



Published in final edited form as:

*Genet Epidemiol.* 2009 September ; 33(6): 479–487. doi:10.1002/gepi.20400.

## Replication of genetic associations as pseudoreplication due to shared genealogy

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### Abstract

The genotypes of individuals in replicate genetic association studies have some level of correlation due to shared descent in the complete pedigree of all living humans. As a result of this genealogical sharing, replicate studies that search for genotype-phenotype associations using linkage disequilibrium between marker loci and disease-susceptibility loci can be considered “pseudoreplicates” rather than true replicates. We examine the size of the pseudoreplication effect in association studies simulated from evolutionary models of the history of a population, evaluating the excess probability that both of a pair of studies detect a disease association compared to the probability expected under the assumption that the two studies are independent. Each of nine combinations of a demographic model and a penetrance model leads to a detectable pseudoreplication effect, suggesting that the degree of support that can be attributed to a replicated genetic association result is less than that which can be attributed to a replicated result in a context of true independence.

### INTRODUCTION

Genetic case-control association studies seek to identify statistical associations between genotype and disease status in samples of unrelated individuals with and without a disease phenotype. Recently, the case-control association design has become common as an approach to the search for susceptibility loci that underlie complex genetic diseases.

As case-control genetic association studies proliferate, it is important to understand the factors that affect the replicability of association results. General acceptance of the importance of an observed association typically requires that the association be detected in additional datasets beyond the one that provided the initial finding. However, many associations identified in one study are not identified in subsequent studies (Ioannidis *et al.*, 2001; Hirschhorn *et al.*, 2002; Lohmueller *et al.*, 2003). While false positives in the initial studies likely contribute to a large fraction of nonreplications, it is also likely that some nonreplications represent true susceptibility loci that replication studies fail to detect (Gorroochurn *et al.*, 2007; Ioannidis, 2007; Zöllner & Pritchard, 2007; McCarthy *et al.*, 2008; Moonesinghe *et al.*, 2008).

The typical difficulties involved in interpreting the replication or nonreplication of any type of statistical finding are compounded in the genetic case-control context by the indirect nature of many genetic association studies. Rather than searching directly for true causal

loci, indirect association studies seek to identify markers whose genotypes are correlated both with genotypes at (unknown) causal loci and with disease status (Kruglyak, 1999; Pritchard & Przeworski, 2001; Neale & Sham, 2004; Zondervan & Cardon, 2004; Hirschhorn & Daly, 2005). These studies derive their utility from the fact that due to shared descent from a common ancestor, disease-affected individuals will often possess both a disease mutation and neighboring marker alleles that were present in the ancestor in whom the disease mutation originally occurred. Thus, identification of a marker associated with disease status can indicate the likely presence on the genome of a nearby causal susceptibility locus.

Indirect associations between a marker and a disease influenced by a nearby susceptibility locus exist as the outcome of a complex stochastic process of mutations, recombinations, and divergences of genealogical lineages that have occurred since the time of the first individual who carried the causal variant (Ardlie *et al.*, 2002; Nordborg & Tavaré, 2002; Balding, 2006; Slatkin, 2008). Disease associations in a population are therefore influenced by the properties of the genetic history of the population since the time of the disease mutation. We argue that this history can also affect the relationship between the outcomes of multiple association studies performed in the population.

Consider a hypothetical scenario illustrating the effect of history on the correlation of outcomes of replicate studies in a single population. Suppose two similar association studies are performed in the population. The samples in the two studies will likely have some degree of shared genealogy, as many individuals from the history of the population are likely to appear in the ancestries of members of both samples. Suppose further that a true causal mutation has given rise to increased disease risk in the population. As a result, certain mutations, recombinations, and divergences of genealogical lineages will occur in the ancestries of many of the individuals who carry both the disease and the causal mutation. Consequently, some of the same events that have led in one sample to the production of an indirect association between a marker and the disease will also have led to an indirect association in a second sample from the population. An example of this correlation in outcomes due to shared genealogy is shown in Figure 1.

We can compare the genetic association context to the scenario of a coin toss. Suppose an unfair coin has probability  $p \neq 0.5$  of landing “heads.” We perform two separate experiments, in each of which we flip the coin  $k$  times and test the null hypothesis that the coin has a fair probability of 0.5. Because the two experiments are independent, the probability that both experiments will reject the null hypothesis is the square of the probability that the first of the studies will reject the null hypothesis. In the case-control setting, however, because of shared ancestry of the individuals in two studies, the outcomes of the studies are not strictly independent, and the probability that both studies will produce a given outcome is greater than the square of the probability that the first study will produce the outcome. Due to the dependence of multiple studies on the same past events, a replication study in a genetic association context can be more accurately described as a form of *pseudoreplication* study. This term is borrowed from the context of ecological field experiments, in which one of its uses is for describing situations where treatment units within an experiment are not truly independent but are viewed as such during statistical analysis (Hurlbert, 1984; Heffner *et al.* 1996).

