A Correlation Network Model for Analyzing Mobility Data in Depression Related Studies

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Abstract: Depression is a serious behavioural disorder that can affect the quality of life. Timely diagnosis and accurate estimation of severity are critical in supporting depression studies and starting early interventional treatment. In this study, we introduce two major contributions. First, we propose a novel computational model that can utilize non-invasive mobility data to recognize individuals suffering from depression disorders. Second, we introduce a new objective index, the Depression Severity Score Index (DSS), which can approximate the seriousness or the degree of severity of depression. The proposed approach is a data-driven model that is built on the mobility data collected from 55 subjects using wearable sensors. In the first step in our proposed approach, a graph model that represents the underlying correlation network is constructed by measuring the pair-wise correlation values between each pair of individuals. Then, we obtain the depression severity index of each subject by utilizing graph properties of the constructed network such as Intra and inter-cluster edges. Our obtained results show that the obtained correlation network model has the potential to identify participants diagnosed with depression from the control group. Moreover, the proposed Depression Severity Score (DSS) has a higher likelihood than the clinical depression score in correctly measuring the depression severity level.

1 INTRODUCTION

In recent years, the prevalence of behavioral disorders such as depression is in increasing trend. Especially, During the COVID-19 pandemic, depression and anxiety disorders are more prevalent than usual in the general population (Mazza et al., 2020). depression would be the second most disability that most people will suffer around the world (Mathers and Loncar, 2006). In addition to this, the cost of healthcare would significantly rise. Furthermore, recent studies show that one out of every five young children is suffering from at least one of the mental health issues including depression, schizophrenia, and ADHD (Li et al., 2021). However, only 25% of them are being diagnosed and treated and the rest of them are undiagnosed. Besides, many children are not aware that they are being affected by mental disorders. According to National Institute of Mental Health (NIMH) statistics, approximately 21 million people have at least one major depressive disorder (unipolar or bipolar depression) (The National Institute of Mental Health (NIMH), 2021). Astonishingly, this number is almost 8% of the total US adult population.

Depression is characterized by a gloomy mood, lack of interest in general everyday activities, low self-esteem, and withdrawal from social gatherings (Thelagathoti and Ali, 2022b) (Thelagathoti and Ali, 2022a). The prevalence of depression for a long time may result in negative outcomes such as poor performance in academics or work location, reduced mobility, self-harm, and unemployment (Li et al., 2021). Especially, suicidal thoughts and self-hurting would dramatically increase. Therefore, it is crucial to identify the condition and facilitate the treatment as early as possible. Without estimating the severity of the depression, it is not viable to provide comprehensive treatment. Assessment of the seriousness of the disorder is as critical as the detection of the disorder. Nevertheless, most of the existing clinical procedures are symptom rating scales such as the MADRS score (Montgomery and Åsberg, 1979) and the Depression Rating Scale (Williams, 1988). In these approaches, severity is estimated by assigning a score or rating for each of the symptoms that are expressed by the indi-

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vidual and observed by the clinician. After an assessment is completed, a final score is calculated which represents the seriousness of the depression. For example, The MADRS score ranges between 0 to 60 in which 0 to 6 is considered as no depression while a value above 34 is treated as severe depression (Montgomery and Åsberg, 1979). The drawback of such rating scales is that the evaluation is controlled by human experience and driven-by patient feedback. In the case of children, it is totally driven-by clinician observation because children are not mature enough to express their symptoms and feelings. Thus, it is the need of the hour to develop objective methods to assess the severity of depression without depending on mere feelings.

