

Bayesian Polynomial Regression Models to Fit Multiple Genetic Models for Quantitative Traits

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Abstract. We present a coherent Bayesian framework for selection of the most likely model from the five genetic models (genotypic, additive, dominant, co-dominant, and recessive) commonly used in genetic association studies. The approach uses a polynomial parameterization of genetic data to simultaneously fit the five models and save computations. We provide a closed-form expression of the marginal likelihood for normally distributed data, and evaluate the performance of the proposed method and existing method through simulated and real genome-wide data sets.

Keywords: marginal likelihood, GWAS, Bayesian model selection, parameterization, additive, dominant, recessive, co-dominant.

1 Introduction

Genome-wide association studies have been a popular approach to discover genetic variants that are associated with increased risk for rare and common diseases (Sebastiani et al. (2009)). The most common variants in the human genome are single nucleotide polymorphisms (SNPs): DNA bases that can vary across individuals. Typically SNPs have two alleles, say A and B, and based on the combination of SNPs alleles in each chromosome pair (the genotype), an individual can be homozygous for the A allele if both chromosomes carry the allele A, homozygous for the allele B if both chromosomes carry the B allele, and heterozygous when the two chromosomes carry the A and B alleles. Genotyping DNA was a slow and expensive process until mid-2000, when high throughput technologies produced microarrays that can generate the genetic profiles of an individual in hundreds of thousands to millions of SNPs, and the technology was the trigger for an explosion of genome-wide association studies (GWAS) to discover the genetic base of common diseases.

Typically in a GWAS the association between each SNP and a quantitative trait is tested using linear regression under a specific genetic model that can assume a genotypic (2 degrees of freedom), dominant, recessive, co-dominant, or additive mode of inheritance of each tested SNP. In a genotypic model the 3 genotypes AA, AB and BB are treated as a factor with 3 levels. The other 4 genetic models compress the 3 genotypes into a numerical variable by either counting the number of minor alleles (additive model), or by recoding the genotypes as AA=0 versus AB, BB=1 (dominant model for

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the B allele), AA, AB=0 versus BB=1 (recessive model for the B allele), AA, BB=0 versus AB=1 (co-dominant model). However, the inheritance pattern is rarely known, and using a suboptimal model can lead to a loss of power (Lettre et al. (2007)).

Selecting the correct genetic model for each SNP is often accomplished by fitting the five models and choosing the model that describes the data best. This approach has several drawbacks. It increases computational burden with genome-wide data as 5 GWASs need to be conducted. Furthermore, testing five models for each SNP increases the burden of multiple testing in addition to the existing issue of multiple comparisons with millions of SNPs. More importantly, the optimal method for choosing the best model is not clear (Lettre et al. (2007)). The common practice is to simply use the additive genetic model. It has been shown that additive models perform reasonably well to detect variants that have additive or dominant inheritance pattern, but they are underpowered when the true mode of inheritance is recessive (Bush and Moore (2012)). Others (Freidlin et al. (2002); Gonzalez et al. (2008); Li et al. (2008); So and Sham (2011)) have proposed to study the maximum of the three test statistics derived under additive, dominant, and recessive models.

We propose a polynomial parameterization of the genetic data that includes the five genetic models as special cases, and we describe a coherent Bayesian framework to select the most likely genetic model given the data. This polynomial parameterization is equivalent to the genetic model described in Servin and Stephens (2007) that adds a dominance effect to the additive model to describe non-additive genetic effects. The advantage of either parameterization is that, in a Bayesian framework, fitting a single model becomes sufficient to test the genotype-phenotype associations without specifying a particular genetic model and this problem has been described in detail in Servin and Stephens (2007). Here, we focus on the specific task of selection of the best genetic model when the specific mode of inheritance is of interest in addition to whether a SNP is associated with the trait.

The next section describes this parameterization and shows that there is a mathematical relationship between the parameters of the polynomial model and each of the five possible genetic models. Section 3 describes the model selection approach that is based on the computation of the marginal likelihood of the five models so that the model with maximum posterior probability can be identified. Section 3 also provides closed form solutions for the marginal likelihood and for the estimates of the parameters of the model with the highest marginal likelihood or Bayes Factor (BF), assuming exchangeable observations that follow normal distributions. The proposed method is evaluated through simulation studies in Section 4, and is applied to two GWAS data sets in Section 5. Conclusions and suggestions for further work are provided in Section 6.

2 Relationship Between the Polynomial Model and Other Genetic Models

Here we show that the five genetic models are specific cases of a general polynomial model, with parameters that satisfy some linear constraints. Let y denote the response

variable in the genetic association study, and consider the polynomial regression model

$$E(y|\beta) = \beta_0 + \beta_1 x_{add} + \beta_2 x_{add}^2$$

where β denotes the vector of regression parameters and x_{add} is the variable that codes for the genotype data as follows:

$$x_{add} = \begin{cases} 0 & \text{if genotype is AA} \\ 1 & \text{if genotype is AB} \\ 2 & \text{if genotype is BB.} \end{cases}$$

Note that the proposed model is equivalent to the additive model with dominance effects described in Servin and Stephens (2007):

$$E(y|\theta) = \theta_0 + \theta_1 x_{add} + \theta_2 x_{het}$$

where $x_{het} = 1$ for heterozygous genotype and 0 otherwise, and $\theta_1 = \beta + 2\beta_2$; $\theta_2 = -\beta_2$. Mathematically, we found the polynomial parameterization more appealing as it allows interpretation of the regression coefficients in terms of the SNP dosage.

2.1 Genotypic Association Model

The genotypic association model is typically parameterized using two indicator variables to describe the effect of the genotypes AB and BB relative to AA:

$$E(y|\gamma) = \gamma_0 + \gamma_1 x_{AB} + \gamma_2 x_{BB}$$

$$x_{AB} = 1 \text{ if genotype is AB (and 0 otherwise)}$$

$$\text{and } x_{BB} = 1 \text{ if genotype is BB (and 0 otherwise).}$$

This parameterization specifies the expected value of y , for each of the 3 genotypes AA, AB, BB as summarized in Table 1. Equating the expected values of y from the 2 different parameterizations produces a system of linear equations:

$$\begin{bmatrix} \gamma_0 \\ \gamma_0 + \gamma_1 \\ \gamma_0 + \gamma_2 \end{bmatrix} = \begin{bmatrix} \beta_0 \\ \beta_0 + \beta_1 + \beta_2 \\ \beta_0 + 2\beta_1 + 4\beta_2 \end{bmatrix}$$

that can be solved as

$$\begin{bmatrix} \gamma_0 \\ \gamma_1 \\ \gamma_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 1 \\ 0 & 2 & 4 \end{bmatrix} \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 1 \\ 0 & 2 & 4 \end{bmatrix} \beta.$$

Therefore, the parameters in the polynomial model and the genotypic association model have a one-to-one relationship. For the other genetic models, some constraints on parameters of the polynomial model are necessary.

2.2 Additive Model

The parameterization of the additive genetic model is $E(y|\alpha_A) = \alpha_{A0} + \alpha_A x_{add}$ and equating the expected values of y in Table 1 leads to the system of linear equations:

$$\begin{aligned}\beta_0 &= \alpha_{A0} \\ \beta_1 + \beta_2 &= \alpha_A \\ 2\beta_1 + 4\beta_2 &= 2\alpha_A\end{aligned}$$

that can be solved if $\beta_2 = 0$, so that $\beta_0 = \alpha_{A0}$, and $\beta_1 = \alpha_A$. Therefore the relationship between the parameters in the polynomial model and additive model requires a linear constraint on the vector β .

