Doctoral Dissertation Proposal Defense
Data-adaptive SNP-set-based Association Tests of Longitudinal Traits

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Dec 15, 2014

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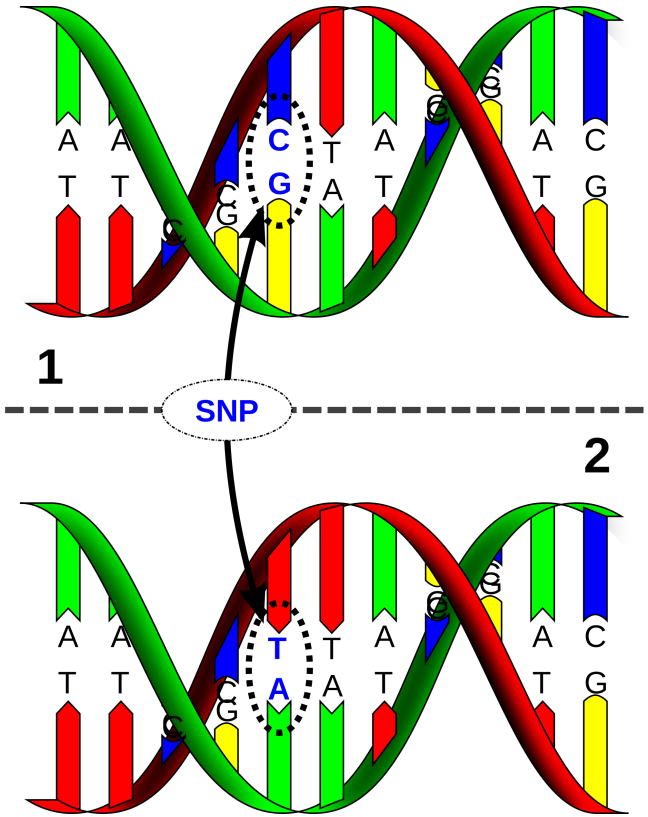
Introduction to GWAS

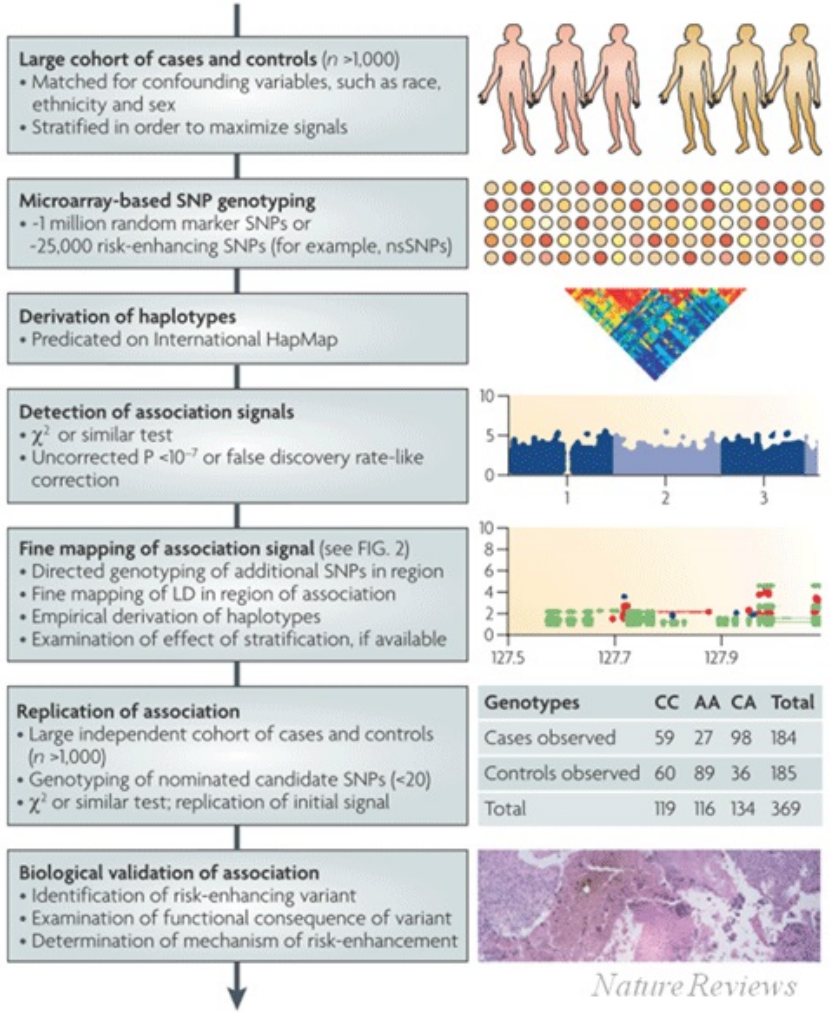
What is SNP?



A Single Nucleotide Polymorphism (SNP) is a DNA sequence variation occurring commonly within a population (e.g. 1%) in which a single nucleotide A, T, C or G in the genome (or other shared sequence) differs between members of a biological species or paired chromosomes.

Introduction to GWAS

A flowchart of GWAS



Introduction to GWAS

How does GWAS result look like?

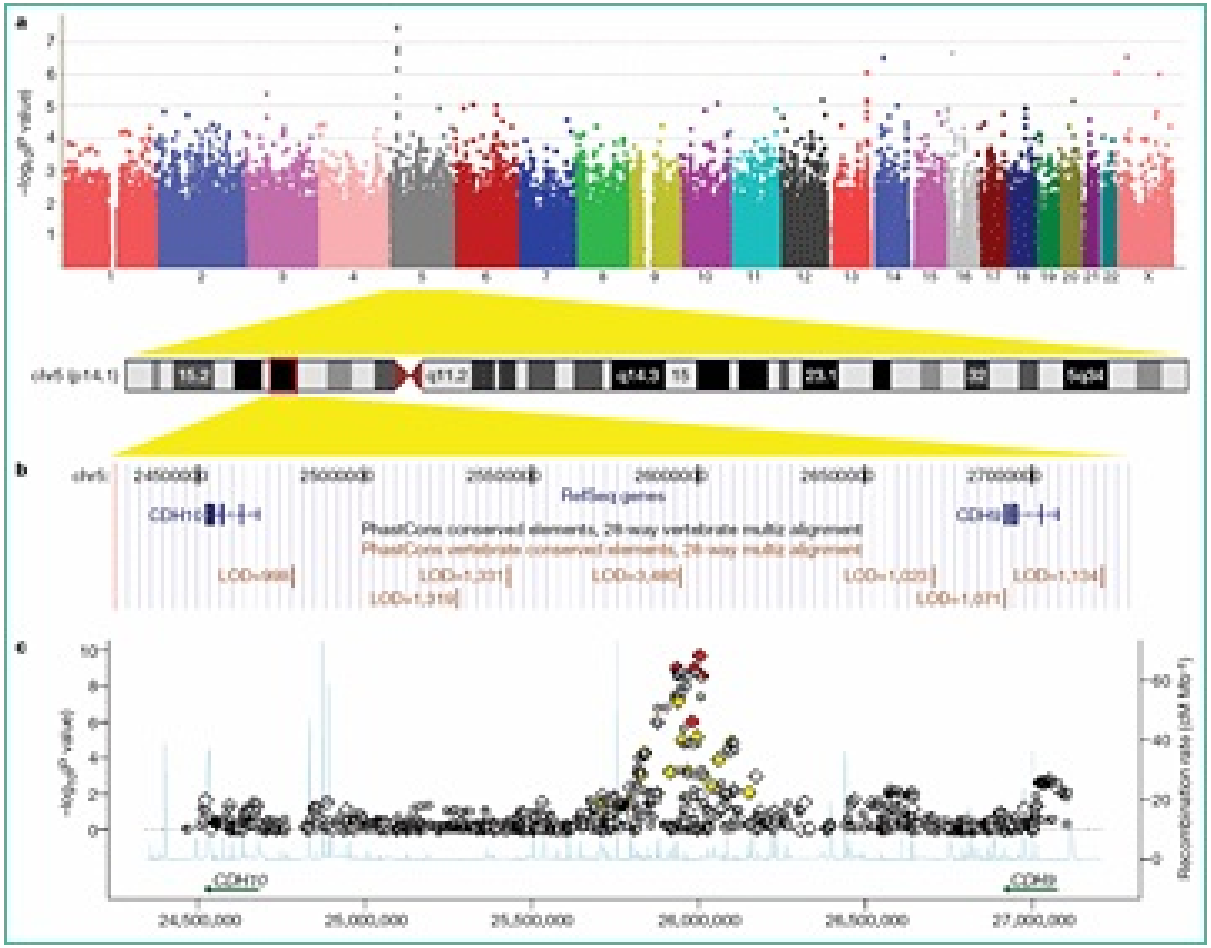


Figure: Common genetic variants on 5p14.1 associate with autism spectrum disorders [WZM+09]

