Applied machine learning for temporomandibular disorders diagnosis

MANUEL MALDONADO - APRIL 2019

Applied machine learning for temporomandibular disorders diagnosis 1

I. Definitions

Project overview

Temporomandibular disorders (TMD) are are a set of conditions that affect the joints and muscles involved in chewing and connecting the lower jaw with the skull. They are a significant public health problem affecting approximately 5% to 10% of the population and is the second musculoskeletal condition after chronic lower back pain (1) leading to chronic pain and limitation in patients. Pain-related TMD can impact the individual's daily activities, psychosocial functioning, and quality of life.

Since 2014, there is a clinical protocol and assessment instruments for the diagnosis of these diseases. The diagnosis is achieved by palpation and **response to several questionnaires that assess the level of pain and the alteration of masticatory function** and associated headaches. These forms were the result of the consensus of a group of experts in the subject from several universities (2).

Some of the drawbacks for the diagnosis based on these questionnaires are:

- The questionnaires are not filled in systematically and strictly
- The extension of these questionnaires. Depending on how the questions are formulated, they can generate up to 400 different answers.
- There is also no common repository where these data are recorded and the sensitivity and specificity of the criteria can be assessed.
- Accuracy in the assessment of pain. Patients chronic pain is associated with psychological alterations that can make the answers not completely objective or measurable.

Problem statement

In 2017, Dr. Berena Uparela released the TMJQuest website, aimed at specialists in the field, dental clinics and institutions interested in the subject. The goal was to digitize the collection of responses to diagnostic questionnaires and provide a common database for researching. Doctors can systematically record the questions answered by their patients and the diagnosis. So, there is available a set of labeled data by physicians.

It is intended to use this data to:

- To offer doctors a preliminary diagnosis using a prediction model. Doctors can obtain a pre-diagnosis as they record their patients' data.
- To identify those questions of the questionnaires that are not relevant for the diagnosis so that the data collection can be made in a more agile way.

- To establish a relationship between the answers to identify those patients whose set of answers do not relate to any of the identified conditions or who present compatible symptoms with more than one.

Metrics

Solution to the described problem is made up of two clearly different parts:

- Application of unsupervised learning to obtain an overview of the data, adaptation of the forms to the diagnosis and to identify outliers. To have a benchmark model for this section is complicated without validation by qualified personnel. The results of this paper will be presented by Dr. Berena Uparela to the scientific committee at the Spanish Society of Craniomandibular Dysfunction and Orofacial Pain (SEDCYDO https://sedcydo.com/) for analysis and validation.
- Design of a predictive model for classification using neural networks. The typical accuracy of a diagnosis for this type of diseases made by a specialist is about 98% (3) so the goal of the suggested prediction should be at least this value. In this situation, the main handicap could be the available data amount (about 600 records) and whether it is possible to reach this accuracy. So, to evaluate the performance of the different classification models to be tested until reaching the best one, it is proposed to use the accuracy indicator.

II. Analysis

Data exploration

This proposal aims to use the data collected from approximately 680 patients. They have been previously filtered to preserve patients privacy. This number increases as the platform that collects them is used so it is possible to improve the generated prediction model with new data in a continuous way.

The available records has been collected through a web form and stored in a relational database. Specifically, the following datasets are available:

- Set of questionnaire questions (parameters.xlsx). This file contains literals of the approximately 400 questions that patients must answer. For the scope of the project these questions have been codified since the original values are not relevant. Also, it makes easier to deal with the file since entries are long text strings and, for the moment, they are only available in Spanish.
- File containing the answers to the previous questions of approximately 680 patients (tmd_data.csv), as well as the diagnosis made by the doctor who has collected the data (label). This file's been generated exporting to CSV format records stored in relational database tables.

First step of the data exploration process was to clearly identify number of features, records and labels as well as to classify different parameters based on data type they store and the range of values that dataset contains for each one. Some of the most relevant indicators are in In [2], In [5] and In [8] cells of notebook.

