

MCIT 590 Final Project, TEAM 27

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Summary

Our project finds clinically similar patients from a given set of patient population. It calculates the similarity between the *index* patient and all other *n* patients.

The program reads in the data from a CSV file and creates a list of clinical encounters. Using the list of clinical encounters, the software builds a clinical utilization for each patient profile (`HashMap`). The unique patient identifier (`patient_number`) is the key and the patient's clinical profile is stored as value. The patient level clinical profile is created by averaging a patient's inpatient visits, outpatient visits, procedures, medications, lab procedures, and emergency visits. These patient clinical utilization profiles are used to compute *similarity* between patients. We used two methods to calculate the similarity between patient's profile, *Euclidean distance* and *Cosine distance*.

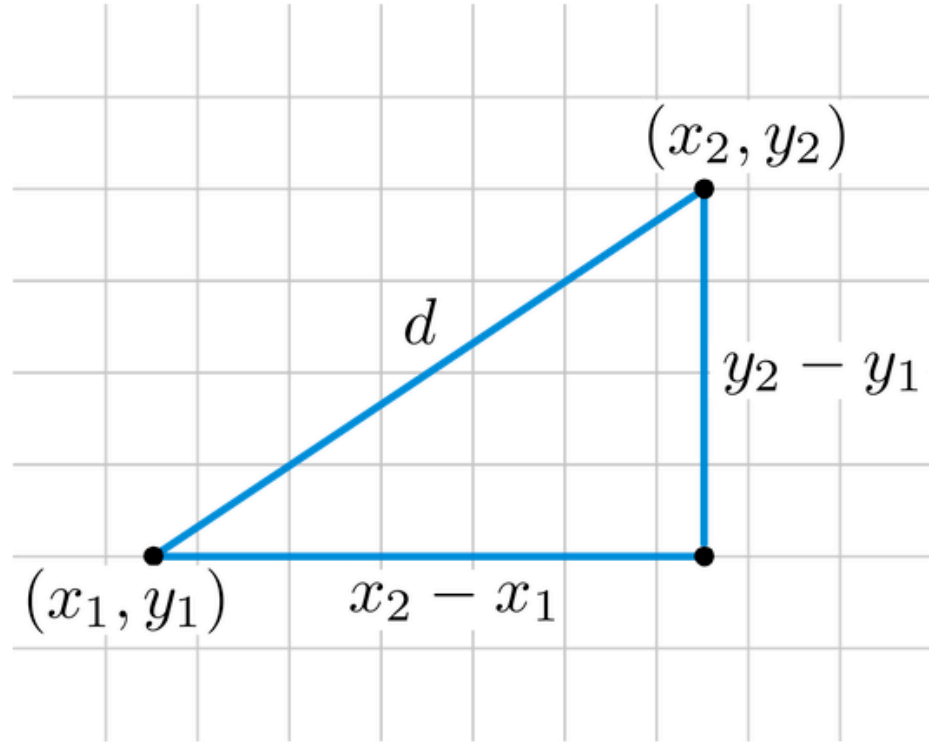
The clinical profile is a vector of patient level measures. We compare the *index* patient's clinical profile with all other patients' clinical profiles to calculate similarity metric and return list of patient's which are within user provided threshold of similarity from *index* patient. The distance measure value ranges from 0 (*most similar*) to 1 (*least similar*)

Distance measures

Euclidean distance

Euclidean distance is the distance between two points and is calculated using the Pythagorean Theorem

$$\sqrt{(x_2 - x_1)^2 + (y_2 - y_1)^2}.$$



(Rosalind 2020).

For the k -dimensional data this formula is generalized to following form

Given, $p_1 = \{p_{1i}, p_{1j}, \dots, p_{1k}\}$ and $p_2 = \{p_{2i}, p_{2j}, \dots, p_{2k}\}$ euclidean distance $d(p_1, p_2)$ is

$$d(p_1, p_2) = \sqrt{\sum_{i=1}^k (p_{1i} - p_{2i})^2}$$

We used scaled version of *euclidean distance* for our software, to force the range of values between 0 and 1 for easy interpretability.

we calculated a maximum possible squared discrepancy for each variable. If m are the number of patients in the given sample, we calculated maximum squared discrepancy for variable i is given by

$$md_i = (\max(p_{1i}, p_{2i}, p_{3i}, \dots, p_{mi}) - \min(p_{1i}, p_{2i}, p_{3i}, \dots, p_{mi}))^2$$

then *scaled euclidean distance* is calculated as,

$$d_s(p_1, p_2) = \sqrt{\sum_{i=1}^k \left(\frac{(p_{1i} - p_{2i})^2}{md_i} \right)}$$

Cosine distance

The Cosine similarity is a measure of similarity in inner product space of two non-zero vectors, which measures cosine of angle between two vectors.

