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November 27, 2017

## Abstract

## Introduction

It has long been known that diversity on Earth is in large part due to the adaptation of organisms to varying environments. We now know that adaptation has a large genetic basis, and that genetic variation is the key to biological diversity. Thus, understanding how and why such genetic variation occurs is a seminal goal of evolutionary biology. Quantifying genetic adaptation is an important aim of population geneticists, and to this end finding methods to detect signals of selection within the genome is of particular interest. Change in the mean phenotype of a population over time can be attributed to many causes including genetic drift or population migration, so detecting signals of selection in particular is no trivial task (cite) .

Until recently, the study of detecting selection has been limited to large-effect alleles, when in fact numerous phenotypic traits of interest are affected by many different loci across the genome. Understanding how to find signals of selection for such polygenic traits has been the subject of much study in recent years. Increased computational capabilities have given us the tools to be able to evaluate the effects of many thousands of loci on a trait, allowing us to evaluate selection in highly polygenic traits, such as height. One of the most important tools developed are Genome-Wide Association Studies (GWAS) which determine which loci across the genome have significant effects on a certain polygenic trait [6]. The effect sizes measured by GWAS for loci on a certain polygenic trait are often denoted  $\alpha$ .

We can express the polygenic phenotype of individuals in a population as the weighted sum of genotypes with additive effect sizes  $\alpha$ . This generalizes to population means, where the mean population phenotype is the weighted sum of effect sizes and frequency of the allele ( $p$ ) at each significant locus ( $l$ ). (cite– Gillepsie? for additive model)

$$\sum_l \alpha_l p_l \tag{1}$$

The additive effect size, then, is key to relating the genotypes of the many loci contributing to the phenotype of interest with the phenotype itself– as shown below, it also plays a key role in statistical tests for polygenic adaptaion. Understanding how  $\alpha$  can be affected by other factors is essential for ensuring that these statistical tests remain as unbiased as possible.

Dominance is one such phenomenon that we hypothesize has a non-trivial effect on  $\alpha$ . Dominance in population genetics refers to when the effect of one allele depends on the presence of another allele at the locus. We can account for the effect of dominance in the effect size by parametrizing  $\alpha$  in terms of the homozygous effect size (A), or effect size of the most frequent homozygote, and the dominance deviation (D), which is the difference in effect size for the heterozygote deviating from  $\frac{1}{2}$  of the homozygous effect size (cite Gillepsie?) :

$$\alpha_\ell = \frac{1}{2}A_\ell + D_\ell(1 - 2p_{1\ell}) . \tag{2}$$

In particular, directional dominance is when alleles with a postive effect size on the trait are systematically dominant and alleles with a negative effect size on the trait are systematically negative. In terms of (2), this means that the signs of A and D are the correlated for a large number of loci. We hypothesized that directional dominance is problematic in tests of polygenic adaptation because the effect size we estimate in the presence of directional dominance depends

on how the allele frequency  $p$  has changed in the recent past. In particular, recessive alleles which have decreased in frequency in the recent past will tend to have larger effect sizes, as shown in Figure 1 in the supplement. Notice that when there is no dominance,  $\alpha$  is constant, but in the presence of directional dominance (positive A and D) for alleles with lower frequency will have a higher effect size.

Given the hypothesized effect that directional dominance has on  $\alpha$ , we suspect that directional dominance will bias statistical tests of polygenic adaptation. We give a short overview of such tests below.

Wright first introduced the parameter  $F_{st}$  as a measure comparing the genetic variation of an allele at a specific site in a subpopulation to that of the entire population [5]. Lewontin and Krakauer, using this parameter developed a novel statistical test based on the fact that under no selection, the expected  $F_{st}$  at a given site will be the same as the population  $F_{st}$ . Further, they concluded that the distribution of  $F_{st}$  across all sites will be chi-squared  $F_{st}$  [7]. The natural conclusion is that sites with statistically different  $F_{st}$  values are candidates for loci that have been acted upon by selection. These conclusions were extended by Spitze, who coined the parameter  $Q_{st}$  as a measure of how the variation of all loci contributing to a phenotype of a subpopulation compares to that of the entire population [2]. Essentially,  $Q_{st}$  is analogous to  $F_{st}$ , except that instead of looking at the variation of one allele at a locus, it measures the ratio of the variation of all loci contributing to a phenotype within a subpopulation to that of the entire population. These early tests for selection utilized the ratio  $\frac{Q_{st}}{F_{st}}$  as a test statistic for detecting signals of selection, where  $F_{st} = Q_{st}$  is the null model, where no selection occurs.

