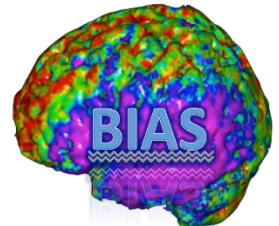
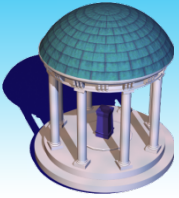




FVGWAS: Fast Voxelwise Genome Wide Association Analysis of Large-scale Imaging Genetic Data

Tutorial: pipeline, software and example



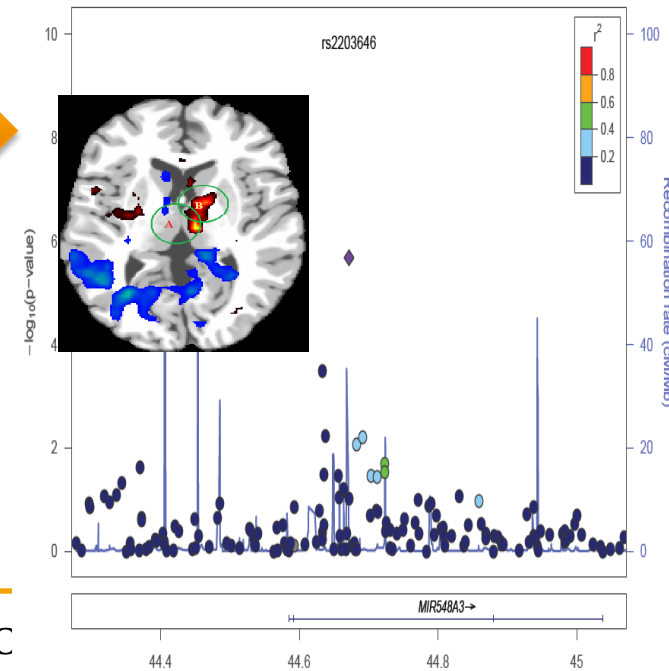
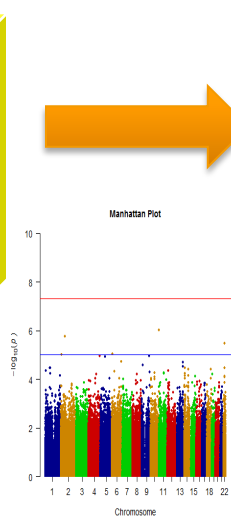
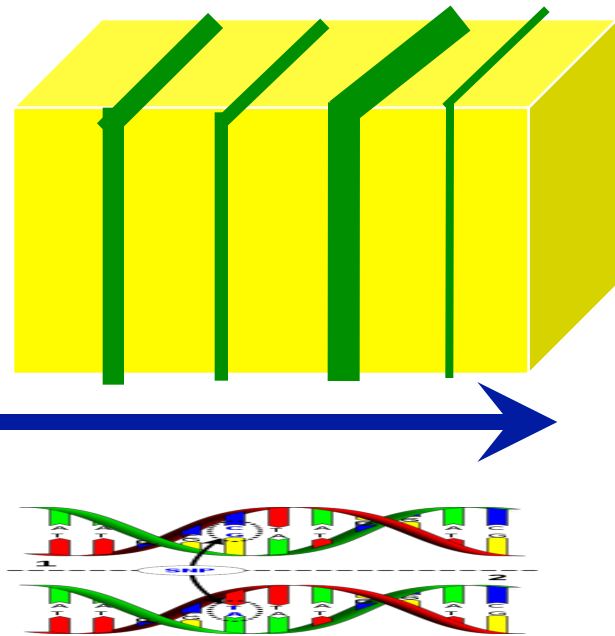


