UTILISING BAYESIAN NETWORKS TO COMBINE MULTIMODAL DATA AND EXPERT OPINION FOR THE ROBUST PREDICTION OF DEPRESSION AND ITS SYMPTOMS

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ABSTRACT
Predicting the presence of major depressive disorder (MDD) using behavioural and cognitive signals is a highly non-trivial task. The heterogeneous clinical profile of MDD means that any given speech, facial expression and/or observed cognitive pattern may be associated with a unique combination of depressive symptoms. Conventional discriminative machine learning models potentially lack the complexity to robustly model this heterogeneity. Bayesian networks, however, may instead be well-suited to such a scenario. These networks are probabilistic graphical models that efficiently describe the joint probability distribution over a set of random variables by explicitly capturing their conditional dependencies. This framework provides further advantages over standard discriminative modelling by offering the possibility to incorporate expert opinion in the graphical structure of the models, generating explainable model predictions, informing about the uncertainty of predictions, and naturally handling missing data. In this study, we apply a Bayesian framework to capture the relationships between depression, depression symptoms, and features derived from speech, facial expression and cognitive game data collected at thymia.

Index Terms— Depression, Bayesian Networks, Multimodal Analysis, Expert Knowledge Integration, Missing Data

1. INTRODUCTION

The healthcare sector is in urgent need of better tools to tackle the challenges of major depressive disorder (MDD) efficiently and effectively. Depression assessments are still based on self-report questionnaires which are prone to bias [1] and where the variability between individuals’ interpretation of questionnaire items is high [2]. Furthermore, clinical interviews and observation are naturally influenced by the clinician’s experience and acumen [3]. Collectively, this means identifying the correct diagnosis and treatment can take many years, with some studies finding untreated depression rates as high as 77% [4]. There is immediate need for a clinical decision support tool offering objective depression metrics, as easily accessible and reliably trackable as physical health ones (e.g. blood test markers). Advances in digital health and phenotyping technologies are therefore being considered integral to improving MDD-associated clinical pathways [4].

In recent years, there has been an acceleration in the number of papers centred around the application of machine learning in the domain of digital health. These works include analyses of speech, facial expressions and cognitive assessments to provide objective measurement criteria to aid in MDD diagnosis [5-7]. A potential shortcoming of such works, however, is that they have almost exclusively been focused on supervised modelling paradigms learning how to partition data based on subjective depression scales, such as the 8-item Patient Health Questionnaire (PHQ-8; [8]), thereby also becoming subject to the same concerns around self-report subjectivity. Moreover, they mainly utilise large multivariate feature spaces and deep learning models which lack transparency regarding how their decisions are being made [9]. Alongside this lack of explainability, such approaches also lack the ability to incorporate expert opinion into the model and are unable to handle missing data robustly.

Bayesian Networks (BN) offer a natural framework to satisfy all the above requirements, which are common in health-care modelling. Indeed, a few recent works have successfully adopted BNs to tackle mental health modelling problems; for example, [10][11]. However, the predictors in these approaches have been simple demographics, biological or environmental factors, as opposed to rich multimodal datasets that can include audio and video data. In this study we propose a novel BN model for joint MDD and depression symptoms classification given a multimodal feature set containing speech, facial expression and cognitive game data gathered at thymia [7]. We then present a range of experiments demonstrating the model’s performance under different realistic use case scenarios, including varying degrees of missing data and integration of expert knowledge.

The main novel contribution of this work is a methodology for incorporating multimodal data in a BN model that achieves strong performance in MDD classification. We also highlight its potential as a clinical decision-support tool by providing results for individual core MDD symptoms.
2. EXPERIMENTAL SETTINGS

This section describes our key experimental settings including the thymia dataset and introduces our Bayesian network.

2.1. Dataset

The experimental data in this study consist of 1,183 participants who performed a series of short online activities within a single session on the thymia Research Platform using their own personal devices (Table 1). We previously presented a portion of this dataset with a smaller number of participants and a focus on audio (acoustic, prosodic and linguistic) and cognitive data gathered from two thymia activities, i.e. an Image Description Task and the n-Back Task, as well as individual PHQ-8 items; see [7]. In the present study, we expand the number of data modalities to include video data recorded during the Image Description Task, as well as additional audio data gathered during a Paragraph Reading Task. Additionally, we include information on the type of personal device that was used to perform the activities as well as on the presence or absence of an MDD diagnosis as self-reported by participants.

2.2. Thymia Activities

We focus on data gathered through three thymia activities: the n-Back Task, the Image Description Task and the Paragraph Reading Task. The first two activities have been previously described in detail in [7]. The Paragraph Reading Task required participants to read aloud a short story (Aesop fable “The North Wind and the Sun” widely used within phonetics) while their voice was being recorded via their device’s microphone. Herein we abbreviate the activity names to “n-Back”, “Image”, and “Paragraph”.

