WELL-BEING & PSYCHOLOGICAL DISTRESS

Genetic and environmental influences on stability, change, and covariance.

by
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SUMMARY

An important goal to psychological research is to advance knowledge on development and sustenance of positive mental health. This study is the first large scale twin study investigating the genetic and environmental influences on stability and change in both psychological well-being and distress during the developmental juncture of young adulthood. The study also aims to illuminate the extent to which genetic and environmental influences on indicators of well-being and distress are overlapping or distinct. The research material consists of self-report data from a population-based sample of Norwegian twins, born between 1967 and 1979, and measured between the ages of 18 and 31. Structural equation modelling techniques primarily developed for genetically informative data were used in all studies. Positive mental health was conceptualised as either subjective well-being (SWB) or global life satisfaction (LS), whereas psychological distress was conceived of as symptoms of anxiety and depression and self-rated sleep problems.

Recent research into well-being and distress has suggested that emotions are regulated by homeostatic processes designed to maintain emotional set-ranges (Sheldon & Lyubomirsky, 2004) or set-points (Headey, Kelley, & Wearing, 1993). Such set-points refer to the most likely values in a person’s temporal distribution of happiness or unhappiness across the lifespan (Sheldon & Lyubomirsky, 2004), representing some kind of a baseline from which the individual deviates in response to environmental circumstances. A person’s emotional well-being or ill-being is thus hypothesised to oscillate around a “neutral” or average level, with homeostatic forces returning it to its original level after occurrence of pleasant or unpleasant events. Some researchers have suggested that this basal affective level is biologically (Headey & Wearing, 1989) or genetically (Lykken & Tellegen, 1996) determined. Others have underscored the importance of environmental contributions such as early nursing environments and parenting styles (e.g. Bowlby, 1951; Ainsworth, 1962). A vast number of studies have shown that effects from life circumstances and events commonly are short-term, however, with most people displaying an amazing ability for adaptation (e.g. Suh, Diener, & Fujita, 1996).

By suggesting that assumingly beneficial interventions, therapeutic, or societal changes essentially produce transitory effects, such evidence of affective adaptation may be highly discouraging to policy makers and individuals, as well as to the psychological and psychiatric enterprise. When interested in reducing ill-being and improving well-being, questions concerning the reality, rigidity, and nature of affective set-points, is tremendously important. Is there a set-point? How set is this set-point? How is the set-point set? Why do some people remain chronically distressed, whereas others stay mentally healthy? Do early life
experiences determine our well-being and ill-being? Are sustainable gains in well-being possible, or is our happiness determined by our unique set of genes?

To address these questions, the first two papers of the present thesis aimed to explore the genetic and environmental risk and protective factors for continuity and change in both well-being and distress in young adults. Paper I explored the magnitude of effects from genes and environment to self-reported SWB, the stability and change in such effects during young adulthood, and sex-specific differences. Paper II investigated the same set of effects for liability to symptoms of anxiety and depression.

The results supported the notion of affective equilibrium levels essentially attributable to a genetic predisposition. For both males and females, considerable stability was found for both well-being and distress, with roughly 80% of the temporal stability being due to additive genetic factors. In contrast, 80% of the time-specific variance was attributable to environmental contributions, indicating that the environment is the main source of change. Thus, levels of well-being and distress were found to change in response to immediate life events, but in most circumstances adapt to an equilibrium, or set-point level. Some new genetic influences emerge, suggesting that the effects of current biological and psychosocial circumstances are of sufficient magnitude to activate different genetic factors over time, and some life circumstances exert long-term effects. Sex differences, both in the set of genes (SWB), and the magnitude of genetic and environmental effects (SWB, psychological distress) were indicated. The major findings from the two longitudinal studies therefore provide strong evidence for the temporal stability of genetic risk factors for SWB and distress in young adults, and substantial sex-specific influences on heritability, stability, and change.

Another important issue in aetiological research on well-being and psychopathology concerns the extent to which risk and protective factors underlying different indicators are common or distinct. Are genetic and environmental determinants of well-being and distress independent or basically overlapping? This question is partly related to the broader and still ongoing debate in psychology concerning the structure of emotions. Many risk and protective factors, both genetic and environmental are not specific to a given phenotype, influencing several correlated phenotypes simultaneously. A second major objective was therefore to further clarify the specificity of the genetic and environmental contributions to the association between well-being and distress.

Using a bivariate model, paper III investigated the extent to which aetiological factors influencing SWB and self-reported sleep problems are distinct or shared. In paper IV this model was extended to explore to what extent the genetic and environmental factors influencing liability to symptoms of anxiety, symptoms of depression, and life satisfaction were overlapping or unique. Two major findings were generated. Firstly, the strong associations between indicators of well-being and distress were to a large extent due to common genetic factors. Secondly, both distinct and overlapping environmental factors were contributing to well-being or ill-being. The results thus indicated substantial overlap in genetic aetiology, for both males and females, and some distinct environmental factors, suggesting that genetic and environmental causes of well-being and ill-being appear to be partly shared, partly distinct.
How may this knowledge be used to improve and promote mental health in individuals and populations? With regard to applied implications, some tentative suggestions and recommendations for future research are presented.

“Happiness and unhappiness are not ends, they are means. They are aspects of mechanisms that influence us to act in the interests of our genes” (Nesse, 2004, p. 1337)
LIST OF PAPERS

**Paper I**

**Paper II**

**Paper III**

**Paper IV**
I INTRODUCTION
1.1. Mental health: Well-being & psychological distress

Prior to the last decades, mental health was typically described in negative terms, with absence of psychopathology commonly regarded as indicative of positive health or well-being. The behavioural and biomedical sciences largely operated on the general assumption that research on disorders, alongside remedies for such problems, would provide knowledge on effective mental functioning (Huppert, 2005). Consequently, research attention predominantly focussed on identification of risk factors for psychological malfunctioning rather than on the reasons for human flourishing.

A growing interest in positive indicators of mental health such as subjective well-being, optimism, gratitude, and life satisfaction, accompanied by increased emphasis on prevention constitutes a major reorientation within the mental health field today and currently, research on both positive and negative health indicators operate conjointly to address the important issues concerning mental health. This reorientation within the mental health field has been characterised as a “paradigm adjustment” (Greenspoon & Saklofske, 2001), but conforms well to the initial WHO definitions of health and mental health (1948) as a “…a state of complete physical, mental and social well-being and not merely the absence of disease and infirmity” (WHO, 2005) and “…a state of well-being in which the individual realizes his or her own abilities, can cope with the normal stresses of life, can work productively and fruitfully, and is able to make a contribution to his or her community” (WHO, 2005). These definitions emphasise the distinction between mental health as the presence of positive health indicators versus mental health as the absence of mental disorder, and underscore that absence of mental disorder may constitute a necessary, but not a sufficient characteristic (Jahoda, 1958; p. 15). Similarly, positive feelings alone may not represent a sufficient criterion for mental health. Positive emotions do not necessarily lead to personal growth and fulfilment, are often transitory and achieved in unsustainable ways (e.g. through drug usage), and the proper expression of mental health often require experience of negative emotions (e.g. disappointing life experiences, traumas, death of a spouse) (Huppert, 2005).