Introduction to GWAS

Common variants and rare variants

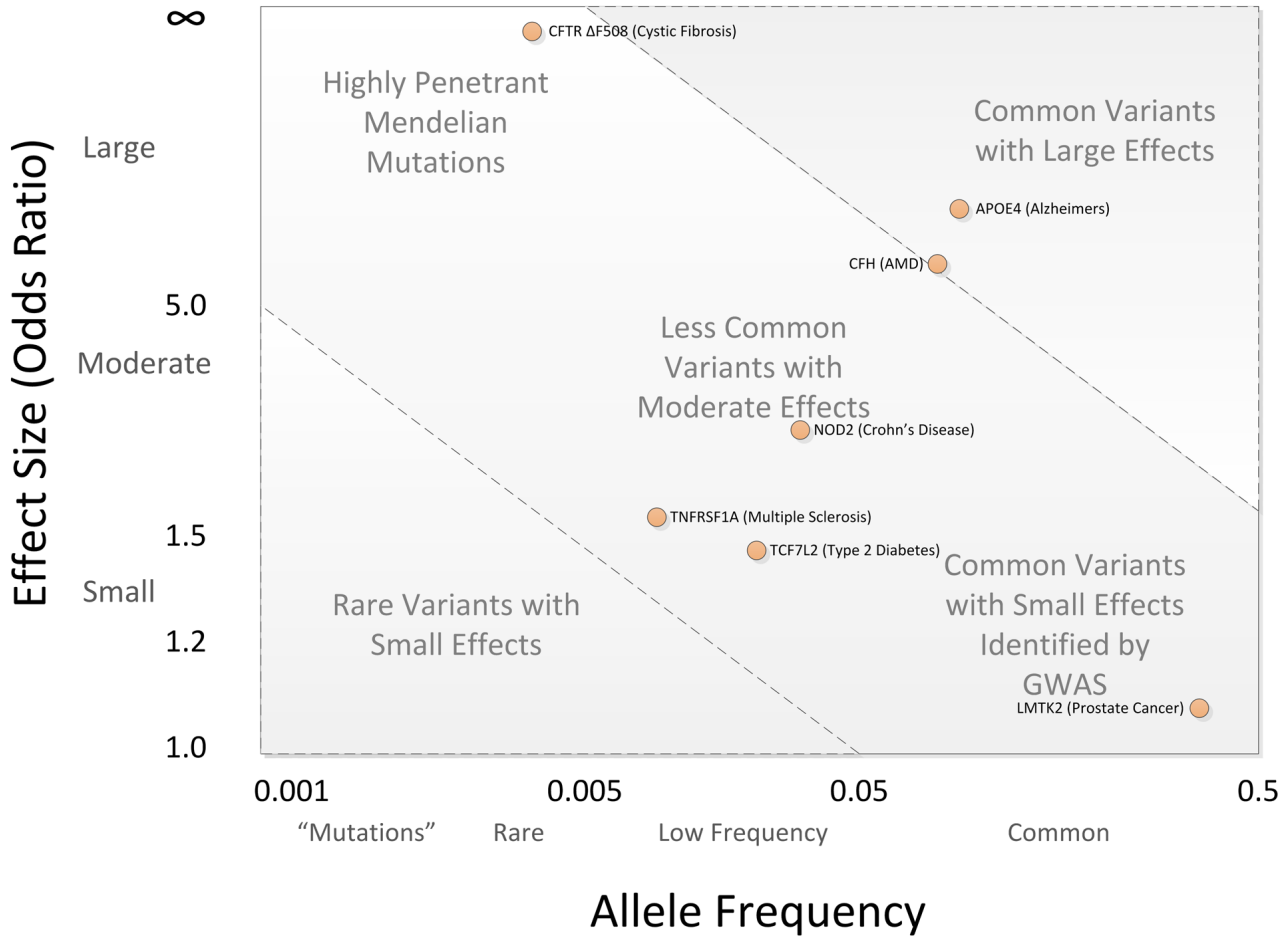


Figure: effect size of Single Nucleotide Variant [BM12]

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single-SNP based association tests

the classical method

For individual i with SNP j coded as x_{ij} ($x_{ij} = 0, 1, 2$ representing copies of minor alleles) and a vector of covariates φ_i,

$$g(\mu_i) = \beta_0 + x_{ij}\beta_j + z_i\varphi_i,$$

However, this method suffers from at least two disadvantages:
1), it will generate millions of tests thus increase the multiple test error correction burden;
2), the coefficient estimate of SNP j will become unstable or even the estimation algorithm cannot converge when SNP minor allele frequency (MAF) becomes smaller, e.g. MAF < 0.01.

SNP-set based association tests I

A brief review

By pooling multiple low MAF SNVs together, the SNP-set based association test can detect the signal(s) from a region (such as a gene) instead of from a single SNV.

Major categories of SNP-set based association tests:

- the so-called "burden test", which used MAF based weighting scheme to combine the sum statistics from multiple SNVs in a region [LL08, MB09];
- the variance-component test, which includes SKAT, C-alpha, SSU, etc [Pan09, NRV+11, WLC+11].
- the Lasso and group-penalized regression based methods [ZSSL10, KPS14].
- the functional linear model and functional principal component analysis based methods [LZX12b, LZX12a, LBX11, FWM+13].

SNP-set based association tests II

A brief review

- the adaptive test combines statistics of burden test and variance-component test, such as SKAT-O, aSum, aSSU, aScore, an exponential combination (EC) framework for set-based association tests, a robust and powerful test using Fisher's method to combine linear and quadratic statistics, a unified mixed-effect model, etc
[HP10, PS11, LEB$^+$12, LWL12, CHG$^+$12, DLS13, SZH13].

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How do longitudinal data look like?

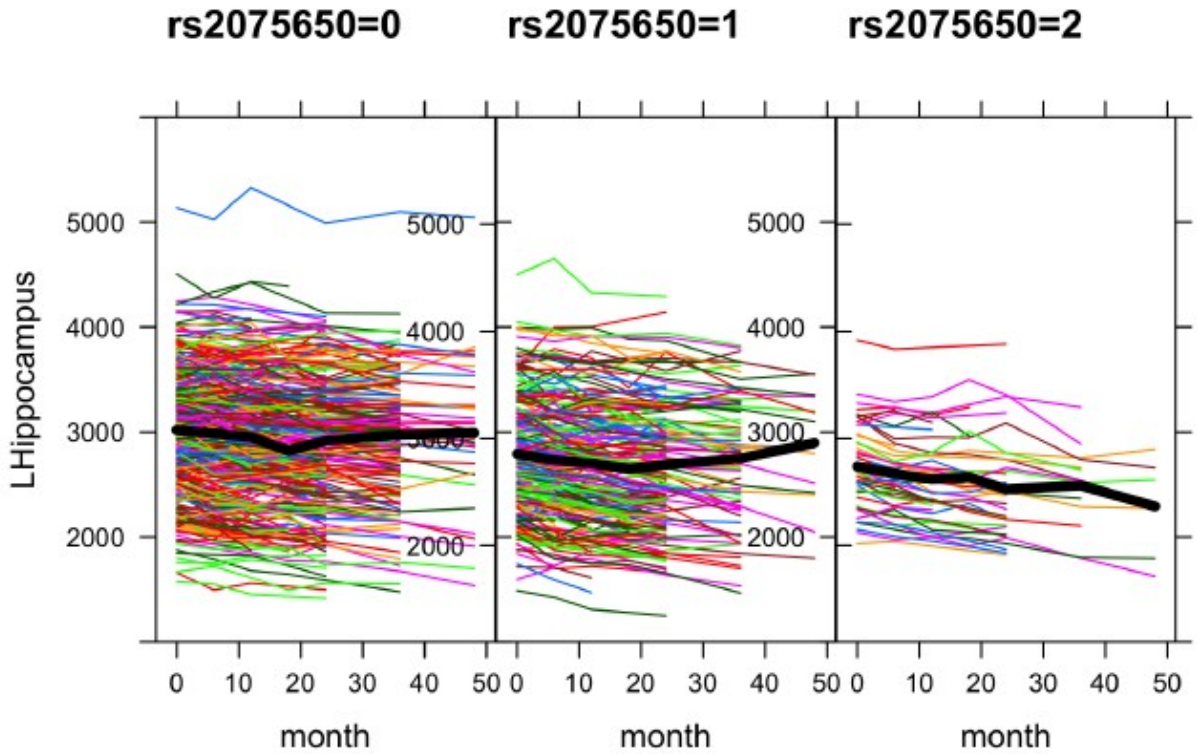

Figure: Trajectories of phenotype left hippocampus volume over time (in months) in three allele groups of SNP rs2075650 [XSP$^+$14]

Why longitudinal? I

A recent study by Xu et al [XSP+14] demonstrates the power gain from longitudinal data analysis over traditional cross-sectional data analysis used in GWAS.

