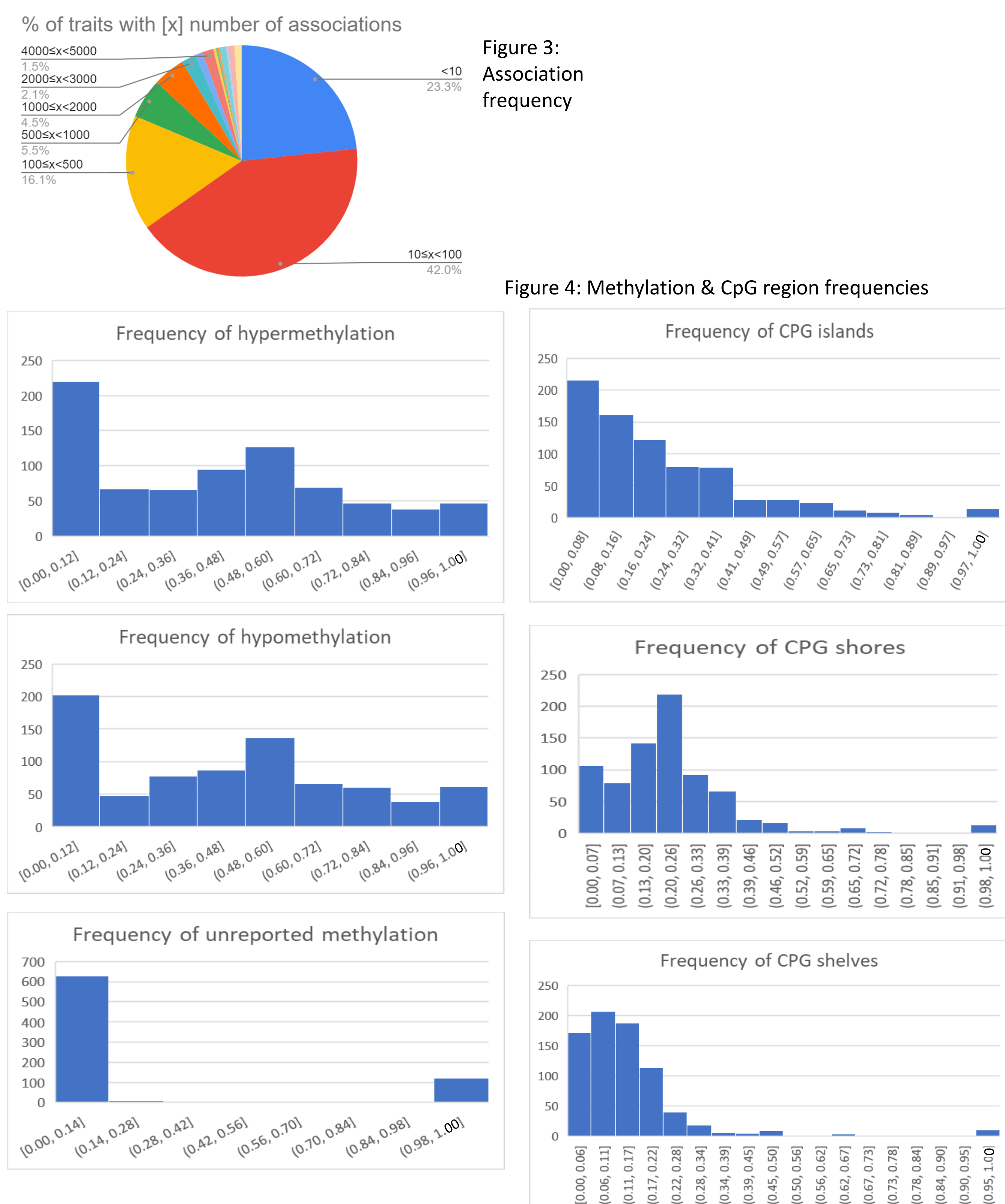


### Introduction

- ❖ Co-occurring diseases
  - ❖ Genes shared between autoimmune diseases(Wen & Yu, 2023), neurodevelopmental conditions(Reichard & Zimmer-Bensch, 2021), neurological and psychiatric disorders(Smeland et al., 2023)
- ❖ EWAS Atlas database compiles results of all studies
  - ❖ Traits, CpGs, associations
- ❖ CpG – Consecutive cytosine and guanine, possible methylation site
- ❖ Methylation – Suppresses the transcription of a gene
- ❖ Relationships can be visualized via a phenotypic network
  - ❖ Networks contain nodes connected by edges