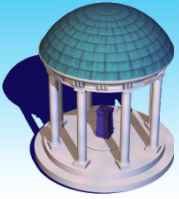
FVGWAS: Pipeline

(I) Spatially Heteroscedastic Linear Model

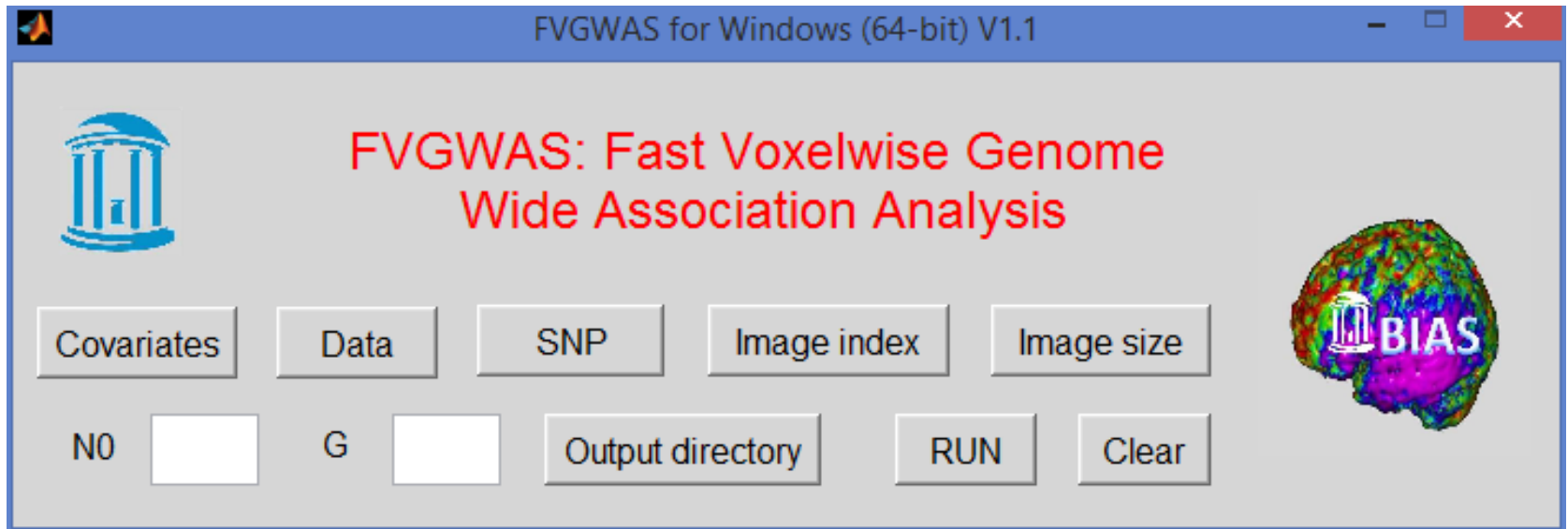
(II) Global Sure Independence Screening Procedure

(III) Detection Procedure

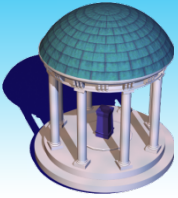




A Software for FVGWAS



<http://www.bios.unc.edu/research/bias/software.html>



A Software for FVGWAS

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FVGWAS: Fast Voxelwise Genome Wide Association Analysis

The Fast Voxelwise Genome Wide Association analysis (FVGWAS) framework to efficiently carry out whole-genome analyses of whole-brain data. FVGWAS consists of three components including a heteroscedastic linear model, a global sure independence screening (GSIS) procedure, and a detection procedure based on wild bootstrap methods. Specially, for standard linear association, the computational complexity is $O(n^*N_V * N_C)$ for voxelwise genome wide association analysis (VGWAS) method compared with $O((N_C + N_V) * n^2)$ for FVGWAS. Our FVGWAS may be a valuable statistical toolbox for large-scale imaging genetic analysis as the field is rapidly advancing with ultra-high-resolution imaging and whole-genome sequencing.



