

Environmental Influences on Well-Being:  
A Dyadic Latent Panel Analysis of Spousal Similarity

Ulrich Schimmack

University of Toronto, Mississauga

Richard E. Lucas

Michigan State University

July 2007

RUNNING HEAD: ENVIRONMENTAL INFLUENCES ON WELL BEING

Authors' Note

We would like to thank Jennifer Tackett, Kelly L. Klump, Lindon Eaves, and Shigehiro Oishi, and Ivana Anusic for helpful comments. The preparation of this article was supported by a standard research grant of the Canadian Social Sciences and Humanities Research Council awarded to the first author. Correspondence regarding this article can be addressed to Ulrich Schimmack at [uli.schimmack@utoronto.ca](mailto:uli.schimmack@utoronto.ca).

Correspondence:

Ulrich Schimmack  
Department of Psychology  
University of Toronto, Mississauga (UTM)  
3359 Mississauga Road North  
Mississauga, Ontario, L5L 1C6, Canada  
phone 905-828-5369 fax 905-569-4326  
email [uschimma@utm.utoronto.ca](mailto:uschimma@utm.utoronto.ca)

## Abstract

This article uses Dyadic Latent Panel Analysis (DLPA) to examine environmental influences on well-being. DLPA requires longitudinal dyadic data. It decomposes the observed variance of both members of a dyad into a trait, state, and an error component. Furthermore, state variance is decomposed into initial and new state variance. Total observed similarity between members of a dyad is decomposed into trait similarity, initial state similarity, new state similarity, and error similarity. Dyadic similarity in new state variance reveals that both members of a dyad change in the same direction, which reveals environmental effects. DLPA is used to examine environmental influences on life satisfaction and domain satisfaction based on 22 annual assessments of married couples in the German Socio-Economic Panel Study ( $Ns = 607$  to  $740$ ). The results show high similarity in new state variance for life satisfaction and objectively identical domains (household income, housing), and less similarity for objectively less similar domains (recreation, health). This finding provides strong evidence for environmental influences on well-being. In addition, the results show high trait similarity. The implications of the latter finding for heritability estimates of well-being in twin studies are discussed.

Keywords: Well Being, Satisfaction, Environment, Longitudinal, Dyadic, Couples

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One of the most interesting and hardest questions in the social sciences is the origin of individual differences. Why are some individuals more or less conscientious, intelligent, healthy, or happy than others? Investigating this important question is difficult because studies of naturally occurring individual differences rely on correlations to make inferences about causality. Personality researchers are well aware of the logical fallacy *cum hoc ergo propter hoc* to infer causality from a single correlation. It is important to note, however, that correlations provide useful information for causal theories, and that a rigorous program of correlational research can reveal causal processes. This article introduces Dyadic Latent Panel Analysis to examine whether environmental factors *cause* individual differences in well-being. After an introduction of the causal model and its implementation in structural equations, Dyadic Latent Panel Analysis is applied to longitudinal panel data to examine the influence of environmental factors on well-being.

*Inferring Causality from Correlations: Monozygotic Twins Reared Apart*

Behavioral genetics research on twins provides the best demonstration of the power of correlational research to demonstrate causality, even when the actual causal variable (i.e., genes) was never observed. Only 40 years ago, the prevalent view in the social sciences was that individual differences are predominantly determined by situational factors that may change rapidly from moment to moment. Today, most social scientists acknowledge that individual differences are stable and that genetic differences explain a substantial portion of individual differences in personality, intelligence, and attitudes (Mischel, 1968; Ross & Nisbett, 1991; Tesser, 1993).

Twin studies allow inferences about causality from correlations because correlations can provide important information about causality. After all, some causal process must produce an observed correlation between two variables (Neale & Cardon, 1992). At the most abstract level, four causal processes that are not mutually exclusive can produce a correlation between two variables, A and B: A may cause B (1), B may cause A (2), or a third variable C causes A (3) and B (4). A single observed correlation is insufficient to estimate the four parameters of the causal model. However, additional assumptions or empirical observations can reduce the number of parameters that need to be estimated. For example, a single correlation between MZ twins reared apart is sufficient to determine causality because twins reared apart cannot influence each other. As a result, it is possible to rule out a causal influence of Twin A on Twin B and vice versa. Furthermore, there is no valid distinction between Twin A and Twin B. As a result, the causal effect of the third variable, C, is equivalent for both. Given  $A \rightarrow B = 0$ , and  $B \rightarrow A = 0$ , and  $C \rightarrow A = C \rightarrow B$ , the causal model reduces from four parameters to one parameter, and it becomes possible to estimate the unknown causal effect based on a single observed correlation. Furthermore, the single parameter can be interpreted as the effect of genes because the only common causal factors between twins reared apart are their genes.

#### *Limitations of Twin Studies with Twins Reared Together*

The example of monozygotic twins reared apart is exceptional. It is more difficult to make inferences about causality when twins share both genetic dispositions and environmental influences (Neale & Cardon, 1992). As noted by Eaves, Fulker, and Heath (1989) "there are effects that cannot be resolved with data on twins by themselves, including the effects of assortment and the shared environment." (p. 113). For example, a zero correlation between biological siblings may suggest that neither genes nor shared environmental influences have a

causal effect. However, it is also possible that genes have a positive effect that makes siblings similar, whereas social influences make them different from each other. For example, aggression may have a 25% heritability, which would contribute  $+0.25$  towards the observed correlation between MZ twins. The actual observed correlation could be close to zero, if other causal factors have a negative influence on the MZ correlation. For example, sibling interaction effects could increase the aggression of the more aggressive twin and decrease the aggression of the less aggressive twin within twin pairs (Plomin, DeFries, McClearn, & McGuffin, 2001). If this negative influence has an effect size of  $r = 0.25$ , the observed correlation between the two MZ twins is close to zero.

Another limitation of twin studies is that they are more suitable to demonstrate genetic than environmental influences on individual differences. The reason is that estimates of environmental influences combine three distinct factors. One factor, the shared environment that has the same influence on both twins produces similarity between twins. For example, parental divorce may have negative effects on the well-being of both twins. The other two factors make twins dissimilar. These two factors are non-shared environment and measurement error. For many individual differences the shared environment between twins is the smallest factor and often makes a negligible contribution. Indeed, twin studies of well-being in adulthood consistently show no effect of the shared environment (Roysamb, Harris, Magnus, Vitterso, & Tambs, 2002; Stubbe, Posthuma, Boomsma, & De Geus, 2005). Thus, estimates of environmental influences are typically limited to influences of the non-shared environment and measurement error.

A major limitation of the standard twin study is that it cannot distinguish between non-shared environmental factors and measurement error. Thus, measurement error may produce

spurious evidence for environmental influences (Schmidt & Hunter, 1996). For example, Stubbe et al. (2005) estimated that 38% of the total variance in life satisfaction was heritable, and that the remaining 62% of the variance was caused by unshared environmental factors and measurement error. Without a precise estimate of the amount of measurement error, the estimate for environmental factors is inflated, and the estimate for heritability is attenuated to an unknown degree. Indeed, longitudinal twin studies found that most of the stable variance in subjective well-being was heritable, whereas environmental influences and measurement error account for most of the unstable variance (Lykken & Tellegen, 1996; Nes, Roysamb, Tambs, Harris, & Reichborn-Kjennerud, 2006). This finding may suggest that environmental influences are transitory, but it may also indicate that a considerable amount of the unstable variance is measurement error. Finally, another limitation of twin studies is uncertainty about the genetic similarity of dizygotic twins and siblings due to the possibility of genetic similarity between parents. This limitation is discussed later in more detail.