The issue of genetic pseudoreplication — the correlation of replicate association studies due to shared genealogies — is important because if correlation among studies is considerable, then it might be inappropriate to regard a replicated genetic association result as having the same level of support as that attributed to a replication in a setting with true independence. Although statistical properties of replication in genetic association studies have frequently

been investigated (Clarke *et al.*, 2007; Gorroochurn *et al.*, 2007; Sullivan, 2007; Zöllner & Pritchard, 2007; Moonesinghe *et al.*, 2008), it has typically been assumed that separate studies have independent outcomes, and the issue of pseudoreplication has not been included in discussions about replication (Vieland, 2001; Hirschhorn & Altshuler, 2002; Hirschhorn *et al.*, 2002; Colhoun *et al.*, 2003; Redden & Allison, 2003; Ott, 2004; Ioannidis, 2007; NCI-NHGRI Working Group on Replication in Association Studies, 2007; McCarthy *et al.*, 2008). Note that the phenomenon that we term “pseudoreplication” is distinct from the phenomenon termed by Gorroochurn *et al.* (2007) “pseudo-failures to replicate.” Whereas Gorroochurn *et al.* (2007) studied replication failures that occurred due to underpowered replication studies, our concern is with the way in which replication of an association result is influenced by the shared descent of the individuals in replicate samples. Our interest is in the relationship between the outcomes of separate studies of the same marker in different sets of individuals, rather than on forms of replication that involve joint analysis of data pooled across studies (Skol *et al.*, 2006).

To quantitatively evaluate the phenomenon of pseudoreplication in simulated genetic association studies, we consider pairs of indirect association studies performed in the same simulated populations. This strategy is similar to that of Ewens *et al.* (2007), who examined the relationship between estimates of the levels of genetic variation observed in two separate samples from the same population. We use a coalescent method to simulate the pair of studies conditional on assumptions about the demographic history of the population; our approach is related to that of Sullivan (2007), who investigated replication using a data-based simulation approach (Wright *et al.*, 2007) rather than using an explicit evolutionary model. Our focus is on pseudoreplication in pairs of studies that both have the same underlying disease effect, and we evaluate the excess probability that both studies detect an indirect association compared to the probability expected under the assumption that the two studies are independent. Although we find that the outcomes of the two studies are often close to independent, we also observe that under the conditions simulated, a pseudoreplication effect does exist, in that replicate studies can have a noticeably higher probability of finding a disease locus than is expected under independence. A consequence of this pseudoreplication effect is that under the conditions simulated, “flip-flop” associations, in which two studies find associations involving opposite variants at the same marker (Lin *et al.*, 2007, 2008; Zaykin & Shibata, 2008), are relatively unlikely to occur at a marker closely linked to a true susceptibility locus.

## METHODS

We simulated pairs of indirect association studies in simulated populations. Each pair of association studies involved two loci — an unknown disease locus and a nearby marker locus tested for association with disease status in both studies. For each pair of simulated studies, we recorded whether both studies, one study, or neither study detected association between the marker and disease status. Our simulation approach was designed to balance the competing issues of providing generally reasonable parameter values, generating enough acceptable simulations quickly, and satisfying the assumption of coalescent methods that relatively few haplotypes are simulated compared to the population size. As the simulations were intended to reflect a scenario of a complex disease with multiple underlying risk factors, high-risk genotypes at the single disease locus simulated were given incomplete penetrance, so that the remaining components of the disease risk due to other variables were not explicitly modeled.

The simulations considered three demographic models of the history of a population. The models were selected as representative among recent coalescent-based approaches to demographic modeling of human population history (Marth *et al.*, 2004; Schaffner *et al.*,

2005; Voight *et al.*, 2005; Plagnol & Wall, 2006; Fagundes *et al.*, 2007). Each model simulates mutation, recombination, and coalescence of genetic lineages backwards in time from the present, conditional on assumptions about the history of the population size. Model 1 involved a constant-sized population of 10,000 diploid individuals, a value with similar magnitude to that reported by studies of various subsets of the human population (Takahata, 1993; Harpending *et al.*, 1998; Yu *et al.*, 2001; Tenesa *et al.*, 2007). Viewed forward in time, Model 2, based on a study of European variation (Marth *et al.*, 2004), involved a population of constant size  $\sim 10,000$  diploid individuals until  $\sim 2000$  generations in the past, at which point an instantaneous jump occurred to size  $1.4 \times 10^5$ ; Model 3, based on African variation (Plagnol & Wall, 2006), involved a constant size of  $\sim 10,000$  diploid individuals until 4280 generations in the past followed by exponential growth to a current size of  $10^6$ .

