# Status update: Detecting epistasis in human complex traits

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## Abstract

Genome wide association studies (GWAS) have become the focus of the statistical analysis of complex traits in humans, successfully shedding light on several aspects of genetic architecture and also biological etiology. Single nucleotide polymorphisms (SNPs) are usually modeled as having linear, cumulative, and independent effects on the phenotype. Though evidently a useful approach, it is often argued that this is not a realistic biological model and that epistasis, the statistical interaction between SNPs, should be included. The purpose of this review is to summarise recent directions in methodology for detecting epistasis, and present evidence for and against the importance of epistasis to complex traits in humans. We also discuss the relevance of epistasis in the context of GWAS, and potential hazards in the interpretation of statistical interaction terms.

## Introduction

**Complex traits** are those that are influenced by many genetic and environmental factors. Almost all diseases that have a significant burden on human health are complex at the population scale. Even classically "**Mendelian**" diseases, such as cystic fibrosis, are at some level complex because numerous genetic effects are involved in modifying the severity of symptoms. Arguably the most important empirical result to emerge from GWAS over the past decade is an indication of what it means for a trait to be "complex", demonstrating that the **mutational target size** for any particular complex trait across the genome is very large, and that the additive genetic variation is comprised of very many variants, almost all of very small effect.

To data, GWAS has enjoyed most success by searching for simple additive effects, where the causal variants exhibit independent, linear, and cumulative effects on the trait. But there are enduring questions about whether this body of research is revealing the full extent of the genetic architecture in complex traits. One aspect of this is whether polymorphisms typically act independently, or if their effects are dependent on other polymorphisms elsewhere in the genome. Defining such genetic interaction, or epistasis, has been the subject of several reviews in the past and we won’t expand on them here, but to summarize briefly, one can discuss epistasis in terms of its functional effect or its statistical effect. In terms of functional epistasis, we are referring to the general observation that the effect of a particular variant depends on the genotype of another variant. In terms of statistical epistasis, we are referring to the interaction variance explained by a combination of causal variants that is not due to their independent effects on their own.

There are several methods for estimating the proportion of the phenotypic variance of a trait that is attributed to independent, additive genetic effects (known as narrow-sense **heritability** (*h*2)). But owing to the technical limitations of accounting for non-additive effects, unequivocal estimation of the phenotypic variation attributable to all additive and non-additive genetic effects (known as broad-sense heritability (*H*2)) is not possible for human traits.1 GWAS are typically performed on traits that have been shown to have a non-zero *h*2, on the assumption that this additive genetic variation in the trait can be dissected into additive effects across the genome. Detecting non-additive genetic effects imposes an assumption that, beyond the additive component of genetic variation, for which there is empirical evidence, there exist more complex components whose existence cannot be verified empirically due to technical limitations.

In essence, there is no strict hypothesis-driven precedent for searching for epistasis as there is for additive effects, and yet the question of epistasis in complex traits is often at the forefront of debate. So why is epistasis of such interest? The major objectives of GWAS can be reduced down to two main categories. The first is to use knowledge of the genomic properties of the causal variants influencing a particular trait to further understand its underlying biology. The second is to use the estimated effects of causal variants to improve prediction of phenotypic outcomes. Should the genetic architecture of a trait be comprised of substantial epistasis then identifying epistatic variants could be beneficial to both of the major objectives of GWAS: identifying instances of functional epistasis could be informative in understanding biological mechanisms; whereas should substantial levels of statistical epistasis exist then genetic prediction of complex traits could potentially be improved beyond the theoretical limit imposed by the estimate of narrow-sense heritability.

To this end, the past few years have seen remarkable activity in the development of methodology and software for the detection of epistasis. In this review we will survey these emerging tools. Following on, we aim to take a cold, hard look at the latest empirical evidence for the importance of epistasis and the potential utility in searching for genetic interactions.

## Methods for detecting epistasis

Despite the severe challenges in robust detection of epistasis for human complex traits (BOX1), the past five years have seen rapid development of methods for studying epistasis in human complex traits2–7. Methods ranging from conventional regression-based methods to nature-inspired algorithms are continually being developed (Figure 1). Most methods use SNP-based tests for pairwise or higher-order interactions in GWAS data via either an exhaustive search of all SNP combinations or testing of a reduced, preselected set. **[Au: please add 1 or 2 sentences as a layman’s introduction to what these methods in essence are trying to detect in order to infer epistasis i.e. what non-additive statistical signal does an ‘interaction’ result in? (I have added clarification to the introduction explicitly mentioning that epistasis results from interactions between variants, hence rationalizing why interactions would be sought by the methods.)]** In a pairwise exhaustive search of a GWAS cohort (typically with a low couple of thousands of samples each genotyped by < 500 000 SNPs), the primary goal is to identify interacting SNPs from a search space of many billions of pairwise tests (strictly *n*(*n*-1)/2 given *n* SNPs). Such a search creates a huge computational burden and also a major statistical challenge of achieving significance thresholds derived following **Bonferroni correction** of the number of tests performed. In addition, methods have been developed to assess interactions between groups of SNPs; for example, SNPs grouped into genes or into functional modules (pathways or networks). As a broad generalization, approaches that search all pairs of SNPs for evidence of all types of epistasis can be termed “**hypothesis free**” whereas those which restrict themselves to searching subsets of SNPs and/or types of epistasis may be termed “hypothesis driven”. Because of the size of the parameter space to search and the number of analyses performed, hypothesis-free approaches pose a major challenge and one of the key achievements in recent years is that computational barriers have been bypassed and an exhaustive search for pairwise interactions has become a more routine exercise8–12. Here we provide an overview of the developments in methodology since an earlier review by Cordell13 with a focus on hypothesis-free, genome-wide methods.

### Regression-based methods

Traditionally methods based on logistic regression or linear regression are used to assess SNP interactions in diseases or **quantitative traits** respectively13,14 (Supplementary information box S1). Given the goal of detecting interactions, one can use SNP genotype models to test interactions directly by comparing the **saturated model** including interactions (LS) against the **reduced model** without (LR) for each pair of SNPs and thus save computing time in estimating genetic parameters unnecessarily. The (LS vs. LR) test is essentially based on the variance explained by four interaction terms and thus consumes four degrees-of-freedom (df). When concerning only additive effects, SNP allelic models can be applied instead in which case the interaction test consumes one df because only the additive-additive interaction term is included and thus could be more powerful if only additive effects are present15.

