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de Kort, J.M.; Dolan, C.V.; Lubke, G.H.; Molenaar, D.

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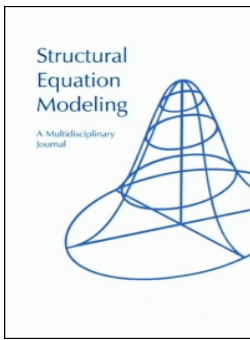
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# Studying the Strength of Prediction Using Indirect Mixture Modeling: Nonlinear Latent Regression with Heteroskedastic Residuals

Johanna M. de Kort,<sup>1</sup> Conor V. Dolan,<sup>1</sup> Gitta H. Lubke,<sup>2</sup> and Dylan Molenaar<sup>3</sup>

<sup>1</sup>*Vrije Universiteit Amsterdam*

<sup>2</sup>*Vrije Universiteit, Amsterdam, and University of Notre Dame*

<sup>3</sup>*University of Amsterdam*

We present a latent regression model in which the regression function is possibly nonlinear, and not necessarily smooth (e.g., a step function), and in which the residual variances are not necessarily homoskedastic. Heteroskedasticity is modeled by making the conditional (on the predictor) residual variance a (user-specified) function of the predictor. We use indirect mixture modeling to estimate the parameters by marginal maximum likelihood estimation, as proposed by Bock and Aitken (1981) in the context of item-response theory modeling and Klein and Moosbrugger (2000) in the context of structural equation modeling. We present a small simulation study to evaluate power and the consequences of model misspecification, and an illustration concerning neuroticism and extroversion. The model can be used to evaluate changes in the strength of the prediction as a function of the predictor.

**Keywords:** heteroskedasticity, indirect mixture, latent regression, marginal maximum likelihood, nonlinearity

In direct applications of finite mixture modeling, the aim is to identify latent classes (mixture components), which are amenable to substantive interpretation (e.g., Dolan, Schmittmann, Lubke, & Neale, 2005; Muthén, Khoo, Francis, & Boscardin, 2003; Schmittmann, Dolan, van der Maas, & Neale, 2005). In indirect applications, mixture modeling is used as a tool to obtain a flexible, tractable form of analysis (e.g., Bauer, 2005; Kelava, Nagengast, & Brandt, 2014; Moosbrugger, Schermelleh-Engel, Kelava, & Klein, 2009). For instance, finite mixture factor

analysis has been used indirectly to accommodate nonnormality (Wall, Gua, & Amemiya, 2012), and directly to identify interpretable latent classes (Dolan & van de Maas, 1998; Lubke & Muthén, 2005). In this article, we use indirect mixture modeling to accommodate nonlinearity and heteroskedasticity in the latent regression model.

We consider the combination of nonlinearity and heteroskedasticity to be of substantive interest to model changes in the strength of prediction. For instance, consider the statement “Social isolation (SI) causes depression (D),” which can be formalized in terms of the linear regression of D on SI. The psychological shorthand narrative is intuitively appealing: the more isolated you are, the more likely you are to be depressed (Cacioppo, Hawkley, & Thisted, 2010). However, it is possible that at low, or even intermediate, levels of depression, depression is less strongly associated with social isolation. This variation in strength of the relationship might be due to heteroskedasticity (e.g.,  $\sigma^2 [D|SI \text{ high}] < \sigma^2 [D|SI \text{ low}]$ ), or due to variation in the value of the regression coefficient,  $\beta$  (e.g.,  $\beta|SI \text{ high} > \beta|SI \text{ low}$ ). The latter results in nonlinearity, whereas the former does not.

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Correspondence should be addressed to Conor V. Dolan, Department of Biological Psychology, Vrije Universiteit, van der Boechorststraat 1, 1081 BT Amsterdam, The Netherlands. E-mail: [c.v.dolan@vu.nl](mailto:c.v.dolan@vu.nl)

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However, both have a bearing on the strength of the regression relationship.

To accommodate nonlinearity, latent polynomial regression is often used. Two main approaches are the (latent) product-indicator approach and the distribution analytic approach (Moosbrugger et al., 2009). Within the product indicator approach latent nonlinearity is specified by including appropriate functions of the observed indicators (Bollen, 1995; Jaccard & Wan, 1996; Jöreskog & Yang, 1996; Kenny & Judd, 1984; Ping, 1996; Schumacker & Marcoulides, 1998). The product-indicator approach requires nonlinear constraints (but see Marsh, Wen, & Hau, 2004), and estimation suitable for nonnormality, given the nonnormality arising from the inclusion of product indicators. Within the distribution analytic approach, the model is estimated by conditioning on latent variables involved in the nonlinear regression terms. This can either be done by formulating the model as an indirect mixture (e.g., the latent moderated structural equation approach; Klein & Moosbrugger, 2000) or by approximating the nonnormal density function of the joint indicator vector (e.g., using quasi-maximum likelihood estimation; Klein & Muthén, 2007). A second indirect mixture approach to nonlinearity was developed by Bauer (2005; see also Pek, Sterba, Kok, & Bauer, 2009). Bauer proposed an exploratory regression model that approximates the nonlinear regression function by means of a weighted combination of linear regression models. This method requires specification of the number of components in the indirect mixture, not of the functional form of the nonlinear function (e.g., curvilinear, quadratic, exponential).

In the methods mentioned so far, heteroskedasticity, if any, is not modeled and not of substantive interest. Generally, in linear regression modeling, heteroskedasticity is viewed as an obstacle to correct statistical inference concerning regression coefficients, which can be addressed by iterated weighted least squares (Greene, 2011; Hooper, 1993) or by a correction of the standard errors (Huber, 1967; White, 1980). However, heteroskedasticity can be of theoretical interest in its own right. For instance, heteroskedasticity is important in the study of ability differentiation (Molenaar, Dolan, & van der Maas, 2011), genotype by environment interaction (Molenaar et al., 2013; van der Sluis, Dolan, Neale, Boomsma, & Posthuma, 2006), and personality (i.e., schematicity hypothesis; Molenaar, Dolan, & de Boeck, 2012). As mentioned earlier, here we are interested in heteroskedasticity (in combination with possible nonlinearity), as it has a bearing on the precision of prediction in the regression model.

Within the context of factor models and item-response theory (IRT) models, Molenaar and colleagues used marginal maximum likelihood (MML) estimation to model nonlinearity and heteroskedasticity (Molenaar et al., 2012; Molenaar et al., 2011; Molenaar, Dolan, & Verhelst, 2010; Molenaar, Dolan, Wicherts, & van der Maas, 2010). This approach is similar to that of Klein and Moosbrugger (2000) as it also exploits the fact that MML estimation in psychometric modeling can be cast in terms of constrained finite mixture modeling (see later).

In this article, we use the indirect mixture modeling approach to fit a nonlinear heteroskedastic latent regression model using MML estimation. In the model, both the regression coefficient and the latent residual variance are deterministic functions of the latent predictor. We show that various forms of heteroskedasticity can be accommodated using smooth or step functions. Similarly, various forms of nonlinearity can be considered including, but not limited to, polynomial functions or smooth functions. The outline of this article is as follows. We first present the formal indirect mixture model. Next, we discuss MML estimation of the model parameters. Then, we present the results of a simulation study to demonstrate the viability of the model in terms of parameter recovery, power, and the effect of misspecification. We apply the model to a real data set pertaining to personality. Finally, we conclude the article with a brief discussion.

