

# Longitudinal Genetic Analysis for Loneliness in Dutch Twins

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In previous studies we obtained evidence that variation in loneliness has a genetic component. Based on adult twin data, the heritability estimate for loneliness, which was assessed as an ordinal trait, was 48%. These analyses were done on loneliness scores averaged over items ('I feel lonely' and 'Nobody loves me') and over time points. In this article we present a longitudinal analysis of loneliness data assessed in 5 surveys (1991 through 2002) in Dutch twins ( $N = 8389$ ) for the two separate items of the loneliness scale. From the longitudinal growth modeling it was found sufficient to have non-zero variance for the intercept only, while the other effects (linear, quadratic and cubic slope) had zero variance. For the item 'I feel lonely' we observed an increasing age trend up to age 30, followed by a decline to age 50. Heritability for individual differences in the intercept was estimated at 77%. For the item 'Nobody loves me' no significant trend over age was seen; the heritability of the intercept was estimated at 70%.

Loneliness can be described as consisting of feelings of social isolation and dissatisfaction with one's social relationships. There is substantial evidence that loneliness is at the heart of a constellation of socioemotional states, which include self-esteem, mood, anxiety, anger, optimism, fear of negative evaluation, shyness, social skills, social support, dysphoria, and sociability (see e.g., Berscheid & Reis, 1998; Cacioppo et al., 2002; Duck et al., 1994; Ernst & Cacioppo, 1999; Hawkey et al., 2005; Peplau & Perlman, 1982; Rook, 1988; Shaver & Brennan, 1991; Weiss, 1973).

Recently, we found that genetic factors influence individual differences in loneliness in adults. By taking an average score of two loneliness items up to five different time points over a 12-year period, we found that the heritability ( $h^2$ ) for variation in loneliness was 48% (Boomsma et al., 2005). The genetic contributions to loneliness were similar in men and women. No qualitative sex differences in heritability were found, indicating that the same genes influence

loneliness in both sexes. In a subsequent linkage analysis, we obtained suggestive evidence that a quantitative trait locus (QTL) on chromosome 12 influences variation in loneliness (Boomsma, Cacioppo, et al., 2006). Comparable heritability estimates were suggested in studies of children (McGuire & Clifford, 2000).

In this article we examine the loneliness items in the Netherlands Twin Register (NTR) with a full genetic growth model, instead of taking an average score over a 12-year period. This analysis makes use of the strength of the study design in which individuals are followed longitudinally so that their status is assessed by multiple measurements (up to five surveys). At each of the five measurement occasions there is a considerable age variation among individuals. At the first occasion mainly adolescents and young adults participated, their age range is 13 to 22 years. At later occasions, new adolescents entered into the study, as well as adult twins. This resulted in an age range of 14 to 85 years at the last measurement occasion. In this article we show how to account for this age variation, with growth specified as a function of age rather than measurement occasion, allowing individually varying ages at each occasion.