Previously an exhaustive search for pairwise interactions at the genome-wide level was considered computationally prohibitive13. Various approaches have been taken to reduce the computational barrier. First, advantage has been taken of modern computing infrastructure and technologies including clusters of computers equipped with multiple CPU cores and/or graphic processing units (GPU)9,11,12,16, parallelization8,10,17 and bitwise computing where SNP genotype data are stored in bitwise data structures to achieve great memory efficiency and computing speed8,18,19. Second, approximate interaction tests have been applied that can be quickly computed and do not miss any important epistatic SNP pairs19. For example F ratio and Kirkwood Superposition Approximation approximate the (LS vs. LR) tests under the assumption of **Hardy-Weinberg Equilibrium** (HWE) for quantitative20 and disease traits19 respectively and can be quickly computed from contingency tables based on SNP genotypes. For convenience, we list some recent applications based on regression and other approaches that can perform fast genome-wide screening of epistasis in GWAS (TABLE 1). Considering the various strengths and weaknesses in these applications, we recommend using the approximate interaction tests as an initial genome-wide screen for putative epistatic interactions and then taking the extra step of re-examining the resultant subset of SNP pairs using the full regression models (e.g. conditional tests) to avoid false positives or redundant signals10,20,21.

An exhaustive genome-wide search is now computationally tractable but still suffers from low power in detection of epistasis13,22,23. Large sample sizes (i.e. many individuals) are generally required for success24. Focusing on interactions involving SNPs with genome-wide significant **marginal effects** confirmed in GWAS **[ somewhere it would be useful to mention the pros/cons: that this set of SNPs is likely to be enriched for SNPs with biological connections to the trait, but that many epistatic interactions may be missed as epistasis only requires that combinations of SNPs, rather than individual SNPs, influence the trait]** may be a practical compromise25,26 in light of limited samples available in most individual GWAS cohorts, because a much less stringent threshold can be applied owing to much reduced multiple tests10,20,27–29. Taking 500 000 SNPs for example, the Bonferroni-corrected threshold on the -log10 scale is 12.4 for an exhaustive search in contrast to 7.0 for a hypothesis-driven search focusing on one SNP with marginal effects, i.e. the approximate 2x difference in threshold is equivalent to a doubled sample size in the focused search. Furthermore, using high-density SNPs could potentially make both exhaustive and focused interaction searches more fruitful as power is a function of interaction effects, sample size and **linkage disequilibrium** (LD) between the SNP and **causal variant** at both loci21,24.

### LD and haplotype-based methods**.**

In disease traits, testing interactions can be translated to testing the difference of inter-locus associations between cases and controls that may be computed faster and more powerful than logistic regression (4 df) mainly because such a difference can be tested using a χ2 statistic with one df13,15,30. A collection of statistics (Supplementary information box S1) are derived to measure the inter-locus association difference between cases and controls using joint genotype frequencies mostly under the HWE assumption, and generally work well for unlinked loci (i.e. no LD between) in rare (e.g. prevalence < 0.01) diseases[ref]. For example, methods based on comparing LDs of pairs of SNPs in cases controls appear to be effective in detecting interactions and an early LD-based statistic31 was recently implemented in a fast tool SIXPAC for genome-wide scans of epistasis18. The LD-based statistics may be adapted to detect interactions between SNP **haplotypes** with an equal (if not better) power15. Unfortunately, only genotypes, rather than haplotypes, are directly observed in GWASs and thus the inference of haplotypes requires the **linkage phase** of SNP genotypes to be estimated in advance which is computationally intensive.

Cautions are recommended when applying these methods in GWASs because diseases are not always rare and focusing on unlinked loci would ignore possible intra-locus interactions21,32, whereas in an exhaustive search HWE does not always hold and LDs do exist in many pairwise SNPs, which could potentially generate inflated false positives15. measures of LD based on correlations (that is, co-occurrence) between pairs of SNPs do not assume HWE or require phasing33 and have been increasingly used in studying epistasis in GWASs15,16,34. For example, for each pair of SNPs, interaction can be tested by a Z-score statistic derived from the difference of their Pearson correlation computed separately in cases and controls16,33. However, simulation studies suggest that the Z-score statistic is still subject to inflated false positives when the two SNPs are highly correlated and/or both with significant marginal effects[ref]15. Similarly, an improved haplotype-based statistic that adopts correct variance calculation and incorporates a weighted average of the joint effects of two SNPs is as powerful as the Z-score statistic33 and can control false positives when only one SNP has marginal effects but not when both SNPs have marginal effects and are in LD15. The inflation is probably due to a method caveat, in which case certain haplotype(s) of the two marginal SNPs in LD can exhibit different association signals in cases and controls with/without interactions. This caveat may be cured using the full logistic regression model that can also correct for **covariates** ignored in the LD and haplotype based methods[ref]34. Therefore a two-step solution using the Z-score statistic for screening interactions genome-wide followed by logistic regression models for testing the promising interactions16 can control false positives without losing the power advantage in the LD and haplotype-based methods.

### Bayesian methods

**Bayes’ theorem** offers a great flexibility to model and stochastically search for epistasis without enumerating all SNP combinations13 (Supplementary information box S2). **[Au: does this then come under the ‘exhaustive’ or ‘hypothesis-driven’ category? It seems to be neither]** Based on a similar rational that the difference of inter-locus genotype frequency distributions between cases and controls may indicate interactions, an early Bayesian tool Bayesian epistasis association mapping (BEAM)35 partitions unlinked SNPs (i.e. SNPs not in LD) into three nonoverlapping groups (i.e. unassociated, associated by marginal effects and by joint effects) according to their posterior probabilities without explicitly testing interactions7,13. The BEAM framework has been improved to use new variables accounting for LD among SNPs and thus allow a full analysis of GWAS data7,36 and further extended to be applicable for quantitative traits via two-way Bayesian partitioning (i.e. partitioning SNPs and samples simultaneously). Nevertheless, additional explicit tests for interactions among SNPs partitioned in the jointly associated group at least may be useful to exclude potential false positive interactions6. Hybrid Bayesian methods appear to be able to improve detection of epistasis in GWASs37–39, e.g. combining the strengths of Bayesian framework and generalized linear model allows fast and stable tests of SNP or haplotype interactions while considering covariates, marginal effects and gene–environment interactions simultaneously38,40. Additionally, the Bayesian model averaging approach may increase power of detection by averaging evidence from multiple plausible models given unknown actual interaction types41.