Our study aims to develop a computational approach that can identify the depressed person from a healthy individual and approximate the severity of the depression. Our model is constructed on the fact that altered mobility is one of the early signs of depression. Recent studies show that the mobility of depressed people is lower than that of healthy people (Garcia-Ceja et al., 2018) (Thelagathoti and Ali, 2022b) (Thelagathoti and Ali, 2022a). This opens the doors to developing computational techniques to classify depressive disorders by utilizing mobility data. For our experiments, we processed the mobility data collected from 55 subjects using body-worn wearable sensors of which 23 of them are suffering from depression and 32 of them are healthy clinical control subjects (Garcia-Ceja et al., 2018). We built the computational model in two stages. In the first stage, a graph-based correlation network is constructed by measuring the pair-wise correlation coefficient between each pair of subjects. The resultant graph inherently separates the depressed group from the healthy group. These two groups are identified and extracted by employing a clustering algorithm. In the second stage, graph properties such as inter and intra-clusters edges are utilized to compute the severity of each participant in the depressed group. Our proposed model is data-driven and does not depend on the group labels present in the dataset. The rest of the document is organized as follows. In section 2, our major contributions are explained while methods are elaborated in section 3. The results are presented in section 4, robustness analysis is performed in section 5, discussion of the results is described in section 6, and limitation are explained in section 7.

2 METHOD

2.1 Overview of the Pipeline

The methodology used for the proposed approach is shown in Fig.1. Overall procedure is divided into 3 stages: data analysis, classification, and severity estimation. In the data analysis stage, the acquired dataset is preprocessed, and extracted relevant features. In the classification step, a graph-based correlation network model is built by utilizing the features extracted in the previous stage. Then the potential clusters are identified in the graph network by applying the MCL clustering algorithm. Since the graph is constructed by incorporating the mobility characteristics of each participant, we believe that the depressed subjects will be grouped into a single cluster while the healthy subjects are expected to be in a different cluster. In the final stage, depression severity is estimated by utilizing graph properties including node degree, inter-cluster density, and intra-cluster density.

2.2 Classification

Dataset description and feature extraction steps are described elsewhere (Thelagathoti and Ali, 2022a). The first objective of this study is to build a classification model that can identify the population of subjects who are diagnosed with either unipolar or bipolar disorder, from their healthy counterparts. The classification task is achieved in two steps. In the first step, a graph-based correlation network is constructed. Then, classification is performed by applying the MCL clustering algorithm. They are further elaborated in the following sections.

2.2.1 Construction of Correlation Network Graph

A network is a graph G = (V, E) is an abstract mathematical representation of associations between
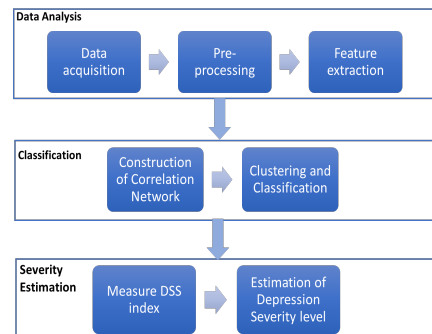

Figure 1: The overview of the methodology.

a group of objects. This graph is represented using a set of nodes or vertices (V) and edges (E) in which nodes denote the individual data item while the edges indicate the interrelationships between the objects (Bondy et al., 1976). A correlation network is a type of graph in which two nodes are connected by an edge depending on the strength of the correlation between those two nodes (Thelagathoti and Ali, 2022b). We hypothesize that the strength of the correlation between a pair of subjects can be determined by using the Pearson correlation coefficient (ρ) (Thelagathoti and Ali, 2022a) (Benesty et al., 2009). Because the Pearson correlation coefficient is a statistical measure to find the linear dependency between two data elements (Benesty et al., 2009). The value of ρ ranges between -1 to +1. Moreover, -1 represents the weakest correlation while +1 indicated the strongest correlation between any two data elements. In order to construct the correlation graph first the correlation coefficient between each pair of 55 participants is measured. Then all 55 subjects are represented as nodes in the graph and two nodes are connected by an edge if and only if the strength of correlation between these two nodes exceeds a certain threshold. The overall methodology for building the correlation network is summarized below.

