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JOINT TEST OF PARAMETRIC AND NONPARAMETRIC EFFECTS IN PARTIAL LINEAR MODELS FOR GENE-ENVIRONMENT INTERACTION

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Abstract: Gene-environment (G×E) interactions play a crucial role in many complex diseases. Many studies have highlighted the importance of the linear and nonlinear effects of G×E interactions to the risk of contracting diseases. Linear effects can be modeled parametrically, whereas nonlinear effects are typically modeled and estimated using nonparametric functions under the framework of partial linear models. Because of the difference in the rates of convergence of the parametric and nonparametric parts, few statistical studies have assessed the simultaneous effects of the linear and nonlinear effects of G×E interactions in the context of a partial linear model. In this study, we consider a hypothesis test to simultaneously detect the linear and nonlinear effects in a generalized partial linear varying-coefficient model. We propose a B-spline backfitted kernel method to estimate the effect of nonlinear interactions. A Wald-type statistic is constructed for the joint testing problem based on the nonparametric generalized likelihood ratio statistic. We show that the joint test statistic asymptotically follows a χ^2-distribution under the null hypothesis of no G×E interaction effect, and a noncentral χ^2-distribution under the alternative. Moreover, the proposed test can simultaneously detect alternatives at optimal rates for both the parametric and the nonparametric components. The utility of the method is demonstrated using extensive simulations and a case study.

Key words and phrases: B-spline back-fitting, genetic association, non-linear G×E interaction, partial linear effect.

1. Introduction

A gene-environment (G×E) interaction is defined as a phenomenon in which the influence of genotypes on phenotypes is different under different environmental conditions (Falconer (1952)). Such interactions are key drivers of epigenetic effects. A growing number of reports have confirmed the role of G×E interaction in many diseases, such as Parkinson's disease (Ross and Smith (2007)) and type-2 diabetes (Zimmet, Alberti and Shaw (2001)). Although linear G×E effects are commonly assumed in many statistical analyses, there is increasing evidence

of nonlinear effects of G×E interactions on the risk of disease (Martinez et al. (2003); Sparrow et al. (2012)). Certain methods for detecting nonlinear G×E effects (e.g., Ma et al. (2011); Wu and Cui (2013)) involve applying varying-coefficient (VC) models to model the effects of nonlinear interactions. A key feature of the VC model is its flexibility in capturing the dynamics of gene effects over a spectrum of environmental changes.

A typical genetic study on G×E interactions collects both continuously and discretely measured environmental variables. For example, a mother's nutrition intake can be considered a continuously measured environmental variable, whereas gender or a person's smoking status can be regarded as a discrete variable when studying the effects of G×E interactions on birth weight. Discrete environmental variables, such as smoking status, do not interact with genes nonlinearly, whereas continuous environmental variables can do so (Ma et al. (2011)). When both types of interactions are considered in a model, a partial linear VC model (PLVCM) can be applied to study the linear and nonlinear effects of G×E interactions, where the former are typically modeled and estimated nonparametrically. Zhang, Lee and Song (2002) considered the PLVCM by introducing a two-step estimation procedure, proposing a root n-consistent estimator for the parametric component. Fan and Huang (2005) proposed a profile likelihood method to estimate parameters based on a local linear method. The PLVCM has been extended to a generalized partially linear VC model (GPLVCM) by Lu (2008) when the response is discrete. Fan and Zhang (2008) reviewed the statistical methods for the VCM and PLVCM, including applications of the VCM to survival, longitudinal, and functional data, as well as time series data.

Let Y be a disease trait that can be quantitative or qualitative. We consider the following GPLVCM:

$$\eta(\mathbf{V};\boldsymbol{\alpha},\boldsymbol{\beta}) = g\{\mu(\mathbf{V})\} = \mathbf{Z}^T\boldsymbol{\alpha}_0 + \beta_0(U) + \{\mathbf{X}^T\boldsymbol{\alpha}_1 + \beta_1(U)\}G, \tag{1.1}$$

where $g\{\cdot\}$ is a given link function; $\mu(\mathbf{V})$ is the conditional mean regression function of Y, given $\mathbf{V} = (\mathbf{Z}, U, G)$, where $\mathbf{Z} = (Z_1, \ldots, Z_q)^T$ is a q-dimensional covariate vector containing both discrete and continuous variables; U is a continuously measured environmental variable of interest; and $\mathbf{X}$ is a p-dimensional vector that is a subset of $\mathbf{Z}$. This vector contains environmental variables that show the linear interactions with G that affects Y, where G is a gene variable (e.g., SNP). In addition, $\boldsymbol{\alpha}_0$ and $\boldsymbol{\alpha}_1$ are parametric coefficients, and $\beta_0(u)$ and $\beta_1(u)$ are nonparametric functions. In particular, $\boldsymbol{\alpha}_1$ models the linear $G \times X$ interaction effect and $\beta_1(u)$ models the nonlinear $G \times U$ effect. These form our

primary focus.

Several methods have been developed to estimate the parameters in model (1.1) based on a local likelihood, such as the two-step estimation procedure (Zhang, Lee and Song (2002)) and the profile likelihood method (Fan and Huang (2005)), which iteratively estimate the linear and nonlinear parts and is very time consuming. These procedures are needed to smooth the bandwidth when the nonparametric component is estimated by a local likelihood. In this study, we propose estimating the linear and the nonparametric parts in two stages using the B-spline backfitted kernel smoothing (BSBK) procedure introduced by Wang and Yang (2007). The BSBK is a two-stage method. In the first stage, we estimate the linear part by approximating the nonparametric functions with B-spline bases. Then, the nonparametric functions can be obtained componentwise, based on the local likelihood, when the linear part and the other components of the nonparametric functions from the B-spline estimation are plugged in. Liu, Yang and Härdle (2013) studied a generalized additive model using the BSBK, which was later extended by Ma and Song (2015) to estimate the varying-index coefficient model. Liu, Cui and Li (2016) applied the BSBK to study a partial linear varying multi-index coefficients model for G×E interactions. The BSBK is considerably faster than the existing two-step method and the profile likelihood method without the requirement of under-smoothing.

Statistical inferences have been studied extensively for the VCM and PLVCM, but these studies deal separately with the parametric and nonparametric components. In our study, the test for the parametric component is formulated as,

$$H_0^P : \boldsymbol{\alpha}_1 = \mathbf{0} \text{ v.s. } H_1^P : \boldsymbol{\alpha}_1 \neq \mathbf{0}. \tag{1.2}$$

The likelihood ratio test statistic (LRT) can be applied (see Fan and Huang (2005); Fan and Zhang (2008)), and has been shown to be asymptotically χ^2-distributed with p degrees of freedom. It is also interesting to assess the interaction between U and G, and to determine whether any nonlinear interactions exist. This results in the following nonparametric component test problem:

$$H_0^{NP} : \beta_1(\cdot) = \mathbf{0} \text{ v.s. } H_1^{NP} : \beta_1(\cdot) \neq \mathbf{0}. \tag{1.3}$$

Fan and Huang (2005) proposed a generalized likelihood ratio statistic (GLRT) that extended the GLRT for the VC model (Fan, Zhang and Zhang (2001); Cai, Fan and Li (2000)). They proved that the GLRT under the null hypothesis converges to a normal distribution, and can be asymptotically approximated by a χ^2-distribution that reveals Wilk's phenomenon for nonparametric and semiparametric models. Because of the difference in the rates of convergence between the

parametric ($\boldsymbol{\alpha}_1$) and the nonparametric parts ($\beta_1(\cdot)$), simultaneous inferences of the effects of linear and nonlinear interactions have not been studied thus far.