The study of well-being and psychological distress thus represent complementary approaches to mental health, and factor analyses have indicated that measures of psychological well-being and ill-being neither represent opposite poles of a unique and unifactorial latent concept, nor completely independent constructs (e.g. Massé, Poulin, Dassa, Lambert, Bélair, & Battaglinin, 1998). Rather they seem to represent correlated dimensions of (at least) a two-dimensional latent construct which may reflect a higher-order concept of mental health.
1.1.1. Mental health in young adulthood

An abundance of research has demonstrated high prevalence of mental health problems in young people (e.g. Lewinsohn, Hops, Roberts, Seeley, & Andrews, 1993). Young adulthood covers a highly transitional life period characterised by more life-changing roles, demographic diversity, instability, and identity decisions than any other life stage (Arnett, 2000). During young adulthood, most leave their childhood home, complete their education, establish a career and many take on family responsibilities and nurse small children. Emergence of psychological problems and insufficient resolution of the many adaptive challenges faced during this developmental juncture may have more critical and lasting consequences than at other stages in life, debilitating social, emotional, and academic development. Research indicates a considerable risk potential for accumulation of complicating factors, recurrences, and future chronicity in young adults with mental health problems (Wittchen, Nelson, & Lachner, 1998). In contrast, positive life experiences may provide the individual with important resources for coping adequately with the life transitions and important choices necessary for building a career, establishing lasting relationships, family life, and a solid base for future challenges. Keyes (2002) uses the terms “flourishing” and “languishing” to indicate either presence or absence of positive mental health. Studying a sample of American youths (aged 12-18), Keyes found flourishing youths to have the fewest depressive symptoms, the least conduct problems, and the highest levels of self-determination, closeness to other people, and school integration. The opposite pattern was characteristic of languishing youths. The findings of Keyes and others highlight the importance of focusing on both positive and negative indicators of mental health. Figure 1 illustrates the mental health spectrum of Keyes schematically and unidimensionally with thresholds from flourishing to mental disorder according to Huppert (2005, p. 322).

Figure 1

![The mental health spectrum](image)

Given that the presence or absence of mental health has critical implications for the individual’s subsequent future, identification and monitoring of risk and protective factors in young adult males and females, are particularly important.
Whereas levels of well-being and satisfaction commonly vary little between the sexes, findings from diverse samples and measures concur in finding sex differences in prevalence, incidence, and morbidity risk for mental health problems such as anxiety and depression from some time during mid-puberty. By late adolescence, the female:male ratio usually approaches 2:1 which is the rate commonly seen in adults (Hankin, Abramson, Moffitt, Silva, McGee, & Angell, 1998). A female preponderance in closely related distress symptoms such as subjective sleep problems is similarly common. Along with partly different challenges facing young adult males and females (associated with e.g. pregnancies, parenting, body image, work life), this underscores the importance of further exploration of sex differences during young adulthood.

1.2. Mental health: Well-being

Since I suppose that very few people come to the psychotherapist for help because life is too much fun, our clinical sampling of the two ends of this distribution is biased. But I am convinced that “high-joy” people exist; and I should be surprised if my readers, in contemplating their range of acquaintances, disagree with me. There are persons who seem able to take considerable pleasure from almost any circumstance not distinctly loaded with aversive components and for whom the most ordinary experiences appear to be a source of considerable gratification. I conjecture that these people are the lucky ones at the high end of the hedonic capacity continuum, i.e. they were “born three drinks” ahead (Meek, 1975, p. 299-300)

Throughout history philosophers have offered a multitude of opinions of what constitutes the good life (Becker, 1992; Ryff, Singer, & Love, 2004), and many nomenclatures and conceptualisations of the nature of well-being have been formulated (Ury, Nitschke, Dolski, Jackson, Dalton, Mueller et al., 2004). Life satisfaction, optimism, quality of life, psychological well-being, and subjective well-being (SWB) are contemporary constructs focusing on the presence of positive psychological characteristics associated with both mental and physical health (Ryff et al., 2004). Currently there are two dominating, although mutually complementing perspectives on well-being in psychological research with distinctions drawn between eudaimonic and hedonic aspects of well-being (Ryan & Deci, 2001). The eudaimonic perspective is strongly inspired by Aristotelian philosophy, focussing on the realization of a person’s “daimon” (true nature, or true potential), actualisation, and human growth. Within this tradition, psychological well-being (PWB)¹ is the standard operational measure. The hedonic perspective is rooted in pleasures, appetites, and affects (Ryan & Deci, 2001), focusing on experiences of life as good, and draws inspiration from the ancient Greeks (e.g. Epicurus) and subsequent philosophers such as Thomas Hobbes (1588-1679) and

¹ PWB consists of six key dimensions including self-acceptance, purpose in life, personal growth, positive relations with others, environmental mastery, and autonomy (Ryff et al., 2004).
Jeremy Bentham (1748-1832). Within this perspective the umbrella term of subjective well-being (SWB) is the central empirical construct.

1.2.1. Subjective well-being

During the past decade SWB has reigned as the primary well-being index in psychological research (Ryan & Deci, 2001), and the index has been recognized as an important additional source for evaluating or monitoring overall societal and economic development (Siegrist, 2003). SWB is a broad term, encompassing the different ways in which people evaluate their lives, and incorporate concepts like life satisfaction, pleasant affect, and feelings of fulfilment (Diener, Scollon, & Lucas, 2003). SWB thus refers to people's multidimensional evaluations of their lives and commonly embraces a tripartite structure, consisting of one cognitive component (life satisfaction) and two affective components, including i) the presence of positive affect, and ii) the relative absence of negative affect (e.g. Diener & Suh, 1997). The latter two components are collectively referred to as the hedonic balance. All three components capture distinct aspects of SWB, but are not entirely independent (Suh et al., 1996), and are assumed to reflect one single underlying dimension, or higher-order construct, which may be summarised as happiness.

1.2.2. Life satisfaction

The different SWB components are considered to be lower-order facets, and are often studied separately (Vittersø & Nilsen, 2002). The cognitive component of life satisfaction (LS) is an important indicator of SWB (e.g. Schimmack & Oishi, 2005; Andrews & Withey, 1976) and is usually conceptualised as a desired and non-specific subjective perception, indicating global well-being, different from evaluative appraisals of specific life-domains such as satisfaction with marriage or work (Diener, Scollon, Oishi, Dzokoto, & Suh, 2000). Global LS is a cognitive product that involves a comparative process between the individual’s current life situation and internalised standards, allowing respondents to use the information they subjectively deem relevant when evaluating their own lives (Cummins & Nistico, 2002).