2.3 Dominant Model

Now, consider the dominant model for the B allele: $E(y|\alpha_D) = \alpha_{D0} + \alpha_D x_{Dom}$, where $x_{Dom}=1$ if genotype is AB or BB (and 0 otherwise). Proceeding as in the previous cases leads to the equations:

$$\begin{aligned}\alpha_{D0} &= \beta_0 \\ \alpha_D &= \beta_1 + \beta_2 = 2\beta_1 + 4\beta_2.\end{aligned}$$

The system has the solution $\alpha_{D0} = \beta_0$ and $\alpha_D = \frac{2}{3}\beta_1$ if the parameters of the polynomial model satisfy the constraint $\beta_1 + 3\beta_2 = 0$.

2.4 Recessive Model

Similarly, consider the recessive model for the B allele: $E(y|\alpha_R) = \alpha_{R0} + \alpha_R x_{Rec}$, where $x_{Rec}=1$ if genotype is BB (and 0 otherwise). In this case, the relations between parameters are:

$$\begin{aligned}\alpha_{R0} &= \beta_0 = \beta_0 + \beta_1 + \beta_2 \\ \alpha_R &= 2\beta_1 + 4\beta_2\end{aligned}$$

with linear constraint $\beta_1 + \beta_2 = 0$, $\alpha_{R0} = \beta_0$ and $\alpha_R = 2\beta_1$.

2.5 Co-dominant Model

Lastly, consider the co-dominant genetic model: $E(y|\alpha_C) = \alpha_{C0} + \alpha_C x_{Cod}$, where $x_{Cod}=1$ if genotype is AB (and 0 otherwise). In this case:

$$\begin{aligned}\alpha_{C0} &= \beta_0 = \beta_0 + 2\beta_1 + 4\beta_2 \\ \alpha_C &= \beta_1 + \beta_2.\end{aligned}$$

The linear constraint is $\beta_1 + 2\beta_2 = 0$, so that $\alpha_{C0} = \beta_0$ and $\alpha_C = \frac{1}{2}\beta_1$.

In summary, there is a one-to-one transformation between the parameters of the polynomial and general model, while the transformation between the polynomial and the other four models (additive, dominant, recessive, and co-dominant) is constrained by a linear contrast of the parameters in the polynomial model.

	Polynomial Model	2-df General Model	Additive Model	Dominant Model	Recessive Model	Co-dominant Model
$E(y AA)$	β_0	γ_0	α_{A0}	α_{D0}	α_{R0}	α_{C0}
$E(y AB)$	$\beta_0 + \beta_1 + \beta_2$	$\gamma_0 + \gamma_1$	$\alpha_{A0} + \alpha_A$	$\alpha_{D0} + \alpha_D$	α_{R0}	$\alpha_{C0} + \alpha_C$
$E(y BB)$	$\beta_0 + 2\beta_1 + 4\beta_2$	$\gamma_0 + \gamma_2$	$\alpha_{A0} + 2\alpha_A$	$\alpha_{D0} + \alpha_D$	$\alpha_{R0} + \alpha_R$	α_{C0}

Table 1: Expected value of the quantitative trait for 3 genotypes in each model.

3 Model Selection via Marginal Likelihood and Parameter Estimation

The polynomial parameterization provides a framework to simultaneously fit different genetic models. Given a sample of genotype data, the question is how to select the most appropriate genetic model. We propose a Bayesian model selection approach in which genetic models are compared based on their marginal likelihood and the model with largest marginal likelihood is selected, assuming that a priori the 5 genetic models are equally likely.

In the polynomial model ($y|\beta = X\beta + \epsilon$ in matrix form), the data are assumed to be exchangeable and follow a normal distribution with:

$$y|X, \beta, \tau \sim N(X\beta, \frac{1}{\tau}I)$$

where I is the identity matrix. A standard normal-gamma prior for the vector of parameters β and precision τ is assumed such that $p(\beta, \tau) = p(\beta|\tau)p(\tau)$, where

$$\tau \sim \text{Gamma}(a_1, a_2)$$

$$\beta|\tau \sim N(\beta_0, (\tau R_0)^{-1})$$

with β_0 , R_0 , a_1 , and a_2 as prior hyperparameters. Specification of these prior hyperparameters can be subjective and represents the prior probability of alternative genetic models. With genome-wide data, most of the tested SNPs are likely to be null SNPs and it is both reasonable and convenient to assume non-informative priors. Therefore the following values for the prior hyper-parameters: $\beta_0 = 0$, $R_0 = I$, $a_1 = 1$, and $a_2 = 1$ will be assumed. If there is strong prior belief about certain genetic models, more informative prior distributions can be chosen and this problem is described at length in Servin and Stephens (2007). The marginal likelihood given this polynomial model M_p can be computed analytically in the equation below:

$$p(y|M_p) = \int p(y|X, \beta, \tau)p(\beta, \tau)d\beta d\tau = \frac{1}{(2\pi)^{\frac{n}{2}}} \frac{a_{2n}^{a_{1n}} \Gamma(a_{1n})}{a_2^{a_1} \Gamma(a_1)} \frac{|R_0|^{\frac{1}{2}}}{|R_n|^{\frac{1}{2}}}$$

with the following updated hyper-parameters:

$$R_n = R_0 + X^T X$$

$$\begin{aligned}\beta_n &= R_n^{-1}(R_0\beta_0 + X^T y) \\ a_{1n} &= a_1 + \frac{n}{2} \\ a_{2n} &= \left[\frac{-\beta_n^T R_n \beta_n + y^T y + \beta_0^T R_0 \beta_0}{2} + \frac{1}{a_2} \right]^{-1}.\end{aligned}$$

Details are for example in O'Hagan and Kendall (1994). In the general genetic model, the vector of parameters γ is a linear transformation of β , $\gamma = \omega\beta$, where the matrix ω is:

$$\omega = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 1 \\ 0 & 2 & 4 \end{bmatrix}.$$

Since γ is a linear transformation of β , once a prior distribution for β is elicited, the prior distribution of γ is derived as:

$$\gamma|\tau = \omega\beta|\tau \sim N(\omega\beta_0, \omega(\tau R_0)^{-1}\omega^T)$$

while the prior for τ does not change with the re-parameterization. If the prior distributions of the parameters vectors are so defined, then it can be shown that $p(y|M_P) = p(y|M_G)$ (see the Supplementary Material for details). In other words, the marginal likelihood is invariant under linear transformations of the regression coefficients.

Derivation of marginal likelihoods for additive, dominant, recessive, and co-dominant models is different, as these models are defined by a linear transformation of the parameters of the polynomial model and an additional constraint. Formally, let $\alpha = \begin{bmatrix} \alpha_0 \\ \alpha_1 \end{bmatrix}$ denote the vector of parameters in any of these models. Then we can define $\alpha = \begin{bmatrix} \alpha_0 \\ \alpha_1 \end{bmatrix} = \begin{bmatrix} \theta_0 \\ \theta_1 \end{bmatrix} | \theta_2 = 0$ where $\theta = \begin{bmatrix} \theta_0 \\ \theta_1 \\ \theta_2 \end{bmatrix} = \omega\beta$ and matrix ω depends on the specific genetic model (see Table 2). If the vector β follows a multivariate normal distribution, θ also follows a multivariate normal distribution, and so does the marginal distribution of θ_2 and α that is a conditional distribution. Starting from the proper prior distributions for the vector of parameters β and precision τ priors, then proper prior distributions for α and τ are found to be:

$$\begin{aligned}\tau &\sim \text{Gamma}(a_1, a_2) \\ \alpha &= \begin{bmatrix} \alpha_0 \\ \alpha_1 \end{bmatrix} = \begin{bmatrix} \theta_0 \\ \theta_1 \end{bmatrix} | \theta_2 = 0 \sim N(\mu_0, \tau^{-1}\Sigma_0^{-1}).\end{aligned}$$