Download Now

FVGWAS-1.0: BIAS (URL)

OR

[See All Files >>](#)

Specifications

License: [BIAS License](#)
[Show more specifications](#) (Domain, Programming Language)

Associations

is from the makers of: [Spatial Statistical Parametric Mapping](#)

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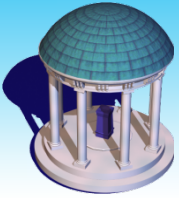
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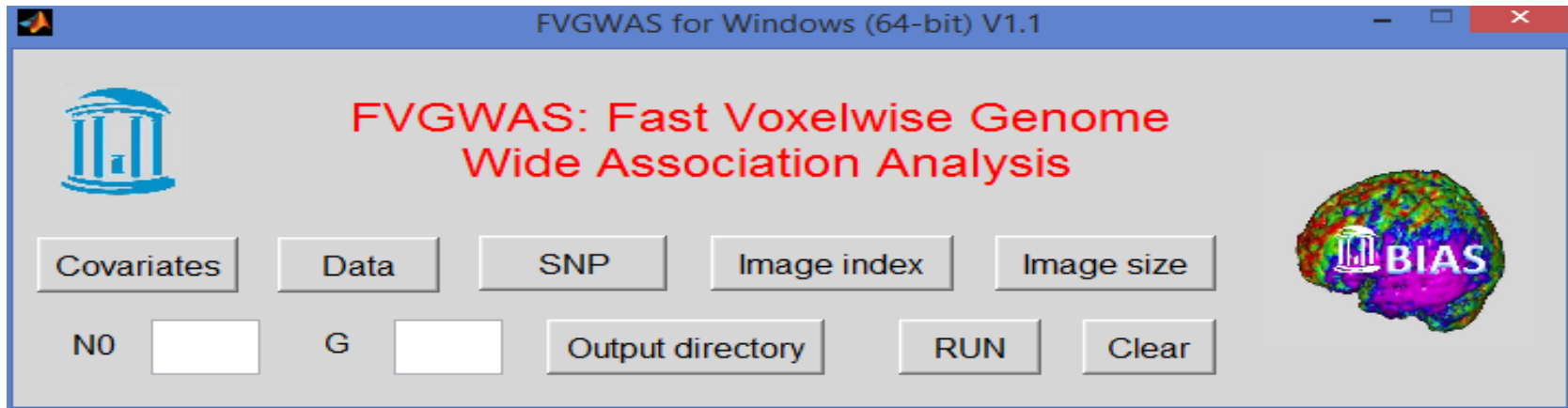
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Documents: 0
Forums: 2 messages in 2 forums
Mailing Lists: 1
News Items: 0
Task Manager: 0 open / 0 total
Tracker: 0 open / 0 total
Total Downloads: 40
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Registered: Jun 10

<https://www.nitrc.org/projects/fvgwas/>



Description of input files



Covariates: $n*d$ design matrix. n is the sample size and d is the number of covariates

Data: image data ($n*V$ matrix). V is the number of voxels (whole brain analysis)
or the number of ROIs (volumetric analysis)

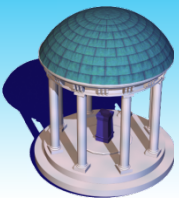
SNP: genetic data ($n*C$ matrix). C is the number of SNPs

Image index: $V*1$ vector. The index of voxels within the brain mask
(Applicable only for whole brain analysis)

Image size: the size of image data, e.g., $1*3$ vector means 3-D image data
(Applicable only for whole brain analysis)

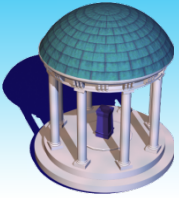
N0: the number of top SNPs

G: the number of bootstrap samples



Example: ADNI Data Volumetric Analysis

- **708** MRI scans of AD (**186**), MCI (**388**), and healthy controls (**224**) from ADNI-1.
- These scans on **462** males and **336** females are performed on a 1.5 T MRI scanners.
- The volumes of **93** ROIs for all subjects are computed.
- Covariates include intercept, gender, age, whole brain volume, and the top 5 principal component scores
- **501,584** SNPs are remained after quality control