## THE INDIRECT MIXTURE MODEL TO TEST NONLINEARITY AND HETEROSKEDASTICITY

### The Linear and Homoskedastic Case

We consider two instances of the latent linear regression model (see Figure 1). We assume that the normally distributed predictor variable ( $\eta_x$ ) is latent with  $L$  indicators and that the dependent variable ( $\eta_y$ ) is either observed (Figure 1 bottom) or latent with  $K$  indicators (Figure 1 top). We assume the dependent variable ( $\eta_y$ ) to be normal conditional on the predictor ( $\eta_x$ ). The number of indicators is arbitrary but assumed to be sufficient to avoid problems of identification. In matrix notation, the model for the  $L$ -dimensional vector of predictor indicators, denoted by  $\mathbf{x}$ , is given by

$$\mathbf{x} = \mathbf{v}_x + \boldsymbol{\lambda}_x \boldsymbol{\eta}_x + \boldsymbol{\varepsilon}_x, \quad (1)$$

where  $\mathbf{v}_x$  is the  $L$ -dimensional vector of intercepts,  $\boldsymbol{\lambda}_x$  is an  $L$ -dimensional vector of factor loadings,  $\boldsymbol{\eta}_x$  is the  $1 \times 1$  vector of the latent predictor (i.e.,  $\boldsymbol{\eta}_x = [\eta_x]$ ), and  $\boldsymbol{\varepsilon}_x$  is the  $L$ -dimensional vector of residuals. Next, the model for the  $K$ -dimensional vector of dependent latent variable indicators, denoted by  $\mathbf{y}$ , given  $K > 1$ , is given by

$$\mathbf{y} = \mathbf{v}_y + \boldsymbol{\lambda}_y \boldsymbol{\eta}_y + \boldsymbol{\varepsilon}_y, \quad (2)$$

with the parameters defined analogously. The preceding model reduces to  $y = v_y + \eta_y$  if  $K = 1$ , as here the variable  $y$  features as the observed dependent. In the standard linear homoskedastic model, the latent dependent variable is regressed on the latent predictor variable as follows:

$$\boldsymbol{\eta}_y = \mathbf{B} \boldsymbol{\eta}_x + \boldsymbol{\zeta}, \quad (3)$$

where  $\mathbf{B}$  is a  $1 \times 1$  matrix containing the regression coefficient  $\beta$ , and  $\boldsymbol{\zeta}$  is a  $1 \times 1$  matrix containing the latent residual

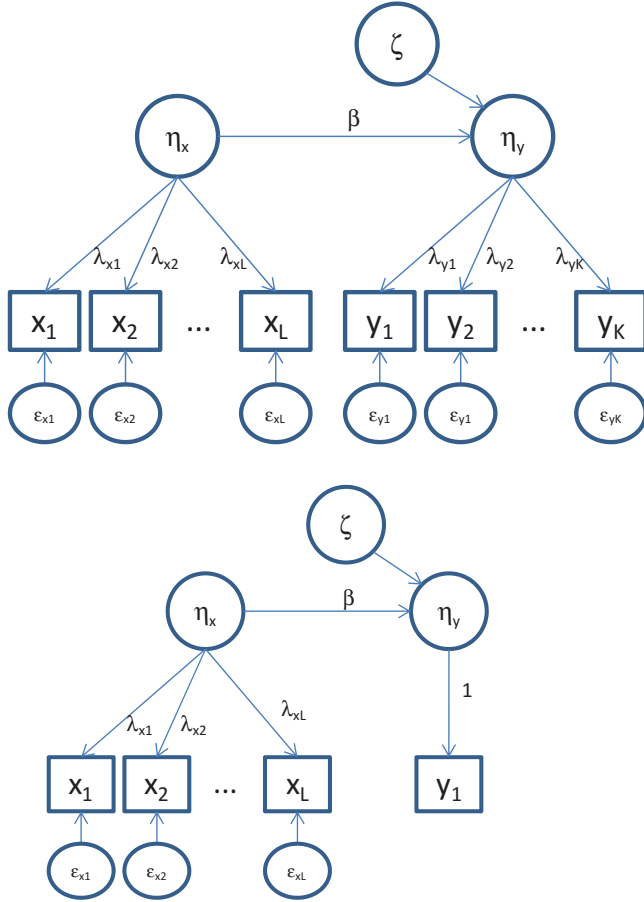


FIGURE 1 Regression models with four predictor and four dependent indicators (top) or one dependent (bottom).

$\zeta$  with variance  $\sigma_\zeta^2$ . Homoskedasticity implies that the variance of  $\zeta$  is constant over the range of  $\eta_x$ .

The Nonlinear and Heteroskedastic Case

We generalize the latent linear regression model to accommodate nonlinearity and heteroskedasticity simultaneously by making the regression coefficient  $\beta$  and the residual variance  $\sigma_\zeta^2$  a function of the predictor  $\eta_x$ :

$$\beta = f_\beta(\eta_x), \tag{4}$$

and

$$\sigma_\zeta^2 = f_\zeta(\eta_x). \tag{5}$$

The choice of the functions  $f_\beta(\cdot)$  and  $f_\zeta(\cdot)$  is arbitrary, and not limited to smooth functions. An obvious smooth function is the  $r$ -degree polynomial regression:

$$\beta = f_\beta(\eta_x) = \gamma_0 + \gamma_1 \eta_x + \gamma_2 \eta_x^2 + \dots + \gamma_r \eta_x^r \tag{6}$$

where the model reduces to standard linear regression if  $\gamma_i = 0$  ( $i = 1, \dots, r$ ). As an example of a discrete function, consider a three-step function:

$$\beta = f_\beta(\eta_x) = \begin{cases} k_0 + k_1 & \text{if } \eta_x \leq -c \\ k_0 & \text{if } -c < \eta_x < c \\ k_0 + k_2 & \text{if } \eta_x \geq c \end{cases} \tag{7}$$

where  $c$  is a chosen, fixed threshold value. To model heteroskedasticity of the latent residual, we could use an  $r$ th order polynomial function:

$$\sigma_\zeta^2 = f_\zeta(\eta_x) = \exp(\phi_0 + \phi_1 \eta_x + \phi_2 \eta_x^2 + \dots + \phi_r \eta_x^r) \tag{8}$$

or equivalently

$$\log(\sigma_\zeta^2) = \log(f_\zeta(\eta_x)) = \phi_0 + \phi_1 \eta_x + \phi_2 \eta_x^2 + \dots + \phi_r \eta_x^r, \tag{9}$$

where the intercept  $\phi_0$  accounts for the latent residual, which is independent of the predictor  $\eta_x$ . In addition,  $\phi_s$  ( $s = 1, \dots, r$ ) are the heteroskedasticity parameters that account for the residual variance as a function of the predictor  $\eta_x$ . As in the case of the regression coefficient, other (discrete) functions can be chosen, such as the step function; for example,

$$\sigma_\zeta^2 = f_\zeta(\eta_x) = \begin{cases} \xi_0 + \xi_1 & \text{if } \eta_x \leq -c, \\ \xi_0 & \text{if } -c < \eta_x < c \\ \xi_0 + \xi_2 & \text{if } \eta_x \geq c. \end{cases} \tag{10}$$

The step function can be used in an exploratory analysis of heteroskedasticity in the extreme of the  $\eta_x$  distribution, where the choice of  $c$  is arbitrary (e.g., setting the threshold  $c$  to equal 1 SD; see the illustration later).

Parameter Estimation

Equations 1 through 5 represent the extended nonlinear latent regression model with heteroskedastic residuals. This model can be fitted by means of MML estimation (Bock & Aitkin, 1981; Klein & Moosbrugger, 2000; Molenaar et al., 2010), in which we condition on  $\eta_x$  and use Gauss–Hermite quadrature (Stroud & Secrest, 1966) to approximate the integral in the log-marginal likelihood.