1.2.3. Measuring well-being

A majority of current research on SWB and LS has been based on simple, cost-efficient self-report items in interviews or questionnaires such as “How satisfied are you with your life?” or “Taken altogether, how happy are you with your life?” (Diener et al., 2003). Much research has been vested in how such global judgements are construed, and on the information people deem relevant when making well-being judgements (Diener et al., 2003). Research generally indicates that most people appear to rely on
multiple sources of information, both temporarily and continuously accessible. Some sources (e.g. academic success) have been shown to mainly provide stable information whereas other sources (e.g. weather) mostly produce temporal changes. A composite well-being judgement is therefore a complex task and may not necessarily reflect a systematic bottom-up computational assessment (Schwartz & Strack, 1999). Computing, weighting, and summing of positive and negative experiences should be time consuming. Yet, most respondents are able to answer global life satisfaction questions in less than a minute (Schwartz & Strack, 1991), suggesting that such judgments may activate a host of heuristic strategies (Diener, Scollon, Oishi, Dzokoto, Suh, 2000). Diener et al. thus suggests that global well-being measures strongly reflect individual differences in dispositional positivity due to allowing the individual to project their norms, general life view, and self-beliefs onto the assessment items. In contrast, concrete or narrow satisfaction ratings are less coloured by general dispositional tendencies, and show stronger links to actual life circumstances and events (Diener et al., 2003). The two kinds of measures (global versus specific) may therefore partly reflect different types of well-being. In recent years, experience sampling methods (e.g. Larson & Fredrickson, 1999) and the Day Reconstruction Method (DRM) (Kahneman, Krueger, Schkade, Schwartz, & Stone, 2004) which uses a daily diary approach has complemented the measuring arena, along with other-report and peer report scales. Neuroscientific measures such as fMRI and EEG (e.g. Urry et al., 2004; Davidson, 2002) studying brain lateralisation of affective valence (positive, negative) are also promising techniques increasingly used within the research field.

1.2.4. Personality, approach, and avoidance

Dispositional theories of SWB make strong predictions concerning the influence from temperament and events, focus on the enduring individual characteristics underlying SWB, and stress the direct importance of personality on SWB (DeNeve & Cooper, 1998). Perhaps the most robust finding in SWB research overall, is the importance of personality and temperament on well-being ratings. SWB is consistently found to be related to stable personality factors (e.g. Costa, McCrae, & Zonderman, 1987), and the association is assumed to reflect a partly biology-based temperamental susceptibility to experience positive and negative affect (Watson & Clark, 1990). The traits of extraversion (Lucas & Fujita, 2000) and neuroticism (Fujita, 1991) have received the most empirical attention. Increasing levels of extraversion are associated with higher levels of SWB, whereas increasing levels of neuroticism are related to declining levels of SWB (e.g. Emmons & Diener, 1985; DeNeve & Cooper, 1998; Diener & Lucas, 1999). Controlling for measurement error, recent studies have revealed correlation estimates around 0.70-0.80 between SWB and extraversion/neuroticism (Diener & Lucas, 1999). Numerous studies have also documented that the cognitive component of LS is positively associated with extraversion and negatively related to neuroticism (e.g. Costa & McCrae, 1980). However, the relationship between these traits and the affective components seems to be stronger (Diener & Lucas, 1999).
Some investigators have proposed that the relationship between these personality traits and well-being is directly (or indirectly) causal (e.g. Schimmack et al., 2002), and personality dispositions are hypothesised to be partly responsible for the temporal stability in well-being generally observed. Gray’s model (1990) posits that extraversion and introversion reflect sensitivities in two neurologically based motivation systems, the behavioural activation system (BAS) associated with positive affect and the behavioural inhibition system (BIS), associated with negative affect (Updegraff, Gable, & Taylor, 2004). These largely distinct affect dimensions may have evolved to address quite different evolutionary tasks. Negative affect may be understood as a component of the withdrawal-oriented (aversive) BIS which is based on punishment sensitivity and facilitates withdrawal from aversive situations when the organism faces a threat (Davidson, 2000). In contrast, positive affect may be linked to the appetitive BAS which is involved in sensitivity to reward, and generates particular types of approach-related positive affect, such as the emotion occurring as the organism approaches a desired goal. Individual differences in these motivation systems may lead to positive and negative experiences influencing well-being and ill-being. A predominance of positive affect is for example suggested to facilitate approach behaviours resulting in a broadening of momentary thought repertoires and building of enduring personal resources (Fredrickson, 2004). High levels of well-being and satisfaction are related to a variety of important positive life outcomes, such as higher levels of relationship and marital satisfaction, success and satisfaction in work settings, improved coping in stressful situations, better health outcomes and longevity (Pavot & Diener, 2004; Danner, Snowdon, & Friesen, 2001).

1.2.5. Genetic factors

Most characteristics, such as basic temperament and personality showing pronounced individual differences, are to a considerable extent influenced by stable genetic factors (Meehl, 1975), and genetic factors seem to predict SWB and LS to a fairly high degree (Roysamb, Harris, Magnus, Vittersø, & Tambs, 2002; Roysamb, Neale, Tambs, Reichborn-Kjennerud, & Harris, 2003; Stubbe, Posthuma, Boomsma, & DeGeus, 2005). The few behavioural genetic studies previously published have indicated considerable genetic influences on SWB (e.g. Lykken & Tellegen, 1996; Roysamb et al, 2002; 2003) and LS (e.g. Stubbe et al., 2005) with heritability explaining as much as 30-50% of the variance in well-being scores. The results are based on research conducted in many different countries, and include many thousands of twins of which the majority is reared together, but some also reared apart. Differences between the studies are largely related to some studies indicating predominantly non-additive (epistatic) genetic effects (Lykken & Tellegen, 1996; Stubbe et al., 2005), whereas others suggest entirely additive genetic influences (Roysamb et al., 2002; 2003). All studies however, generally find non-genetic variance to essentially be accounted for by unique environmental influences unique to each individual.
1.2.6. Socio-demographic factors

Broadly speaking, associations between SWB/LS and socio-demographic factors are weak, with such factors typically accounting for only a minor portion of the variance. Although various socio-demographic factors may play different roles in different countries, depending on living conditions, income distribution, and social security (Daukantaitė & Zukauskiene, 2006), small or negligible effects have been found for factors such as age, sex, race, and ethnicity. The socio-demographic factors showing the most robust relationship to SWB are marital status, employment status, educational level, and income level (e.g. Diener et al., 1999). Numerous studies have evidenced higher levels of SWB in married couples, and unmarried people who live with a romantic partner (Mastekaasa, 1992; 1994). Explanations for this robust finding generally include both social causation and social selection processes, and both explanatory theories have received some empirical support (House, Umberson, & Landis, 1988; Horwitz, White, & Howell, 1996).

People in wealthy countries commonly report higher levels of well-being than people from poorer countries although the effect is minor. Income levels show small, but positive correlations with SWB in wealthy nations (Diener et al., 2003) with the richest people reporting the highest levels of SWB, and the poor reporting relatively more negative affect. Nonetheless, increases in well-being levels do not seem to follow increases in income, whether measured within or between nations (Diener & Suh, 1997).

1.2.7. Stability and change

SWB and each of its facets appear to be moderately consistent across situations (Diener & Larsen, 1984) and the lifespan (Magnus & Diener, 1991). This stability may partly reflect a dispositional tendency (trait) to experience life positively or negatively (“top-down approach”), and partly a cumulative effect of specific, positive life events (“bottom-up approach”) (e.g. Brief, Butcher, George, & Link, 1993). Longitudinal reports of SWB suggest, however, that life events do not have a substantial influence on SWB over longer time intervals (10 years) (Costa et al., 1987; Diener et al., 1992), and the effect of most life events diminishes within 3 months (Suh et al., 1996). Exposure to life events are also fairly stable due to being, at least partly, generated by personality factors (Headey & Wearing, 1989) and genetic influences (e.g. Kendler, Neale, & Kessler, 1993). Most people adapt to circumstantial changes and return to some kind of a biologically or genetically determined equilibrium level, leading some researchers to suggest that well-being is regulated by homeostatic processes designed to maintain emotional set-points (Headey & Wearing, 1989).

