Genetic algorithms for feature selection in the children and adolescents depression context

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Abstract—**Depression is the leading cause of disability in the world and, according to the World Health Organization, is the leading cause of illness and disability in the adolescence. Previous research has found that half of all people who developed mental disorders had their first symptoms up to age 14. However, what are the most important characteristics to determinate whether or not someone has depression? Genetic algorithms have been used quite efficiently in the problem of feature selection from a dataset. Thus, the main objective of this work is to use genetic algorithms to search for the most relevant features to improve the performance of classifiers to assist in the diagnosis of depression in children and adolescents. The dataset used in this work contains information on 166 children and adolescents between 10 and 16 years of age, of whom 67 are males and 99 are females with different depressive symptoms. The genetic algorithm found, in its best result, a set of 55 features out of the 112 in the dataset. The feature referring to how one feels with her/his own appearance was the most used in the solutions returned by the genetic algorithms. The use of the dataset composed of the 55 features selected by the genetic algorithms improved the performance of the classifiers by 6 to 20 percentage points, reaching f-measure values between 90% and 96%, which is a very significant result in the depression diagnosis context.**

Index Terms—**genetic algorithms, depression, children and adolescents, feature selection, machine learning.**

I. Introduction

Depression, according to the World Health Organization (WHO)[1], is different from oscillations in habitual humor or short-term feelings in response to daily life challenges. This disorder could become a very serious health problem, mainly if it is long term and moderate to high intensity. Depression is the most common reason to get someone incapable to work, then it is an economically influencing factor too.

More than 300 million people are depressive in the whole world, an increase of about 18% in the 2005-2015 decade. Besides depression causes too much pain and suffering to the person and interferes is her/his professional, scholar, and familial activities and performance. The American Psychiatric Association (APA)[2] affirms that one out of six persons (about 16.67%) will undergo depression in a moment in her/his lifetime. This estimative leads to an impressive number of more than one billion people affected by depression and its consequences around the planet.

The World Health Organization points out in recent studies that depression has been a major cause of illness and disability in adolescence. According to Wang et al. [1], Comijs et al. [2], and Yoon et al. [3], half of all people who develop mental disorders had their first symptoms up to the age of 14. That is, caring for children and adolescents with mental health disorders can prevent deaths and/or suffering throughout life. This disorder is characterized by a high risk of suicide, considered to be the second most common cause of death among people aged 15-29 years [4].

In its worst case, depression can lead the person to suicide: about 800 thousand people die that way every year. Suicide is the second main death reason among people around 15 to 29 years of age. The WHO alerts that, in spite of the existence of effective treatments, less than half of depressed people in the world (in many countries, less than 10%) receive those treatments. The barriers to an effective treatment include (but are not limited to) lack of resources (monetary ones and specialized health professionals) and social stigma associated with the mental disorders in general.

Besides, another remarkable obstacle to effective treatment of depression is the imprecise evaluation, mainly the diagnostics. Many depressed people get incorrect diagnostics being not treated as so. On the other side, many people get diagnostics of depression but they are not. This fact leads to the incorrect prescription of medicine to who need it not and lack of medication to whom really need it. Hence, there are effective pharmacological and psychological treatments for depression, but they need to be correctly prescribed to the people who need them. And this points to the cruciality of a precise diagnostic.

Depression can occur at any moment in the lifetime, but it arises for the first time, commonly, around the end of the adolescence and the 25 years of age. Therefore, research on that stuff is essential in order to aid in the diagnostic and treatment of that disorder, especially in the age it first occurs. So, the main goal of this work is to find out, by the means of genetic

[1]http://www.who.int/mediacentre/factsheets/fs369/en/

[2]https://www.psychiatry.org/psychiatrists/practice/quality-improvement/quality-measures-for-mips-quality-category

algorithms, the most relevant features to the classification of depression symptomatology in order to help in the diagnosis of depression in children and adolescents. In this context, from the selected features this work analyses the classification performance of $k-$NN ($k-$Nearest Neighbor), SVM (Support Vector Machines), and Random Forest classifiers.

