

Haplotypes and Imputation

When multiple markers/SNPs are genotyped in a gene or gene region, the SNPs may be in linkage disequilibrium (LD). Each individual test of association with a marker is correlated with all tests for other markers in LD with that marker.

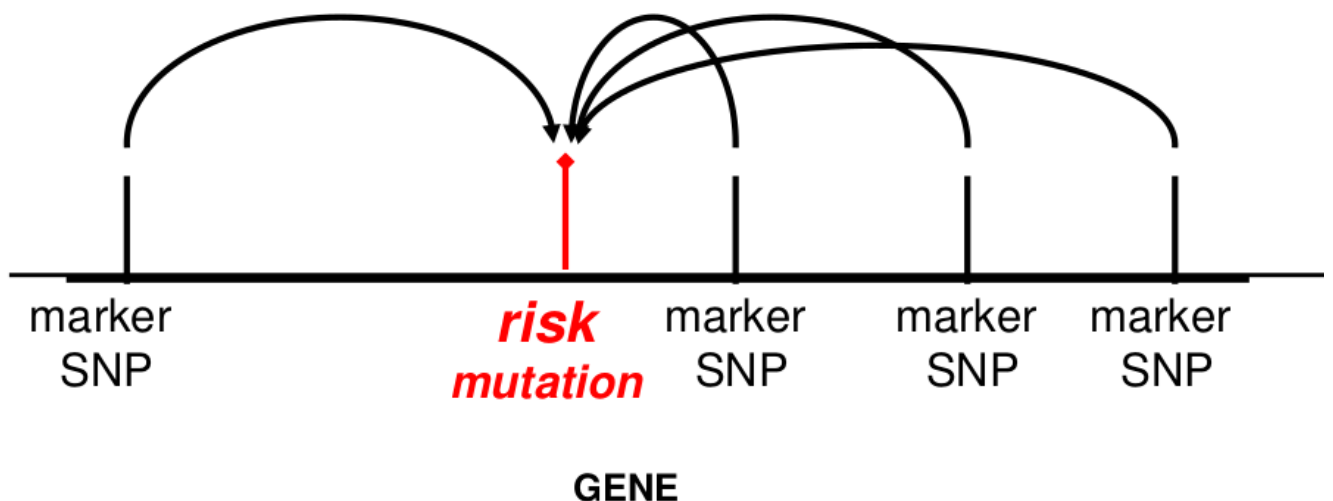
So, instead of testing the individual markers for association, we may want to test haplotypes of markers for association.

Review: A haplotype is a combination of alleles at multiple loci that are transmitted together on the same chromosome. It should provide the alleles present on the locus and which alleles are on the same chromosome. For example, if we have 2 SNPs with alleles (A, a) and (B, b) then we have $2 \times 2 = 4$ possible haplotypes: AB, Ab, aB, ab.

For linked SNPs within a gene or small chromosomal region there are typically far fewer haplotypes observed than are theoretically possible (as a consequence of LD).

Reasons to Care About Haplotypes

1. We haven't typed the casual variant. The haplotype that the variant lies on is a better surrogate for the variant than any one SNP in the haplotype.



2. The "causal" genetic variant is actually the haplotype, not any one variant -- The haplotype confers risk rather than an individual SNP allele.

- Options include:
 - All SNPs on a chromosome
 - All SNPs on a "haplotype block" (chromosome segment where all variants are in high LD)
 - Sliding windows of 2-5 SNPs across region of interest
- Unless there is high LD, there will be more haplotypes than SNPs -> create haplotypes from SNPs that are in LD

Regression with Haplotypes/Likelihood-Based Tests

Take the following example with 3 SNPs and 4 observed Haplotypes, where each person i has 2 haplotypes:

	Coding			
Observed haplotype pair:	H_1	H_2	H_3	H_4
H_1H_1	2	0	0	0
H_1H_2	1	1	0	0
H_2H_2	0	2	0	0
H_1H_3	1	0	1	0
H_2H_4	0	1	0	1
H_3H_4	0	0	1	1

We can use variables to count the number of each haplotype type per person. This coding works for any type of multi-allelic marker, not just haplotypes.

We can use a linear regression model with the haplotype counts as predictors:

$$E(Y_i) = \beta_0 + \beta_1 H_{2i} + \beta_2 H_{3i} + \beta_3 H_{4i} + \dots + \beta_k X_{ki}$$

Note we do not include H_1 in the model. Since $H_1 + H_2 + H_3 + H_4 = 2$, we already know H_1 once we know the remaining haplotypes. Think of H_1 as a reference haplotype.

Each individual will have a 0, 1, or 2 for each of the 3 indicator variables for the haplotypes.

