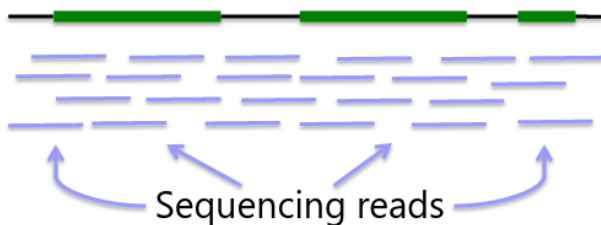


Sequencing Data and Analysis of Rare Variants

Genotyping arrays can be obtained at pre-selected sites for each sample. Ex. Genotyping sites known to be polymorphic based on prior sequencing.

Sequencing is obtaining "every" base in the exome or genome for each sample. Most of the sequence is identical across samples. This is used to find locations that are polymorphic, or differ across samples.

Whole Genome Sequencing

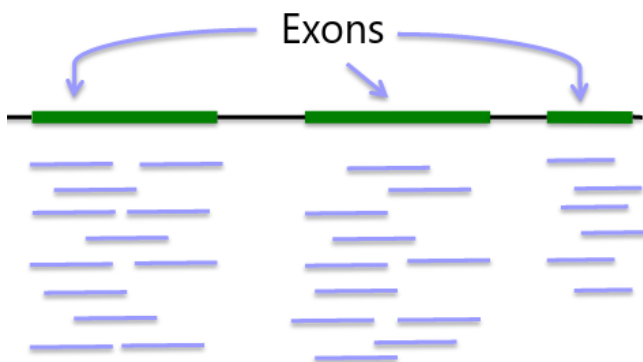


Genome: ~3GB per individual

Advantage - whole genome coverage

Disadvantage - cost ~\$1000 for 30x, limited interpretability

Whole "Exome" Sequencing



Exome: ~33MB per individual

Advantage: Covers protein coding regions, interpretable variation, cost ~\$500

Disadvantage: Missing 99% genome coverage

VCF Format

Variant Calling File (VCF) is a standard format for storing sequencing data. It includes genotypes for all sites where at least one individual had alleles different from references alleles for all individuals in the study.

Every VCF file has three parts in the following order:

- Meta-information lines or Header (begins with ##)
- Last Meta-information line: Record Header (line beginning with #CHROM)
- Data lines (Body) contain marker and genotype data (one variant per line)
 - A data line is called a VCF record
 - Each VCF record has the same number of tab-separated fields as the record header line
 - The symbol "." is used to denote missing data

Meta information

(a) VCF example

```
##fileformat=VCFv4.1
##fileDate=20110413
##source=VCFtools
##reference=file:///refs/human_NCBI36.fasta
##contig=<ID=1,length=249250621,md5=1b22b98cdeb4a9304cb5d48026a85128,species="Homo Sapiens">
##contig=<ID=X,length=155270560,md5=7e0e2e580297b7764e31dbc80c2540dd,species="Homo Sapiens">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##ALT=<ID=DEL,Description="Deletion">
##INFO=<ID=SVTYPE,Number=1,Type=String,Description="Type of structural variant">
##INFO=<ID=END,Number=1,Type=Integer,Description="End position of the variant">
```

Record header line ↓

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	SAMPLE1	SAMPLE2
1	1	.	ACG	A,AT	40	PASS	.	GT:DP	1/1:13	2/2:29
1	2	.	C	T,CT	.	PASS	H2;AA=T	GT	0 1	2/2
1	5	rs12	A	G	67	PASS	.	GT:DP	1 0:16	2/2:20
X	100	.	T		.	PASS	SVTYPE=DEL;END=299	GT:GQ:DP	1:12:.	0/0:20:36

First 8 columns: variant information

9th column is format of sample information

Subject data

The first nine columns of the data record give information about the variants:

1. CHROM - the chromosome number/id
2. POS - the genome coordinate of the first base in the variant.
Within a chromosome, VCF records are sorted in order of increasing position.
3. ID - a semicolon-separated list of marker identifiers (often rsid)
4. REF - the reference allele expressed as a sequence of one or more A/C/G/T nucleotides (e.g. "A" or "AAC")
5. ALT - the alternate allele expressed as a sequence of one or more A/C/G/T nucleotides (e.g. "A" or "AAC"). If there is more than one alternate allele, the field is a comma-separated list of all alternate alleles.