#### *Inferring Causality from Correlations: Spousal Similarity*

The study of dyads that are not genetically related overcomes some of the problems inherent in the study of dyads that share genetic and environmental influences in traditional behavioral genetics studies. This article focuses on spousal similarity, but the discussion of spousal similarity can be generalized to other genetically unrelated dyads (e.g., roommates, co-workers, neighbors, etc.). Studies of spouses can separate environmental influences from measurement error because environmental influences on spouses are revealed as shared environment effects, which are not confounded with measurement error. For example, if household income were a positive predictor of well-being, then spouses should have similar levels of well-being because spouses share the same household income.

It is possible to consider spouses as a special case of a traditional behavioral genetics study. In a typical behavioral genetics study of biologically related dyads, genetic similarity is set to a fixed value based on the degree of genetic relatedness (e.g., 1 for MZ twins, .5 for DZ twins, .25 for grandparent-grandchild). For spouses the genetic similarity due to genetic relatedness is zero, under the standard assumption of random mating. The possibility that spouses are genetically similar due to assortative mating is considered later. The ability to fix genetic similarity to zero provides the ability to reveal environmental influences on individual differences with fewer assumptions than studies that have to separate dyadic similarity into a genetic and a shared environmental factor.

In this regard, the advantage of studying spouses for uncovering environmental factors is similar to the advantage of studying mono-zygotic twins reared apart for uncovering genetic factors. For mono-zygotic twins reared apart the environmental influences can be set to zero, and similarity can be directly interpreted as evidence for genetic influences. For spouses the genetic similarity can be set to zero, and similarity can be interpreted directly as evidence for environmental factors. In this regard, studies of spousal similarity are similar to adoption studies, in that the genetic relatedness between biological and adopted children is also zero, and any similarity between them can be directly interpreted as evidence for environmental effects.

Given the lack of evidence for shared environment effects on well-being of adult twins, it is important to emphasize that shared environment effects for spouses are fundamentally different from shared environment effects for adult twins. In a study of adult twins, shared environment captures mostly past environmental factors (e.g., parental influences). In contrast, spousal similarity reveals current environmental influences (e.g., household income, social

influences of spouses on each other, etc.). Thus, shared environment factors for spouses are to a large extent part of the unshared environment variance in twin studies.

One reason for the failure to find shared environment effects in twin studies may be that well-being is influenced primarily by recent environmental factors. Consistent with this hypothesis, twin studies often find a decrease in shared environment effects during adolescence (McCartney, Harris, & Bernieri, 1990). This finding suggests that recent environmental factors that are not shared with a twin become more important over time. In twin studies, these environmental factors are part of the non-shared environment. In studies of spousal similarity, some of these environmental factors are revealed as shared environment factors.

The difference between shared environment with a twin and shared environment with a spouse is illustrated in a study of marital satisfaction in female twins and their husbands (Spotts et al., 2004). The study found that the shared environment with a co-twin had no influence on marital satisfaction (i.e., genes were sufficient to explain twin similarity in marital satisfaction). At the same time, shared environmental factors between spouses, reflected in high spousal similarity, made a substantial contribution to marital satisfaction. In other words, the current shared environment with a spouse influenced marital satisfaction, but the past shared-environment with a twin did not. It seems likely that these results would generalize to other indicators of well-being.

#### *Assortative Mating*

Spousal similarity is not sufficient to prove environmental influences on individual differences. The reason is that spousal similarity may be due to assortative mating; that is, the tendency to select a spouse with similar attributes. For example, spouses are similar in height and individual differences in height are highly heritable (Silventoinen, Kaprio, Lahelma, Viken, &

Rose, 2003). Thus, spousal similarity in height erroneously suggests an environmental influence on height during adulthood, if one neglects assortative mating as an alternative causal mechanism. However, it is equally problematic to assume that spousal similarity is caused by assortative mating, when it is in fact due to shared environmental influences. "Incorrect or untested assumptions about assortative mating for example, will usually lead to incorrect conclusions about genetic architecture and environmental transmission" (Heath & Eaves, 1985, p. 16). In this regard, it is noteworthy that twin studies of well-being have implicitly assumed that spouses are not genetically related, although spouses tend to have similar levels of well-being (Bookwala & Schulz, 1996; Schimmack & Lucas, 2007; Tambs & Moum, 1992). Thus, existing heritability estimates may be biased by incorrect assumptions about the genetic similarity between twins.

Despite the critical importance of separating environmental influences and assortative mating as causes of spousal similarity, this issue has been neglected in empirical studies of well-being. The main reason is probably that most dyadic studies are cross-sectional, and cross-sectional studies make it difficult or impossible to distinguish environmental influences and assortative mating. Longitudinal dyadic studies overcome this limitation (Schimmack & Lucas, 2007). The reason is that assortative mating and shared environment effects make different predictions about the time course of spousal similarity. Assortative mating predicts spousal similarity at the beginning of the marital relationship. It predicts spousal similarity during later stages of the relationship only to the extent that the factors that produced initial similarity remain stable over time. In contrast, changes in the characteristics that produced assortment would reduce spousal similarity. For example, spouses tend to assort on physical attractiveness (Feingold, 1988). However, physical attractiveness changes gradually over time (Alley, 1993;

Zebrowitz, Olson, & Hoffman, 1993). Thus, an assortative mating model predicts that spousal similarity in physical attractiveness decreases over time. To illustrate, assume that spousal similarity in attractiveness at the beginning of marriage is  $r = .4$ , and that physical attractiveness has a 10-year stability of  $.8$ . Due to the changes in attractiveness over time, spousal similarity in attractiveness after 10 years of marriage would be only  $r = .25$  (i.e.,  $.4 * .8 * .8$ ). Effects of the shared environment make a different prediction. If spouses were similar in the factors that produce changes in attractiveness over time, spousal similarity in attractiveness would be higher than  $.25$ , because similarity in the changing variance is added to the similarity that exists due to initial similarity. Whether spousal similarity in attractiveness after 10-years is higher or lower than initial similarity ( $r = .4$ ) depends on the effect size of spousal similarity in the new variance that produces changes in attractiveness over time.

In general, a longitudinal study of spousal similarity can be used to distinguish four factors of spousal similarity: (a) spousal similarity in traits that do not change over time, (b) initial spousal similarity in states that change over time, (c) spousal similarity in new state variance that produces changes in state variance over time, and (d) shared measurement error between spouses. Spousal similarity in new state variance that is not present at the beginning of marriage provides strong evidence for environmental influences (Schimmack & Lucas, 2007).