The remaining text is organized in the following way: in the second section the theoretical framework with the main concepts related to depression and the algorithms used in this paper are presented, followed by the works related to the addressed problem in the third section; the fourth section describes the methodology and aspects related to the dataset. In the fifth section the results and discussions are presented; and, finally, in the sixth section, the final considerations about this paper are exposed.

II. FEATURE SELECTION BY MEANS OF GENETIC ALGORITHMS

Datasets composed of hundreds of features (attributes) have become common in the classification problems and this is the case of the depression symptomatology classification. In general, machine learning algorithms used to classification have the quality of their results diminished if all features in the dataset are used to train them[5]. The feature selection methods arose precisely to circumvent this problem. They search for the relevant attributes, removing irrelevant, redundant or noisy data. Thus, in general, the computational and classification performances of the machine learning algorithms are improved by feature selection. [6]. Besides, the comprehensibility of the models generated by some kinds of algorithms, like those that build decision trees or that generate rules, is augmented [5].

Genetic algorithms (GA) are a search technique based on Darwinian natural selection: the fittest is more likely to survive and leave offsprings for the next generation of a population [7, 8]. In genetic algorithms, the population is represented by the individuals (chromosomes) that are selected and submitted to the genetic operators crossover ("recombination") and mutation. The next generation of a population is formed in a way that the fittest individuals are more likely to survive and reproduce (natural selection). So, the evolution of a population is led by the "quality" of each individual as a solution to the problem in question, which is called the fitness.

The GA are adequate to hard problems in which becomes computationally impracticable to find the optimal solution to the problem, since the GA population covers several regions of the search space, without having to realize all the possible combinations. That is the case of feature selection because all possible combinations of features should be evaluated as a possible solution to the problem. Genetic algorithms have been used in a very efficient way in the selection of features from a dataset [9, 10, 11].

III. RELATED WORK

The literature presents many works that use genetic algorithms to select features in order to optimize different classification processes. Different works in different areas have applied genetic algorithms in different kinds of data..The common objective is to get better model accuracy with the use of GA for feature selection. This is the case of the following works related to the depression and other mental diseases diagnosis.

Hosseinifard et al. [12] studied the non-linear analysis of EEG (electroencephalogram) signals to discriminate patients between depressed and controls (individuals without depression symptoms). Forty-five depressed and unmedicated patients, plus 45 subjects without the disorder, participated in the study. To discriminate the two groups, the support vector machines (SVM), linear discriminant analysis and logistic regression were used. Classification accuracy of 89% was achieved by the SVM classifier improved by the features selected by genetic algorithms. This study shows that non-linear EEG analysis may be a useful method for discriminating depressed patients and normal individuals if used with feature selection. .

Galván-Tejada et al. [13] propose a methodology to detect people with depression from the movement data generated by the patient's activity, obtained from wearable devices like smartwatches.Using this signal as an information source, an approach is taken to extract statistical features, in time and spectral evolution of the signal. Subsequently, a selection of features is made by means of GA to reduce the amount of information necessary to give a quick and non-invasive diagnosis. The results show that the feature selection approach can reach a value of 0.647 for the area under the curve (AUC) using only two features. These results allowed the authors to conclude that using the signal of activity of a smart band, it is possible to distinguish depressive people, what is a preliminary and automated tool that helps specialists in the diagnosis of depression almost in real-time.

Vinutha et al. [14] use a database with 5542 instances, collected by the National Alzheimer's Coordination Center (NACC) in India. The authors used GA to select the best subset of scores needed for clinical diagnosis, and these scores were evaluated by the logistic regression model using AUC, precision and mean square error (MSE). The simulations performed showed that a high precision classification (0.9427), AUC (0.9713) and lower error rate (0.041) can be achieved by combining four neuropsychological scores. This set of features are predominantly selected by the GA in different executions and, therefore, have a significant role in the screening of subjects affected by the Mild Cognitive Impairment mental disorder.