The dynamic equilibrium model (Headey & Wearing, 1989), proposes a biologically determined “set point” of SWB, with homeostatic forces returning it to its original level after occurrence of pleasant or unpleasant events. This idea is partly derived from the finding that people eventually seem to adapt to both good and bad conditions (e.g. Brickman & Campbell, 1971; Brickman, Coates, & Janoff-Bulman, 1978), and in the
long run are destined to “hedonic neutrality”. The effect has been termed “the hedonic treadmill” effect (Brickman & Campbell, 1971) or hedonic adaptation (Frederick & Lowenstein, 1999), and substantial empirical support for the theory has been accumulated (Diener, 2000).

However, questions concerning the strength of this dispositional or homeostatic system remain unanswered and the dispositional perspectives have been criticised for diminishing the importance of external influences. Evidence clearly points to some external influences on SWB. People vary considerably in their emotional tone and seem to have a basal level of well-being (trait), but also vary substantially in response to life events (state) (Huppert, 2005). When predicting SWB on a short-term basis, personality factors have been found to be weaker predictors than situational influences. There are nation-level differences and shifts in life satisfaction levels according to societal changes (Inglehart & Klingemann, 2000), and some people do not seem to adapt to permanent changes following certain experiences, such as widowhood (Lucas, Clark, Georgellis, & Diener, 2003) and unemployment (Lucas, Clark, Georgellis, & Diener, 2004). Some researchers have also documented substantial success when using various happiness-increasing interventions (Sheldon, Kasser, Smith, & Share, 2002). As such, SWB is probably best explained by integrative models including the effects of life circumstances as well as global personality dimensions (e.g. Brief et al., 1993).

In response to accumulating evidence, Lyubomirsky, King, and Diener (2005) has recently advanced a model of longitudinal well-being specifying three major determinants of well-being at any given point in time: i) the individual’s specific set point or set range (reflecting personality and temperament), ii) the individual’s current life circumstances (demographic, contextual, geographic), and iii) the individual’s current intentional activities (behavioural, cognitive, conative). A central assumption is that hedonic adaptation occurs more quickly with respect to circumstantial changes than to activity changes. Circumstantial boosts seem to be short-lived due to people taking the new circumstances for granted and cease to derive positive experiences from them. In contrast, intentional activities lead to more diverse and varied experiences, and may bring about an expanding array of new opportunities and possibilities leading to sustained positive effects. Intentional activity may also directly counteract the tendency toward adaptation (Sheldon & Lyubomirsky, 2006).

The only previous longitudinal study of SWB specifically, comparing monozygotic (MZ) and dizygotic (DZ) twins (aged 20 and 30), found that 44% and 52% of the variance in well-being was attributable to genetic influences (Lykken & Tellegen, 1996). Over a 10 year period SWB scores correlated 0.50, indicating substantial stability in SWB during the transitional years between age 20 and 30. Based on considerable differences in cross-time correlations for MZ and DZ twins, the authors estimated genetic effects to explain approximately 80% of the variance in stable SWB. Long-term SWB thus seems predominantly determined by genetically based dispositions. Due to the big difference between correlations for MZ and DZ twins, the authors suggested that happiness is an “emergenic trait”, non-additive rather than additive. SWB is thereby understood, not as a summed effect of polymorphic genes, but resulting from interactions arising from a certain constellation of genes. The study by Lykken and Tellegen was based on a very
small sample however, and correlation analyses only. The precision with which this study could split additive and non-additive genetic effects was therefore rather limited. Also, this small study was not able to explore possible sex-specific effects. A cross-sectional Norwegian twin study obtained similar heritability estimates to those of Lykken & Tellegen, but found the genetic effects to be additive rather than non-additive. The results also suggested sex-specific genetic mechanisms, indicating a partly different set of genes and different magnitude of the genetic and environmental influences in males and females (Røysamb et al., 2002; 2003). Further studies exploring differential effects in males and females, and stability in such factors over time are thus highly warranted.

1.3. Mental ill-health: Psychological distress

Most people describe their lives as happy (Diener & Diener, 1996). Nevertheless, major cross-sectional community surveys report high prevalence of mental disorder ranging from 25% (Robins & Regier, 1991) to 37% (Kessler, McGonagle, Zhao, Nelson, Hughes, Eshleman, Wittchen, & Kendler, 1994) in young adults, with rates depending on diagnostic criteria and age ranges used in the studies (Narrow, Rae, Robins, & Regier, 2002). Comparable estimates have been shown in the Nordic populations (Kringlen, Torgersen, & Cramer, 2001; Alto-Setälä, Maruunen, Tuulio-Henriksson, Poikolainen, & Lönnquist, 2001). Even more prevalent are sub-diagnostic states of anxiety and depression (distress). Symptoms of anxiety and depression commonly rate as the most common complaints seen in psychiatric and general medical practice overall (Kendler, Heath, Martin, & Eaves, 1986), and symptoms are associated with reduced quality of life (Atkinson, Zibin, & Chuang, 1997), increased health services utilization (Simon, VonKorff, & Barlow, 1995), subsequent disorder (e.g. anxiety, mood and sleep disorders) (Cuijpers & Smit, 2004), large-scale economic costs (Broadhead, Eugene, Blazer, George, & Chiu, 1990), and excess mortality (Harris & Barraclough, 1998).

In this thesis mental ill-health or psychological distress is indexed by symptoms of anxiety and depression, and by self-rated sleep problems. Along with sub-diagnostic symptoms of anxiety and depression, subjective sleep problems often rate as the second most common symptom of psychological distress, being reported by as much as one third of the population (e.g. Heath, Eaves, Kirk, & Martin, 1998). Numerous studies have evidenced close associations between sleep problems, symptoms of anxiety, and symptoms of depression, with sleep problems found to reflect a general negative affectivity dimension shared between anxiety and depression (Watson & Clark, 1991). The symptoms are strongly related to the personality trait of neuroticism, possibly reflecting the withdrawal-oriented (aversive) BIS system which facilitates escape, disengagement, or withdrawal from aversive situations (Davidson, 2000), and may represent an evolved mechanism involved in allocating effort proportional to propitiousness (Nesse, 2000). When risks are considerable or efforts likely to be wasted,
low mood or anxiety may block investments, or facilitate fight or flight, and keep the individual awake.

1.3.1. Symptoms of anxiety and depression

Symptoms of depression include feelings of sadness, worry, and despair, whereas symptoms of anxiety are closer related to feelings of fear and apprehension and are often accompanied by physical sensations such as nausea and palpitations. Both types of symptoms may be understood as components of the withdrawal-oriented (aversive) BIS system, but may have evolved to address somewhat different evolutionary tasks. Clinical mood and anxiety disorders are usually defined as categorical diagnoses, but temporal fluctuations across threshold and sub-threshold levels are typically found (Merikangas, Zhang, Avenevoli, Acharyya, Neuenschwander, & Angst, 2003) with a majority displaying persistent anxiety and depression throughout the life span and few displaying time-limited symptoms. Those who meet sub-threshold diagnostic criteria at an early age often continue to manifest symptoms (Merikangas et al., 2003). Research thus supports the existence of a continuum or spectrum concept of anxiety and depression symptomatology (e.g. Kendler, Heath, Martin, & Eaves, 1987), as differences between subsyndromal states and formal categorical diagnoses are generally quantitative, and not qualitative.