To facilitate parameter estimation, we reformulate the models in Figure 1 into an equivalent specification, which is displayed in Figure 2. Specifically, given the model for the indicators of  $\eta_x$  in Equation 1, the conditional mean vector of the  $x$  indicators is given by  $\mu_x | \eta_x = \mathbf{v}_x + \lambda_x \eta_x$ , and the conditional covariance matrix is given by  $\Sigma_x | \eta_x = \Theta_x$ . When considering both nonlinearity and heteroskedasticity in the latent regression of  $\eta_y$  on  $\eta_x$  the model for the indicator vector of  $\eta_y$  conditional on  $\eta_x$ , is defined as  $\mathbf{y} | \eta_x = \mathbf{v}_y + \lambda_y f_\beta(\eta_x) \eta_x + \lambda_y \zeta + \boldsymbol{\varepsilon}_y$ , where  $f_\beta(\eta_x)$  is

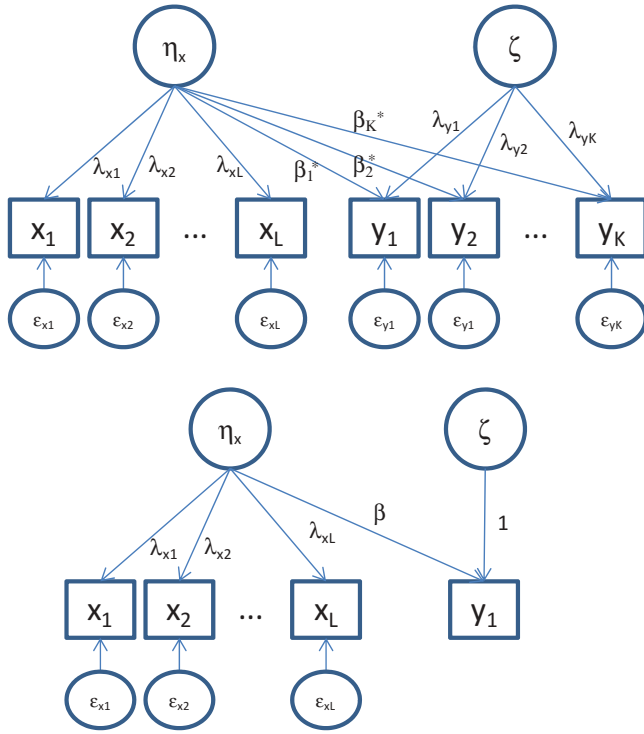


FIGURE 2 Regression models with four predictor and four dependent indicators (top) or one dependent indicator (bottom) in an equivalent (to Figure 1) specification. Note that  $\beta_k^* = \beta \times \lambda_{y_k}$  where  $k = 1, \dots, K$ .

specified as discussed earlier. In the case of a second-order polynomial, we have  $f_\beta(\eta_x) = \gamma_0 + \gamma_1 \eta_x$ ; that is,

$$\begin{aligned} y|\eta_x &= \mathbf{v}_y + \lambda_y (\gamma_0 + \gamma_1 \eta_x) \eta_x + \lambda_y \zeta + \varepsilon_y = \\ &= \mathbf{v}_y + \lambda_y (\gamma_0 \eta_x + \gamma_1 \eta_x^2) + \lambda_y \zeta + \varepsilon_y, \end{aligned}$$

which reveals the quadratic nature of the regression model.

The vector of the conditional means of the dependent indicators is defined as  $\boldsymbol{\mu}_y|\eta_x = \mathbf{v}_y + \lambda_y f_\beta(\eta_x) \eta_x$ . The model-implied conditional covariance structure depends on the  $f_\zeta(\eta_x)$ , as follows:  $\boldsymbol{\Sigma}_y|\eta_x = \lambda_y [f_\zeta(\eta_x)] \lambda_y^t + \boldsymbol{\Theta}_y$ , where, for instance,  $f_\zeta(\eta_x) = \exp(\phi_0 + \phi_1 \eta_x)$ . To formulize the MML function we stack the indicator vectors of the predictor and dependent latent variable,  $\mathbf{x}$  and  $\mathbf{y}$ , into the vector  $\mathbf{z}$ . In addition, the conditional mean vector of  $\mathbf{x}$  and  $\mathbf{y}$  is stacked into  $\boldsymbol{\mu}_{\eta_x}$  and the conditional covariance matrix is the block matrix  $\boldsymbol{\Sigma}_{\eta_x}$ . Then, the conditional distribution of the data of subject  $i$ ,  $\mathbf{z}_i$ , is defined as

$$\begin{aligned} h(\mathbf{z}_i|\eta_x, \boldsymbol{\tau}) &= (2\pi)^{-M/2} \left| \boldsymbol{\Sigma}_{\eta_x} \right|^{-1/2} \\ &\exp\left(-\frac{1}{2} (\mathbf{z}_i - \boldsymbol{\mu}_{\eta_x})' \left[ \boldsymbol{\Sigma}_{\eta_x} \right]^{-1} (\mathbf{z}_i - \boldsymbol{\mu}_{\eta_x})\right). \end{aligned}$$

By integrating out  $\eta_x$ , we obtain the marginal density of the observed variables for subject  $i$

$$k(\mathbf{z}_i|\boldsymbol{\tau}) = \int_{-\infty}^{\infty} h(\mathbf{z}_i|\eta_x, \boldsymbol{\tau}) \times \varphi(\eta_x) d\eta_x,$$

where  $\varphi(\eta_x)$  is a standard normal density function. Approximating the log of this density using Gauss–Hermite quadratures, we obtain

$$\log L(\boldsymbol{\tau}|\mathbf{z}) \approx \sum_{i=1}^M \log \left( \sum_{q=1}^Q W_q^* \times h(\mathbf{z}_i|N_q^*, \boldsymbol{\tau}) \right), \quad (11)$$

where  $M$  is the number of subjects and  $\boldsymbol{\tau}$  is the parameter vector. In addition,  $N_q^* = \sqrt{2} N_q$  and  $W_q^* = \frac{1}{\sqrt{\pi}} W_q$  where  $N_q$  and  $W_q$  are the  $Q$  nodes and weights ( $q = 1, \dots, Q$ ), respectively of the Gauss–Hermite quadrature approximation. Note that  $0 < W_q^* < 1$  and  $\sum_{q=1}^Q W_q^* = 1$ , so that the log-marginal likelihood function,  $\sum_{q=1}^Q W_q^* \times h(\mathbf{z}_i|N_q^*, \boldsymbol{\tau})$  has the form of a  $Q$ -component mixture distribution with the weights featuring as mixing proportions, and  $h(\mathbf{z}_i|N_q^*, \boldsymbol{\tau})$  featuring as the  $q$ th mixture component distribution. The model as defined earlier is implemented in OpenMx (Boker et al., 2011) within the R program (R Development Core Team, 2012).<sup>1</sup>

## SIMULATION STUDY

We explored the viability of this model by means of a small simulation study, in which we considered parameter recovery, power, and the effects of misspecification. We limited the simulation study to the second-order polynomial non-linearity model and the second-order polynomial heteroskedasticity model, as defined in Equations 6 and 8. To make the relevant comparisons, we considered four instances of the model: the full model (i.e., the model with the regular regression parameters  $\gamma_0, \phi_0$ , and the nonlinearity parameter  $\gamma_1$ , and heteroskedasticity parameter  $\phi_1$ ); the heteroskedasticity model (i.e., the model with parameters  $\gamma_0, \phi_0$ , and  $\phi_1$ ); the nonlinearity model (i.e., the model with parameters  $\gamma_0, \phi_0$ , and  $\gamma_1$ ); and the basic model (i.e., the standard regression model with only parameters  $\gamma_0, \phi_0$ ). We denote these models as FULL, NON-L, HETERO, and BASIC, respectively.