2.3. Features

Data from the three thymia activities was processed to extract a total of 322 features which included: 8 cognitive features (n-Back), 97 video features (Image), 88 extended Geneva Minimalistic Acoustic Parameter Set (eGeMAPS) acoustic and prosodic features (from both Image and Paragraph), 24 linguistic features (Image), as well as an additional curated set of 17 fine-grained acoustic features (Paragraph). Details on the cognitive, eGeMAPS and speech features were previously provided and can be found in [7]. The video features were extracted using Visage Technologies Software. The software extracted features related to facial translation, rotation and gaze in the 3D space, action units

2.4. Bayesian Network Model

Bayesian Networks (BNs) are probabilistic graphical models that specify the joint distribution by defining a set of conditional independence rules that can be easily mapped to a Directed Acyclical Graph (DAG). Our BN model is composed of four groups of variables: CONFOUNDS, CONDITION, SYMPTOMS and ACTIVITY measures (Figure 1).

The CONFOUNDS group includes age and gender as demographic variables, and emotions. An estimated face scale was also provided to normalise values, allowing for changes in a participant’s distance from the screen and camera.

The fine-grained acoustic features consist of summary statistics of the formant trajectories extracted from specific voiced audio segments of the Paragraph audio recordings. We used audio segments corresponding to three sets of words chosen to isolate the following vowel sounds: /i/ (‘wind’, ‘which’, ‘he’, ‘his’, ‘him’), /u/ (‘should’, ‘could’, ‘took’, ‘two’), /a/ (‘hard’, ‘last’, ‘and’, ‘at’).

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1The thymia Research Platform allows the hosting of complex, remote, multimodal studies on a smart device. During various activities (e.g. questionnaires, cognitive games etc.), data from the device’s camera, keyboard, mouse/trackpad and/or touch screen can be streamed to a secure backend. The platform is fully HIPAA-compliant, 2018 EU GDPR-compliant, is ISO27001-certified and NHS Toolkit-compliant.
The condition variable indicates the presence or absence of a depression diagnosis. To capture the variation of depression incidence across age groups and genders, we model the condition $C$ as a Bernoulli distribution:

$$p(C|A, G) = \text{Ber}(C| \text{logistic}(f_c(A, G)))$$  \hspace{1cm} (1)

where

$$f_c(A, G) = \omega_{c,0} + \omega_{c,a} A + \omega_{c,g} G.$$  \hspace{1cm} (2)

The symptom variables represent the individual PHQ-8 items. In order to simplify the model, each symptom is converted from its original 4-point scale to a binary scale indicating ‘low’ and ‘high’ symptom levels. The symptom-specific binarisation thresholds are calculated from a logistic regression of each individual symptom on the condition variable. In order to capture inter-symptom conditional dependencies, the symptom variables are embedded in an inter-symptom DAG estimated using the DirectLiNGAM graph discovery algorithm [17]. Each binary symptom variable $S_s$, with $s \in \{0, 1, \ldots, 7\}$, is modelled as a Bernoulli distribution:

$$p(S_s|A, G, C, P_s) = \text{Ber}(S_s| \text{logistic}(f_s(A, G, C, P_s)))$$  \hspace{1cm} (3)

where $P_s$ is a column vector of $k_s$ parent symptoms of $S_s$ as specified by the inter-symptom DAG and

$$f_s(A, G, C, P_s) = \omega_{s,0} + \omega_{s,a} A + \omega_{s,g} G + \omega_{s,c} C + \omega_{s,p} P_s$$  \hspace{1cm} (4)

with $\omega_{s,p} \in \mathbb{R}^{k_s}$. In the following we use $S$ to indicate the column vector of all binary symptoms.

The activity measures are derived from the feature sets described in the previous section by applying two processing steps. First, standard rescaling is applied to all features individually. Second, supervised PCA [18] is applied to each feature set independently using the condition variable as target. The first two principal components of each feature set are then selected, yielding a total of 16 activity measures (2 from N-Back, 10 from Image, 4 from Paragraph). Each activity measure variable $M_m$, with $m \in \{0, 1, \ldots, 15\}$, is modelled as a Gaussian distribution

$$p(M_m|A, G, D, C, S) = \mathcal{N}(M_m|f_m(A, G, D, C, S), \sigma^2_m)$$  \hspace{1cm} (5)

where

$$f_m(A, G, D, C, S) = \omega_{m,0} + \omega_{m,a} A + \omega_{m,g} G + \omega_{m,d} D + \omega_{m,c} C + \omega_{m,s} S$$  \hspace{1cm} (6)

with $\omega_{m,s} \in \mathbb{R}^8$. In the following we use $M$ to indicate the column vector of all activity measures.

The full BN model describing the joint probability distribution over all the variables described above is then given by

$$p(M, S, C, A, G, D) = \prod_{m=0}^{15} p(M_m|A, G, D, C, S) \times \prod_{s=0}^{7} p(S_s|A, G, C, P_s) \times p(C|A, G) \times p(A) \times p(G) \times p(D).$$  \hspace{1cm} (7)

### 2.5. Model Implementation and Training

We implemented the BN model using the probabilistic programming library NumPyro [19]. Model training was performed via the Markov Chain Monte Carlo (MCMC) inference of model parameters using the No-U-Turn sampler (NUTS) algorithm in NumPyro, with 4 Markov chains and 1000 samples per chain. We used the following prior distributions for the model parameters: Dirichlet($K = 4, \alpha = 1$) for the group frequencies of the age variable; Beta($\alpha = 1, \beta = 1$) for the Bernoulli probabilities of the gender and device variables; $\mathcal{N}(\mu = 0, \sigma = 1)$ for all $\omega$ parameters in Equations (2), (4) and (6); LogNormal($\mu = 0, \sigma = 1$) for the $\sigma_m$ parameters in Equation (5).

