Supplementary 2: Deep Neural Network Analysis

Introduction

As outlined in the associated manuscript, a DNN approach to the present dataset is motivated by its dimensionality and lack of aetiological model with which to 'subjectively' select a feature set feasibly capable of predicting outcome.

Architecture Selection

Hyperparameter Selection

A persistent challenge in neural network development is the expansive nature of parameters in the model. Architectures and characteristics of them are all experimenter dependant. As such, we attempted to some extent objectify our model selection process to provide credence to our claims that non-linear models fail to accurately predict outcome in this cohort. Based upon initial trial training runs we established a 3-dimensional parameter space to explore the most efficient network:

- No. units in the hidden layers.
    - 20 and 80
- No of hidden layers.
    - 1, 3, and 5.
- Activation function
    - SelfNormalising*, Leaky ReLU, TanH

- Self-normalising network structures are unique in their model weight initialisation and normalisation of weights at each training epoch, method of dropout as well as their activation function.
- Fixed hyperparameters based on pilot modelling were:

- Dropout rate = 0.5 (Alpha Dropout rate = 0.5 in the case of the self-normalising network)
- Partition ratio of 0.7 (70% for training the data 30% for validation) for hyperparameter sweeps, 0.9 for cross-validation, randomly allocated each new network initialisation.

The model selection process

Step 1. Selecting optimal hyperparameters: Within the 2 x 3 x 3 hyperparameter space each possible combination was iterated over to 2000 epochs with early-stopping and checkpointing at the optimal binary cross entropy to establish the most optimal network hyperparameters. AUROCs for each network in its optimally trained state were then compared to establish the most clinically useful predictive network for further evaluation. Figure 1 and 1a show evaluation metrics and training characteristics for the parameter sweep and optimal model for the functional group and Figure 2 and 2a for the pathophysiological group.

Step 2. Cross-Validation: In order to achieve an accurate assessment of the DNNs predictive capacity we then employed a 10-fold cross-validation process of the model selected through hyperparameter sweeps. The dataset was divided into 10 subdivisions at random and a model trained on a 0.9 partition ratio and validated against a 0.1 validation set. This was repeated 10 times with every single observation being used to validate the efficacy of the model. The variation of each successful model in each scenario tested are shown in Table 1.

Step 3. Assessing alternative feature combinations: Given the DNNs failure to predict based solely on the baseline dataset we assessed the capacity of increasing and decreased complexity of feature space i.e. the predictors in the model and compared the ability to predict outcome with little change.