NIAGADS

RESEARCH USE STATEMENT AND NON-TECHNICAL SUMMARY

Research Use Statement for Application for Genomic Data from NIAGADS

Please limit to 2,200 characters max. The statement should include the following components:

- Objectives of the proposed research;
- Study design;
- Analysis plan, including the phenotypic characteristics that will be evaluated in association with genetic variants

Research Use Statement:

The aim of this study is to investigate the consistency of generating a polygenic risk score for Alzheimer's disease (AD) across different cohort using different genotyping platform. This investigation aims to identify the most biologically relevant SNPs (rather than statically relevant) that can be used to predict individuals at high risk of developing AD, with the long-term goal of creating an early diagnostic test and aid development of personalized therapeutic interventions.

Access to three genotyping datasets have been requested to use alongside my own generated dataset using the Brains for Dementia Research cohort. Polygenic risk score analysis will be performed on each dataset independently to derive the best SNP model to predict AD in that cohort. The SNP models derived for each cohort will then be applied to see how well they predict AD in the other datasets. Finally, a combined SNP model will be derived from those SNPs in common across the dataset, with the accuracy in prediction compared to the other SNP models. Only the AD diagnosis status will be used in this analysis alongside the genotyping data provided for each cohort. The datasets may be subjected to imputation to increase SNP coverage if required.

I will contact NIAGADS to start the process of submitting derived data, in this case the final SNP model to generate polygenic risk scores for Alzheimer's disease when a publication has been accepted, so the data will become available to the public in compliance with the timeline indicated in the GDS.

Non-Technical Summary for Application for Genomic Data from NIAGADS

Investigators will provide a non-technical summary of their proposed research. If the project is approved, this statement will be publicly available for lay audiences to read the purpose and objectives of the research. Please limit to 1,100 characters.

Polygenic risk score analysis is now being used to investigate which variations in the DNA predict high risk of developing AD, however currently this analysis is being carried out on single cohorts, with very little in the data produced identifying consistent variants that can be used for an early diagnostics test. The purpose of this study is to identify a genetic model that accurately predicts risk of developing AD. This will be accomplished by analyzing the DNA data from different cohorts to generate risk score model that will consistently predict those individuals with AD with a high accuracy across all datasets. It is hope this may lead to an early diagnostic test for AD and therapeutic interventions.