### Setting

We set the number of indicators of the latent predictor ( $\eta_x$ ) to equal  $L = 4$ , and the number of indicators of the latent dependent variable ( $\eta_y$ )  $K = 4$  or  $K = 1$  (given  $K = 1$ ,  $\eta_y$  is simply equal to the dependent  $y$ ). To fit the models, we used the following identifying (scaling) constraints; in each

<sup>1</sup> The OpenMx script is available at [www.dylanmolenaar.nl](http://www.dylanmolenaar.nl).



model the variance of  $\eta_x$  was fixed to 1. Additionally, given  $K = 4$ , the first factor loading of  $\eta_y$  was fixed to 1. To generate data, we set all 4 factor loadings associated with  $\eta_x$  to equal .5 and the factor loadings associated with  $\eta_y$  to equal 1. We fixed all latent variable means (i.e.,  $E[\eta_x]$ ,  $E[\eta_y]$ ) to equal zero, consistent with the data generating model. We set the variances of  $\varepsilon_x$  to equal .5 for all predictor indicators, and the variances of  $\varepsilon_y$  to equal 1 (but zero in the case of  $K = 1$ ). Next, we set the baseline regression parameter ( $\gamma_0$ ) to equal .4, and the baseline residual term ( $\phi_0$ ) to equal ( $\pm$ ) .29, depending on whether the residual variance increased or decreased with the predictor.

To evaluate parameter recovery, power, and effects of misspecification of the model, we simulated data under the NON-L, HETERO, or FULL model, for both  $K = 4$  and  $K = 1$ . Prior to the simulation study, we established the number of quadrature points needed for accurate estimation, and checked the Type I error rate. We found that 25 points were sufficient and we established that the empirical Type I error rate was equal to the nominal  $\alpha$  (results available on request). We varied the values of the parameters of interest

to be either small, medium, or large, and either positive or negative (i.e.,  $\gamma_1 = \pm.1; \gamma_1 = \pm.15; \gamma_1 = \pm.2$ , and  $\phi_1 \approx \pm.22; \phi_1 \approx \pm.31; \phi_1 \approx \pm.40$ ). Figure 3 depicts the effects. The upper half shows the simulated nonlinearity effects and the lower half shows the simulated heteroskedasticity effects. In the simulation we used all possible combination of effects (i.e., one or two effects present, positive or negative). This scheme led to 24 different parameter settings for both  $K = 4$  and  $K = 1$ . We set the sample size to  $N = 300$  and conducted 1,000 replications per parameter setting.

## RESULTS

### Parameter Recovery

To check parameter recovery, we calculated the means and the standard deviations of the parameter estimates obtained under the true (data generating) model. Tables 1 through 3 show the means and standard deviations of the estimates obtained using the three models. Generally, the parameter

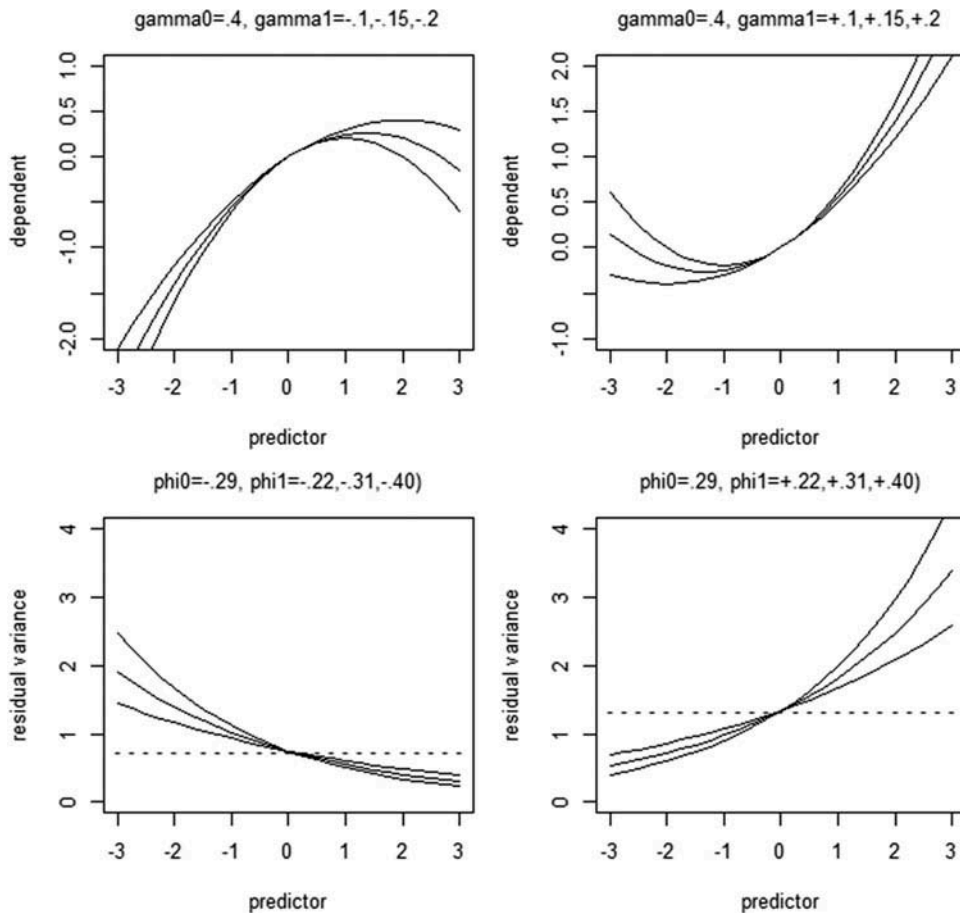


FIGURE 3 Overview of simulated effects. Top left and top right: nonlinearity of the regression relationship (e.g., top left  $\gamma_0 = .4$ ,  $\gamma_1 = .1, .15$ , or  $.20$ , where  $\beta = g_0 + g_1 \eta_x$  and  $E[\eta_y | \eta_x] = \beta \eta_x = \gamma_0 \eta_x + \gamma_1 \eta_x^2$ ; see Equation 6). Bottom left and bottom right: heteroskedastic residual variance as function of  $\eta_x$  (e.g., bottom right  $\phi_0 = .29$ ,  $\phi_1 = .22, .31$ , or  $.40$ , where the residual variance  $\sigma_\varepsilon^2 | \eta_x = \exp[\phi_0 + \phi_1 \eta_x]$ ; see Equation 8).

TABLE 1  
Mean and Standard Deviations of Parameter Estimates Given  $K = 1$  and  $K = 4$  Dependent Variable Indicators, Given Nonlinearity

Effect	Direction	$K = 1$			$K = 4$		
		$\gamma_0$	$\phi_0$	$\gamma_1$	$\gamma_0$	$\phi_0$	$\gamma_1$
Small		.40	-.29	(-).10	.40	-.29	(-).10
	$\gamma_1 < 0$	.40(.06)	-.30(.09)	-.10(.05)	.40(.07)	-.31(.17)	-.10(.05)
	$\gamma_1 > 0$	.40(.06)	-.30(.09)	.10(.05)	.40(.07)	-.32(.17)	.10(.05)
Medium				(-).15			(-).15
	$\gamma_1 < 0$	.40(.06)	-.31(.09)	-.15(.05)	.40(.07)	-.31(.17)	-.15(.05)
	$\gamma_1 > 0$	.40(.06)	-.30(.09)	.15(.05)	.40(.07)	-.30(.17)	.15(.05)
Large				(-).20			(-).20
	$\gamma_1 < 0$	.40(.06)	-.30(.09)	-.20(.05)	.40(.07)	-.31(.17)	-.20(.05)
	$\gamma_1 > 0$	.40(.06)	-.30(.09)	.20(.05)	.40(.07)	-.30(.17)	.20(.05)

Note. The true model (denoted NON-L) was fitted. Results are based on 1,000 replications ( $n = 300$  per replication).

