("foo.csv", g, delimiter=",")
# print type(rec_df.iloc [[0]][' weight'])
#apply Finnish Risk Factor Assesment:
def apply_FRA_age(row):
if row['age'] > 45:
return row['age'] * 0
                                                                                                                           \label{eq:search_sex} \begin{split} \operatorname{search\_sex} &= \operatorname{SelectField}(\operatorname{'Sex'}, \operatorname{choices} = [(\operatorname{'1'}, \operatorname{'Female'}), \\ &(\operatorname{'2'}, \operatorname{'Male'}), \operatorname{('3'}, \operatorname{'BOTH'})]) \end{split}
          search_forms.py
                                                                                                                          search_dm_type = SelectField('DM Type', choices = [('1', 'Type 1 diabetes mellitus'), ('2', 'Type 2 diabetes mellitus'),

('3', 'Other specified diabetes mellitus'),('4',' Diabetes mellitus due to underlying condition'),('5',' Drug or chemical induced diabetes mellitus'),

('6',' ANY')])
from\ flask\_wtf\ import\ FlaskForm\ from\ wtforms\ import\ StringField,\ IntegerField,\ TextAreaField,
SubmitField, RadioField, SelectField, DecimalField from wtforms.fields.html5 import TelField
from\ wtforms.validators\ import\ Input Required,\ Length,\ Any Of
           ,NumberRange
class SearchForm(FlaskForm):
```

```
'61–70'), ('7', '71–80'), ('8', '81–90'),('9', '91–100'),('ANY', 'ANY')])
                                                                                                                             submit_search = SubmitField("SEARCH")
                                                                                                                                                                <img src="{{url-for('static', filename='
img/tech1.jpg')}}" alt="">
          _navbar.html
<div class="navbar-fixed">
                                                                                                                                                             </div>
                                                                                                                             <br>
        <div class="nav-wrapper blue darken-2">
                                                                                                                                                             <a href="#">
           <a href="#" data-activates="mobile-demo" class="
    button-collapse show-on-large"><i class="
    material-icons">menu</i></a>
<img style="padding-top: 7px; padding-right: 3px"
    src="{{url.for('static', filename='img/
        upm_OpH.icon.ico')}}" alt=""> <a href="/" id
        = "sp.name" class="brand-logo">CHITS</a>
                                                                                                                                                                <span class="name white-text">
                                                                                                                                                                          Diabetes Recommender System</
                                                                                                                                                             </a>
                                                                                                                                                             <a href="#">
<a href="#">
<span class="School white-text">UPM
                                                                                                                                                            - CHITS</span>
               = "sp_name" class="brand=logo">CH11S</a>

<a href="/">
<home</i>+HOME</a>
<a href="/recommender">
<a href="/recommender">
<a href="/recommender">
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                                                                                                                                                                             <br><br><br><
                                                                                                                                                        </div>
                                                                                                                                          <a class="subheader">NAVIGATION</a>
                           </a>
                                                                                                                                         > (li><a href="/"><i class="material-icons left"> home</i> HOME</a> <a href="/faq"><i class="material-icons left"> left"> local_hospital</i> <fra>fAQ</a> <a href="/recommender"> <i class="material-icons left"> local_hospital</i> <fra>fAQ</a> <a href="/recommender"> <i class="material-icons left"> local_pharmacy</i> TREATMENT
                 <a href="/search"> <i class="material-icons left">person_pin</i>SEARCH</a>
               <a href="/statistics"> <i class="material-icons left">insert_chart</i> STATISTICS</a></li
                                                                                                                                        icons left">local_pharmacy</i> TREATMENT </a> <a> <a href="/search"> <i class="material-icons left">person_pin</i> <SEARCH</a> <a href="/statistics"><i class="material-icons left">insert_chart</i> </i> <STATISTICS</a>
            </div>
                                                                                                                                          <div class="divider"></div>
<a class="subheader">LINKS</a>
</div>
                                                                                                                                                                cli><a href="https://telehealth.ph/
project-chits/">CHITS</a>
    >
                                                                                                                              <div class="user-view">
                                  <div class="background">
          dashboard.html
                                                                                                                                                                Consultations: \{\{value\}\} - \{\{i\}\} < /span
{\% \text{ extends 'dashboard\_layout.html' \%}}
                                                                                                                                             \{\% \text{ endfor } \%\}
{% block body %}
                                                                                                                                           </div>
                                                                                                                                         </div>
                                                                                                                          </div>
<div class="row">
  carrons class="row">
cdiv class="col s12 l12 m12 ">
cdiv class="card-panel blue darken-4 z-depth-4
animated bounceInLeft">
cspan class="light white-text">PATIENTS WITH
DIABETES CONSULTATIONS
                                                                                                                             <div class="divider"></div>
                                                                                                                                div class="divider"></div>
<div class="row">
<div class="col s12 16 m12">
<div class="col s12 16 m12">
<div class="card-panel red z-depth-4 center animated zoomInDown">
<span class="light white-text"> Highest Recorded
                </span>
         </div>
                                                                                                                                             </div>
                                                                                                                                                        dL < /h4 >
                                                                                                                                                   <a class="waves-effect waves-light btn modal-trigger" href="#modal_fbs">Click here to
  </div>
                                                                                                                                                              view profile</a>
<div class="divider"> </div>
                                                                                                                                        </div>
</div>
                                                                                                                                        <div id="modal_fbs" class="modal">
                                                                                                                                        canvas></div>
</div>
<div class="divider"> </div>
                                                                                                                                                 {% for index, row in highest_fbs_profile .iterrows
                                                                                                                                                            () %}
<div class="row">
<div class="col s12 l3 m12">
                                                                                                                                                     Weight: {{row['weight]}
                                                                                                                                                     ']}} kg 
Height: {{row['height
    <div class="card-panel z-depth-4"><canvas id="pie-
chart" height="220"></canvas></div>
                                                                                                                                                    </div>
       row['hc']}}class="white-text">Age: {{row['age']}}
                     animated zoomInDown">
                                                                                                                                                     p> Gender: {{row['gender
                     <h6 class="light white-text">Top 3 Non-DM
                                                                                                                                                                ']}}
                     Diagnosis [Out of {{dataset_count}} Consultations] </h6>
                                                                                                                                                     Hba1C Result: {{row['}
                                                                                                                                                     HBA1C']}}%
cp class="white-text">FBS Result: {{row[' FBS']}} mg/dL
                      <span class="white-text"> Number of
```

```
icd_E11">E011 < /a > 
                                                                                        class="tab"><a class="violet-text" href
="#icd_E13">E013</a>
           {% endfor %}
                                                                                 </div>
                                                                              </div>
        a >
                                                                                       chart_icd_Drug_Chemical_induced" width="800"
         </div>
                                                                                 chart-icd_Drug-chemical-induced with 800 height="300"></div>
<div id="icd_E10"><canvas id="doughnut-chart-icd_type1" width="800" height="300"></canvas></div>
<div id="icd_E11"><canvas id="doughnut-chart-icd_type2" width="800" height="300"></div>
<div id="icd_E11"><canvas id="doughnut-chart-icd_type2" width="800" height="300"></div>
      </div>
    <div class="col s12 l6 m12">
     div>
            Recorded HbalC result</ri>
<div class="divider"></div>

<hetalphase="divider"></div>

<hetalphase="divider"></fd>

<hetalphase="divider">

<hetalphase="divider">

                                                                                 <div id="icd_E13"><canvas id="doughnut-
chart_icd_otherDM" width="800" height
                                                                                        ="300"></div>
            }}%</h4>
<a class="waves-
                                                                               </div>
                  ff/o</nla/
ass="waves-effect waves-light btn modal-
trigger red" href="#modal_hba1c">Click
here to view profile</a>
                                                                            </div>
                                                                           </div>
          </div>
                                                                                 <div class="row">
                                                                            </div>
      <div id="modal_hba1c" class="modal">
<div class="modal-content teal">
           <h4 class="white-text">Patient Profile</h4><div class="row">
                                                                                       Diabetes Mellitus Diagnosis by Gender</h6>
                                                                              </div>
             {% for index, row in highest_hbalc_profile .
iterrows() %}
                Weight: {{row['weight]}
                ']}} kg 
Height: {{row['height
                ']}} cm
Waist Circumference:
                {{row['wc']}}
Hip Circumference: {{
                row['hc']}}Age: {{row['age']}}</
                p> class="white-text">Gender: {{row['gender]}
                                                                                 <div id="E08_gender" ><canvas id="bar-chart-
grouped_E08" width="800" height="350"></</pre>
                      ^{\prime }]\}\} 
                Hba1C Result: {{row['}
                HBA1C']}}%

class="white-text">FBS Result: {{row[']}}

                                                                               canvas></div>
<div id="E09_gender"><canvas id="bar-chart-
                                                                               <div id="E09_gender"><canvas id="bar-chart-
grouped_E09" width="800" height="250"></
canvas></div>
<div id="E10_gender"><canvas id="bar-chart-
grouped_E10" width="800" height="250"></
</pre>
                      FBS']\}\}\ mg/dL 
           \{\% \text{ endfor } \%\}
                                                                               canvas></div>
<div id="E11_gender" ><canvas id="bar-chart-grouped_E11" width="800" height="250"></
           </div>
         </div>
         <div class="modal-footer">
                                                                                     canvas></div>
           <a href="#!" class="modal-action modal-close
waves-effect waves-green btn-flat">Exit</
                                                                               <div id="E13.gender" ><canvas id="bar-chart-
grouped_E13" width="800" height="250"></
                                                                                     canvas></div>
         </div>
                                                                            </div>
  </div>
                                                                           </div>
</div>
 </div>
<div class="divider"> </div>
                                                                           </div>
 <div class="row";
="270"></canvas></div>
 </div>
 <div class="col s12 l12 m12">
                                                                          <div class="divider"> </div>
  <div class="card-panel"><canvas id="specific-dm-cases
-pie-chart" width="800" height="350"> </canvas</pre>
                                                                           ></{\rm div}>
 </div>
 <div class="col s12 m12 l12">
                                                                           </div>
  <div class="col s12 l12 m12">
                                                                             <div class="card-panel z-depth-4"><canvas id="
age_group_bar-chart-grouped" width="800" height
="200"></canvas></div>
             h6>
    </div>
    </div>
                                                                           </div>
        cli class="tab"><a class="green-text" href="#
  icd_E10">E010</a>
cli class="tab"><a class="orange-text" href="#</pre>
```