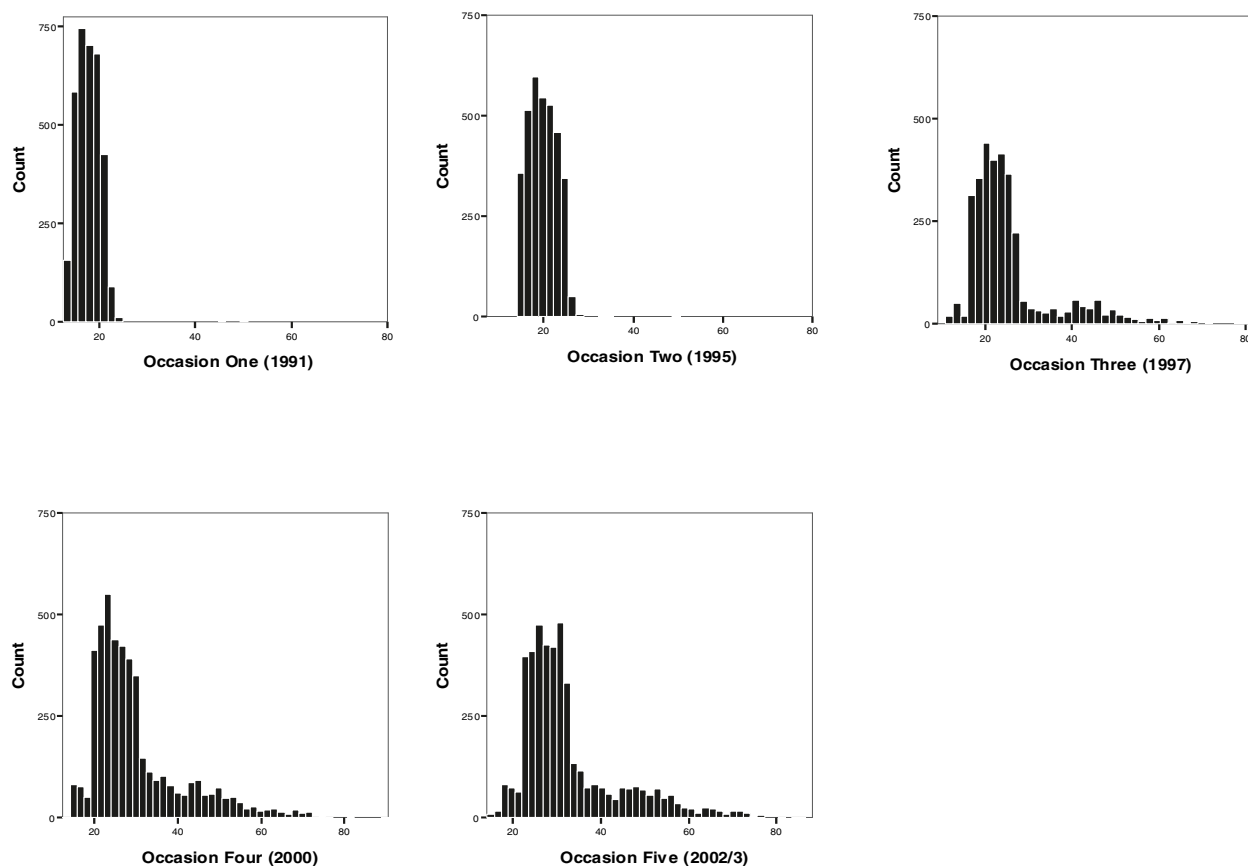
## Methods

### Subjects and Phenotypes

In 1991 the NTR started a longitudinal survey study of health and lifestyle in adolescent and adult twins and their family members (Boomsma, Vink, et al., 2002; Boomsma, de Geus, et al., 2006). Surveys were mailed to twin families every 2 to 3 years. Adolescent and young adult twins were recruited through City Council registrations in 1990 to 1991 and in 1992 to 1993. After 1993 an effort was also made to recruit additional adult and older twins through a variety of approaches. New twins could enter the study at any

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**Figure 1**  
Age distribution at the five measurement occasions.

point in time. Details on response rates, response bias, and demographic characteristics of the sample can be found elsewhere (Koopmans et al., 1999; Stubbe et al., 2005; Vink et al., 2004;). Surveys were mailed out in 1991, 1993, 1995, 1997, 2000, 2002/3 and 2004/5. Five surveys (not the 1993 and 2004 surveys) contained the Young Adult Self Report (YASR; Achenbach, 1990). Based on factor analyses (Boomsma et al., 2005), we selected two YASR items (item 12: ‘I feel lonely’, and item 33: ‘Nobody loves me’), which could be answered on a 3-point scale (never, sometimes, often). For over 35% of the same-sex twin pairs zygosity was assessed based on DNA or blood group polymorphisms. Table 1 summarizes the

number of participating twins by sex and zygosity. A total of 4591 pairs participated (793 incomplete and 3798 complete pairs). Table 2 gives an overview of the longitudinal participation rate. Subjects could take part from one to five times.