In the work presented in Ashish et al. [15], data for training and validation were collected during the years 2004 and 2005 in a government psychiatric hospital in India. The main objective of the study was to develop a software prototype to classify and diagnose depression, as well as to identify the main symptoms responsible for depression since it involves the collection of data from patients by physicians that may interfere in reporting subjectively. A neuro-fuzzy system model was developed for this purpose with optimized

performance through two approaches: in the former, a back-propagation algorithm was considered, and in the second, genetic algorithms were used. The authors conclude that the GA approach was more accurate in the diagnosis than the retro-propagation and that computer-based diagnostic software can help clinicians to make decisions.

IV. MATERIALS AND METHODS

A. Description of the dataset

The dataset used in this study was obtained in a partnership with the federal institution Graduate Program in Psychology: Cognition and Behavior of the Federal University of Minas Gerais (UFMG). The dataset contains information from local children and adolescents, with different depressive symptoms, aged between 10 and 16 years. Figure 1 illustrates the composition of the dataset used in the study.

Figure 1. Combination of attributes that make up the database.

In addition to attributes such as age and gender, attributes like schooling, who lives with the patient, time of contact with parents, use of medications, scores obtained by answering the Young Self report (YSR) [16] Children's Depression Inventory(CDI) [17] also constitute the dataset. There are also demographic characterization data, how many hours per week are spent with the parents, whether the patient or parents already had psychological or psychiatric care and the parents' schooling. Other issues considered important by the mental health community [18] have been included too: factors such as anxiety, social problems, inattention, aggressiveness, and conduct problems.

The attributes are mostly ordinal, where the answers to each question are represented by a number that corresponds to a list of possible answers.

B. Preprocessing

In order to obtain a more consistent model, before actually starting the application of the feature selection algorithms and classification, the preprocessing of the data was done. The strategies adopted in this step were: to delete attributes that do not contribute to profiling, to merge attributes, to optimize or to create new representation encodings, to treat the possibility of missing data, and to analyze inconsistent instances that do not fit the identified groups.

All data preprocessing was performed using the Python 3 programming language, through the Jupyter Notebook environment. Sequentially, the steps of the dataset preprocessing were:

- Removal of attributes in which most of the values (>90%) were missing.
- Data inconsistency handling.
- Numeric encoding for nominal.
- Binarization of the values of some attributes.
- Discretization of the values of some attributes.
- Identification and manipulation of the classification attribute (class): initially there was not an obvious attribute in the dataset that classified the patients according to their symptomatology. With the application of the CDI questionnaire to patients, a new attribute is obtained, the "CDI Sum". This new attribute is equivalent to a score of the interviewed patient at the end of the inventory.

Figure 2 presents the distribution of the interviewed individuals, considering the feature "CDI Sum". The "CDI Sum" attribute assumes values in the $[0, 46]$ range and it does not determine the existence or absence of depression, but it gives information to assist a professional in the assessment. Nevertheless, there is no unanimity on the cut-off value that determines a subdivision, since this value may vary according to the sample. The recommendation of Kovacs [19] is to use the 85 percentile for the indication of "high" symptomatology. So, 63 individuals were classified with "high" and the other 103 with "low" symptomatology.
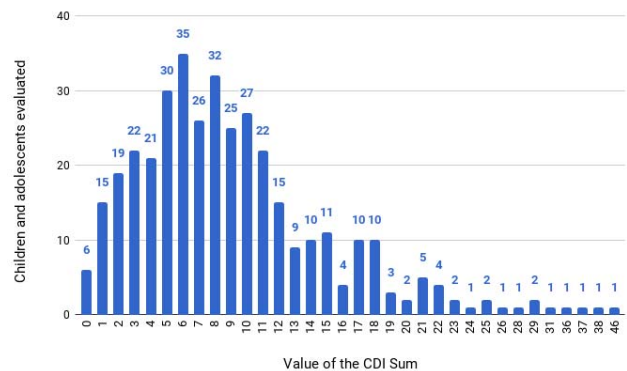

Figure 2. CDI Sum distribution.

After the data preprocessing, each individual was repre-

sented by an instance with 113 features, including symptomatology (High/Low) and the dataset totalized 166 instances.