Given, $p_1 = \{p_{1i}, p_{1j}, \dots, p_{1k}\}$ and $p_2 = \{p_{2i}, p_{2j}, \dots, p_{2k}\}$, the *cosine* similarity is calculated as,

$$\cos(\theta) = \frac{\sum_{i=1}^k p_{1i} p_{2i}}{\sqrt{\sum_{i=1}^k p_{1i}^2} \sqrt{\sum_{i=1}^k p_{2i}^2}}$$

cosine distance is calculated as $1 - \cos(\theta)$

Project Flow

The user runs the MainFrame.java file and the window below is displayed.

Clustering Patients Finder

Patient_ID	Race	Gender	Age	Num_Procedures	Num_Medications	Num_LabTests	Num_Outpatient	Num_Inpatient	Num_ER_Visits
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Import Data

Index Patient: (Patient ID)

Method for Distance Calculation

☒ Euclidean

☐ Cosine

Patient Distance Threshold (0 - 1):

Submit

Total Number of Patients: 0

The "Import Data button" allows the user to select the "diabetic_data.csv" provided patient data. The `MainFrame` then executes the `DataReader` class to read data into `ClinicalEncounters` class. Then methods in `PatientProcessor` class are executed to build `HashMap` of `Patient` class. Data from the `Patient` class is displayed in the window as below.

Clustering Patients Finder

Patient_ID	Race	Gender	Age	Num_Procedures	Num_Medications	Num_LabTests	Num_Outpatient	Num_Inpatient	Num_ER_Visits
23593320	AfricanAmerican	Male	(70-80)	1.0	8.5	34.5	0.0	0.0	0.0
87950655	Caucasian	Female	(80-90)	0.0	11.0	71.0	4.0	0.0	0.0
176163458	Caucasian	Female	(50-60)	0.0	19.0	5.0	0.0	0.0	1.0
98436573	Caucasian	Female	(80-90)	0.0	17.0	47.0	0.0	0.0	0.0
85853466	Caucasian	Female	(50-60)	0.0	16.0	38.0	0.0	1.0	0.0
43385490	Caucasian	Female	(70-80)	2.5	9.5	27.0	0.0	0.0	0.0
49545981	Caucasian	Female	(40-50)	1.0	28.0	59.0	0.0	0.0	0.0
95684031	Caucasian	Female	(50-60)	4.0	6.0	33.0	0.0	0.0	0.0
46400202	AfricanAmerican	Male	(60-70)	2.0	19.0	46.0	0.0	0.0	0.0
33686028	Caucasian	Male	(70-80)	0.0	18.5	50.0	0.0	0.5	0.0
62915535	Caucasian	Female	(30-40)	2.0	20.0	62.0	0.0	1.0	0.0
85460247	Caucasian	Male	(50-60)	1.0	17.0	65.5	0.5	0.0	0.0
2621502	Caucasian	Female	(50-60)	3.0	19.5	41.5	0.0	0.5	0.0
98829810	Caucasian	Female	(40-50)	0.0	3.0	57.0	0.0	1.0	1.0
104597028	Caucasian	Female	(40-50)	2.0	21.0	44.0	0.0	0.0	0.0
16095849	Caucasian	Male	(20-30)	0.0	8.0	3.0	0.0	0.0	0.0
61735860	Hispanic	Female	(70-80)	0.0	12.0	46.5	4.0	0.0	0.0
86246712	Caucasian	Male	(60-70)	0.0	18.0	24.0	0.0	0.5	0.0
30671307	Caucasian	Female	(50-60)	0.0	17.5	70.5	0.0	0.5	0.5
108529245	Caucasian	Male	(70-80)	3.0	9.0	60.0	0.0	4.5	0.0
186649349	Caucasian	Male	(50-60)	1.0	19.0	1.0	2.0	0.0	0.0
2752524	Caucasian	Male	(70-80)	1.0	7.0	3.0	4.0	0.0	1.5

Import Data

Index Patient: (Patient ID)

Method for Distance Calculation

☒ Euclidean

☐ Cosine

Patient Distance Threshold (0 - 1):

Submit

Total Number of Patients: 71518

Once the data is imported the user can view and select an index patient for comparison against all other patients.