- Patients dataset has **681 samples with 401 features each.**
- Parameters ['Q74', 'Q76', 'Q78', 'Q80', 'Q82', 'Q84', 'Q86', 'Q88', 'Q90', 'Q92','Q94', 'Q96', 'Q100', 'Q101', 'Q102'] **have no value at all**, so they've been deleted from the dataset.
- Parameters ['Q74', 'Q76', 'Q78', 'Q80', 'Q82', 'Q84', 'Q86', 'Q88', 'Q90', 'Q92', 'Q94', 'Q96', 'Q100', 'Q101', 'Q102', 'Q131', 'Q133', 'Q135', 'Q137', 'Q152', 'Q154', 'Q156', 'Q158', 'Q176', 'Q178', 'Q180', 'Q182', 'Q197', 'Q199', 'Q201', 'Q203', 'Q210', 'Q212', 'Q218', 'Q220', 'Q222', 'Q224', 'Q349', 'Q350', 'Q352', 'Q353', 'Q355', 'Q356', 'Q358', 'Q359', 'Q362', 'Q365', 'Q368', 'Q371'] **have only one different value** so have been used to test if, by removing them from the dataset, results changed.
- Parameters ['Q10', 'Q19', 'Q49', 'Q50', 'Q51', 'Q103', 'Q104', 'Q105', 'Q106', 'Q107', 'Q108', 'Q114', 'Q115', 'Q116', 'Q160', 'Q161', 'Q162'] contain a range of int type values that have been regularized using log transform (In [12])
- All other parameters contain **boolean data type**
- Label dataset contains 11 different values. One hot encoding has been apply in order to build a prediction model with deep learning. (In [26])
- **Outliers** detection was implemented and **6 records** were deleted from dataset, as they were present as outliers in more than one feature (In [13])

Exploratory visualization

- **Original dataset**

	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	...	Q392	Q393	Q394	Q395	Q396	Q397	Q398	Q399	Q400	Label
0	1	1	0	1	0	1	1	0	1	2	...	0	0	1	0	1	0	1	0	0	Cefaleas/TMD
1	1	0	1	1	1	1	1	1	1	6	...	1	0	1	0	1	0	1	0	0	DM. Referido
2	0	0	0	0	0	0	0	1	0	3	...	1	1	1	1	0	1	0	0	0	DDSRSLA
3	0	0	0	1	0	0	0	0	1	4	...	1	0	1	0	1	1	1	0	0	DDCRCBI
4	1	0	0	0	1	1	0	0	0	5	...	1	0	0	1	1	1	0	0	1	DDSRCLA
5	0	0	0	0	0	0	0	0	0	2	...	1	1	0	0	0	1	1	0	0	DDCR
6	1	1	1	1	1	1	1	1	1	3	...	0	0	0	1	1	1	0	0	0	Mialgia
7	1	0	1	1	1	1	1	1	1	2	...	1	0	0	1	1	1	0	0	1	Mialgia Local
8	0	0	0	0	0	0	0	0	1	7	...	1	0	1	1	0	0	1	1	0	DDCR
9	1	0	1	1	1	1	1	1	1	3	...	0	0	0	0	1	0	1	0	1	Artralgia

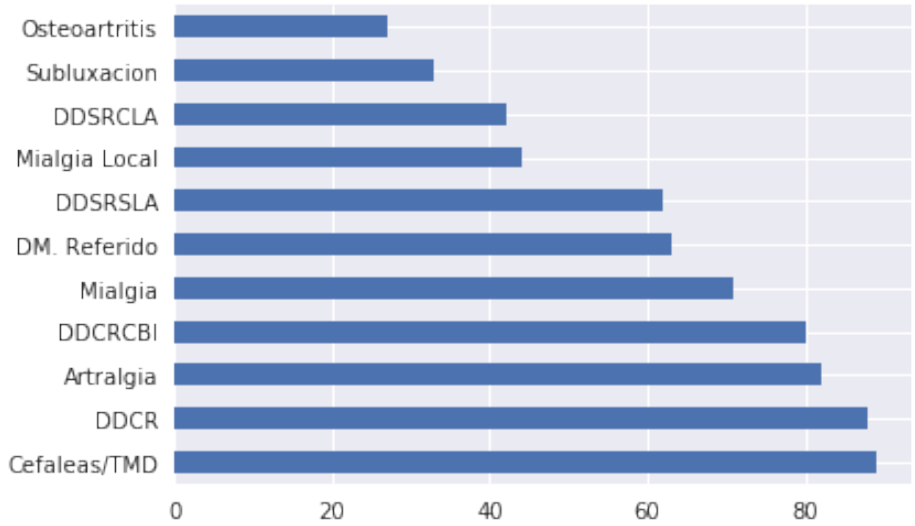
10 rows × 401 columns

- **Dataset description**

	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	...	Q391	Q392	
count	681.00000	681.000000	681.000000	681.000000	681.000000	681.000000	681.000000	681.000000	681.000000	681.000000	...	681.000000	681.000000	68
mean	0.63583	0.349486	0.355360	0.555066	0.509545	0.538913	0.506608	0.475771	0.725404	3.809104	...	0.646109	0.509545	
std	0.48155	0.477158	0.478974	0.497324	0.500276	0.498850	0.500324	0.499780	0.446639	1.945275	...	0.478527	0.500276	
min	0.00000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	1.000000	...	0.000000	0.000000	
25%	0.00000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	2.000000	...	0.000000	0.000000	
50%	1.00000	0.000000	0.000000	1.000000	1.000000	1.000000	1.000000	0.000000	1.000000	4.000000	...	1.000000	1.000000	
75%	1.00000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	6.000000	...	1.000000	1.000000	
max	1.00000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	7.000000	...	1.000000	1.000000	