In this work, we assess the overall effects of G×E interactions: that is, we simultaneously determine whether $\boldsymbol{\alpha} = \mathbf{0}$ and $\beta_1(\cdot) = \mathbf{0}$. We frame this joint test problem as follows:

$$H_0^{PNP} : \boldsymbol{\alpha}_1 = \mathbf{0}, \beta_1(\cdot) = \mathbf{0} \text{ v.s. } H_1^{PNP} : \boldsymbol{\alpha}_1 \neq \mathbf{0} \text{ or } \beta_1(\cdot) \neq 0. \tag{1.4}$$

The challenge posed by the joint test is that the parametric and nonparametric components have different convergence rates. We can easily obtain the $\sqrt{n}$-consistent parametric estimator $\widehat{\boldsymbol{\alpha}}_1$, but cannot do so for the nonparametric estimator $\widehat{\boldsymbol{\beta}}_1(\cdot)$. Recently, Cheng and Shang (2015) proposed a joint test for the parametric and nonparametric functions at fixed points, instead of assessing the functions entirely. Their testing problem is defined as

$$H_0 : \boldsymbol{\alpha}_1 = \mathbf{0}, \beta_1(u_0) = \beta_1^0(u_0) \text{ vs. } H_1 : \boldsymbol{\alpha}_1 \neq \mathbf{0} \text{ or } \beta_1(\mathrm{u}_0) \neq \beta_1^0(\mathrm{u}_0),$$

where u_0 is a given fixed point and $\beta_1^0(\cdot)$ is a given function. In our setting, the test for the function at some given points is not meaningful. We are more interested in testing whether the entire function is zero. This motivates our joint hypothesis test defined in (1.4).

The remainder of this paper is organized as follows. We introduce the model, the method of estimation, and the statistical properties of the estimators in Section 2. In Section 3, we lay out the hypothesis testing framework and derive the asymptotic distribution of the test statistic. Out simulations and a real data analysis are described in Sections 4 and 5, followed by a discussion in Section 6. All technical details are provided in the Appendix and the online Supplementary Material.

2. Model and Estimation

We denote the conditional mean of Y, given $\mathbf{V} = (\mathbf{Z}, U, G)$, by $\mu(\mathbf{v}) = E(Y|\mathbf{V} = \mathbf{v})$. For an ordinary generalized linear model (GLM), the conditional density of Y, given $\mathbf{V} = \mathbf{v}$, belongs to an exponential family,

$$f_{Y|V}(y|\mathbf{v}) = \exp[y\xi(\mathbf{v}) - b\{\xi(\mathbf{v})\} + c(y)],$$

for known functions $b\{\cdot\}$ and $c(\cdot)$, where $\xi(\mathbf{v})$ is the canonical parameter. In this study, we consider the model defined in (1.1).

Under the quasi-likelihood framework, where only the relationship between the mean and the variance is specified, we can estimate the conditional mean by replacing the conditional log-likelihood $\log\{f_{Y|V}(y|\mathbf{v})\}$ with a quasi-likelihood

function $Q\{\mu(\mathbf{v}), y\}$. Let the conditional variance of Y, given $\mathbf{V}$, be $\mathrm{Var}(Y|\mathbf{V} = \mathbf{v}) = \sigma^2 V(\mu(\mathbf{v}))$, with an unknown function $V(\cdot)$. Thus, the quasi-score function can be given by (see Carroll et al. (1997) and Cai, Fan and Li (2000))

$$\frac{\partial}{\partial u} Q(u, y) = \frac{y - u}{V(u)}. \tag{2.1}$$

2.1. Parameter estimation in GPLVCM

We define $\tilde{\mathbf{Z}} = (\mathbf{Z}^T, \mathbf{X}^T G)^T$, $\boldsymbol{\alpha} = (\boldsymbol{\alpha}_0^T, \boldsymbol{\alpha}_1^T)^T$, and $\boldsymbol{\beta}(u) = (\beta_0(u), \beta_1(u))^T$. The $\mathbf{X}$ variables contain the environmental variables that interact linearly with G. Thus, $\mathbf{X}$ is a subset of $\mathbf{Z}$, and the dimensionality of $\mathbf{X}$ is smaller than that of $\mathbf{Z}$. Model (1.1) can then be simplified as follows:

$$\eta(\mathbf{V}; \boldsymbol{\alpha}, \lambda) = \beta_0(U) + \beta_1(U) G + \tilde{\mathbf{Z}}^T \boldsymbol{\alpha}, \tag{2.2}$$

where λ contains the parameters used to estimate the nonparametric functions $\beta_0(U)$ and $\beta_0(U)$. Consider the knot sequence $\xi_1 = \cdots = 0 = \xi_r < \xi_{r+1} < \cdots < \xi_{r+N_n} < 1 = \xi_{r+N_n+1} = \cdots = \xi_{N_n+2r}$, where the number of interior knots $N = N_n$ increases with the sample size n. Let $J_n = N + r$. We denote by $\mathcal{J}$ the space of the B-spline basis function of order r ($r \geq 3$) (de Boor (2001)), with the B-spline basis $\mathbf{B}_r(u) = (B_{s,r}(u) : 1 \leq s \leq J_n)^T$, $u \in [a_u, b_u]$, where $[a_u, b_u]$ is the support of U. Then, $\beta_l(u)$, $l = 0, 1$, are approximated using the following spline functions:

$$\tilde{\beta}_l(u) \approx \sum_{s=1}^{J_n} B_{s,r}(u) \lambda_{s,l} = \mathbf{B}_r^T(u) \lambda_l,$$

where $\lambda = (\lambda_1^T, \lambda_2^T)$, with $\lambda_l = (\lambda_{s,l}, 1 \leq s \leq J_n)^T$. Then, $\boldsymbol{\alpha}$ and the B-spline coefficients λ are estimated by

$$(\widehat{\boldsymbol{\alpha}}^T, \widehat{\lambda}^T)^T = \underset{\boldsymbol{\alpha} \in \boldsymbol{\Theta}_\alpha, \lambda \in \mathbb{R}^{2J_n}}{\arg\min} \ell_n(\boldsymbol{\alpha}, \lambda), \tag{2.3}$$

with the log-likelihood function given as

$$\ell_n(\boldsymbol{\alpha}, \lambda) = \sum_{i=1}^{n} Q(g^{-1}\{\tilde{\eta}(\mathbf{V}_i; \boldsymbol{\alpha}, \lambda)\}, Y_i), \tag{2.4}$$

where $\tilde{\eta}(\mathbf{V}; \boldsymbol{\alpha}, \lambda) = \tilde{\mathbf{Z}}^T \boldsymbol{\alpha} + \tilde{\beta}_0(U) + \tilde{\beta}_1(U) G$, $\tilde{\boldsymbol{\beta}}(u) = (\tilde{\beta}_0(u), \tilde{\beta}_1(u))^T$, and $\boldsymbol{\Theta}_\alpha$ is the parametric space of $\boldsymbol{\alpha}$.

The consistency of the spline estimators for the nonparametric functions $\tilde{\beta}_l(u)$, $l = 0, 1$ can be established. As in Wang and Yang (2007) and Liu, Cui and Li (2016), we use the BSBK estimator to establish the asymptotic normality. We define $\widehat{\eta}_{-0}(\mathbf{V}_i; a, b) = \tilde{\mathbf{Z}}_i^T \widehat{\boldsymbol{\alpha}} + \tilde{\beta}_1(u_i) G_i + a + b(u_i - u)$, $\widehat{\eta}_{-1}(\mathbf{V}_i; a, b) = \tilde{\mathbf{Z}}_i^T \widehat{\boldsymbol{\alpha}} +$

$\tilde{\beta}_0(u_i) + aG_i + b(u_i - u)G_i$, and $\widehat{\ell}_l(a,b) = \sum_{i=1}^n Q(g^{-1}\{\widehat{\eta}_{-l}(\mathbf{V}_i; a, b)\}, Y_i)K_{h_l}(u_i - u)$, where $K(\cdot)$ is a kernel function and h_l is the bandwidth, for $l = 0, 1$. We can obtain the BSBK estimator of $\beta_l(u)$ as $\widehat{\beta}_l(u) = \widehat{a}$ using local linear fitting, as follows:

$$(\widehat{a}, \widehat{b}) = \underset{(a,b)\in\mathcal{A}}{\arg\min}\, \widehat{\ell}_l(a,b), \tag{2.5}$$

where $\mathcal{A} \subset \mathcal{R}^2$ is a subset.