6. QUAL - The Phred-scaled probability that a REF/ALT polymorphism exists at this site given sequencing data. A value of 10 indicates a 1 in 10^1 chance of error, 50 indicates 10^5 chance of error, etc.

$$p(\text{error}) = \frac{1}{10^{Q/10}} = 10^{-Q/10}$$

7. FILTER - Either "PASS" or a semicolon-separated list of failed quality control filters

8. INFO - Values in INFO are defined in the header. Contains additional information about the variant represented as tag-value pairs, where the tag and value are separated by an equals sign, and pairs are separated by colons. Usually it is information summarized from the samples, but can also include information from other sources such as population frequencies from a database.

9. FORMAT - Explanation of information in FORMAT are defined in the header. As for INFO, a colon-separated list. Describes the format of the data reported for each sample in the file.

There are many tools that can be used with VCF and BCF (binary version of VCF), such as bcftools and plink.

"Missing Heritability"

GWA studies are great for identifying SNP associations, but usually loci identified have small effects on traits. Much of the phenotypic variation or risk due to genetics ("heritability") is unexplained.

Unexplained variance/risk may be due to:

- Many additional variants with very small effects
- Non-SNP variants such as structural variants not typed by current GWAS chips.
- Epigenetic factors: methylation
- Over-estimation of heritability due to:
 - Genetic interaction
 - Dominance effects
 - Shared environment
- **Rare variants that we have not yet been tested**

Rare Variants

There are a lot of different rare variants, they are very common! Rare variants are more likely to be functional/deleterious. The best way to find rare variants is to sequence.

Recent expansion of the human population supports the theory of causal rare variants (there's 8 billion people today). Multiple causal rare variants have been found within genes. Animal studies suggest larger effects of rarer variants.

MAF (Minor Allele Frequency) cutoff can be used to define a "rare" variant (this level makes a difference in analysis).

Association Analysis with Rare Variants

The problem with single variant tests such as regression methods is that there are too few observations to provide a stable test.

We can combine rare variants by grouping them by gene region or functional information (exomes, non-synonymous or nonsense, predicted function), which can improve power.

(Lee et al, 2014)

Table 2. Summary of Statistical Methods for Rare-Variant Association Testing

	Description	Methods	Advantage	Disadvantage	Software Packages ^a
Burden tests	collapse rare variants into genetic scores	ARIEL test, ⁵⁰ CAST, ⁵¹ CMC method, ⁵² MZ test, ⁵³ WSS ⁵⁴	are powerful when a large proportion of variants are causal and effects are in the same direction	lose power in the presence of both trait-increasing and trait-decreasing variants or a small fraction of causal variants	EPACTS, GRANVIL, PLINK/SEQ, Rvtests, SCORE-Seq, SKAT, VAT
Adaptive burden tests	use data-adaptive weights or thresholds	aSum, ⁵⁵ Step-up, ⁵⁶ EREC test, ⁵⁷ VT, ⁵⁸ KBAC method, ⁵⁹ RBT ⁶¹	are more robust than burden tests using fixed weights or thresholds; some tests can improve result interpretation	are often computationally intensive; VT requires the same assumptions as burden tests	EPACTS, KBAC, PLINK/SEQ, Rvtests, SCORE-Seq, VAT
Variance-component tests	test variance of genetic effects	SKAT, ⁶¹ SSU test, ⁶² C-alpha test ⁶³	are powerful in the presence of both trait-increasing and trait-decreasing variants or a small fraction of causal variants	are less powerful than burden tests when most variants are causal and effects are in the same direction	EPACTS, PLINK/SEQ, SCORE-Seq, SKAT, VAT
Combined tests	combine burden and variance-component tests	SKAT-O, ⁶⁴ Fisher method, ⁶⁵ MiST ⁶⁶	are more robust with respect to the percentage of causal variants and the presence of both trait-increasing and trait-decreasing variants	can be slightly less powerful than burden or variance-component tests if their assumptions are largely held; some methods (e.g., the Fisher method) are computationally intensive	EPACTS, PLINK/SEQ, MiST, SKAT
EC test	exponentially combines score statistics	EC test ⁶⁷	is powerful when a very small proportion of variants are causal	is computationally intensive; is less powerful when a moderate or large proportion of variants are causal	no software is available yet