It is possible that spousal similarity in new state variance reflects pure environmental effects or gene x environment interactions. For example, all spouses may respond with an increase in well-being in response to an increase in household income. Alternatively, the effect of an increase in household income on spouse's well-being may be moderated by genetic dispositions that influence materialistic values. In this article, we do refer to all effects that involve environment as environmental effects and do not distinguish between main effects of

environment or interaction effects of environment with genetic dispositions. Spousal similarity in new state variance that emerges over the course of marriage is necessary and sufficient to demonstrate environmental effects on well-being.

#### *Dyadic Latent Panel Analysis of Spousal Similarity*

Several articles have made important contributions to the modeling of longitudinal data (Cole, Martin, & Steiger, 2005; Ehrhardt, Saris, & Veenhoven, 2000; Kenny & Zautra, 1995; Ormel & Schaufeli, 1991; Rudinger & Rietz, 1998). The main common element of these models is that they decompose the total variance of a construct into three components, a stable trait component that does not change over time, an unstable state component that changes over time, and a third component that reflects error variance. This model is typically applied to a single construct to examine the contribution of trait and state factors to stability and change of a single construct (Ehrhardt et al., 2000; Ormel & Rijdsdijk, 2000). An extension of the model to two constructs can be used to decompose the observed covariation between two constructs into covariations of the three variance-components (Kenny & Zautra, 1995; Ormel & Schaufeli, 1991). Dyadic Latent Panel Analysis uses this approach to examine the contribution of different variance components to observed spousal similarity.

Figure 1 provides a visual representation of Dyadic Latent Panel Analysis (DLPA). Like many structural equation models, DLPA starts with a measurement model that separates the observed variance ( $O$ ) into two latent factors that represent reliable variance ( $R$ ) and error variance ( $E$ ). This decomposition is done for all repeated measures of wives ( $O_w$ ) as well as all repeated measures of husbands ( $O_H$ ). Although it is unusual to have a measurement model with a single observed variable, the longitudinal nature of the data makes it possible to separate reliable

and error variance (Cole et al., 2005; Heise, 1969; Kenny & Zautra, 1995; Rudinger & Rietz, 1998).

$$(1) \text{ Observed Variance (O) = Reliable Variance (R) + Error Variance (E)}$$

The next assumption of DLPA is that reliable variance (R) is fully determined by two latent factors: a trait factor (T) that captures the influence of stable dispositions, and a state factor (S) that allows for changes over time. Again, this decomposition of reliable variance is applied to all repeated measures of wives ( $R_W$ ) and husbands ( $R_H$ ).

$$(2) \text{ Reliable Variance (R) = State Variance (S) + Trait Variance (T)}$$

DLPA further distinguishes two components of state variance: old state (OS) variance that is shared with the state variance on the previous assessment and new state (N) variance that reflects valid changes in state variance from one assessment to the next. Figure 1 does not directly show OS. Rather, the amount of OS depends on the amount of state variance on the previous occasion ( $S_{n-1}$ ) and the stability of state variance, which is represented by the autoregressive path coefficient of state variance at Time n-1 to state variance at Time n,  $\beta_{oldS}$ . OS equals the product of state variance on the previous occasion and the square of the autoregressive parameter, which reveals the amount of state variance that is explained by state variance on the previous occasion,  $OS_n = S_{n-1} * \beta_{oldS}^2$ .

$$(3) \text{ State Variance (S}_n\text{) = Old State Variance (S}_{n-1}\text{ * } \beta_{oldS}^2\text{) + New State Variance (N)}$$

The decomposition of state variance into old and new variance is not possible for the first assessment. In Figure 1, this variance is the initial state (IS) variance.

The three equations imply that the model in Figure 1 has five parameters to model stability and change of wives' well-being and five parameters to model husbands' well-being.

$$(4a) O_H = T_H + IS_H * \beta^2_{HoldS} + N_H + E_H$$

$$(4b) O_W = T_W + IS_W * \beta^2_{WoldS} + N_W + E_W$$

In addition to these 10 parameters, DLPA decomposes observed spousal similarity into similarity in four variance components:

1. Trait similarity ( $T_{sim}$ ) is the correlation between the two trait factors  $T_H$  and  $T_W$ .
2. Initial state similarity ( $I_{sim}$ ) is the correlation between the state factors on the first assessment  $IS_H$  and  $IS_W$ .
3. New state similarity ( $N_{sim}$ ) is the similarity in the new state factors  $N_H$  and  $N_W$ .
4. Error similarity ( $E_{sim}$ ) is the similarity in the error variances  $E_H$  and  $E_W$ .

For the current purpose of examining environmental influences on well-being, new state similarity is crucial. New state similarity reveals that spouses change in the same direction. The amount of new state variance over short time intervals is likely to be small (Ehrhardt et al., 2000). Thus, even high spousal similarity in new state variance can only make a small contribution to observed spousal similarity. However, these small effects on a single occasion accumulate over longer time intervals due to high short-term stability of well-being (Ehrhardt et al., 2000). Thus, it is also important to examine the cumulative amount of new state similarity.

This can be done by examining spousal similarity in state variance on the last occasion. Over long time intervals, most of the state variance is independent of initial state variance. Therefore, spousal similarity in state variance on the last occasion reveals the total environmental contribution to observed spousal similarity.

Spousal similarity in the error variance also reveals changes, but these changes are limited to a single occasion and reflect temporary fluctuations or shared method variance. The nature of initial state similarity is ambiguous. It may reveal effects of assortment or prior environmental influence before the first assessment. Spousal similarity in trait variance may reveal genetic similarity due to assortment, but could also be due to stable environmental factors.

In short, DLPA requires the estimation of 14 parameters: 5 parameters for wives' trait, initial state, new state, and error variance, and wives' state stability, 5 parameters for husbands' trait, initial state, new state, and error variance, and husbands' state stability, and 4 parameters for spousal similarity in trait, initial state, new state, and error variance. The actual number of parameters estimated in DLPA may be larger, depending on assumptions about stationarity of model parameters, as explained in the next section.

### *Model Identification*

Conditions for the identification of the DLST model are the same as for models with repeated assessments of a single individual (Cole et al., 2005; Kenny, 1975). A key assumption of the model is that the four variances, trait, initial state, new state, and error, are independent. The assumption that error variance is independent of state and trait variance is common to structural equation models with a measurement model. The assumption of independence of state and trait variance is implied in the definition of trait and state variance as variance that is stable (trait) and variance that changes over time (state).

Another important assumption is stationarity (Kenny, 1975). The stationarity assumption implies that the strength of causal processes that produce stability and change remains stationary over the different waves of assessment. This assumption implies that stability (and change) over the same time lag is the same. For example, the correlation between wave 1 and wave 2 is the same as the correlation between future waves with the same time interval (e.g., wave 5 and wave 6). Stationarity also implies that the amount of true variance remains constant from wave to wave. An additional assumption is that error variance remains constant across waves; that is, the reliability of assessments is stationary.