We set the space $\mathcal{M}$ as a collection of functions with a finite L_2-norm on $[a_u, b_u] \times \mathcal{R}$ by $\mathcal{M} = \{\kappa(u,g) = \beta_0(u) + \beta_1(u)g, E\beta_l(U)^2 < \infty, l = 0, 1\}$. For $1 \le j \le p+q$, let $g_0(u,g)$ be a minimizer in $\mathcal{M}$ for the following optimization problem:

$$\kappa_0(\tilde{Z}_j) = g_0(u,g) = \underset{\kappa\in\mathcal{M}}{\arg\min}\, E\{\tilde{Z}_j - \kappa(U,G)\}^2,$$

where E represents the conditional expectation of Z_j, given (U, G). Let $P_j(\tilde{Z}_j) = \kappa_0(\tilde{Z}_j)$ and $\mathbf{P}(\tilde{\mathbf{Z}}) = (P_1(\tilde{Z}_1), \ldots, P_{p+q}(\tilde{Z}_{p+q}))^T$. Let $\widehat{\mathbf{Z}} = \tilde{\mathbf{Z}} - \mathbf{P}(\tilde{\mathbf{Z}})$. Let $q_j(x) = (\partial^j/\partial x^j)Q\{g^{-1}(x), y\}$, for $j = 1, 2, 3$. Then, $q_1(x) = \{y - g^{-1}(x)\}\rho_1(x)$, $q_2(x) = \{y - g^{-1}(x)\}\rho_1'(x) - \rho_2(x)$, and $\rho_j(x) = \{dg^{-1}(x)/dx^j\}/V\{g^{-1}(x)\}$. We define the covariance matrix of $\boldsymbol{\alpha}$ as

$$\Sigma_{\alpha^0} = E\left\{\rho_2(\mathbf{V})^{-1}\widehat{\mathbf{Z}}\widehat{\mathbf{Z}}^T\right\}^{-1}.$$

Here, Σ_{α^0} can be simplified as $\Sigma_{\alpha^0} = \rho_0 E\{\widehat{\mathbf{Z}}\widehat{\mathbf{Z}}^T\}^{-1}$ if the error variance $\rho(\mathbf{V})$ is a constant ρ_0. Let $\mu_k = \int t^k K(t)dt$, and $\nu_k = \int t^k K^2(t)dt$. Then, we can establish the asymptotic normality for the parametric estimator $\widehat{\boldsymbol{\alpha}}$ and the nonparametric estimator $\widehat{\beta}_l(u)$. Theorems 1 and 2 below are special cases of the theorems in Liu, Gao and Cui (2016) when the dimension of the loading parameter is one. We omit the proofs of these theorems.

Theorem 1. *Suppose that assumptions* (A.1)–(A.5) *in the Appendix hold,* $nN^{-4} \to \infty$ *and* $nN^{-2r-2} \to 0$*; then,*

$$\|\widehat{\boldsymbol{\alpha}} - \boldsymbol{\alpha}\|_2 = O_p(n^{-1/2}).$$

Furthermore, as $n \to \infty$*,*

$$n^{1/2}(\widehat{\boldsymbol{\alpha}} - \boldsymbol{\alpha}) \xrightarrow{\mathcal{L}} N(\mathbf{0}, \Sigma_{\alpha^0}),$$

where $\boldsymbol{\alpha}$ *is the true parameter of* $\boldsymbol{\alpha}$*.*

Theorem 2. *Suppose that assumptions* (A.1)–(A.5) *in the Appendix hold,* $nN^{-4} \to \infty$ *and* $nN^{-2r-2} \to 0$*; then, for* $l = 0, 1$*,*

$$(nh_l)^{1/2}\left\{\widehat{\beta}_l(u) - \beta_l(u) - b_l(u)h_l^2\right\} \xrightarrow{\mathcal{L}} N(0, v_l(u)), \text{ as } n \to \infty,$$

where $v_0(u) = \nu_0\{E[\rho_2(\mathbf{V})|U=u]\, f(u)\}^{-1}$, $v_1(u) = \nu_0\{E[\rho_2(\mathbf{V})G|U=u]\, f(u)\}^{-1}$, *and* $b_l(u) = \mu_2\beta_l''(u)/2$.

3. Hypothesis Test

Our model can simultaneously assess the effects of linear and nonlinear G×E interactions. This can be achieved by simultaneously testing the parametric and nonparametric components $\boldsymbol{\alpha}_1$ and $\beta_1(\cdot)$, which allows us to jointly discover trends in the interactions of the linear and nonlinear environmental effects. We consider the following more general hypothesis test to detect whether $\boldsymbol{\alpha}_1$ and $\beta_1(u)$ are simultaneously equal to specific parametric forms:

$$H_0 : \boldsymbol{\alpha}_1 = \boldsymbol{\alpha}_1^*, \beta_1(\cdot) = \beta_1^*(\cdot) \text{ v.s. } H_1 : \boldsymbol{\alpha}_1 \neq \boldsymbol{\alpha}_1^* \text{ or } \beta_1(\cdot) \neq \beta_1^*(\cdot), \tag{3.1}$$

where $\boldsymbol{\alpha}_1^*$ are given constants, and $\beta_1^*(\cdot)$ is a given parametric form with unknown parameters, such as the linear form $\beta_1^*(u) = \delta_0 + \delta_1 u$. Note that hypothesis (1.4), that is, $H_0^{PNP} : \boldsymbol{\alpha}_1 = \mathbf{0}, \beta_1(\cdot) = \mathbf{0}$, is a special case of hypothesis (3.1). To make the work more general, we develop the testing procedure following this general setup.

3.1. Generalized likelihood ratio test

To test the nonparametric function $\beta_1(\cdot)$, that is,

$$H_0^{NP} : \beta_1(\cdot) = \beta_1^*(\cdot) \text{ v.s. } H_1^{NP} : \beta_1(\cdot) \neq \beta_1^*(\cdot), \tag{3.2}$$

we can construct a generalized likelihood ratio (GLR) test. Let $\widehat{\boldsymbol{\alpha}} = (\widehat{\boldsymbol{\alpha}}_0^T, \widehat{\boldsymbol{\alpha}}_1^T)^T$ be the BSBK estimate of $\boldsymbol{\alpha}$ proposed in Section 2.1. Let $\widehat{\boldsymbol{\beta}}_{H_0}(u)$ and $\widehat{\boldsymbol{\beta}}_{H_1}(u)$ be the estimates of $\boldsymbol{\beta}_1(u)$ under H_0 and H_1, respectively. Let the log-likelihood functions under H_0 and H_1 in hypothesis test (3.2) be $\ell_n(H_0) = \sum_{i=1}^n Q(g^{-1}\{\widehat{\eta}_{H_0}(\mathbf{V}_i; \widehat{\boldsymbol{\alpha}}, \widehat{\boldsymbol{\beta}})\}, Y_i)$ and $\ell_n(H_1) = \sum_{i=1}^n Q(g^{-1}\{\widehat{\eta}_{H_1}(\mathbf{V}_i; \widehat{\boldsymbol{\alpha}}, \widehat{\boldsymbol{\beta}})\}, Y_i)$, respectively, where $\widehat{\eta}_{H_0}(\mathbf{V}_i; \widehat{\boldsymbol{\alpha}}, \widehat{\boldsymbol{\beta}}) = \widehat{\beta}_{0,H_0}(U_i) + \widehat{\boldsymbol{\alpha}}_{H_0}^T \tilde{\mathbf{Z}}_i + \widehat{\beta}_{1,H_0}(U_i)G_i$, and $\widehat{\eta}_{H_1}(\mathbf{V}_i; \widehat{\boldsymbol{\alpha}}, \widehat{\boldsymbol{\beta}}) = \widehat{\beta}_{0,H_1}(U_i) + \widehat{\boldsymbol{\alpha}}_{H_1}^T \tilde{\mathbf{Z}}_i + \widehat{\beta}_{1,H_1}(U_i)G_i$. We define the following GLR test statistic:

$$T_{NP} = -2(\ell_n(H_0) - \ell_n(H_1)). \tag{3.3}$$

To facilitate expression, we use the same bandwidth h for all coefficients. We denote the support of U as Ω, and the length of Ω as $|\Omega|$. Then, $\sigma_n^2 = 2h^{-1}|\Omega| \int \{K(u) - 0.5K * K(u)\}^2 du$ and $\mu_n = h^{-1}|\Omega|(K(0) - 0.5\nu_0)$, where $K * K(u)$ denotes the convolution of $K(u)$. Following the same arguments as in Fan, Zhang and Zhang (2001), we can show that under some regular conditions, $\sigma_n^{-1}(T_{NP} - \mu_n)$ is asymptotically normally distributed.