Burden Tests

- Instead of testing rare variants individually, group variants likely to have similar function
- Score presence or absence of rare variants per individual -- use rare variant score to predict trait values
- Makes the assumption that the effect of all rare variants is in the same direction
- If all variants grouped in a test are causal, leads to a large increase in power
- Success (power) depends on:
 - Number of associated variants contributing to signal
 - Number of neutral (null) variants
 - direct of effects

CAST

- Compare the frequency of cases and controls with at least one mutation within a gene or region
- Can be thought of as an indicator approach
 - $X_i = 1$ when subject i has at least one rare variant in the region/gene
 - $X_i = 0$ when a subject i has no rare variants
- CAST score can be tested against any type of outcome in regression framework
- Assumes same effect whether a single or multiple rare variants occur in a region in an individual

Unweighted Sum / CMC

- An extension of CAST
- An unweighted sum of the rare variants in a gene or region
 - Commonly used to collapse rare variants into a score of minor alleles
- Regression (linear or logistic) used to test association with the rare variant score (sum)
- All variants included in the sum are assumed to have the same magnitude and direction of effect

RVT1

- An extension of CAST/CMC
- Instead of the sum, uses the proportion of sites at which an individual carries a rare variant as the predictor
- Accounts for missing data:
 - n_i - Number of rare variants for which subject i has been genotyped
 - r_i - Number out of the n_i sites where individual i carries at least one rare allele
 - Score is r_i / n_i

Weighted Sum of the Variants

$$X_i = \sum_{m=1}^M G_{i,m} W_m$$

□ $G_{i,m}$ is the genotype for individual i at SNP m

□ W_m is the weight for SNP m

$$\hat{W}_m = \frac{1}{\sqrt{n_m f_m (1-f_m)}}$$

Risk Allele Frequency:

$$f_m = \frac{a_m}{2n_m}$$

For case-control outcomes:

$$f_m = \frac{a_m^u + 1}{2n_m^u + 2}$$

a_m : total number of minor (or risk) alleles for the SNP m

n_m : total number of subjects for SNP m

a_m^u : number of minor (or risk) alleles in the unaffected subjects for SNP m

n_m^u : total number of unaffected subjects for SNP m

$G_{i,m}$: is the number of risk variants for SNP m in individual i

Madsen and Browning proposed using a weight based on the inverse of the MAF in the unaffected sample. Lower MAF SNPs have a larger weight. Makes the assumption that the rarer variants have a large phenotypic effect.

- Weights can be developed using any criterion; Allele frequency, function, previous evidence. There is no "best" way
- Use weight in a regression to include covariate and use for quantitative outcomes
- Allows variants to be treated differently based on beliefs about likelihood of functionality
- Still assumes all variants have effect in same direction

Variable Threshold (VT) Model

- Addresses arbitrary MAF cutoff of other burden tests
- Calculates test statistics across many MAF cutoffs
- Chooses maximum test statistic over all MAF cutoffs
- Controls for over fitting using permutation
 - Computationally expensive
- Regression framework -- quantitative or qualitative outcome, covariates
- All variants in MAF bin have the same direction of effect: Weights:
 - 0 for variants that are excluded based on MAF
 - 1 for variants included

Variance Component Tests (SKAT)

Sequence Kernel Association Test

- Test of the joint effects of multiple variants in a region on a phenotype
- Regression framework: allows for inclusion of covariates
- Does not require permutation
- Does not get an estimate of effect size (beta)

We want to test $H_0: \beta_1 = \beta_2 = \dots = \beta_m$ Or $t = 0$

Assume:

$$\beta_j \sim f(\mu = 0, \sigma^2 = w_j \tau)$$

τ is a variance component and w_j is a pre-specified weight for variant j , usually chosen to be a function of the MAF.