- Assumption 1: N is the number of subjects under the study. In this manuscript, we have considered 55 participants from the 'Depresjon' dataset (Garcia-Ceja et al., 2018) as the population under the study.

- Assumption 2: K is the number of proposed features that will be used to build the correlation network. We have proposed 48-hour-wise features.

- Assumption 3: Pi and Pj are individual random subjects taken from the population of N subjects where $((i, j) \leq N$ and $(i, j) > 0$.

- Assumption 4: ρ[i,j] implies the Pearson pairwise correlation coefficient value between subjects I and j. CM is a Correlation Matrix that is that is generated after finding ρ[i,j] for all i and j. In other words, CM[i,j] contains ρ value between subjects i and j.

- Assumption 5: T is a predefined threshold that has to be set by the user to determine the strength of the correlation that needs to be established for constructing a correlation graph. In general, anything above 0.5 is considered a strong correlation.

- Assumption 5: SM is a significance matrix that is obtained after applying threshold T.

- Step 1: Compute the pair-wise Pearson correlation between each pair of subjects

- Step 2: Step 1 generates CM which is of size 55x55. For example, CM[3,9] represents the correlation coefficient value (ρ between participants 3 and 9.

- Step 3: choose T in such a way that only strongly associated subjects are connected in the final graph. In this study, we have chosen 0.7 as a threshold to build the graph.

- Step 4: SM is generated after applying T. SM is an adjacency matrix obtained from CM using the following equation.

$$SM[i,j] = \begin{cases} 1, & \text{if } (CM)(Pi, Pj)) \geq T \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

The value at SM[i,j] = 1 indicates that Pi and Pj will be connected by an edge in the graph because Pi and Pj are associated with respect to their mobility data. Conversely, the value of 0 at SM[i,j] represents that Pi and Pj are weakly correlated. Therefore, Pi and Pj will not be connected in the final graph.

- Step 5: SM is an adjacency matrix which is an abstract representation of a graph. Instinctively, the correlation graph is formed by utilizing the SM adjacency matrix by incorporating 55 subjects as nodes and the value at SM[i,j] to connect edges between any two subjects.

2.2.2 Clustering and Classification

In the previous step, only a correlation network graph is constructed. In this step, actual classification will be performed. In the context of this study, the aim of the classification is to identify depressive subjects from their healthy counterparts. The uniqueness of the correlation graph is that the graph is formulated in such a way that subjects who are similar concerning their mobility characteristics will come together and be strongly connected in the network. At the same time, weakly associated subjects become distant apart. It means that the correlation graph is inherently constructed in a way that strongly connected subjects are connected edges while the weakly connected subjects are not directly connected in the network. Therefore, after constructing a correlation graph it is enough to extract communities (clusters) that are homogeneous concerning their mobility profiles.

To extract well-connected clusters, we have employed the MCL community detection algorithm. MCL is a popular community detection algorithm that detects strongly connected communities in a graph by randomly walking through all the nodes (Cai et al., 2010). A community (cluster) is a subgraph where

all the nodes in the subgraph are densely connected while all nodes between the communities are sparsely connected (Emmons et al., 2016). Since we have built the graph by analyzing the motor activity of each participant, identified clusters will possess similar motor behavior characteristics. It is expected that all the subjects who possess homogeneous mobility patterns clustered into a single community.