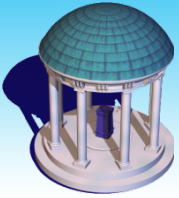
Lunch FVGWAS in MatLab

The screenshot displays the MATLAB R2014a environment. The Command Window shows the following commands and output:

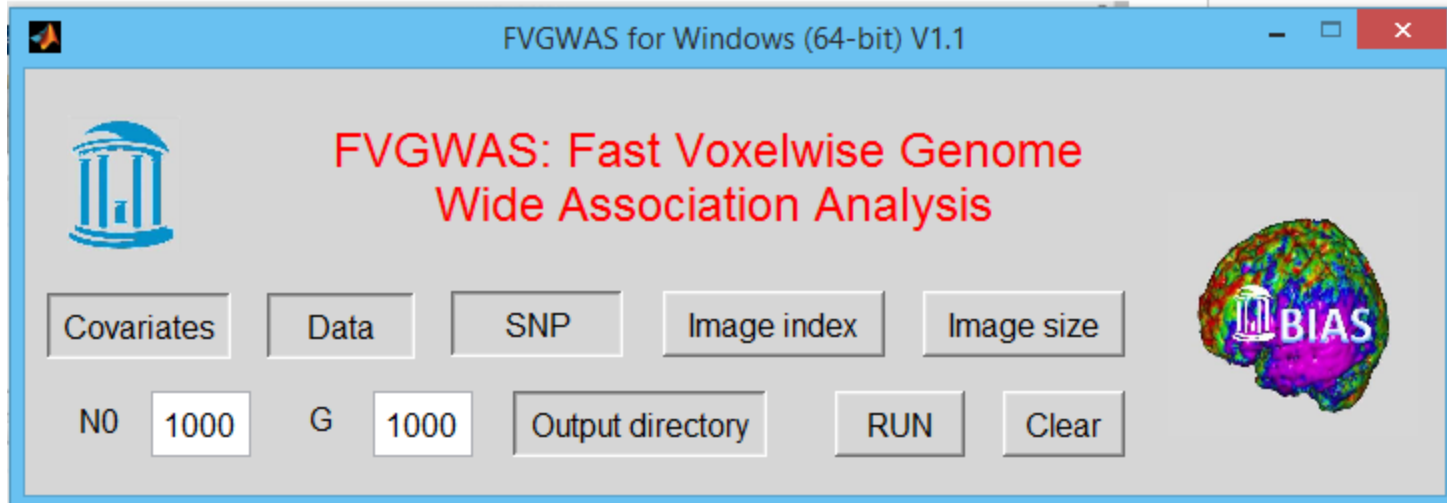
```
>> cd E:\FVGWAS-1.0
>> FVGWASgui
fx >>
```

The FVGWAS GUI window, titled "FVGWAS for Windows (64-bit) V1.1", contains the following elements:

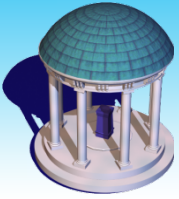
- Logo of the University of North Carolina.
- Title: "FVGWAS: Fast Voxelwise Genome Wide Association Analysis".
- Buttons for "Covariates", "Data", "SNP", "Image index", and "Image size".
- Input fields for "NO" and "G".
- Buttons for "Output directory", "RUN", and "Clear".
- A 3D brain model with a "BIAS" label.