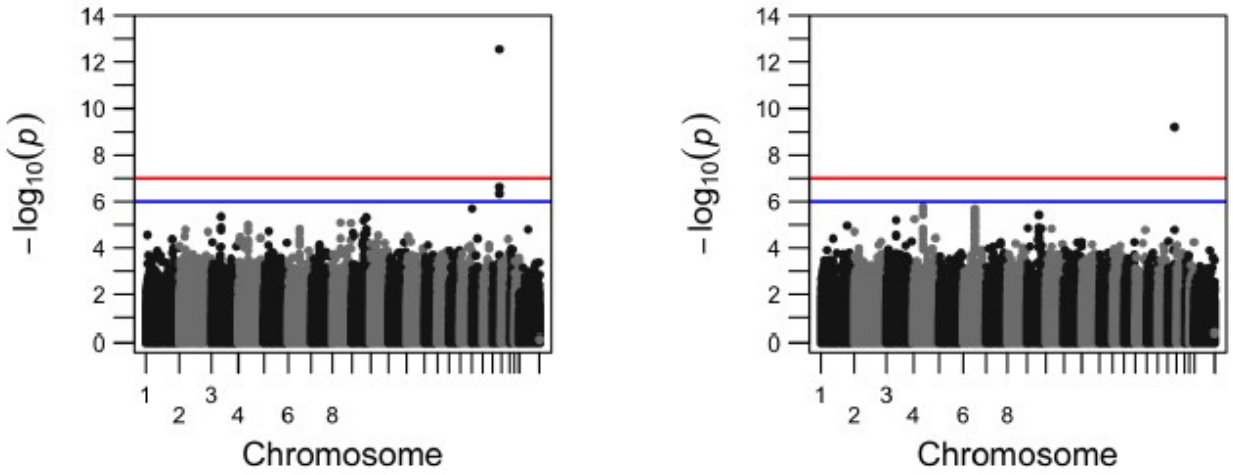

Figure: Comparison of the Manhattan plots for genome-wide p-values for phenotype left hippocampus volume from longitudinal analysis (left) and from cross-sectional analysis (right) [XSP+14]

Why longitudinal? II

Power

Model	rs2075650			rs439401		
	$P = 10^{-8}$	$P = 10^{-10}$	$P = 10^{-15}$	$P = 10^{-8}$	$P = 10^{-10}$	$P = 10^{-15}$
LME-RSI	1	1	0.859	0.872	0.677	0.148
GEE-Robust	1	1	0.857	0.871	0.676	0.170
Baseline	0.736	0.448	0.038	0.077	0.015	0

LME-RSI: a linear mixed-effects model with random slope and intercept; LME-RI: a linear mixed-effects model with only a random intercept term; GEE-Robust: GEE with the sandwich covariance estimator; GEE-Naive: GEE with the model-based covariance estimator; Baseline: a linear model at the baseline testing for the main effects of an SNP.

doi:10.1371/journal.pone.0102312.t008

Figure: Simulation results at significance level P with different methods [XSP+14]

A brief review of major longitudinal data analysis methods I

Major categories of longitudinal data analysis methods:

- random effect models
  Random effect model is a two-stage models, which treat probability distributions for the response vectors of different individuals as a single family and the random-effects parameters which hold the same for the same individual as another distribution [LW82].
- marginal effect models
  Marginal effect model is an extension to quasi-likelihood method. Rather than giving subject-specific(SS) estimates as in random effect models, marginal effect models by GEE give population-averaged (PA) estimates.
- transitional (Markov) models
  The transitional (Markov) model, describes the conditional distribution of each response y_{ij} as an explicit function of first q prior observations $y_{ij-1}, \ldots, y_{ij-q}$ from history response vector: $H_{ij} = \{y_{ik}, k = 1, \ldots, j-1\}$ and covariates x_{ij}. The integer q is referred as the order of the Markov models.

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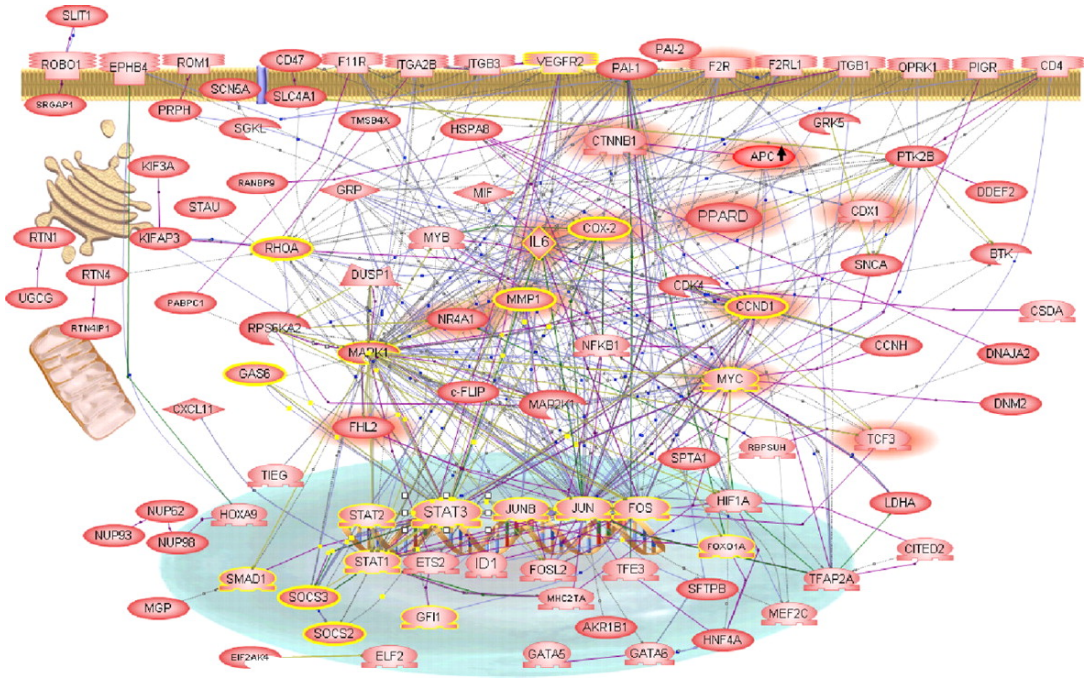
A big picture



The advantage of using Gene-Set/Pathway based association test in GWAS:

- it utilizes the information of biological pathway to help localize the association signal(s) from close related genes
- it further aggregates multiple Genes/RVs against testing each Gene/RV separately, which will boost the statistical power

Types of Gene-Set/Pathway based association test in GWAS

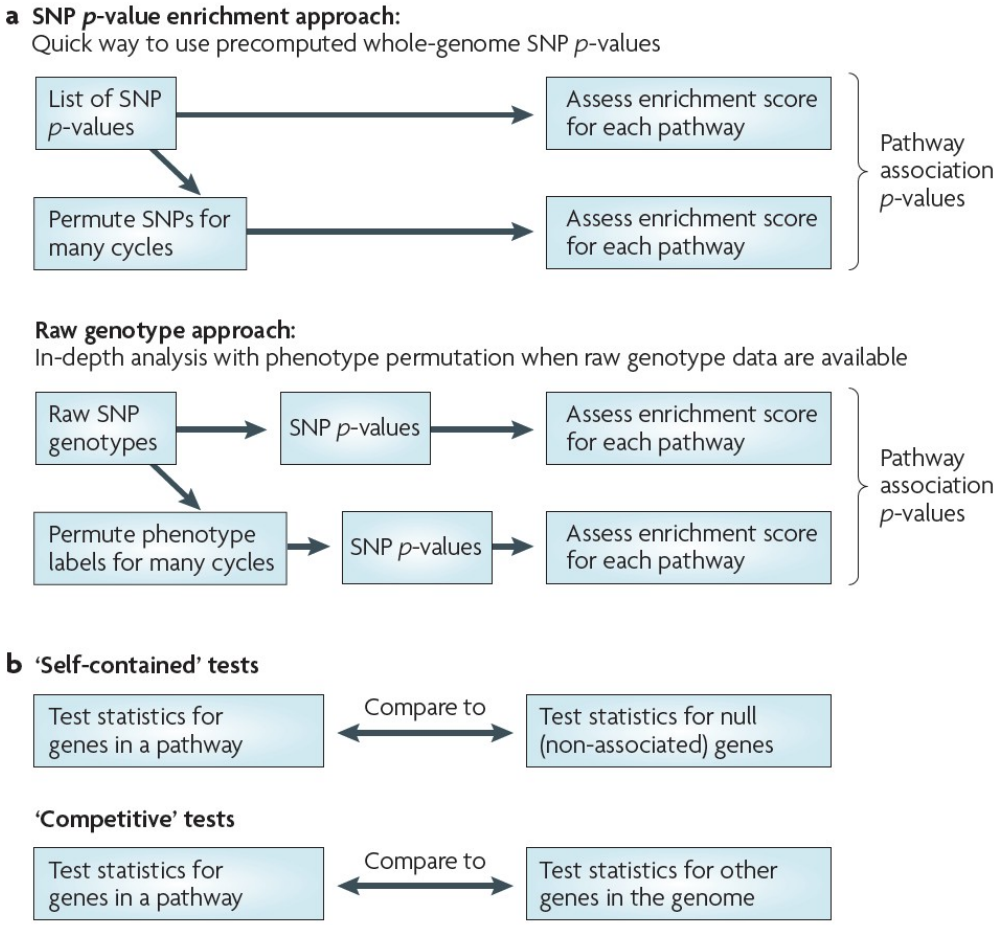


Figure: Types of pathway association method [WLH10]