Much later, Berg and Coop introduced a comprehensive test statistic, called  $Q_x$ , based on these central ideas to test for selection [1]. This statistic depends on  $F_{st}$  and a generalized analogy to  $Q_{st}$ , expressed in terms of  $\alpha$  and the allele frequencies  $p$  over loci  $l$  and  $l'$ , summed over populations  $m$ .  $V_a$  is the additive genetic variance of the entire population, and  $\bar{p}_l$  is the mean frequency.

$$Q_x = \frac{1}{V_A F_{ST}} \sum_{m=1}^M \sum_{\ell=1}^L \sum_{\ell'=1}^L \alpha_{\ell} \alpha_{\ell'} (p_{m\ell} - \bar{p}_{\ell}) (p_{m\ell'} - \bar{p}_{\ell'}) \quad (3)$$

The distribution of this statistic is expected to be chi-squared. Notice that the additive effect size  $\alpha$  is the weighting factor for loci in the expression for  $Q_x$ .

In the presence of directional dominance, we hypothesized a bias in tests for polygenic adaptation that depends on  $\alpha$ . Alleles which are systematically dominant and which have recently increased in frequency (large  $p$ , positive D) will tend to have smaller effect sizes, while alleles which are recessive which have recently decreased in frequency (small  $p$ , negative D) will tend to have larger effect sizes. In the latter case, the test for polygenic selection advanced by Berg and Coop (3) will tend to make false positive judgements for selection, because the statistic will be calculated over alleles which do not actually increase the effect size.

Height is one polygenic trait with many well-defined significant alleles via GWAS [3]. It has also been shown to exhibit directional dominance [4]. We aim to quantify the hypothesized bias, first with simulated populations, then with height genotype data from the UK Biobank.

## Theory/Methods

Using the expression for the test statistic  $Q_x$  (3), we can substitute the expression for  $\alpha$  (2) and manipulate the expression algebraically to derive the following expansion for the test statistic, in terms of the homozygous effect (A) and the dominance deviation (D):

$$\begin{aligned}
& \sum_{l=1}^L \left( \frac{1}{2} A_l (p_{1l} - \epsilon_l) \right)^2 + \sum_{l=1}^L \sum_{l' \neq l}^L \left( \frac{1}{4} A_l (p_{1l} - \epsilon_l) A_{l'} (p_{1l'} - \epsilon_{l'}) \right) \\
& + \sum_{l=1}^L A_l D_l (1 - 2p_{1l}) (p_{1l} - \epsilon_l)^2 + \sum_{l=1}^L \sum_{l' \neq l}^L \left( \frac{1}{2} A_l D_{l'} (1 - 2p_{1l'}) (p_{1l} - \epsilon_l) (p_{1l'} - \epsilon_{l'}) \right. \\
& \quad \left. + \frac{1}{2} D_l A_{l'} (1 - 2p_{1l}) (p_{1l} - \epsilon_l) (p_{1l'} - \epsilon_{l'}) \right) \\
& + \sum_{l=1}^L (D_l (1 - 2p_l) (p_{1l} - \epsilon_l))^2 + \sum_{l=1}^L \sum_{l' \neq l}^L D_l (1 - 2p_l) (p_{1l} - \epsilon_l) D_{l'} (1 - 2p_{l'}) (p_{1l'} - \epsilon_{l'})
\end{aligned} \tag{4}$$

We can loosely consider the single summation terms to be variances corresponding to the expansion of additive effects multiplied by additive effects, additive times dominance, and dominance times dominance, and the double summation terms as covariances of these quantities. We expect the inflation of the test statistic due to dominance effects to come from the last two terms. Note that when dominance is not present ( $D = 0$ ) the expansion reduces to the expression Berg and Coop present when  $\alpha$  is treated as a constant [1].

Using this expansion, we have created simulations to characterize our hypothesized dominance bias. We used simulated populations under a couple of assumptions: first, that the values of the dominance deviations and homozygous effects are constant throughout the population. While this is not true in general, (why is this justified? cite??) Second, that  $F_{st}$  for these simulated approximations can be roughly estimated by the number of generations elapsed over the population size. Third, that the distribution of allele frequencies after one generation can be approximated by a normal distribution centered at the ancestral frequency with variance  $F_{st} * \epsilon * (1 - \epsilon)$  where  $\epsilon$  is the ancestral frequency. (CITE THESE ASSUMPTIONS???)

All simulations were performed in R.