For each demographic model, we considered three penetrance models for the disease locus — recessive, additive, and dominant. For each of the nine combinations of a demographic model and a penetrance model, we simulated 100,000 pairs of indirect association studies, each with a disease locus and a nearby marker locus that was tested for disease association. To simulate pairs of studies, we first independently selected a recombination rate per base pair  $r$ , a mutation rate per base pair  $\mu$ , a probability of disease  $p_L$  for the low-risk homozygous genotype at the disease locus, a probability of disease  $p_H$  for the high-risk homozygous genotype at the disease locus, and a population disease frequency  $p_D$ . Values for these parameters were selected uniformly within specified ranges:  $[5 \times 10^{-9}, 2.75 \times 10^{-8}]$  for  $r$ ,  $[1 \times 10^{-9}, 2 \times 10^{-8}]$  for  $\mu$ ,  $[0, 0.4]$  for  $p_L$ ,  $[0.4, 1]$  for  $p_H$ , and  $[0.15, 0.4]$  for  $p_D$ .

Given the demographic model, recombination rate, and mutation rate, we used the ms coalescent simulator (Hudson, 2002) to simulate 4000 haplotypes, each of length  $s = 300,001$  base pairs. The ms approach simulates an infinitely-many-sites model in which  $\mu s$  is a mutation rate for a whole sequence and in which recurrent mutations are not allowed at individual sites. For the population mutation and recombination parameters, we used  $\theta = 4N\mu s$  and  $\rho = 4Nr(s - 1)$ , where  $N$  was the present population size for the appropriate model ( $10^4$  for Model 1,  $1.4 \times 10^5$  for Model 2,  $10^6$  for Model 3).

The ms command to generate one simulation of Model 1 was `ms 4000 1 -t  $\theta$  -r  $\rho$  300001`, where  $\theta$  and  $\rho$  were random values based on simulated choices of  $\mu$  and  $r$ . The command for Model 2 was `ms 4000 1 -t  $\theta$  -r  $\rho$  300001 -eN 0.00357 0.07143`; the value 0.00357 represents the time at which the population size changed (in units of  $4N$ ), and 0.07143 represents the ancient population size (in units of  $N$ ). The command for Model 3 was `ms 4000 1 -t  $\theta$  -r  $\rho$  300001 -G 4303.9 -eG 0.00107 0.0`. The value 4303.9 represents the exponential population growth rate (population size at time  $t$  measured in units of  $4N$  generations is given by  $Ne^{-(4303.9)t}$ ), 0.00107 represents the time of onset of growth in units of  $4N$  generations, and 0.0 indicates a constant size in the period prior to growth.

The 4000 simulated haplotypes were paired randomly to obtain 2000 diploid individuals. Scanning from left to right, polymorphic sites were tested as potential disease loci, choosing the derived allele as the high-risk allele. For a given site, treating the site as the disease locus, disease status was simulated for each of the 2000 individuals based on the genotype of the individual and the probabilities  $p_L$  and  $p_H$ , using the penetrance model to determine the probability of disease for heterozygotes ( $p_L$  for the recessive model,  $p_L/2 + p_H/2$  for the additive model, and  $p_H$  for the dominant model). If the fraction of affected individuals was found to lie in the interval  $[p_D - 0.01, p_D + 0.01]$ , then the site was chosen as the disease locus. If no suitable disease locus was found in the simulated 300 kb region, then the simulation was discarded and a new simulation was generated.

Once the disease status was specified for each individual, two disjoint case-control samples, representing two association studies, were selected randomly from the individuals, without replacement. Each sample included 100 cases and 100 controls (each simulation generated enough cases and controls that two disjoint samples could always be selected). All sites with minor allele frequency greater than or equal to 0.05 in the full set of 2000 simulated individuals were then identified as potential marker loci (excluding the disease locus as a possible marker locus). If more than 150 such loci were produced in a single simulation, then 150 of the possible marker loci were selected at random (possibly fewer than 150 for the last simulation, as a target number of pairs of association studies was reached). For each marker locus, contingency tables involving the three possible marker genotypes and case/control status were generated separately in both simulated studies. A  $3 \times 2$   $G$  test statistic for association (Sokal & Rohlf, 1995) was then calculated for each study, and associations significant at the 0.05 level were identified based on the chi-squared distribution with two degrees of freedom (cutoff of 5.991, henceforth denoted  $c$ ). Denoting the entries in the contingency table by  $m_{00}$ ,  $m_{01}$ , and  $m_{11}$  for the numbers of occurrences of the three genotypes in cases (where “1” represents the derived allele at the marker locus and “0” is the ancestral allele) and  $n_{00}$ ,  $n_{01}$ , and  $n_{11}$  for the corresponding values in controls, we identified marker allele 0 as disease-associated if we observed  $n_{00} + n_{01} < m_{00} + m_{01}$  and  $n_{01} + n_{11} > m_{01} + m_{11}$ , marker allele 1 as disease-associated if  $n_{00} + n_{01} > m_{00} + m_{01}$  and  $n_{01} + n_{11} < m_{01} + m_{11}$ , and neither allele as disease-associated otherwise. We recorded the parameters for the simulated scenario, the allele more strongly associated with disease in each of the two studies, and the  $G$  statistics for the two studies ( $G_1$  for one study arbitrarily labeled as the first study, and  $G_2$  for the other study).