```
text: 'Number of Consultations per diagnosis [Total
                                                                                                      Consultations: ' + dm_specific_cases_total +']'
                                                                                           }
 <div class="divider"> </div><br>
                                                                                        }
                                                                                   });
<div class="row">
 FAMILY HISTORY OR PAST HISTORY
                                                                                           dm_cases_ave_age_values.push('{{value}}');
{% endfor %}
          </span>
          Some data for males
                                                                                       {\tt new\ Chart} ({\tt document.getElementById} ("{\tt dm\_cases\_bar-chart}
                 may not appear due to the small population. To
view data on males, click on the female label of
                                                                                           -horizontal"), {
type: 'horizontalBar',
                                                                                           data: {
    labels: dm_cases_ave_age_labels,
                   each graph 
       </div>
                                                                                              datasets: [
                                                                                                   label: "Average Age by Gender", background
Color: ["#e<br/>53935", "#1565c0"], 
</div>
<div class="divider"> </div>
                                                                                                   data: dm_cases_ave_age_values
                                                                                             ]
options: {
                                                                                              legend: { display: false },
                                                                                              title: {
                                                                                                display: true,
text: 'Average Age by Gender with DM
          canvas></div>
                                                                                                text: 'Average Age
Consultations'
 </div>
<div class="col s12 l6 m12">
  cdiv class="cond-panel z-depth-4"><canvas id="
    dm_history_gender_count_by_gender_ph_fh-bar-chart
    -grouped" width="800" height="300"></canvas
    ></div>
                                                                                      });
 </div>
                                                                                       /*year_months_graph*/
                                                                                        var year_months = [];
var data_year_months = []
   {% for i,value in dm_cases_year_month.iteritems() %}
 </div>
                                                                                           year_months.push('{{i}}');
data_year_months.push('{{value}}');
 <div class="row">
                                                                                          {% endfor %}
                                                                                         new\ Chart (document.get Element By Id ("year\_months\_graph") \\
                                                                                          "), {
type: 'line',
 data: {
                                                                                            labels: year_months,
                                                                                            datasets: [{
    data: data_year_months,
    label: "Consultations",
    borderColor: "#3e95cd".
          canvas></div>
 </div>
     </div>
     <div class="row">
                                                                                                  fill: false
    <div class="row">
    <div class="col s12 112 m12 ">
    <div class="col s12 112 m12 ">
    <div class="card-panel z-depth-4"><canvas id="
        dm.ph.fh.age.group.bar-chart-grouped" width
        ="800" height="200"></canvas></div>
                                                                                               },
                                                                                            ]
                                                                                          options: {
    </div>
                                                                                             title : {
                                                                                              display: true,
text: 'Number of Diabetes Consultations'
     </div>
\{\% \text{ endblock } \%\}
                                                                                       });
{% block script%}
                                                                                      /*cases_count*/
                                                                                      <script type="text/javascript">
 var dm_specific_cases =
 var dm_specific_values= [];
var dm_specific_cases_total = 0
     {\( \formalfont{\text{or} i in \ dm_cases_specific_count \( \formalfont{\text{w}} \)} \)
\( \dm_specific_cases \text{.push}('\{\{i [0]\}')'; \)
\( \dm_specific_values \text{.push}('\{\{i [1]\}\}'); \)
\( \dm_specific_cases_total = \dm_specific_cases_total + \delta \)
                                                                                          {% endfor %}
                                                                                         new\ Chart (document.getElementBy Id ("dm\_cases\_graph"),
       {{i[1]}};
{% endfor %}
                                                                                           {
type: 'horizontalBar',
                                                                                           data: {
    labels: dm_cases,
  {\tt dm\_specific\_cases\_total} \ = \ {\tt dm\_specific\_cases\_total} \ . \\ {\tt toString}
                                                                                              datasets: [
 {\tt new\ Chart} ({\tt document.getElementById} ("specific-dm-cases-
                                                                                                   label: "Number of cases"
        pie-chart"), {
                                                                                                   backgroundColor: ["#3e95cd", "#8e5ea2", "#3
cba9f", "#e8c3b9", "#c45850", "#3e95cd",
"#8e5ea2", "#3cba9f", "#e8c3b9", "#c45850
     type: 'pie',
     data: {
       labels: dm_specific_cases,
       \substack{,\\ \text{"\#3e95cd", "\#8e5ea2", "\#3cba9f", "\#e8c3b9", "\#c45850", "\#3e95cd", "\#8e5ea2", "\#3cba9f}
                                                                                                             "#e8c3b9","#c45850","#3e95cd"],
                                                                                                   data: dm_values
       }]
                                                                                             ]
     },
     options: {
                                                                                           options: {
   legend: { display: false },
        title: {
          display: true,
```

```
title : {
                                                                                                             text: 'Population by Gender with Family History or
               display: true,
text: 'Number of Consultations per Specific
                                                                                                                      Past History DM'
                                                                                                          }
                       Diagnosis'
                                                                                                 });
   });
      //gender_count
      var dm_cases_gender= [];
      var dm_values_gender = [];
                                                                                                      var dm_history_gender_count_by_gender_ph_fh_labels= [];
        {% for i.value in cases_gender.iteritems() %}
                                                                                                     var dm_history_gender_count_by_gender_past_history_values
              \begin{array}{l} dm\_cases\_gender.push(`\{\{i\}\}');\\ dm\_values\_gender.push(`\{\{value\}\}'); \end{array} 
                                                                                                          dm_history_gender_count_by_gender_family_history_values
                                                                                                              = \Pi;
        {% endfor %}
                                                                                                    \label{eq:count_by_gender_count_by_gender} \{\% \  \, \text{for i,value in} \quad \text{dm_history\_gender\_count\_by\_gender}.
      new\ Chart(document.getElementById("pie-chart"),\ \{
                                                                                                            \label{eq:count_by_gender_ph_fh_labels.push} $$ \dim_{i=1}^{n} (i_{i_{i}})^{n}; $$
          type: 'pie',
data: {
              labels: dm_cases_gender,
                                                                                                            if('\{\{i[1]\}\}' == '1')
             datasets: [{ label: "Gender",
                                                                                                            dm_history_gender_count_by_gender_past_history_values
_push('{{value}}');
                 backgroundColor: ["#f44336", "#3e95cd"],
                 data: dm_values_gender
             }]
                                                                                                             dm_history_gender_count_by_gender_family_history_values
                                                                                                                      .push('{{value}}');
           options: {
   title : {
                display: true,
text: 'Population by Gender with DM
                                                                                                      /*console.log('{{i [0]}}');
console.log('{{i [1]}}' == '1');
console.log('{{value}}');*/
{% endfor %}
          }
     });
                                                                                                     new Chart(document.getElementById("
var dm_cases_female= [];
var dm_cases_male = [];
                                                                                                             dm.history_gender_count_by_gender_ph_fh-bar-chart
-grouped"), {
                                                                                                           type: 'bar',
data: {
var dm_cases_age_group = [];
 \label{eq:constraint}  \{\% \ for \ a\_group, value \ in \ dm\_cases\_age\_grp.iterrows() \ \%\} \\  dm\_cases\_female.push(`\{\{\ value[`M']\ \}\}') \\  dm\_cases\_age\_group.push(`\{\{\ a\_group\ \}\}') \\  \{\% \ endfor \ \%\} 
                                                                                                              labels:
                                                                                                                       dm\_history\_gender\_count\_by\_gender\_ph\_fh\_labels
                                                                                                                        .slice (1, 3),
                                                                                                              datasets: [
                                                                                                                     label: "Past History"
                                                                                                                     background Color: "\#3e95cd",
  -grouped"), {
type: 'bar',
                                                                                                                             dm\_history\_gender\_count\_by\_gender\_past\_history\_values
        data: {
    labels: dm_cases_age_group,
                                                                                                                    label: "Family History",
backgroundColor: "#8e5ea2",
           datasets: [
                label: "Female",
backgroundColor: "#e53935",
data: dm_cases_female
                                                                                                                             dm_history_gender_count_by_gender_family_history_values
                label: "Male",
backgroundColor: "#0d47a1",
                                                                                                              ]
                                                                                                           },
                 data: dm_cases_male
                                                                                                     });
           ]
        options: {
   title : {
                                                                                                       var dm_ph_fh_cases_female= []
             display: true,
text: 'Age Group by Gender with DM Consultations
                                                                                                 var dm_ph_fh_cases_male = [];
var dm_ph_fh_cases_age_group = [];
                                                                                                 {% for a_group,value in dm_history_gender_age_grp.iterrows () %} dm_ph_fh_cases_female.push('{{ value['F'] }}') dm_ph_fh_cases_male.push('{{ value['M'] }}') dm_ph_fh_cases_age_group.push('{{ a_group }}')
  });
                                                                                                  {% endfor %}
  var dm_history_sex_labels= [];
var dm_history_sex_values = [];
{% for i,value in dm_history_gender.iteritems() %}
    dm_history_sex_labels.push('{{i}}');
    dm_history_sex_values.push('{{value}}');
                                                                                                     \begin{array}{c} {\rm new~Chart(document.getElementById("} \\ {\rm dm\_ph\_fh\_age\_group\_bar-chart-grouped"}),~\{ \end{array}
                                                                                                            type: , data: {
                                                                                                                     'bar',
                                                                                                              labels: dm_ph_fh_cases_age_group,
                                                                                                              datasets: [
     {% endfor %}
                                                                                                                  {
                                                                                                                     label: "Female",
backgroundColor: "#e53935",
data: dm_ph_fh_cases_female
    new Chart(document.getElementById("dm_ph_fh_gender"),
      type: 'pie',
data: {
                                                                                                                 }, {
    label: "Male",
    backgroundColor: "#0d47a1",
    data: dm_ph_fh_cases_male
         labels: dm_history_sex_labels,
         label: "Average Age",
backgroundColor: ["#8e5ea2", "#3cba9f"],
data: dm_history_sex_values
                                                                                                              ]
                                                                                                            }.
                                                                                                           options: {
   title : {
         }]
                                                                                                                 display: true,
text: 'Age Group by Gender with Family History
      options: {
          title: {
            display: true,
                                                                                                                          or Past History DM'
```