**Longitudinal Genetic Analysis**

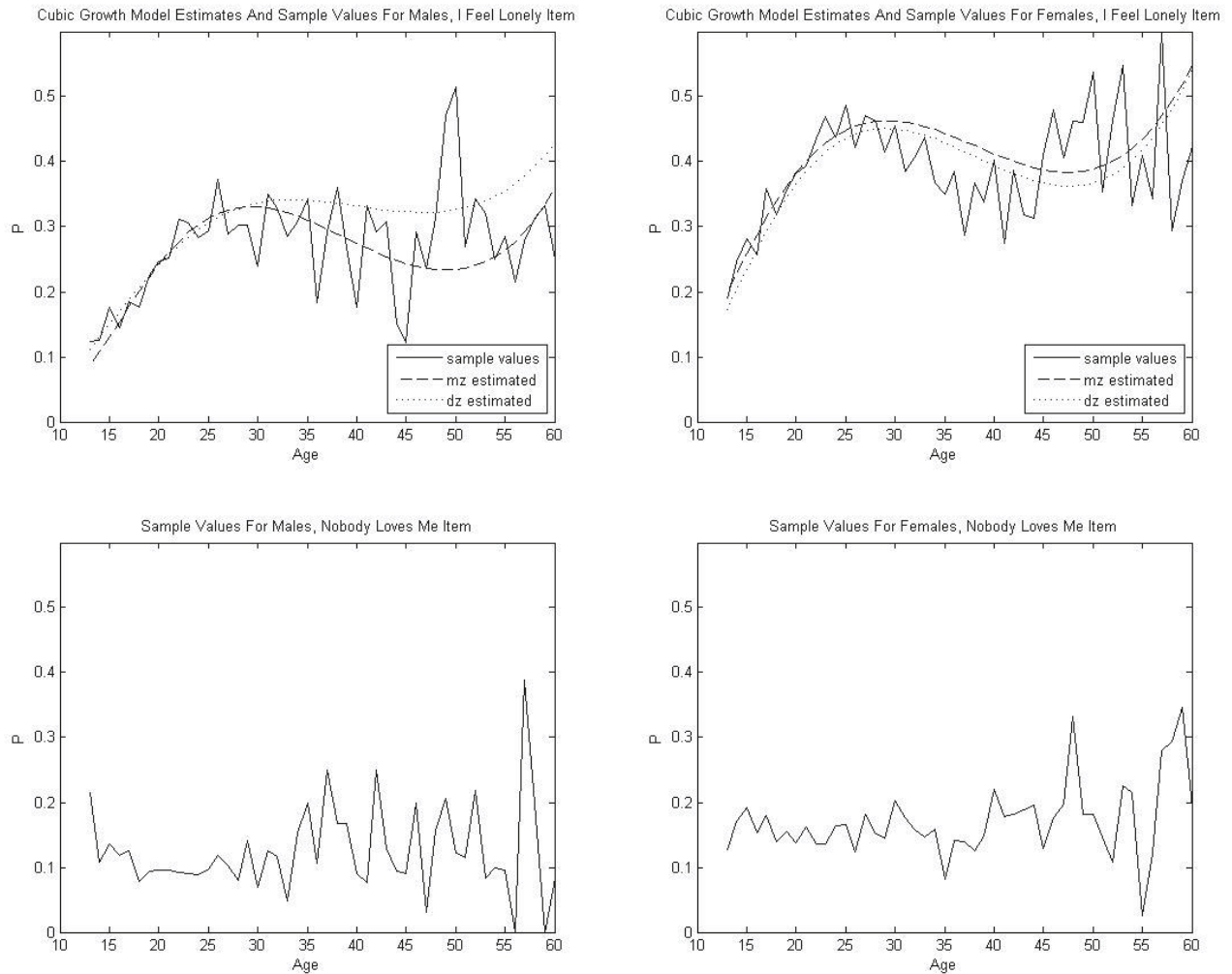
Individuals are followed longitudinally so that their loneliness status is assessed by multiple (one to five) measurements. At each of the five measurement occasions there is considerable age variation among individuals. At the first occasion, the age range is 13 to 22 years. Together with new adolescents entering into the study, later occasions also include adult twins resulting in an age range of 14 to 85 at the last measurement occasion. The age distribution for every measurement occasion is shown in Figure 1.

Figure 2 shows the observed proportions of individuals at different ages who endorse each of the two items (shown as jagged curves). The proportions are plotted for the combined categories ‘sometimes’ and ‘often’. The item ‘I feel lonely’ shows an increase in early adulthood, followed by a decrease in middle-aged subjects, with a possible upturn thereafter. The item ‘Nobody loves me’ shows no trend over time. It

**Table 1**  
Full Sample: Number of Twins According to Sex and Zygosity

	Twins Total <i>N</i>	Twins MZ	Twins DZ-SS	Twins DOS
Females	5108	2542	1460	1106
Males	3281	1327	966	988

Note: MZ is monozygotic and DZ is dizygotic



**Figure 2**

Estimated item proportions and estimated probabilities as a function of gender and age.

should be emphasized that the proportions have high variability at the ends of the age range because of a limited number of older subjects.