1.3.2. Risk factors

Anxiety and depression are heterogeneous states resulting from complex interplay between multiple genes and both environmental and developmental epigenetic components (Hamet & Tremblay, 2005). Heritability estimates of self report symptoms of anxiety and depression are commonly ranging between .3 and .5 (e.g. Kendler et al., 1986), although varying somewhat according to age and sex (Scourfield, Rice, Thapar, Harold, Martin, & McGuffin, 2003), measurement instrument, and informants included in the study (Happonen, Pulkkinnen, Kaprio, van der Meere, Viking, & Rose, 2002). Non-genetic effects account for half of the phenotypic variance or more. Important environmental influences include factors such as exposure to a disturbed family environment, premature parental loss, divorce, childhood sexual abuse, lifetime trauma, dysfunctional self-schemata, low social support, recent stressful life events, and marital status/problems (see Kendler, Gardner, & Prescott, 2003; 2006). A female preponderance in prevalence and incidence for anxiety and depression is consistently reported, leaving female gender an important vulnerability factor. A large meta-analysis of major depression, including more than 20 000 subjects, found no consistent sex differences in heritability although the correlation between male and female genetic effects indicated only a partial overlap (Sullivan, Neale, & Kendler, 2000). Recently, however, Kendler, Gatz, Gardner, & Pedersen (2006) demonstrated both qualitative and quantitative sex-specific genetic effects for major depression in a large population-based sample of Swedish twins with heritability estimated to be larger in females than in males.
The report included only cross-sectional analyses, however, and data from middle aged and elderly twins only, providing only suggestive evidence that sex-specific genetic and environmental factors may operate also at other life stages and over time, and highlighting the need for further studies of such effects in other samples and age groups.

1.3.3. Co-occurrence

Whether categorically or dimensionally defined, anxiety and depression co-occur. The comorbidity rate for anxiety and mood disorders, as well as sub-threshold symptoms of anxiety and depression is substantial, with meta-analyses estimating depressed patients to have an overall prevalence rate of 57% for any anxiety disorder (e.g. Clark, 1989). Several large scale epidemiological studies have indicated that the comorbidity or co-occurrence between the most common mental disorders is accounted for by two broad underlying factors reflecting externalising (anti-social personality disorder, substance abuse/dependence) and internalising (anxiety, depressive) disorders (Krueger, 1999). The internalising factor has been shown to be divisible into two sub-dimensions, one referring to a combination of pervasive anxiety and sadness (anxious-misery), including major depression (MD), dysthymia, and generalised anxiety disorder (GAD), and one reflecting phobic avoidance (fear), including animal and situational phobia (Krueger, 1999; Kendler, Prescott, Myers, & Neale, 2003; Hettema, Prescott, & Kendler, 2004). The stability of this latent 3-factor structure has been found to be substantial (Vollebergh, Iedema, Bijl, de Graaf, Smit, & Ormel, 2001).

A series of studies have also indicated that anxiety and unipolar mood disorders largely share a common genetic diathesis, rendering individuals at risk for development of both types of disorders (Mineka, Watson, & Clark, 1998). Twin studies of both children (e.g. Rice et al., 2002) and adults (Kendler et al., 1987) support a substantial shared genetic predisposition to anxiety and depression that reflects individual differences in negative affectivity and subjective psychological distress (Mineka et al., 1998). Genetic risk factors for GAD and MD are shown to be highly correlated (e.g. Kendler et al., 1996; Kendler, Gatz, Gardner, & Pederson, 2006b), and evidence suggests that this general vulnerability may be indexed in part by the personality trait of neuroticism. Neuroticism is a strong predictor of comorbidity among internalising disorders such as MD and GAD (Hettema, Neale, Myers, Prescott, & Kendler, 2006), and recent biometric evidence suggests a considerable overlap between genetic factors for neuroticism and genetic factors for MD and GAD (Hettema et al., 2004; 2006; Fanous, Gardner, Prescott, Cancro, & Kendler, 2002; Kendler et al., 2006b), as well as between neuroticism and sub-threshold symptoms of anxiety and depression (Jardine, Martin, Henderson, & Rao, 1984). Shared genetic factors have for example been found to account for 91% and 76% of the correlation between neuroticism and MD in males and females, respectively (Kendler, Gardner, Gatz, & Pederson, 2006). In addition, the promoter region of the serotonin transporter gene (5-HTT) appears to be linked to neuroticism, anxiety and depression (Lesch, Bengel, Heils, Zhang Sabol, Greenburg et al., 1996), and to moderate the influence of life events on depression (Caspi, Sugden,
Moffitt, Taylor, Craig, Harrington et al., 2003). Liability to symptoms of anxiety, symptoms of depression, and neuroticism may therefore be partly linked to a common genetic diathesis.

1.3.4. Stability and change

Previous research has indicated that between 40% and 76% of the variance in self-reported depression symptoms partly reflect stable and heritable personality traits (Duncan Jones, Fergusson, Ormel, & Horwood 1990). Nevertheless, few studies have reported on the contribution from genetic factors to the cross-time correlation in anxiety and depressive symptoms (e.g. Rijsdijk, Schnieder, Ormel, Sham, Goldberg, & Spector, 2003; Carmelli, Swan, Kelly-Hayes, Wolf, Reed, & Miller, 2000), and none have investigated a pure young adult sample. Analysing two-wave data from elderly male twins Carmelli et al. (2000) reported that the stability of symptoms was attributable to continuity of genetic influences, and Rijsdijk et al. (2003), studying female twins estimated the contribution of genetic factors to be considerable (73%). An Australian study of an age heterogeneous sample of Australian twins (aged 20-96) including both males and females, found genetic influences operational at age 20 to essentially explain continuity in anxiety and depression (Gillespie, Kirk, Evans, Heath, Hickie, & Martin, 2004), although smaller age-dependent genetic effects were observed for female respondents at the ages of 30 (anxiety) and 40 and 70 (depression). These studies suggest that genetic vulnerability to anxiety and depression are rather stable across time. There is however, a need for research on narrower age groups and on sex-specific genetic and environmental effects on stability and change.

1.3.5. Subjective sleep problems

Subjective sleep problems cover a range of complaints of which difficulties in initiating or maintaining sleep, or non-restorative sleep rate as the most frequent. It is generally measured by self report, as such representing a subjective phenomenon that does not have to be validated against objective sleep measures (e.g. polysomnography) (Jansson & Linton, 2006).