```
options: {
 });
                                                                                                                                                                                                                                                                     title: {
                                                                                                                                                                                                                                                                          display: true,
text: 'Type 1 diabetes mellitus'
                                                                                                                                                                                                                                                            }});
   var ICD10_underlying_cond_labels = [];
                         dm_history_ave_age_labels.push('{{i}}');
dm_history_ave_age_values.push('{{value}}');
                                                                                                                                                                                                                                                      var ICD10_underlying_cond_values = [];
           \{\% \ \mathrm{endfor} \ \%\}
                                                                                                                                                                                                                                                      {% for i,value in ICD10_underlying_cond.iteritems()
    new Chart(document.getElementById("bar-chart-horizontal"), {
    type: 'horizontalBar',
                                                                                                                                                                                                                                                                          %}
                                                                                                                                                                                                                                                                ICD10_underlying_cond_labels.push('{{i}}');
ICD10_underlying_cond_values.push('{{value}}');
                      labels: dm_history_ave_age_labels,
                                                                                                                                                                                                                                                      {% endfor %}
                       datasets: [
                                    label: "Population (millions)", backgroundColor: ["#e53935", "#3e95cd"], data: dm_history_ave_age_values
                                                                                                                                                                                                                                         \label{eq:chart_document.getElementById} \begin{picture}(t) the condition of the conditio
                                                                                                                                                                                                                                                          type: 'horizontalBar',
                     ]
                                                                                                                                                                                                                                                        data: {
    labels: ICD10_underlying_cond_labels,
              },
              options: {
    legend: { display: false },
    title: {
                                                                                                                                                                                                                                                                datasets: [
                                                                                                                                                                                                                                                                            label: "Number of Consultations",
backgroundColor: ["#3e95cd", "#8e5ea2","#3
cba9f","#e8c3b9","#c45850",
"#d81b60","#4a148c",
"#0d47a1","#006064",
"#f4d835","#ff6f00",
"#f4511e","#00e676",],
data: ICD10_underlying_cond_values
                            display: true,
text: 'Average Age by Gender with Family History
/Past History'
                     }
});
           var ICD10_type2_labels = [];
var ICD10_type2_values = [];
                                                                                                                                                                                                                                                              ]
                                                                                                                                                                                                                                                        options: {
            \begin{cases} \text{% for i,value in } ICD10\_type2.iteritems() \% \} \\ ICD10\_type2\_labels.push(`\{\{i\}\}'); \\ ICD10\_type2\_values.push(`\{\{value\}\}'); \end{cases} 
                                                                                                                                                                                                                                                                legend: { display: false },
title: {
                                                                                                                                                                                                                                                                      display: true,
text: 'Diabetes mellitus due to underlying
                                                                                                                                                                                                                                                                                           condition?
            {% endfor %}
    });
                                                                                                                                                                                                                                                     var ICD10_otherDM_labels = [];
var ICD10_otherDM_values = [];
                  data: {
                           labels: ICD10_type2_labels,
                         datasets: [
                                         \begin{array}{l} label\colon "Number\ of\ Consultations",\\ backgroundColor\colon ["\#3e95cd",\ "\#8e5ea2","\#3\\ cba9f","\#e8c3b9","\#c45850"], \end{array} 
                                                                                                                                                                                                                                                      \begin{cases} \text{% for i,value in } & ICD10\_otherDM.iteritems() \% \} \\ & ICD10\_otherDM\_labels.push(`\{\{i\}\}'); \\ & ICD10\_otherDM\_values.push(`\{\{value\}\}'); \end{cases} 
                                         data: ICD10_type2_values
                                }
                        ]
                                                                                                                                                                                                                                                      {% endfor %}
                   },
                  options: {
   title : {
                                                                                                                                                                                                                                              new Chart(document.getElementById("doughnut-
                                                                                                                                                                                                                                                            chart_icd_otherDM"), {
type: 'doughnut',
                                display: true,
text: 'Type 2 diabetes mellitus
                                                                                                                                                                                                                                                            data: { labels: ICD10_otherDM_labels,
                  }});
                                                                                                                                                                                                                                                                    datasets: [
                                                                                                                                                                                                                                                                          {
                                                                                                                                                                                                                                                                                 label: "Number of Consultations", background
Color: ["#3e95cd", "#8e5ea2", "#3 cba9f", "#e8c3b9", "#c45850"
            var ICD10_type1_labels = [];
           var ICD10_type1_values = [];
            \begin{cases} \% \ for \ i,value \ in \ ICD10\_type1.iteritems() \ \% \} \\ ICD10\_type1\_labels.push(`\{\{i\}\}'); \\ ICD10\_type1\_values.push(`\{\{value\}\}'); \end{cases} 
                                                                                                                                                                                                                                                                                  data: ICD10_otherDM_values
                                                                                                                                                                                                                                                                          }
                                                                                                                                                                                                                                                            options: {
   title : {
            {% endfor %}
                                                                                                                                                                                                                                                                          display: true,
text: 'Other specified diabetes mellitus'
            new Chart(document.getElementById("doughnut-
                                                                                                                                                                                                                                                            }});
                                chart_icd_type1"), {
                   type: 'doughnut',
                                                                                                                                                                                                                                                      var ICD10_Drug_Chemical_induced_labels = [];
                         labels: ICD10_type1_labels,
                                                                                                                                                                                                                                                      var ICD10_Drug_Chemical_induced_values = [];
                                       label: "Number of Consultations",
backgroundColor: ["#3e95cd", "#8e5ea2", "#3
cba9f", "#e8c3b9", "#c45850"],
data: ICD10_type1_values
                                                                                                                                                                                                                                                     \begin{cases} \% \ for \ i, value \ in \ ICD10\_Drug\_Chemical\_induced. \\ iteritems() \ \% \end{cases} \\ ICD10\_Drug\_Chemical\_induced\_labels.push(`\{\{i\}\}'); \\ ICD10\_Drug\_Chemical\_induced\_values.push(`\{\{value, value, 
                },
```

```
{% endfor %}
                                                                                                      {\tt new\ Chart} ({\tt document.getElementById} ("bar-chart-
                                                                                                        grouped_E09"), {
type: 'horizontalBar',
                                                                                                        data: {
    labels: E09_labels,
 new Chart(document.getElementById("doughnut-
     chart_icd_Drug_Chemical_induced"), {
   type: 'doughnut',
   data: {
                                                                                                           datasets: [
                                                                                                              {
                                                                                                                 label· "Male"
        labels: ICD10_Drug_Chemical_induced_labels,
                                                                                                                 backgroundColor: "#3e95cd",
        datasets: [
                                                                                                                 data: E09_M_values
                                                                                                              }, {
           {
              label: "Number of Consultations",
backgroundColor: ["#3e95cd", "#8e5ea2", "#3
cba9f", "#e8c3b9", "#c45850"],
data: ICD10_Drug_Chemical_induced_values
                                                                                                                 ,{
label: "Female",
backgroundColor: "#8e5ea2",
                                                                                                                 data: E09_F_values
                                                                                                              }
                                                                                                          ]
        ]
                                                                                                        options: {
   title : {
     },
     options: {
   title : {
                                                                                                              display: true,
text: 'Drug or chemical induced diabetes mellitus'
           display: true,
text: 'Drug or chemical induced diabetes mellitus'
                                                                                                           }
     }});
                                                                                                  });
                                                                                                  var E10_M_values =
/* unique array JS*/
function onlyUnique(value, index, self) {
                                                                                                   var E10_F_values =[]
var E10_labels =[]
        return self.indexOf(value) === index;
                                                                                                   {% for i,value in ICD10_type1_withgender.iteritems()
                                                                                                      \begin{array}{ll} E10\_labels.push('\{\{i\,[0]\}\}') \\ & \text{if}\,('\{\{i\,[1]\}\}' == "M")\{\\ & E10\_M\_values.push('\{\{value\}\}') \end{array} \\ \end{array} 
  var E08_M_values =[]
  var E08_F_values =[]
var E08_labels =[]
  {% for i, value in
            \begin{array}{ll} ICD10\_dm\_underlying\_cond\_with gender.iteritems() \\ \% \end{array} 
                                                                                                              E10_F_values.push('{{value}}')
     \begin{array}{l} {\rm E08\_labels.push('\{\{i\,[0]\}\}')} \\ {\rm if\,('\{\{i\,[1]\}\}'=="M")\{} \\ {\rm E08\_M\_values.push('\{\{value\}\}')} \end{array} 
                                                                                                     {% endfor %}
                                                                                                     E10_labels = E10_labels. filter ( onlyUnique );
             E08_F_values.push('\{\{value\}\}')
                                                                                                      {\tt new\ Chart}({\tt document.getElementById}("{\tt bar-chart-model}) \\
                                                                                                        grouped_E10"), {
type: 'horizontalBar',
    {% endfor %}
                                                                                                        data: {
    E08_labels = E08_labels. filter ( onlyUnique );
                                                                                                           labels: E10_labels,
                                                                                                           datasets: [
     {\tt new\ Chart} ({\tt document.getElementById} ("bar-chart-
                                                                                                              {
                                                                                                                 label: "Male"
       grouped_E08"), {
type: 'horizontalBar',
                                                                                                                 backgroundColor: "#3e95cd",
       data: {
                                                                                                                 data: E10_M_values
          labels: E08_labels ,
                                                                                                                 label: "Female",
         datasets: [
                                                                                                                 backgroundColor: "#8e5ea2",
data: E10_F_values
                label: "Male",
                backgroundColor: "#3e95cd",
data:E08_M_values
                                                                                                          ]
             }, {
   label: "Female"
                                                                                                        options: {
   title : {
               backgroundColor: "#8e5ea2",
data: E08_F_values
                                                                                                              display: true,
text: 'Type 1 diabetes mellitus'
         ]
     },
options: {
  title : {
    display: true,
    text: 'Diabetes mellitus due to underlying
        condition'
                                                                                                           scales: {
yAxes: [{
                                                                                                         scaleLabel:
                                                                                                           display: true
                                                                                                        xAxes: [{
                                                                                                                             ticks: {
                                                                                                                                min: 0.
 });
                                                                                                                                stepSize: 1,
                                                                                                                                max: 10
   \begin{array}{l} \mathrm{var} \ \mathrm{E09\_M\_values} = [] \\ \mathrm{var} \ \mathrm{E09\_F\_values} = [] \\ \mathrm{var} \ \mathrm{E09\_labels} = [] \end{array} 
                                                                                                               scaleLabel:
                                                                                                                 display: true
                                                                                                            },
}]
}
  {% for i, value in
           ICD10\_Drug\_chemical\_induced\_with gender.iteritems
           () %}
    E09_labels.push('{{i[0]}}')
if ('{{i[1]}}' == "M"){
E09_M_values.push('{{value}}')
                                                                                                 });
             E09_F_values.push('{{value}}')
                                                                                                     var \ E11\_M\_values = []
                                                                                                   var E11_F_values =[]
var E11_labels =[]
    {% endfor %}
                                                                                                    {% for i,value in ICD10_type2_withgender.iteritems()
                                                                                                    %}
E11_labels.push('{{i [0]}}')
if ('{{i [1]}}' == "M"){
    E09_labels = E09_labels. filter ( onlyUnique );
```