Clustering Patients Finder

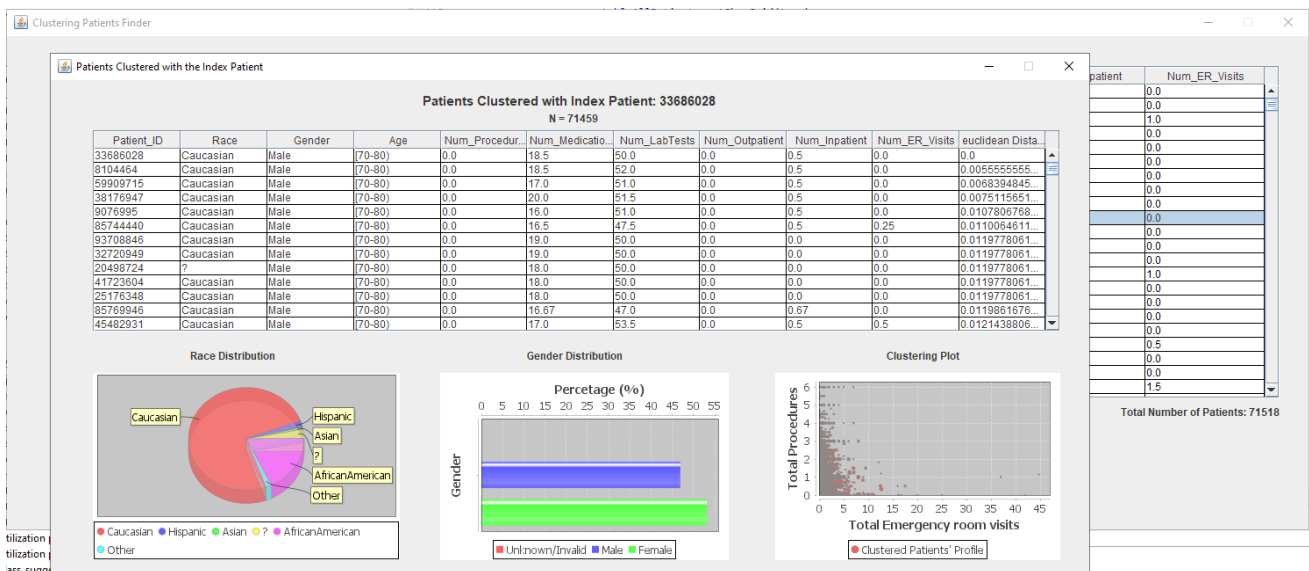
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2752524	Caucasian	Male	(70-80)	1.0	7.0	3.0	4.0	0.0	1.5

Total Number of Patients: 71518

Import Data Index Patient: (Patient ID) 23593320 Method for Distance Calculation: ☒ Euclidean ☐ Cosine Patient Distance Threshold (0 - 1):

Submit

Once the user has selected the index patient, the user can either copy and paste or type in the patient ID into the Index Patient box. Additionally the user can choose Euclidean or Cosine distance calculations. Finally the user must enter a threshold value of 0 - 1 and then click submit. The MainFrame then executes PatientProcessor and Patient classes to develop profile HashMap. Finally the methods in `DataAnalysis`, `ClusteringFrame`, `Plots`, `DataDisplay`, `mapValueComparator` are called to calculate similarity values and display those values into three JCharts seen below.



The window then displays Race Distribution of patients, Gender distribution, and the Clustering plot.

Project Setup and Component Installation:

Step 1:

Follow video installing Window Builder SWING:

<https://www.youtube.com/watch?v=K7R68JFd024>

Alternative:

- (1) Browse to: <https://www.eclipse.org/windowbuilder/>
- (2) Drag install icon in an open Eclipse window.
- (3) If installation does not start automatically the Eclipse Marketplace Window will open:
- (4) In search box type "Window Builder"
- (5) Follow instructions for installation:

Eclipse Marketplace

Eclipse Marketplace

Select solutions to install. Press Install Now to proceed with installation. Press the "more info" link to learn more about a solution.

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WindowBuilder




WindowBuilder 1.9.3

*** NEW VERSION 1.9.3 *** WindowBuilder is composed of SWT Designer and Swing Designer and makes it very easy to create Java GUI applications without spending a... [more info](#)

by [Eclipse Foundation](#), EPL

[SWT](#) [swing](#) [wysiwyg](#) [graphical](#) [WindowBuilder](#) ...


★ 531



Installs: **363K** (13,248 last month)

Installed

WindowBuilder




WindowBuilder Nightly Build 1.9.4.pre

Nightly Build! Install if you want to use the latest patches before a release is available. It can be unstable. WindowBuilder is composed of SWT Designer and... [more info](#)

by [Eclipse Foundation](#), EPL


[SWT](#) [swing](#) [wysiwyg](#) [graphical](#) [WindowBuilder](#) ...

★ 4



Installs: **3.01K** (1,044 last month)

Installed




Spark Builder Generator 0.0.21

Generates a builder according to the GoF pattern for Java domain objects. Features Generates a builder with custom name patterns Can generate staged builder ... [more info](#)

by [Unknown](#), MIT

[Builder Pattern](#) [builder](#) [code generator](#) [SparkTools](#) [design pattern](#) ...