Theorem 3. *If assumptions* (A.1)–(A.5) *in the Appendix hold,* $nN^{-4} \to \infty$*, and* $nN^{-2r-2} \to 0$*, then, under* H_0 *in* (3.2)*, when* $nh^{9/2} \to 0$*,*

$$\sigma_n^{-1}(T_{NP} - \mu_n) \xrightarrow{\mathcal{L}} N(0,1),$$

where $\sigma_n^2 = 2h^{-1}|\Omega| \int \{K(u) - 1/2K * K(u)\}^2 du$ *and* $\mu_n = h^{-1}|\Omega|\{K(0) - 1/2\nu_0\}$*.*

Let $\boldsymbol{\xi}_1 = \sqrt{n}\Sigma_{\alpha_1^*}^{-1/2}(\widehat{\boldsymbol{\alpha}}_1 - \boldsymbol{\alpha}_1^*)$, $\boldsymbol{\xi}_2 = \sigma_n^{-1}(T_{NP} - \mu_n)$, and $\boldsymbol{\xi} = (\boldsymbol{\xi}_1^T, \boldsymbol{\xi}_2)^T$, where $\Sigma_{\alpha_1^*}$ is the asymptotical covariance of $\widehat{\boldsymbol{\alpha}}_1$. $\Sigma_{\alpha_1^*}$ is the bottom-right block diagonal matrix of Σ_{α^*} with dimension $p \times p$. This motivates us to construct the following test statistic to simultaneously assess both the parametric and the nonparametric parts:

$$T_n = \|\boldsymbol{\xi}\|_2^2. \tag{3.4}$$

Lemma 1. *Suppose that assumptions* (A.1)–(A.5) *in the Appendix hold; then, under* H_0 *in* (3.1)*,*

$$\mathrm{COV}(\boldsymbol{\xi}_1, \boldsymbol{\xi}_2) \xrightarrow{P} 0.$$

Lemma 1 states that $\boldsymbol{\xi}_1$ is asymptotically unrelated to $\boldsymbol{\xi}_2$.

Theorem 4. *If assumptions* (A.1)–(A.5) *in the Appendix hold, under* H_0 *in* (3.1)*,*

$$T_n \xrightarrow{\mathcal{L}} \chi_{p+1}^2.$$

Theorem 4 states that T_n has an asymptotic χ^2-distribution with $p+1$ degrees of freedom. Note that Cheng and Shang (2015) obtained a similar result for fixed points. However, we can test the entire function instead of testing it at fixed points.

3.2. Power approximation

In this section, we examine the power of the joint test using the following sequence of local alternatives:

$$H_{1n} : \boldsymbol{\alpha}_1 = \boldsymbol{\alpha}_1^* + \boldsymbol{\alpha}_{1n} \text{ or } \beta_1(\cdot) = \beta_1^*(\cdot) + \beta_{1n}(\cdot), \tag{3.5}$$

where $\beta_{1n}(\cdot)$ is a vector-valued function. Before discussing (3.5), we first consider the alternative of testing the nonparametric component:

$$H_{1n}^{NP} : \beta_1(\cdot) = \beta_1^*(\cdot) + \beta_{1n}(\cdot). \tag{3.6}$$

Theorem 5. *If assumptions* (A.1)–(A.5) *in the Appendix hold,* $nN^{-4} \to \infty$*, and* $nN^{-2r-2} \to 0$*, and if* $nh^4 \to 0$ *and* $nh^{1/2}E[\rho(\mathbf{V})\beta_{1n}(U)^2G^2] \to C(\beta)$*, where*

$C(\beta)$ is a constant, then, under H_{1n}^{NP} in (3.6),

$$\frac{(T_{NP} - \mu_n - d_{2n})}{\sigma_n} \xrightarrow{\mathcal{L}} N(0,1),$$

where $d_{2n} = nE[\rho(V)\beta_{1n}(U)^2 G^2]$.

Let $\phi = \phi_\alpha + \phi_\beta$, where $\phi_\alpha = \lim_{n\to\infty} n\boldsymbol{\alpha}_{1n}^T \Sigma_\alpha^{-1} \boldsymbol{\alpha}_{1n}$ and $\phi_\beta = \lim_{n\to\infty} d_{2n}$. The following theorem states the asymptotic distribution of the statistic T_n under H_{1n} in (3.5).

Theorem 6. *Suppose that the assumptions in Theorem 5 hold and* $n^{-1/2}\|\boldsymbol{\alpha}_{1n}\| \to C$, *where C is a constant. Then, under H_{1n} in* (3.5), *the statistic T_n in* (3.4) *converges to a noncentral χ^2-distribution with degrees of freedom $p+1$ and noncentrality ϕ.*

Theorem 6 implies that the test can simultaneously detect alternatives with orders $\boldsymbol{\alpha}_{1n} = n^{-1/2}C$ and $\beta_{1n}(u) = n^{-1/2}h^{-1/4}\beta_c(u)$, with a given constant C and a given function $\beta_c(u)$. This simultaneously yields the parametric and nonparametric convergence rates (see Hardle and Mammen (1993); Gao and Gijbels (2008)).

4. Monte Carlo Simulation

The finite-sample performance of the proposed method was evaluated by simulation. In example 1, we assumed a quantitative trait, but assumed a binary disease trait in example 2.

Example 1 (continuous response). Consider the following PLVCM model:

$$Y = \boldsymbol{\alpha}_0^T \mathbf{Z} + \beta_0(U) + \{\boldsymbol{\alpha}_1^T \mathbf{X} + \beta_1(U)\}G + \varepsilon,$$

where $\mathbf{Z} = (Z_0, Z_1, Z_2, Z_3)^T$ and $\mathbf{X} = (Z_1, Z_2, Z_3)^T$. We generated Z_0, Z_1, and Z_2 from an independent normal distribution $N(0,1)$, Z_3 from a Bernoulli distribution $Ber(1, 0.5)$, and U from a uniform distribution $U(0,1)$. G was coded as $(2,1,0)$ corresponding to genotypes (AA, Aa, aa), respectively . We set the minor allele frequency (MAF) $p_A = (0.1, 0.3, 0.5)$ and assume a Hardy–Weinberg equilibrium. Single nucleotide polymorphism (SNP) genotypes AA, Aa, and aa were simulated from a multinomial distribution with frequencies p_A^2, $2p_A(1-p_A)$, and $(1-p_A)^2$, respectively, for the three genotypes. The error ε follows a normal distribution $N(0, \sigma^2)$. We set $\boldsymbol{\alpha}_0 = (0.7, 0.6, 0.8, 0.5)^T$, $\boldsymbol{\alpha}_1 = (0.6, 0.8, 0.5)^T$, $\beta_0(u) = \cos(\pi u)$, and $\beta_1(u) = \sin(\pi u)$. We assess the performance of the joint test under $H_0 : \boldsymbol{\alpha}_1 = \mathbf{0}, \beta_1(\cdot) = 0$ in (1.4). Note that we first tested whether both terms are zero, because researchers are typically interested in whether an

Table 1. Testing size with $\sigma = 0.1, 0.5, 1.0$, $p_A = 0.1, 0.3, 0.5$, and $n = 200, 500, 1{,}000$.

	$n = 200$			$n = 500$			$n = 1{,}000$		
σ	p_A=0.1	p_A=0.3	p_A=0.5	p_A=0.1	p_A=0.3	p_A=0.5	p_A=0.1	p_A=0.3	p_A=0.5
1.0	0.063	0.060	0.057	0.056	0.061	0.054	0.057	0.053	0.052
0.5	0.063	0.063	0.060	0.058	0.065	0.055	0.055	0.052	0.052
0.1	0.067	0.058	0.059	0.057	0.060	0.054	0.056	0.053	0.051

overall interaction effect exists. We also evaluated the power under a sequence of alternative models indexed by τ, that is, $H_1^\tau : \boldsymbol{\alpha}_1^\tau = \tau\boldsymbol{\alpha}_1, \beta_1^\tau(\cdot) = \tau\beta_1(\cdot)$.