```
E11_M_values.push('{{value}}')
                                                                                  E13_labels = E13_labels. filter ( onlyUnique );
            }
else {
                                                                                  new Chart(document.getElementById("bar-chart-
grouped_E13"), {
  type: 'horizontalBar',
            E11_F_values.push('{{value}}')
                                                                                    data: {
                                                                                      labels: E13_labels,
      {% endfor %}
                                                                                      datasets: [
     {\rm E11\_labels} = {\rm E11\_labels}. \ {\rm filter} \ ( \ \ {\rm onlyUnique} \ );
                                                                                           label: "Male"
                                                                                           backgroundColor: "#3e95cd",
data: E13_M_values
       {\tt new\ Chart} ({\tt document.getElementById} ("bar-chart-
                                                                                        }, {
   label: "Female",
        grouped_E11"), {
type: 'horizontalBar',
                                                                                           backgroundColor: "#8e5ea2", data: E13_F_values
        data: {
          labels: E11_labels,
                                                                                        }
          datasets: [
                                                                                      ]
             {
               label: "Male",
                                                                                    },
                                                                                    options: {
   title: {
               backgroundColor: "#3e95cd",
               data: E11_M_values
                                                                                        display: true,
text: 'Other specified diabetes mellitus'
               ,  {
  label:  "Female",
               backgroundColor: "#8e5ea2",
data: E11_F_values
                                                                                           scales: \{
                                                                                     yAxes: [{
scaleLabel: {
          1
                                                                                      display: true
        options: {
   title : {
                                                                                    }
}],
            title: \(\)\ display: true, text: 'Type 2 diabetes mellitus'
                                                                                    xAxes: [{
                                                                                                     ticks: }
                                                                                                      min: 0,
                                                                                                      stepSize: 1,
max: 10
   });
                                                                                          scaleLabel: {
    var E13_M_values =[]
var E13_F_values =[]
var E13_labels =[]
                                                                                           display: true
                                                                                       },
}]
}
     \{\% \  \, \text{for i,value in } \  \, \text{ICD10\_otherDM\_withgender.iteritems()} \\ \% \} 
                                                                                   }
     E13_labels.push('{{i [0]}}')
if ('{{i [1]}}' == "M"){
                                                                               });
            E13_M_values.push('{{value}}')
            else {
             E13_F_values.push('{{value}}')
                                                                            </script>
      {% endfor %}
                                                                                {% endblock %}
      dashboard_layout.html
                                                                              }
                                                                             main, footer { padding-left: 300px;
<!DOCTYPE html>
<html>
<head>
                                                                                @media only screen and (max-width: 992px) {
                                                                                  header, main, footer {
   padding-left: 0;
    <meta http-equiv="Content-Type" content="text/html;</pre>
      charset=UTF-8"/>
<meta name="viewport" content="width=device-width
            , initial-scale=1, maximum-scale=1.0"/>
                                                                                  /* nav */
         link href="https://fonts.googleapis.com/icon?
family=Material+Icons" rel="stylesheet"> -->
                                                                            @media only screen and (min-width: 993px) {    .side-nav {
                                                                                top: 66px;
    k rel= "stylesheet" type= "text/css" href= "{{
    url_for('static', filename='css/materialize.css')
    }
                                                                                      </style>
                                                                             <title>CHITS Diabetes Recommender System</title>
</head>
                                                                            <body>
                                                                              <header>
                                                                                 <div class="navbar-fixed">
                                                                              <nav>
                                                                                 <div class="nav-wrapper blue darken-2">
          <style type="text/css">
              body {
    display: flex;
                                                                                   <a href="#" data-activates="mobile-demo" class="button-collapse"><i class="material-icons">
    min-height: 100vh;
    flex-direction: column;
                                                                                   main {
    flex: 1 0 auto;
```

}

```
nbsp CHITS</a>
                                                                                                                                                                         <div>Icons made by <a href="https://www.
flaticon.com/authors/wissawa-khamsriwath"
    itle="Wissawa Khamsriwath">Wissawa
Khamsriwath</a>
Khamsriwath
/a> from <a href="https://
www.flaticon.com/" title="Flaticon">www.
flaticon.com</a> is licensed by <a href="http://creativecommens.or/licenses/by.</pre>
         </div>
         </div>
     </nav>
                                                                                                                                                                                      http://creativecommons.org/licenses/by/3.0/" title="Creative Commons BY 3.0"
                                                                                                                                                                                       target="_blank">CC 3.0 BY</a></div>
</div>
                                                                                                                                                                           </div>
     </div>
                                                                                                                                                                     <div class="footer-copyright">
                          >
                                                                                                                                                                          <div class="container">
                                   <div class="user-view">
                                                                                                                                                                               2018 UPM.RJBC
                                        <div class="background blue darken-2">
                                                                                                                                                                      </div>
                                       ^{</\mathrm{div}>}_{<\mathrm{br}>}
                                                                                                                                                                 </footer>
                 \begin{array}{c} </{\rm div}> \\ </{\rm li}> --> \end{array}
                                                                                                                                               <script src="https://code.jquery.com/jquery-2.1.1.min.js</pre>
                                                                                                                                                               ></script>
                                                                                                                                                 <script type="text/javascript">
$(document).ready(function(){
    $('. slider '). slider ();
}
                  <li><a class="subheader">NAVIGATION</a><<li
                 $(document).ready(function(){
                                                                                                                                                           $ ('. parallax').parallax()
                                                                                                                                                       });
                $(document).ready(function() {
                                                                                                                                                  $('select').material_select();
});
                  left">person_pin</i>SEARCH</a><a href="/statistics"><i class="material-icons left">insert_chart</i>STATISTICS</a>
                                                                                                                                                            $(document).ready(function(){
                                                                                                                                                       $ ('. collapsible ') . collapsible ()
                               <div class="divider"></div>
  <a class="subheader">LINKS</a></
                                                                                                                                                   });
                                                                                                                                                       (document).ready(function() {
// the "href" attribute of the modal trigger must specify
                                                  li>

https://telehealth.ph/
project-chits/">CHITS</a>
                                                                                                                                                                      the modal ID that wants to be triggered
                                                                                                                                                       $ ('. modal').modal();
     </header>
   <!-- <div class ="container"> -->
                 <main>
                                                                                                                                                 </script>
     {% block body%}
                                                                                                                                                   <script src="https://cdnjs.cloudflare.com/ajax/libs/Chart.</pre>
  {% endblock %}
<!-- </div>
-->
                                                                                                                                                   js/2.7.1/Chart.min.js"></script>
<script defer src="https://use.fontawesome.com/releases/
v5.0.8/js/all.js" integrity="sha384-
 </main>
                                                                                                                                                                 SlE991lGASHoBfWbelyBPLsUlwY1GwNDJo3jSJO04KZ33K2bwfV9YBauFfnstreeter and the state of the state
   <footer class="page-footer blue darken-2">
                                                                                                                                                                    crossorigin="anonymous"></script>
                      <div class="container">
<div class="row">
                               div class="row">
<div class="col 16 s12">
<h5 class="white-text">SUPPORT</h5>

Please send an email to: <a class="grey-text">class="grey-text">class="grey-text">grey-text</a>
                                                                                                                                                   <script type="text/javascript" src="{{ url.for('static ',
      filename = 'js/graphs.js') }}"></script>
{% endblock %}
                                                -text text-lighten-4" href="mailto:
rbcabrera1@up.edu.ph">rbcabrera1@up
                                                                                                                                                   .edu.ph</a>
                               </div>
                                 <div class="col l4 offset -l2 s12">
                                                                                                                                                   <script type="text/javascript" src="{{ url.for('static ',
     filename = 'js/init.js') }}"></script>
                                    <h5 class="white-text">Links</h5>
                                    <a class="grey-text text-lighten-3"
                                                    href="https://telehealth.ph/project-chits/" target="_blank">CHITS</a>>
                                                                                                                                               </body>
                                                                                                                                               </html>
                                    </div>
                                                                                                                                                         <div class="col l4 m12 s12 hide-on-med-and-down
    animated slideInLeft"> <imp src="{{url.for('
        static', filename='img/business.png')}}" alt
    =""></div>
<div class="col l8 m10 s10">