If all assumptions are made, DLPA estimates 14 parameters because parameters are constrained across waves. As a result, new waves do not add new information, but help to obtain more precise parameter estimates (Cole et al., 2005). However, additional waves can also be used to test stationarity assumptions (Kenny & Zautra, 1995). If more than 8 waves are available, it is possible to assume stationarity for the first four waves, and for the second four waves, and to compare parameter estimates for the two sets of waves. Significant differences between parameter estimates reveal changes in variance components or stability. For example, stability may increase with age. In the present study with 22 waves of data, the waves were split into two halves of 11 waves to test stationarity.

### *Model Implementation*

There are two reasons for the lack of applications of trait-state-error models to empirical data since Ormel and Schaufeli (1991) introduced the model. First, the model requires relatively large sample sizes and multiple waves to produce reliable estimates (Cole et al., 2005). Second, the assumption of stationary state variance requires non-linear constraints, which were difficult to implement in linear structural equation programs (Rudinger & Rietz, 1998; Schilling, 2006).

Recent advances in software development overcome this limitation. We used the software program MPLUS 4.2 (Muthén & Muthén, 2007) which makes it easy to implement non-linear constraints.<sup>1</sup> Users simply write the non-linear constraint in a single command line:

$$\text{Initial State Variance} = \text{Initial State Variance (IS)} * \beta^2_{\text{oldS}} + \text{New Variance}$$

### *Spousal Similarity in Well-Being*

Before embarking on a dyadic multi-wave longitudinal study, it is useful to examine spousal similarity cross-sectionally. Environmental factors are more likely to play a role, if a cross-sectional study reveals spousal similarity. Several studies have indeed found moderate to high spousal similarity in life satisfaction (Bookwala & Schulz, 1996; Schimmack & Lucas, 2007; Tambs & Moum, 1992). However, cross-sectional studies do not reveal whether spousal similarity is due to assortative mating or environmental influences. In fact, different researchers have attributed spousal similarity in life satisfaction to assortative mating (Tambs & Moum, 1992) or environmental influences (Bookwala & Schulz, 1996). A DLPA of longitudinal data is needed to test these hypotheses empirically.

Studies of domain satisfaction are rare, with the exception of marital satisfaction, which also shows high spousal similarity (Spotts et al., 2004). The investigation of spousal similarity in domain satisfaction is particularly interesting because life domains vary in the similarity of the objective factors that could influence spouses' subjective evaluation of a life domain. Some life domains (e.g., household income, housing) are objectively identical for both spouses. Thus, high degrees of spousal similarity should be observed, if domain satisfaction were influenced by the common objective circumstances. In contrast, other domains are objectively less similar (e.g., health, recreation). Influences of the objective individual differences in these domains on satisfaction in these domains should produce less spousal similarity. Thus, a model of

environmental influences on well-being predicts higher spousal similarity for objectively more similar domains than objectively less similar domains. To test this hypothesis, DLPA was used to examine spousal similarity in satisfaction with four domains: two domains were objectively identical for spouses (household income, housing), and two domains were objectively less similar (health, recreation).

## Method

### *Data Set*

The data analyses are based on all waves of the German Socio-Economic Panel (SOEP) from 1984 to 2005 (Wagner, Frick, & Schupp, 2006). The SOEP is an ongoing panel study based on a nationally representative household sample. For the present study, the sample is limited to participants who were married in 1984 and who had complete data for all 22 waves from 1984 to 2005. The sample sizes varies from  $N = 604$  to  $N = 740$  due to the different number of missing data for different items. The dependent variables were satisfaction ratings on an 11-point scale ranging from 0 = completely dissatisfied to 10 = completely satisfied. At the beginning of the interview, respondents answered questions about domain satisfaction. Only domains that were included on all 22 waves were used for this article. Two domains were objectively identical (household income, housing) and two domains were not objectively identical (recreation, health). At the end of the interview, respondents answered a single question about satisfaction with life in general.

## Results

### *Life Satisfaction*

The results for life satisfaction are presented first with a detailed discussion of various models that make different assumptions about stationarity. The discussion of these models

illustrates how assumptions can be tested and the influence of different assumptions on model parameters. Furthermore, the results can be compared to those of previous studies that have examined stability and change of individuals' life satisfaction in the SOEP (Ehrhardt et al., 2000), and with Schimmack and Lucas's (2007) study of dyadic similarity based on patterns of observed correlations without an explicit causal model.

*Model 1.* Model 1 is the most restrictive model. It assumes complete stationarity for all assessments. In addition, it assumes equal spousal similarity in error variance and new state variance for all waves. Overall model fit is typically evaluated on the basis of a variety of fit indices (Schermelleh-Engel, Moosbrugger, & Müller, 2003). Acceptable fit requires a Comparative Fit Index (CFI) greater than .95, a Root Mean Square Error of Approximation (RMSEA) smaller than .06, and a Standard Root Mean Residual (SRMR) smaller than .08. Based on these indices, the fit of Model 1 could be considered acceptable (Table 1). Table 2 shows the standardized parameter estimates for this model. Rather than reporting error variance, the amount of reliable variance (1 - error variance) is reported. Furthermore, trait variance and state variance are reported as the proportion of the reliable variance rather than the total variance. The amount of new variance is not reported, but can be inferred from state stability (i.e., new variance = 1 - stability<sup>2</sup>). For example, a stability of .9 implies that 81% of the variance is old and 19% of the variance is new.

Consistent with previous studies, husbands' and wives' parameter estimates revealed a reliable trait component, a reliable state component, a reliable error component, and high annual stability of state variance (Ehrhardt et al., 2000). Furthermore, parameter estimates are similar for husbands and wives, indicating that the processes that produce stability and change in life satisfaction are similar across gender. The most important new findings were the four parameter

estimates for spousal similarity in trait, initial state, new state, and error variance. In addition, Table 2 shows spousal similarity in (old and new) state variance on the last assessment. This measure reveals the cumulative effect of new spousal similarity over time.

The most important finding is that there is high (i.e.,  $r > .5$ , Cohen, 1988) spousal similarity in new state variance, which also leads to high spousal similarity in final state variance. This finding provides unequivocal evidence for environmental influences (including gene x environment interaction effects) on life satisfaction because it cannot be attributed to genetic relatedness or initial spousal similarity due to assortment. In addition, the results show high spousal similarity in trait variance. This finding suggests that assortative mating also contributes to spousal similarity in life satisfaction, although it is also possible that stable environmental factors contribute to spousal similarity in the trait component. Finally, spousal similarity in the error component is relatively small. This finding suggests that a large portion of the error variance is indeed random error variance, which by definition cannot be shared between spouses. At the same time, the presence of spousal similarity in the error components reveals that not all of this variance is random error variance. Some variance must be due to occasion specific factors that are shared between spouses. Overall fit is not sufficient to demonstrate that a causal model produced accurate parameter estimates (McDonald & Ho, 2002; Tomarken & Waller, 2003). The following models relax some of the assumptions made in Model 1 and examine the impact on model fit and parameter estimates.