The process of simulating populations using *ms*, choosing a disease locus, sampling two sets of cases and controls, and choosing one or more marker loci was repeated until 100,000 pairs of association studies — each pair involving the same population, the same disease locus, and the same marker locus, but different individuals — were obtained. Under the assumption that two studies of the same disease and marker locus in the same population are independent, the probability that both studies produce significant associations is the product of the probability that the first study produces a significant association and the probability that the second study produces a significant association. Thus, under this hypothesis, our simulations would be expected to produce  $Pr[G_1 > c \text{ and } G_2 > c] = Pr[G_1 > c] Pr[G_2 > c]$ , and our primary interest was in evaluating the excess probability  $Pr[G_1 > c \text{ and } G_2 > c] - Pr[G_1 > c] Pr[G_2 > c]$  attributable to pseudoreplication. We also evaluated the excess using  $Pr[G_1 > c \text{ and } G_2 > c] / (Pr[G_1 > c] Pr[G_2 > c])$ , the ratio of the conditional probability  $Pr[G_2 > c | G_1 > c]$  to the unconditional  $Pr[G_2 > c]$ . To assist in interpreting the pseudoreplication effect, we also examined  $Pr[G_1 > c]$ ,  $Pr[G_1 > c \text{ and } G_2 > c]$ , and  $Pr[G_1 > c] Pr[G_2 > c]$ .

## RESULTS

The nine models tended to produce similar results for  $Pr[G_1 > c]$ , the power to detect association in a single study, though they varied in the distance over which power was reasonably high (Figure 2). These differences among models in the distance over which association was detectable likely result from the difference across models in the extent of allelic association. As expected based on previous theoretical and simulation-based predictions (Slatkin, 1994; Kruglyak, 1999; Zöllner & von Haeseler, 2000; McVean, 2002), the constant model (Model 1) produced a greater extent of association along the genome than did the instantaneous expansion and exponential expansion models (Models 2 and 3).

For each of the nine models, power  $Pr[G_1 > c]$  depended in a sensible way on the various parameters, as can be seen for the role of the distance between the marker and the disease locus in Figure 2. The effects of the other parameters for a representative model,



demographic Model 2 with a recessive disease effect, are shown in Figure 3. Lower recombination rate led to increased power, reflecting the greater level of association produced between the marker and the disease locus when their recombination distance was smaller. Mutation rate had little impact on  $Pr[G_1 > c]$ , as the effect of mutation rate was mainly to influence the speed at which suitable disease and marker loci were simulated, rather than to substantially influence the properties of the scenarios that were ultimately accepted. Disease frequency also had relatively little effect in most simulated models. However, power increased with decreasing penetrance  $p_L$  for the low-risk homozygous genotype, with increasing penetrance  $p_H$  for the high-risk homozygous genotype, and with increasing relative risk  $p_H/p_L$ .

Considering  $Pr[G_1 > c \text{ and } G_2 > c]$  and  $Pr[G_1 > c] Pr[G_2 > c]$ , similar effects of the various parameters are observed (Figure 4). However, comparing the top two rows of Figure 4, it is apparent that  $Pr[G_1 > c \text{ and } G_2 > c]$  is typically greater than  $Pr[G_1 > c] Pr[G_2 > c]$ . The bottom two rows of Figure 4 demonstrate that  $Pr[G_1 > c \text{ and } G_2 > c] - Pr[G_1 > c] Pr[G_2 > c]$  is almost always positive and that  $Pr[G_1 > c \text{ and } G_2 > c] / (Pr[G_1 > c] Pr[G_2 > c])$  is almost always greater than 1. Particularly for the scenarios with the highest power — small  $r$ , small  $p_L$ , large  $p_H$ , large  $p_H/p_L$ , and small distance between the marker and the disease locus — the pseudoreplication effect  $Pr[G_1 > c \text{ and } G_2 > c] - Pr[G_1 > c] Pr[G_2 > c]$  is noticeably greater than zero. Considering  $Pr[G_1 > c \text{ and } G_2 > c] / (Pr[G_1 > c] Pr[G_2 > c])$ , the power to detect association in the second study when conditioning on having detected association in the first study is often magnified by a factor of 2 to 5 compared to the unconditional power. A generally similar magnitude of the pseudoreplication effect is observed in all nine models, extending over a longer distance in the constant-sized Model 1 compared to instantaneous expansion Model 2 and exponential expansion Model 3 (Figure 5).