We used the BIC criterion to select the number of interior knots, while fixing the order of the basis function as cubic to approximate the unknown functions, as described in Ma and Song (2015). The BSBK estimator $\widehat{\beta}_l(u)$ is sensitive to the choice of the bandwidth h_l, for $l = 0, 1$. Bandwidth selection has been extensively studied (see Sepanski, Knickerbocker and Carroll (1994); Ruppert, Sheathers and Wand (1995)). To avoid estimating high-order derivatives, we employed a bandwidth selector based on the MSE criterion, called the empirical bias bandwidth selection (EBBS) (Ruppert (1997); Carroll, Ruppert and Welsh (1998); Liu, Jiang and Zhou (2014)).

Table 1 reports the size ($\tau = 0$) under different standard deviations ($\sigma = 0.1, 0.5, 1.0$), different MAFs ($p_A = 0.1, 0.3, 0.5$), and different sample sizes ($n = 200, 500, 1{,}000$). We can see that the sizes tend to 0.05 as the sample size n increases. The same phenomenon is observed as the MAF approaches 0.5 and the standard deviation increases. Figure 1 shows the size and power function ($\tau > 0$) at the 0.05 significance level, based on 500 Monte Carlo simulations with different sample sizes and MAFs. The empirical type 1 errors in the three scenarios are very close to the nominal level 0.05. We observe a drastic power increase when the MAF increases from 0.1 to 0.3 in all scenarios. The sample size and error variance also have a significant impact on the testing power, as shown in the figure. Overall, the results indicate that our method can reasonably control the false positive rate and has appropriate power to detect the joint association signal.

Example 2 (Binary response). This simulation design assumes an underlying GPLVCM model for binary responses, with the logistic regression model given as,

$$\text{logit}\{P(Y = 1|\mathbf{Z}, U, G)\} = \boldsymbol{\alpha}_0^T\mathbf{Z} + \beta_0(U) + \{\boldsymbol{\alpha}_1^T\mathbf{X} + \beta_1(U)\}G, \tag{4.1}$$

where U and G are generated in the same manner as in Example 1, $\mathbf{Z} =$

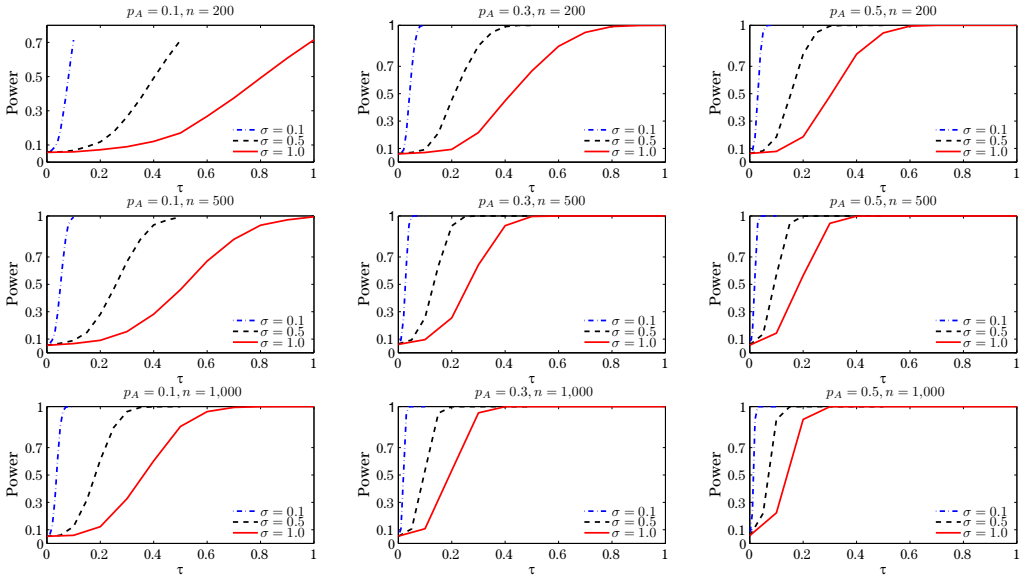

Figure 1. The empirical size and power function of test statistic T_n for the simultaneous inference of parametric and nonparametric parameters under different simulation settings.

$(Z_0, Z_1, Z_2, Z_3)^T$ is generated from an independent normal distribution $N(0, 1)$, and $\mathbf{X} = (Z_1, Z_2, Z_3)^T$, $\boldsymbol{\alpha}_0 = (0.7, 0.6, 0.8, 0.5)^T$, and $\boldsymbol{\alpha}_1 = (0.6, 0.8, 0.5)^T$. We set $\beta_0(u) = \cos(\pi u)$ and $\beta_1(u) = \sin(\pi u)$. Figure 2 shows the size ($\tau = 0$) and power function ($\tau > 0$) at a significance level of 0.05 based on 1,000 Monte Carlo simulations with different sample sizes and $P_A = 0.3$. Similar results to those in example 1 are observed for $P_A = 0.1$ and $P_A = 0.5$, and hence are omitted. The results demonstrate the finite sample performance of the proposed joint test statistic.

Intuitively, we expect a power gain for the joint test when both the parametric and nonparametric components contribute something, as pointed out by one reviewer. When one component has a weak signal, the joint test signal could be diluted. To demonstrate this, we conducted further simulations. We simulated data assuming three scenarios. In scenario 1 (denoted as S1), both the parametric and nonparametric components are assumed to have an effect. In scenario 2 (S2), there is only parametric interaction effect, while the nonparametric effect is assumed to be zero. In S3, no parametric effect is assumed and only the nonparametric effect is included. Scenarios S2 and S3 are extreme cases. The corresponding data-generating model under the alternative in the three scenarios

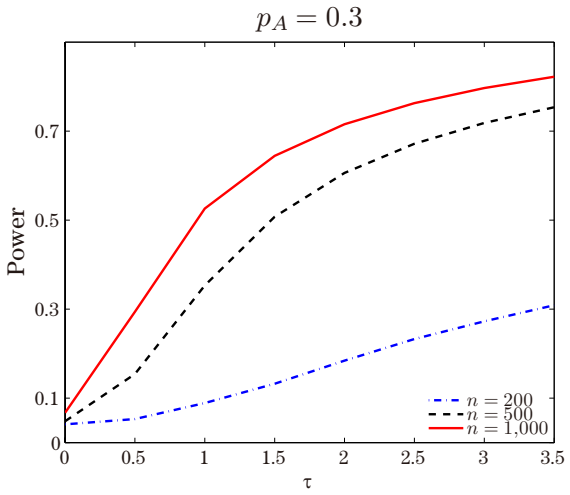

Figure 2. The empirical size and power function of the test statistic T_n for the simultaneous inference of both parametric and nonparametric parameters with binary response with different sample sizes.

are given as follows, where each component is described in Example 1:

(S1). $H_1^\tau : Y = \boldsymbol{\alpha}_0^T \mathbf{Z} + \beta_0(U) + \tau\{\boldsymbol{\alpha}_1^T \mathbf{X} + \beta_1(U)\}G + \varepsilon.$

(S2). $H_1^\tau : Y = \boldsymbol{\alpha}_0^T \mathbf{Z} + \beta_0(U) + \tau\boldsymbol{\alpha}_1^T \mathbf{X}G + \varepsilon.$

(S3). $H_1^\tau : Y = \boldsymbol{\alpha}_0^T \mathbf{Z} + \beta_0(U) + \tau\beta_1(U)G + \varepsilon.$

where the data $(\mathbf{Z}, U, G)$ are generated as in Example 1; $\mathbf{X}$ is a subset of $\mathbf{Z}$; and the model in H_1^τ is a sequence of alternative models indexed by τ, for $\tau = 0, 0.01, \ldots, 0.1$. For this simulation, we focus on cases with a sample size $n = 500$, MAF=0.3, and error variance $\sigma^2 = 1$ in all three scenarios. Similar performance is observed under other settings, and hence are omitted.

We consider the following three hypothesis testing problems:

(1). Joint test, denoted by "JointTest", i.e., $H_0 : \boldsymbol{\alpha}_1 = 0, \beta(\cdot) = 0$.

(2). Partial parametric test, denoted by "ParTest", i.e., $H_0 : \boldsymbol{\alpha}_1 = 0$.

(3). Partial nonparametric test, denoted by "NonparTest", i.e., $H_0 : \beta(\cdot) = 0$.