## Results/Discussion

Simulations of the expansion (4) were performed with population size 10000 over 100 generations, starting at an ancestral frequency of 0.5, an homozygous effect size of 0.5, and a dominance deviation value of 0. The distribution of  $Q_x$  was simulated under these conditions for 1000 replicates.

## Supplement

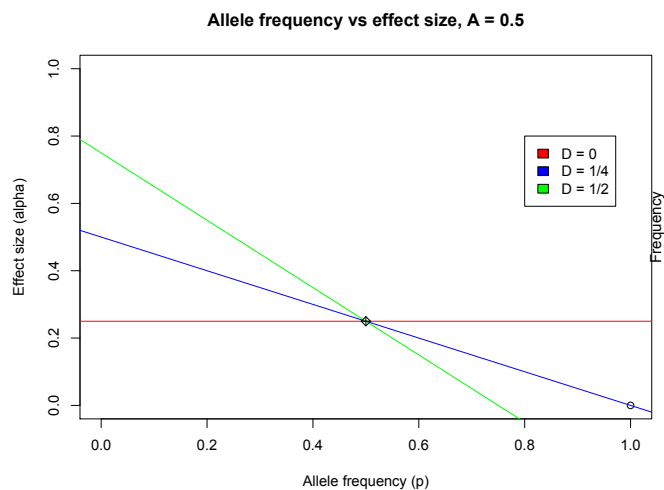


Fig. 1: Effect sizes for various dominance deviation values under directional dominance

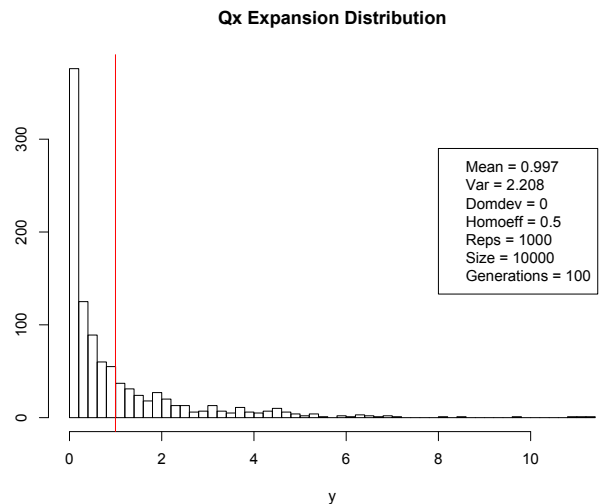
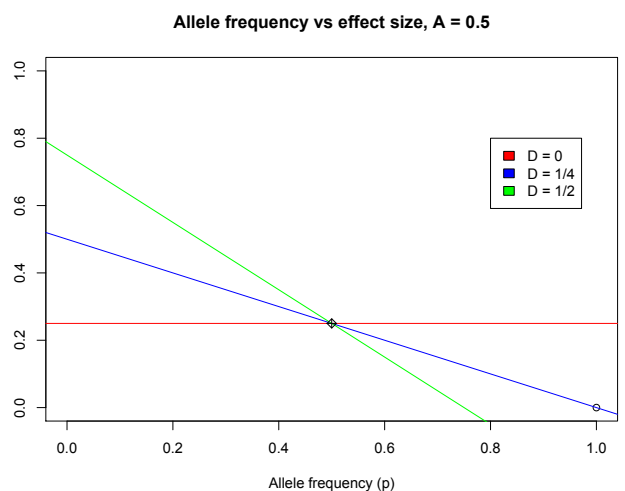
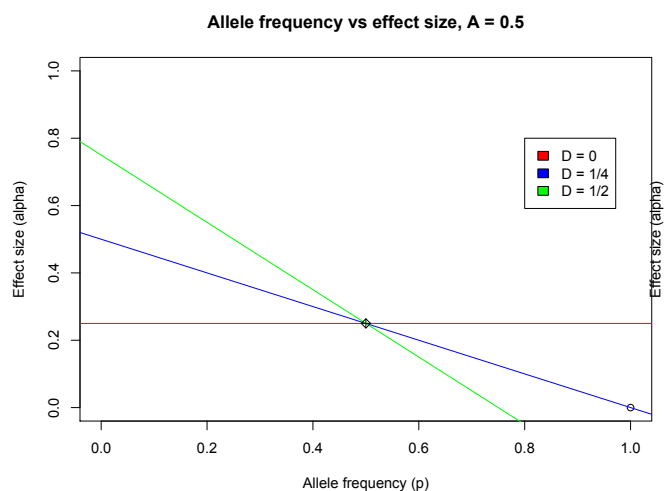


Fig. 2:  $Q_x$  Expansion Distribution



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