μ_0 and Σ_0^{-1} can be obtained by using properties of the conditional multivariate normal distribution (Eaton (1983)) and are summarized in Table 3. Using these derived priors, the marginal likelihood for the additive, dominant, recessive, and co-dominant models (M_A , M_D , M_R , and M_C , respectively) can be computed in closed form. The derivation of the marginal likelihood for the dominant model is detailed in the Supplementary Material. Derivation of the marginal likelihood for the additive, recessive, and co-dominant

	2-df General Model	Dominant Model	Recessive Model	Codominant Model	Additive Model
ω	$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 1 \\ 0 & 2 & 4 \end{bmatrix}$	$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 1 \\ 0 & 1 & 3 \end{bmatrix}$	$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 2 & 4 \\ 0 & 1 & 1 \end{bmatrix}$	$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 1 \\ 0 & 1 & 2 \end{bmatrix}$	$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 1 \\ 0 & 0 & 1 \end{bmatrix}$

Table 2: Specification of ω for five genetic models.

model is similar. Note that the derivation relies on the use of proper prior distributions for the parameters of the polynomial model.

Assuming that the 5 genetic models are a priori equally likely, the Bayes rule to model selection is equivalent to choosing the genetic model with the highest marginal likelihood or BF relative to the null model (i.e. ratio of marginal likelihood of one of the five models and the null model) (Kass and Raftery (1995)). Once the most likely model is selected, the parameter estimates of any of the five genetic models are the means of the posterior distributions. The regression parameters in the polynomial model are estimated by $\beta_n = R_n^{-1}(R_0\beta_0 + X^T y)$ and using the one-to-one relationship, the parameters in the general model can be estimated by $\gamma_n = \omega\beta_n$. The relation between parameters of the polynomial models and the dominant, recessive, co-dominant, and additive models can be used to derive their posterior estimates. Specifically, from the set of relations:

$$\begin{aligned} \beta|\tau &\sim N(\beta_n, (\tau R_n)^{-1}) \\ \theta = \omega\beta|\tau &\sim N(\theta_n = \omega\beta_n, \omega(\tau R_n)^{-1}\omega^T) \\ \alpha = \begin{bmatrix} \theta_0 \\ \theta_1 \end{bmatrix} | \theta_2 = 0 &\sim N(\mu_n, \tau^{-1}\Sigma_n^{-1}) \end{aligned}$$

and using the properties of the conditional multivariate normal distribution, the point estimates μ_n for any model are found to be:

$$\mu_n = \begin{bmatrix} \theta_{n0} \\ \theta_{n1} \end{bmatrix} + [S_{12}][S_{22}]^{-1}[0 - \theta_{n2}]$$

where $\omega(\tau R_n)^{-1}\omega^T = \tau^{-1} \begin{bmatrix} S_{11} & S_{12} \\ S_{21} & S_{22} \end{bmatrix}$, and $\dim(S_{11}) = 2 \times 2$, $\dim(S_{12}) = 2 \times 1$, $\dim(S_{21}) = 1 \times 2$, and $\dim(S_{22}) = 1 \times 1$. Table 3 summarizes the specification of ω and formulas for computing prior and updated hyper-parameters and marginal likelihood for different genetic models discussed in this section as well as the null model.

4 Simulation Studies

Three simulation studies were conducted to assess false and true positive rates of the Bayesian procedure with polynomial models and compared to the frequentist approach in which the association with minimum p-value is selected. Simulation study (1) was designed to evaluate the false positive rates of the polynomial model approach for various

	Prior Hyper parameters	Posterior Hyper parameters	Marginal Likelihood
M_P	$\beta_0 = [\beta_{00} \beta_{01} \beta_{02}]^T$ $R_0 = \begin{bmatrix} r_{11} & r_{12} & r_{13} \\ r_{21} & r_{22} & r_{23} \\ r_{31} & r_{32} & r_{33} \end{bmatrix}$ a_1 a_2	$\beta_n = R_n^{-1}(R_0\beta_0 + X^T y)$ $R_n = R_0 + X^T y$ $\alpha_{1n} = \alpha_1 + n/2$ $\alpha_{2n} = \left(\frac{-\beta_n^T R_n \beta_n + y^T y}{2} \right)^{-1}$ $\frac{\beta_0^T R_0 \beta_0}{2} + \frac{1}{\alpha_2} \Big)^{-1}$	$p(y M_P) = \frac{1}{\alpha_2^{\alpha_1} \Gamma(\alpha_1)}$ $\frac{1}{(2\pi)^{n/2} R_0 ^{1/2}}$ $\alpha_{2n}^{\alpha_{1n}} \Gamma(\alpha_{1n})$
M_G	$\gamma_0 = \omega \beta_0$ $R'_0 = \omega(R_0)^{-1} \omega^T$ a_1 a_2	$\gamma_n = \omega \beta_n$ $R'_n = \omega(R_n)^{-1} \omega^T$ $\alpha_{1n} = \alpha_1 + n/2$ $\alpha_{2n} = \left(\frac{-\beta_n^T R_n \beta_n + y^T y}{2} \right)^{-1}$ $\frac{\beta_0^T R_0 \beta_0}{2} + \frac{1}{\alpha_2} \Big)^{-1}$	$p(y M_G) = \frac{1}{\alpha_2^{\alpha_1} \Gamma(\alpha_1)}$ $\frac{1}{(2\pi)^{n/2} (\omega^{-1})^T R_n \omega^{-1} ^{1/2}}$ $\alpha_{2n}^{\alpha_{1n}} \Gamma(\alpha_{1n}) = p(y M_P)$
M_D	Let $\omega \beta_0 = \theta_0 = \begin{pmatrix} \theta_{00} \\ \theta_{01} \\ \theta_{02} \end{pmatrix}$ $\omega(\tau R_0)^{-1} \omega^T = S_0 =$ $\tau^{-1} \begin{pmatrix} s_{01}^{11} & s_{02}^{12} & s_{03}^{13} \\ s_{02}^{21} & s_{02}^{22} & s_{02}^{23} \\ s_{03}^{31} & s_{03}^{32} & s_{03}^{33} \end{pmatrix}$ $\mu_0 = \begin{pmatrix} \theta_{00} \\ \theta_{01} \end{pmatrix} -$ $\begin{pmatrix} s_{03}^{13} \\ s_{02}^{23} \end{pmatrix} (s_{03}^{33})^{-1} \theta_{02}$ $\Sigma_0^{-1} = \begin{pmatrix} s_{01}^{11} & s_{02}^{12} \\ s_{02}^{21} & s_{02}^{22} \end{pmatrix} -$ $\begin{pmatrix} s_{03}^{13} \\ s_{02}^{23} \end{pmatrix} (s_{03}^{33})^{-1} \begin{pmatrix} s_{01}^{31} & s_{02}^{32} \end{pmatrix}$ $a_1; a_2$	Let $\omega \beta_n = \theta_n = \begin{pmatrix} \theta_{n0} \\ \theta_{n1} \\ \theta_{n2} \end{pmatrix}$ $\omega(\tau R_n)^{-1} \omega^T = S_n =$ $\tau^{-1} \begin{pmatrix} s_{n1}^{11} & s_{n2}^{12} & s_{n3}^{13} \\ s_{n2}^{21} & s_{n2}^{22} & s_{n2}^{23} \\ s_{n3}^{31} & s_{n3}^{32} & s_{n3}^{33} \end{pmatrix}$ $\mu_n = \begin{pmatrix} \theta_{n0} \\ \theta_{n1} \end{pmatrix} -$ $\begin{pmatrix} s_{n3}^{13} \\ s_{n2}^{23} \end{pmatrix} (s_{n3}^{33})^{-1} \theta_{n2}$ $\Sigma_n^{-1} = \begin{pmatrix} s_{n1}^{11} & s_{n2}^{12} \\ s_{n2}^{21} & s_{n2}^{22} \end{pmatrix} -$ $\begin{pmatrix} s_{n3}^{13} \\ s_{n2}^{23} \end{pmatrix} (s_{n3}^{33})^{-1} \begin{pmatrix} s_{n1}^{31} & s_{n2}^{32} \end{pmatrix}$ $a_{1n} = a_1 + n/2$ $a_{2n} = \left(\frac{-\mu_n^T \Sigma_n \mu_n + y^T y}{2} \right)^{-1}$ $\frac{\mu_0^T \Sigma_0 \mu_0}{2} + \frac{1}{a_2} \Big)^{-1}$	$p(y M_i) = \frac{1}{\alpha_2^{\alpha_1} \Gamma(\alpha_1)}$ $\frac{1}{(2\pi)^{n/2} \Sigma_n ^{1/2}}$ $\alpha_{2n}^{\alpha_{1n}} \Gamma(\alpha_{1n})$ where i = dominant, recessive codominant or additive
M_N	$\beta_0 = [\beta_{00}]$ $R_0 = (r_{11})$ a_1 a_2	$\beta_n = R_n^{-1}(R_0\beta_0 + 1^T y)$ $R_n = R_0 + 1^T y$ $\alpha_{1n} = \alpha_1 + n/2$ $\alpha_{2n} = \left(\frac{-\beta_n^T R_n \beta_n + y^T y}{2} \right)^{-1}$ $\frac{\beta_0^T R_0 \beta_0}{2} + \frac{1}{\alpha_2} \Big)^{-1}$	$p(y M_{null}) = \frac{1}{\alpha_2^{\alpha_1} \Gamma(\alpha_1)}$ $\frac{1}{(2\pi)^{n/2} R_0 ^{1/2}}$ $\alpha_{2n}^{\alpha_{1n}} \Gamma(\alpha_{1n})$