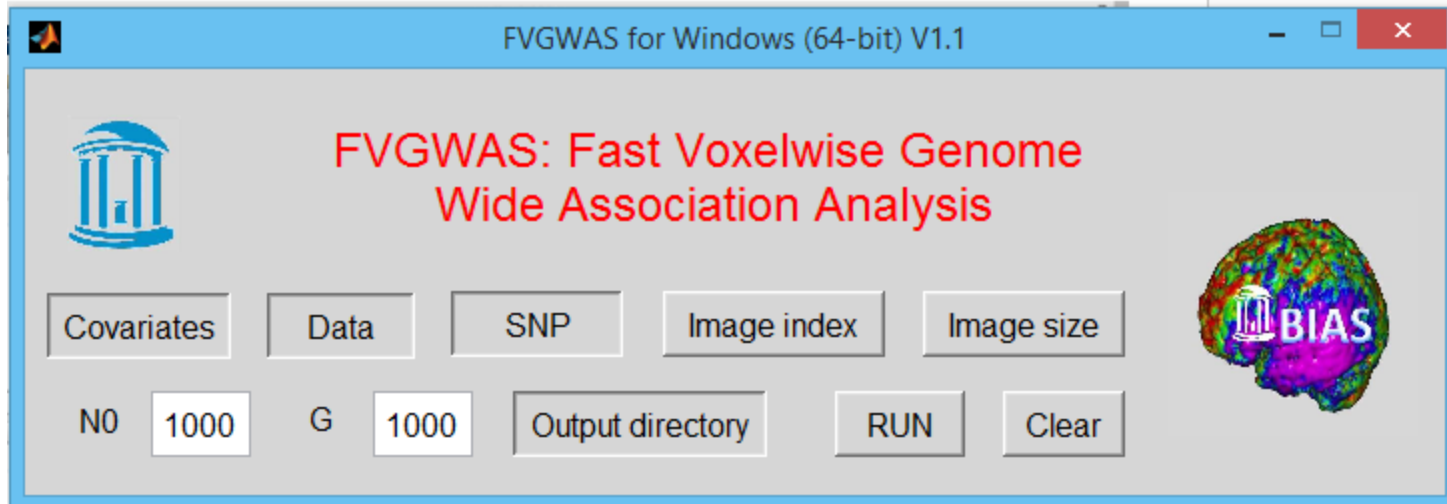
Load Data into FVGWAS



- Click the button **Covariates**: load “volumetric_covariate.mat”
- Click the button **Data**: load “volumetric_image_roidata.mat”
- Click the button **SNP**: load “volumetric_snpdata.txt”
- Set **N0**: 1000
- Set **G**: 1000
- Click the button **Output directory**: set “E:/FVGWAS-1.0/Oput”
- Click the button **RUN**



Output files of FVGWAS

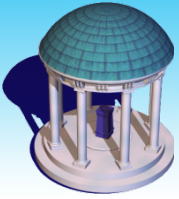


❑ “GSISresults.mat”

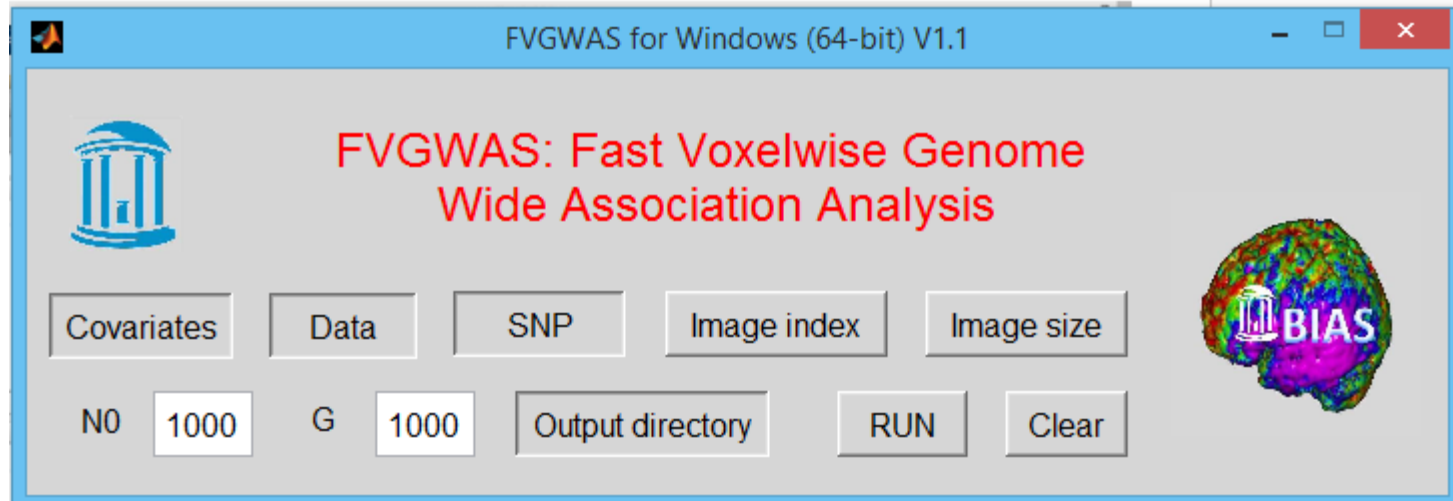
results of GSIS step, variable “pp” contains the $-\log_{10}\{p\text{-values}\}$ of all SNP data.