C. Feature selection

For the selection of the best features, the Non-dominated Sorting Genetic Algorithm II (NSGA-II), an algorithm that can work with several objectives simultaneously, was chosen. The choice of NSGA-II was motivated because it is the most referenced version of a multiobjective GA [20] in the literature. Its implementation was done in Python, using the DEAP library, made available by the *Université Laval* [21].

For the purpose of using genetic algorithms is needed to define the representation of the individuals, a fitness function to evaluate "how good" is an individual as a solution to the problem, and a set of parameters like crossover and mutation probabilities, size of the population, a stop criteria, and so forth. The following are the main implementation choices for the GA.

1) Representation of the individuals: an individual represents a possible solution to the problem being solved. Figure 3 presents an example of the representation of individuals used in this work. Each individual is represented by an array of 112 positions (each one representing a feature of the dataset) that can store the value 0 or 1, indicating the absence or the presence, respectively, of that particular feature.
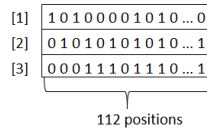

Figure 3. Representation of three individuals.

2) Fitness: the fitness function must produce a value that that indicates how "good" (adapted) is an individual as a solution to the problem. Hence, a good fitness function is crucial to the GA performance. It is used to compare two individuals and so to distinguish between a promising solution and another not so suitable to the problem [22]. In this work, a classifier is used to classify the dataset corresponding to the features represented by an individual created by the GA. So, a good fitness function must evaluate the performance of the classifier. There are dozens of metrics to evaluate the performance of a classifier, ranging from the error metrics like the mean squared error to those derived from a confusion matrix like the precision, recall (sensitivity), accuracy, etc [5]. The F-measure[3] was chosen as the metric to provide the fitness function values because it is a simple metric that harmonizes between precision and recall values, that are commonly used to evaluate classifiers.

The $k-$NN was used as the classifier for not requiring an additional cost of hyperparameters adjustments, what turns feasible the execution of a large set of experiments in a smaller amount of time than would be required to tune the

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[3]$f - measure = \frac{2 \times precision \times recall}{(precision + recall)}$

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hyperparameters of the majority of others classifiers. $k-$NN was also used by Santos et al. [23] and showed to be efficient.

3) Parameters of the experiments: preliminary tests were performed to determine which intervals of the parameters' values would be most appropriate for the experiments. The number of generations of the GA was defined as the stop criterion. The experiments were carried out with 10 different random seeds for each set of parameters in order to increase the reliability of the results that were averaged over ten runs. The parameters and their values are shown in Table I.

Table I
EXPERIMENTS PARAMETERS

Population initialization	Random
Representation	Binary
Crossover operator	Two Points
Crossover probability *(Pc)*	65%, 70%, 75%, 80%
Mutation operator	One Point
Mutation probability *(Pm)*	1%, 5%, 10%
Population size	200, 300, 500, 1000
Number of generations	200, 300, 500, 1000
Crossover selection method	Tournament (size = 2)
Composition of the new generation	Non dominated individuals
Stop criterion	Number of generations

V. RESULTADOS E DISCUSSÕES

After the end of one GA run there is a set of candidate solutions for the problem (the population) with an average value for fitness. The best set of parameters was that of the GA run that the population had the best average fitness. Figure 4 shows the behavior of fitness during evolution for the best set of parameters: population of 500 individuals, 500 generations, crossover probability of 0.75. and mutation probability of 0.05.
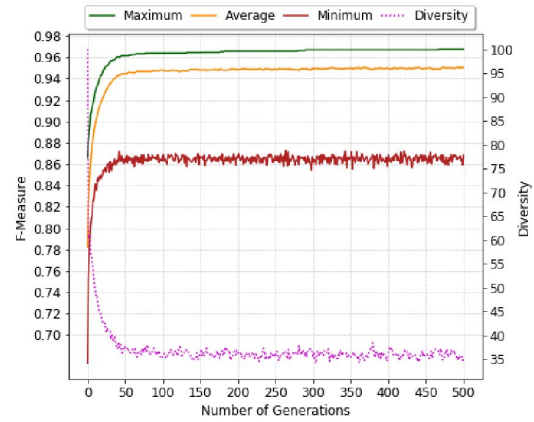

Figure 4. Experiments. Fitness and diversity as the population is evolved through generations. Results are the average of 10 runs.