### 2.6. Model Evaluation

We performed a stratified 5-fold cross-validation to evaluate model performance in a range of inference tasks. The same proportion of gender, age groups and PHQ-8 distribution was kept across the training and test sets for each fold. We use the area under the receiver operating characteristic curve (ROC-AUC) as our evaluation metric.

### 3. RESULTS AND DISCUSSIONS

Given the generative nature of a BN model, any of its variables or groups of variables can be chosen as targets in a prediction task. Of particular interest is the task of predicting condition and symptoms given the observation of other variables in the model. We performed a set of experiments to evaluate the model performance in this joint prediction task.

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**Table 1.** Sociodemographic, depression and activity distributions in the experimental data.

| Group   | #Participants | Age Mean | Age SD | Device Phone | Device PC | PHQ-8 Mean | PHQ-8 SD | Cumulative Activity Time | Activity Time |
|---------|---------------|----------|--------|--------------|-----------|-------------|---------|--------------------------|---------------|
| control | 481           | 34       | 14     | 46           | 948       | 4.8         | 3.9     | 10:55:38                 | "6 days, 6:47:37" |
| patient | 90            | 37       | 13     | 12           | 177       | 13.1        | 5.2     | 2:11:36                  | "1 day, 7:21:46" |


under several realistic scenarios (Figure 2). Overall, the experiments showed an increase in predictive performance with the amount of observed variables in the model, and a generally higher performance for CONDITION than SYMPTOMS. The lowest performance was found when the CONFONDS, age and gender, are the only available information, with an average ROC-AUC of 0.58 for CONDITION and 0.55 for the SYMPTOMS. Conversely, when all ACTIVITY measures are available, the average ROC-AUC increases up to 0.75 for CONDITION and 0.63 for SYMPTOMS.

Additionally, we evaluated the performance when only subsets of ACTIVITY measures or data modalities are available as input to the model (Figure 2). These experiments correspond to common real-life scenarios in which a participant does not perform the full set of activities or opts out of audio/video recording. This set of experiments revealed an increase in model performance as more activities are observed, with paragraph measures having the strongest positive impact. Likewise, performance increases the more data modalities that are included, with audio having the strongest positive impact.

Finally, we performed a set of experiments where all ACTIVITY measures plus one SYMPTOM are observed (Figure 2). This simulates the scenario in which reliable information about the presence or absence of a symptom is available to the clinician using the model. In this scenario, we observed that the predictive performance further improves for both CONDITION and the other unknown SYMPTOMS.

Fig. 2. Model performance in the joint prediction of condition and symptoms given the observation of other sets of variables. Averages (with 95% CI) across 5 cross-validation test folds are shown. Dashed lines highlight model performances when all measures are observed.

The main purpose of our BN model is to serve as a support tool for clinical decision-making. The model allows integration of multimodal information from thymia activities with expert knowledge provided by the clinician using it. Given its ability to generate predictions despite missing information, this model naturally lends itself to be used as part of an iterative screening process. For example, the clinician may decide to administer only a subset of activities to a patient, then consult the model predictions and decide whether other information may be needed to support a diagnosis, subsequently administering additional activities, asking the patient about their sleep patterns or investigating other symptoms (Figure 3).

4. CONCLUSIONS

This work represents a proof-of-concept for a BN model, demonstrating its performance as a robust MDD prediction tool utilising multimodal speech, vision or cognitive data. We also highlight the potential of this model under different real-world operating conditions. A limitation of the current model is the reduced set of confounding variables. Future research will explore a larger set of confounds, such as life events that could affect mood (e.g. loss or change of jobs) or health problems that could affect voice (e.g. having a cold). An additional limitation of the current model is the lack of time dynamics, which limits its scope to static one-off predictions. In future work, we aim to collect a longitudinal dataset and to expand the model to a dynamic BN, in order to enable its application to other clinical reasoning tasks where time is a critical factor, such as prognosis. Finally, given the large heterogeneity of symptoms in MDD and their overlap with many other conditions (e.g. anxiety or PTSD), digital phenotype research needs to ensure that the proposed phenotypes are sensitive and specific to MDD. Hence, the next steps for future research will be to work with clinician benchmarks and control datasets that include various differential diagnoses.

Fig. 3. Raw model predictions of condition probability in two sample participants, one patient and one control, for four sets of inputs: A = confounds, B = confounds + n-back, C = confounds + n-back + paragraph, D = confounds + n-back + paragraph + sleep symptom. Error bars denote 95% credible intervals.
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