8 rows × 400 columns

- **Diseases distribution**



- **Final dataset after normalization and removing features and normalization**

	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	...	Q391	Q392	Q393	Q394	Q395	Q396	Q397	Q398	Q399	Q400
0	1	1	0	1	0	1	1	0	1	0.292481	...	1	0	0	1	0	1	0	1	0	0
1	1	0	1	1	1	1	1	1	1	0.903677	...	0	1	0	1	0	1	0	1	0	0
2	0	0	0	0	0	0	0	1	0	0.500000	...	1	1	1	1	1	0	1	0	0	0
3	0	0	0	1	0	0	0	0	1	0.660964	...	1	1	0	1	0	1	1	1	0	0
4	1	0	0	0	1	1	0	0	0	0.792481	...	0	1	0	0	1	1	1	0	0	1

Algorithms and techniques

This project's been divided into 2 different sections (apart from data exploration). On the one hand, it is intended to apply what has been learned in the unsupervised learning module to preprocess and analyze the available data and, on the other, to develop a classification model based on Deep Learning by implementing a neural network. Considering that data are non-linear, non-stationary and the independent between them, in addition to the limited number of outputs (11 different diseases are going to be detected) I considered that a solution based on a neural network was suitable to the described problem.

The process followed and used tools/techniques have been the following:

1. Import of necessary libraries and datasets.
2. Data Exploration using ***Pandas***: Statistical analysis of data and parameters.
3. Data preprocessing using ***Sklearn***: Identify parameters susceptible for preprocessing (log transform), data cleaning, obtain training and test sets form original dataset and outliers detection.
4. Use of **correlation matrix** and **coefficient of determination R^2 with decision tree regressor** to identify features that could be inferred from others.

5. Dimensionality reduction based on above results.
6. Clustering: Calculate **silhouette score** to determine if number of clusters are related with number os diseases to detect. Use of ***K-means*** **and** ***Principal Component Analysis*** (finally discarded) and clustering representation using **parallel coordinates**.
7. **Neural network architecture**: Iterative cycle for the development (using ***Keras***) of the prediction model, performance testing based on suggested evaluation metrics and improvement. Make predictions on the validation datasets.
8. Deletion of candidate features (suggested based on previous tasks) to check if prediction model is able to perform as well as original one.
9. Development of **prediction function** based on previous model ready to be used by the TMJQuest website

Benchmark

As we have previously shown, to have an accurate benchmark model is complicated without the help and validation by specialists in the subject. The conclusions of this project related to the possibility of reducing the questionary of questions that patients fill in are mere suggestions that should be analyzed by an expert committee. The prediction model tries to be only an additional help for physicians, who must confirm the suggested diagnosis with a deeper patient exploration.

III. Methodology

Data preprocessing

Since the dataset structure was relatively well prepared for use in the project (all parameters have numerical, most of them with on with a limited range, or boolean values) there are no further considerations other than those described in the data exploration section.