### Data-filtering methods

Hypothesis-driven approaches aim to select a subset of SNPs for interaction tests based on either existing biological knowledge (e.g. databases of pathways and protein-protein interactions5,24,42), or statistical features (e.g. marginal effects24 and SNP genotype frequencies43,44), or fast algorithms18,45–48. Methods based on **variance heterogeneity** among SNP genotypes can effectively select potentially interacting SNPs for quantitative traits but could miss SNPs that are interacting but have limited variance heterogeneity and require further work to confirm either gene-gene or gene-environment interactions involved49,50. Besides the apparent speed advantage, filtering-based methods can have greater power than exhaustive searches because of much reduced multiple testing, as well as functional interpretation when considering only SNPs with putative biological connections to the trait. However, caution is recommended when applying filtering because of potential biases (either upwards or downwards) caused by limitations in the algorithms and existing knowledge that may be subject to publication bias4 and may be context-dependent51,52. Furthermore, it is debatable what threshold is appropriate after filtering as it might alter the null distributions of test statistics53.

### Artificial intelligence algorithms

Many attempts have been made to adopt or improve algorithms from other disciplines to address the **large P small N problem** in detecting epistasis3,5,6,13, particularly when moving beyond pairwise interactions to consider higher-order interactions where regression-based methods3 may suffer from increasingly computational complexity and data sparsity47,54. Machine learning and data mining algorithms **[Au: machine learning or data mining or both? Please be clear throughout this section which methods are of which type (and/or see my suggestion for expanding the table to more comprehensively list the methods)]** often employ certain classifiers for data reduction and/or feature selection to reduce both the computational and statistical burden of an exhaustive search6,55,56, but previously were not all scaled up for GWASs or for explicitly testing interactions and could miss interactions between SNPs without marginal effects if marginal effects are included in a classifier13,55,56. While most existing algorithms (e.g. **Multifactor Dimensionality Reduction**, **tree-based methods** and **entropy-based methods**) are being scaled up by modern computing technologies57–61, their classifiers are also being improved to be applicable for complex quantitative traits57,62–65, to allow the use of risk scores aggregating multiple interactions72, and to account for SNPs without marginal effects66,67.

Improved computing efficiency also facilitates the combination of complementary algorithms. For example, using tree-based methods for screening and Multifactor Dimensionality Reduction for interaction testing can improve the overall performance68–70, and the Reconstructability Analysis method uses entropy-based heuristics to search and evaluate structures of various interaction models constructed by graph theory61. New algorithms such as Ant Colony Optimization, which mimics how ant colonies find the shortest route to foods71, are being adopted for epistasis studies but are not currently transparent about how interactions are tested. Nevertheless, the detection of higher-order interactions appears very challenging to machine-learning and data-mining methods too considering that interactions are not explicitly tested in many cases. When interactions are explicitly tested, e.g. using Reconstructability Analysis, detection of three-way interactions requires multilayer hypothesis tests and thus is as difficult as regression methods4,72, in addition to issues of excessive computing demand, exponentially increased multiple tests and insufficient sample sizes13. Despite some progress, it seems likely that new approaches will be needed for robust genome-wide detection of higher-order interactions.

### Group- and module-based methods

Testing interactions based on SNPs grouped into genes or functional modules can dramatically reduce the multiple test burden (e.g. only ~2 x 108 pairwise tests are required for 20,000 genes) and thus increase the power of detection23,73, including testing for higher-order interactions74. In addition, proper grouping of SNPs may collectively capture causal variants that are not well tagged by individual SNPs75. However, this may be complicated by a number of factors (e.g. group definitions and correlations among SNPs and SNP pairs)76. A common practice is to use genes to group SNPs and derive gene-based variables factoring in SNP correlations for interaction tests via regression77, or for analogous LD-based approaches15 that test the difference of correlation of a pair of genes between cases and controls78,79. Alternatively, one can first compute all pairwise interactions between SNPs in each group and derive gene-based interaction *P* values by integrating the pairwise interaction *P* values73.

These gene-based studies suggest that it is important to incorporate external LD information via **imputation** to increase the chance of capturing unobserved causal variants and to use a composite value from a set of signals (instead of the single best signal, for example) to detect multiple interactions between a pair of genes. Of note, gene-based methods implicitly assume no intragenic interactions, which may not necessarily hold21,32. One can also use pre-computed pairwise SNP interactions to build statistical interaction networks and aggregate multiple gene–gene interactions and marginal effects using network analysis algorithms such as SNPrank80 to identify functionally important pathways3. However, the issues associated with the gene-based approaches (e.g. intragenic interactions and correlated SNP pairs) also need to be addressed.

### Multi-trait and multi-level integration

Collectively analyzing multiple complementary traits may help the detection of **pleiotropic epistasis** to infer shared pathways and/or regulatory mechanisms but this domain remains fundamentally unexplored due to its potential complexity81,82. Pleiotropic epistasis could be identified in human complex traits by simply looking for SNP–SNP interactions shared across related traits21 or using a gene-based method with a latent variable representing multiple traits83. On the other hand, emerging evidence of epistasis identified through expression quantitative trait locus (**eQTL**) and other ‘omics’ studies may potentially link functional interactions and help to understand the underlying molecular mechanisms84,85. A BEAM derived Bayesian partition method that uses three latent variables for gene expressions (i.e. tens of thousands traits), SNPs and individuals to model them simultaneously could be a good alternative to regression based methods [ref]. However, integration of statistical and functional interactions is not straightforward86 and may require system biology approaches87. **[Au: this concept would benefit from extra information somewhere, e.g. the differences between statistical and functional epistasis, why there is limited overlap between the two and how systems biology approaches could bridge this gap. This can be brief, but it is important to include. This is also relevant for comprehending your ‘evolution of complex traits’ section, when these issues are mentioned but not explained]**

### Comparing alternative analytical approaches

So far we have briefly discussed only the major methodological developments in the past five years. The methods almost all consider only genotyped SNPs with precise genotypes (i.e. they are unable to handle imputed SNPs with probability-attached genotypes at the genome-wide level) and thus are unable to support meta-analysis of multiple GWAS data based on imputation, which is a key future challenge to increase the power of detection of epistasis. Another challenge is to incorporate the sex chromosome currently ignored in epistasis studies[ref]. Obviously, it is very difficult to recommend the ‘best’ applications without careful comparisons because of huge variation among them, including interaction definitions and null distributions53. Several attempts have been made to evaluate different methods55,56,88–92, suggesting community-wide efforts93 may be essential to fulfill the task. Furthermore, consensus significance thresholds for either genome-wide or focused searches and standards for replication and reporting have become fundamentally important to improve the overall quality of future epistasis studies including result sharing. As a general guidance, we reiterate the recommendation of the two step solution for a genome-wide search for epistasis, i.e. using approximate but fast interaction tests for initial screening and the full regression models to test for significance in either a disease or quantitative trait.

