

Introduction

- Imaging genetics combines modern statistical genetics approaches with quantitative neuroimaging-derived phenotypes
- The unique nature of neuroimaging phenotypes presents certain challenge in using existing statistical genetics software

Aims

Develop imaging genetics tools that will

- Accept neuroimaging data formats
- Implement standard genetic analyses

Heritability

Genetic correlation

QTL

GWAS

- Accept populations of random complexity
- Capable of performing Meta and Mega Genetic analysis

Methods

Sequential Oligogenic Linkage Analysis Routines (SOLAR) is the basis for the new software – SOLAR-Eclipse (SE).

SE development in-progress

New data type module for reading NIFTI and GIFTI

JNI interfaces for easy pipeline integration

Performance optimization for parallel processing

Mega-genetic analysis capability

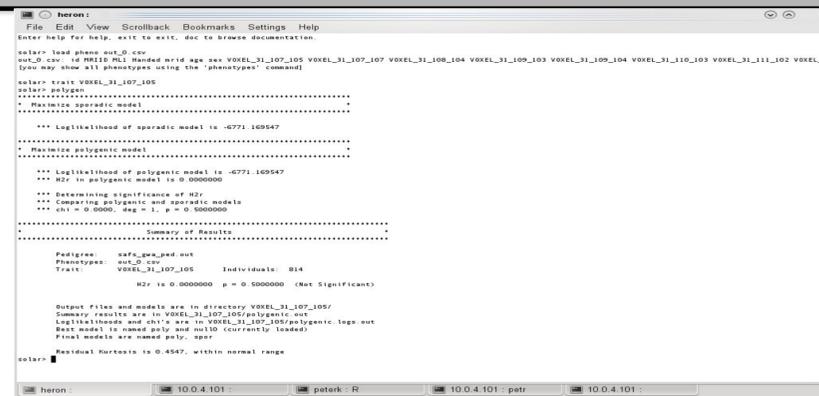


Figure 1. Solar interface

Progress

- [R]-like visual interface with support for shell and TCL scripts
- SE new phenotype file format was created to accommodate binary voxel-and-vertex wise data types (Figure 2)
- New command lines were developed to accommodate for parallel processing of binary phenotypes using mask command

Results

- Mega-genetic analysis can be performed by combining diverse sample into a single pedigree (Figure 3).

Different pedigrees are combined into a superfamily
 Class variable is added to identify separate pedigrees
 Samples for which raw data is available can be combined into a single pedigree.
 Sporadic effects are calculated individually for each sample.
 Inverse normal transformation is used to Z-normalize each dataset.
 Heritability estimates for each population and a combined pedigree are calculated to test significance of population-specific difference and the combined significance of heritability or fixed effects.

- Solar phenotype files read binary traits (Figure 2)
- Mask command provides for parallelization

Limitations

- Memory is a limiting factor for large studies
- Memory chunking is supported as ad-hoc solution

ID	Age	Sex	DTIFA:NIFTI	GMT:GIFTI
A00001	21	M	Gobs_fa.nii.gz:1	Gobs_gmt.gii.gz:1
A00002	34	F	Gobs_fa.nii.gz:3	Gobs_gmt.gii.gz:2
A00003	24	M	Gobs_fa.nii.gz:2	Gobs_gmt.gii.gz:3

Figure 2. Example for the new phenotype file CSV file format. Semicolon is used to provide identification of the file type in the header and the sequence of the volume/surface in the combined file.

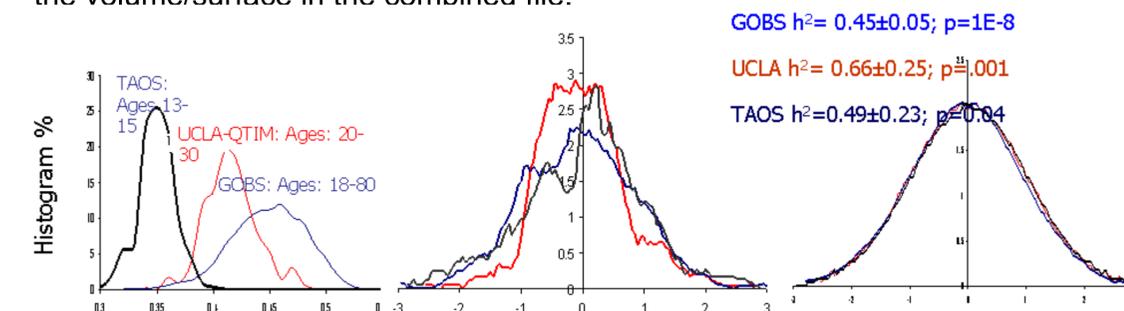


Figure 3. Mega-genetic processing

Mega Analysis

$$h^2 = 0.47 \pm 0.05; p = 10^{-16}$$

Meta Analysis SE-Weighted

$$h^2 = 0.48 \pm 0.07; p = 0.004$$

Meta Analysis N-Weighted

$$h^2 = 0.44 \pm 0.03; p = 10^{-6}$$

Figure 4. Mega- versus Meta-genetic analysis

Conclusion

We are developing SOLAR-Eclipse into an imaging genetic software toolkit.

See our workshop at Imaging Genetics Conference

<http://www.imaginggenetics.uci.edu>

Funding provided by NIH-NIBIB EB015611