A logistic random effects growth model (see, e.g., Fitzmaurice et al., 2004) is used to model the individual development in item endorsement probabilities over time. To account for the within-occasion age variation in the growth model, growth is specified as a function of age rather than occasion, allowing individually varying ages at each occasion. A growth function allowing a cubic polynomial is used to permit a flexible growth shape. With the example of a binary outcome  $u_{it}$  for occasion  $t$  and individual  $i$ , the logistic growth model is expressed in terms of item endorsement probabilities as a cubic function of the log odds of endorsing the item versus not endorsing it,

$$\log [P(u_{it} = 1 | i, s_i, q_i, c_i, x_{it}) / P(u_{it} = 0 | i, s_i, q_i, c_i, x_{it})] = i_i + s_i * (x_{it} - d) + q_i * (x_{it} - d)^2 + c_i * (x_{it} - d)^3, \quad [1]$$

where  $x_{it}$  represents the age of the subject and  $d$  is a centering constant chosen as age 30. Here, the ‘random effect’ intercepts  $i_i$ , linear slopes  $s_i$ , quadratic slopes  $q_i$ , and cubic slopes  $c_i$  are allowed to vary across individuals and the goal is to estimate their means, variances and heritability. In these data it was found sufficient to have non-zero variance for the intercept only while the other effects have zero variance. Within a twin pair, two growth equations are considered, allowing the two random intercepts to correlate and assuming a normal distribution. Families with only one twin are also included. The growth model in equation [1] implicitly assumes that any cohort (period) effects are ignorable so that an individual of a certain age is at the same point on the growth curve irrespective of the measurement occasion. For example, a 20-year-old is assumed to be at the same growth curve point at the first occasion as a 20-year-old at the last occasion, 11 to 12 years later.

The data from the six twin groups of monozygotic males and females (MZM and MZF) and dizygotic

**Table 2**

Longitudinal Participation: Number of Twins

Number of times twins participated	
1	2973
2	2386
3	1558
4	959
5	513

males and females and pairs of opposite sex (DZM, DZF, DOSMF, and DOSFM) are analyzed together using maximum-likelihood estimation with two dimensions of numerical integration in the Mplus program (Muthén & Muthén, 1998–2007). Scripts are available from Muthén on request. Genetic modeling is carried out for a pair of twins by imposing an ACE (additive genetic, common environmental and unique environmental) model on variances and covariances of the random intercepts  $i_{1ik}$ ,  $i_{2ik}$  for Twin 1 and Twin 2,

$$V(i_{1ik}) = V(i_{2ik}) = a_k^2 + c_k^2 + e_k^2, \quad [2]$$

where  $k$  represents male or female, and

$$Cov(i_{1ik}, i_{2il}) = f * a_k * a_l + c_k * c_l, \quad [3]$$

where  $f$  is 1.0 for MZ twins and .5 for DZ twins (Boomsma, Busjahn, et al., 2002).

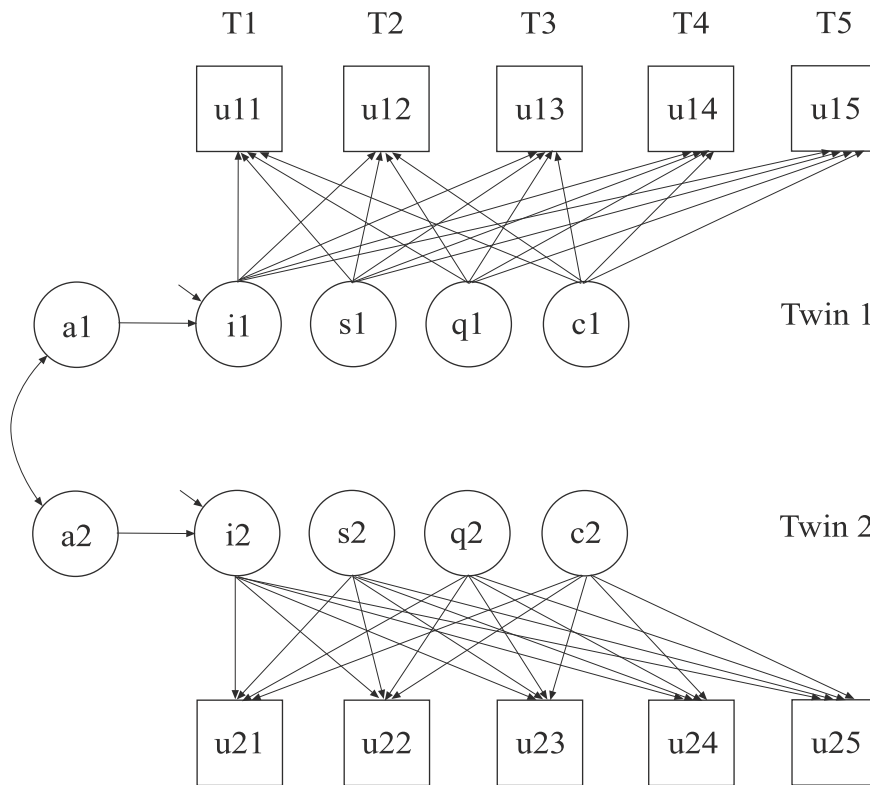
The covariance expression in [3] includes dizygotic twins of opposite sex. As is seen from [2] and [3], the covariance matrix for the random effects is allowed to vary across sex. In addition, the means of the random effects are allowed to vary across both sex and zygosity. For each sex, the heritability is estimated as