Implementation

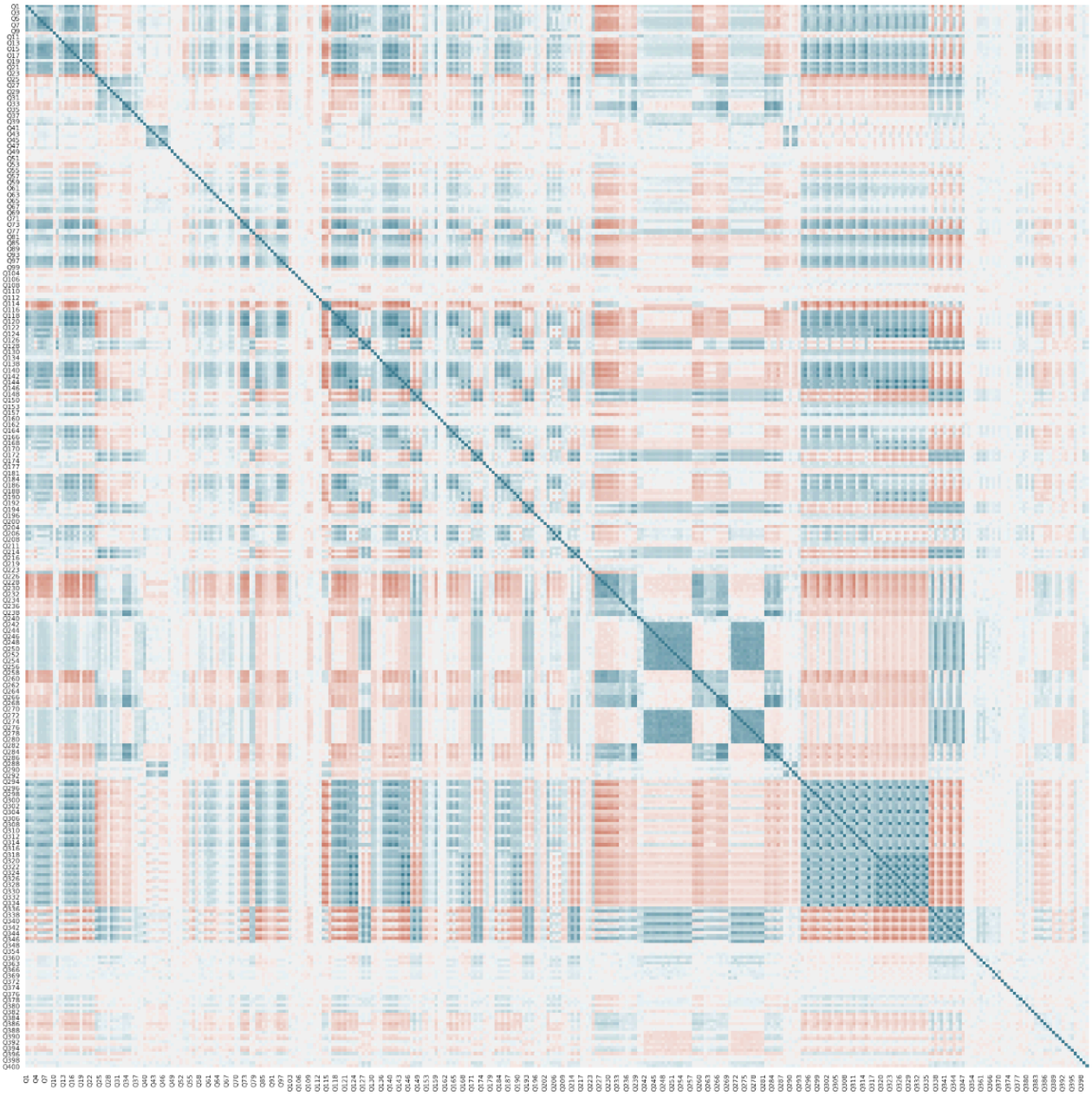
There were three main goals for this project:

- Identify those features that has no impact on patient diagnosis in order to remove them from dataset.
- Identify overlapping diseases or not detected ones.
- Develop a prediction model as accurate as physicians.

We are going to describe the followed process to achieve these goals.

Two first goals were intended to be achieved by using unsupervised learning techniques. Correlation matrix and heatmap were used in order to identify those features susceptible of being

guessed from another ones. Form the very beginning it was clear that a strong correlation existed between certain features.



Correlation matrix and coefficient of determination R^2 where combined to get a list of features that contains those features which were detected by both processes upper a certain threshold. Threshold was established in 0.9 in both cases, although using 0.8 could have lead to delete more features. Using a more conservative approach it been preferred as we are only considering a quantitative approach of questions made to patients. Probably there are a set of questions not related with the final diagnosis but useful for patient classification.

Clustering was performed to identify how clearly records present in dataset were classified. To achieve this, silhouette score for number of clusters between 2 and 14 was used. Getting the highest

value for 11 clustered (as 11 was the number of diseases to diagnosis) would have been expected but all obtained values were really low.

To identify why, we worked on a process of applying dimensionality reduction using Principal Component Analysis (***PCA***) and clustering using ***K-means***, but after several tests a clear conclusion was not reached. The large number of parameters in the data set made this task difficult.

We then tried to graphically represent the dataset in a way that could show different diseases grouped by, for which the utility of ***Pandas*** library parallel coordinates was used but, again, the amount of parameters and the impossibility of representing it all in a legible way has prevented obtaining the conclusions marked in the objectives of the project.

This is currently, an unfinished outcome of the project.