Figure 3 shows the power functions of the three tests under three different scenarios. In all cases, the size ($\tau = 0$) of the three tests can be reasonably controlled. In S1, where both the parametric and nonparametric effects are present,

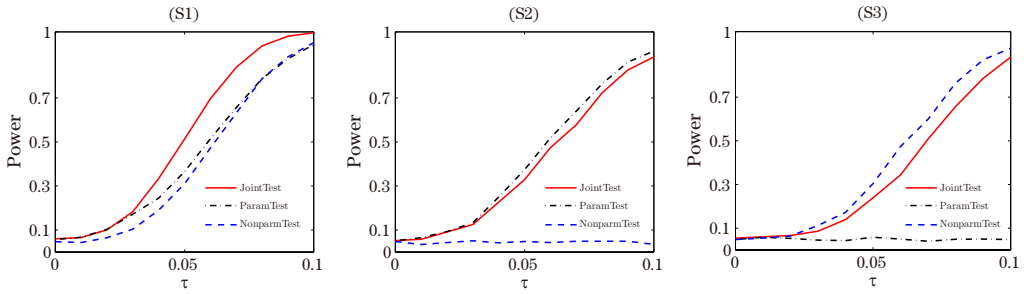

Figure 3. Plot of testing size and power for "JointTest" (solid line), "ParamTest" (dotted line) and "NonparamTest" (dot-dashed line) under scenarios S1, S2 and S3.

we observed better power of the joint test than that of the two partial tests, highlighting the power gain when both components contribute something. In S2, where includes only a parametric effect, the partial size for the nonparametric test is well controlled (dotted line). The power of JointTest is sightly smaller than that of ParTest, owing to the signal dilution from the nonparametric component. In S3, where no parametric effect exists, the partial size for the parametric test is well controlled (dot-dashed line). The power of JointTest is sightly smaller than that of NonparTest, owing to the signal dilution from the parametric component.

From this simulation, we see that the joint test achieves a power gain when both the parametric and nonparametric components contribute something. In extreme cases, where one component does not show any effect or shows a weak effect, the joint test will incur a power loss, owing to potential signal dilution by the weaker effect. Although we cannot theoretically show the conditions under which the joint test has larger power than that of the individual tests, this simulation result does illustrate the power gain of the joint test and gives us some practical insight into the proposed test.

5. Case Study

We applied the proposed GPLVCM model to a data set from the Gene Environment Association Studies initiative (GENEVA, `http://www.genevastudy.org`), funded by the trans-NIH Genes, Environment, and Health Initiative (GEI), to show the utility of the proposed method. Birth weight was the primary variable of interest of the trait. Fetal growth is not only determined by fetal genes, but is also controlled by complex interactions between fetal genes and the maternal uterine environment. In this example, we focused on a Thai population, with 1,126 subjects genotyped with the Omni1-Quad_v1-0_B plat-

Table 2. List of SNP ID, gene to which the SNP belongs, MAF, alleles (minor allele is shown as bold font), and p-values for SNP *rs1490352* on chromosome 6, under the marginal and joint tests.

SNP ID	Gene	MAF	Alleles	p-values		
				JointTest	ParTest	NonparTest
rs1490352	NKAIN2	0.4082	**G**/A	4.349E-07	0.259	5.087E-08

form. Because the mother's glucose level can have a significant impact on fetal growth, we chose *b_CordPGC_mg* (the fetus-cord glucose level) as the varying environmental variable U to try to understand whether fetal genes respond to the mother's glucose level to influence birth weight. The discrete variable, denoted by Z_1, contains the gender of the fetus. The continuous variables, denoted by Z_2 and Z_3, respectively, contain *m_HtM_OGTT* (the mother's mean OGTT height) and *m_OneHrPG_CLC_mg* (the mother's one-hour OGTT glucose). We set $\mathbf{Z} = (Z_1, Z_2, Z_3)^T$ and $\mathbf{X} = (Z_2, Z_3)^T$. To show the utility of the method, we picked chromosome 6 for the demonstration. There are 43,261 SNPs following the removal of those with minor allele frequencies less than 0.05 or p-values < 0.001 for testing the Hardy-Weinberg equilibrium. Our goal is to determine whether there are any SNPs associated with birth weight in the Thai population and if so, how the SNPs respond to mother's glucose level (the environment) changes to influence birth weight, and to further determine the mechanism of interaction.

We tested to determine whether any SNP was associated with birth weight based on the joint test, that is, $H_0 : \boldsymbol{\alpha}_1 = 0$ and $\beta_1(\cdot) = 0$. We individually tested each SNP and applied the local false discovery rate (LFDR) (see Efron et al. (2001); Storey (2002); Storey and Tibshirani (2003)) to adjust the multiple testing. We used the R package "fdrtool" with "bootstrap" method (Strimmer (2008)) to calculate the local FDR, and then estimated the proportion of null p-values for the joint test, calculated as $\eta_0 = 0.7237$. The bandwidth constant was chosen as $c = 0.4125$ in the bandwidth calculation formula $h = c \times sd(U) \times n^{-2/9}$. We used the same notation as given in Section 4: the proposed joint test (denoted by "JointTest"); partial parametric test (denoted by "ParTest"); and partial nonparametric test (denoted by "NonparTest"). The Q-Q plot of the $-\log_{10}$(p-values) for these three tests are depicted in Figure 4. It can be seen that the chosen bandwidth does not lead to inflated p-values. Based on the proportion of null p-value estimate $\eta_0 = 0.7237$, there is only one SNP (*rs1490352*) showing statistical significance.

Table 2 shows the SNP *rs1490352* with the SNP ID, MAF, alleles, and

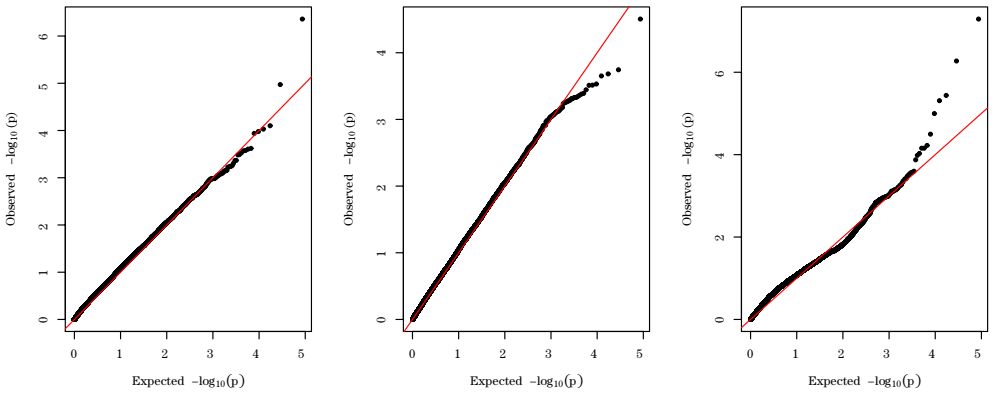

Figure 4. The QQ-plot of the -log10(p-values) for the "JointTest" (left), "ParTest" (middle) and "NonparTest" (right) with a chosen bandwidth constant $c = 0.4125$.

the p-value of each for the joint and separate tests. Alleles in bold represent minor alleles. We also separately tested the two interaction effects. We see that the joint test yielded p-values closer to those of the nonparametric testing. The parametric component is not statistically significant. The weak effect of the parametric component may dilute the joint test signal, leading to a slightly larger p-value of the joint test than that of the nonparametric test. This result is consistent with and supported by our simulation study.

6. Discussion

The evaluation of G×E interactions is an important topic in research on genetic association studies. With the development of statistical models, for example, the partially linear varying-coefficient model, we can assess the nonlinear G×E interactions in a model-based framework. In this study, we proposed and verified a joint testing framework to assess the effects of G×E interactions including linear and nonlinear interactions. Note that the joint test is equivalent to assessing the total genetic effect (the main genetic effect is embedded into the nonparametric function. See below for further explanation). In a genetic association study, the natural choice is to assess the total genetic effect first, then assess the effects of the interaction. This is another motivation, in addition to the gain in power offered by the proposed joint testing framework. Linear and nonlinear interactions can be assessed separately if the null hypothesis of the joint test is rejected.

We theoretically assessed the distribution of the joint test statistic under the

proposed estimation framework. Both the simulation and the real data analysis demonstrated the utility of the method. Novel genetic insight can be obtained from the joint test. In contrast to the work of Cheng and Shang (2015), where the parametric and nonparametric functions were jointly assessed at fixed points, we assess the two components globally. Although the parametric and nonparametric components have different convergence rates, the proposed test can simultaneously yield their respective optimal rates. In addition to the application of G×E interactions, our work also contributes to the theory of semiparametric inferences.