## Overview of empirical evidence for epistasis

The literature is replete with reports of epistasis influencing human traits, but often the evidence supporting such claims is difficult to evaluate. Different methods and experimental designs have been used, ranging from filtering approaches such as hypothesis-driven candidate gene testing, to hypothesis-free exhaustive searches. And indeed epistasis has been reported for a wide spectrum of complex traits and diseases. Here we provide a summary of some of these findings.

### Hypothesis-free studies

The Wellcome Trust Case–Control Consortium (WTCCC) data has been fruitful for identifying marginal additive effects of modest size, and indeed exhaustive two-locus searches have also been applied. Wan *et al*.19 performed a genome-wide search for pairwise interactions in each of the seven traits studied, and reported thousands of significant interactions in total. The vast majority of statistical interactions were between SNPs within the MHC region affecting type 1 diabetes or rheumatoid arthritis, which may be attributable to haplotype effects, where interactions in close proximity to one another are simply tagging a single haplotype which harbors a single causal variant. It was also observed that many interactions had a specific pattern of epistasis known as multiplicative effects, where the interacting loci had marginal additive effects that were larger than expected in combination with one another. Often such an interaction can be removed simply by transforming the scale on which the trait is measured, often referred to as a scale effect. However, some of the multiplicative interactions were between SNPs that have not previously been identified by GWASs, and this lends empirical support to the idea that searching for epistasis may confer increased statistical power to detect marginal effects. Such a situation can arise if two variants have additive effects that are too small to be captured by a standard GWAS, but they have a large interaction term which can be captured when searching for interactions. Using a larger cohort of control samples, a reduced statistical model that searched for only additive x additive interactions, and more stringent controls for population stratification, Lippert *et al*.94 also performed exhaustive scans for epistasis in the seven diseases in WTCCC. Their results largely echoed those presented in Wan *et al*., reporting very many effects in the MHC for autoimmune traits. But again there was no attempt at replication to verify these statistical claims, nor to explore the possibility of haplotype effects.

Prabhu and Pe’er used their computationally efficient software, SIXPAC, to search for epistasis influencing bipolar disorder, and identified a pair of interacting SNPs that had not previously been shown to have an effect from GWASs. They attempted to replicate these results in an independent cohort and although the interacting regions showed some evidence for replication, the actual discovery SNPs did not.

In an attempt to maximize detection power, one method is to choose traits for which genetic effects are expected to be large, such as is the case in gene expression95. Using the Brisbane Systems Genetics Study96 (BSGS) data of 846 individuals with gene expression levels measured in whole blood, 501 instances of epistatic effects could be detected using an exhaustive pairwise search method, of which 30 could be significantly replicated in two independent samples97. An important conclusion from the study was that even after correcting for power discrepancy, substantially more phenotypic variance was attributable to additive effects than to non-additive effects

The trend that emerges is that there are hints of epistasis being uncovered through exhaustive searches for epistasis underlying complex traits, but as of yet there is rather little evidence that this approach detects epistatic interactions that are easily interpreted and statistically replicated in comparison to additive effects. Though the absence of evidence is not necessarily evidence for its absence, it is reasonable to conclude at this stage that there do not exist large non-additive effects influencing complex traits that had thus far eluded the detection.

### Hypothesis-driven studies

An alternative approach to performing exhaustive searches is to overcome the problem of having a very stringent threshold by restricting the search to a few candidate loci. Candidate loci are typically chosen because either they are suspected to have a biological role in the trait of interest, or because they have statistical evidence for additive effects from previous GWASs. Arising from these strategies are some examples of epistasis with strong statistical support, many examples with weak statistical support, and a few reports that declare no evidence for epistasis.

Reports for putative interactions in studies driven by biological hypotheses are rife. The sheer volume of reports of epistasis is exemplified by an important study by Combarros *et al*.98, where they collated data from over 100 publications that reported epistasis of some form influencing the risk of Alzheimer’s disease (and related traits such as its age of onset). These reports comprised multiple experimental designs, sample sizes, and statistical methods, but they demonstrate that, using a standardized statistical test, 27 of the putative pairs of SNPs had interaction terms at the nominal significance level of *P* < 0.05 (mostly involving the pathogenic ε4 allele of apolipoprotein E (*APOE4*). Although, ostensibly, this is more than what is expected by chance, Combarros *et al*. pointed out that there are many limitations to how these studies were conducted; notably, most of the studies did not adjust for relevant covariates or potential confounding from population stratification, nor did they show evidence of replication.

Owing to the variability in design and reproducibility of epistasis studies, the Epistasis Project was created to provide a regularised framework for replication of claims of epistasis in a large, well-controlled study. To date, a few reports of epistasis from candidate gene studies have been discovered99–101 or shown to replicate102 in the Epistasis Project cohort, but perhaps the main conclusion from this work is that epistasis must be cautiously reported and interpreted because in the absence of solid replication the majority of identified epistatic interactions might be false positives.

Beyond the Epistasis Project other statistically robust examples of epistasis have also been shown. For example, Rhinn *et al.*103 designed a study to identify differential gene expression caused by *APOE4* and independent of *APOE4* in conferring a risk for late-onset Alzheimer’s disease. In doing so, they demonstrated two genetic interactions where SNPs regulating *FYN* and *RNF219* each decreased the risk of Alzheimer’s disease in *APOE4* non-carriers, but not in *APOE4* carriers. This finding was also statistically replicated in independent samples. The successful strategy of restricting the search to genetic effects that control **endophenotypes** resonates with the outcomes from many of the hypothesis-free studies, supporting the notion that examples of functional epistasis exhibit relatively little non-additive variance, thus making them hard to identify in highly polygenic complex traits.

Multiple sclerosis (MS) is another complex trait in which epistasis has been demonstrated to have an impact. Because the *HLA-DR2* haplotype in the MHC region showed complete LD over a long distance in multiple ethnic populations it was hypothesised that selection was maintaining the co-segregation of two alleles due to epistasis. *In vivo* studies in humanised mice confirmed that separation of the two alleles led to an MS-like phenotype104, and subsequent analysis in human populations showed increased incidence of MS amongst individuals exhibiting recombination between the interacting loci105; both studies thus provide support for a role for this allelic pair in protecting from MS.