Only a very small number of pairs of studies with  $G_1 > c$  and  $G_2 > c$  had the property that opposite high-risk alleles were identified at the marker locus in the two studies. For each of the nine models, the fraction of pairs of studies with  $G_1 > c$  and  $G_2 > c$  and opposite high-risk alleles was less than  $5 \times 10^{-4}$ ; considering only those studies with  $G_1 > c$  and  $G_2 > c$ , in each of the nine models the fraction of studies with opposite high-risk alleles was less than 1%. This result has the consequence that the excess observed in Figure 4 for  $Pr[G_1 > c \text{ and } G_2 > c]$  compared to  $Pr[G_1 > c] Pr[G_2 > c]$  is due to genuine pseudoreplication of associations with the same marker allele, rather than to scenarios in which opposite alleles at the marker locus were associated with disease in the two separate studies.

## DISCUSSION

In simulations of pairs of association studies performed in the same population, we have observed the existence of a noticeable “pseudoreplication” effect, in which the shared ancestry of individuals in two different association studies of the same genomic region induces a correlation in the outcomes of the two studies. We have found that the pseudoreplication effect sometimes produces a considerable magnification of the power to detect association in a second study when conditioning on having detected it in an initial study, and that the excess probability that two studies identify a disease association is greater in scenarios with higher power to detect true disease associations. The excess probability of replication of a disease association was greatest at short distances between the marker tested and the disease locus, and for disease alleles with high relative risk. Small populations have more genealogical sharing among individuals than do large populations; thus, the pseudoreplication effect was greatest for the scenario with the smallest population size (Model 1), in which the set of cases included in the two replicate studies comprised a substantial fraction of affected individuals in the full population.

The occurrence of genealogical correlation between studies might have contributed to a low probability for “flip-flop” associations when disease loci were truly present. As we have observed, genealogical correlation leads to increased probability that two association studies of the same marker and disease will produce the same outcome in the same population, thereby decreasing the probability of divergent outcomes. Although recent studies have shown that flip-flop associations can indeed occur in the presence of true disease associations (Lin *et al.*, 2007, 2008; Zaykin & Shibata, 2008), our simulations suggest that the scenarios that produce such flip-flops near a disease locus might be quite rare.

The pseudoreplication phenomenon has the consequence that the level of statistical support provided by genetic association replications is less than that provided by truly independent replicates, an important result for the practice of association meta-analyses. Thus, the existence of pseudoreplication suggests that new strategies should be developed for estimating the degree of correlation between pseudoreplicated genetic association experiments, and for taking this correlation into account when agglomerating the results of separate studies. To minimize the correlation, it may also be advisable to focus on larger populations, for which the pseudoreplication effect is expected to be smallest.

It is worthwhile to note, however, that our simulations differed in various ways from common practices in replication studies. To match our simulations to the typical setting in which a derived disease allele arises on an existing haplotypic background, we chose the derived allele for the disease variant, so that the results are not directly applicable to the fraction of situations in which disease alleles are ancestral. Loci were simulated under selective neutrality, so that potentially important scenarios with deleterious disease alleles were not considered. To utilize the demographic models chosen with a coalescent simulation approach, the sample size in our simulated studies was small compared to that of studies of typical magnitude, as was the power to detect disease association. However, the main effect of an increase in sample size is an increase in statistical power, and conditions that we have simulated that have different power levels suggest that the pseudoreplication effect is most easily observed when power is high.

An additional limitation is that we considered replication in the same population, whereas replication studies are often performed in a separate population. Due to a smaller degree of genealogical sharing for individuals from separate populations compared to individuals from the same population, the degree of correlation between studies is likely to be smaller than for pairs of studies in the same population. However, the use of different populations introduces the possibility that the history of mutations, recombinations, and divergences of genealogical lineages might differ between populations; for a true disease mutation in two populations, the power to detect the mutation via indirect association studies might vary between the two populations due to differences in their linkage disequilibrium histories (Figure 6; Hirschhorn *et al.*, 2002; Colhoun *et al.*, 2003; Ioannidis, 2007).

Also unlike many situations in practice, the choice to perform a second study in our simulations was not made conditional on the outcome of the first study. Thus, our framework did not take into account issues such as the potential for overestimation of effect size in the initial study and the consequent potential for overestimation of power in the replication study — the “winner’s curse” (Gorroochurn *et al.*, 2007; Yu *et al.*, 2007; Zöllner & Pritchard, 2007). Our simulations also only considered the genealogical aspects of the properties of replication studies in unstructured populations; other factors — such as population structure, difference in sample sizes, heterogeneity of mechanisms that produce the same disease, differences in phenotyping, and gene-gene and gene-environment interactions — also influence outcomes of replication studies, as do differences in markers genotyped or other differences in the genotyping procedure. It remains to evaluate the

comparative magnitude of the pseudoreplication phenomenon in conjunction with an investigation of the effects of these various other factors.