For 4 haplotypes, the general (Omnibus) test for association would be:

$$H_0: \beta_1 = \beta_2 = \beta_3 = 0; \text{ df} = 3$$

If we reject the null, then do tests on individual haplotypes

Global (omnibus) tests of haplotype association provide some protection from the multiple testing problem, as it tests whether the haplotype distribution is associated with phenotype.

In reality we rarely know haplotypes with certainty. Instead, for each individual haplotype estimation produces the probability of each possible haplotype pair. Can use the same model, but replace the observed haplotype counts with the expected counts (determined by probabilities).

SNP Imputation

The most recent application of haplotypes is imputation. The idea is we use a **reference population** that has denser genotyping of whole genome sequencing on your subset of SNPs plus many additional SNPs to impute the SNPs not typed on your chip.

A **reference population** is a set of individuals who have been genotyped or sequenced in a comprehensive manner. Typically these are for the whole genome sequenced (all the SNPs are included in the sample, plus many additional).

The HapMap project was the first available reference population. HRC created a large reference panel of human haplotypes by combining together sequencing data from multiple cohorts (current release consists of 64,976 haplotypes at ~39 million SNPs). TOPmed has a set of haplotypes from 97,256 genome sequenced individuals, more diverse than HRC.

Reference sample has genotypes on many SNPs:



Your sample has genotypes for SNPs on a commercial chip:



Using the set of reference haplotypes,
you can infer genotypes at loci that are
not typed in your own sample:



The two commonly used methods for imputation are IMPUTE and Minimac, and some organizations have "imputation servers" so you can impute your GWAS data to large sequenced data sets without needing powerful on-site computers.

"Dosage"

Genotype imputation does not assign a genotype to each individual, instead for each individual it assigns a probability for each of the possible genotypes at each genetic variant.

Analysis is then performed on the "dosage" - the expected genotype. The most common model is additive, but one could also use a dominant or recessive dosage.

AA	AT	TT
0	1	2
0.02	0.10	0.88

Additive model dosage= $0 \times 0.02 + 1 \times 0.10 + 2 \times 0.88 = 1.86$

"Best Guess Genotype"

Another method is "best guess" genotype. This is the genotype with highest probability. It ignores uncertainty in genotype assignment. We usually impose a posterior probability threshold; if $p < Q$, genotype is set to missing (typically set to .8, .9 or .95)

Imputation Accuracy

The overall quality of imputed data depends on how well matched the reference samples are to the samples you are trying to impute.

The concordance of imputed genotypes with true (unknown) genotypes also depends on how much information about the ungenotyped SNPs (how strong is the LD between ungenotyped and genotyped SNPs?)

For high information the concordance reaches nearly 100%, for low information regions it can be much lower.

Imputation R^2 is an estimate of the squared correlation between imputed and true genotypes. It can be estimated by the obs/exp variance ratio: ratio of empirical genotype dose variance to expected (binomial) genotype variance.

$$R^2 = \text{var}(\hat{G}) / \text{var}(G)$$

Due to excess homozygosity in a well imputed variant, R^2 will occasionally be more than 1.

This imputation quality measure is also a measure of the correlation between the imputed genotypes and true genotypes.

Typically:

- $R^2 \geq .8$ is good imputation
- $R^2 < .3$ is bad imputation
- $.3 \geq R^2 < .8$ is moderate quality imputation can be used in analysis

Good imputation:

- Has a imputed genotype dosage close to the individuals true (unknown) genotype
- Allele frequency estimated from the imputed genotypes is close to the true frequency
- Under HWE, genotypes should have frequency q^2 , $2pq$, p^2 and genotype variance $2pq$ (binomial distribution)
- The best possible imputation will have a sample variance of G_{hat} which is the same as the binomial variance, and $R^2 = 1$

The worst possible imputation is when we have no information about the genotypes other than the allele frequency (which can be estimated from the reference haplotypes). In this case, the imputation would assign everyone the genotype probabilities q^2 , $2pq$, p^2 . Thus everyone would have the same genotype dosage:

$$1 \times 2pq + 2 \times p^2 = 2p$$

Variance would be 0 because there is no LD between SNPs, and thus correlation would be 0.

Why Impute Genotypes?

- Fill in missing genotype data
- Can test ungenotyped SNPs (with some error) for association
- Analysis of individual SNPs are easier to interpret than haplotypes
- **Simplifies combining results from genome-wide association studies using different genotyping platforms**

We can also combine studies to increase sample size, and thus the power. The problem is when studies use different reference SNPs, which is why the common SNPs across platforms is small.

There are 2 ways to combine studies:

- Combined (joint or pooled)
 - Combine individual data from multiple cohorts
 - Often not feasible because of patient confidentiality
- Meta analysis
 - Combining evidence for association across studies
 - Can combine test statistics, p-value or effect size estimates (i.e. regression parameters)

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