*Model 2.* Model 2 relaxes the assumption of equal total variances, while assuming stationarity for the ratio of variance components. Kenny and Zautra's (1995) refer to this model as a quasi-stationary model. For example, if state variance, trait variance, and error variance at time 1 are 1, the total variance at time 1 is 3. If total variance at time 2 is 2.1, the equal ratio

assumption implies that trait, state, and error variance are .7 at time 2. In other words, the reduction of total variance by .9 is equally divided between the three variance components, with each contributing a reduction of .3.

Model 2 was implemented by first scaling observed variables to have equal variances, and then fit a fully constrained model to the rescaled variables. The scaling was implemented by first creating latent factors that were arbitrarily scaled to the variance of one observed variable. The other observed variables were free to load on this latent factor, and all structural parameters were constrained to be the same for all waves. This model uses the freely varying factor loadings of the observed variables on the latent factor to transform equal latent variances into unequal observed variances. This model requires an additional scaling parameter for N-1 waves for the wives and for the husbands. Thus, the model has 42 ( $2*22 - 2$ ) fewer degrees of freedom as Model 1. Table 1 shows that Model 2 produces a notable improvement in fit over Model 1, indicating that total variances are not the same across assessments. A visual inspections of observed variances showed that decreasing variances, especially over the first waves, account for this finding (Ehrhardt et al., 2000). Interestingly, Table 2 shows that Model 2 produces essentially the same parameter estimates as Model 1. The reason is that the assumption of equal total variances has no influence on the standardized relation among variables. Thus, standardized parameter estimates are identical. Although Model 2 has good overall fit, it is possible that the change in total variances is not equally divided among trait, state, and error variance. In fact, it is highly unlikely that this is the case. Thus, the following models examine how changes in each of the variance components individually influence model fit and parameter estimates.

*Model 3.* Model 3 relaxed the stationarity assumption of equal trait variances. That is, the amount of trait variance could vary across assessments. To allow for unequal trait variance, the

variance of the trait factor was set to 1 and the relation between true variances of each wave and the trait factor was allowed to vary freely across waves. This model has the same degrees of freedom as Model 2. However, model fit is much worse than the previous model. This finding shows that unequal trait variances alone cannot account for the unequal observed variances. Inspection of Table 3 shows that parameter estimates for Model 3 were fairly similar to the previous model.

*Model 4.* Model 4 relaxed the assumption of equal error variances across assessments. This model essentially assumes that the decrease in total variance is due to decreasing error variance and therewith increasing reliabilities. Ehrhardt et al. (2000) demonstrated that reduced error variances account at least partially for the changes in total variance. Table 1 shows that Model 5 fits the data better than Model 1, but not as well as Model 2, although the difference between Model 2 and Model 5 was small. This finding suggests that unequal error variances contribute to the changes in total variance, but are not sufficient to explain all of the changes. Nevertheless, the crucial parameter estimates of spousal similarity are again very similar to the previous model.

*Model 5.* Model 5 relaxed the stationarity assumption of equal state variance. Furthermore, it relaxed the assumption of stationarity for the stability of state variance. The reason is that it makes little sense to assume that the ratio of new and old state variance remains the same, when total state variance changes. Table 1 shows that Model 5 fitted the data as well as Model 2 and 4. Table 2 shows that this model produces some notable differences in parameter estimates. The most notable discrepancy was the stability of state variance that ranged from .38 to .95 for wives, and .38 to .97 for husbands. Furthermore, the parameter estimates showed a clear trend to increase over time with stabilities in the first five waves below .6 (36% shared variance) and stabilities in the last five waves above .8 (64% shared variance). The reason for this increase in

stability is that the model used the amount of new state variance to model the reduction in total variance. If less new variance is added over time, state variance decreases and stability increases. The model also produced different results for spousal similarity in new state variance, which varied from .13 to .88. A clear trend was noticeable suggesting that spousal similarity in new variance increases over time. Thus, while there is less new variance, spouses tend to be more similar in the new state variance added on later waves. In other words, the greater amount of new variance in the beginning was more unique to each spouse.

Closer inspection of parameters in Model 4 revealed a large discrepancy between spousal similarity in the first and second wave. Whereas initial spousal similarity was high (.71), it dropped considerably due to the large amount of non-shared new variance that was added at time 2, as implied by the low stability of state variance in the beginning. As a result, spousal similarity in state variance at time 2 was only .25. Then spousal similarity in state variance climbs back to .60 on the last wave, due to increasing spousal similarity in new variance and increasing stability of state variance. This pattern of spousal similarity is difficult to explain because wave 1 and wave 2 are essentially random chosen moments in the lives of married couples. A plausible explanation for this finding is that the problem arises from the assumption of equal error variances across waves. A more plausible interpretation of the finding is that low stability over the first waves is in fact due to larger error variance, which by definition is unstable (Ehrhardt et al., 2000). Thus, it seems unlikely that Model 5 provides accurate parameter estimates, despite good model fit.

*Model 6.* Model 6 differed from previous models in that it did not relax a stationarity assumption of a single parameter across all waves. Rather, it relaxes the stationarity assumption for all parameters for the first and second half of the waves. A comparison of the parameter

estimates from the first half and the second half reveals linear trends in parameter estimates. Model fit was better than the fit of the fully constrained Model 1, indicating some significant changes in parameters.

Table 4 shows the parameter estimates for the first and second half, and the effect size of the difference between the two parameter estimates (Cohen, 1988). Effect sizes are based on Fisher  $r$ - $z$  transformations of correlations and computing the difference between the two  $z$ -values. For parameter estimates of variances, the square root of the variance was used. The reason for this transformation is that the square root reveals the path coefficients for the assumed causal effects. For example, the square root of reliability coefficients reveals the causal effect of reliable variance on observed variance. Table 4 also reports the boundaries of the 99% confidence interval. If two confidence intervals are not overlapping, two parameters can be considered significantly different from each other.

Most parameter estimates were fairly similar, and effect sizes of differences between parameter estimates were small ( $Q < .40$ ). The only statistically significant difference was the 10% increase in reliability for husbands. Especially, estimates of spousal similarity were quite similar across the two halves. The most notable effect was an increase in stability of state variance. However, this increase has to be interpreted with caution because it was not statistically reliable and because it may be inflated by the models' assumption that error variances of the first 11 waves are equal.

In sum, a series of models were used to obtain parameter estimates using different assumptions of stationarity. The results lead to the following conclusion.

1. The reliability of the single-item life satisfaction item ranges from .5 to .7, and tends to increase over time.

2. Trait and state variance contribute about equally to the reliable variance, although state variance tends to make a stronger contribution.

3. The annual stability of state variance of life satisfaction is high, suggesting that individual differences in life satisfaction change only slowly over time. Furthermore, state stability may increase over time.

4. There is high ( $r > .5$ ) spousal similarity in trait, initial state, new state, and final state variance. Most of the state variance at the end of the study is cumulative new state variance, because initial state variance predicts only a small portion (2%, i.e.,  $[\text{.91}^{22}]^2$ ) of the final state variance.

5. Finally, it is noteworthy that parameter estimates for wives and husbands were very similar. This finding suggests that similar factors influence husbands' and wives' life satisfaction.