❑ “voxelclusterandSNP.mat”

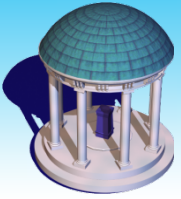
variable “rawpvalue” is a $C \times N_0$ matrix including the raw p-values of top N_0 SNPs.
variable “pv” is a $C \times N_0$ matrix, including the corrected p-values.



Results summary of FVGWAS

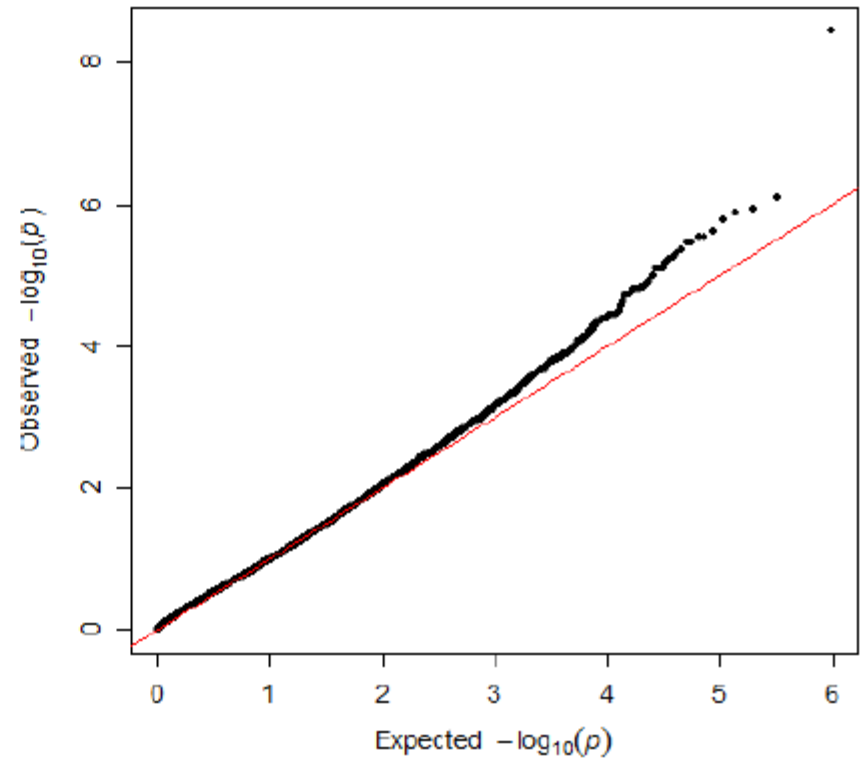
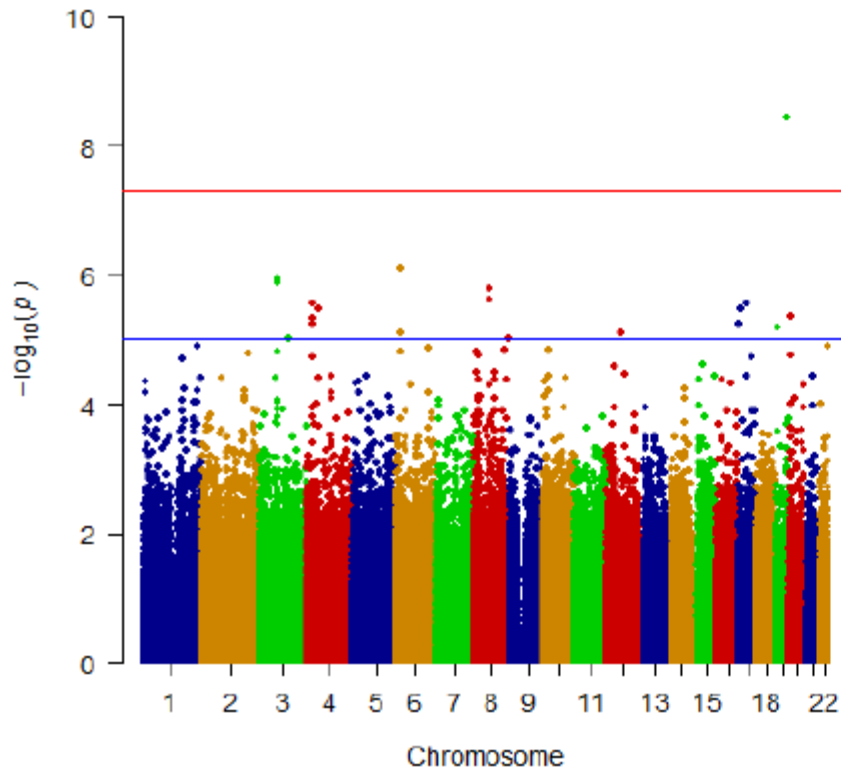