A brief review of current Gene-Set/Pathway based association tests in GWAS I

- GSEA modification in GWAS; GSEA-SNP;i-GSEA4GWAS
- modification of Fishers method for combing SNP P-values for gene-level or gene-set-level association
- gene set ridge regression in association studies (GRASS)
- association list go annotator (ALIGATOR), which is a 'p-value enrichment approach' requiring only pre-computed SNP p-values, uses Fisher's exact test on SNP with minimum p-value for the gene-level association
- the SNP ratio test (SRT),tests the ratio of significant SNPs in a pathway and compute the empirical p-value based on permutation
- supervised principal component analysis with a Gumbel extreme value mixture distribution as test statistic distribution and simulation-based standardization procedure for pathway size single-marker level assuming an additive SNP effect, then uses Fisher's combination test to combine individual p-values of markers and corrected by Brown's approximation to better control type I error

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Dissertation Aims

- Aim 1: Data-adaptive SNP-set-based association tests (aSPU) for longitudinal data analysis within GEE framework;
  - (a), for CVs;
  - (b), for RVs.
- Aim 2: Pathway-based longitudinal aSPU family tests: Path-aSPU
- Aim 3: Package/software development

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Public Health Significance I

1. Due to the **complexity** in genetics association with phenotype, e.g. specific association effect directions and sizes, a given test favoring one scenario may or may not perform well in other scenarios [Pan09, DLS13, PKZ+14, SZH13]. In other words, there is **no single test** the most powerful among all testing scenarios.

   Therefore, a few data-adaptive tests were developed as an ad hoc strategy, e.g. some tests tried to combine the advantage of burden test and variance-component test; some other tests tried to use a set of pre-determined weights for individual RVs.

   Compared to the previous limited sense data-adaptive tests, our proposed method will be more extensive and generalized in **data adaptability**. The new tests will provide a relative high power in almost all data scenarios;

Public Health Significance II

2. There is not yet a **SNP-set** based **data-adaptive** association test method for **longitudinal** data analysis in GWAS: we will propose such a new method to fill in this gap;
3. CVs and RVs are **both** important in finding the missing heritability of human complex disease. Our proposed new method will have the ability to handle both of them (either CVs or RVs);
4. Currently, there are **no** statistical methods designed for pathway-based association test in **longitudinal data settings**, not to mention the **data-adaptive** property. We will extend the SNP-set based method to **Gene-set/Pathway based method** to fill in the gap;
5. We will produce an R package or independent Linux command-line based software implementing proposed methods to facilitate the community usage.

In conclusion, my dissertation work will provide useful methods/tools for identifying the underlying genetic factors explaining the heritability of human complex disease, and in the long run this will contribute to the prevention, diagnosis and cure of complex diseases.

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Aim 1(a)

To develop a data-adaptive longitudinal association test within GEE framework for **common variants**, which will be done in either sliding-window based or gene-based manner for real GWAS data.

Aim 1(a) I

Method: introduction to notation and formula

Suppose for each subject $i = 1, \ldots, n$, we have k total longitudinal measurements

$$y_i = (y_{i1}, y_{i2}, \ldots, y_{ik})'$$

with y_{im} as a element, p SNPs of interest as a row vector

$$x_i = (x_{i1}, x_{i2}, \ldots, x_{ip})$$

with x_{ij} coded as 0,1 or 2 for the count of the minor allele, and

$$z_i = (z_{i1}, z_{i2}, \ldots, z_{iq})$$

as a row vector for q variates.

Thus, we have:

$$X_i = \begin{pmatrix} x_i \\ x_i \\ \vdots \\ x_i \end{pmatrix}, Z_i = \begin{pmatrix} 1 & z_i \\ 1 & z_i \\ \vdots & \vdots \\ 1 & z_i \end{pmatrix}$$

X_i is a $k \times p$ matrix, and Z_i is a $k \times (q+1)$ matrix.

Aim 1(a) II

Method: introduction to notation and formula

We then have the GLM equation as,

$$g(\mu_i) = \eta_i = Z_i\varphi + X_i\beta = H_i\theta$$

The consistent and asymptotically Normal estimates of β and φ can be obtained by solving the GEE [LZ86]:

$$U(\varphi, \beta) = \sum_{i=}^{n} U_i(\varphi, \beta) = \sum_{i=1}^{n} (\frac{\partial \mu_i}{\partial \theta'})' V_i^{-1} (Y_i - \mu_i) = 0,$$

with

$$\frac{\partial \mu_i}{\partial \theta'} = \frac{\partial g^{-1}(H_i\theta)}{\partial \theta'}, V_i = \phi A_i^{\frac{1}{2}} R_w A_i^{\frac{1}{2}},$$

and

$$A_i = \begin{bmatrix} v(\mu_{i1}) & 0 & \cdots & 0 \\ 0 & v(\mu_{i2}) & 0 & 0 \\ \vdots & 0 & \ddots & \vdots \\ 0 & 0 & \cdots & v(\mu_{ik}) \end{bmatrix}$$

Aim 1(a) III

Method: introduction to notation and formula

With a canonical link function and a working independence model, we have a closed form of the U vector with **two parts** corresponding to SNPs and covariates, and its covariance estimator:

$$U = \left(U'_{.1}, U'_{.2}\right)' = \sum_i (Z_i, X_i)' (Y_i - \mu_i)$$

$$\widetilde{\Sigma} = \widehat{\mathrm{Cov}}(U) = \sum_i (Z_i, X_i)' \widehat{\mathrm{var}(Y_i)} (Z_i, X_i) = \sum_i (Z_i, X_i)' (Y_i - \hat{\mu}_i)(Y_i - \hat{\mu}_i)' (Z_i, X_i) = \begin{pmatrix} V_{11} & V_{12} \\ V_{21} & V_{22} \end{pmatrix} \quad (1)$$

Aim 1(a) IV

Method: introduction to notation and formula

Our goal is to detect whether there is any association between the longitudinal trait and the SNPs via testing on hypothesis

$$H_o : \beta = (\beta_1, \beta_2, \ldots, \beta_p)' = 0$$

We have under the null hypothesis with $g(Y_i) = Z_i\varphi$ to obtain φ and predict $\hat{\mu} = g^{-1}(Z\hat{\varphi})$. We hereby have score vector under the null hypothesis, with a working independence model, is:

$$U(\hat{\varphi}, 0) = (U'_{.1}, U'_{.2})' = \sum_{i=1}^{n} (U'_{i1}, U'_{i2})'$$

where

$$U_{.1} = \sum_i Z_i'(Y_i - \hat{\mu}_i), U_{.2} = \sum_i X_i'(Y_i - \hat{\mu}_i)$$

As U asymptotically follows a multivariate normal distribution under H_0, then the score vector for β also has an asymptotic normal distribution:

$$U_{.2} \sim N(0, \Sigma_{.2}),\ \Sigma_{.2} = \widehat{Cov}(U_{.2}) = V_{22} - V_{21}V_{11}^{-1}V_{12}$$

, where V_{xx} are defined in Equation 1.

Aim 1(a) V

Method: introduction to notation and formula

Several classical tests:

- **The Wald Test:** The Wald Test known as $T = \hat{\beta}' \text{cov}\,(\hat{\beta})\,\hat{\beta}$ is most commonly used, where $\hat{\beta}$ is the estimate of β after fitting the full GEE model with $g(\mu_i) = Z_i\varphi + X_i\beta$. Under H_0, we have $T \sim \chi^2_p$. The Wald test is more time consuming by fitting full model, may fail to converge with many SNPs put on RHS of the regression-like equation to test, and more importantly, the type I error tends to inflate in such case [PKZ$^+$14, ZXSP14].
- **The Score Test:** $T = U'_{.2}\Sigma^{-1}_{.2}U^{-1}_{.2}$, where $U_{.2}$ and $\Sigma_{.2}$ are discussed above; the statistic is asymptotically equivalent to the Wald test with the same null distribution $T \sim \chi^2_p$. Since we only need to fit the null model with covariates, it is computationally easier and less likely to have numerical convergence problems. More importantly, the score test controls the type I error well [PKZ$^+$14, ZXSP14].
- **The UminP Test:** $T = \max_j \frac{U^2_{.2,j}}{\Sigma_{.2,jj}}$ for $j \in 1, 2, \ldots, p$, of jth SNP effect. The $\Sigma_{.2,jj}$ is the jth entry on the diagonal of $\Sigma_{.2}$. With max T, we can get minimal p-value accordingly. A simulation method based on the asymptotic normal distribution of the score vector can be used to calculate its p-value [PKZ$^+$14, ZXSP14]. An asymptotic multivariate normal distribution numerical integration based method provided an alternative to calculate its p-value [PHS09, Pan09].