TABLE 2  
Mean and Standard Deviations of Parameter Estimates Given  $K = 1$  and  $K = 4$  Dependent Variable Indicators, Given Heteroskedasticity

Effect	Direction	$K = 1$			$K = 4$		
		$\gamma_0$	$\phi_0$	$\phi_1$	$\gamma_0$	$\phi_0$	$\phi_1$
Small		.40	(-).29	(-).22	.40	(-).29	(-).22
	$\phi_1 < 0$	.40(.06)	-.30(.09)	-.22(.10)	.40(.07)	-.32(.17)	-.23(.13)
	$\phi_1 > 0$	.40(.08)	.27(.08)	.23(.10)	.40(.09)	.27(.14)	.23(.11)
Medium				(-).31			(-).31
	$\phi_1 < 0$	.40(.06)	-.31(.09)	-.31(.10)	.40(.07)	-.31(.17)	-.30(.13)
	$\phi_1 > 0$	.40(.08)	.27(.09)	.31(.10)	.40(.09)	.27(.14)	.31(.11)
Large				(-).41			(-).41
	$\phi_1 < 0$	.40(.06)	-.30(.09)	-.41(.10)	.40(.07)	-.32(.18)	-.40(.13)
	$\phi_1 > 0$	.40(.08)	.27(.09)	.40(.10)	.40(.09)	.27(.14)	.41(.12)

Note. The true model (denoted *Hetero*) was fitted. Results are based on 1,000 replications ( $n = 300$  per replication).

TABLE 3  
Mean and Standard Deviations of Parameter Estimates Given  $K = 1$  and  $K = 4$  Dependent Variables Indicators, Given Nonlinearity and Heteroskedasticity

Effect	Direction	$K = 1$				$K = 4$			
		$\gamma_0$	$\phi_0$	$\gamma_1$	$\phi_1$	$\gamma_0$	$\phi_0$	$\gamma_1$	$\phi_1$
Small		.40	-.29	(-).10	-.22	.40	-.29	(-).10	-.22
	$\gamma_1 < 0 \phi_1 < 0$	.40(.06)	-.31(.10)	-.10(.05)	-.22(.10)	.40(.07)	-.32(.17)	-.10(.05)	-.22(.13)
	$\gamma_1 > 0 \phi_1 < 0$	.40(.06)	-.31(.09)	.10(.05)	-.22(.10)	.40(.07)	-.32(.17)	.10(.05)	-.22(.13)
			.29	(-).10	.22		.29		.22
	$\gamma_1 > 0 \phi_1 > 0$	.40(.08)	.27(.09)	.10(.06)	.23(.10)	.40(.09)	.26(.14)	.10(.06)	.23(.11)
Medium				(-).15				(-).15	
	$\gamma_1 < 0 \phi_1 > 0$	.40(.08)	.27(.09)	-.10(.06)	.23(.10)	.40(.09)	.26(.14)	-.10(.06)	.23(.13)
	$\gamma_1 < 0 \phi_1 < 0$	.40(.07)	-.31(.10)	-.15(.05)	-.31(.10)	.40(.07)	-.32(.17)	-.15(.05)	-.31(.13)
	$\gamma_1 > 0 \phi_1 < 0$	.40(.07)	-.31(.10)	.15(.05)	-.32(.05)	.40(.08)	-.32(.17)	.15(.05)	-.31(.13)
			.29	(-).15	.31		.29	(-).15	.31
	$\gamma_1 > 0 \phi_1 > 0$	.40(.08)	.27(.09)	.15(.06)	.31(.10)	.41(.09)	.26(.14)	.15(.06)	.31(.11)
Large				(-).20				(-).20	
	$\gamma_1 < 0 \phi_1 > 0$	.40(.08)	.27(.09)	-.15(.06)	.31(.10)	.40(.09)	.26(.14)	-.15(.06)	.31(.12)
	$\gamma_1 < 0 \phi_1 < 0$	.40(.08)	-.31(.17)	-.20(.05)	-.40(.10)	.40(.08)	-.32(.17)	-.20(.06)	-.41(.13)
	$\gamma_1 > 0 \phi_1 < 0$	.40(.07)	-.31(.10)	.20(.05)	-.41(.12)	.40(.08)	-.31(.17)	.20(.06)	-.40(.14)
			.29	(-).20	.41		.29	(-).20	.41
	$\gamma_1 > 0 \phi_1 > 0$	.40(.09)	.27(.09)	.20(.07)	.40(.10)	.40(.09)	.26(.14)	.20(.07)	.41(.12)
	$\gamma_1 < 0 \phi_1 > 0$	.40(.08)	.27(.09)	-.20(.06)	.40(.11)	.40(.09)	.26(.14)	-.19(.07)	.41(.12)

Note. The true model (denoted Full) was fitted. Results are based on 1,000 replications ( $n = 300$  per replication).



values are recovered correctly. The parameter estimates pertaining to the residual variance ( $\phi_0$ ,  $\phi_1$ ) are slightly biased. However, the differences are negligible in the light of the standard deviations of the estimates. For instance, in Table 2, given  $K = 1$ , the expected value of  $\phi_0$  is .29 (in absolute value) and the mean estimated values vary between .27 and .31 (in absolute value), with a standard deviation of about .09. The estimates of the parameter pertaining to the regression function are accurate.

## Power

We evaluated the power of the likelihood ratio test to detect various effects. Given either nonlinearity or heteroskedasticity, we fitted the true data generating model (either NON-L or HETERO) and the alternative BASIC model. The likelihood ratio was based on minus twice the difference in likelihood values (BASIC vs. NON-L or HETERO; i.e., 1 *df* test). Given both effects, we fitted the true model (FULL) and the BASIC model. The likelihood ratio was based on minus twice the difference in likelihood values (BASIC vs. FULL; i.e., 2 *df* test). Table 4 contains the empirical power estimates based on 1,000 replications. Given medium effect sizes (i.e.,  $\phi_1 = \pm.31$  and  $\gamma_1 = \pm.15$ ), the power ( $df = 2$ ,  $\alpha = .05$ ) to detect both effects simultaneously is good (power = .89 or better). The power to

detect heteroskedasticity ( $\phi_1 \neq 0$ ) or nonlinearity ( $\gamma_1 \neq 0$ ) is sufficient (i.e., 1 *df* tests) given median effect sizes with power varying between .83 and .97 ( $\gamma_1 = \pm.15$ ) and .69 and .90 ( $\phi_1 = \pm.31$ ). Given small effect sizes (i.e.,  $\phi_1 = \pm.22$  and  $\gamma_1 = \pm.1$ ) the 1 *df* tests are appreciably lower (ranging from .46–.68 to detect heteroskedasticity, ranging from .54–.63 to detect heteroskedasticity). Similarly, power of the 2 *df* tests is insufficient given small effects (ranging from .59–.87). Clearly  $N = 300$  is too small a sample size to detect these effects with adequate power.

The 2 *df* tests have lower power if the effects are opposite effect (e.g., negative nonlinearity and positive heteroskedasticity). For instance, given small effects and  $K = 1$ , the power is .87 and .71 given consistent effects, and .79 and .66 given opposite effects (see Table 4 rows 13–16). Interestingly, this finding is consistent with the effects on the unconditional distribution of the data. Specifically, heteroskedasticity and nonlinearity consistently give rise to nonnormality, as evaluated using the Shapiro–Wilks test (results available on request). However, when both effects are present in opposite directions, nonnormality is harder to detect, which suggests that opposite effects on the distribution appear to cancel out. This suggests that apparent normality per se does not rule out the presence of heteroskedasticity in combination with opposite-effect nonlinearity.

## Misspecification

We considered misspecified models to gauge the effect of the misspecification on the other parameters. We focused on the effects of the misspecification (dropping a parameter) on the other parameters as we wanted to establish the bias in the other parameters that this causes. We do not consider the effect on the goodness of fit per se as the results in Table 4 address this issue (in terms of power). We simulated data using three data generating models with either one effect (HETERO or NON-L), or both effects (FULL) present. We fitted misspecified models, which excluded these effects, as shown in Table 5. We simulated 1,000 data sets with the medium effect sizes for both  $K = 4$ , and  $K = 1$  with positive heteroskedasticity and positive nonlinearity.