#### *Domain Satisfaction*

The domain satisfaction data were analyzed with all models. However, only the results of the model with separate parameter estimates for the first and second half (Model 6) are reported because this model (a) provides robust estimate of parameter estimates and (b) tests the stationarity assumption for all parameter estimates. Overall model fit was acceptable for all domain satisfaction, although some domains produced better fit than others (Table 4).

The parameter estimates for the four domains are shown in Tables 5 to 8. A general finding is that parameter estimates tend to be quite similar for the first and second half of the study as well as for wives and husbands. A second general observation is that all domains replicate the pattern of increasing reliabilities from the first to the second half of the study. Similarly, state stability tends to increase.

The most important finding is that estimates of spousal similarity in state variance vary across domains in a theoretically predicted direction. Domains that are objectively identical for both spouses showed very high spousal similarities with estimates ranging from .73 to .83. In contrast, domains that are objectively less similar produced less spousal similarity. The lowest similarity was obtained for health satisfaction, .22 to .26. A difference between a .82 and a .22 correlation is very large,  $Q = 1.87$  (Cohen, 1988). Thus, the results provide strong support for the hypothesis that spousal similarity in the state variance of domain satisfaction reflects the influence of environmental factors on domain satisfaction.

A second important finding is that spouses are also similar in the trait component of domain satisfaction, and that trait similarity often exceeded state similarity. This finding cannot be attributed to differences in reliabilities because both estimates are based on latent factors that control for measurement error.

### Discussion

The main contribution of this article was to provide unequivocal empirical evidence for environmental influences on life satisfaction and domain satisfaction because spouses' life satisfaction and domain satisfaction changed in the same direction. Furthermore, the amount of spousal similarity varied as a function of the domain. Spousal similarity was higher for objectively identical domains than for objectively less similar domains. This finding has important implications for theories of SWB. The most important implication is that SWB judgments are neither unstable judgments that are based on irrelevant information (Schwarz & Strack, 1999), nor entirely due to the result of immutable genetic dispositions (Lykken & Tellegen, 1996). As a result, SWB can provide meaningful information about the quality of

individual's life as assessed from the subjective perspective of the individual's living these lives, and these judgments can inform public policies (Diener et al., 2006; Veenhoven, 1994).

Beyond these broader implications, the present study also raises important questions about the interpretation of previous studies of environmental versus genetic influences on SWB. These implications are discussed separately for the findings regarding state similarity and trait similarity in life satisfaction.

#### *Spousal Similarity in the State Component of Life Satisfaction*

Behavioral genetics studies typically find that genetic factors explain 40% to 50% of the variance in SWB (Lykken & Tellegen, 1996; Nes et al., 2006; Stubbe et al., 2005). Furthermore, the studies suggest that the shared environment with a co-twin has no influence on SWB. As a result, the remaining variance is either due to environmental influences unique to each twin or measurement error. Furthermore, even reliable environmental influences may be due to short-lived temporary changes. The uncertainty about the nature of the variance that is not explained by genetic factors has led some authors to suggest that these factors are relatively unimportant for the understanding of individual differences in SWB. In a well-publicized quote, Lykken and Tellegen (1996) compared happiness to height and concluded that "trying to be happier is as futile as trying to be taller and therefore counterproductive" (p. 189). The present findings show that non-heritable variance is far from irrelevant. Consistent with several other studies, this study shows that state variance in happiness changes only gradually over time (Ehrhardt et al., 2000; Fujita & Diener, 2005; Schimmack & Oishi, 2005; Veenhoven, 1994). More importantly, this study shows that environmental factors, directly or in interaction with genetic dispositions, cause some of the changes in life satisfaction and satisfaction with some life domains. Although the exact environmental factors remain unclear, it is plausible that some of these environmental

factors are under people's control. For example, some people may invest time and resources in their home, leading to higher satisfaction with their home. Thus, the present results strongly suggest that trying to be happier is as productive as trying to be healthier. Although it may be difficult to achieve this goal, environmental barriers (e.g., few jobs that pay \$1000/hour, few six-bedroom houses in Manhattan, and the price of a Porsche) may be as important as genetic dispositions.

One limitation of the present work is that the present findings do not show the effect size of environmental effects on SWB. The reason is that various causal models can explain spousal similarity in SWB. One causal model assumes that shared environment factors have independent and equal effects on both spouses. Based on this model, spousal similarity would be equivalent to the amount of variance that is explained by shared environmental factors. For life satisfaction, this would imply that 60% of the state variance is explained by the shared environment between spouses. The remaining variance could be due to unshared environmental factors or even genetic factors, if genetic factors also contribute to changes in life satisfaction (Nes et al., 2006).

However, an alternative causal model could assume that spousal similarity is only partially an environmental effect. According to this model, husbands' genes have a strong influence on husbands' SWB, but the same genes also influence wives' SWB. For example, a husband may have a genetic disposition to be sensitive to stress. During times of stress this disposition leads to a marked decrease in the husband's life satisfaction, but it also has a negative influence on the wife. A similar process could produce an influence of wives' genetic dispositions on husbands' life satisfaction. This model can predict quite high spousal similarity with relatively weak environmental effects. However, two findings suggest that spousal similarity in state variance is caused by shared environment effects. First, the higher spousal similarity in domain satisfaction

in objectively identical domains than in objectively less similar domains is more consistent with a shared environment effect. Second, longitudinal behavioral genetics studies suggest that genes make a small contribution to state variance (Lykken & Tellegen, 1996; Nes et al., 2006).

Nevertheless, it is important to note that estimates of effect sizes depend on unproven assumptions about the causal model that produces spousal similarity. An important avenue for future research is to search for environmental predictors of spousal similarity in state variance, and to examine whether genetic disposition moderate these environmental influences (Caspi et al., 2003).

#### *Spousal Similarity in the Trait Component of Life Satisfaction*

The present findings of high spousal similarity in the trait component of life satisfaction and satisfaction with some domains also has important implications for the interpretation of behavioral genetics studies. The reason is that existing studies implicitly assumed that spouses do not have similar genetic dispositions for happiness, or at least did not explicitly consider the possibility of genetic similarity between spouses.

To evaluate the implications of the present findings of high spousal similarity in the trait component of SWB for genetic models, it is necessary to distinguish between two models of assortative mating (Neale & Cardon, 1992). The social homogamy model assumes that spousal similarity is limited to the environmental component of the phenotype. This is a highly restrictive and implausible assumption for the trait component of life satisfaction. The assumption has also been proven incorrect for traits with much lower levels of spousal similarity such as height and weight (Silventoinen et al., 2003). Thus, it is more plausible to assume that spousal similarity in the trait component of life satisfaction is due to phenotypic assortment. That is, spouses actively select partners with similar characteristics. Based on this model, it is possible to infer genetic

similarity between spouses from the observed similarity between spouses with a simple formula (Neale & Cardon, 1992).

$$\text{Genetic Similarity} = \text{Phenotypic Similarity} * \text{Heritability } (h^2)$$

Previous studies have suggested that 80% of the trait variance in SWB is heritable (Lykken & Tellegen, 1996; Nes et al., 2006). As a result, a phenotypic assortative mating model suggests that the phenotypic trait similarity of  $\sim .8$  in the present study implies that 64% of the trait similarity in life satisfaction is due to genetic similarity (i.e.,  $.8 * .8$ ). This high degree of genetic similarity between spouses has important implications for the genetic similarity between DZ twins and siblings, which can be derived from another formula used in behavioral genetics research (Reynolds, Baker, & Pedersen, 1996).

$$\text{DZ Genetic Similarity} = 0.5 * (1 + \text{Parents' Genetic Similarity}).$$

According to this formula, genetic similarity for the trait component increases from the standard estimate of 50% under the assumption of random mating to 82% ( $1.64 / 2$ ) based on the previous estimate of 64% genetic similarity between parents for the trait component of life satisfaction. As a result, an additive genetic model that takes genetic similarity between parents into account predicts that DZ correlations are  $.82 * \text{MZ correlations}$ , as compared to the standard prediction that they are half of the MZ correlations under the random mating assumption. Thus, an additive genetic model with phenotypic assortment predicts an MZ correlation of  $.8$  and a corresponding DZ correlation of  $.66$ .