★ 54





Installs: **11.8K** (372 last month)


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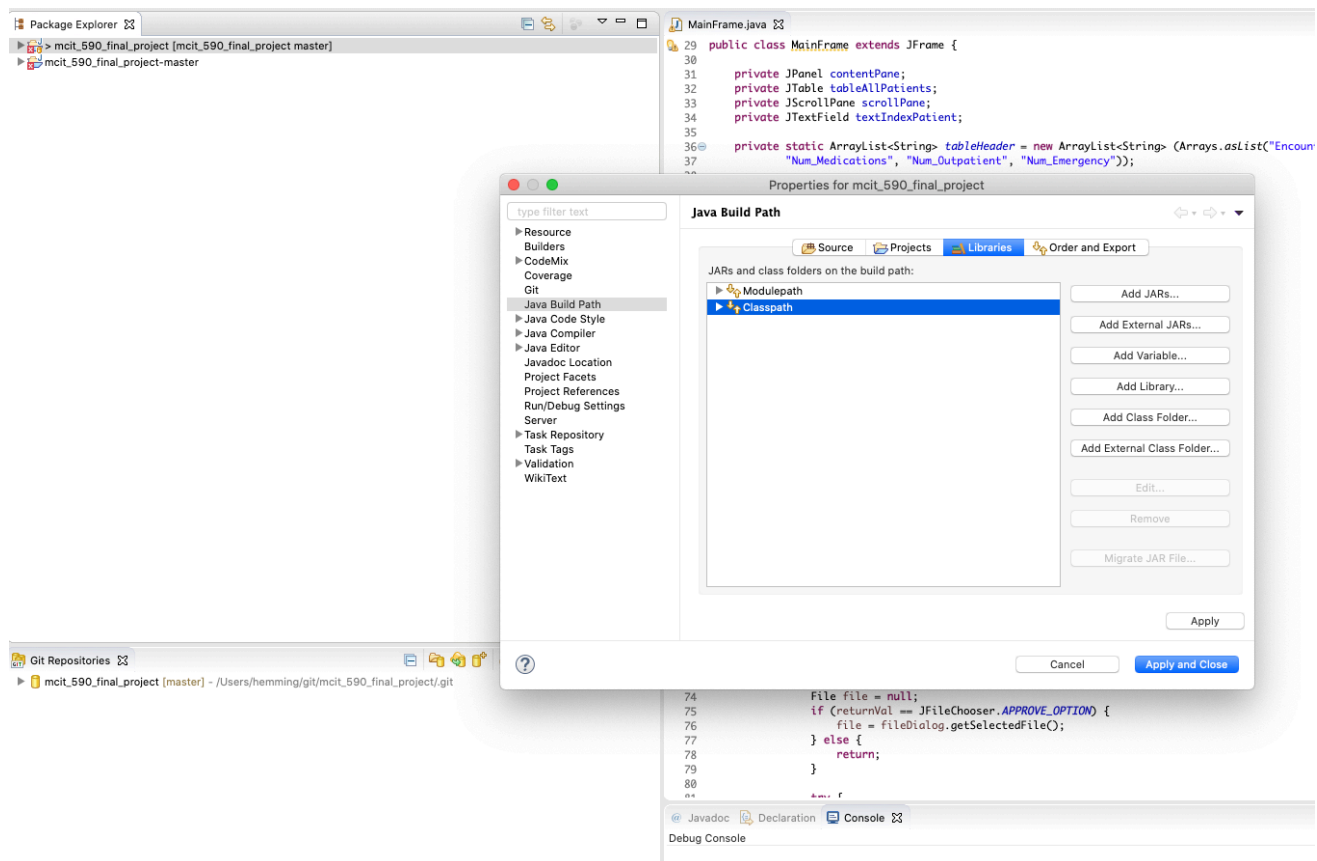
Cancel

Finish

Step 2:

J Common and J Chart Installation

- (1) Navigate to [jfreechart-1.0.19-install.pdf](#)
- (2) Follow instructions on page 31, A3 for Eclipse installation.
- (3) Jcommon-1.0.23.zip and jfreechar-1.0.19.zip included for installation.
- (4) Once you add J Chart and J Common to your eclipse libraries, you may need to add the Library path into your project. See instructions below.



- (1) Right Click project, Select properties
- (2) Navigate to build path
- (3) Select Libraries
- (4) Add Library from Eclipse Libraries, this was completed during Jchart and JCommon installation.

References:

Hu, J., Wang, F., Sun, J., Sorrentino, R., & Ebadollahi, S. (2012). A healthcare utilization analysis framework for hot spotting and contextual anomaly detection. *AMIA ... Annual Symposium proceedings. AMIA Symposium, 2012*, 360–369.

Rosalind 2020. <http://rosalind.info/glossary/euclidean-distance/>

Machine Learning Plus 2020. <https://www.machinelearningplus.com/nlp/cosine-similarity/>

Chris Emmery 2020. <https://cmry.github.io/notes/euclidean-v-cosine>