An alternative strategy for narrowing the search to overcome large significance thresholds is to only test for epistasis amongst SNPs that have known marginal effects. Though not routine, many GWASs report that they performed follow-up analysis of epistasis amongst their hits, but although the number of positive findings remains very low, some successes have been reported. Strange *et al*.26 looked for epistasis amongst significant marginal effects from a GWAS for psoriasis, and demonstrated that the risk alleles at the *HLA-C* and *ERAP1* loci only conferred effects if they were both present. A similar pattern of epistasis was uncovered using the same strategy by Evans *et al*.25 in a GWAS for ankylosing spondylitis, this time between *ERAP1* and a large additive effect at *HLA-B27*. In both cases, the same patterns replicated in independent samples, and these are perhaps the first statistically robust examples of epistasis influencing human complex traits.

One pitfall of these examples of epistasis is that they are evident on the **observed scale** of the disease trait, but because the interaction is between SNPs with large effects, it could be the case that on the **liability scale** of disease the contribution to risk is purely additive. For example, suppose that a disease manifests only once a certain threshold of deleterious effects are present. Even if each causal variant contributes an additive risk, an individual homozygous for risk alleles at two loci with large effects might reach that threshold, whereas individuals with any other combination of alleles at these two loci will not, giving the appearance of epistasis. This is indeed a philosophical quandary when dealing with **binary phenotypes**, because on the observed scale one is implicitly using an epistatic threshold model, in the sense that the contribution of a genetic effect to an individual’s disease risk depends on the sum of risk alleles elsewhere in the genome.106 Theory demonstrates that this effect is more likely to be observed when disease prevalence in the population is low, as is the case for most complex diseases.

It should be noted that though epistatic signals have been uncovered when candidate loci are selected based on marginal effects, this strategy often isn’t successful. For example Lucas *et al*.107 restricted the search for epistatic effects influencing risk of myocardial infarction by hypothesizing that either SNPs that had weak marginal effects or SNPs that had known marginal effects for a number of related. Though the sample size was reasonably large and the search space was drastically reduced, no statistically significant epistatic signals were uncovered. Similar conclusions have been drawn for other complex traits, including type 2 diabetes108, body mass index (BMI)109 and serum uric acid levels110.

Although we have only focused on a few examples here, the picture that is emerging is that compelling statistical support is absent for the vast majority of reported epistatic interactions. Potentially through some level of ascertainment bias, those epistatic effects that appear to be statistically robust predominantly have large marginal effects, and contribute relatively little in terms of phenotypic variance from interaction terms alone. Given the current empirical evidence, one can hypothesise that the number of instances of epistasis may indeed be large, but that the contribution of gene interactions to the variance of complex traits is rather small.

## Conclusions

Though plenty remains to be done, a massive body of scientific discovery has been achieved through the additive genetic paradigm,111 in spite of its simplicity and seeming disconnection from realistic biological models. Although we can present a clear view on how to continue the progress in detecting epistasis in complex traits (through increased sample sizes, increased SNP density and rigorous standards of reporting (BOX 2)), it remains unclear to what extent epistasis will offer a solution to the major questions being posed about the genetics of human complex traits at this stage.

Nevertheless, the search for epistasis is fast becoming a relatively effortless one. Sophisticated computational techniques have made the analysis fast, interpretable, and potentially routine at the individual GWAS level. The next challenge is to greatly improve power of detection via meta-analyses of multiple GWASs that are readily available. Therefore we believe that given this low cost to high potential benefit scenario the search for epistasis is indeed warranted.

## Box 1: Why is epistasis theoretically difficult to detect?

Supposing that the component of trait variance caused by non-additive genetic effects is comprised of numerous small effects (as is the case for the additive genetic component) the statistical power to detect them is, in principle, much lower than that of detecting additive effects for a number of reasons, as described below. Note that these challenges to the detection of epistasis apply particularly to humans and other outbred species; it is possible that these challenges can be greatly reduced or even eliminated altogether in studies of model organisms112.

##### Linkage disequilibrium

The variance explained by a SNP detected in a GWAS is unlikely to be equal to the variance explained by the true causal variant that is being tagged by the marker. The additive variance at the observed marker will decrease linearly with decreasing LD r2 between itself and the causal variant, where r is the strength of correlation between the causal variant and observed SNP. Thus if effect sizes are small then GWAS is dependent upon there being high LD between causal variants and observed SNPs. However, the **dominance variance** at the observed SNP reduces by a factor of r4, thus the dependence on high LD between observed SNPs and unobserved causal variants is much higher when detecting dominance effects. Extending this to two loci to consider epistasis, the additive by additive (AxA) variance on average reduces by r4 across both loci, the additive by dominance (AxD) variance by r6, and the dominance by dominance (DxD) variance by r8. The consequence of these constraints is that any given SNP-genotyping microarray has substantially greater coverage of the genome when searching for additive effects than when searching for epistatic effects and indeed dominance. To overcome this problem one needs denser genotyping or high-quality imputed genotypes or sequence data to identify non-additive effects at the same power as additive effects.

##### Curse of dimensionality

The search for additive effects is performed in a single dimensional search space, that is, our search is constrained to the number of markers in the experiment. In principle, searching for epistasis involves expanding from one dimension to two or more dimensions, thus the parameter space increases exponentially. This problem, where any signal becomes drowned out by the noise, is known as the "curse of dimensionality". There are several strategies that one can use to scan the genome for epistatic effects as discussed in the main text, but they typically involve expansion of the search space and a higher multiple testing penalty than is required for detecting non-epistatic effects. Therefore, in order to obtain the same power of detection as searching for additive effects, the sample size must increase and/or the variance explained by epistatic effects must be larger.

##### Model complexity

Modelling the additive effect of a SNP on a phenotype is achieved through a model that uses only one degree of freedom. However, for two loci there are four interaction terms (AxA, AxD, DxA, DxD), thus under the hypothesis that each of the four epistatic effects is equal in magnitude28,29,113 the model complexity for the statistical test increases. Comparing the power of detection between genetic loci of equal variance that comprise either additive effects or epistatic effects, the increased number of degrees of freedom used by the epistatic test will lead to a less extreme *P* value despite capturing the same amount of variance as in the scenario for the additive test. The simple way to overcome this problem is to increase the sample size.

##### Replication

Replication is key to confirming the statistical veracity of associations. Relative to testing for additive effects,the increased dependence of epistasis on high LD between observed SNPs and causal variants means that there is likely to be an ascertainment bias in a discovery sample for markers in higher LD in the sample than they are in the population, simply due to sampling. Thus, taking an independent sample from the population one resamples the LD, and it is unlikely that the same ascertainment for high LD will occur. In this context we expect the replication rate of epistasis to be substantially lower than for additive effects. Performing detection and replication on very dense SNP-genotyping microarrays, imputed genotypes, or sequence data will overcome this problem.