Table 3: Specification prior hyper-parameters, updated hyper-parameters, and marginal likelihood for each model. M_P =Polynomial Model, M_G =Genotypic Model, M_D =Dominant Model, M_R =Recessive Model, M_C =Codominant Model, M_A =Additive Model, and M_N =Null Model.

selection criteria. Real genotype data from two GWASs of different sample sizes were used and the quantitative trait in each set was randomly permuted to create data sets with no true positive associations. Simulation study (2) was designed to compare sensitivity and specificity of our proposed method and the standard approach by simulating genetic data that mimic the GWAS setting with causal SNPs (i.e. SNPs truly associated with the trait) having different modes of inheritance, each SNP explaining the same proportion of the trait variability. Simulation (3) modified the design of simulation (2) and let SNPs explain varying proportions of the trait variability.

4.1 Simulation Study (1)

Data: Two real datasets were used. The first data set consisted of genotype data of 201 unrelated offspring of centenarians from the New England Centenarian Study (NECS) (<http://www.bumc.bu.edu/centenarian/>) (Sebastiani and Perls (2012)). The genotype data were described in Sebastiani et al. (2012). The quantitative trait in this analysis was a neuroticism score measured in the NEO-Five Factor Inventory (NEO-FFI), which is a 60-item (12 items per domain) measure of five personality dimensions (neuroticism, extraversion, openness, agreeableness, and conscientiousness) (Costa and McCrae (1992)). Previous studies have shown that the estimated heritability of neuroticism is approximately 25% (Bae et al. (2013); Pilia et al. (2006)). The second data set consisted of 843 unrelated African-American subjects with sickle cell anemia enrolled in the Cooperative Study of Sickle Cell Disease (CSSCD) (<https://biolincc.nhlbi.nih.gov/studies/csscd/>) (Gaston and Rosse (1982)). In this cohort, the trait is the percent of fetal hemoglobin in the total hemoglobin. The percent fetal hemoglobin is a major modulator of hematologic and clinical complications of sickle cell anemia (Akinshaye et al. (2011)). Studies have shown that there is a strong genetic basis of fetal hemoglobin and a well-established gene that affects this trait is *BCL11A* (Bae et al. (2012)). The estimated heritability ranges from 60.9% to 89% (Garner et al. (2000); Pilia et al. (2006)). Both studies were approved by the institutional review board of each participating institution, and standard quality control procedures were performed on both genotype data (Bae et al. (2012); Sebastiani et al. (2012)).

Methods: Initially 254,612 and 486,331 autosomal SNPs were available for analysis in the two cohorts (NECS and CSSCD), respectively. It is well known that SNPs in close proximity tend to be correlated with each other (Slatkin (2008)), and this non-random correlation can bias the assessment of false positive rates. In order to avoid this problem, SNPs whose pairwise correlation was $r^2 > 0.2$ were removed using the PLINK software (Purcell et al. (2007)). After this pruning, 50,894 and 140,864 independent SNPs were left for analysis in the NECS and CSSCD sample, respectively. In both sets, 50,000 SNPs were randomly chosen from each set and 10,000 simulations were performed by permuting the trait values at random. Two approaches were evaluated in this simulation study: 1) the proposed method, in which the best genetic model was selected based on the maximum BF for each SNP; and 2) the frequentist approach, in which five genetic models were fitted and the best model was selected based on the minimum p-value for each SNP. For the genotypic model (2 degrees of freedom) in the frequentist approach, the minimum of the two p-values was chosen. Various threshold criteria for the two approaches were explored and the number of significant associations detected for varying thresholds was recorded. False positive rates were computed as the rates of significant associations.

4.2 Simulation Study (2)

Data: In order to assess the true positive rates of our proposed method and the standard approach, genetic data were simulated with known causal SNPs, each explaining the same proportion of the trait variance. A modification of the simulation procedure

described in Yip and Lange (2011) was used to simulate the data but an additional source of variability was introduced as well as SNPs with dominant and recessive mode of inheritance, in addition to additive effects. Several scenarios were considered by using different sample sizes ($N=1,000, 10,000, 20,000, 50,000,$ and $100,000$) and different heritability (Ober et al. (2001)) of the quantitative traits ($h^2=0.2, 0.4,$ and 0.6). Heritability is defined as the proportion of the total variance of the trait that is explained by the genetic effect and the higher the heritability the larger the genetic contribution to the trait. A total of 500,000 SNPs were simulated in each run and included 100 causal SNPs: 34 with additive effects, 33 with dominant effects, and 33 with recessive effects. We assumed that each causal SNP explained 1/100 of the total genetic variance so that, for example, when the total heritability was 0.2 and 20% of the total phenotypic variance was due to the genetic variance, each causal SNP explained 1/100 of the total genetic variance and hence the SNP-specific heritability was 0.002.

Methods: The following steps describe the simulation scheme.

Step 1. Generate minor allele frequency for each SNP

The minor allele frequency (MAF: frequency of B allele) for each SNP was randomly drawn from a Beta distribution $Beta(2, 8)$, which represents the distribution of commercially available chips (Yip and Lange (2011)). We also used a standard quality control procedure by excluding any SNPs with MAF less than 0.01.

Step 2. Generate the genotype

Genotypes for each SNP (AA, AB, BB) were generated assuming Hardy-Weinberg equilibrium. Essentially, if p is the prevalence of the A allele in the population, Hardy-Weinberg equilibrium (HWE) law states that the prevalence of the three genotypes will be $p^2, 2p(1-p), (1-p)^2$ (Weinberg (1908)). These expected genotype frequencies were used to simulate the genotype data, given p .