From Figure 4, it can be seen that the percentage of diversity (indicating the number of individuals generated that are different from their parents) converged to approximately 38% in the generation 50. In addition, there were no significant improvements in maximal fitness of individuals from generation 150, approximately, to the end of the run. Similar

behavior is observed for the individuals with worse fitness, who converged near generation 50.

Accounting for all 1920 tests performed (192 × 10 randomizations) with the genetic algorithms, the features' frequency of occurrence in the individuals of the last generation of the population of each run were computed. Thus, the features were collected in 1920 × 500 individuals. Figure 5 presents the list of the 20 most frequent features[4].
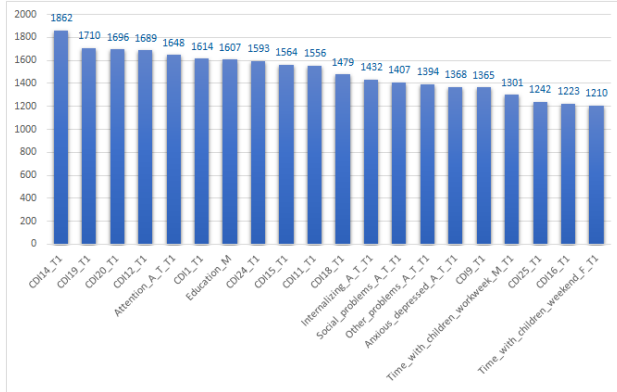

Figure 5. Frequencies of the 20 features most used by GA in the 1920 experiments.

Among the most used features, it is possible to highlight the presence of feelings regarding self-esteem, own illness, loneliness, and even suicidal thoughts, as well as familiar issues such as the mother's schooling. The most frequent feature was the $CDI14\_T1$ which indicates how one feels about his/her own appearance. These results corroborate the findings in Babore et al. [24], Ju and Lee [25], Ticusan [26], and Yoon et al. [27] that self-esteem is an important factor for depression and suggest continuous interventions to increase self-esteem in adolescence, which greatly reduces the degree of depression.

The best-performing GA found a set of 55 features (out of 112 from the dataset) which were those used by the best individual (f-measure = 96.75%). Comparing these 55 features to the 20 most frequent features in all GA runs (Figure 5), is noticed that the best GA made use of 19 from the 20 features that had the highest frequencies. That is, 95% of the 20 best features were used by the best GA. This fact evidences the correct choice of the best set of parameters by the genetic algorithm in the feature selection problem.

In order to evaluate the performance of classifiers using only the 55 features selected by GA, tests were performed with k-NN, SVM and Random Forest (RF). Ten-fold cross-validation and the analysis of the f-measure, precision, and sensitivity (recall) metrics were performed. The SVM and RF hyperparameters were adjusted by grid search:

[4]A list with the descriptions of the 20 topmost features can be found at https://drive.google.com/file/d/1gkycs6RJ-VXRaXIZvRiwRHI$_I VGnYmP-$/$view$

- k-NN: The value of the parameter k, that indicates the number of neighbors considered to classify an instance, was adjusted in the range of [1 to 20] (running 10-fold cross-validation) and $k-$NN had the best performance with $k = 1$.
- SVM: the $Cost$ and γ parameters were adjusted by traversing the [2^{15}, 2^{-15}] range using a RBF (Radial Basis Function) or linear kernel. The best values were $\gamma = 0.1665$, Cost $= 0.6987$, and linear kernel.
- Random Forest: The best parameter values for the classifier were: Max_depth = 10, Max_features = 7, Min_samples_split = 10, Bootstrap = True, and Criterion = entropy.