Sleep problems represent a non-specific condition associated with a vast number of medical and mental disorders, and may be related to a multitude of genetic and environmental influences. Twin surveys from Finland (Partinen, Kaprio, Koskenvuo, Putkonen, & Langinvainio, 1983) and Australia (Heath, Eaves, et al., 1998) have revealed more similar sleep patterns, sleep duration, and subjective sleep quality in monozygotic than dizygotic twins. Familial clustering is also documented in studies using electroencephalogram (EEG) recordings, polysomnography (PSG), investigating body movements, slow wave sleep and rapid eye movement (REM) density (Linkowski, Kerkhofs, Hauspie, & Mendlowicz, 1991). Previous twin studies suggest that at least 33% of the variance in sleep quality and general sleep disturbance is accounted for by genetic factors, with non-shared environmental factors accounting for the remaining
variance (Heath, Kendler, Eaves, & Martin, 1990; Hublin, Kaprio, Partinen, & Koskenvuo, 2001). Lifestyle factors such as smoking, educational level, marital status, number of children, and consumption of tea, coffee and alcohol explain only a minor proportion of the variance (4%) in subjective sleep disturbance (Heath et al., 1998), whereas stress factors (e.g., job stress, commuting, chronic financial strain, family conflicts) and life events (e.g., significant loss) are considerably more important (e.g. Hall, Buysse, Nowell, Nofzinger, Houck, Reynolds et al., 2000; Ohayon & Zulley, 2001).

1.3.6. Sleep problems, distress, and mental disorders: Co-occurrence

Sleep complaints are strongly associated with most psychiatric disorders (Kupfer, 1995), and diagnostic criteria for depression have always included sleep problems as a central characteristic (Perlis, Giles, Buysse, Thase, Tu, & Kupfer, 1997). Epidemiological and clinical studies have shown that between 40% and 60% of subjects with insomnia also suffer from a concomitant mental disorder (e.g. Breslau, Roth, Rosenthal, & Andreski, 1996), with sleep problems usually representing an associated symptom that do not warrant a separate diagnosis (Ohayon, 1997). In mood disorders specifically, sleep disturbance plays a prominent role, with a majority (80%) having sleep disturbances, either chronically or during exacerbations of their psychiatric disorders (Reynolds & Kupfer, 1987). Insomnia symptoms may also increase the risk of relapse or development of a new onset disorder. A likely hypothesis is that sleep problems and mood related problems share a common aetiology making the same individuals vulnerable to both conditions. Previous results based on non-twin samples have suggested that sleep problems reflect a non-specific negative affectivity dimension shared between anxiety and depression (Watson & Clark, 1991), and biometric studies exploring the commonality and specificity in genetic and environmental influences are warranted.

1.4. Quantitative Genetics: A methodological framework

“The meaning of genetic variation among normal individuals (as opposed to genetic defects that cause a disorder) also has to be thought through with care. An innate difference among people is not the same thing as an innate human nature that is universal across species. Documenting the way that people vary will not directly reveal the workings of human nature, any more than documenting the ways that automobiles vary will directly reveal how car engines work. Nonetheless, genetic variation certainly has implications for human nature…” (Pinker, p. 49)

The current study is based on quantitative behavioural genetic methodology and the next section aims to outline some of the basic concepts, assumptions, and techniques inherent in quantitative genetics and quantitative genetic analysis so that readers not
familiar with the methodology may understand and interpret the results presented in the later sections.

1.4.1. The emerging field

Recognition of the importance of genetics is one of the most profound and dramatic changes within the behavioural sciences during the past few decades (Plomin, DeFries, McClearn, & McGuffin, 2001). The history of heredity and genetics in psychology has had a much longer history, however, and the past century has seen a series of changes in the prevailing views on the genetic and environmental aetiology underpinning mental health and behaviour, as well as development of increasingly more sophisticated approaches to the analysis of such processes.

The first mathematical tools for the description of resemblance in relatives that gave rise both to much of modern statistics and to population genetics was developed in the 19th century by Sir Francis Galton (1822-1911) in collaboration with Karl Pearson (1857-1936). The Belgian statistician, Adolph Quetelet (1796-1874) had previously applied statistical methods and the normal probability curve to biological and social data, and Galton assumed that results similar to those of Quetelet could be obtained for mental characteristics (Schultz & Schultz, 1987). In 1893, Galton founded the “Committee for Conducting Statistical Inquiries into the Measurable Characteristics of Plants and Animals”, and the committee came to include W. F. R. Weldon and Karl Pearson, who later extended Galton’s statistical work and created the discipline of biometry. Pearson and Weldon were supporters of a strict Darwinian evolution, and regarded the study of evolution as essentially a statistical problem. Darwin had conceptualised evolution as a continuous and gradual process, understanding inheritance to essentially be of the blending type, in which offspring generally will be intermediate between their parents. Although acknowledging the existence of heritable and discontinuous variants, Darwin had believed these to be of little importance.

Considerable interest and debate surrounded the notions of hereditary transmission and “Darwinian blending”. A serious limitation in Darwin’s evolution theory around 1900 concerned the theory not being capable of explaining the gradual generational loss of variation among individuals. For Darwin’s evolutionary theory to work, the differences among individuals had to be heritable. Galton had acknowledged the idea of discontinuous evolution and the biologist William Bateson (1861-1926) was an ardent proponent of this idea. Bateson, was a traditional biologist and critical of the statistical

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2 The study of biometry or biostatistics applies statistics to a broad range of topics in biology. The field was critical in the formation of the foundation theories of modern biology. The methods used by biometricians such as Weldon and Pearson were not committed to a specific theory of hereditary transmission, but did provide very accurate phenotypic predictions (Morrison, 2002).
biometrical approach (Morrison, 2002). Rediscovery of Mendelian laws of heredity for discrete traits in 1900 seemed to provide the missing link in Darwin’s theory of inheritance. As opposed to Darwin’s theory, Mendelian theory was based on the notion of discontinuous variation, and Bateson used the theory as a support for his own theory of discontinuous evolution. Many geneticists, however, such as Pearson and the biometrists strongly opposed the Mendelian view and assumed that most differences among individuals were continuous rather than discrete. The vigorous debate that developed between Mendelianism and the (largely Darwinian) biometry partly persisted until the 1930s, and was not just about to different theories of inheritance, but also about whether biometrical methods were useful for biology and whether the results obtained from such methods were compatible with Mendelianism (Morrison, 2002).

The basis or initiation of what came to be known as “biometrical genetics” or “quantitative genetics” was introduced in papers by Ronald A. Fisher (1918) and his contemporary Sewall G. Wright (1921). Fisher derived statistical methods accounting for Mendelian heritability ratios, and is thus credited with reconciling Darwinian and Mendelian views on heredity and evolution, as well as to reconcile Mendelian and biometric approaches to the problem of heredity (Morrison, 2002). In “Correlation between relatives on the supposition of Mendelian inheritance” Fisher presented the first account on how correlations between relatives could be explained based on the Mendelian laws of inheritance by assuming what is now known as the polygenic model. This model assumes that variation for a certain trait is caused by a huge number of individual genes, each inherited according to Mendel’s laws (Neale & Cardon, 1992). Fisher thus provided a mathematical theory which could reconcile familial correlational observations with a specific theory of inheritance. Wright developed path analysis which is a method permitting diagrammatic presentation of linear structural models and may be considered as a form of structural linear regression analysis which can be used to i) explain the interrelationship among observed variables, and ii) evaluate the relative influences of multiple determinants of a specific variable through the use of latent, unobserved as well as observed effects (Rao & Province, 2000).