To make predictions for cross-sectional studies that cannot distinguish trait, state, and error variance, it is necessary to make further assumptions about the contribution of trait variance to observed variance. Numerous studies, including the present one, suggest that the trait component accounts for no more than 50% of the total variance (Ehrhardt, et al., 2000; Lykken & Tellegen,

1996; Nes et al., 2006; Schimmack & Oishi, 2005; Veenhoven, 1994). Assuming 50% trait variance, the predicted twin similarities in cross-sectional studies are .40 for MZ twins ( $.8 * .5$ ) and .33 ( $.66 * .5$ ) for DZ twins. Importantly, the difference between the similarities of DZ and MZ twins shrinks with the contribution of trait variance to observed variance. Thus, the predicted difference between MZ and DZ twins ( $.40 - .33 = .07$ ) is even smaller for cross-sectional studies of total variance. Contrary to this prediction, all behavioral genetics studies found considerably larger differences between MZ and DZ correlations, ranging from .18 (Nes et al., 2006) to .29 (Stubbe et al., 2005) to .36 (Lykken & Tellegen, 1996). These large discrepancies suggest that a simple additive genetic model is inconsistent with the existing data. Several studies came to the same conclusion even assuming no genetic relatedness between parents (Lykken & Tellegen, 1996; Stubbe et al., 2005). The present findings make it even less likely that an additive genetic model can explain the data. The present conclusion is also consistent with other recent findings that non-additive genetic effects contribute to personality traits related to SWB such as extraversion and neuroticism (Keller, Coventry, Heath, & Martin, 2005). A non-additive genetic model of life satisfaction has several important implications. Arguably the most important implication is that even strong genetic assortment between parents does not have strong effects on their children's SWB (Maes et al., 1997; Truett et al., 1994). The reason is that children inherit parents' genes, but not the complex interactions between genes that produce non-additive genetic effects. Thus, tall parents can expect to have tall children, because height is largely determined by additive genetic effects, but parents with a happy disposition cannot expect their children to inherit the same happy disposition, because SWB appears to be mostly influenced by non-additive genetic factors. This is another reason why Lykken and Tellegen's (1996) analogy between height and happiness is misleading.

*Future Applications of Dyadic Latent Panel Analysis*

This article demonstrates that DLPA can provide important information about environmental influences on well-being. Future research can apply DLPA to dyadic longitudinal data in other domains and for different types of dyads. It is therefore instructive to compare DLPA to other methods that have been used to analyze longitudinal dyadic data. The most common model is arguable the cross-lagged panel model (Rogosa, 1980). The main difference between the cross-lagged panel model and DLPA is that the cross-lagged panel model assumes that there is no trait component. This is an extremely restrictive and implausible assumption. Other problems also plague cross-lagged panel analysis as a method to make inferences about causality (Rogosa, 1980).

A few studies have applied a simplex model to longitudinal twin data (Gillespie, Evans, Wright, & Martin, 2004; Neale & Cardon, 1992). Like the cross-lagged panel model, a simplex model implicitly assumes that trait variance is zero (Schilling, 2006). This assumption goes against the broader assumption that genes can produce individual differences over long time intervals. Thus, it seems preferable to model longitudinal twin data with DLPA that does not make a priori assumptions about the amount of trait variance.

DLPA can also be extended to examine similarity among larger groups (e.g., families, workgroups). For example, similarity in new state variance unique to a particular dyad (e.g., father-child) suggests different environmental effects (e.g., social interactions) than similarity in new state variance that is shared across all members of a group (e.g., household income).

*Limitations*

The main limitation of DLPA is that it can only reveal environmental factors that are shared between members of a dyad. In this regard, DLPA is overly conservative and is likely to

underestimate environmental effects. Thus, it is important to compare the results of DLPA with results from other studies, most prominently twin studies. Twin studies overestimate environmental effects whenever measurement error cannot be estimated. Thus, twin similarity and spousal similarity provide a range for plausible estimates of environmental effects.

A practical limitation is that DLPA requires dyadic data with repeated assessments over a sufficiently long interval to observe changes in state variance. Thus, DLPA cannot be applied to most data sets in psychological research. However, the cost of conducting research with small samples or two-wave retest studies over short time periods is that these studies are unable to reveal causal processes. It is important to realize that this is a limitation of the data and not of correlational research in general. By demonstrating the power of DLPA to demonstrate environmental influences, we hope that more studies with adequate data will become available. For now, DLPA can be applied to existing data sets such as the SOEP and other household panel studies.

Another limitation of DLPA is that it does not reveal the nature of environmental factors. In this regard, DLPA is akin to traditional behavioral genetics studies. Behavioral genetics studies demonstrated that genes are important, but could not reveal which genes are important. Currently, molecular genetics studies are starting to provide answers to this question. Similarly, DLPA only demonstrates that shared environmental factors influence well-being, but it does not reveal the nature of these factors. To examine the nature of these factors, it is necessary to include relevant predictor variables in the longitudinal study. For example, Lucas, Clark, Georgellis, and Diener (2004) demonstrated that unemployment has negative effects on individuals' life satisfaction. This environmental effect on individuals' life satisfaction may contribute to dyadic similarity if unemployment of one spouse also causes changes in the other

spouse's life satisfaction. To test this hypothesis, additional predictor variables can be included in a DLPA to examine whether they contribute to spousal similarity.