Table II shows the percentage values of f-measure (mean $\pm$ standard deviation in the $10-$fold cross-validation tests) for the classifiers with and without feature selection. On average, all classifiers performed better with feature selection, with increases between 2 (RF) and 8 ($k-$NN) percentage points, considering the class with low symptomatology (Low), $k-$NN had a higher performance increase than Random Forest: 8 percentage points against 2. For the class with high symptomatology (High), all classifiers performed better, with more significant gains: 6 percentage points to Random Forest, 7 to SVM, and 20 to $k-$NN. This behavior is also similar to the metric components of f-measure, precision and recall (sensitivity), as shown in the tables III and IV, but more markedly for sensitivity with high symptomatology (Table IV, class High). In any application, such gains are important but much more in aiding the diagnosis.

It is important to note that $k-$NN had the best results with the selection of features in relation to the others in the three metrics evaluated. This performance is not expected for the type of problem addressed here (classification), especially if compared to SVM. One of the reasons for this increase is that the genetic algorithm evolved based on the performance of $k-$NN. However, this fact also shows that, although $k-$NN has been used to accelerate the evolution process, according to Subsection IV-C, the data set chosen by genetic algorithms was useful to the other classifiers since their performance was substantially improved or maintained, according to the results.

Table II
F-MEASURE (%) FOR THE CLASSIFIERS

	With feature selection			Without feature selection		
	$k-$NN	SVM	RF	$k-$NN	SVM	RF
High	96.13 (±0.05)	91.09 (±0.08)	82.76 (±0.09)	76.33 (±0.10)	84.06 (±0.13)	76.69 (±0.14)
Low	96.13 (±0.03)	94.65 (±0.04)	89.79 (±0.06)	87.97 (±0.05)	91.5 (±0.07)	87.71 (±0.06)
Average	94.78 (±0.04)	92.87 (±0.06)	86.27 (±0.09)	82.15 (±0.10)	87.78 (±0.11)	82.2 (±0.12)

VI. FINAL CONSIDERATIONS

Given the importance of accurate diagnosis of the depression disorder and the alarming numbers of people, among them, children and adolescents, who are suffering from this

Table III
PRECISION (%) FOR THE CLASSIFIERS

	With feature selection			Without feature selection		
	$k-$NN	SVM	RF	$k-$NN	SVM	RF
High	95.48 (±0.06)	90.80 (±0.07)	81.32 (±0.12)	86.74 (±0.11)	89.31 (±0.11)	78.83 (±0.18)
Low	95.52 (±0.04)	95.52 (±0.06)	88.12 (±0.09)	83.66 (±0.06)	89.36 (±0.08)	85.35 (±0.11)
Average	95.50 (±0.05)	93.16 (±0.07)	84.72 (±0.11)	85.20 (±0.09)	89.34 (±0.10)	82.09 (±0.15)

Table IV
SENSITIVITY (RECALL) (%) FOR THE CLASSIFIERS

	With feature selection			Without feature selection		
	$k-$NN	SVM	RF	$k-$NN	SVM	RF
High	92.14 (±0.07)	92.14 (±0.10)	78.81 (±0.18)	69.29 (±0.13)	80.48 (±0.16)	73.57 (±0.21)
Low	97.00 (±0.04)	94.09 (±0.04)	89.27 (±0.06)	93.09 (±0.06)	94.09 (±0.06)	88.18 (±0.09)
Average	94.57 (±0.06)	93.12 (±0.08)	84.04 (±0.14)	81.19 (±0.15)	87.28 (±0.14)	80.88 (±0.18)

disorder, works that help in the diagnosis are increasingly relevant. The proposal to improve the quality of the models generated by classifiers using the genetic algorithms approach to feature selection showed to be promising in face of the improvement of the metrics evaluated.

The results show that the use of the selected features data increased the performance of the evaluated classifiers between 6 and 20 percentage points in the detection of high symptomatology, which is very significant in the aid in diagnosis. Although the results are promising, the methodology must be tested with other classifiers and data, in addition to more extensive experimentation with the adjustment of the various parameters involved. Since SVM performance is generally much better than k-NN, even higher increasing rates are expected to be achieved using it instead of $k-$NN.

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