        The system analyzes the patient's profiles and
            faq.html
{\% \text{ extends 'layout.html' }\%}
{% block body %}
 <div class="container">
                                                                                                                                                              The system analyzes the patient's profiles and attempts to find a patient similar to current
    <div class="section">
<h5 class="light">How does the system recommend?</
                                                                                                                                                                           patient. The system compares the patient's weight, height, waist circumeference, hip
                     h5>
              <div class="divider"></div>
                                                                                                                                                                            circumference, age, gender, HbA1c Result, and
                                                                                                                                                                            FBS result.
         <div class="row">
```

```
The data for the analysis was collected from CHITS (
                                                                                                            Community Health Information Tracking System ). The data extraction and analysis was done
             The algoritm used to find similar patients is called Cosine Similarity. <a href="http://mlwiki.org/index.php/Cosine_Similarity" target="_blank">Click here for more information on how the algorithm works</a>
                                                                                                             using Python and SQL.
                                                                                                   <a href="/statistics" class="waves-effect waves-light red btn">DATA ANALYSIS</a>
           <\!\!\mathrm{p} class="light animated fade
In"> Once the system finds similar patients, it provides
                                                                                                  </div>
                  the top 5 nearest patients and gives out patient profile information and treatment as \,
                                                                                                  <div class="col 14 m12 s12 hide-on-med-and-down
animated slideInRight"> <img src="{{url_for('
static', filename='img/analytics.png')}}" alt</pre>
                  recommendation.

<strong>WARNING:</strong> The recommendation
given by the system does not guarantee
                                                                                                          =""></div>
                                                                                                 </div>
                                                                                              </div>
                   improving the patient's condition. It is still recommended to consult a doctor for proper
                                                                                             <div class="section">
<h5 class="light">Multiple Platforms</h5>
<div class="divider"></div>
                   medication
                                                                                                   <br>>
        <a href="/recommender" class="waves-effect waves-
light btn">GET RECOMMENDATION</a>
                                                                                                  <div class="row">
  <div class="col 14 m12 s12 hide-on-med-and-down</pre>
                                                                                                 animated slideInLeft"><img id = "image-test"
src="{{url.for('static', filename='img/devices.png
')}}" alt=""></div>
<div class="col l8 m12 s12 animated fadeIn"> The
      </div>
   </div>
                                                                                                         system may be used in all types of platforms from mobile, tablets and desktop/laptop computers. </
                                                                                                </div>
                                                                                              </div>
   <div class="section">
<h5 class="light">DASHBOARD DATA</h5>
<div class="divider"></div>
                                                                                          </div>
       <div class= "row" >
<div class="row" >
<div class="col 18 m12 s12" >

                                                                                          {% endblock %}
       index html
                                                                                                      </div>
                                                                                                  <!--
{% extends 'layout.html' %}
                                                                                                     {% block body %}
<div class=" slider">
                                                                                                      </div>
     slides">
                                                                                                   <img style="filter: blur(5px);" class = "
    slider_bg" src="http://www.hiplink.com/
    images/easyblog_shared/Blog-Images/
    shutterstock_253752736.jpg" />
                                                                                                  </div>
                                                                                                  <!-- Icon Section -->
           <div class="caption center-align">
<h3>Diabetes Recommender System</h3>
                                                                                                   <div class="row container">
  <div class="col m4">
        </div>
                                                                                                    {\tt material-icons">local\_hospital</i></}
                  >
                    <h6 class="center" style="font-size:85%;">
                                                                                                                  Diabetes Recommender System</h6>
<div class="divider"></div>
           facebook.jpg" />
<div class="caption left-align">
<h3>Better Lifestyle</h3>
<h5 class="light grey-text text-lighten-3">for a

The system allows patients to improve their
                                                                                                                            lifestyle by recommending medical/non-medical treatments.<br/>br> <br/>br>
                   better tomorrow.</h5>
        </div>
                                                                                                                            Can be used as a decision support system by Health Professionals or as
           li>
<img style="filter: blur(5px)" class = "slider_bg"
src="{{url_for('static', filename='img/12.jpg')}}" />
<div class="caption left-align">
<h3>Be Active</h3>
<h5 class="light grey-text text-lighten-3">to be
physically fit.</h5>
</div
                                                                                                                            a guide to patients
                                                                                                                 </\mathrm{div}>
                                                                                             </div>
        </div>
                                                                                                         <div class="col m4">
                                                                                               ="material-icons">tag_faces</i></h2
                                                                                                                  <h6 class="center">Patient-Centered</h6
                                                                                                        <h5 class="light grey-text text-lighten-3">to
improve diet habits.</h5>
                                                                                                                         profile to recommend you the best
```

```
regimen that suits your needs. 
                                                                                                                                                                                                                                </div>
                                    </div>
                                                                                                                                                                                                                            </div>
                             </div>
                                                                                                                                                                                                                     </div>
                                                                                                                                                                                                                                     <div class="parallax">
                             <div class="col m4">
                    <img style="filter: grayscale(60%);" src="{{
    url_for('static', filename='img/Eating-
    Burger-Junk-Food.jpg')}}" />
                                   <h6 class="center">Research and Development
                                                                                                                                                                                                                       </div>
                                      /h6><div class="divider">/div>class="light">Researchers may view
trends in diabetes cases in the
                                                                                                                                                                                                               </div>
                                                                                                                                                                                                                   <div class="row">
                                                                                                                                                                                                           <div class="col s12 m12 l12">
                                              Philippines for further research and analysis. This may enable them to
                                                                                                                                                                                                                                <canvas id="line-chart" width="300" height
="80"></canvas>
                                                              develop proper healthcare managment plan to improve healthcare systems
                                                                                                                                                                                                          </div>
                             </div>
                                                                                                                                                                                                              </div>
                        </div>
 <br>
                                                                                                                                                                                                               <br> <br>>
           Philippinos ;
<br/>
                                                                                                                                                                                         {% endblock %}
                layout.html
                                                                                                                                                                                           <!-- < div class = "container" > -->
 <!DOCTYPE html>
                                                                                                                                                                                                             <main>
 <html>
                                                                                                                                                                                               {% block body%}
         {% endblock %}
                                                                                                                                                                                            <!-- </div>
                                                                                                                                                                                         </main>
                                                                                                                                                                                            url_tor('static', filename='css/materianze.css')
}}">
k rel= "stylesheet" type= "text/css" href= "{{
    url_for('static', filename='css/style.css')}}">
k rel= "stylesheet" type= "text/css" href= "{{
    url_for('static', filename='css/icon.css')}}">
k rel= "stylesheet" type= "text/css" href= "{{
    url_for('static', filename='css/icon.css')}}">

                                                                                                                                                                                                                          <div class="row">
<div class="col 16 s12">
                                                                                                                                                                                                                                     div class="col 16 s12">
<a href="https://doi.org/10.12">div.class="white-text">SUPPORT</a>/h5>
<a href="https://doi.org/10.12">div.class="grey-text text-lighten-4">grey-text text-lighten-4">grey-text text-lighten-4" href="mailto:rbcabrera1@up.edu.ph">rbcabrera1@up.edu.ph">rbcabrera1@up.edu.ph</a>//p>
                                            url_for('static', filename='css/animate.css')
</div>
                                                                                                                                                                                                                                    <div class="col l4 offset -l2 s12">
<h5 class="white-text">Links</h5>
                           <style type="text/css">
                     body {
display: flex;
                                                                                                                                                                                                                                            <a class="grey-text text-lighten-3"</li>
                                                                                                                                                                                                                                                            chits/" target="_blank">CHITS</a
                    min-height: 100vh;
flex-direction: column;
              }
                                                                                                                                                                                                                                       </div>
              main {
                    flex: 1 0 auto;
                                                                                                                                                                                                                        <!-- <div>Icons made by <a href="https://
                                                                                                                                                                                                                                       - <div>Icons made by <a href="https://www.flaticon.com/authors/wissawa-khamsriwath" title="Wissawa Khamsriwath">Wissawa Khamsriwath</a>> from <a href="https://www.flaticon.com/" title="Flaticon">www.flaticon.com/a> is licensed by <a href="http://creativecommons.org/licenses/by/3.0/" title="Creative Commons BY 3.0" target="_blank">CC 3.0 BY</a> <>/div>
                      \operatorname{span}\{
                            margin: 0em;
                                                                                                                                                                                                                                         ></div>
                     </style>
                                                                                                                                                                                                                          <div>Icons made by <a href="http://www.
freepik.com" title="Freepik">Freepik</a>
from <a href="https://www.flaticon.com/"
title="Flaticon">www.flaticon.com</a> is
licensed by <a href="http://
creativecommons.org/licenses/by/3.0/" title
="Creative Commons BY 3.0" target="
_blank">CC 3.0 BY</a></div>
    <title>CHITS Diabetes Recommender System</title>
 </head>
 <body>
    {% include '_navbar.html' %}
```