Lastly, we note that our simulations focused only on pseudoreplication for marker loci closely linked to true disease loci. What about pseudoreplication of false positives, at markers not located near a causal locus? Suppose that a true disease mutation exists somewhere in the genome. Because many affected individuals in the population possess the disease mutation, “cryptic relatedness” (Devlin & Roeder, 1999; Voight & Pritchard, 2005) might exist, in which pairs of affected individuals would share a greater degree of recent ancestry compared to pairs in which one or both individuals was unaffected. As a result, a second sample of cases might contain more individuals from a part of the population pedigree that was overrepresented in an initial sample. Because of shared ancestry between the two sets of cases, alleles at sites distant from the disease locus that had high frequencies in the first sample would be more likely to have high frequencies in the second sample. Thus, in principle, a false positive finding might be replicated in a second study; similarly to the scenario of pseudoreplication of true positives, shared genealogy might contribute to pseudoreplication of false positives. It is therefore possible that because of pseudoreplication resulting from cryptic relatedness across samples, false positive findings might recur in separate studies more often than is generally appreciated. Simulations of distant markers or whole genomes rather than the single short region considered here will be required for quantitative examination of this potentially important phenomenon.

## Acknowledgments

We thank S. Zöllner and two reviewers for comments on a draft of the manuscript and M. Slatkin for comments and for suggesting the use of the term “pseudoreplication.” This work was supported by NIH grants R01 GM081441, R01 HL090564, and T32 HG00040, by a Burroughs Wellcome Fund Career Award in the Biomedical Sciences, and by an Alfred P. Sloan Research Fellowship.

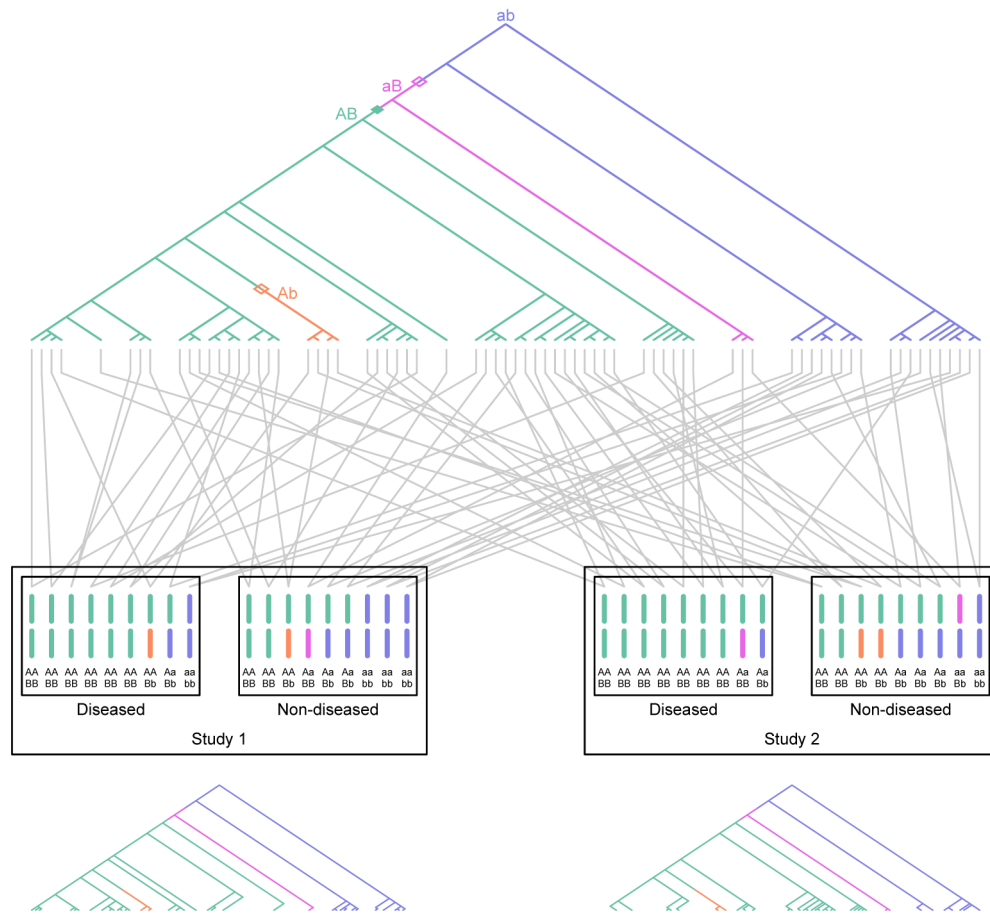
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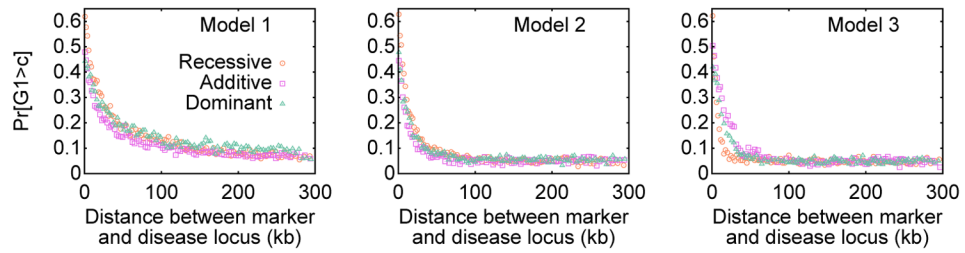