2.3 Severity Estimation

In the case of behavioral disorders such as depression, it is not sufficient to determine the onset of the illness. It is critical to estimate the severity of the disorder immediately after diagnosing the disorder. However, most of the existing clinical diagnostic approaches are human-driven and controlled by human analysis along with patient feedback (Montgomery and Åsberg, 1979) (Williams, 1988). These methods do not provide an objective estimation of the seriousness of the depression. Furthermore, extensive human effort combined with frequent hospital visits is essential. To avoid these limitations, we are proposing a novel depression severity index namely Depression Severity Score (DSS) computed by utilizing the motor activity data collected using wearable sensor instruments. This section further illustrates the proposed methodology to measure the DSS index. The basis for DSS calculation is in the abundance of various graph properties that can be extracted from the acquired correlation graph in the previous step. We have formulated the DSS index by utilizing graph attributes such as inter-cluster density and intra-cluster density for each vertex. The intra-cluster density of a vertex is the sum of edges incident from the vertex in a cluster to each other vertex within the same cluster. Similarly, the inter-cluster density of a vertex is referred to the total number of edges incident from each vertex in that cluster to each other vertex that does not belong to the same cluster. To compute DSS we have adopted the notion of a core node and a bridge node suggested by Wang. et.al.(Cai et al., 2010). The following procedure elaborates on the approach to estimating depression severity.

- Assumptions:
  - Let G = (V, E) be a correlation graph obtained in earlier steps.
  - The classification task aims to detect all possible clusters in G. C = S1,..., Sm are a set of clusters identified in the classification task where Si is a subset of V and m is number of clusters identified by classification task.
  - Core node - A vertex Pi in cluster Sm is said to be the 'Core node' if for all edges Pi $\longrightarrow$ Pj

where Pi belongs to Sm and Pj also belongs to Sm. In other words, all its edges are connected to nodes that belong to the same cluster.
  - Bridge node - A vertex Pi in a cluster Sm is said to be the 'Bridge node' if for all edges Pi $\longrightarrow$ Pj where Pi belongs to Sm, Pj belongs to Sn (where m=! n). It means that its edges are connected to nodes that do not belong to the same cluster and also to other clusters in the neighborhood of that vertex.

- Depression Severity Score is calculated as follows

$$DSS(Pi) = \frac{\text{sum of inter-cluster edges}}{\text{sum of intra-cluster edges}} \quad (2)$$

where sum of inter-cluster edges of Pi is defined as the total number of edges that are incident from Pi in a cluster to all other nodes in the same cluster. Conversely, sum of intra-cluster of Pi is defined as the total number of edges that are incident from Pi to all other nodes in a different cluster.

- Interpretation of DSS :

In this study, we propose to formulate DSS as a binary index in which the value is either 0 or 1. However, the result of equation 2 is not a binary number but rather its s spectrum where the value DSS(Pi) ranges between 0 and 1. The interpretation of DSS binary categorization is shown in Table 1. If the DSS index for Pi is 0 or above, then we consider the subject Pi as the core node in the graph. It indicates that node Pi does not have any edges incident to the nodes in another cluster and it's strongly connected to the nodes within the same cluster. On the other hand, If Pi is > 0 then Pi is treated as a bridge node which means the node is connected to the other nodes in the same cluster as well to the nodes in neighborhood clusters. Although we use DSS as a binary index, we believe that the DSS index can be used as a supplementary tool for clinicians and healthcare professionals in the severity estimation of depressive disorder. Furthermore, experts in the medical domain can modify the DSS index for a fine-grained assessment of depression.

Table 1: Severity estimation and Interpretation.

DSS(Pi) value	Node category	Interpretation
DSS(Pi) = 0	Core Node	Depression Severity High
DSS(Pi) > 0	Bridge Node	Depression Severity Low

(a) Correlation Network graph.

(b) Classification.

(c) Severity Estimation.

(d) Robustness Analysis.