Under the proposed GPLVCM model, the joint test of the effects of the G×E interaction is equivalent to testing the total genetic effect. If we take $\beta_1(u) = \beta_1 + f(u)$, where $f(u)$ can be linear or nonlinear in u, $\beta_1(u)G = \beta_1 G + f(u)G$. It can be seen that the term $\beta_1(u)G$ contains the marginal effect of G on Y. If we use a B-spline to approximate the basis functions of $\beta_1(u)$, a change in the normalized basis functions can be obtained with the first column of the basis functions containing all ones (Schumaker (1981)). Such a transformation does not change the nature of the spline functions, but allows us to separate the marginal and interaction-related effects. Thus, the main genetic effects and those of nonlinear G×E interactions can be tested separately under the proposed framework.

Our method was motivated and demonstrated by a genetic association study. It can be applied to other studies, where a partial linear structure can be fitted. Partial linear models have been extensively studied in the literature. While most studies focus on the estimation problem, little research has been dedicated to testing the significance of the joint parametric and nonparametric effects. Our work fills this gap beyond the application of assessing G×E interactions. In addition, it can be extended to generalized partially linear additive models (e.g., Zhang and Liang (2011) and Ma and Yang (2011)) and partially linear varying multi-index coefficient models (Liu, Cui and Li (2016)). This extension allows us to assess the nonlinear G×E effect when more than one continuous environmental variable of interest is considered.

Supplementary Material

The technical details, including proofs of the major theorems and lemmas used in this paper, can be found in the Supplementary Material.

Acknowledgments

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Appendix: Proofs

Notations: For any vector $\boldsymbol{\xi} = (\xi_1, \ldots, \xi_s)^T \in \mathcal{R}^s$, $\|\boldsymbol{\xi}\|_\infty = \max_{1\le l\le s} |\xi_l|$. For any nonzero matrix $\mathbf{A}_{s\times s}$, denote its L_r norm by $\|\mathbf{A}\|_r = \max_{\boldsymbol{\xi}\in\mathbb{R}^s, \boldsymbol{\xi}\neq 0} \|\mathbf{A}\|_r \|\boldsymbol{\xi}\|_r^{-1}$. For any matrix $\mathbf{A} = (A_{ij})_{i,j=1}^{s,t}$, $\|\mathbf{A}\|_\infty = \max_{i\le i\le s} \sum_{j=1}^t |A_{ij}$. Let $C^{(p)}[a_u, b_u] = \{\psi : \psi^{(p)} \in C[a_u, b_u]\}$ be the space of pth-order smooth functions. Denote the space of Lipschitz continuous functions for any fixed constant c_0 by $\mathrm{Lib}([a_u, b_u], c_0) = \{\psi : |\psi(x_1) - \psi(x_2)| \le c_0|x_1 - x_2|, \forall x_1, x_2 \in [a_u, b_u]\}$. The following assumptions are required to show the consistency and asymptotic normality of our estimators:

Assumptions:

A.1 The random variable U has compact support $[a_u, b_u]$. The density function $f_u(\cdot)$ of random variable U is bounded away from zero on Ω, and there exists a constant $0 < c_0 < \infty$ such that $f_u(\cdot) \in \mathrm{Lib}([a_u, b_u], c_0)$.

A.2 The nonparametric function $m_l \in C^{(p)}[a_u, b_u]$, $l = 0, 1$.

A.3 $c_x \le \|E\{\mathbf{Z}^T\mathbf{Z}|U = u\}\|_2 \le C_x$.

A.4 The kernel function $K(\cdot)$ is a symmetric density function with compact support $[-1, 1]$ and $K \in \mathrm{Lib}([a_u, b_u], c_K)$ for some constant c_K.

A.5 The functions $u^3K(u)$ and $u^3K'(u)$ are bounded, and $\int u^4K(u)du < \infty$.

Denote $q_k(\tilde{\eta}_i)$ by $q_k\{\tilde{\eta}(\mathbf{V}_i; \boldsymbol{\alpha}_0, \lambda)\}$, $k = 1, 2$, $i = 1, \ldots, n$. Let $\mathbf{q}_k = (q_k(\tilde{\eta}_1), \ldots, q_k(\tilde{\eta}_n))^T$ and $\mathbf{W}_{q_2}$ be a diagonal matrix with diagonal elements $\mathbf{q}_2\{\tilde{\eta}\}$. Define

$$\begin{aligned} \mathbf{U} &= E[q_2(\tilde{\eta}_i)D_iD_i^T], & \widehat{\mathbf{U}} &= \frac{1}{n}\mathbf{D}^T\mathbf{W}_{q_2}\mathbf{D}, \\ \mathbf{U}(\mathbf{Z}) &= E[q_2(\tilde{\eta}_i)D_i(\mathbf{Z})D_i(\mathbf{Z})^T], & \widehat{\mathbf{U}}(\mathbf{Z}) &= \frac{1}{n}\mathbf{D}(\mathbf{Z})^T\mathbf{W}_{q_2}\mathbf{D}(\mathbf{Z}), \end{aligned} \tag{A.1}$$

where $D_i = (\mathbf{B}_r(U_i)^T\tilde{X}_{i,l}, l = 1, \ldots, 2p)^T$, $D_i(\mathbf{Z}) = (\mathbf{Z}_i^T, D_i^T)^T$, $\mathbf{D} = (D_1, \ldots, D_n)^T$ which is an $n \times pJ_n$ matrix, and $\mathbf{D}(\mathbf{Z}) = (D_1(\mathbf{Z}), \ldots, D_n(\mathbf{Z}))^T$ which is an $n \times 2(q + pJ_n)$ matrix.

The proofs of Theorems 1 and 2 are omitted here; they are special cases in Liu, Gao and Cui (2016). The details are shown in the Supplementary Materials. To prove Theorem 3, we define "oracle" estimation. Similar to (2.5), we can obtain the "Oracle" kernel estimator of $\beta_l(u)$ as $\widehat{\beta}_l^O(u) = \widehat{a}^O + \widehat{b}^O u$ by local linear fitting:

$$(\widehat{a}^O, \widehat{b}^O) = \underset{(a,b)\in\mathcal{A}}{\arg\min}\, \tilde{\ell}(a,b), \tag{A.2}$$

where $\tilde{\ell}(a,b) = \sum_{i=1}^n Q(g^{-1}\{\widehat{\eta}_{-l}^O(\mathbf{V}_i; a^O, b^O)\}, Y_i) K_{h_l}(u_i - u)$, $\widehat{\eta}_{-0}^O(\mathbf{V}_i; a, b) = \widehat{\boldsymbol{\alpha}}^T \tilde{\mathbf{Z}}_i + \beta_1(u_i) G_i + a + b(u_i - u)$ and $\widehat{\eta}_{-1}^O(\mathbf{V}_i; a, b) = \widehat{\boldsymbol{\alpha}}^T \tilde{\mathbf{Z}}_i + \beta_0(u_i) + a G_i + b(u_i - u) G_i$. The "Oracle" means that we already know the true functional structure before estimating function $\beta_l(u)$.