Step 3. Select the causal SNPs

100 causal SNPs from the total SNPs were randomly chosen and assigned the mode of inheritance randomly to the selected SNPs.

Step 4. Determine the effect size for each causal SNP

The effect size a_j for each j^{th} causal SNP ($j=1, 2, \dots, 100$) was computed from the formula:

$$h_j^2 = \frac{\sigma_{Add,j}^2 + \sigma_{Dom,j}^2}{\sigma_{Total}^2} = \frac{2p_j(1-p_j)[a_j + d_j(1-2p_j)]^2 + [2p_j(1-p_j)d_j]^2}{\sigma_{Total}^2}$$

where $\sigma_{Add,j}^2$ is the additive genetic variance of the j^{th} causal SNP, $\sigma_{Dom,j}^2$ is the dominance genetic variance of the j^{th} causal SNP, σ_{Total}^2 is the total phenotypic variance, p_j is the MAF for the j^{th} causal SNP, a_j is the additive genetic effect at the j^{th} causal SNP, and d_j is the dominance genetic effect at the j^{th} causal SNP. The parameter h_j^2 is the locus-specific heritability, which was assumed to be $\frac{h^2}{100}$. This is the amount of heritability that is contributed by the j^{th} causal SNP and hence all causal SNPs contribute to the total heritability by an equal amount. In the above formula, note that the genetic variance is decomposed into the additive and dominance variance component.

The additive genetic variance implies that each additional copy of an allele contributes a fixed amount of effect a_j to the trait. Under this assumption, the trait value of the heterozygote (AB) would be the midpoint between the two homozygotes (AA and BB). On the other hand, when there exists dominance genetic variance, the trait value of the heterozygote will deviate from the midpoint between the two homozygotes, and the degree of deviation is expressed by the quantity d_j . Therefore, it follows that $d_j = 0$ for any SNP with additive effect, and $d_j = a_j$ for any SNP with dominant effect, and $d_j = -a_j$ for any SNP with recessive effect. We also assumed $\sigma_{Total}^2 = 1$. Note that only the three genetic models (additive, dominant, and recessive) were considered.

Step 5. Generate the phenotypic value based on the causal SNPs

Let y_i denote the phenotypic value for i^{th} individual. For each causal SNP, the SNP contribution to the trait was randomly generated as

$$X_{ij} \sim N(a_j G_{ij}, \frac{\sigma_{Total}^2}{100})$$

where a_j is the effect of the j^{th} causal SNP (computed in the previous step) and G_{ij} is genotype coding for the i^{th} individual at the j^{th} causal SNP that was generated in Step 2. For an additive causal SNP, G_{ij} = number of minor allele (0, 1, 2). For a dominant causal SNP, $G_{ij} = 1$ if the genotype is AB or BB (0 otherwise). For a recessive causal SNP, $G_{ij} = 1$ if the genotype is BB (0 otherwise). Then, the phenotypic value is:

$$y_i = \sum_j X_{ij}$$

and $E(y_i) = \sum_j a_j G_{ij}$ and $Var(y_i) = \sigma_{Total}^2 = 1$.

Step 6. Perform association tests using our method and the standard approach

Step 7. Repeat 100 times

In each simulated data set, the empirical false positive rates in the two approaches were evaluated to determine thresholds for p-values and BF with the same false positive rates. Specifically, in each simulated set the number of false positive associations (significant associations of null SNPs) in the frequentist results with p-values $p < 1 \times 10^{-7}$, 5×10^{-7} , 1×10^{-6} , and 5×10^{-6} were counted and the BF thresholds that produced the same number of false positive associations in the Bayesian approach were detected. Using these p-values and BF thresholds that produced the same empirical false positive rates, the power of the two approaches was evaluated. Two types of power were considered: (1) the number of causal SNPs detected as associated regardless of whether the correct genetic model was identified and (2) the number of causal SNPs detected with the true genetic model.

4.3 Simulation Study (3)

Data and Methods: The limitation of Simulation Study (2) is the assumption that each SNP accounts for the same proportion of the trait variability. Therefore, the scheme of the Simulation Study (2) was modified to let causal SNPs explain varying proportions

of the trait variability. In this modified design, the genetic variances of dominant and recessive SNPs were increased, while decreasing the genetic variance of additive SNPs. This trade-off was necessary to maintain the same total heritability used in Simulation Study (2) for proper comparison later. The following two cases were considered: 1) when h_j^2 was halved for additive SNPs and 2) when h_j^2 was quartered for additive SNPs. In case 1), this resulted in increasing h_j^2 by 25% for both dominant and recessive SNPs. In case 2), this resulted in increasing h_j^2 by 37.5% for both dominant and recessive SNPs. Under these changes, the effect sizes were generated based on Step 4 in the previous section and the rest of the simulation design remained the same.

a) Bayesian Polynomial Model Approach

	BF>100	BF> 500	BF>1000	BF>1500	BF>3000	BF>5000
NECS data	9.0×10^{-4}	1.4×10^{-4}	8.0×10^{-5}	4.0×10^{-5}	2.0×10^{-5}	0.0×10^{-0}
CSSCD data	6.8×10^{-4}	1.2×10^{-4}	6.0×10^{-5}	4.0×10^{-5}	2.0×10^{-5}	0.0×10^{-0}

b) Frequentist Approach

	$p < 10^{-3}$	$p < 10^{-4}$	$p < 10^{-5}$	$p < 10^{-6}$	$p < 10^{-7}$	$p < 10^{-8}$
NECS data	3.4×10^{-3}	4.0×10^{-4}	4.0×10^{-5}	0.0×10^{-0}	0.0×10^{-0}	0.0×10^{-0}
CSSCD data	3.3×10^{-3}	3.8×10^{-4}	4.0×10^{-5}	0.0×10^{-0}	0.0×10^{-0}	0.0×10^{-0}

Table 4: Median false positive rates in the NECS and CSSCD data in 10000 permutations (Simulation Study 1). BF=Bayes Factor; p=p-value.

Results: Table 4 shows the median false positive rates at varying significance thresholds in the two sets included in Simulation Study (1). Setting the thresholds to maximum BF > 1500 in our approach and minimum p-value < 10^{-5} in the standard approach yields the same median false positive rate of 4×10^{-5} in both data sets. This translates into 2 false positive associations among 50,000 SNPs.

Figures 1-3 summarize the results of Simulation Study (2) for the scenario in which the total heritability is 0.4 and the sample sizes are 10,000, 20,000, and 50,000. The full set of results can be found in the Supplementary Materials. With a sample of 1000, neither approach detects any causal SNPs, while almost all causal SNPs are detected when the sample size is 100,000, regardless of the heritability. Figure 1 shows the distribution of the empirical false positive rate for different p-value thresholds and Figure 2 shows the distribution of the BF that would produce the same empirical false positive rates of the frequentist procedure. Figure 3 shows the box plot of the true positive rate (proportion of detected causal SNPs) of the two approaches at varying significance thresholds. Finally, Table 5 shows the mean number of additive, dominant, and recessive SNPs that are correctly identified (out of 34, 33, and 33, respectively) in the two approaches at successive thresholds.