## Box 2: What constitutes a significant epistatic interaction?

Evidently, detection of epistasis is extremely challenging. But with sample sizes increasing rapidly, and the growing availability of high-density SNP-genotyping microarrays and sequencing, we are entering an era in which detection of epistasis is now feasible. Here we provide some guidance for the robust identification of epistatic interactions that can be trusted by the scientific community.

##### Replication is necessary

As with additive genetic effects, following the discovery of epistatic genetic effects, the gold standard for reporting them is to show that the same SNPs replicate with the same direction of effect on the phenotype in an independent sample.

##### Sufficiently stringent significance thresholds

If independent samples are not available for replication, stringent significance thresholds are of utmost importance. Based on there being effectively around 1 million independent loci in the genome, GWASs have adopted a standard significance threshold of p = 5x10-8. With the emergence of rapid computational methods for performing exhaustive pairwise scans, we suggest a significance threshold of p = 0.05 / 0.5(1x106)2 = 1x10-13.

##### Discount the possibility of scale effects

Ideally quantitative analysis should be performed on phenotypes that are normalized through rank transformation, and it should be demonstrated that any detected non-additive effects persist following transformation to a biologically relevant scale.114 For binary phenotypes the analysis of epistasis is most convincing when shown to be present on the liability scale of risk.

##### Discount the likelihood of haplotype effects

In a typical pairwise scan inflation of test statistics for interaction terms between neighbouring SNPs on the same chromosome can arise due to haplotype effects, and this is often inseparable from epistatic effects.21 Ideally the two tested SNPs should neither be in LD with each other nor should both be in LD with some other, potentially unobserved, variant. This latter caveat is impractical in the absence of sequence data and we suggest that interacting SNPs should be in LD r2<0.1, and D’<0.1 to reduce the possibility of haplotype effects underlying any signals.

## Box 3: The missing heritability

By definition, epistasis does not have a direct role to play in the problem of the missing heritability. The missing heritability pertains to the problem that there are insufficient additive effects discovered to account for the additive genetic variance estimated to exist for that trait. SNPs that interact can have marginal additive (and dominance) effects, but the nexus to declaring that they interact is that they have an epistatic effect that does not contribute to additive genetic variation. In principle, the total additive genetic variance accounted for by interacting SNPs can be captured by a standard, suitably powered GWAS searching for additive effects.

The metric of missing heritability emerges from two variables: the tally of genetic effects uncovered and the estimate of the trait's h2. In each case epistasis may have a subtle part to play. Firstly, some theoretical studies postulate that if, for some interacting loci, the epistatic variance is large compared to the additive variance, searching for epistatic effects might be one way to uncover loci with additive variance with more power than searching for the additive effects directly.115 Such instances might arise if the trait has a large **mutational target size** and is under direct selection.113 This scenario does not posit that epistatic variance contributes to additive variance, rather, searching for epistasis may lead to the identification of variants either rare or with small additive effects that would otherwise go undetected in a standard GWAS. Some empirical evidence exists to support this hypothesis,19,21 however it is unlikely to be a widespread phenomenon116 and theory shows that even in complex multi-locus epistatic patterns marginal additive effects are necessary to produce measurable additive variance for a trait.117

Secondly, because the direct estimation of non-additive genetic variation is almost always intractable, its contribution to the resemblance between relatives is unknown.1 Thus, it is possible that under certain experimental designs heritability estimates are inflated through contamination from non-additive variation.118 To what extent is this realistically a problem and how reliably can it be measured? A recent theoretical study gained much attention after demonstrating that redundancy amongst biological pathways could create an illusion of additive genetic variance in twin studies23 (provided that large common environmental effects were present119). Indeed it is a known issue in such study designs that, although it is not the most parsimonious model, a combination of non-additive variation and common environmental variation can lead to a significant additive parameter.120

To overcome this problem one can attempt to use family-based studies to estimate additive effects directly, and one can use contrasts between different types of relatives. For example, full siblings will share 0.5 additive variance and 0.25 dominance variance, while parent-offspring will share 0.5 additive and 0 dominance variance. If the correlation between degree of shared additive variation and phenotypic similarity is high across all types of relatives then this would be strong evidence for heritability estimates being uncontaminated by non-additive variance. Height shows consistent estimates of heritability between twin studies and family studies,121 but h2 estimates for BMI are much higher from twin studies than from family studies,122 suggesting that height is probably mostly influenced by additive effects but there is the potential for non-additive effects to play an important role in BMI.

## Box 4: Genetic prediction

A potential direct translation of large-scale genetic studies into medical practice is to use knowledge of an individual’s genetic profile to predict phenotypic outcomes.123 There are two main limiting factors in the accuracy of predicting phenotypes through genetic profiles. First, the maximum prediction accuracy is limited by the trait heritability.124 And second, the accuracy in which the genetic profile predicts the phenotype is dependent on the accurate estimation of the underlying genetic effects.125 In this context, is the inclusion of epistatic effects into genetic scores important for improving genetic prediction in complex traits?

With estimates of narrow-sense heritability obtainable for complex traits, one can estimate the maximum prediction accuracy under the assumption of perfect knowledge of all additive genetic effects. Conversely, our inability to estimate broad-sense heritability therefore makes it difficult to quantify the potential improvements that the inclusion of non-additive effects might incur. For highly heritable traits it is unlikely that non-additive genetic variance will form a large component of phenotypic variance, and therefore the inclusion of epistatic effects in genetic profile scores will not improve prediction accuracy. However one might speculate that non-additive variance could have a significant influence on the phenotypic outcome of more lowly heritable traits, and this may include endophenotypes such as methylation126,127 or gene expression levels.96

Another limiting factor in the inclusion of epistatic effects for genetic prediction is that, even assuming a significant non-additive genetic component, it is demonstrably hard to obtain reliable estimates of epistatic genetic effects. Nevertheless, it is not necessary to construct genetic predictors from significant effects as estimated through GWA studies alone. Using a relaxed threshold for the inclusion of additive effects into a genetic predictor has been shown to improve prediction accuracy for schizophrenia,128 demonstrating that an underlying polygenic architecture will comprise numerous small effects that fail reach a stringent significance threshold. Daetwyler *et al*.125 showed that in addition to heritability, the prediction accuracy is also a function of the ratio of the number of effects influencing the trait (often modeled as the number of independent markers in the genome) and the sample size.125,129 Therefore, for most complex traits that are polygenic in nature it is necessary to use extremely large sample sizes.130 In principle one could use this approach to also include epistatic effects, but because the effective number of independent pairwise genomic regions is dramatically higher131 than independent regions, a corresponding increase in sample size may be required to obtain gains in prediction accuracy equivalent to an additive model.