$$h_k^2 = a_k^2 / (a_k^2 + c_k^2 + e_k^2). \quad [4]$$

It should be noted that the heritability estimate of the growth model is not affected by changes of the centering constant  $d$  in [1].

The model is shown in diagrammatic form in Figure 3, where for simplicity a same-sex twin pair is considered and the common environment component is left out. For MZ twins the correlation between the additive genetic components  $a_1$  and  $a_2$  is 1.0 and for DZ twins the correlation is .5. It is seen that the analysis is carried out in a ‘wide data’ format using a multivariate single-level model as opposed to a ‘long data’ format using a univariate two-level model. The growth model is similar to parallel process growth modeling often used in latent growth curve analysis.

The analyses of each of the two items ‘I feel lonely’ and ‘Nobody loves me’ used the following steps. First, due to the low prevalence of the highest category ‘often’, the items were first analyzed in both a



**Figure 3**  
Genetic growth model diagram.

dichotomized form ('never' vs. 'sometimes-often') and in their original three-category form (using the conventional proportional-odds specification; Agresti, 2002). The choice had little effect on the heritability estimates and results are presented for the original three-category form. Second, the choice of a linear, quadratic, or cubic model was assessed via likelihood-ratio chi-square testing. This resulted in a cubic model for the item 'I feel lonely' and a linear model for the item 'Nobody loves me'. The cubic model fitted the male sample proportions very well, while the female proportions were underestimated in the 35 to 45 age range. This misfit disappeared when restricting the growth model to subjects no older than 60 years of age. This restriction removed only a small fraction of the sample (340 observations — not subjects — out of 18,981 observations). Third, the need for a random linear slope in addition to a random intercept was assessed by Bayesian information criterion (BIC; Schwartz, 1978) and found not to be needed for either item. Fourth, in addition to gender differences in means, gender differences in variances and covariances of the intercepts were investigated by BIC and found to be ignorable for both items. Fifth, age differences in heritability were studied by analyzing two subsamples (age  $\leq 35$  [3683 families], and  $35 < \text{age} \leq 60$  [787 families]).

## Results

Figure 2 shows the observed proportions of individuals at different ages who endorse each of the two items (shown as jagged curves). The proportions are plotted for the combined categories 'sometimes' and 'often'. For both items, the curves in women show a higher degree of loneliness than the curves in men. The item 'I feel lonely' shows an increase in early adulthood, followed by a decrease in middle-aged subjects, with a possible upturn thereafter. Female and male twins both show an increase in loneliness up to a peak at ages 25 to 30, followed by a decline and a low around age 50. The item 'Nobody loves me' shows no trend over time.

No sex differences in covariance structure were observed. The correlations in MZ and DZ twins for the intercept were .78 and .36 for the 'I feel lonely' item and .69 and .36 for the 'Nobody loves me' item, suggesting an additive genetic model for both items.

Indeed, for both items, the C component of the ACE model for growth was found small and insignificant. For the 'I feel lonely' item the heritability was estimated as .77 ( $SE = 0.03$ ), and for the item 'Nobody loves me' the heritability was .70 ( $SE = 0.05$ ).

The analyses of the subsamples of older and younger subjects indicated heritability differences due to age. For the 'I feel lonely' item, these growth analyses used a quadratic function given the more limited curvature in those age ranges. For the 'I feel lonely' item, analyses of the two age groups resulted in heritabilities of .74 (.08) for ages less than or equal to 35 and .41 (.23) for ages greater than 35 but less than or

equal to 60. For the 'Nobody loves me' item heritabilities were estimated as .74 (.11) for ages less than or equal to 35 and .54 (.10) for ages greater than 35 but less than or equal to 60. However, it should be noted that the group aged between 35 and 60 years is small compared to the other group.