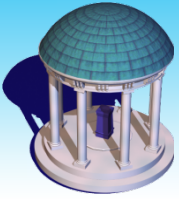
- ❑ Run “**manhattanplot.m**” in MatLab to generate the GWAS results
Output file: “SNP_ROlandSNP_nonsmoothing_hg19_ALL708_SC.txt”
- ❑ Run “**manp.R**” in R to plot the Manhattan plot and QQ plot



ADNI Data Analysis: Volumetric Analysis

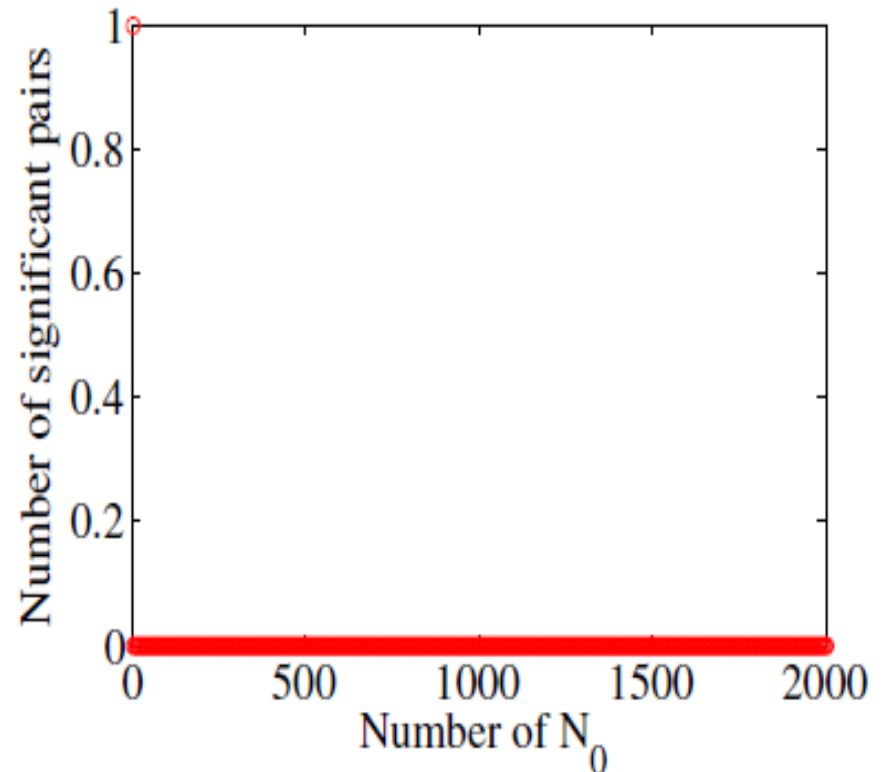
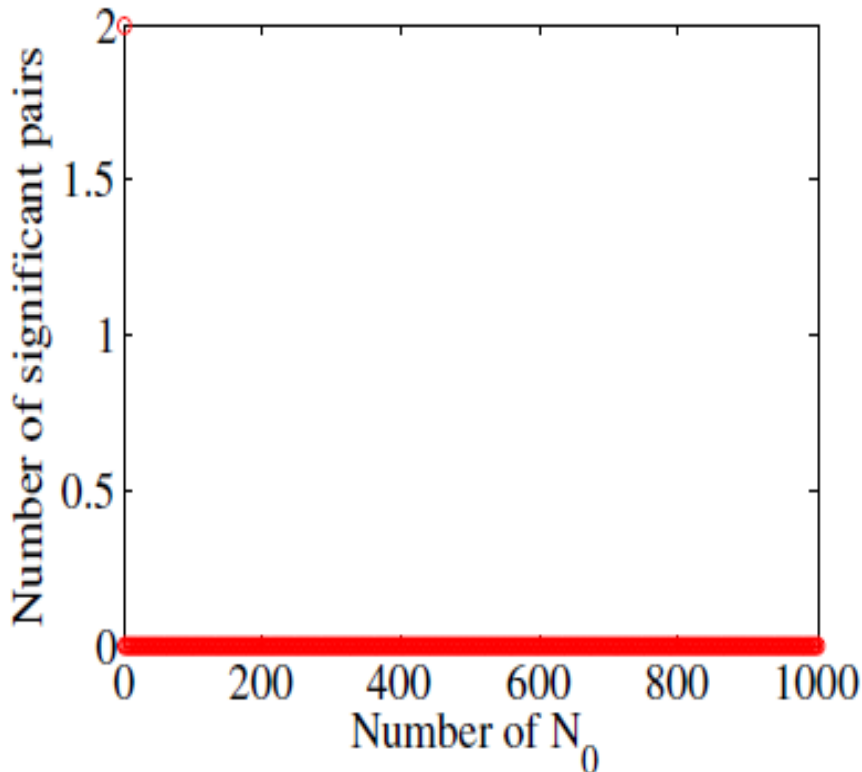
Manhattan Plot

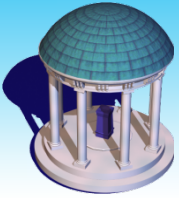




ADNI Data Analysis: Volumetric Analysis

Numbers of significant SNP–ROI pairs based on the corrected p-values





ADNI Data Analysis: Volumetric Analysis

**Top SNPs associated with volumes of
HL/HR —Hippocampus Left/Right and AL/AR — Amygdala Left/Right**

ROI	Best SNP	CHR	BP	p-Value	Gene
HL	rs2075650	19	45395619	1.4E-07	TOMM40
	rs6896317	5	142949513	5.5E-05	TRIO
	rs439401	19	45414451	7.6E-04	APOE
HR	rs2075650	19	45395619	2.7E-07	TOMM40
	rs6896317	5	142949513	5.5E-05	TRIO
	rs439401	19	45414451	1.2E-03	APOE
AL	rs2075650	19	45395619	1.5E-05	TOMM40
	rs6896317	5	142949513	5.8E-05	TRIO
	rs405509	19	45408836	1.4E-03	APOE
AR	rs2075650	19	45395619	1.4E-08	TOMM40
	rs6896317	5	142949513	4.7E-07	TRIO
	rs405509	19	45408836	1.1E-03	APOE