Aim 1(a) I

Method: A new class of tests and a data-adaptive test in longitudinal data settings

A general form of score-vector-based statistic can be generalized as:

$$T_w = W'U = \sum_{j=1}^{p} W_j U_j$$

where $W = (W_1, \ldots, W_p)'$ is a vector of weights for the p SNVs [LT11].
with special cases:

$$T_{Sum} = 1'U = \sum_{j=1}^{p} U_j, \qquad T_{SSU} = U'U = \sum_{j=1}^{p} U_j^2,$$

These two tests are called Sum test and SSU test [Pan09].

Aim 1(a) II

Method: A new class of tests and a data-adaptive test in longitudinal data settings

If we choose weight to be

$$W_j = U_{.2,j}^{\gamma-1}$$

for a series of integer value $\gamma = 1, 2, \ldots, \infty$, leading to the sum of powered score (U) tests called **SPU** tests:

$$T_{SPU(\gamma)} = \sum_{j=1}^{p} U_{.2,j}^{\gamma-1} U_{.2,j}$$

When $\gamma \to \infty$ as an extreme situation, where ∞ is assumed to be an even number, we have

$$T_{SPU(\gamma)} \propto ||U||_\gamma = \left(\sum_{j=1}^{p} |U_{.2,j}|^\gamma \right)^{\frac{1}{\gamma}} \to ||U||_\infty = \max_{j=1}^{p} |U_{.2,j}| \equiv T_{SPU(\infty)}.$$

In our experience, SPU(γ) test with a large $\gamma > 8$ usually gave similar results as that of SPU(∞) test [PKZ+14], thus we will only use $\gamma \in \Gamma = \{1, 2, \ldots, 8, \infty\}$ for the whole dissertation work.

Aim 1(a) III

Method: A new class of tests and a data-adaptive test in longitudinal data settings

Simulation-based P-value estimation of $T_{SPU(\gamma)}$

Suppose T is short notation of $T_{SPU(\gamma)}$ for a specific γ and $\hat{\Sigma}_{.2}$ is the covariance matrix of the score vector $U_{.2}$ based on original data (see Equation 1). We draw B samples of the score vector from its null distribution:

$$U_{.2}^{(b)} \sim MVN\left(0, \hat{\Sigma}_{.2}\right),$$

with $b = 1, 2, \ldots, B$, and thus obtain a statistics under null hypothesis: $T^{(b)} = \sum_{j=1}^{p} U_{.2,j}^{(b)\gamma}$. We then can calculate the p-value of $T_{SPU(\gamma)}$ as

$$P_{SPU(\gamma)} = \sum_{b=1}^{B} \frac{I(T^{(b)} \geq T^{obs}) + 1}{B + 1}.$$

Aim 1(a) IV

Method: A new class of tests and a data-adaptive test in longitudinal data settings

The aSPU test

Although we have a list of SPU(γ) statistics and p-values, we are not sure which one is **the most powerful** in a specific data situation. Thus, it will be convenient to have a test which data-adaptively and automatically **select/combine the best** SPU(γ) test(s).

We hereby propose an adaptive SPU (aSPU) test to achieve such purpose. Accordingly, we will have the aSPU test statistic:

$$T_{aSPU} = \min_{\gamma \in \Gamma} P_{SPU(\gamma)},$$

Aim 1(a) V

Method: A new class of tests and a data-adaptive test in longitudinal data settings

Simulation-based P-value estimation of T_{aSPU}
Similarly,

$$P^{(b)}_{SPU(\gamma)} = \sum_{b_1 \neq b}^{B} \frac{I(T^{(b_1)}_{SPU(\gamma)} \geq T^{(b)}_{SPU(\gamma)}) + 1}{(B-1)+1}$$

for every γ and every b. Then, we will have $T^{(b)}_{aSPU} = \min_{\gamma \in \Gamma} P^{(b)}_{SPU(\gamma)}$, and the final p-value of aSPU test is:

$$P_{aSPU} = \sum_{b=1}^{B} \frac{I(T^{(b)}_{aSPU} \leq T^{obs}_{aSPU}) + 1}{B+1}.$$

It is worth noting again that the same B simulated score (U) vectors have been used in calculating the P_{aSPU}.

Aim 1(a) VI

Method: A new class of tests and a data-adaptive test in longitudinal data settings

Other versions of aSPU test

- **aSPUw test**
  The SPUw test is a *diagonal-variance-weighted* version of the SPU test, defined as:

$$T_{SPUw(\gamma)} = \sum_{j=1}^{p} \left(\frac{U_{.2,j}}{\sqrt{\hat{\Sigma}_{.2,jj}}} \right)^{\gamma}$$

- **aSPU(w).Score test**

$$T_{aSPU.Score} = \min\left\{ \min_{\gamma \in \Gamma} P_{SPU(\gamma)}, P_{Score} \right\},$$

Aim 1(a) I

Method in data simulation

Simulation of genotype data

1. a latent vector $G_i = (G_{i1}, \ldots, G_{ip})'$ was first drawn from a **multivariate Normal distribution** $N(0, R)$, where R had a AR(1) correlation structure with its (i, j)th element in terms of purely correlation $r_{ij} = \mathrm{Corr}(G_{if}, G_{ig}) = \rho^{|f-g|}$ between any two latent components, G_{if} and G_{ig} for $f \neq g$. In our simulations we set $\rho = 0.8$.;
2. the latent vector G_i was dichotomized to yield a haplotype with each latent element G_{ij} dichotomized to 0 or 1 with probability $\mathrm{Prob}(G_{ij} = 1) =$ MAF of jth SNP; the MAFs were randomly drawn from a uniform distribution: for causal SNPs the MAFs were set between 0.3 and 0.4; for null SNPs the MAFs were set between 0.1 and 0.5;
3. we combined two independent haplotypes to form the genotype $X_i = (X_{i1}, \ldots, X_{ip})'$ for subject i. The haplotypes for different subject were generated independently.

Aim 1(a) II

Method in data simulation

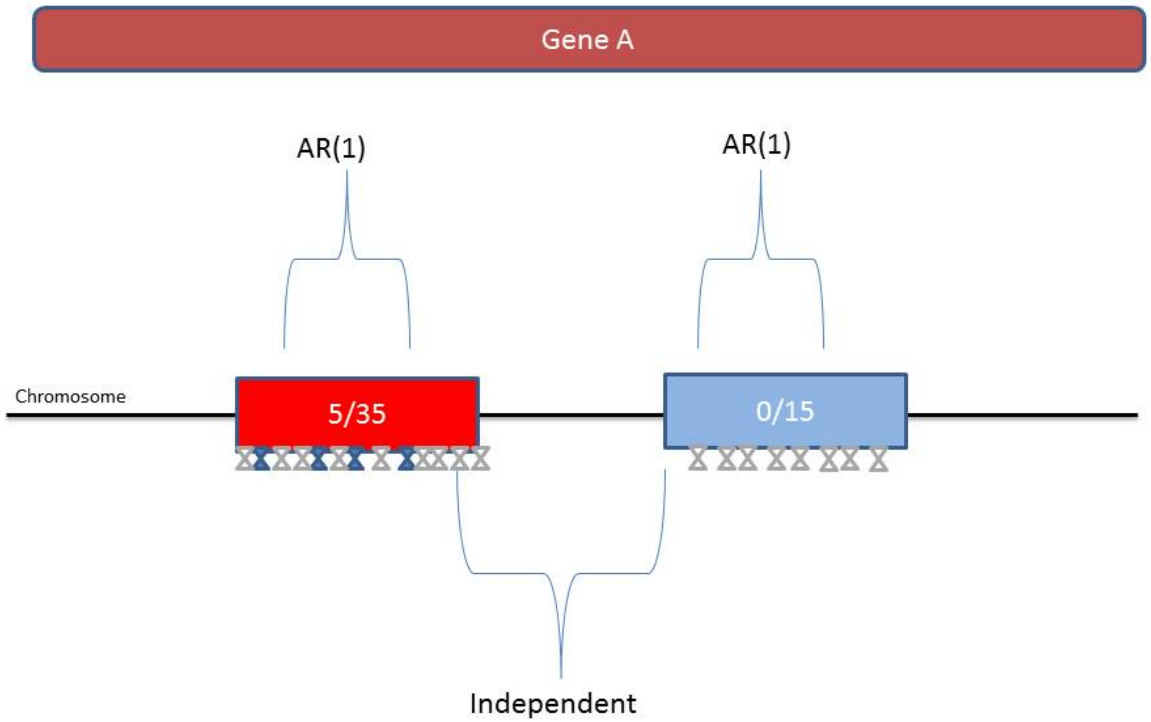

Figure: Demo graph of genotype simulation

Aim 1(a) III

Method in data simulation

Simulation of phenotype data

We setup the mixed effect model to achieve the AR(1) correlation structure as:

$$y_{im} = \mu_i + b_i + \underbrace{\rho e_{i,m-1} + s_{i,m}}_{e_{i,m}}, \tag{2}$$

with $m = 1, \ldots, k$ indexes the longitudinal measurements within subject i;
$\mu_i = Z_i\varphi + X_i\beta = H_i\theta$ as in quantitative trait case; b_i is the random intercept representing the subject-level random effect, and

$$\rho e_{i,m-1} + s_{i,m} = e_{i,m},$$

where ρ is lag-one autocorrelation coefficient, so we can plugin our estimate from real data here by setting up $\rho = 0.7$. We assume the following distribution:

$$b_i \sim N(0, \sigma_b^2)$$
$$e_{i,m} \sim N(0, \sigma_e^2)$$
$$s_{i,m} \sim N(0, (1-\rho^2)\sigma_e^2)$$

Aim 1(a) IV

Method in data simulation

Under this assumption, the variance-covariance matrix across longitudinal measurements becomes (assuming $k = 4$ for the number of longitudinal measurements):

$$\Sigma_{4\times 4} = Var\begin{pmatrix} b_i + e_{i1} \\ b_i + \rho e_{i1} + s_{i2} \\ b_i + \rho e_{i2} + s_{i3} \\ b_i + \rho e_{i3} + s_{i4} \end{pmatrix} = \sigma_b^2 \begin{pmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 1 \end{pmatrix} + \sigma_e^2 \begin{pmatrix} 1 & \rho & \rho^2 & \rho^3 \\ \rho & 1 & \rho & \rho^2 \\ \rho^2 & \rho & 1 & \rho \\ \rho^3 & \rho^2 & \rho & 1 \end{pmatrix} \quad (3)$$

Aim 1(a) V

Method in data simulation

Connect phenotype data with genotype data
Let we first introduce the below splitting of the phenotype variance:

$$Var(y_{im}) = Var(X_{ij})\beta_j^2 + \sigma_{oth}^2 = 2f(1-f)\beta_j^2 + \sigma_{oth}^2 \tag{4}$$

Now let we look at the relationship between genetic heritability (narrow-sense heritability) and equation (4):

$$h^2 = \frac{Var(A)}{Var(P)} \tag{5}$$

In our situation for jth SNP, this can be extended to:

$$h_j^2 = \frac{Var_j(A)}{Var(P)} = \frac{Var(X_{ij})\beta_j^2}{Var(y_{im})} = \frac{Var(y_{im}) - \sigma_{oth}^2}{Var(y_{im})} \approx \frac{Var(y_{im}) - \sigma_b^2 - \sigma_e^2}{Var(y_{im})} \tag{6}$$

Aim 1(a) VI

Method in data simulation

Summary of parameter setup in simulation studies

After this point, by systematically solving the equations (4) and (6), we can easily calculate the β_j for jth SNP once we have determined the value of h_j^2, σ_b^2, σ_e^2 and f. Usually a h_j^2 for a single SNP j will not be high for complex disease and we used $h_j^2 = 0.001$ in our simulation study to control β_j, with other parameters set as: $\sigma_b^2 = 1$, $\sigma_e^2 = 1$ and $k = 4$ representing the number of longitudinal measurements for a single subject. Without special indication, we will use the simulated data set with 1000 replicates; significance level is set at 0.05.

Aim 1(a) I

Preliminary simulation results

- **Tests under default simulation settings with varying sample size**

n	Score	UminP	SumP	SumP.w	SSU	aSPU	aSPUw	aSPU.sco	aSPUw.sco
500	0.038	0.056	0.058	0.053	0.044	0.052	0.051	0.050	0.048
1000	0.047	0.054	0.048	0.049	0.065	0.065	0.064	0.059	0.057
2000	0.055	0.041	0.053	0.053	0.059	0.052	0.055	0.058	0.058
3000	0.055	0.054	0.057	0.060	0.065	0.063	0.054	0.056	0.059

Table: Type I error under using working independence R_w

Aim 1(a) II

Preliminary simulation results

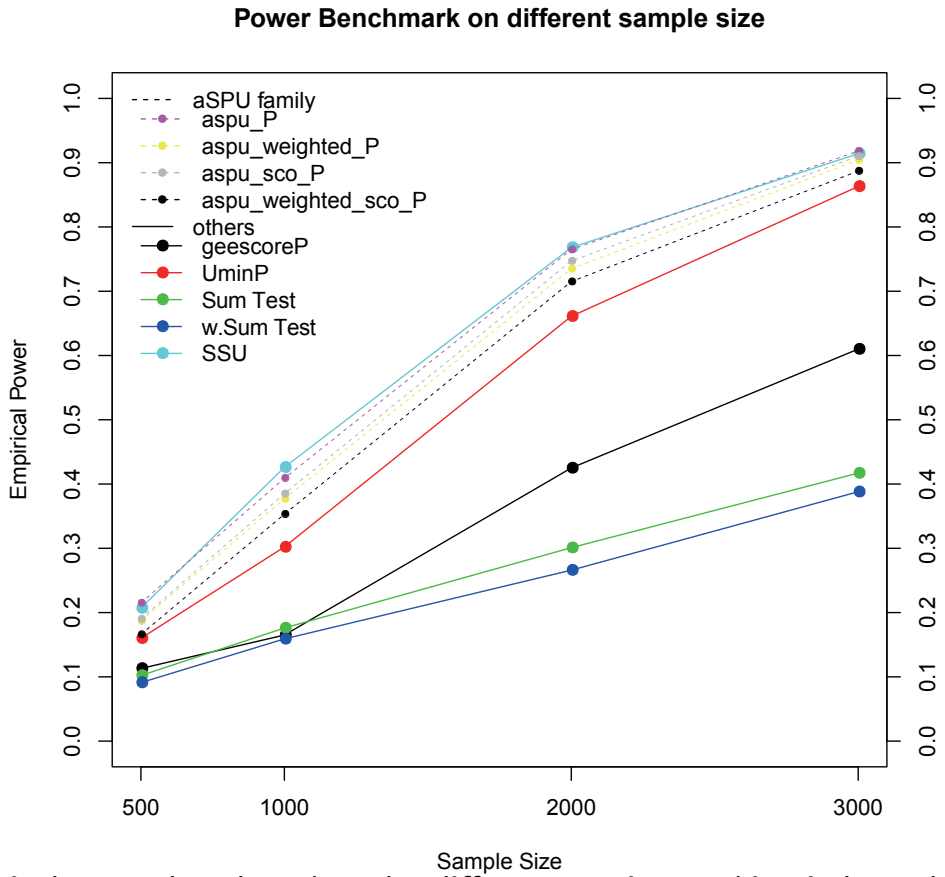

Figure: Empirical power benchmark under different n using working independence R_w

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Aim 1(b)

Extend the data-adaptive longitudinal association test within GEE framework to work for **rare variants** in a gene-based manner.

Aim 1(b) I

Method

For CVs we have:

$$U_{.2}^{(b)} \sim MVN\left(0, \hat{\Sigma}_{.2}\right)$$

with $b = 1, 2, \ldots, B$, and thus obtain a statistics under null hypothesis: $T^{(b)} = \sum_{j=1}^{p} U_{.2,j}^{(b)\gamma}$. We then calculate the p-value of $T_{SPU(\gamma)}$ as $P_{SPU(\gamma)} = \sum_{b=1}^{B} \frac{I(T^{(b)} \geq T^{obs})+1}{B+1}$.

The above algorithms will hold in RV case by large, except that the $U_{.2}^{(b)}$ may **not** follow the multivariate Normal distribution any longer. As a remedy, we propose a permutation algorithm that generates the empirical null distribution of $U_{.2}^{(b)}$ and in the same time **maintain the relationship** between longitudinal traits and possible covariates such as age, gender, etc, for subject i. The algorithm will also be robust to **missing data** as this is a usual case in longitudinal data settings.