(e) Mobility across different groups.
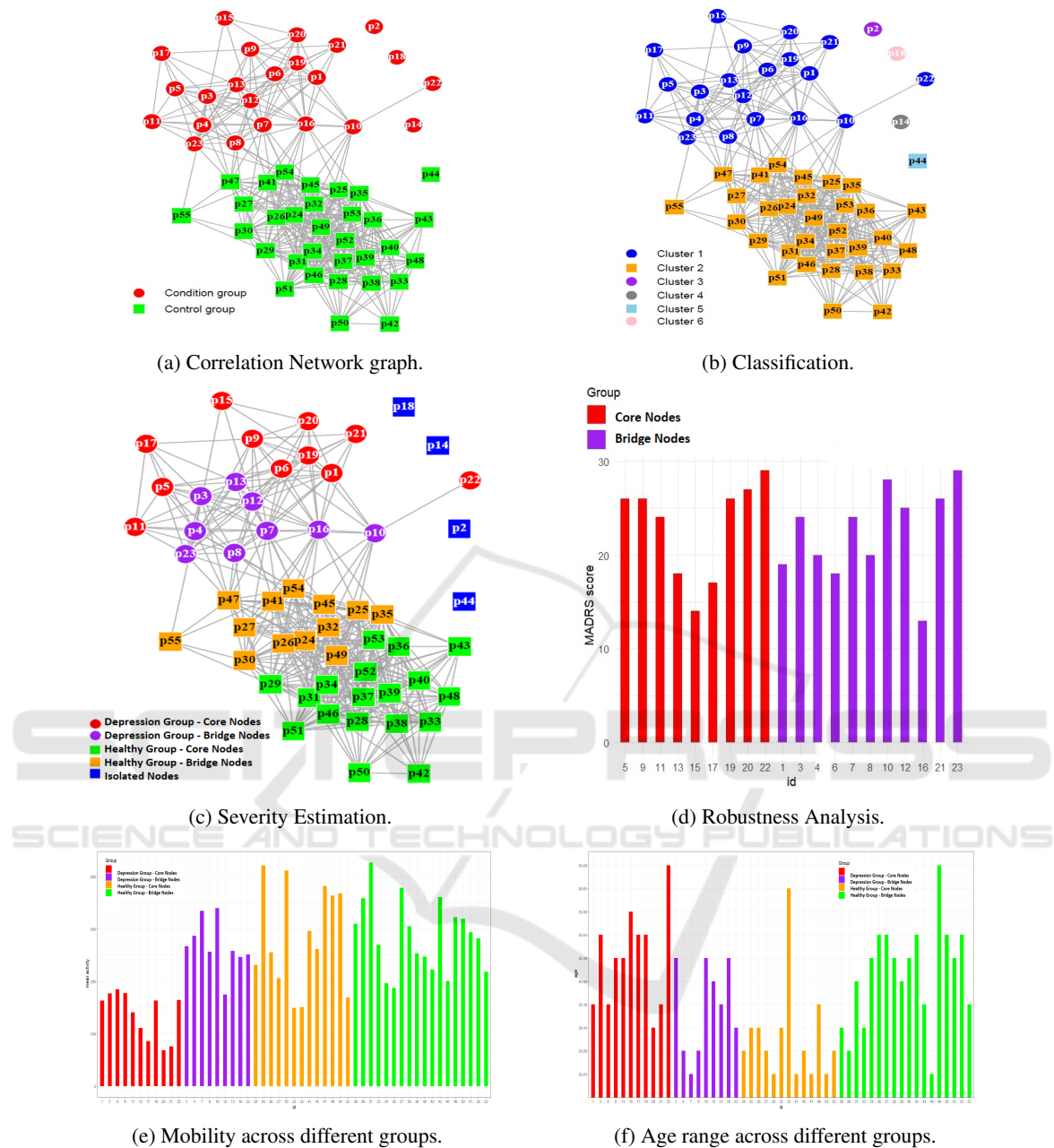

(f) Age range across different groups.

Figure 2: Classification and Severity estimation.

3 RESULTS

The study includes 55 participants of which 23 individuals belong to the condition group while 32 individuals belong to the control group. The novelty of our approach is that we did not use the group label (condition or control group) which is already present in the dataset. We have built on the fact that the mobility of the condition group is lower and distinguishable than the control group. Furthermore, we have utilized graph properties in order to estimate the severity of the depression. The results of our experiments are described in the following sections.