## Discussion

Nearly every adolescent and adult has experienced the ebb and flow of the pain of loneliness. Unsurprisingly, then, Weiss' (1973) pioneering work on loneliness emphasized the circumstances and feelings associated with intense loneliness. Subsequent research has found environmental predictors of loneliness across the lifespan, including childhood trauma (Kochenderfer-Ladd & Wardrop, 2001), peer acceptance (Renshaw & Brown, 1993), ethnic attachment (Kim, 1999), social network size and diversity (Hawkey & Cacioppo, 2007), and bereavement (Grimby, 1993). Intergenerational similarities in loneliness have also been observed, a finding linked to environmental factors such as attachment and child-rearing practices (Lobdell & Perlman, 1986) rather than genetic transmission between generations. Although these factors are labeled as 'environmental' or 'situational', behavior genetics research suggests that the individual variation attributed to these factors may have a genetic basis (e.g., Jockin et al., 1996; Middeldorp et al., 2005).

The question of heritability for loneliness is important in light of sociodemographic changes in the structure of social relationships in industrialized societies over the past several decades. According to the middle projections by the U.S. Census Bureau (1996), for instance, the number of people living alone will grow to almost 29 million by 2010 — more than a 30% increase since 1980. In the General Social Survey, respondents in 2004 were three times more likely to report having no one with whom to discuss important matters than were respondents in 1985 (McPherson et al., 2006). The modal respondent reported three confidants in 1985 and no confidants in 2004. Similarly, in a large Dutch study (Breedveld et al., 2006) it was found that between 1975 and 2005 there was a decrease in the number of hours spent on social contacts from 12.7 to 9.1 hours per week (mainly a decrease in seeing friends).

Despite the demographic changes and associated variations in loneliness, the overall levels of loneliness do not appear to have increased as dramatically as the loss of social confidants and contacts might suggest (cf. Rubenstein & Shaver, 1982; Steffick, 2000). Recent evidence from cross-sectional studies showing that variation in loneliness has a significant genetic component (Boomsma, Cacioppo, et al., 2006; Boomsma et al., 2005; McGuire & Clifford, 2000) may explain at least in part this dissociation. In the present study, we performed a 12-year longitudinal analysis of loneliness in 8389 Dutch twins for two

separate items. Results underscored the importance of studying heritable as well as environmental influences on variations in loneliness. In our data we observe a sex difference with women more often than men endorsing the 'I feel lonely' and an age related increase in the endorsement of this item. For the 'I feel lonely' item heritability was estimated to be 77%. For the item 'Nobody loves me' heritability was estimated to be 70% but no trend with age was observed. The heritability estimates mainly reflect the large influence of genetic factors in young adults (below age 35 years). The estimates in older adults (above age 35 years) were 41% for the 'I feel lonely' item and 54% for the 'Nobody loves me' item. However, the number of older participants was much lower than the sample below age 35 years.

In the longitudinal analyses of the individual items, we observe a difference in heritability estimates compared to our initial results of the loneliness scores averaged over items and measurement occasions (heritability of around 50% vs. a heritability of over 70%). This higher heritability from the longitudinal growth modeling might be explained by the fact that this model can isolate time-specific variation from growth factor variation. If the time-specific reliability of the items is rather low, summing up the sum of 2 items over only a few time points (many subjects have participated only two times) will not give a highly reliable score, which will lead to a lower heritability estimate (if each person had been observed over more time points reliability might improve). We tried out this idea by two analyses. First, summing over the two items for each time point and doing a growth model ACE analysis, simply assuming that the five sums for each twin are continuous variables, gave a heritability estimate in the neighborhood of the current ones. Second, summing also across time points and dividing by the number of occasions observed, gave a lower heritability, as observed in our previous studies. So, in conclusion, a strength of the growth model is that the time-specific, 'irrelevant' variation in the items — the unreliability — is purged from the ACE analysis.

It is important to emphasize, too, that high heritability does *not* imply environmental influences are unimportant for health and well-being. Experimental manipulations of loneliness have shown it to have dramatic effects on a range of outcomes including mood, shyness, anxiety, hostility, and self esteem (Cacioppo, Hawkley et al., 2006), and longitudinal studies statistically controlling for basal levels of loneliness have shown that loneliness promotes increases in depressive symptomatology (Cacioppo, Hughes et al., 2006) and increases in the morning rise in cortisol (Adam et al., 2006). The current results, however, underscore the importance of considering heritable as well as environmental influences in future research on the etiology of loneliness.

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