1.4.2. Changes in prevailing views

There has been a series of shifts in the views on the genetic and environmental aetiology for mental health and behaviour. Despite quantitative genetic methodology and principles of population genetics being developed already at the beginning of the century, a preoccupation with environmental contributions to human behaviour continued in the behavioural sciences until the 1960s (Rutter, Moffit, & Caspi, 2006). The behaviourist movement from the 1920s to the 1960s proclaimed that behaviour should be understood entirely independently of biology, genetics, and evolutionary history and the movement exerted a profound influence on most theories of learning

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3 In 1866, Gregor Mendel demonstrated that traits in pea plants followed laws of dominant and recessive inheritance (1. Mendelian law), and showed that inheritance of one gene is not affected by inheritance of another gene (2. Mendelian law).

4 The quantitative genetics tradition study how multiple-gene effects lead to quantitative traits.
and development for several decades. Numerous studies documented associations between environmental risk factors such as adverse life experiences and later development of mental ill-health. In the 1950s and 60s research such as Bowlby’s (1951) and Ainsworth’s (1962), evidencing overwhelming effects from parental behaviour on children’s mental health development, was highly influential (Rutter et al., 2006). During this time, a majority of researchers investigating risk and protective factors for mental health seem to have accepted the idea of lasting, and often irreversible effects from early childhood experiences (Rutter, 2002b). Rutter (2002b) summarises the period between the 20’s and 70’s as a research phase characterised by “a serious neglect of the need to provide rigorous tests of environmental mediation hypotheses and a comparable ignoring of the need to differentiate between person effects on the environment and environmental effects on the individual” (p. 9). He also underscores a general failure within the mental health field to appreciate the continuities in environmental disadvantage, resulting in erroneous conclusions concerning the persistence of early environmental sequlae during this time period.

From the late 1960s there was a considerable growth in behavioural and psychiatric genetics. Methodological strategies improved, and twin and adoption studies clearly evidenced the importance of genetic influences on development of psychopathology. By the early 1980s, environmental effects were considered less influential. This major shift was considerably due to three specific challenges, namely i) research documenting the impact of children on family functioning (e.g. Bell, 1968), ii) behavioural genetic research evidencing that environmental experiences typically tend to make children growing up in the same family dissimilar rather than similar (Plomin & Daniels, 1987), and iii) that many associations between environmental risk factors and psychopathology was genetically mediated (Rutter et al., 2006).

Development and refinement of molecular genetic strategies in the 1990s led many researchers to initially believe in the possibility for identification of specific genes with causal effect on the development of psychopathology. These expectations have not been met. A large number of twin, adoption, and extended family designs using quantitative genetic methodology have unambiguously evidenced multiple genetic and environmental influences on individual differences in liability. Mendelian genetics described heredity for discontinuous traits that exhibited clear patterns of segregation (Evans, Gillespie, & Martin, 2002). A majority of the traits or phenotypes relevant to biological psychology are rather characterised by a continuous distribution and influences from multiple genes and environmental effects. Consequently they are known as multi-factorial, quantitative, or complex traits. Complex traits generally result from a combined action of several genetic loci (polygenetic) with contributions from low-penetrant, common alleles and from environmental factors that may be immeasurable, or unknown (Ober, Abney, & McPeek, 2001), making the study of individual genetic effects immensely difficult (Evans et al., 2002). Due to small effects, genetic heterogeneity, and complex patterns of interplay with environmental factors, as well as to psychometric difficulties related to phenotypic definitions, it has become abundantly clear that finding susceptibility genes to multi-factorial traits, in a robust and replicable manner, is highly complicated, if at all possible (Merikangas & Risch, 2003).
1.4.3. Quantitative behaviour genetic analysis

Recent quantitative genetic research in psychopathology and psychological characteristics emphasise a multi-factorial (i.e. multiple genetic and environmental processes individually and interactively influence their development) and polygenetic (i.e. many genes with differing effect sizes are involved in genetic variation) aetiology, and assumes risk factors to be probabilistic with effects extending throughout the normal distribution (Rutter et al., 2006). These properties enable use of statistical approaches based on the properties of the normal curve and estimation of the relative proportions of phenotypic variance which is attributable to genetic and environmental contributions (Evans et al., 2002).

Adoption and twinning are naturally occurring events that provide experimental situations which may be exploited to quantify the relative effects of nature and nurture. If genetic influences are affecting a quantitative trait, phenotypic resemblance of relatives should increase with increasing genetic relatedness (Plomin et al., 2001). Quantitative genetics thus uses the known genetic relationship between family members to estimate the contribution of unknown genes and environmental factors to the observed population variance of a given trait.

Genetic epidemiology is commonly divided into quantitative genetic epidemiology, gene finding research and molecular genetics. Quantitative genetic epidemiology includes family, twin, and adoption studies, and in this thesis we focus exclusively on twin studies. Twin studies compare the phenotypic resemblance in monozygotic (MZ) and dizygotic (DZ) same and opposite-sexed twins. When using such designs, current available techniques allow for partitioning of the genetic variance into additive genetic effects (A) (i.e. the effect of one allele is added to the effects of another allele) and non-additive effects (D) (reflecting interactions between alleles at the same locus [dominance] or interacting alleles across loci [epistasis]), or a combination. Environmental variance may similarly be separated into either shared (C) (common) or non-shared (E) (individual) effects, in which the former refers to non-genetic influences tending to make siblings similar, whereas the latter tend to make them unalike.

Figure 2

![Diagram showing phenotypic variance components](image)

\[ \mathbf{P} = aA + dD + cC + eE \]
Traditionally, quantitative traits were analysed using analysis of variance and intra-class correlations. Recent advances in statistical modelling such as structural equation modelling (SEM) is a more general and flexible model-fitting approach in which the effects ($a, c, d, e$) caused by A, C, D, and E are modelled as regression coefficients in a linear regression of measured variables on unobserved, latent sources of variance (Figure 2). Estimates of these effects are derived by parameterizing the model according to the differential degree to which pairs of MZ and DZ twin pairs are correlated for genetic effects.

In the classic twin design it is impossible to estimate four variance components by means of only three observed statistics in any given model due to C and D being entirely negatively confounded. Consequently, only one of them may be estimated in a given model, and models including the D component are fit only when the ratio of MZ to DZ correlations exceeds 2.0 (Plomin, Chipuer, & Loehlin, 1992). Parameter estimates, or variance component estimates for the structural equation models can be obtained by using a fitting function in which the difference between the observed covariance matrix and the matrix implied by the model is quantified. Such fitting functions provide an estimate of how well any given model fits the data as well as the significance of each model parameter. The significance of a variance component is evaluated by dropping the given variance component from the full model and comparing the fit between the models.

Current quantitative behaviour genetics has moved beyond just measuring heritability. The new SEM techniques enable multivariate analysis of the aetiology underlying co-occurrence or comorbidity, developmental analysis, sex limitation effects, inclusion of covariates in linkage analysis, and estimation of heritability and linkage that is dependent on a certain exposure to environmental risk factors (Kendler, 2005; Boomsma, Bushjahn, & Peltonen, 2002). Recently, SEM has also been used to perform combined linkage and association studies.

"Genes not only push us towards exceptional conditions of mental functioning but scatter us within the normal range, producing much of the variation in ability and temperament that we notice in the people around us". Importantly however, most effects of genes are probabilistic and their effects vary depending on the environment" (Pinker, p. 46).