3.1 Classification

In the context of this article, the main aim of the classification task is to identify the subgroups that are in-

herently present in the population. The classification task is performed in two stages. In the first stage, a correlation network is constructed as shown in Fig .2(a), by incorporating 48 features derived in the earlier step and by using a predefined threshold T of 0.7. In the second stage, a clustering algorithm is employed to bring out the inherent clusters from the correlation network. We have employed the MCL algorithm to highlight the clusters in the graph network as depicted in Fig. 2(b). The graph displayed in Fig.2(b) demonstrates that two subgroups (condition and control) were fairly separated and established as separate communities (clusters). Although we have not used labels for classification, we are referring to the class label for the sake of accuracy estimation. Apart from the isolated nodes, p1 through p23 which are marked in blue belong to the condition group while p24 through p55 which are marked in orange belong to the control group.

3.2 Severity Estimation

The classification task identified two major subgroups as shown in Fig.2(b) . One of the subgroups is the condition group while the other is the control group. Since all the subjects belonging to the control group are healthy and not diagnosed with depression, illness severity has been estimated only for the condition group (p1 through p23). The DSS index is measured using equation 2 for each participant from the condition group. By utilizing the severity estimation procedure mentioned in Table 1, all the nodes in the condition group are split up into core nodes and bridge nodes as shown in Fig.2(c). we have computed score for each person in control group and categorized them into two groups as shown in Fig. 2(c). (orange and green color nodes). However, the description and interpretation of these nodes are out of the scope of this document.

4 ROBUSTNESS ANALYSIS

This section describes the validation analysis performed on the obtained results. This manuscript presents results in two folds. First, classification between condition and control group without utilizing label. Second, severity estimation of the condition group those who are suffering from a depressive disorder.

4.1 Robustness of Classification

In traditional label-driven classification tasks such as supervised machine learning techniques, the outcome is solely dependent on labels present in the dataset. Therefore, the classification results are subject to bias because of the labels present in the dataset. Furthermore, in medical datasets, it is not practical to expect a label for every observation as its high time intensive and requires huge human effort. To mitigate this problem, our classification task is data-driven rather than label-driven. However, we use existing class labels to analyze the robustness of our methodology. Table 2 illustrates the performance of the classification task by comparing our outcome against the known label. The above results demonstrate that none of the subjects were misclassified. Apart from the two major groups some participants got isolated and not connected to the network. Out of 55 subjects under the study, 4 of them are isolated.

4.2 Robustness of Severity Estimation

In this section, severity estimation results of the condition group are validated against the clinical rating scale which is already present in the dataset. The classification task identified 20 subjects belonging to the condition group out of a total of 23 subjects. Then, the severity estimation task divided them into two categories as shown in Table 1. To validate our results from the clinical context, participants with high severity of depression are expected to possess a high MADRS score whereas subjects with low severity are expected to have a low MADRS rating. According to MADRS ratings shown in Fig.2(d), our results prove that core nodes are rated with a low MADRS score while bridge nodes are rated with a MADRS rating. Furthermore, the results demonstrate that the likelihood of a DSS index reflecting a clinical rating scale such as MADRS is very high.

Table 2: Classified category vs dataset label.

Actual group	Classified group			
	Condition	Control	Isolated	Total
Condition	20	0	3	23
Control	0	31	1	32
Total	20	31	4	55

5 DISCUSSION

This research aimed to build a computational model which is driven by the mobility data instead of the class label present in the dataset. Most of the previous studies utilized supervised machine learning algorithms in which a classifier is trained on the existing data with a known class label then the trained model will be used to predict future instances. The disadvantage of this approach is that the training step expects all the class labels to be present in the dataset. It implies that the dataset must contain a label indicating the health status of the subject. However, in the real world, it is a tedious job to append health status to each observation. Furthermore, the model should be able to produce useful results even though the labels are not available in the dataset. Our current work in this paper attempts to bridge this gap. Since our model does not necessitate a label to be annotated for each observation, it works only by including mobility data.