The mean and standard deviation of the quantitative traits were 2.55 and 1.10 when the total heritability was 0.4. Several points are noteworthy. The first point is that, as

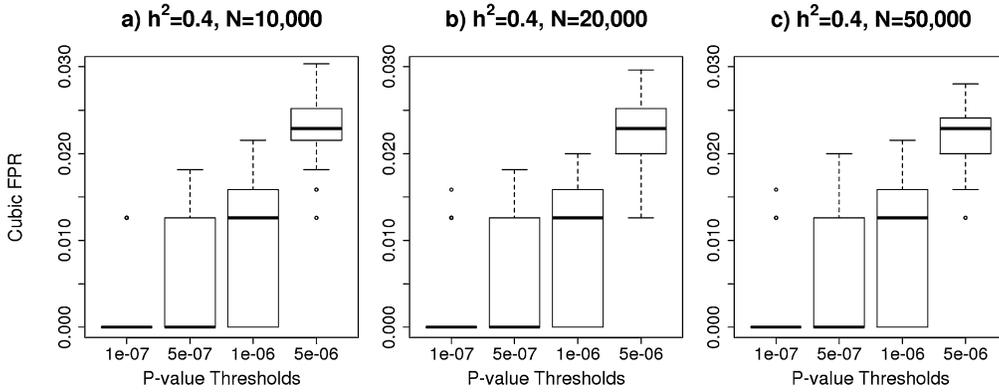


Figure 1: Box plot of cubic root of empirical false positive rates (y-axis) for different p-value thresholds (x axis), and increasing sample sizes. The results are based on the simulation scenario when the heritability was 0.4 and the sample sizes were 10,000, 20,000, and 50,000 (panel a, b, and c, respectively).

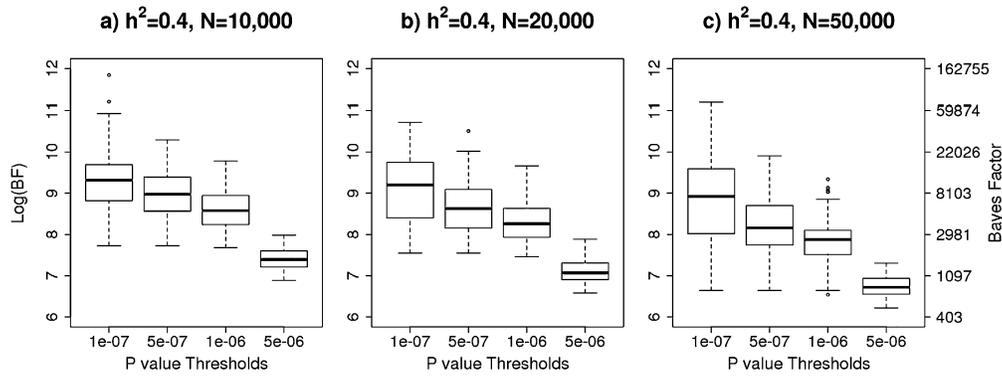


Figure 2: Box plot of log-transformed BF (y-axis) for different p-values thresholds (x-axis) and increasing sample sizes. The results are based on the simulation scenario when the heritability estimate was 0.4 and the sample sizes were 10,000, 20,000, and 50,000 (panel a, b, and c respectively).

expected, lower heritability of the trait results in a smaller number of detections. Even when the total heritability was relatively high ($h^2=0.6$), both approaches detected about half of the causal SNPs with $N=10,000$. At the most stringent significance threshold of $p < 1 \times 10^{-7}$, the Bayesian approach correctly identified 53.75 causal SNPs on average and the frequentist approach correctly identified 46.52 causal SNPs on average when heritability is 0.6 and N is 20,000 (see Supplementary Materials for detail). This result is consistent with findings from other authors that large sample sizes are needed to

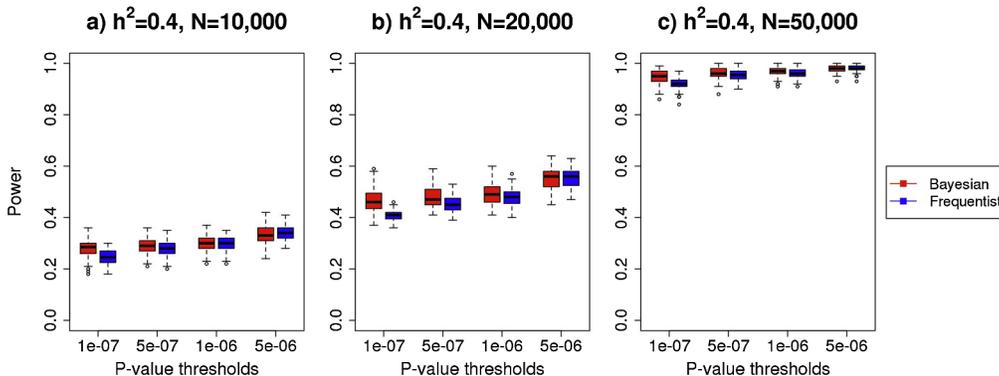


Figure 3: Box plot of power of the two approaches at different significance thresholds (Red: Bayesian approach; Blue: Frequentist approach). The results are based on the simulation scenario when the heritability estimate was 0.4 and the sample sizes were 10,000, 20,000, and 50,000 (panel a, b, and c, respectively).

detect many casual variants that explain a small proportion of variability. For example, in Park et al. (2010) authors have shown that they need approximately $N=25,000$ to detect 25 loci out of 201 causal variants with 80% power for a highly heritable trait.

Secondly, we observed that the false positive rate of decision rules based on BF decreases as the sample size increases, given a fixed BF threshold. This property has also been noted in Matthews (2011) and Wakefield (2012) and implies that we can relax the thresholds for BF as we increase the sample size and better leverage the increased sample size than frequentist procedures. Figure 2 illustrates this property graphically. For example, at a fixed p-value threshold 1×10^{-7} , the median BF threshold needed to obtain the same false positive rate decreases from 11122 to 9866 to 7489 as the sample size increases from 10,000 to 20,000 to 50,000. A similar pattern is observed at all levels of false positive rates. In contrast, no such pattern is observed in the frequentist approach, and the false positive rates are invariant to sample sizes given a fixed p-value threshold in the standard approach.

The third important point is that the Bayesian method we propose has a slightly greater power for more stringent (lower) thresholds (see Figure 3) than the frequentist approach. This result holds for all sample sizes and all levels of heritability considered in the simulations (see Supplement Figures S3 and S6). Also, at this stringent threshold, the Bayesian approach recovered more correct genetic models when the sample sizes were 20,000 and 50,000 (Table 5). Although our method recovers less often than the frequentist approach SNPs with an additive genetic effect, it identifies more often SNPs with a dominant and recessive effect. When the sample size was 10,000, the Bayesian approach recovered slightly fewer genetic models. In addition, both approaches identified nearly 0 models that had either dominant or recessive inheritance pattern when $N=10,000$ in simulation study (2). We speculated that this may be due to the lack of power to detect rare variants. For example, if we assume $MAF=0.01$, under HWE the