We limit our discussion to the  $K = 1$  condition, as the  $K = 4$  results are similar. First, we consider the results obtained when the misspecified models were fit to data generated using the HETERO model (i.e.,  $\phi_1 \neq 0$ ,  $\gamma_1 = 0$ ). In the BASIC model (i.e., fixing  $\phi_1$  to zero), the variance parameter  $\phi_0$  is somewhat biased (–.25 vs. –.29), as is to be expected. The results of fitting the NON-L model ( $\phi_1$  fixed to 0, and  $\gamma_1$  estimated), demonstrates that  $\gamma_1$  is hardly affected by the misspecification: –.03 ( $SD = .05$ ) versus 0. Considering data generated under the NON-L model (i.e.,  $\phi_1 = 0$ ,  $\gamma_1 \neq 0$ ), we find that fitting the BASIC model (i.e.,  $\phi_1$  fixed to zero) results in a bias in the variance parameter  $\phi_0$  (–.24 vs. –.29). Fitting the HETERO model (i.e.,  $\phi_1 \neq 0$ ,  $\gamma_1 = 0$ ) demonstrates that  $\phi_1$  is hardly affected by the misspecification (estimate = .06;  $SD = .10$ ), but that  $\gamma_0$  is

TABLE 4  
Empirical Power to Detect Effects Given  $\alpha = .05$ ; 1 *df* Test ( $\gamma_1 \neq 0$  or  $\phi_1 \neq 0$ ) and 2 *df* Test ( $\gamma_1 \neq 0$  and  $\phi_1 \neq 0$ ), Given  $K = 1$  and  $K = 4$   
Dependent Variable Indicators

Effect size	Direction	$K = 1$	$K = 4$
Small	$\gamma_1 < 0$	.63	.55
	$\gamma_1 > 0$	.61	.54
Medium	$\gamma_1 < 0$	.89	.86
	$\gamma_1 > 0$	.83	.97
Large	$\gamma_1 < 0$	.98	.97
	$\gamma_1 > 0$	.99	.97
Small	$\phi_1 < 0$	.67	.46
	$\phi_1 > 0$	.68	.55
Medium	$\phi_1 < 0$	.89	.69
	$\phi_1 > 0$	.90	.82
Large	$\phi_1 < 0$	.99	.91
	$\phi_1 > 0$	.99	.95
Small	$\gamma_1 < 0, \phi_1 < 0$	.87	.75
	$\gamma_1 > 0, \phi_1 < 0$	.79	.69
	$\gamma_1 > 0, \phi_1 > 0$	.71	.63
	$\gamma_1 < 0, \phi_1 > 0$	.66	.59
Medium	$\gamma_1 < 0, \phi_1 < 0$	.99	.97
	$\gamma_1 > 0, \phi_1 < 0$	.97	.95
	$\gamma_1 > 0, \phi_1 > 0$	.95	.93
	$\gamma_1 < 0, \phi_1 > 0$	.91	.89
Large	$\gamma_1 < 0, \phi_1 < 0$	1	1
	$\gamma_1 > 0, \phi_1 < 0$	1	1
	$\gamma_1 > 0, \phi_1 > 0$	1	.99
	$\gamma_1 < 0, \phi_1 > 0$	.99	.98

Note. Results are based on 1,000 replications ( $n = 300$  per replication).

TABLE 5  
Parameter Estimates in Misspecified Models, Given  $K = 1$  or  $K = 4$  Dependent Variable Indicators

True Model	Fitted Model	$K = 1$			$K = 4$				
		$\gamma_0$	$\phi_0$	$\gamma_1$	$\phi_1$	$\gamma_0$	$\phi_0$	$\gamma_1$	$\phi_1$
HETERO		.40	-.29	.00	-.31	.40	-.29	.00	-.31
	BASIC	.40(.06)	-.25(.09)	-.03(.05)		.39(.07)	-.26(.17)	-.02(.05)	
NONL	NON-L	.40(.06)	-.27(.09)			.40(.07)	-.27(.17)		
		.40	-.29	.15	.00	.40	-.29	.15	.00
FULL	BASIC	.40(.06)	-.24(.09)		.06(.10)	.40(.07)	-.25(.17)		-.04(.12)
	HETERO	.38 (.06)	-.25(.09)			.389 (.07)	-.25(.17)		
FULL		.40	-.29	.15	-.31	.40	-.29	.15	-.31
	BASIC	.40(.06)	-.20(.09)	.13(.05)	-.23(.10)	.40(.07)	-.20(.17)	.13(.05)	-.26(.13)
	HETERO	.45(.06)	-.24(.09)			.45(.08)	-.25(.17)		
	NON-L	.39(.06)	-.23(.09)			.39(.07)	-.25(.17)		

Note. Results are based on 1,000 replications ( $n = 300$  per replication).

slightly biased (.38 vs. .40). Overall misspecification could result in appreciable bias. However, the misspecification of heteroskedasticity ( $\phi_0 = 0$  and  $\gamma_1 \neq 0$  rather than  $\phi_1 \neq 0$  and  $\gamma_1 = 0$ ) produced little bias in the regression parameters ( $\gamma_1$  is estimated close to its true value of 0), and vice versa. This suggests that the parameter sets  $\{\gamma_0, \gamma_1\}$  and  $\{\phi_0, \phi_1\}$  are relatively independent.

### ILLUSTRATION

#### Data

We fitted the model to a subset of items from the Big Five Personality questionnaire 5PFT (Elshout & Akkerman, 1975). The 5PFT consists of five scales, each including 14 items measured with 7-point Likert scales. The data were obtained from Smits, Dolan, Vorst, Wicherts, and Timmerman (2011), and were collected in a sample of first-year psychology students in the Netherlands between 1982 and 2007. Smits et al. (2011) demonstrated that the 5PFT dimensions correspond to the five dimensions of the NEO PI (Costa & McCrae, 1985). We analyzed the data of the male students ( $N = 2,764$ ) 18 to 25 years old. We created two subsamples of  $n = 1,382$ , a discovery and a replication sample.

Based on item reliability, we selected a subset of four predictors and four observed outcome items from the Neuroticism and the Extroversion scale. The reliabilities (Cronbach's  $\alpha$ ) of these small scales are .78 (Extroversion) and .84 (Neuroticism) in the first sample, and .78 (Extroversion) and .85 (Neuroticism) in the second sample. The means and the standard deviations in the two samples are shown in Table 6.

#### Models

To illustrate the model, we used two different functions to model heteroskedasticity and nonlinearity. First, we used the

TABLE 6  
Overview of Means and Standard Deviations in the Two Samples Used in the Illustration

	Sample 1 ( $n = 1,382$ )		Sample 2 ( $n = 1,382$ )	
	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>
Age	20.59	1.87	20.6	1.88
YE1	4.44	1.52	4.46	1.52
YE2	4.10	1.59	4.15	1.57
YE3	4.33	1.53	4.42	1.48
YE4	4.56	1.48	4.59	1.48
YN1	3.36	1.42	3.33	1.39
YN2	3.18	1.62	3.12	1.62
YN3	3.70	1.51	3.63	1.51
YN4	3.10	1.56	3.00	1.50

Note. YE1 to YE4 are the indicators of extraversion; YN1 to YN4 are the indicators for neuroticism.

first-order polynomial function using the regression parameters  $\gamma_0, \gamma_1$ , and heteroskedasticity parameters  $\phi_0, \phi_1$ . Second, we used the step function using the parameters  $\kappa_0, \kappa_1, \kappa_2$  (see Equation 7) for the stepwise regression, and stepwise heteroskedasticity parameters  $\xi_0, \xi_1, \xi_2$  (see Equation 10). For the step function, the cutoff points were set at  $-1 SD$  and  $+1 SD$  of the item scores. We first fitted the full models in which both effects were present (denoted either S-FULL or L-FULL), and we then fitted the nonlinearity model (NON-L) and the heteroskedasticity model (HETERO). Finally, we fitted the standard latent regression model. In total, we fitted seven different models: BASIC, L\_HETERO, L\_NON-L, L\_FULL, and S\_HETERO, S\_NON-L, S\_FULL. In the polynomial and the step function model, we applied the likelihood ratio test to determine whether we could drop the heteroskedasticity, the nonlinearity parameter, or both by making the following comparisons. For both the polynomial model and the step function model we first compared the FULL model with the BASIC

model using an omnibus test (both effects). Second, we compared the FULL model with the HETERO and NON-L model. Finally, we compare the HETERO and NON-L model with the BASIC model. Given the exploratory nature of these analyses, we adopted an  $\alpha$  of .05 and used the replication sample to replicate results obtained in the discovery sample. To determine which model best fit the data, we compared the overall fit of the models using Akaike's information criteria (AIC). All models were fitted to the Neuroticism and Extroversion data (discovery sample and the replication sample) in OpenMx (Boker et al., 2011) by maximizing the likelihood function given in Equation 11.