We have designed this model in two stages. First, a correlation network graph is constructed. Second, the MCL algorithm is employed to detect communities in the graph. The correlation between each pair of subjects is measured using the Pearson correlation coefficient with respect to 48 features. The intuitive idea behind the construction of a correlation network is that if any two subjects are connected by an edge, then they are correlated concerning their mobility data. In other words, two subjects are connected by an edge if they possess similar mobility composition. Since our method is not machine learning based, we do not use a confusion matrix as a method of finding the accuracy metric. But cluster quality metrics such as modularity can be used. Yet, a quality metric such as modularity does not make sense in the case of biomedical datasets. Therefore, we have validated our results against the clinical score available in the dataset.

In addition to the classification and severity estimation, we have performed an enrichment analysis to verify if there are common and distinguishable demographic properties between or within the subgroups. Enrichment analysis is a powerful computation tool that has been heavily used in biomedical informatics. In the past, researchers have mainly used this technique to interpret gene expression data and compare groups that display similar biological parameters (Mclean et al., 2016). In this study, we have compared the age and average motor activity of each person concerning between subgroups and within the subgroup. The results of this analysis are shown in Fig.2(e) and Fig.2(f). Enrichment analysis reveals some interesting facts that are significant to consider. For example,

most of the participants in the high depression severity zone are younger than the high severity zone. Conversely, the mobility profiles of high-depression zone subjects are lower than low depression subjects.

6 LIMITATIONS AND FUTURE WORK

The primary focus of this work is to identify different subgroups that are inherently present in the data by utilizing their mobility data. A methodology is a data-driven approach rather than label-driven. Although our results are promising, there are certain limitations in this study. First, even though the correlation between the DSS index and MADRS clinical score is very high, it is not always true. In other words, a few participants' DSS index is not reflecting the MADRS score. This might be because of the fact that the MADRS score might be always an accurate measure of depression especially when the patients are under antidepression medication treatment (Montgomery and Åsberg, 1979). In addition to that, in the medical domain, it is always not viable to get 100% accurate results. However, our model has been proposed based on the mobility data rather than depending on the feelings or experiences of the clinician. Secondly, the dataset contains only 23 subjects belonging to the depression group. We do not reject the limitation of a limited sample. Nevertheless, our future work is acquiring larger datasets that include multiple psychological disorders such as depression, and ADHD.

7 CONCLUSION

Depression is a serious mental health disorder that can negatively impact a person's daily routine and cause a significant reduction in life span. Prolonged diagnosis can cause deterioration in the mental health condition and eventually reduces the possibility of treating the illness or limit its effectiveness. Unfortunately, there is no objective clinical test that can detect depression disorder and estimate its severity level. Existing clinical procedures are predominantly driven by clinician observation and self-reporting symptoms from the patient or his/her family members. Nevertheless, many researchers have developed several computational methods to address the problem. However, most of these approaches are supervised and driven by class labels there are present in the dataset. Appending a label for every observation takes huge human

effort and is impractical in real-world scenarios.

In this study, we introduce a novel data-driven computational method that can classify depression and estimate its severity level without using a class label. The proposed model is motivated by the fact that reduced mobility is an early indication of depression. At first, a graph-based correlation network is constructed using the mobility data collected from wearable sensors and employing a clustering algorithm to extract strongly connected communities (clusters) in the graph. The advantage of employing the correlation network model is that its underlying graph inherently possesses the potential communities, and they can be identified by s suitable community detection clustering algorithm such as MCL. The obtained network also has several graph-theoretic properties that can be utilized to further analyze the mobility data. Taking advantage of such properties, we have developed a new metric, Depression Severity Score index (DSS), by using graph metrics including inter and intra-cluster density. The obtained results demonstrate that the correlation between measured DSS and clinical depression rating score is high. We envision that DSS can be used as a supplementary tool for clinicians and healthcare professionals in obtaining objective diagnostic assessment.

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