		Bayesian				Frequentist				
	N	Significance Threshold	A	D	R	Total	A	D	R	Total
Simulation Study (2) - Uniform Contribution	10000	1×10^{-7}	15.6	0.7	0.9	17.2	17.3	0.3	0.3	17.9
		5×10^{-7}	16.0	0.8	1.0	17.7	19.8	0.6	0.6	21.0
		1×10^{-6}	16.3	0.9	1.2	18.4	20.8	0.7	0.8	22.3
		5×10^{-6}	17.5	1.3	1.9	20.7	22.4	1.1	1.6	25.2
	20000	1×10^{-7}	25.0	4.9	6.4	36.3	28.2	2.4	3.5	34.2
		5×10^{-7}	25.0	5.6	7.5	38.0	28.2	4.1	5.4	37.7
		1×10^{-6}	25.0	6.2	8.1	39.3	28.2	4.9	6.6	39.7
		5×10^{-6}	25.0	8.8	11.0	44.8	28.3	7.5	10.1	45.9
	50000	1×10^{-7}	30.0	27.1	30.5	87.6	31.2	23.2	28.6	82.9
		5×10^{-7}	30.0	27.6	31.1	88.8	31.2	24.4	30.3	85.8
		1×10^{-6}	30.0	27.8	31.4	89.3	31.2	24.6	31.0	86.7
		5×10^{-6}	30.0	28.5	32.0	90.5	31.2	25.4	31.9	88.5
Simulation Study (3) - Case 1)	10000	1×10^{-7}	3.5	1.4	1.9	6.8	3.2	0.7	0.8	4.7
		5×10^{-7}	3.8	1.5	2.1	7.4	4.9	1.0	1.4	7.3
		1×10^{-6}	4.1	1.8	2.4	8.3	5.7	1.3	1.8	8.9
		5×10^{-6}	5.5	2.9	3.7	12.0	8.5	2.5	3.2	14.2
	20000	1×10^{-7}	16.5	10.4	13.1	40.0	18.9	6.3	8.1	33.2
		5×10^{-7}	17.0	11.5	14.5	43.1	21.2	9.0	11.5	41.7
		1×10^{-6}	17.4	12.3	15.4	45.1	21.9	10.2	13.3	45.4
		5×10^{-6}	18.5	14.7	18.7	51.9	23.6	12.9	17.7	54.2
	50000	1×10^{-7}	26.3	29.4	32.7	88.4	29.0	26.6	32.2	87.8
		5×10^{-7}	26.3	29.4	32.8	88.5	29.0	26.8	32.6	88.4
		1×10^{-6}	26.3	29.5	32.8	88.7	29.0	26.9	32.7	88.5
		5×10^{-6}	26.3	29.5	32.9	88.8	29.0	26.9	32.9	88.8
Simulation Study (3) - Case 2)	10000	1×10^{-7}	0.3	2.0	2.8	5.1	0.2	0.9	1.1	2.2
		5×10^{-7}	0.3	2.3	3.1	5.7	0.5	1.7	2.1	4.2
		1×10^{-6}	0.4	2.6	3.4	6.3	0.6	2.1	2.7	5.5
		5×10^{-6}	0.7	3.9	5.0	9.6	1.2	3.5	4.5	9.2
	20000	1×10^{-7}	3.9	13.5	16.8	34.2	3.4	8.8	11.2	23.5
		5×10^{-7}	4.4	14.5	18.0	36.9	5.3	11.7	15.2	32.2
		1×10^{-6}	4.8	15.2	19.0	39.0	6.4	12.7	16.9	35.9
		5×10^{-6}	6.3	17.8	22.3	46.4	9.3	15.6	21.4	46.3
	50000	1×10^{-7}	20.9	29.7	32.9	83.5	24.2	27.4	32.7	84.3
		5×10^{-7}	21.3	29.7	32.9	84.0	25.3	27.5	32.9	85.6
		1×10^{-6}	21.5	29.7	33.0	84.2	25.6	27.5	33.0	86.0
		5×10^{-6}	21.8	29.7	33.0	84.5	26.1	27.5	33.0	86.5

Table 5: Mean number of additive, dominant, and recessive SNPs correctly identified (out of 34, 33, and 33, respectively) in the two approaches when heritability is 0.4. A=additive; D=dominant; R=recessive.

expected count of the homozygote group for the minor allele is only 1. As the sample size increased, there was a substantial increase in identification of dominant and recessive variants. Results from simulation study (3) also support this conjecture. Increased effect sizes for SNPs with dominant and recessive effects resulted in more detection of these variants at the cost of loss of power for additive SNPs. However, loss of power for additive SNPs was much greater than increased power for dominant and recessive SNPs when the sample size was 10,000. This result suggests that we need much higher sample sizes to detect dominant and recessive variants, compared to the additive SNPs.

5 Application to Real Data

Using the thresholds that yielded the same false positive rate in the two methods (maximum $\text{BF} > 1500$ and minimum $p < 1 \times 10^{-5}$) in simulation study (1), we compared the results obtained with the two methods in the cohorts described in the earlier section, using the SNP sets generated after pruning the dependent SNPs. In the NECS data, out of 50,894 tested SNPs, nine SNPs were found associated with neuroticism using the polynomial model approach, whereas only five SNPs were significant using the standard approach (Table 6). Four SNPs were common in both analyses. For these four SNPs, the genetic models selected agreed in the two approaches. This result suggests that the Bayesian model selection procedures work well in the case of small sample sizes and can potentially discover more variants.

In the CSSCD data, out of 140,864 tested SNPs, ten SNPs were associated with fetal hemoglobin in both approaches, and eight SNPs were common in both (Table 6). For these eight SNPs in common, five of them agreed in the genetic model selection between the two approaches, but three SNPs (rs2239580, rs12469604, and rs2034614) had discrepant results. For rs2239580, the Bayesian procedures selected the dominant model, while the standard approach identified the genotypic model. For rs12469604, the Bayesian procedure selected the dominant model, while the additive model had the minimum p-value. For rs2034614, the co-dominant model had the maximum BF and the genotypic model had the minimum p-value.

Using our Bayesian polynomial model approach in the NECS data, 4 SNPs had dominant models, 3 SNPs had additive models, 1 SNP had a co-dominant model and 1 SNP had a recessive model. In the CSSCD data, 3 SNPs had dominant models, 3 SNPs had co-dominant models, 3 SNPs had recessive models, and 1 SNP had an additive model. These results suggest that different variants may influence the trait through different genetic models. Some of these associations would not have been captured if an additive model alone was used, and this highlights the need to examine all possible genetic models in a computationally efficient manner to ensure that we do not miss any interesting findings.

6 Conclusion

We propose a Bayesian approach to simultaneously detect the SNPs associated with a continuous trait and the mode of inheritance. Our Bayesian approach uses a polynomial parameterization of the SNP dosage that can simultaneously represent different genetic models and a coherent framework for model selection based on comparing different models by their posterior probability (The Wellcome Trust Case Control Consortium (2007); Marchini et al. (2007); Servin and Stephens (2007); Guan and Stephens (2008); Wakefield (2008); Newcombe et al. (2009); Stephens and Balding (2009); Clark et al. (2010); Lorenzo Bermejo et al. (2011); Maller et al. (2012); Xu et al. (2012)). Crucial to our approach is the use of proper prior distributions on the parameters of the polynomial model, from which the prior distributions of specific genetic models can be derived. In contrast to this coherent Bayesian approach, it is important to emphasize