```
<div>Icons made by <a href="https://www.
                                                                                                       $progress.find(".amount").text();
                           Pixel perfect">Pixel perfect title="
Pixel perfect">Pixel perfect title="
Pixel perfect">Pixel perfect</a> from <a
href="https://www.flaticon.com/" title="
Flaticon">www.flaticon.com</a> is
                                                                                                       $progress.find (".amount").hide();
if (animate!== false) {
    $progress.animate({
                           licensed by <a href="http://creativecommons.org/licenses/by/3.0/" title="Creative Commons BY 3.0" target="blank">CC 3.0 BY</a></div>
                                                                                                             "height": percentageAmount + "%"
}, 1200, function () {
    $(this).find(".amount").fadeIn(200);
                                                                                                       });
} else {
  -->
                                                                                                             $progress.css({
    "height": percentageAmount + "%"
                  </div>
               </div>
               <div class="footer-copyright">
<div class="container">
        2018 UPM.RJBC
                                                                                                             $progress.find(".amount").fadeIn(200);
                                                                                                       }
                                                                                                 }
                  </div>
                                                                                                 $(document).ready(function () {
            </div>
                                                                                                       thermometer();
                                                                                                 });
 <script src="https://code.jquery.com/jquery-2.1.1.min.js</pre>
  "></script>
<script type="text/javascript">
$(document).ready(function(){
$('. slider '). slider ();
                                                                                                            });
      });
                                                                                                   </script>
   $(document).ready(function(){
    $('. parallax').parallax();
                                                                                                    <script src="https://cdnjs.cloudflare.com/ajax/libs/Chart.
    js/2.7.1/Chart.min.js"></script>
<script defer src="https://use.fontawesome.com/releases/
    v5.0.8/js/all.js" integrity="sha384-</pre>
      });
    $(document).ready(function() \{ \\ $('select').material\_select(); \\ \end{aligned} 
                                                                                                             SIE991IGASHoBfWbelyBPLsUlwY1GwNDJo3jSJO04KZ33K2bwfV9YBauFfn: "crossorigin="anonymous"></script>
                                                                                                     {% block script%}
      $(document).ready(function(){
$('. collapsible ') . collapsible ();
                                                                                                     });
      $(document).ready( function () {
$('#myTable').DataTable();
                                                                                                      });
                                                                                                    <script type="text/javascript" src="{{ url.for('static ',
    filename = 'js/layout.js') }}"></script>
<script type="text/javascript" src="{{ url.for('static ',
    filename = 'js/init.js') }}"></script>
<script type="text/javascript" src="{{ url.for('static ',
    filename = 'js/raphael-2.1.4.min.js') }}"></script</pre>
      "use strict";
      war $thermo = $("#thermometer"),

$progress = $(".progress", $thermo),

$goal = $(".goal", $thermo),
            percentage Amount;\\
                                                                                                        \begin{aligned} & goalAmount = goalAmount \mid \mid parseFloat(\$goal.text()), \\ & progressAmount = progressAmount \mid \mid parseFloat( \end{aligned}
      sprogress.text()),
percentageAmount = Math.min(Math.round(
progressAmount / goalAmount * 1000) / 10, 100);
//make sure we have 1 decimal point
                                                                                                  </body>
                                                                                                  </html>
      $goal.find(".amount").text();
        recommender.html
\{\% \text{ extends 'dashboard_layout.html' }\%\}
                                                                                                                    </div>
                                                                                                                          <div class="input-field col s12 m6 l6">
{% block body %}
                                                                                                                    {{ form.height }}
<label for="first_name">Height(cm)</label>
   <div class="row">
      <form class="col s12 m12 l7 animated slideInLeft"
                                                                                                                    \{\% \text{ for error in form.height.errors } \%\}
               method="POST" action="{{ url_for('recommender
                                                                                                                   <h6 style="color:red;">{{ error }}</h6>{% endfor %}
            ') }}" >
{{ form.csrf.token }}
<fieldset class="z-depth-5">
                                                                                                                 </div>
      <legend><div class="card-panel teal">
                                                                                                               </div>
            <span class="white-text">Patient Information</
span>
</div></legend>
                                                                                                                 <div class="row">
<div class="input-field col s12 m6 l6">
                                                                                                                    {{ form.wc}}
<label for="first_name">Waist Circumference(cm
             <div class="row">
                                                                                                                            )</label>
                                                                                                                   \mbox{\ensuremath{\%}} for error in form.wc.errors \mbox{\ensuremath{\%}} <h6> style="color:red;">{{ error }}</h6> {\mathcal{%}} endfor \mbox{\ensuremath{\%}}
                   <div class="input-field col s12 m6 l6">
                  {{ form.weight }}
<label for="first_name">Weight(kg)</label>
                                                                                                                </div>
                  <div class="input-field col s12 m6 l6">
                                                                                                                    {{ form.hc }}
                  \{\% \text{ endfor } \%\}
```

```
<label for="first_name">Hip Circumference(cm)
                                                                                                                                                                              </button>
                                              </label>
                                                                                                                                                                            </div>
                                                                                                                                                                                    </fieldset>
                            {% for error in form.hc.errors %}
                            </form>
                                                                                                                                                                                    <br>>
                                                                                                                                                                                                 </div>
                     </div>
                                                                                                                                                                                                    <div class="row">
                                                                                                                                                                                                     </span>
                  <div class="input-field col s12 m6 l6">
                       {{ form.age }}
<label for="first_name">Age</label>
                                                                                                                                                                                                       {% endfor %}
                                                                                                                                                                                                          <
                                                                                                                                                                                                              | 1> 
| div class="collapsible-header"><i class="fas fa-weight"></i>&nbsp Weight</div> 
| div class="collapsible-body">| light">The more fatty tissue you have, the more resistant your cells become to
                            </div>
                                  <div style="padding: 20px;">
<label style="font-size: 120%;">Sex:</label
                                                                                                                                                                                                                   the more resistant your cents become insulin.
<a href="https://www.mayoclinic.org/diseases-conditions/diabetes/symptoms-causes/syc-20371444">Source</a
                                                   \{\% \text{ for subfield in form.sex } \%\}
                                                        {{td>{{ subfield (class_="with-gap")}
                                                      }
{td>{{ subfield.label }}
                                                                                                                                                                                                                                    ></div>
                                                                                                                                                                                                          \{\% \text{ endfor } \%\}
                                                                                                                                                                                                               <div class="collapsible-header"><i class="fas</pre>
                                                                                                                                                                                                              cliv class="collapsiole-neader"><1 class="fa-plus"></i>>&nbsp Height</div></div class="collapsible-body">Obese people are more likely to develop type 2 diabetes. Extra weight
                                             \begin{array}{l} \{\% \ {\rm for \ error \ in \ form.sex.errors \ \%} \\ < h6 \ {\rm style="color:red;">} \{\{ \ {\rm error \ }\} \} < / h6 \end{array} 
                                                                                                                                                                                                                              sometimes causes insulin resistance and is
common to people with type 2 DM. BMI
                                            {% endfor %}
                                                                                                                                                                                                                              is used to see if you are at risk of type 2 diabetes. It is computed as BMI = kg/m <sup>2</sup>  <a href="https://www.niddk.nih.gov/health-information/">https://www.niddk.nih.gov/health-information/</a>
                                     </div>
                                                                                                                                                                                                                              diabetes/overview/symptoms-causes">
Source</a></div>
                    </div>
                                                                                                                                                                                                         <div class="divider"></div>
                                                                                                                                                                                                              li>
<div class="collapsible-header"><i class="fas fa-heartbeat"></i>/i>&nbsp Waist and Hip Circumference</div>
<div class="collapsible-body">The waist-to-hip ratio (WHR) is a quick measure of fat distribution that may help indicate a person's overall health. People who carry more weight around their middle than their hips may be at a higher risk of developing certain health conditions. According to the
                                                                                                                                                                                                          >
                       <div class="row">
                             <div class="col s12 m12 l4"> <h5 class="grey-
text">Lab Results</h5> </div>
              <div class="col s12 m12 l8">
                  </span>
                  </div>
                                                                                                                                                                                                                                 health conditions. According to the
World Health Organization (WHO),
              </div>
       </div>
                                                                                                                                                                                                                                world Health Organization (WHO), having a WHR of over 1.0 may increase the risk of developing conditions that relate to being overweight, including heart disease and type 2 diabetes. 
><a href="https://www.medicalnewstoday.com/articles/319439.html">https://www.medicalnewstoday.com/articles/319439.html
                       <div class="row">
<div class="input-field col s12 m12 l6">
                            {{ form.hba1c}}
<label class="active" for="first_name">HBA1C
                                             (\%)</label>
                                                                                                                                                                                                                                 php">Source</a></div>
                                                                                                                                                                                                           \label{eq:condition} $$ \{\%$ for error in form.hbalc.errors $\%$ <h6 style="color:red;">${\{ error }}</h6> <{\% endfor $\%} 
                                                                                                                                                                                                            <
                                                                                                                                                                                                               <div class="collapsible-header"><i class="fas
fa-sort-numeric-up"></i>&nbsp Age
                                                                                                                                                                                                                   </div>
<div class="collapsible-body"><p class="
                                                                                                                                                                                                                                   light">Your risk increases as you get older. This may be because you tend to
                       </div>
                                                                                                                                                                                                                                   exercise less, lose muscle mass and gain weight as you age 
<a href="https://www.mayoclinic.org/diseases-conditions/diabetes/symptoms-causes/">https://www.mayoclinic.org/diseases-conditions/diabetes/symptoms-causes/</a>
                             <div class="input-field col s12 m12 l6">
                            {{ form.fbs }}
<label class="active" for="first_name">Fasting
                                             Blood Sugar(mg/dL) </label>
                                                                                                                                                                                                                                    syc-20371444">Source</a></div>
                                                                                                                                                                                                          {% for error in form.fbs.errors %}
                                        <h6 style="color:red;">{{ error }}</h6>
                                                                                                                                                                                                              <div class="collapsible-header"><i class="fas
fa-male"></i>&nbsp <i class="fas fa-
female"></i>&nbsp Gender</div>
<div class="collapsible-body">Sex-related differences in
lifettyla may lead to differences."
                            {% endfor %}
                             </div>
                     </div>
                                                                                                                                                                                                                                   light">Sex—related differences in the risk of developing diabetes mellitus 
<a href="http://www.who.int/bulletin/volumes/91/9/12-113415/en/">Source</a></div>
<div class="right">
      <br/>
<
```