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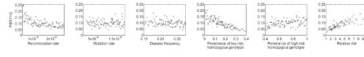


**Figure 1.** Schematic of two association studies performed in the same diploid population. Two loci are considered, a disease-susceptibility locus with alleles  $A$  and  $a$ , and a marker locus with alleles  $B$  and  $b$ . The genealogy of sampled copies of the susceptibility locus in two association studies is shown. The most recent common ancestor of the sampled copies has haplotype  $ab$ . Open diamonds represent recombinations, the closed diamond represents a mutation, and distinct colors represent distinct two-locus haplotypes. The  $A$  allele is a true disease-susceptibility allele; allele  $B$  is indirectly associated as it lies on the haplotype on which the first  $A$  mutation occurred. Gray lines represent the pairing of haplotypes to form diploid individuals. For the purpose of illustration with a small sample size as shown in the figure, disease status is assigned to individuals according to a multiplicative model with penetrance  $1/6$  for low-risk  $aa$  homozygotes and relative risk 2 for heterozygotes. The figure shows that both association studies performed in the population reflect disease associations with allele  $B$ . The genealogies at the bottom represent the subgenealogies for the individuals included in the two separate studies. They display a high degree of correlation in the history of events responsible for indirect associations between  $B$  and disease.



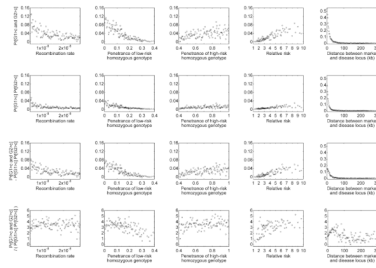
**Figure 2.**

$Pr[G_1 > c]$  as a function of the distance between the marker and the disease locus. The plots display nine combinations of demographic model (Models 1, 2, 3) and penetrance model (recessive, additive, dominant). For each of the nine combinations, the 100,000 simulated studies were binned into 100 groups each consisting of 1000 studies. The probability evaluated from the studies in a bin is plotted at the mean of the 1000 values placed in the bin.