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Footnote

1 An annotated Mplus syntax file is available from the first author upon request.

Table 1

*Model Fit of Models 1-6 for Life Satisfaction (N = 725)*

Model	Chi	df	CFI	RMSEA	SRMR
M1: Fully Constrained	1923	978	.953	.037	.083
M2: UE Total Variance	1360	936	.979	.025	.063
M3: UE Trait Variance	1815	936	.956	.036	.069
M4: UE Error Variance	1380	936	.978	.026	.057
M5: UE State Variance & Stability	1340	896	.978	.026	.070
M6: Split Wave	1710	967	.963	.033	.076

Table 2

*Parameter estimates of Models 1-5 for Life Satisfaction.*

Parameter	M1	M2	M3	M4	M5
<b>Wives</b>					
Reliability	.61	.61	.56-.63	.45-.70	.58-.72
Trait Variance	.41	.38	.28-.45	.43	.40-.74
State Variance	.59	.62	.55-.72	.57	.26-.60
Annual Stability	.90	.90	.91	.90	.39-.95
<b>Husbands</b>					
Reliability	.62	.62	.56-.70	.49-.72	.57-.74
Trait Variance	.35	.33	.21-.47	.37	.37-.80
State Variance	.65	.67	.53-.79	.63	.20-.63
Annual Stability	.91	.91	.91	.91	.38-.97
<b>Similarity</b>					
Trait	.76	.75	.72	.76	.79
Initial State	.78	.95	.78	.84	.71
Final State <sup>a</sup>	.67	.67	.63	.60	.60
New State	.61	.59	.63	.60	.13-.88
Error	.29	.20	.29	.16-.47	.29

<sup>a</sup> Final state similarity is not a free parameter. It is determined by initial state similarity, new state similarity, and state stability.

Table 3

*Parameter Estimates for Life Satisfaction.*

Parameter	1-11	12-22	<i>Q</i>
Wives			
Reliability	.58 [.54 .62]	.64 [.61 .67]	.10
Trait Variance	.50 [.37 .63]	.39 [.27 .51]	-.15
State Variance	.50 [.37 .63]	.61 [.49 .73]	.17
Annual Stability	.87 [.83 .92]	.92 [.89 .94]	.26
Husbands			
Reliability	.57 [.54 .61]	.67 [.64 .70]	.17
Trait Variance	.43 [.30 .56]	.38 [.25 .50]	-.07
State Variance	.57 [.44 .70]	.62 [.50 .75]	.08
Annual Stability	.88 [.84 .92]	.92 [.89 .94]	.21
Similarity			
Trait	.77 [.69 .86]		
Initial State	.74 [.61 .87]	.62 [.53 .71]	-.23
New State	.61 [.52 .70]	.63 [.55 .72]	.03
Final State <sup>a</sup>	.64 [.56 .73]	.63 [.57 .69]	-.02
Error	.32 [.28 .36]	.25 [.21 .29]	-.09

Table 4

*Fit Indices for Domain Satisfaction.*

Domain	N	Chi	Df	CFI	RMSEA	SRMR
Household Income	680	1890	967	.959	.037	.069
Housing	607	1899	967	.954	.040	.070
Recreation	693	1691	967	.958	.033	.057
Health	740	1377	967	.979	.024	.042

Table 5

*Parameter Estimates for Household Income.*

Parameter	1-11	12-22	<i>Q</i>
Wives			
Reliability	.62 [.59 .66]	.70 [.67 .73]	.15
Trait Variance	.35 [.23 .48]	.49 [.37 .61]	.19
State Variance	.65 [.52 .77]	.51 [.39 .63]	-.22
Annual Stability	.87 [.83 .91]	.93 [.90 .95]	.33
Husbands			
Reliability	.60 [.63 .67]	.68 [.65 .71]	.14
Trait Variance	.43 [.30 .56]	.45 [.34 .57]	.03
State Variance	.57 [.44 .70]	.55 [.43 .66]	-.03
Annual Stability	.87 [.83 .90]	.91 [.88 .94]	.19
Similarity			
Trait	.93 [.88 .98]		-
Initial State	.81 [.73 .88]	.80 [.73 .86]	-.03
New State	.82 [.77 .88]	.79 [.73 .86]	-.09
Final State	.82 [.77 .87]	.79 [.75 .84]	-.09
Error	.33 [.29 .37]	.28 [.24 .32]	-.06

Table 6

*Parameter Estimates for Housing.*

Parameter	1-11	12-22	<i>Q</i>
Wives			
Reliability	.66 [.62 .70]	.67 [.63 .70]	.02
Trait Variance	.34 [.23 .46]	.34 [.21 .47]	.00
State Variance	.66 [.54 .77]	.66 [.53 .79]	.00
Annual Stability	.83 [.79 .88]	.91 [.88 .94]	.34
Husbands			
Reliability	.67 [.63 .70]	.67 [.63 .70]	.00a
Trait Variance	.43 [.31 .56]	.43 [.31 .56]	.00a
State Variance	.57 [.44 .69]	.57 [.43 .66]	.00a
Annual Stability	.82 [.77 .87]	.91 [.88 .94]	.37
Similarity			
Trait	.89 [.84 .96]		-
Initial State	.86 [.79 .93]	.83 [.77 .89]	-.11
New State	.83 [.79 .88]	.73 [.65 .81]	-.26
Final State	.83 [.79 .88]	.74 [.69 .79]	-.24
Error	.40 [.35 .44]	.22 [.18 .26]	-.20

Table 7

*Parameter Estimates for Recreation.*

Parameter	1-11	12-22	<i>Q</i>
Wives			
Reliability	.57 [.53 .61]	.65 [.62 .69]	.13
Trait Variance	.32 [.15 .48]	.31 [.16 .47]	-.01
State Variance	.68 [.52 .85]	.69 [.53 .84]	.02
Annual Stability	.86 [.81 .92]	.93 [.91 .95]	.37
Husbands			
Reliability	.54 [.51 .57]	.62 [.58 .65]	.13
Trait Variance	.20 [.02 .38]	.27 [.07 .47]	.09
State Variance	.80 [.62 .98]	.73 [.53 .93]	-.17
Annual Stability	.90 [.87 .94]	.93 [.90 .96]	.19
Similarity			
Trait	.89 [.62 .1.00]		-
Initial State	.43 [.28 .58]	.45 [.35 .55]	.02
New State	.49 [.39 .59]	.46 [.35 .57]	-.04
Final State	.48 [.38 .57]	.46 [.39 .54]	-.03
Error	.20 [.16 .24]	.18 [.15 .22]	-.02

Table 8

*Parameter Estimates for Health.*

Parameter	1-11	12-22	<i>Q</i>
<b>Wives</b>			
Reliability	.58 [.55 .62]	.68 [.64 .71]	.17
Trait Variance	.59 [.49 .65]	.63 [.56 .70]	.07
State Variance	.41 [.35 .51]	.37 [.30 .44]	-.05
Annual Stability	.83 [.78 .89]	.83 [.76 .89]	.00
<b>Husbands</b>			
Reliability	.62 [.59 .70]	.66 [.63 .69]	.07
Trait Variance	.46 [.37 .56]	.54 [.45 .63]	.11
State Variance	.54 [.44 .63]	.46 [.37 .55]	-.11
Annual Stability	.85 [.81 .89]	.87 [.82 .92]	.08
<b>Similarity</b>			
Trait	.47 [.36 .58]		-
Initial State	.24 [.06 .42]	.11 [-.05 .27]	-.13
New State	.26 [.13 .39]	.22 [.09 .35]	-.04
Final State	.26 [.13 .38]	.22 [.12 .32]	-.04
Error	.14 [.10 .18]	.08 [.04 .13]	-.06

Figure Captions

*Figure 1.* Dyadic Latent Panel Analysis of Spousal Similarity