There has been use of epistatic effects for the prediction of complex traits in many model organism species. It was shown that including a network of epistatic effects in chicken lines132 for prediction in independent samples133 marginally improved prediction over the use of additive effects only. A number of reports have shown similar conclusions for several traits in plants also134–136, whereas others demonstrate that inclusion of epistatic effects yields no improvement in prediction accuracy,137 or that additive effects alone are sufficient to explain most genetic variation.138

## Figure 1

## Types of methods to detect epistasis in GWAS. Outline of different types of methods in two major groups based on SNPs and groups of SNPs respectively.

**[Au: regression connectivity corrupted?]**

Regression

LD

Frequentist

Genome-wide

Haplotype

Partition

Hybrid

Bayesian

Knowledge

Filtering

Statistics

SNP-based

Algorithm

Machine learning

Artificial Intelligence

Gene

Data mining

Module

Group-based

**Table 1**

A partial list of publicly available applications for genome-wide analysis of epistasis in GWAS\*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name** | **Type** | **Trait** | **Main feature** | **URL** |
| PLINK | Regression | both | PLINK epistasis module has been a benchmark application for new tool developments | http://pngu.mgh.harvard.edu/~purcell/plink/epi.shtml |
| FastEpistasis | Regression | both | An efficient parallel extension to the PLINK epistasis module | <http://www.vital-it.ch/software/FastEpistasis/> |
| BOOST | Regression | dis | Bitwise implementation, approximate tests for screening and logistic regression for testing | <http://bioinformatics.ust.hk/BOOST.html> |
| epiGPU | Regression | qt | GPU-enhanced contingency table based approximate tests | <http://sourceforge.net/projects/epigpu/> |
| PIAM | Regression | dis | Multithread parallel enhanced, contingency table based approximatetests | <http://www.ihs.ac.cn/xykong/PIAM.zip> |
| eCEO | Regression | dis | Bitwise implementation and cloud computing enhanced Chi square tests | http://www.comp.nus.edu.sg/~wangzk/eCEO.html |
| SNP-SNP interactions | Regression | dis | Logic regression based epitasis test at the gene level, based on concepts of SNP intersection and union | http://www.ualberta.ca/~yyasui/homepage.html |
| BiForce | Regression | both | Bitwise and multithread implementation and approximate tests | <http://bioinfo.utu.fi/biforcetoolbox> |
| EPIBLASTER | LD | dis | GPU-enhanced, LD-based screening and logistic regression for testing | <http://www.mpipsykl.mpg.de/en/epiblaster/index.html> |
| SIXPAC | LD | dis | Bitwise implementation of Probably Approximately Complete search algorithm and LD-based test | <http://www.cs.columbia.edu/~snehitp/sixpac/> |
| iLOCi | LD | dis | Parallel implementation of LD-based score test | http://www4a.biotec.or.th/GI/tools/iloci |
| SHEsisEpi | Haplotype | dis | GPU and multithread enhanced odds ratio tests | http://analysis2.bio-x.cn/SHEsisMain.htm |
| GenomeMatrix | Haplotype |  | Haplotype-based odds ratio test for interactions | <https://sph.uth.edu/hgc/faculty/xiong/software-B.html> |
| IndOR | Haplotype | dis | Independence-based odds ratio tests using a biological definition of epistasis | http://www.sites.univ-rennes2.fr/laboratoire-statistique/EMILY/IndOR/ |
| HAPAL | Haplotype | dis | Mapping haplotype-haplotype interactions with adaptive LASSO | http://www.stt.msu.edu/~cui/software.html |
| BEAM series | Bayesian | both | Bayesian partition model considering LD | <http://sites.stat.psu.edu/~yuzhang/> |
| BhGLM | Bayesian | both | Bayesian hierarchical Generalized Linear Model for haplotype interactions | <http://www.ssg.uab.edu/bhglm/> |
| SNPTEST | Bayesian | dis | Bayesian model averaging approach to model interactions involving known risk loci | http://www.stats.ox.ac.uk/∼marchini/software/gwas/gwas.html |
| MDR series | Data mining | dis or both | The MDR framework combines attribute selection and classification with cross-validation for modelling interactions, with a number of derived methods including pMDR, MdrPDT, FAM-MDR, MB-MDR (R package). | <http://www.multifactordimensionalityreduction.org/>  http://ritchielab.psu.edu/ritchielab/software/mdr-downloads/  http://www.statgen.ulg.ac.be/software/FAM-MDR/FAM-MDR.zip |
| SNPHarvester | Filtering | dis | Stochastic search for significant SNP groups then test interactions using logistic regression | http://bioinformatics.ust.hk/SNPHarvester.html |
| EDCF | Filtering | dis | Clustering frequent genotype combinations for testing interactions | http://www.cs.ucr.edu/∼minzhux/EDCF.zip |
| Relief series | Filtering | dis | Using an ensemble of tuned ReliefF filters to select SNPs for interaction tests | https://code.google.com/p/ensemble-of-filters/ |
| SNPruler | Machine learning | dis | Using predictive rule to infer disease-associated epistatic interactions | http://bioinformatics.ust.hk/SNPRuler.zip |
| Random Jungle | Machine learning | dis | A computational and memory efficient implementation of random forest with added features to improve classification | http://imbs-luebeck.de/imbs/de/node/227 |
| SNPInterForest | Machine learning | dis | An improved random forest framework able to identify interactions between SNPs without marginal effects | https://gwas.biosciencedbc.jp/SNPInterForest/index.html |
| RAPID | Data mining | dis | Identify correlated SNP pairs after projecting their correlations to distance between two points in a Euclidean space | <http://bix.ucsd.edu/projects/rapid> |
| TEAM | Data mining | both | Using Minimum Spanning Tree incrementally updates the contingency tables for epistatic tests without scanning all individuals | <http://www.csbio.unc.edu/epistasis/> |

\*: dis: disease trait; qt: quantitative trait; both: applicable to either disease or quantitative traits

**[Additional ideas for display items (we can accommodate a maximum of 7)**

**- A figure to more schematically illustrate the logic of the different types of epistasis detection method? E.g. this could be made of a few panels, one for each major method shown. Each panel could start with some schematic chromosomal loci with SNPs marked, and then diagrammatically show how the loci are analysed. For example, regression methods would exhaustively compare all SNP pairs) perhaps shown by a dense web of connecting lines. Filtering methods would only carry forwards a subset of SNPs for comparisons, and group-based methods could colour sets of SNPs in different colours for set-set comparison. For the LD/haplotype/Bayesian/AI methods, I’m not clear of the details, so these would be especially enlightening to schematically illustrate.**

**- A summary table of the results/evidence discussed in the in the “Overview of empirical evidence”… section?]**

## Glossary

**Complex trait**: A trait where variation between individuals is controlled by several or many genes and different environmental effects, potentially with interactions between these different effects.