## RESULTS

### Results Using the Polynomial Model

Table 7 gives an overview of the fit measures and likelihood ratio tests obtained in fitting the models to the two data sets. We found that in the polynomial model the omnibus test of both effects (nonlinearity and heteroskedasticity) was significant in the discovery sample and replicated in the replication sample: comparison of L\_FULL with BASIC, discovery sample,  $\chi^2(2) = 11.73$ ,  $p = .0028$ ; replication sample,  $\chi^2(2) = 15.69$ ,  $p = .0004$ . Additional comparisons showed that the nonlinearity parameter  $\gamma_1$  was not significant: L\_FULL versus L\_HETERO model, discovery sample 1,  $\chi^2(1) = .35$ ,  $p = .55$ ; replication sample,  $\chi^2(1) = 1.21$ ,  $p = .27$ ; whereas the heteroskedasticity parameter  $\phi_1$  was significant: L\_FULL versus L\_NONL model, discovery sample,  $\chi^2(1) = 8.34$ ,  $p = .004$ ; replication sample,  $\chi^2(1) = 7.37$ ,  $p = .007$ . Given these tests, we considered L\_HETERO the model of choice. Further comparison of the L\_HETERO model with the BASIC model also showed that the heteroskedasticity parameter  $\phi_1$  was significant: L\_HETERO to BASIC, discovery sample,  $\chi^2(1) = 11.38$ ,  $p = .0007$ ; replication sample 2,  $\chi^2(1) = 14.47$ ,  $p = .0001$ . We concluded that the L\_HETERO model gives the best account of the data. It is important to note that the comparison of the L\_NON-L model with the BASIC model (i.e., the test of nonlinearity without taking into account heteroskedasticity) suggests that nonlinearity is present in the second sample: discovery sample, L\_NON-L to BASIC,  $\chi^2(1) = 3.39$ ,  $p = .065$ ; replication sample,  $\chi^2(1) = 8.31$ ,  $p = .004$ . This demonstrates the importance of considering simultaneously heteroskedasticity and nonlinearity.

### Results Using the Step Function Model

In the step function model, the omnibus tests of both effects were significant: comparison of S\_FULL with BASIC, discovery sample,  $\chi^2(4) = 62.78$ ,  $p < .0001$ , replication sample,  $\chi^2(4) = 35.64$ ,  $p < .0001$ . Additional comparisons showed that the step regression parameters,  $\kappa_1$  and  $\kappa_2$ , and the step

heteroskedasticity parameters,  $\zeta_1$  and  $\zeta_2$  (see Equation 10), were significant: S\_FULL versus S\_HETERO, discovery sample,  $\chi^2(2) = 29.03$ ,  $p < .0001$ ; replication sample,  $\chi^2(2) = 17.48$ ,  $p = .001$ ; S\_FULL versus S\_NON\_L, discovery sample,  $\chi^2(2) = 55.15$ ,  $p < .0001$ ; replication sample,  $\chi^2(2) = 26.06$ ,  $p < .0001$ . Using the step function model, the FULL model provided the best account of the data.

Comparing the AIC of the two models of choice (L\_HETERO and S-FULL) showed that the S-FULL fitted the data best (discovery sample: AIC L\_HETERO = 14657.03, AIC S\_FULL = 14611.63; replication sample: AIC L\_HETERO = 14522.87, AIC S\_FULL = 14507.70). Comparing the parameter estimates of the two models (Table 8), the difference in the implied regression relation and residual variance are apparent. We plotted the regression relation and residual variance of the BASIC model, the L\_HETERO, and the S\_FULL model in Figure 4. Based on the parameters of L\_HETERO model, the regression relation of the polynomial function is equal to the regression relation of the basic model. However, the residual variance is larger at the lower region of extroversion than in the higher region of extroversion (i.e.,  $\sigma^2[\text{neuroticism} \mid \text{low extroversion}] > \sigma^2[\text{neuroticism} \mid \text{high extroversion}]$ ). This implies a stronger relation between neuroticism and extroversion in the high regions of extroversion. For the S\_FULL model, we note that the regression relation is only present at the lower and higher regions of extroversion ( $SD < -1$  or  $SD > 1$ ), whereas in the midrange (between  $-1 SD$  and  $+1 SD$ ), there seems to be no relation between the two constructs. Additionally, we note that the residual variance is largest in the midrange, and smallest at the high tail of the distribution, which implies a stronger relation between neuroticism and extroversion in the high regions of extroversion.

## DISCUSSION

In this article, we used the indirect mixture modeling approach to model latent heteroskedasticity and nonlinearity in latent regression using MML estimation. The approach is based on the MML estimation as presented by Bock and Aitkin (1981) in the context of IRT modeling, and by Klein and Moosbrugger (2000) in the context of structural equation modeling (see also Moosbrugger et al., 2009). Molenaar, Dolan, and de Boeck (2012; see also Molenaar, Dolan, & Verhelst, 2010) used this approach to model heteroskedasticity and nonlinearity in IRT and factor models.

The possibility to model nonlinearity and heteroskedasticity simultaneously is interesting for both statistical and theoretical reasons. As shown in the simulation study, ignoring heteroskedasticity in presence of nonlinearity leads to biased estimation of the nonlinearity in the regression relation. In the illustration, we showed the consequence of ignoring heteroskedasticity. Failing to model simultaneously

TABLE 7  
Fit Measures and Likelihood Ratio Test Statistics in the Analysis of Neuroticism and Extroversion

Data	Function	Model	AIC	-2LL	df	Model Comparison									
						Compared With BASIC			Compared With FULL						
						LRT	Diff	df	LRT	Diff	df	p	p		
Discovery	Polynomial	BASIC	14666.41	36522.41	10929										
		L_HETERO	14657.03	36511.03	10928	11.38	1	.0007	0.35	1	.555	*			
		L_NON-L	14665.02	36519.02	10928	<b>3.39</b>	1	.066	8.34	1	.004				
	Step	L_FULL	14658.68	36510.68	10927	11.73	2	.0028							
		S_HETERO	14636.67	36488.67	10927	33.74	2	4.71e-8	29.03	55.15	2	4.96e-7	*		
		S_NON-L	14611.63	36514.79	10927	62.78	2	.022							
Replication	Polynomial	S_FULL	36459.63	10925	7.55e-13	4									
		BASIC	14535.34	36393.34	10929										
		L_HETERO	14522.87	36378.87	10928	14.47	8.31	1	.0001	1.21	1	.271	*		
	Step	L_NON-L	14529.03	36385.03	26	15.69	1	.004	7.37	1	.007				
		L_FULL	14523.65	36377.65	27			.0001							
		S_HETERO	14521.18	36375.18	10927	18.16	9.58	2	.0001	17.48	2	.001	*		
	S_NON-L	14529.76	<b>36383.76</b>	36357.70	35.64	2	.008	26.06	2	2.19e-6					
	S_FULL	14507.70		10925		4	3.43e-7								

Note. Top part of the table contain the results obtained with the two models in the discovery sample ( $n = 1,382$ ); bottom part contains the results obtained in the replication sample ( $n = 1,382$ ).