```
>
                                                                                                                                          after an overnight fast. A fasting blood
                      <div class="collapsible-header"><i class="fas
fa-sort-numeric-up"></i> &nbsp
                                                                                                                                          sugar level less than 100 mg/dL (5.6 mmol/L) is normal. A fasting blood
                         HBA1C</div>
<div class="collapsible-body">This blood test indicates your average blood sugar level for the past
                                                                                                                                          sugar level from 100 to 125 mg/dL (5.6 to 6.9 mmol/L) is considered prediabetes. If it's 126 mg/dL (7 mmol/L) or higher on two separate tests, you
                                   two to three months. It measures the percentage of blood sugar attached to
                                                                                                                                          have diabetes. <a href="https://www.mayoclinic.org/diseases-"
                                   hemoglobin, the oxygen—carrying protein in red blood cells. The higher
                                                                                                                                          conditions/diabetes/diagnosis-
treatment/drc-20371451">Source</a
                                  your blood sugar levels, the more
hemoglobin you'll have with sugar
attached. An A1C level of 6.5 percent
or higher on two separate tests
                                                                                                                                           ></div>
                                                                                                                           indicates that you have diabetes. An A1C between 5.7 and 6.4 percent indicates prediabetes. Below 5.7 is
                                                                                                                       indicates prediabetes. Below 5.7 is considered normal.mellitus <a href="https://www.mayoclinic.org/diseases-conditions/diabetes/diagnosis-treatment/drc-20371451">Source</a>
                                                                                                                       </div>
                   </div>
                                                                                                                 </div>
  <li>
                                                                                                           </div>
                      <div class="collapsible-header"><i class="fas
                                 fa-sort-numeric-up"></i> & nbsp
                          FBS</div>
<div class="collapsible-body">light">A blood sample will be taken
                                                                                                       {% endblock %}
                                                                                                             \begin{array}{c} {\rm darken-2">BMI</div>} \\ <{\rm div~class="collapsible-body"><div~style="height: 130px"~id="g1"></div>} \\ <{\rm script~type="text/javascript">} \end{array}
        result.html
{% extends 'layout.html' %}
                                                                                                                 window.onload = function () {
{% block body %}
                                                                                                                       var g1 = new JustGage({
   id: "g1",
   value: {{bmi}},
   min: 0,
   <div class="row">
         v class="row">
<div class="col s12 m12 l12">
<div class="card-panel blue darken-2 z-depth-4
animated slideInRight">
<span class="white-text"> HERE ARE THE
RESULTS OF THE ANALYSIS
                                                                                                                             max: 30,
                                                                                                                             title: "{{bmi_res}}", relativeGaugeSize: true
                </span>
                                                                                                                      });
                                                                                                              }
</script> </div>
             </div>
          </div>
                                                                                                              <div class="col s12 l9 m12">

cul class="collapsible">

                                                                                                             </div>
      <div class="collapsible-header active blue darken-2"
                                                                                                           </div>
                   white-text"><i class="material-icons">info</i>>Patient Data</div>
         <div class="collapsible-body">
<div class="row">
<div class="row">
<div class="row">
<div class="col s12 l3 m12">
<span>Weight:{{form.weight.data}} kg</span>
                                                                                                              <div class="row">
                                                                                                               <div class="row">
<div class="col s12 l12 m12">

{% for t in list_treatments %}
                   br> <span>Height:{{form.height.data}} cm</span
                            ><br>
              </div>
                                                                                                                       <div class="collapsible-header active blue darken
               <div class="col s12 l4 m12">
                                                                                                                                -2 white-text">
<i class="material-icons">add_circle</i>
              <span>Waist Circumference:{{form.wc.data}} cm
                       span><br>
                <span>Hip Circumference:{{form.hc.data}} cm</
span><br/>cbr>
                                                                                                                                          Recommendation \{\{\text{loop.index}0+1\}\}
              </div>
                                                                                                                                   </div>
                                                                                                                       <div class="collapsible-body">
              <div class="col s12 l2 m12">
                <h6>Patient Information:</h6>
<div class="divider"></div>
<div class="divider"></div>
<div class="row">
<div class="row">
<div class="col s12 l3 m3">
<span>Weight: {{t['weight']}} kg</span
              </div>
                       <div class="col s12 l3 m12">
                      <\!\operatorname{span}\!>\!\operatorname{HBA1C}\!:\!\{\{\operatorname{form.hba1c.data}\}\}\%\!<\!/\operatorname{span}
                               ><br>
                      <span>FBS:{{form.fbs.data}} mg/dL</span</pre>
                                                                                                                                       <br>
                               ><br>
                                                                                                                                         <span>Height: {{t['height']}} cm
                    </div>
                                                                                                                                    span></div>
             </div>
      </div>
                                                                                                                                    <div class="col s12 l3 m3">
<span>Waist Circumference: {{t['wc
      ']}} cm</span>
                                                                                                                                              <br>>
                                                                                                                                   <span>Hip Circumference: {{t['hc']}} cm
             <br/> <div class="col s12 l3 \, m12"> <<br/> <ul class="collapsible" data-collapsible="
                                                                                                                                            span>
                           accordion">
                                                                                                                                    </div>
          <div class="collapsible-header active white-text blue">–text blue
```

```
<div class="col s12 l3 m3">
                                          \begin{array}{l} <\!\!\operatorname{span}\!\!>\!\!\operatorname{Age:}\; \{\{\operatorname{t}['\operatorname{age'}]\}\} <\!\!/\operatorname{span}\!\!> \\ <\!\!\operatorname{br}\!\!> \end{array}
                                                                                                                                                                                            </div>
                                   <span>Gender: \{\{t['gender']\}\}</span>
                                                                                                                                                                                                      <div class="row">
                                                                                                                                                                                                <h6>Treatment Result:</h6>
<br/>
<br/>
<br/>
div class="divider"></div>
<br/>
<br/>
<br/>
<br/>
class="col s12 112 m12">
<span><br/>
<br/>
TPN']}}</span>
<br/>
<br/>
<br/>
<br/>
<br/>
(div)
                                          </div>
                                          <div class="col s12 l3 m3">
<span>HBA1C: {{t['HBA1C']}}}%</span>
                                            <span>FBS: {{t['FBS']}} mg/dL</span>
                                                                                                                                                                                                 </div>
                                     </div>
                                 <div>
                                     <h6>Similarity Score: {{res[loop.index0]
                                                                                                                                                                                            </div>
                                                  ][1]}}%</h6>
                                 </div>
                                      <br>
                                                                                                                                                                                            <a href="https://www.diabetes.ca/diabetes-
and-you/healthy-living-resources/
diet-nutrition/basic-meal-planning"
target="_blank" class="waves-effect
waves-light red btn">Diet and
                                     <div class="row">
                                          Exercises Management Plan</a>
                                               <span><b>Complain Notes</b>: {{t['}
                                                                                                                                                                               </div>
                                                      | CN']}}
| CN']}
| CN']
| CN']}
| CN']
| CN
                                                                                                                                                                          {% endfor %}
                                                               <span><b>Diabetes Diagnosis</br>
b>: {{t['DIAG_DM']}}
span> <br/>
<span><b>NON-DM Diagnosis
                                                                                                                                                                   √/div>
                                                                                                                                                                </div>
                                                                             </b>: {{t['DIAG_NONDM
']}}</span> <br>>
                                          </div>
                                                                                                                                                       {% endblock %}
            search.html
                                                                                                                                                                     </form>
{% extends 'layout.html' %}
                                                                                                                                                                               <div class="col s12 m9 l9">
{% block body %}
                                                                                                                                                                       <div class="row">
                     <form class="col s12 m3 l3 animated slideInLeft"
    method="POST" action="{{ url_for('search')}</pre>
                                                                                                                                                                                 <thead>
                                                                                                                                                                                     <tr>
                   }}" >
{{ s_form.csrf_token }}
                                                                                                                                                                                             <fieldset class="z-depth-5">
          <legend><h5 class="grey-text">SEARCH</h5></
                       legend>
                                                                                                                                                                                                 \begin{array}{l} <\!\!\operatorname{th}>\!\!\operatorname{Age}<\!\!/\operatorname{th}> \\ <\!\!\operatorname{th}>\!\!\operatorname{Sex}<\!\!/\operatorname{th}> \end{array}
                   <div class="row">
                          DM DiagnosisNON - DM Diagnosis
                          </div>
                                                                                                                                                                                      </thead>
                          {% if search_df is defined%}
                                                                                                                                                                                   {% for i, value in search_df.iterrows() %}
                          <div class="input-field col s12 m12 l12">
{{ s.form.search_sex}}
<label>SEX</label>
                                                                                                                                                                                     \langle tr \rangle
                                                                                                                                                                                        {{value['
                                                                                                                                                                                       </div>
                                 <div class="input-field col s12 m12 l12">
                                                                                                                                                                                       <div class="right">
              </div>
                                                                                                                                                                                        >{{value|'gender']}}

{{value|'DIAG_DM']}}

{{value|'DIAG_NONDM']}}

       </div>
       </fieldset>
```

```
\{\% endfor \%\}
                                                                                                                                                                </div>
                         {% endif %}