Aim 1(b) II

Method

The permutation algorithm can be implemented as follows:

1. identify the max k across all n subjects, which is the number of longitudinal measurements, e.g. $k = 4$.
2. detect if the data has missing values, if yes, fill the missing value with NA to complement the data dimension (for example, subject i with $Y_i = (y_{i,1},,,y_{i,4})'$ has two missing measurements at time 2 and time 3. After missing value complementing, it becomes $Y_i = (y_{i,1}, \mathrm{NA}, \mathrm{NA}, y_{i,4})'$). Now we should have all the subjects with each Y_i of dimension equal to $k \times 1$.
3. complement H_i to be of full dimension, i.e. $k \times (p + q + 1)$, for covariates and SNVs. Now we should have $\begin{pmatrix} Y_i & H_i \end{pmatrix}$ as an augmented matrix of dimension $k \times (p + q + 2)$ for each subject i, where $H_i = (Z_i, X_i)$. For total n subjects, we have row-wise binded matrix

$$M = \begin{pmatrix} Y_1 & H_1 \\ Y_2 & H_2 \\ \vdots & \vdots \\ Y_n & H_n \end{pmatrix}$$

of dimension $nk \times (p + q + 2)$.

Aim 1(b) III

Method

4. permute the SNV chunk among different individuals, i.e. the X_i in $\begin{pmatrix} Y_i & Z_i, X_i \end{pmatrix}$ with the X_j in $\begin{pmatrix} Y_j & Z_j, X_j \end{pmatrix}$, where $i \neq j$.
5. with permuted

$$M^{*(b)} = \begin{pmatrix} Y_1 & Z_1, X_1^{*(b)} \\ Y_2 & Z_1, X_2^{*(b)} \\ \vdots & \vdots \\ Y_n & Z_1, X_n^{*(b)} \end{pmatrix}$$

   we refit the GEE model and get the $U_{.2}^{*(b)}$
6. repeat step 4 - 5 B times to produce $U_{.2}^{*(b)}$ with $b = 1, 2, \ldots, B$.

Aim 1(b) I

Methods in data simulation

The simulation strategy of RV data is almost the same with previous strategy for generating CV data , except that:

1. the MAF of RVs, regardless of casual one or null one, are set between **0.001** and **0.01**.
2. the casual RVs are **not** excluded from later test as we expect the whole-genome sequencing or exome sequencing/Chip platform will identify high density SNVs including the real casual ones.

We will use the same simulated longitudinal phenotype data as for CVs.

Aim 1(b) I

Preliminary simulation results

If we still use the CVs' strategy on RVs, we will have

- **Simulation-based Test under default settings with varying sample size**

n	pSSU	pSSUw	pScore	pSum	mvn.UminP	UminP	SPU(1)	SPUw(1)	SPU(2)	SPUw(2)	aSPU	aSPUw	aSPU.sco	aSPUw.sco
500	0.053	0.054	0.052	0.049	0.047	0.022	0.052	0.026	0.063	0.025	0.056	**0.021**	0.059	**0.035**
1000	0.055	0.040	0.042	0.048	0.054	0.049	0.048	0.046	0.061	0.044	0.045	0.045	0.053	0.047
2000	0.054	0.050	0.048	0.049	0.046	0.045	0.053	0.044	0.063	0.061	**0.066**	**0.062**	**0.062**	**0.062**
3000	0.045	0.044	0.039	0.060	0.053	0.055	0.057	0.058	0.058	0.052	0.049	0.055	0.055	0.057

Table: Empirical type I error using simulation-based method in RV analysis. mvn.UminP: UminP method based MVN distribution; UminP: UminP method based on simulation.

Aim 1(b) II

Preliminary simulation results

- **Permutation-based Test under default settings with varying sample size**

  As noted before, there are some minor issues in using simulated-based aSPU method to test RVs, we thus tested the aSPU performance based on permutation algorithm. The type I error is shown below.

n	pSSU	pSSUw	pScore	pSum	mvn.UminP	UminP	SPU(1)	SPUw(1)	SPU(2)	SPUw(2)	aSPU	aSPUw	aSPU.sco	aSPUw.sco
500	0.053	0.054	0.052	0.049	0.047	0.046	0.050	0.049	0.056	0.061	0.054	0.053	0.060	0.056
1000	0.055	0.040	0.042	0.048	0.054	0.056	0.048	0.049	0.056	0.043	0.047	0.045	0.052	0.051
2000	0.054	0.050	0.048	0.049	0.046	0.046	0.049	0.043	0.053	0.052	0.063	0.057	0.058	0.056
3000	0.045	0.044	0.039	0.060	0.053	0.050	0.058	0.058	0.047	0.048	0.049	0.053	0.049	0.053

Table: Empirical type I error using permutation-based method in RV analysis. mvn.UminP: UminP method based MVN distribution; UminP: UminP method based on permutation.

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Aim 2

To extend the data-adaptive longitudinal association test within the GEE framework to work for common variants or rare variants in a gene-set/pathway-based manner, i.e. **pathway-based association test**.

Aim 2 I

Method

A pathway analysis involves multiple genes (e.g. 20 as a typical number). As the genes within a pathway may contain different numbers of RVs, we need to modify the aSPU test to **adjust for various gene length** to avoid dominant influence from a large (or small) gene.

Suppose we let the short notation $U_{g.}$ to represent $U_{.2}$ for the RVs X_i'part in the whole score vector, and $U_{g.} = (U_{g,1}, U_{g,1}, \ldots, U_{g,p_g})'$ is the score vector for gene g with p_g RVs of itself. Given a pathway (or gene set) S, the gene-specific SPU statistic is as follows:

$$T_{SPU(\gamma;g)} \propto ||Ug.||_\gamma = \left(\frac{\sum_{j=1}^{p_g} |U_{g,j}|^\gamma}{p_g} \right)^{\frac{1}{\gamma}} \tag{7}$$

Then accordingly, the pathway-based SPU statistic is

$$T_{Path-SPU(\gamma,\gamma 2;S)} = \sum_{g \in S} (T_{SPU(\gamma;g)})^{\gamma 2} \tag{8}$$

Aim 2 II

Method

The pathway-based aSPU statistic is thus

$$T_{Path-aSPU(S)} = min_{\gamma,\gamma 2} P_{Path-SPU(\gamma,\gamma 2;S)} \tag{9}$$

We propose to use $\gamma 2 \in \Gamma 2 = \{1, 2, 4, 8\}$. The $1, 2, 4, 8$ will cover Sum-like test, SSU-like test, and two more tests preferring the sparse-casual-gene situation (e.g. only 2 or 3 genes are associated with traits in a pathway, say with 20 genes).

Aim 2 I

Methods in data simulation

- We will simulate a pathway with 20 genes; each gene g will contain p_g RVs with p_g randomly draw from a uniform distribution $U(5, 30)$; 10 of the 20 genes will be randomly selected to be causal, with each casual gene containing 1 causal RV.
- We will test Path-aSPU family on the simulated data to evaluate the type I error and power, with comparison to other existing tests like GRASS [CHP+10],which executes lasso regression (L1-norm) of eigenSNPs within each gene to achieve variable selection, while performing ridge regression (L2-norm) of eigenSNPs at the gene-set-level to achieve gene effect estimates shrinkage simultaneously; ALIGATOR [HGP+09], the association list go annotator, which is a 'p-value enrichment approach' requiring only pre-computed SNP p-values, uses Fisher's exact test on SNP with minimum p-value for the gene-level association; Plink [PNTB+07], which is a very popular GWAS analysis tool and plinkSet module within it implements the set-based associate test; the famous GSEA test in association study settings by [WLB07].

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Aim 3

To provide an R package or Linux command-line based software program to enable convenient implementation of above methods. The package/software will be released to public (e.g. CRAN) eventually.

Aim 3

Method

1. the package/software will be straightforward to install and use for 1st-time user
2. the package/software will have the ability to run in a very flexible parallel computation framework, e.g. can use single node with multiple cores or use multiple nodes with multiple cores. The parallel protocol we will adopt is either SOCKET or MPI.
3. the package/software will have state-of-the-arts technique to enable efficient implementation of aSPU algorithms, such as hash table, radix sort, memory-efficient task send & collect among nodes, some intensive loops consider calling C++ code, etc.
4. the package/software will have a help document with demo examples

Real Data Introduction

The real data used in my dissertation will be obtained from the Atherosclerosis Risk in Communities (ARIC) Study (https://www2.cscc.unc.edu/aric/).

The Cohort Component of the ARIC study began in 1987. A total of 15,792 participants received an extensive examination, including medical, social, and demographic data. These participants were re-examined every three years with the first screen (baseline) occurring in 1987-89, the second in 1990-92, the third in 1993-95, and the fourth exam was in 1996-98. In 2009, the NHLBI funded a fifth exam, which is currently being conducted.