TABLE 8  
Parameter Estimates for the Two Data Sets Used in the Illustration of the Model

Data	Function	Model	Parameter estimates					
			Non-linearity			Heteroskedasticity		
			$\gamma_0$	$\gamma_1$		$(\log)\phi_0$	$(\log)\phi_1$	
Data 1	Polynomial	BASIC	-.49(.03)	—		.68(.08)	—	
		HETERO	-.49(.03)	-.05(.03)		.66(.08)	.81(.06)	*
		NON-L	-.48(.03)	-.02(.03)		.68(.08)	.82(.07)	
		FULL	-.50(.03)			.66(.08)		
	Step	BASIC	$\kappa_0$	$\kappa_1$	$\kappa_2$	$\xi_0$	$\xi_1$	$\xi_2$
		HETERO	-.49(.03)	—	—	.68(.08)	—	—
		NON-L	-.52(.02)	-.40(.15)	-.25(.15)	.77(.07)	.08(.07)	-.41(.04)
		FULL	-.21(.13)	-.62(.14)	-.66(.12)	.67(.05)	.11(.07)	-.42(.04)
Data 2	Polynomial	BASIC	$\gamma_0$	$\gamma_1$		$(\log)\phi_0$	$(\log)\phi_1$	
		HETERO	-.45(.03)	—	—	.77(.08)	—	—
		NON-L	-.45(.03)	-.08(.03)	—	.75(.08)	.81(.06)	*
		FULL	-.43(.03)	-.03(.03)		.76(.08)	.84(.07)	
	Step	BASIC	$\kappa_0$	$\kappa_1$	$\kappa_2$	$\xi_0$	$\xi_1$	$\xi_2$
		HETERO	-.45(.03)	—	—	.77(.08)	—	—
		NON-L	-.52(.02)	-.38(.15)	-.15(.16)	.80(.00)	-.18(.08)	-.39(.00)
		FULL	-.22(.12)	-.61(.15)	-.75(.13)	.76(.08)	-.15(.09)	-.41(.04)
		FULL	-.06(.12)			.72(.06)		

heteroskedasticity and nonlinearity, we would have concluded that the relationship between extroversion and neuroticism was nonlinear, but we would not have been able to assess the effect of heteroskedasticity. As shown in the real data example, fitting the polynomial function would have led to a different conclusion.

We consider the flexibility in specifying the function to model nonlinearity and heteroskedasticity a useful feature of this approach. In the illustration, we demonstrated that using different functions to model the latent regression and latent residual provided greater insight into the underlying regression relation. Using the polynomial function, it appeared that the residual variance decreased with extroversion, and that the regression relation was constant over the range of extroversion. However, using the step function, we found that the residual variance was larger in the midrange of extroversion and smaller in the tails. Additionally, we showed that the regression relation was strong in the tails and absent in the midrange of extroversion. This observation underscores the importance of flexibility in the specification of the function with which heteroskedasticity and nonlinearity are modeled.

To establish the viability of the model, we investigated the performance of the model in a small-scale simulation study. We established that parameter recovery is accurate and that given reasonable sample sizes, power is acceptable. We observed lower power given opposite effects of nonlinearity and heteroskedasticity. This can be explained in terms of the detection of nonnormality in the data with regular tests such as the Shapiro–Wilks test. When the

effects of nonlinearity and heteroskedasticity are in opposite directions, their effects on the distribution cancel out. The simulation study also showed that misspecification of the model does not lead to incorrect statistical inferences when estimating a parameter known to be zero. Given these results, we consider the model to be viable. However, we note that ignoring either heteroskedasticity or nonlinearity when both effects are known to be present in data does lead to biased estimation of the strength of the regression relation.

This study has the following limitations. First, we only considered a limited number of indicators of both the predictor and the dependent, although many psychological phenomena are measured with more indicators (e.g., items in the questionnaire). The addition of indicators is relatively straightforward. Second, we also considered a limited number of factors, although psychological theories often concern numerous constructs. Generalization of the model to multiple factors might be accomplished via the use of multivariate Gauss–Hermite quadratures. Within the MML framework, extension of the model might only be feasible for a small number of factors (up to five; see Wood et al., 2002). For larger models, a Bayesian estimation procedure is a viable option (e.g., Arminger & Muthén, 1998; Molenaar & Dolan, 2014). Third, we limited the simulation study to the first-order heteroskedasticity and first-order nonlinearity model. As discussed in Molenaar et al. (2010), and demonstrated in our example, the model can be extended to polynomial functions, other nonlinear functions, and step functions. As such, a variety of nonlinear



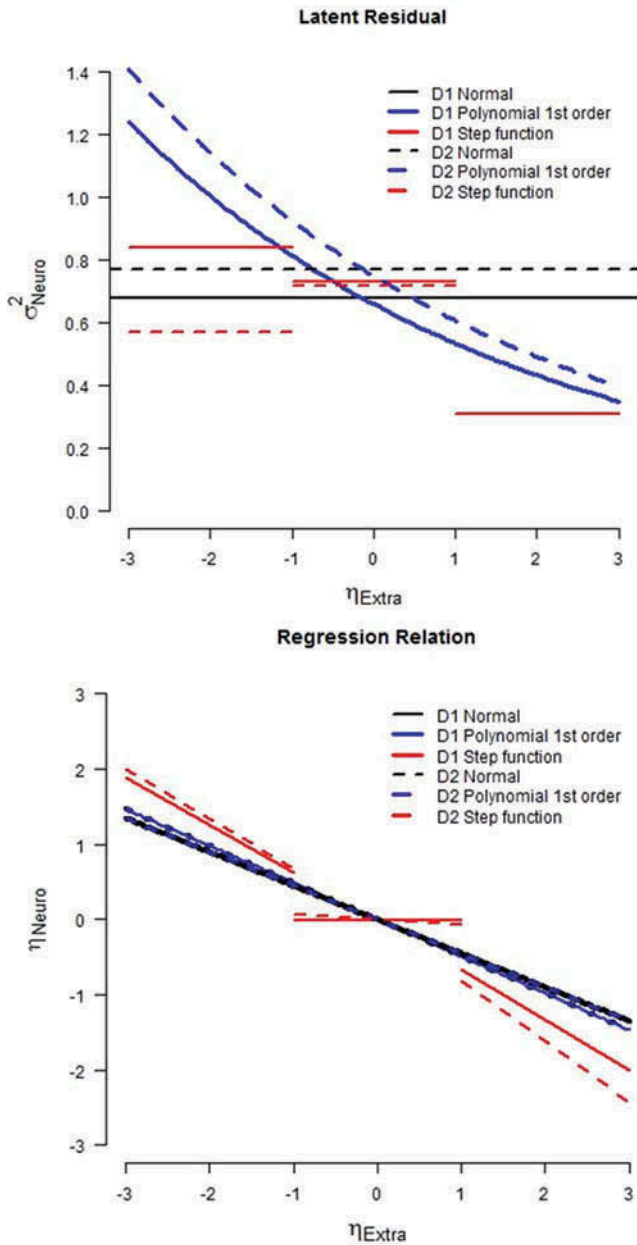


FIGURE 4 Effect of the parameter estimates on the latent residual variance (top) and the regression relation (bottom). Parameter values of best fitting model are used, as given in Table 8.

relations can be considered and tested in practice. This method requires the specification of functions to accommodate nonlinearity and heteroskedasticity. For a more exploratory approach to nonlinearity of the regression function based on indirect mixture modeling, we refer to Bauer (2005; Pek et al., 2009), and for a recent exploratory data mining approach that can handle nonlinearity, we refer to Miller, Lubke, McArtor, and Bergeman (in press). Finally, we have assumed that the predictor and conditional dependent variable (i.e., conditional on  $\eta_{\text{Extra}}$ ) are normally

distributed. Kelava et al. (2014) presented a nonlinear latent regression model with nonnormal predictors.

## ORCID

Conor V. Dolan  <http://orcid.org/0000-0002-2496-8492>  
Dylan Molenaar  <http://orcid.org/0000-0002-7168-3238>

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