a) NECS Data								
Bayesian								
SNP	Chr/Gene	BF_G	BF_A	BF_D	BF_R	BF_C	BF_{max}	
rs850610	1/C1orf203	1.0e5	8.0e4	1.2e6	1.5e1	1.5e3	1.2e6	
rs7666974	4/unknown	7.6e2	1.4e-1	7.4e1	7.5e1	1.2e4	1.2e4	
rs2333166	4/unknown	4.6e2	3.9e2	3.4e3	3.8e-1	1.5e3	3.4e3	
rs2801185	1/ESRRG	2.2e2	4.4e1	4.9e-1	2.0e3	4.0e-1	2.0e3	
rs1869676	8/unknown	1.4e3	5.0e3	1.0e1	2.0e3	3.7e1	5.0e3	
rs8064944	17/unknown	2.2e2	1.0e1	4.3e3	2.9e-1	4.4e-1	4.3e3	
rs3746314	19/C19orf12	1.8e3	2.4e3	9.4e2	3.7e1	9.9e-1	2.4e3	
rs9555139	13/unknown	6.5e2	2.2e3	6.7e1	1.5e2	1.5e1	2.2e3	
rs12770017	10/unknown	1.4e2	3.0e-1	1.9e3	1.2e-1	1.9e1	1.9e3	
rs1530239	2/IKZF2	7.9e1	5.8e1	7.0e-1	2.1e1	5.9e1	5.9e1	
Frequentist								
SNP	Chr/Gene	P_{Het}	P_{Hom}	P_A	P_D	P_R	P_C	P_{min}
rs850610	1/C1orf203	2.0e-7	2.4e-4	2.5e-7	1.9e-8	3.3e-2	2.1e-5	1.9e-8
rs7666974	4/unknown	8.4e-4	7.7e-1	1.5e-1	5.3e-2	6.9e-4	1.9e-6	1.9e-6
rs2333166	4/unknown	5.8e-6	2.3e-1	5.5e-5	5.5e-6	4.4e-1	8.7e-6	5.5e-6
rs2801185	1/ESRRG	7.3e-1	3.1e-6	1.9e-3	1.0e-1	2.8e-6	6.2e-1	2.8e-6
rs1869676	8/unknown	8.1e-1	1.5e-1	3.5e-4	2.4e-1	1.1e-4	3.2e-4	1.1e-4
rs8064944	17/unknown	4.0e-4	2.7e-4	2.2e-2	2.1e-4	2.8e-1	5.2e-1	2.1e-4
rs3746314	19/C19orf12	2.2e-2	1.5e-3	8.8e-4	2.2e-3	6.0e-3	1.0e-1	8.8e-4
rs9555139	13/unknown	4.2e-1	6.2e-2	8.2e-3	7.0e-2	1.2e-2	6.1e-2	8.2e-3
rs12770017	10/unknown	2.6e-4	1.1e-3	9.6e-1	7.9e-4	3.8e-1	6.0e-2	2.6e-4
rs1530239	2/IKZF2	3.5e-2	1.4e-3	3.7e-6	3.1e-3	2.3e-5	5.0e-4	3.7e-6
b) CSSCD Data								
Bayesian								
SNP	Chr/Gene	BF_G	BF_A	BF_D	BF_R	BF_C	BF_{max}	
rs6709302	2/BCL11A	1.7e4	1.9e5	7.4e3	3.8e2	2.1e1	1.9e5	
rs7631659	3/unknown	1.2e4	3.4e1	4.4e-1	1.6e5	2.2e-1	1.6e5	
rs13043968	20/unknown	1.9e3	1.2e1	2.5e-1	3.1e4	2.1e-1	3.1e4	
rs2239580	14/COCH	2.5e3	1.1e3	3.0e4	1.5e-1	2.8e4	3.0e4	
rs6932510	6/RPS6KA2	5.9e2	2.1e3	5.9e3	3.1e-1	3.7e3	5.9e3	
rs1890911	14/unknown	2.5e2	8.5e-1	1.5e-1	4.4e3	3.3e-1	4.4e3	
rs12469604	2/unknown	6.1e2	2.2e3	2.9e3	6.3e-1	1.8e3	2.9e3	
rs2034614	12/PRICKLE1	1.8e2	1.5e2	1.7e3	1.6e-1	2.8e3	2.8e3	
rs2301819	4/TBC1D14	8.4e1	5.0e1	1.9e2	1.9e-1	2.0e3	2.0e3	
rs9642124	7/unknown	3.8e1	4.8e-2	3.2e1	9.2e-1	1.8e3	1.8e3	
rs11794652	9/FUBP3	9.9e1	4.2e2	5.2e1	6.0e2	2.1e-1	6.0e2	
rs7975463	12/unknown	3.5e1	1.3e1	1.8e2	8.4e-2	8.9e2	8.9e2	
Frequentist								
SNP	Chr/Gene	P_{Het}	P_{Hom}	P_A	P_D	P_R	P_C	P_{min}
rs6709302	2/BCL11A	1.2e-4	2.5e-7	1.3e-8	8.0e-7	2.6e-5	1.5e-2	1.3e-8
rs7631659	3/unknown	9.1e-1	7.6e-8	7.0e-3	1.5e-1	7.5e-8	9.2e-1	7.5e-8
rs13043968	20/unknown	8.9e-1	5.4e-7	2.1e-2	2.8e-1	4.9e-7	6.7e-1	4.9e-7
rs2239580	14/COCH	1.7e-7	2.1e-1	4.9e-6	2.3e-7	5.7e-1	3.2e-7	1.7e-7
rs6932510	6/RPS6KA2	4.9e-6	2.5e-1	6.4e-6	3.3e-6	3.9e-1	6.5e-6	3.3e-6
rs1890911	14/unknown	6.7e-1	4.7e-6	1.5e-2	3.7e-1	2.6e-6	2.5e-1	2.6e-6
rs12469604	2/unknown	1.2e-5	2.3e-1	6.6e-6	7.2e-6	2.8e-1	1.4e-5	6.6e-6
rs2034614	12/PRICKLE1	7.7e-6	5.6e-1	9.4e-5	1.2e-5	8.7e-1	9.0e-6	7.7e-6
rs2301819	4/TBC1D14	1.9e-5	7.0e-1	3.5e-3	1.3e-4	3.7e-1	1.3e-5	1.3e-5
rs9642124	7/unknown	4.0e-4	8.7e-1	9.8e-1	1.6e-2	1.4e-2	1.6e-5	1.6e-5
rs11794652	9/FUBP3	9.9e-2	3.3e-6	7.9e-6	2.8e-3	1.1e-5	4.8e-1	3.3e-6
rs7975463	12/unknown	7.6e-6	2.8e-1	6.5e-3	4.6e-5	6.2e-1	1.2e-5	7.6e-6

Table 6: Significant results using two approaches in the a) NECS and b) CSSCD data. BF=Bayes Factor ;P=p-value; G=genotypic; A=additive; D=dominant; R=recessive; C=co-dominant; Het=heterozygote genotype factor in the genotypic model; Hom=homozygote genotype factor in the genotypic model. SNPs that were significant in both approaches are highlighted in gray.

that the frequentist approach does not have a clear way to compare the genotypic model (2 degrees of freedom) to the other four specific genetic models (1 degree of freedom). The evaluation of the method in simulated data shows that the Bayesian method we propose has a slightly higher power when we limit to false positive rates at very small values and this is a particularly attractive property in genome-wide association studies in which the large number of SNPs analyzed requires to set the false positive rate to extremely small numbers. An additional attractive feature of this method is the gain in computations: The proposed method codes five genetic models simultaneously using a single polynomial parameterization instead of fitting five different genetic models for each SNP. This contrasts with the standard approach in which recoding of the SNP genotype and conducting 5 analyses is necessary to evaluate all five models concurrently.

An important theoretical implication of this particular parameterization is that it shows that different genetic models are functionally related. We have shown that there is a mathematical relationship between the parameters of the polynomial model and each of the five genetic models. This relation also suggests that when all five genetic models are evaluated the effective number of tests per SNP is less than 5. In practice, GWASs suffer from severe correction for multiple testing, and evaluation of several genetic models for each SNP aggravates this issue. However, our work suggests that the correction for multiple testing should be less severe as the effective number of tests is less than the number of models fitted, when evaluating all five genetic models, although it is not immediately obvious how Bonferroni type corrections should benefit from this result.

The proposed work can be particularly useful for genome-wide data consisting of millions of SNPs. This work, at the current state, is limited to the case where the trait is quantitative, as we can obtain closed form solutions for the marginal likelihood and BF. More work is needed to evaluate a similar approach when the trait of interest is binary or time-to-event. In particular, when performing logistic regression in the GWAS context, alternative measures of associations such as approximate Bayes Factor or Bayesian false-discovery probability (Wakefield (2007, 2008, 2009)) can be considered.

Supplementary Material

Supplementary Materials: Bayesian Polynomial Regression Models to Fit Multiple Genetic Models for Quantitative Traits (DOI: [10.1214/14-BA880SUPP](https://doi.org/10.1214/14-BA880SUPP); .pdf).

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