                  </div>
                  </div>
                                                                                                                                                           {% endblock %}
                                                                                                                                                          ( SELECT concept_id,encounter_id,person_id,value_text FROM obs
              dataset_extract.sql
                                                                                                                                                          FROM obs
WHERE concept_id = 44 AND (
value_text LIKE '%metformin%' OR
value_text LIKE '%insulin%' OR
value_text LIKE '%Glibenclamide%' OR
value_text LIKE '%glipizide%' OR
value_text LIKE '%glipizide*' OR
value_text LIKE '%glibenclamide%' OR
value_text LIKE '%glibenclamide%' OR
value_text LIKE '%glimepiridee%' OR
value_text LIKE '%glimepiridee%' OR
value_text LIKE '%acarbose%'
)
  //GET DATASET FOR RECOMMENDER SYSTEM
 SELECT obs.person_id, obs.concept_id, obs.encounter_id,obs.
               value_numeric , person.gender,person.birthdate, obs.value_text,obs.date_created
 FROM obs
OR ( value_text LIKE '%diabetes%' AND concept_id = 84) ) sub
                                                                                                                                                         ) sub
ON obs.person_id = sub.person_id AND obs.encounter_id =
    sub.encounter_id
INNER JOIN person ON person.person_id = obs.person_id
WHERE obs.concept_id = 21 OR obs.concept_id = 23 OR obs.
    concept_id = 26 OR obs.concept_id = 27
OR obs.concept_id = 44 OR obs.concept_id = 43 OR obs.
    concept_id = 84 OR obs.concept_id = 40
OR obs.concept_id = 41 ORDER BY obs.person_id
 OR (value_text LIKE '%diabetes%' AND concept_id = 84)
 ) sub
ON obs.person_id = sub.person_id AND obs.encounter_id =
 sub.encounter_id
INNER JOIN person ON person_id = obs.person_id
WHERE JOHN person ON person are besoned a consept-id and where obs.concept_id = 21 OR obs.concept_id = 23 OR obs. concept_id = 26 OR obs.concept_id = 27
OR obs.concept_id = 44 OR obs.concept_id = 43 OR obs. concept_id = 84 OR obs.concept_id = 40
OR obs.concept_id = 41 ORDER BY obs.person_id
                                                                                                                                                           //GET UNIQUE IDS with PAST HISTORY OR FAMILY
                                                                                                                                                          HISTORY
SELECT DISTINCT obs.person_id,obs.concept_id,person.
                                                                                                                                                                         {\tt gender, person. birthdate, obs. concept\_id, obs. value\_coded,}
                                                                                                                                                                         obs.voided
                                                                                                                                                          obs.voided
FROM obs
INNER JOIN person ON obs.person.id = person.person.id
WHERE concept.id = 465 AND (value_coded = 1 OR
value_coded = 2) AND obs.voided = 0 ORDER BY obs
        matching
 SELECT DISTINCT obs.person_id, obs.encounter_id,person.
                                                                                                                                                                         .person_id
              birthdate,person.gender
FROM obs
INNER JOIN
                                                                                                                                                                              if row_dist_id ['gender'] == 'M':
    n_df.set_value(index_dist_id,'isMale',1)
    n_df.set_value(index_dist_id,'isFemale',0)
              Dataset_Generator.pv
  # coding: utf-8
                                                                                                                                                                                      n_df.set_value(index_dist_id ,'isMale',0)
n_df.set_value(index_dist_id ,'isFemale',1)
  # # IMPORT PANDAS AND ENTER HC Name
                                                                                                                                                                                     index_data, row_data in data.iterrows():

if row_dist_id ['person_id'] == row_data['
    person_id'] and row_dist_id ['encounter_id']
    == row_data['encounter_id']:

if row_data['concept_id'] == 21:
    n_df.set_value(index_dist_id,'weight',
        row_data['value_text'])

elif row_data['concept_id'] == 23:
    n_df.set_value(index_dist_id,'height',
        row_data['value_text'])

elif row_data['concept_id'] == 26:
    n_df.set_value(index_dist_id,'we',
        row_data['value_text'])

elif row_data['concept_id'] == 27:
    n_df.set_value(index_dist_id,'he',
        row_data['value_text'])

elif row_data['concept_id'] == 40:
    n_df.set_value(index_dist_id,'CN',
        row_data['value_text'])

elif row_data['concept_id'] == 41:
    n_df.set_value(index_dist_id,'HN',
        row_data['value_text'])

elif row_data['concept_id'] == 43:
    n_df.set_value(index_dist_id,'DN',
        row_data['value_text'])

elif row_data['concept_id'] == 44:
    n_df.set_value(index_dist_id,'TN',
    row_data['value_text'])

elif row_data['concept_id'] == 44:
    n_df.set_value(index_dist_id,'TN',
    row_data['value_text'])

elif row_data['concept_id'] == 84:
    if "diabetes" in row_data['value_text'].

lower():
    n_df.set_value(index_dist_id,'
 # In[1]:
                                                                                                                                                                              for index_data, row_data in data.iterrows():
 import pandas as pd
 # In[2]:
 def create_dataset( file ):
           # # LOAD CSV TO DATAFRAME
 # In[3]:
          dist_id = pd.read_csv(file+"/"+file+"_dist_pid_eid.csv")
data = pd.read_csv(file+"/"+file+"_raw_ds.csv")
          \# # CREATE DATASET
          # In[4]:
          columns = ['person.id','encounter.id','weight', 'height
','wc','hc','isMale','isFemale','birthdate','age','
CN','HN','DN','DIAG_DM','DIAG_NONDM','TPN']
n_df = pd.DataFrame(columns=columns)
          for index_dist_id, row_dist_id in dist_id.iterrows():
    #print index_dist_id, row_dist_id ['person_id'],
    row_dist_id ['encounter_id']
    n_df.set_value(index_dist_id, 'person_id', row_dist_id')
                                                                                                                                                                                                                   lower():
n_df.set_value(index_dist_id,
                                                                                                                                                                                                                                 DIAG_DM',row_data['value_text
                    ['person_id'])
n_df. set_value(index_dist_id ,'encounter_id',
                                                                                                                                                                                                          else ·
                                                                                                                                                                                                                  n_df.set_value(index_dist_id ,'
DIAG_NONDM',row_data['
                    row_dist_id ['encounter_id'])
n_df.set_value(index_dist_id ,'birthdate', row_dist_id
                                                                                                                                                                                                                                  value_text'])
                                   ['birthdate'])
```

```
n\_df \ ['birthdate'] \ = pd.to\_datetime (n\_df \ ['birthdate'],
                                                                                                 errors='coerce')
n_df['birthdate']. dt.strftime('%m/%d/%Y')
                                                                                                 # In[8]:
                                                                                                 \begin{array}{ll} n\_df\left['\,age'\right] &= pd.to\_datetime(n\_df['birthdate'])\\ now &= dt.date.today()\\ n\_df\left['\,age'\right] &= ((now-n\_df['birthdate'])/365).dt.days \end{array}
     # In[5]:
                                                                                                 # In[9]:
     n_df
                                                                                                 n_df
     # In[6]:
                                                                                                 # In[10]:
     n_df ['weight']. fillna (0, inplace=True)
n_df ['height']. fillna (0, inplace=True)
n_df ['wc']. fillna (0, inplace=True)
n_df ['hc']. fillna (0, inplace=True)
                                                                                                 {\tt n\_df.to\_csv(\ file +"/"+file+"\_dataset.csv",index=False)}
                                                                                            file = "g"
                                                                                            while file != 'exit':
file = raw_input("ENTER FILE:")
     # In[7]:
     import datetime as dt
       Dataset_Concat.pv
                                                                                           path =r'A_DATASET' # use your path
allFiles = glob.glob(path + "/*.csv")
frame = pd.DataFrame()
# coding: utf-8
                                                                                           | list_ = [] | for file_ in allFiles: | df = pd.read_csv(file_,index_col=None, header=0) | list_ .append(df) | frame = pd.concat(list_)
\# # The glob module finds all the path
names matching a specified pattern according to the rules used by the Unix shell,
# In[1]:
                                                                                            # # Save DF as CSV #
import pandas as pd
import glob
                                                                                            # In[6]:
\# # append all df to a list. concat list to create single DF
                                                                                            #index = False to avoid index column in csv file
                                                                                            frame.to_csv(" final_dataset .csv".index=False)
       init.js
                                                                                              $(document).ready(function() \{ \\ $('select').material\_select(); \\ 
(function($){
                                                                                              });
  $(function(){
     $('.button-collapse').sideNav();
                                                                                            $(document).ready(function(){
    $('ul.tabs').tabs();
});
   }); // end of document ready
})(jQuery); // end of jQuery name space
       style.css
                                                                                            h3,h5,h6 {
/* Custom Stylesheet */
                                                                                              text-transform: uppercase;
                                                                                               font-weight: 900;
 * Use this file to override Materialize files so you can
         update
 \ast the core Materialize files in the future
                                                                                              @media (max-width: 400px) {
                                                                                                 font-size: 22px;
 * Made By MaterializeCSS.com
                                                                                              @media (min-width: 1200px) {
font-size: 75px;
.icon-block {
   padding: 0 15px;
.icon-block .material-icons {
font-size: inherit;
                                                                                            i.icon-grey {
                                                                                                 color: grey;
#sp_name{
                                                                                           span{
 text-transform: uppercase;
                                                                                              font-weight: light
  margin: 0 0 1rem;
                                                                                            /*@media only screen and (min-width: 1200px) {
  tbody {
  display:block;
  height: 500px;
   @media (max-width: 400px) {
     font-size: 22px;
  @media (min-width: 1200px) {
font-size: 75px;
                                                                                               overflow: auto:
                                                                                              thead, thody tr {
                                                                                              display:table;
```

```
width:100%;
table—layout:fixed;
}
thead {
width: calc( 100% - 1em )
}
table {
width:100%;
}

graphs.js

try{
new Chart(document.getElementById("line-chart"), {
type: 'line',
data: {
labels: [2015,2016,2040],
datasets: [{
    data: [3.5,6,12],
    label: "Philippines",
    borderColor: "#3e95cd",
    fill: false
}

}*/
for table

*/

*/
options: {
    title: {
    display: true,
    text: 'Diabetes Cases (in millions)'
    }
}

catch(err) {
    console.log("Error")
}
```

XI. Acknowledgement

I would like to thank God first for everything. Without you, none of these would be possible. I thank you for helping me achieve my goals all these years.

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