For the the prediction model implementation, an iterative process has been followed. First of all, on hot encode was performed over labels dataset in order to get and 11 nodes output layer. Then, from a basic neural network architecture with an input and an output layer, changes have been added based on the results obtained of each combination (mainly accuracy against training a testing datasets). The details of the final implementation can be found in the attached notebook, In [24] - I [27] cells. Specifically, different adjustments have been performed related to:

- Number of hidden layers
- Input and hidden layers size
- Activation functions
- Kernet initializers
- Optimizers
- Adding/Removing dropout layers
- Using regularization
- Number of epochs

The used model that produces the outcomes described in next section (which does not have to be the final candidate since at the time of publication of this report is still working on its improvement) is as follows:

```
X_train_reduced, X_test_reduced, y_train, y_test = train_test_split(reduced_dataset, dummy_y, test_size=0.3)
classifier = Sequential()
# First Hidden Layer
classifier.add(Dense(64, activation='relu', kernel_initializer='random_normal', input_dim=len(reduced_dataset.columns)))
classifier.add(Dropout(0.2))
# Second  Hidden Layer
classifier.add(Dense(32, activation='relu', kernel_initializer='random_normal'),)
classifier.add(Dropout(0.2))
# Output Layer
classifier.add(Dense(number_of_diseases, activation='softmax', kernel_initializer='random_normal'))
classifier.add(Dropout(0.2))
classifier.summary()
```

```
_________________________________________________________________
Layer (type)                 Output Shape              Param #
=================================================================
dense_1 (Dense)              (None, 32)                11264
_________________________________________________________________
dropout_1 (Dropout)          (None, 32)                0
_________________________________________________________________
dense_2 (Dense)              (None, 16)                528
_________________________________________________________________
dropout_2 (Dropout)          (None, 16)                0
_________________________________________________________________
dense_3 (Dense)              (None, 11)                187
_________________________________________________________________
dropout_3 (Dropout)          (None, 11)                0
=================================================================
Total params: 11,979
Trainable params: 11,979
Non-trainable params: 0
```

Finally, based on the prediction model, a prediction function was implemented. By supplying a list of answers to the questions list, it provides the diagnosed disease.

Refinement

From the beginning of the process of the prediction model development, it became pretty clear that the main problem was going to be to deal with overfitting. Virtually all combinations of layers, sizes, activation functions, optimizers, adding or removing dropout, parameter tuning, etc. have been oriented to reduce overfitting.

I had to include several changes in the original NN architecture due to high overfitting once we started to use the reduced dataset. Original architecture achieved only an about 77% accuracy using testing set, although training data accuracy was quite similar to using full dataset. Some of the changes were:

- Use ***L1 and L2 regularizations***: Did not work. In fact, we got worse results.
- Increase output size of layers. It improved accuracy (testing set) by more than 10 points.
- Change output layer activation function from ***sigmoid*** to ***softmax***. It worked really well.

After doing that, accuracy for the prediction model using the reduced set of data is even a little bit better than using the full dataset.

Final results are shown in the next section.

IV. Results

Based on the project goals described above, the project **most relevant results** are the following:

- There is available a prediction model providing and **accuracy over 95% in detection of temporomandibular diseases**.
- There is available a prediction function, ready to use, to get a diagnosis based on a set of answers
- Above results have been obtained from a reduced features dataset, where **more than 20% of original questions made to patients have been removed without impact in prediction** (399 features were reduced to 317).

V. Conclusion

Free-form visualization

The main project outcome, in its current state, is that it is possible to develop an accurate prediction model based on the data collected in the dataset. At this time, **the prediction model provides an accuracy of more than 95% against the validation data**. Not only this, it has also been possible to achieve this accuracy by using a set of reduced features, that has gone **from 400 features in the original dataset, to 317, which means a reduction of more than 20%.**

Given that, data are directly collected from questionnaires that doctors carry out to patients , this means a promising considerable saving of time for both of them.

Reflection

The hardest problem to deal with provided dataset has been the large number of features and to establish relationships between them. Since project definition, it was clearly shown that techniques learned in the "Unsupervised Learning" module could be very useful to provide doctors and dentists a detailed analysis of the data collection and classification process and how to improve it. However, I have not been able to reach relevant conclusions in this regard, apart from remove some of the features. Honestly, this goal has not been achieved by the current status of the project.

On the other hand, the developed prediction model seems very promising. There is still some overfitting but I am sure that it can be reduced.

Improvement

At this moment, there are one significant goal of the project that have not still been achieved: The determination of those combinations of answers that could lead to non clear disease classification.

Improving accuracy and reducing overfitting is another way of improving the project. Probably it is going to be easier as we get more patient records in the future.

1) National Institute of Dental and Craniofacial Research. Facial Pain. http://www.nidcr.nih.gov/DataStatistics/FindDataByTopic/ FacialPain/ (accessed 7/28/2013).
2,3) International RDC/TMD Consortium Network and Orofacial Pain Special Interest Group