Under the null hypothesis Q is a mixture of chi-squared distributions.

Variance component score test statistic:

$$Q = (\mathbf{y} - \hat{\boldsymbol{\mu}})' K (\mathbf{y} - \hat{\boldsymbol{\mu}}) \text{ where } K = G W G'$$

$$\hat{\boldsymbol{\mu}} = \hat{\gamma}_0 + X \hat{\gamma}_1 \text{ for continuous traits}$$

$$\hat{\boldsymbol{\mu}} = \text{logit}^{-1}(\hat{\gamma}_0 + X \hat{\gamma}_1) \text{ for binary traits}$$

$\hat{\gamma}_0$ and $\hat{\gamma}_1$ are estimated under H_0 by regression Y on X

$W = \text{diag}(w_1, w_2, \dots, w_m)$: Weights of the m variant sites

Matrix K is $n \times n$ (n individuals) with ij^{th} element equal to:

$$K(G_i, G_j) = \sum_{k=1}^m w_k G_{ik} G_{jk}$$

$K(G_i, G_j)$ measures the similarity of individuals i and j for the m markers

For the weights the original paper recommends this weight for variant j :

$w_j = \text{Beta}(\text{MAF}_j, \alpha_1, \alpha_2)$, with $\alpha_1 = 1$ and $\alpha_2 = 25$ or Madsen-Browning uses $\alpha_1 = .5$ and $\alpha_2 = .5$

SKAT-O

The goal is to combine the best features of SKAT and burden tests into one test with optimal power. Burden tests have good power when all variants have similar effect size & direction. SKAT has better power when many variants are null and/or effects in opposite directions.

- Unified test statistic is a weighted sum of the burden test statistic Q_B and the SKAT statistic

$$Q_S = \rho Q_B + (1 - \rho) Q_S$$

- The weight ρ can be interpreted as the correlation of regression coefficients of the variants
 - If close to 1: collapse all variants and use burden test
 - If close to 0: all different, SKAT is most powerful
- Asymptotic distribution is mixture of chi-square 1df (for Q_B) and mixture of chi-squares (for Q_S)
- P-value can be computed analytically with numerical integration

Significance Thresholds for Rare Variant Tests

Depends on:

- Type of sequence study
 - Targeted
 - Exome
 - Whole genome
- Type/numbers of tests performed
 - One test per gene
 - Multiple tests per gene -- whether different or same tests were run on SNP sets
 - Are the tests independent
- Testing a region already known to have a signal
 - Using independent samples
 - Using the same samples that identified the region

Bonferroni for the number of tests performed can also be applied. Though it is likely to be conservative, even if tests are independent -- some tested genes/regions do not have sufficient variation. Unless the study is very large, p-values likely to be less significant than expected under H_0 : no association.

Conditional Analysis

For regression-based tests, a conditional analysis amounts to including the associated common variant AND the rare variant score in the same model.

Let $X_i = \sum_{m=1}^M G_{i,m} W_m$ be the rare variant score for person i .

Let Z_i be the genotype (0,1,2) of the common variant previously associated with the trait Y_i for person i .

Model: $E(Y_i) = \beta_0 + \beta_1 Z_i + \beta_2 X_i$

To test whether the rare variant score is associated with the trait conditional on the common variant:

$H_0: \beta_2 = 0$

If the test is significant then the association between Y_i and common variant Z_i does not fully explain the association observed between Y_i and rare variant score X_i , i.e. the rare variant is not just a proxy for the common variant or vice-versa.