Dominance variance:

**Genetic architecture**: The complete description of the genetic factors influencing trait variation, such as number of genetic loci, their effects, allele frequencies actions and interactions.

**Epistasis:** Statistical interactions between loci in their impact on a trait such that the impact of a particular single locus genotype depends on the genotype at other loci.

**Mutational target size:** Fraction of the genome in which new mutations potentially cause variation for a trait. For most complex traits this is large suggesting many loci can potentially influence trait variation.

**Mendelian disease**: Where the disease state is completely or largely determined by variation at a single gen locus inherited in a Mendelian fashion.

**Heritability**: The proportion of the trait variation for a particular trait in a particular population and environment that is under genetic control. The **narrow-sense heritability (h2)** refers to the proportion of variation due to the additive effects of genes whereas the **broad-sense heritability (H2)** is the proportion due to all genetic effects.

**Bonferroni correction:** The simplest and perhaps most conservative method to control family error rate (*α*) by correcting for the number (*n*) of independent hypothesis tests when *n* is large, i.e. the corrected threshold *Pcorrected* = *α*/*n.*

**Hypothesis free analysis:** No assumption is made about the loci involved in epistasis or their effects and so all possible pairs of SNPs are tested (an **exhaustive search**). **Hypothesis driven analysis** limits the combinations of loci tested according to some prior hypothesis (for example that only loci with a marginal effect should be tested or only those loci in a particular pathway).

**Quantitative traits:** Phenotypes (e.g. height) vary continuously, in contrast to qualitative traits in which phenotypes are discrete (e.g. disease or healthy).

**Saturated and reduced models:** There are nine joint genotypes for a pair of SNPs each with three genotypes (e.g. AA, Aa and aa). These can be modelled in full using nine parameters: one as the baseline (e.g. aa/aa), two for each SNP (e.g. AA/aa and Aa/aa) and four for interactions (e.g. AA/Aa, AA/AA, Aa/Aa, Aa/AA). The saturated model fits all the nine parameters, whereas the reduced model fits the first five parameters and excludes the four interaction parameters.

**Hardy–Weinberg Equilibrium**: A principle stating that allele and genotype frequencies of variants in a population will remain constant from one generation to the next in the absence of evolutionary disturbing factors such as mutation and genetic drift.

**Marginal effect:** The average effect of a locus across all other loci and environmental effects (also known as main effect).

**Linkage disequilibrium (LD)**: The nonrandom association of alleles of two or more loci in a population owing to limited recombination. LD is often used to measure the relationship of genetic markers of the loci – a high LD means the markers are closely related (i.e. co-occurring) so one marker can predict the other(s). Markers in high LD with an unobserved causal variant can increase the power of detection of associations. Several methods can be used to calculate LD, of which correlation is the simplest and robust approach.

**Causal variant:** A genetic variant directly modifies a phenotype and/or causes a change of disease risk. Owing to the limited amount of variation interrogated by SNP genotyping microarrays, SNPs in GWASs typically merely tag the causal region rather than themselves being the causal variant.

**Haplotype:** A combination of alleles (DNA sequences) inherited from a single parent. A haplotype can be within one locus or across multiple loci, with or without physical coupling on the DNA strand.

**Linkage phase:** The information of combinations DNA alleles in a diploid individual inherited from the mother or father (also known as gametic phase).

**Covariate:** A variable that may confound the outcome variable of a statistical model, e.g. age is a covariate of human height.

**Bayes’ Theorem:** A probability theory by the Reverend Thomas Bayes to calculate conditional probabilities based on prior distributions of parameters in a model and the observed experimental data.

**Variance heterogeneity:** Variance of a quantitative trait may differ between the three possible genotypes of a biallelic SNP in the presence of genetic interactions, which can therefore be used to screen for potential interacting SNPs.

**Large P small N problem:** A statistical challenge to estimate a large number of parameters based on a small number of samples.

**Multifactor Dimensionality Reduction:** A data mining algorithm that can reduce a high-dimensional multi-locus model of multifactorial classes (i.e. SNP genotype combinations) into a one-dimensional model of one variable of either high risk (potential interacting) or low risk classes based on the ratio of cases and controls in each class. The algorithm uses cross-validation iteratively to define the best classification.

**Tree-based methods:** Model-free or non-parametric machine learning approaches for conducting regression and classification analyses by recursive partitioning variables into tree structures. Popular applications in epistasis studies include random forest, random jungle, classification and regression trees.

**Entropy-based methods:** Entropy is a key measure of uncertainty associated with a random variable in information theory. Entropy-based methods examine the information/entropy difference between different models with and without interactions to detect epistasis.

**Imputation:** Statistical inference of unobserved SNP genotypes based on a reference panel of known haplotypes in a population (e.g. human 1000 Genomes Project). Imputation can greatly narrow down the distance between SNPs and causal variants and thus increase the power of detection of associations.

**Pleiotropic epistasis:** Statistical interaction signals shared in multiple traits.

**Endophenotype:** A heritable trait genetically correlated with a disease trait. Often a trait that be measured in all individuals whether diseased or not and which potentially provides a predictor of disease status.

**Polygenic architecture:** A trait genetic architecture under which many genes of small effect contribute to trait variation.

**Binary phenotype**: Disease traits often have two major states, diseased or healthy. They may nonetheless be complex traits where transition to the disease state is influenced by an underlying **liability** to disease that is controlled by many genetic loci and environmental effects.

**eQTL:** An expression quantitative trait locus controls variation in expression of a particular gene. An eQTL may lie adjacent to the gene being controlled (*cis* acting control) or some distance away (*trans* acting).

The Wellcome Trust Case–Control Consortium **[Au: please briefly mention the diseases being studied and an overview of the approach(es) involved]**

**observed scale**

**liability scale**

rank transformation

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