As in Liu, Cui and Li (2016), assuming that the nonparametric functions $\boldsymbol{\beta}(u)$ are known, we can construct a GLR statistic based on the "Oracle" estimator $\widehat{\boldsymbol{\beta}}^O(u)$. Consider hypothesis test (3.5). Let $\widehat{\beta}_{l,H_0}^O(u)$ and $\widehat{\beta}_{l,H_1}^O(u)$ be the "Oracle" estimates under H_0 and H_1, the same as in Section 2.1, respectively. The resulting likelihoods under H_0 and H_1 in hypothesis test (3.5) are

$$\ell_n^O(H_0) = \sum_{i=1}^n Q(g^{-1}\{\widehat{\eta}_{H_0}^O(\mathbf{V}_i; \widehat{\boldsymbol{\alpha}}, \widehat{\boldsymbol{\theta}})\}, Y_i),$$
$$\ell_n^O(H_1) = \sum_{i=1}^n Q(g^{-1}\{\widehat{\eta}_{H_1}^O(\mathbf{V}_i; \widehat{\boldsymbol{\alpha}}, \widehat{\boldsymbol{\theta}})\}, Y_i),$$

where $\widehat{\eta}_{H_0}^O(\mathbf{V}_i; \widehat{\boldsymbol{\alpha}}, \widehat{\boldsymbol{\theta}}) = \mathbf{Z}_i^T \widehat{\boldsymbol{\alpha}}_{0,H_0} + \mathbf{X}_i^T \widehat{\boldsymbol{\theta}}_{0,H_0}^O(U_i) + \mathbf{Z}_i^T \widehat{\boldsymbol{\alpha}}_{1,H_0} G_i$ and $\widehat{\eta}_{H_1}^O(\mathbf{V}_i; \widehat{\boldsymbol{\alpha}}, \widehat{\boldsymbol{\theta}}) = \mathbf{Z}_i^T \widehat{\boldsymbol{\alpha}}_{0,H_1} + \mathbf{X}_i^T \widehat{\boldsymbol{\theta}}_{0,H_1}^O(U_i) + \{\mathbf{Z}_i^T \widehat{\boldsymbol{\alpha}}_{1,H_1} + \mathbf{X}_i^T \widehat{\boldsymbol{\theta}}_{1,H_1}^O(U_i)\} G_i$. We define the following Oracle-version of the GLR test statistic as

$$T_{NP}^O = 2(\ell_n^O(H_1) - \ell_n^O(H_0)). \tag{A.3}$$

Let $a_K = \{K(0) - 1/2 \int K^2(u)du\}[\int \{K(u) - 1/2 K * K(u)\}du]^{-1}$, where $K * K(u)$ denotes the convolution of K.

Proof of Theorem 3: According to Lemma S.9 in the Supplementary Materials,

$$\ell_n^O(H_0) - \ell_n(H_0) = O_p(\log n),$$
$$\ell_n^O(H_1) - \ell_n(H_1) = O_p(\log n),$$

which implies that

$$T_{NP} = T_{NP}^O + O_p(\log n).$$

Lemma S.10 in the Supplementary Materials states that under the assumptions

of Theorem 3,

$$\sigma_n^{-1}(T_{NP}^O - \mu_n) \xrightarrow{\mathcal{L}} N(0,1),$$

where $\sigma_n^2 = 2h^{-1}|\Omega| \int \{K(u) - 1/2K * K(u)\}^2 du$ and $\mu_n = h^{-1}|\Omega|\{K(0) - 1/2 \int K^2(u)du\}$. This results directly in Theorem 3.

Proof of Lemma 1: Invoking the proof of Theorem 1 and 3,

$$n^{1/2}\Sigma_\alpha^{-1/2}(\widehat{\boldsymbol{\alpha}} - \boldsymbol{\alpha}^*) = n^{-1/2}\Sigma_\alpha^{-1/2}\sum_{i=1}^n(\tilde{\mathbf{Z}}_i - \mathbf{P}(\tilde{\mathbf{Z}}_i))\varepsilon_i + o_p(1),$$
$$\sigma_n^{-1}(T_{NP} - \mu_n) = v^{-1}\Upsilon(n) + o_p(1),$$

where $\varepsilon_i = q_1(\eta^*_{i,H_0})$, $\Upsilon(n) = (1/n)h^{-1/2}\sum_{i\neq j}^n \varepsilon_i\varepsilon_j \check{\mathbf{X}}_i^T\Gamma(U_i)\check{\mathbf{X}}_j\{2K((U_i-U_j)/h) - \tilde{K}((U_i-U_j)/h)\}$, and $v^2 = 2|\Omega|\int\{K(t) - 1/2\tilde{K}(t)\}^2dt$ are defined in the proof of Lemma S.10 in the Supplementary Materials. Let

$$\mathbb{I}_{1n} = \sum_{k\neq i,j}^n (\tilde{\mathbf{Z}}_k - \mathbf{P}(\tilde{\mathbf{Z}}_k))\varepsilon_k$$
$$\sum_{i\neq j}^n \varepsilon_i\varepsilon_j\check{\mathbf{X}}_i^T\Gamma(U_i)\check{\mathbf{X}}_j\left\{2K\left(\frac{U_i-U_j}{h}\right) - \tilde{K}\left(\frac{U_i-U_j}{h}\right)\right\},$$
$$\mathbb{I}_{2n} = \sum_{i\neq j}^n \varepsilon_i^2\varepsilon_j(\tilde{\mathbf{Z}}_i - \mathbf{P}(\tilde{\mathbf{Z}}_i))\check{\mathbf{X}}_i^T\Gamma(U_i)\check{\mathbf{X}}_j\left\{2K\left(\frac{U_i-U_j}{h}\right) - \tilde{K}\left(\frac{U_i-U_j}{h}\right)\right\}.$$

It is easy to see that $E[\mathbb{I}_{1n}] = 0$ and $E[\mathbb{I}_{2n}] = 0$. Therefore,

$$\mathrm{COV}(\boldsymbol{\xi}_1, \boldsymbol{\xi}_2) = n^{-1/2}v^{-1}\Sigma_\alpha^{-1/2}(\mathbb{I}_{1n} + \mathbb{I}_{2n}) + o_p(1),$$

which results directly in $\mathrm{COV}(\boldsymbol{\xi}_1, \boldsymbol{\xi}_2) \xrightarrow{P} 0$.

Proof of Theorem 4: Theorem 1 and Theorem 3 imply that

$$\|\boldsymbol{\xi}_1\|_2^2 \xrightarrow{\mathcal{L}} \chi_p^2, \text{ and } \boldsymbol{\xi}_2^2 \xrightarrow{\mathcal{L}} \chi^2.$$

Theorem 4 follows from Lemma 1.

Proof of Theorem 5: We proved in Lemma S.11 that under H_1^{NP} in (4.1),

$$\sigma_n^{-1}(T_{NP}^O - \mu_n - d_n) \xrightarrow{\mathcal{L}} N(0,1), \tag{A.4}$$

where $d_{2n} = nE[\rho(V)\boldsymbol{\theta}_n(U)^T\check{\mathbf{X}}\check{\mathbf{X}}^T\boldsymbol{\theta}_n(U)]$. According to Lemma S.9 in the Supplementary Materials,

$$\ell_n^O(H_0) - \ell_n(H_0) = O_p(\log n),$$
$$\ell_n^O(H_1) - \ell_n(H_1) = O_p(\log n),$$

which implies that

$$T_{NP} = T_{NP}^{O} + O_p(\log n). \tag{A.5}$$

Thus, Theorem 5 can be shown by (A.4) and (A.5).

Proof of Theorem 6: From Theorem 1,

$$\begin{aligned}\boldsymbol{\xi}_1 &= \sqrt{n}\Sigma_{\alpha_1}^{-1/2}(\widehat{\boldsymbol{\alpha}}_1 - \boldsymbol{\alpha}_1^*) \\ &= \sqrt{n}\Sigma_{\alpha_1}^{-1/2}(\widehat{\boldsymbol{\alpha}}_1 - \boldsymbol{\alpha}_1) + \sqrt{n}\Sigma_{\alpha}^{-1/2}(\boldsymbol{\alpha}_1 - \boldsymbol{\alpha}_1^*),\end{aligned}$$

which implies that $\boldsymbol{\xi}_1$ is asymptotically normally distributed with mean $\sqrt{n}\Sigma_{\alpha_1}^{-1/2}\boldsymbol{\alpha}_{1n}$ and variance one. Along the lines of the proof of Lemma 1, we can prove that $\boldsymbol{\xi}_1$ and $\boldsymbol{\xi}_2$ are asymptotically uncorrelated under H_{1n}. It is easy to see that $\|\boldsymbol{\xi}_1\|_2^2$ converges to a noncentral chi-squared distribution with q degrees of freedom and noncentrality parameter $\phi_\alpha = \lim_{n\to\infty} n\boldsymbol{\alpha}_{1n}^T\Sigma_{\alpha_1}^{-1}\boldsymbol{\alpha}_{1n}$. This implies that T converges to a noncentral chi-squared distribution with $q+1$ degrees of freedom and noncentrality parameter $\phi = \phi_\theta + \phi_\theta$, where $\phi_\theta = \lim_{n\to\infty} d_{2n}$.

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