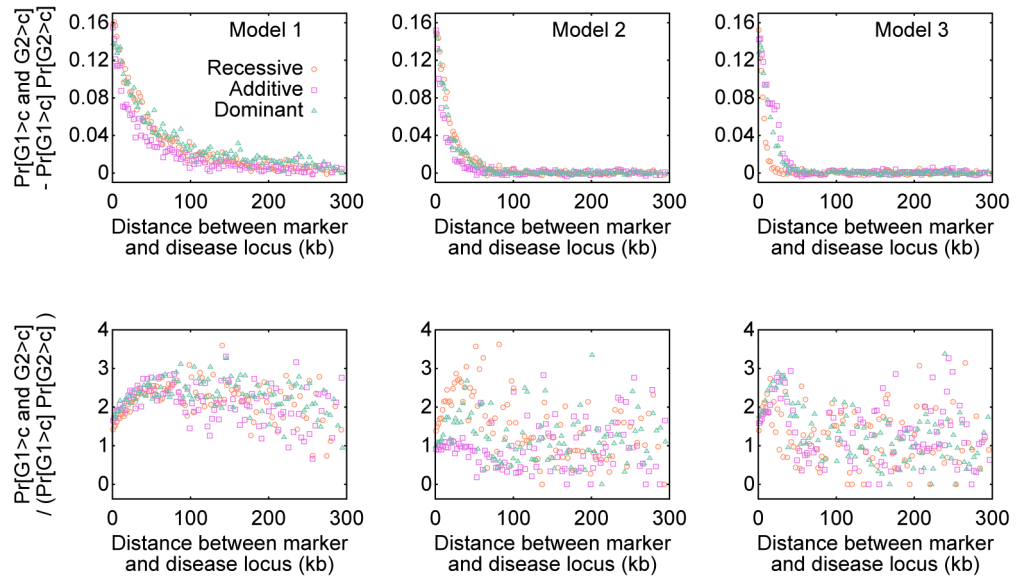


**Figure 3.**  $Pr[G_1 > c]$  as a function of recombination rate ( $r$ ), mutation rate ( $\mu$ ), disease frequency ( $p_D$ ), penetrance of the low-risk homozygous genotype ( $p_L$ ), penetrance of the high-risk homozygous genotype ( $p_H$ ), and relative risk ( $p_H/p_L$ ). For each of these variables, the 100,000 simulated studies were binned into 100 groups each consisting of 1000 studies. The probability evaluated from the studies in a bin is plotted at the mean of the 1000 values placed in the bin. The plots are based on demographic Model 2 with the recessive disease model.



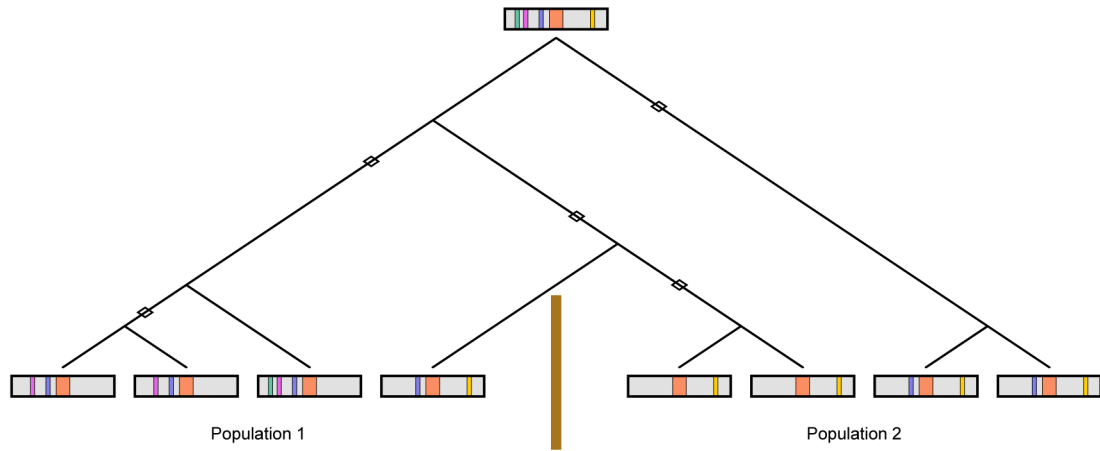


**Figure 4.**  $Pr[G_1 > c \text{ and } G_2 > c]$ ,  $Pr[G_1 > c] Pr[G_2 > c]$ ,  $Pr[G_1 > c \text{ and } G_2 > c] - Pr[G_1 > c] Pr[G_2 > c]$ , and  $Pr[G_1 > c \text{ and } G_2 > c]/(Pr[G_1 > c] Pr[G_2 > c])$  as functions of recombination rate ( $r$ ), penetrance of the low-risk homozygous genotype ( $p_L$ ), penetrance of the high-risk homozygous genotype ( $p_H$ ), relative risk ( $p_H/p_L$ ), and distance between the marker and the disease locus. For each of these variables, the 100,000 simulated pairs of studies were binned into 100 groups each consisting of 1000 pairs. The quantities evaluated from the studies in a bin are plotted at the mean of the 1000 values placed in the bin. The plots are based on demographic Model 2 with the recessive disease model.



**Figure 5.**

$Pr[G_1 > c \text{ and } G_2 > c] - Pr[G_1 > c] Pr[G_2 > c]$  and  $Pr[G_1 > c \text{ and } G_2 > c] / (Pr[G_1 > c] Pr[G_2 > c])$  as functions of the distance between the marker and the disease locus. The plots display nine combinations of demographic model (Models 1, 2, 3) and penetrance model (recessive, additive, dominant). For each of the nine combinations, the 100,000 simulated pairs of studies were binned into 100 groups each consisting of 1000 pairs. The quantity evaluated from the studies in a bin is plotted at the mean of the 1000 values placed in the bin.



**Figure 6.**

Schematic of a possible pattern of linkage disequilibrium in two populations. A disease mutation (orange) occurs on an ancestral chromosome that contains several marker alleles (green, purple, blue, yellow). Over time, recombination events (open diamonds) break down the correlations between the disease mutation and the marker alleles. However, the recombination history is different for populations 1 and 2, separated by a barrier to gene flow (brown vertical line). Consequently, if the purple or blue allele were examined in population 1, then a disease association might be found, but it might not be replicated in population 2. A similar situation applies for the yellow allele, with the roles of the populations reversed.