Figure 1:  
Sample network

### Results



### Discussion/ Conclusions

- ❖ Preliminary analysis indicates that most traits(65.3%) have under 100 associations
- ❖ Low reported methylation rates
- ❖ CpG shores and shelves more common than islands
- ❖ Smaller sample used since full dataset is too large to analyze
- ❖ Cancers and non-cancer diseases within sample tend to cluster
  - ❖ Ex. Adenoma, oral cancer, colorectal cancer; schizophrenia & multiple sclerosis
- ❖ Some unclassified traits cluster, most are isolated
  - ❖ Fewer edges between clustered traits
- ❖ Isolated traits have fewer edges than clustered traits
- ❖ Understanding of correlated traits provides insight for diagnosis and treatment of co-occurring diseases

### Methods

- ❖ Data source: EWAS Atlas
- ❖ Analysis methods: Excel & Python Networkx package
- ❖ Preliminary Excel analysis of data
  - ❖ Traits sorted by number of associations, CpG site frequencies, methylation frequency
  - ❖ CpG frequency classified as islands, shores, shelves
- ❖ Sample of 10,000 traits from 643,806 in database used for Networkx analysis
  - ❖ Traits color coded, connected by shared CpGs (grey)
  - ❖ Networks made for all traits of a type
  - ❖ Types include cancer, non-cancer disease, behavior, phenotype, unclassified
- ❖ Graphs made for cancer, non-cancer diseases, unclassified

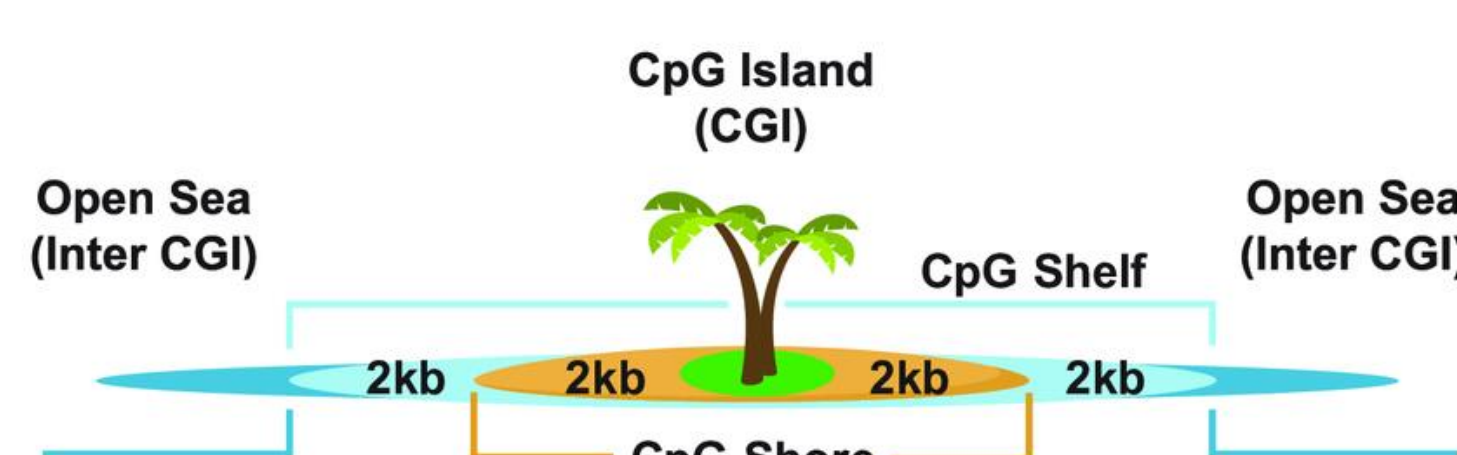


Figure 2: Diagram of CpG frequency terms(Bassal, 2023)

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