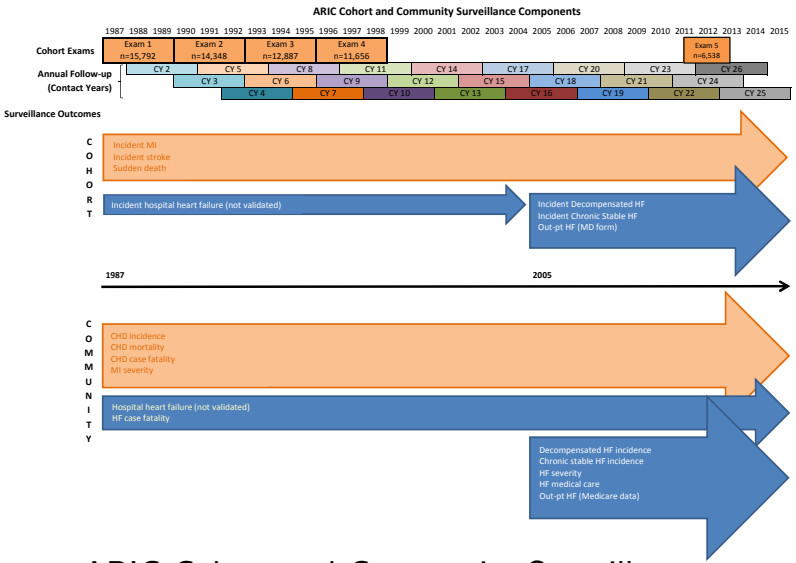

Figure: ARIC Cohort and Community Surveillance Components. Figure adopted from the ARIC website

We will apply our proposed method on ARIC data. Specifically, we will use the four closely cardiovascular-disease-related traits measured in ARIC cohort data, which are **total cholesterol** (tch), **High-density lipoprotein** (HDL), **Low-density lipoprotein** (LDL) and **triglycerides** (trgs). We will exclusively use Caucasian samples ($n = 11478$). For the covariates, we will include but not limited to subject's demographic information such as age, gender, BMI, etc.

References I


William S Bush and Jason H Moore, *Genome-wide association studies*, PLoS computational biology **8** (2012), no. 12, e1002822.


Lin S Chen, Li Hsu, Eric R Gamazon, Nancy J Cox, and Dan L Nicolae, *An exponential combination procedure for set-based association tests in sequencing studies*, The American Journal of Human Genetics **91** (2012), no. 6, 977–986.


Lin S Chen, Carolyn M Hutter, John D Potter, Yan Liu, Ross L Prentice, Ulrike Peters, and Li Hsu, *Insights into colon cancer etiology via a regularized approach to gene set analysis of gwas data*, The American Journal of Human Genetics **86** (2010), no. 6, 860–871.


Andriy Derkach, Jerry F Lawless, and Lei Sun, *Robust and powerful tests for rare variants using fisher's method to combine evidence of association from two or more complementary tests*, Genetic epidemiology **37** (2013), no. 1, 110–121.


Ruzong Fan, Yifan Wang, James L Mills, Alexander F Wilson, Joan E Bailey-Wilson, and Momiao Xiong, *Functional linear models for association analysis of quantitative traits*, Genetic epidemiology **37** (2013), no. 7, 726–742.


Peter Holmans, Elaine K Green, Jaspreet Singh Pahwa, Manuel AR Ferreira, Shaun M Purcell, Pamela Sklar, Michael J Owen, Michael C O'Donovan, and Nick Craddock, *Gene ontology analysis of gwa study data sets provides insights into the biology of bipolar disorder*, The American Journal of Human Genetics **85** (2009), no. 1, 13–24.


Fang Han and Wei Pan, *A data-adaptive sum test for disease association with multiple common or rare variants*, Human heredity **70** (2010), no. 1, 42–54.


Sunkyung Kim, Wei Pan, and Xiaotong Shen, *Penalized regression approaches to testing for quantitative trait-rare variant association*, Frontiers in genetics **5** (2014).


Li Luo, Eric Boerwinkle, and Momiao Xiong, *Association studies for next-generation sequencing*, Genome research **21** (2011), no. 7, 1099–1108.

References II


Seunggeun Lee, Mary J. Emond, Michael J. Bamshad, Kathleen C. Barnes, Mark J. Rieder, Deborah A. Nickerson, N. H. L. B. I G. O Exome Sequencing Project-E. S. P Lung Project Team , David C. Christiani, Mark M. Wurfel, and Xihong Lin, *Optimal unified approach for rare-variant association testing with application to small-sample case-control whole-exome sequencing studies.*, Am J Hum Genet **91** (2012), no. 2, 224–237 (eng).


Bingshan Li and Suzanne M. Leal, *Methods for detecting associations with rare variants for common diseases: application to analysis of sequence data.*, Am J Hum Genet **83** (2008), no. 3, 311–321 (eng).


Dan-Yu Lin and Zheng-Zheng Tang, *A general framework for detecting disease associations with rare variants in sequencing studies*, The American Journal of Human Genetics **89** (2011), no. 3, 354–367.


Nan M Laird and James H Ware, *Random-effects models for longitudinal data*, Biometrics (1982), 963–974.


Seunggeun Lee, Michael C. Wu, and Xihong Lin, *Optimal tests for rare variant effects in sequencing association studies.*, Biostatistics **13** (2012), no. 4, 762–775 (eng).


Kung-Yee Liang and Scott L Zeger, *Longitudinal data analysis using generalized linear models*, Biometrika **73** (1986), no. 1, 13–22.


Li Luo, Yun Zhu, and Momiao Xiong, *Quantitative trait locus analysis for next-generation sequencing with the functional linear models*, Journal of medical genetics **49** (2012), no. 8, 513–524.


———, *Smoothed functional principal component analysis for testing association of the entire allelic spectrum of genetic variation*, European Journal of Human Genetics **21** (2012), no. 2, 217–224.


Bo Eskerod Madsen and Sharon R. Browning, *A groupwise association test for rare mutations using a weighted sum statistic.*, PLoS Genet **5** (2009), no. 2, e1000384 (eng).

References III


Benjamin M Neale, Manuel A Rivas, Benjamin F Voight, David Altshuler, Bernie Devlin, Marju Orho-Melander, Sekar Kathiresan, Shaun M Purcell, Kathryn Roeder, and Mark J Daly, *Testing for an unusual distribution of rare variants*, PLoS genetics **7** (2011), no. 3, e1001322.


Wei Pan, *Asymptotic tests of association with multiple snps in linkage disequilibrium*, Genetic epidemiology **33** (2009), no. 6, 497–507.


Wei Pan, Fang Han, and Xiaotong Shen, *Test selection with application to detecting disease association with multiple snps*, Human heredity **69** (2009), no. 2, 120–130.


Wei Pan, Junghi Kim, Yiwei Zhang, Xiaotong Shen, and Peng Wei, *A powerful and adaptive association test for rare variants*, Genetics (2014), genetics–114.


Shaun Purcell, Benjamin Neale, Kathe Todd-Brown, Lori Thomas, Manuel AR Ferreira, David Bender, Julian Maller, Pamela Sklar, Paul IW De Bakker, Mark J Daly, et al., *Plink: a tool set for whole-genome association and population-based linkage analyses*, The American Journal of Human Genetics **81** (2007), no. 3, 559–575.


Wei Pan and Xiaotong Shen, *Adaptive tests for association analysis of rare variants.*, Genet Epidemiol **35** (2011), no. 5, 381–388 (eng).


Jianping Sun, Yingye Zheng, and Li Hsu, *A unified mixed-effects model for rare-variant association in sequencing studies*, Genetic epidemiology **37** (2013), no. 4, 334–344.


Kai Wang, Mingyao Li, and Maja Bucan, *Pathway-based approaches for analysis of genomewide association studies*, The American Journal of Human Genetics **81** (2007), no. 6, 1278–1283.


Michael C. Wu, Seunggeun Lee, Tianxi Cai, Yun Li, Michael Boehnke, and Xihong Lin, *Rare-variant association testing for sequencing data with the sequence kernel association test.*, Am J Hum Genet **89** (2011), no. 1, 82–93 (eng).

References IV


Kai Wang, Mingyao Li, and Hakon Hakonarson, *Analysing biological pathways in genome-wide association studies.*, Nat Rev Genet **11** (2010), no. 12, 843–854 (eng).


Kai Wang, Haitao Zhang, Deqiong Ma, Maja Bucan, Joseph T Glessner, Brett S Abrahams, Daria Salyakina, Marcin Imielinski, Jonathan P Bradfield, Patrick MA Sleiman, et al., *Common genetic variants on 5p14. 1 associate with autism spectrum disorders*, Nature **459** (2009), no. 7246, 528–533.


Zhiyuan Xu, Xiaotong Shen, Wei Pan, Alzheimer's Disease Neuroimaging Initiative, et al., *Longitudinal analysis is more powerful than cross-sectional analysis in detecting genetic association with neuroimaging phenotypes*, PloS one **9** (2014), no. 8, e102312.


Hua Zhou, Mary E Sehl, Janet S Sinsheimer, and Kenneth Lange, *Association screening of common and rare genetic variants by penalized regression*, Bioinformatics **26** (2010), no. 19, 2375.


Yiwei Zhang, Zhiyuan Xu, Xiaotong Shen, and Wei Pan, *Testing for association with multiple traits in generalized estimation equations, with application to neuroimaging data*, NeuroImage **96** (2014), 309–325.