1.4.4. Genetic effects

Genetic effects or heritability ($h^2$) refers to the total part of the phenotypic variance attributable to genetic differences, and comprises both additive and non-additive effects. If there is no dominance effect, the alleles are said to act additively such that the genotypic effect of a given heterozygote is exactly half the sum of the genotypic effect of two homozygotes (Evans et al., 2002). The heritability coefficient is statistically estimated from correlations or variance-covariance matrices in a given population and do not enable us to infer to what extent genes or environmental factors affect a single individual. Thus, $h^2$ is: i) never individual-specific, ii) sample-specific, and iii) does not
necessarily translate into tangible biological differences (e.g. mutations. It refers to the genetic contribution to differences between individuals in a given population at a specific time, and is either estimated in a broad or narrow sense, with broad-sense heritability referring to effects from both A and D, and narrow-sense heritability referring only to additive genetic effects.

The genetic effect from the latent variables A and D contribute to resemblance in co-twins. MZ twins share all their genes, and the effects of A and D are therefore perfectly correlated in MZ co-twins, whereas DZ co-twins share on average 50% of their segregating genes giving a correlation of 0.5. If some alleles act in a dominant pattern, the correlation between genetic dominance effects will be 0.25. Epistasis reduces the DZ correlation to an extent depending on the number of loci involved and their relative effect on the phenotype (Neale & Cardon, 1992). Genetic influence is implied if the MZ correlation is significantly greater than the DZ correlation, and $h^2$ of the phenotype can be estimated from twice the difference between MZ and DZ correlations.

1.4.5. Environmental effects

"Life is a pinball game in which we bounce and graze through a gantlet of chutes and bumpers. Perhaps our history of collisions and near misses explains what made us what we are? One twin was once beaten up by a bully, the other one was home sick that day. One inhaled a virus, the other didn't. One twin got the top bunk bed, the other got the bottom bunk bed" (Pinker, 2002, p. 396)

Environmental effects are either conceptualised as shared (common) or non-shared (individual). The C construct includes all environmental factors contributing to similarity between co-twins regardless of zygosity, and is correlated 1.0 in all zygosity groups. Contributions from C are suggested if both the MZ and DZ correlations are significant and of similar size, and if twice the DZ correlation is greater than the MZ correlation. The E construct refers to all environmental factors contributing to differences between twins including random measurement error, thus the estimated effect of E constitutes the residual variance after the effects of A and C have been removed and thus tend to overestimate the non-shared environmental influences due to including measurement error.

Quantitative genetic research on mental health, personality, and psychopathology has quite consistently indicated that family resemblance is mainly attributable to genetic factors rather than to shared environment. Estimated magnitude of effects from shared environment influences are commonly small or negligible, and quite consistently less than that of the non-shared effects. However, as the non-shared environmental estimate also subsumes measurement error, there is sometimes more balance between shared and non-shared effects when accounting for error of measurement, and continuities over time (Rutter, 2000b).

Importantly, the apparent non-importance of shared environmental influences that is estimated for many phenotypes, does not necessarily imply that family environment or
parenting have little or negligible effect on children’s mental health. Both shared and non-shared environmental influences are inferences that derive from evidence that environmental factors make siblings alike or different. Estimated shared or non-shared environmental influences have nothing to do with whether the environmental factor is residing within or outside the family. Family features might quite possibly exert large non-shared effects because a given feature (e.g. conflict) impinges more strongly on one sibling than the other (Rutter, 2002).

1.4.6. Genetic and environmental factors: Stability and change

Genetic factors are often implicitly assumed to represent static influences throughout the lifespan, contributing to stability over time, whereas change is assumed to reflect the effects of environmental influences. It is not unreasonable however, to suppose that environmental factors are involved in generating stability over time (Saudino & Plomin, 1996). The theory of psychoanalysis for instance, assumed life-long influences from early childhood experiences on adult personality, and limited opportunities for change in adolescence and adult life.

Assuming that only environmental influences provide a potential for current or enduring change may be similarly premature. Genetic influence implies neither immutability nor stability (Pedersen & Reynolds, 1998). New genetic effects may emerge at any point in life as genetic expression is dynamic and may change in both quality and quantity with development (Plomin, 1986), with different genes coming in to play at different developmental stages throughout life. Genetic change may be conceptualised as the degree to which genetic influences affecting a given trait at a certain age differs from genetic influences affecting the same trait at another age. Such temporal genetic effects might be involved in the specific timing of certain age-related events, and presumed examples of genetic change occur during phases such as puberty and menopause, in which different genes governing hormone production become active and later on inactive. Similarly, there are marked age trends in the onset of some disorders (Rutter, 2002). The genetic effects on change are also a reminder that although the DNA does not change, different life-situations at different ages might make different genetic factors salient. The genes contributing to happiness for adolescents are not necessarily the same as those contributing to happiness among their grandparents. Even moderately stable traits may be influenced by differing sets of genes at different life stages (Plomin, 1986). Thus, both genetic and environmental factors may represent both sources of change and continuity in behavioural development.

In longitudinal behavioural genetic research, genetic and environmental correlations across different ages may be estimated, and genetic change is indicated whenever the genetic cross-time correlation is less than unity. Stability in genetic and environmental factors may similarly be estimated by means of behavioural genetic model fitting procedures. Such procedures enable estimation of to what extent the observed stability is attributable to genetic or non-genetic influences. Importantly, however, high genetic correlations do not imply that genes are contributing substantially to the given
phenotypic stability. There might be the very same set of genes that contribute to a
given trait over time, but its influence might be minor compared to that of the
environmental contributions. Thus, longitudinal twin studies allows for estimation of
how genetic and environmental effects can contribute to phenotypic stability and the
extent to which these influences are themselves, stable.

“Despite the sizable plasticity of Homo sapiens and the dynamic quality of such conceptions
as norms of reaction, zone of development, or plasticity, not everything is possible in
ontogenetic development. Although open, development inherently also is limited”
(Baltes, 199, p. 367)

1.4.7. Genetic and environmental factors: Co-occurrence

Data from both MZ and DZ twins permit estimation of effects from genes and
environment on multivariate associations between different variables (Neale & Cardon,
1992). Most genes involved in complex traits are likely to have pleiotropic effects (i.e.
genetic factors affect several different phenotypes) on a number of related quantitative
traits and recent research has indicated that vulnerability often is tied to “families” of
disorders, conditions, and dimensions as indicated for example by the accumulating
evidence on shared risk factors for many mental disorders. Behavioural inhibition for
example represent a risk factor for developing anxiety related problems, but
simultaneously serve as a protective factor against antisocial disorder (Rutter, 2002).
Thus, an underlying set of genes or environmental factors may be related to a very
specific trait only, but most often appear to increase vulnerability or protection to a
whole spectrum of disorders and conditions, influencing several correlated phenotypes
simultaneously.

A purpose closely related to the decomposition of co-occurrence or comorbidity into
genetic and environmental factors, is to quantify the extent to which the total genetic
and environmental variance is specific to a single phenotype, and to what extent it is
shared by other phenotypes under study.

The extent to which the same or different genes and environmental influences
contribute to a phenotypic correlation is often measured as genetic and environmental
correlations between the given phenotypes. The genetic and environmental correlation
can be quite different from the genetic or environmental covariance. For example, the
genetic contribution to two given traits may be minor, implying low genetic covariance.
Yet, the genetic correlation could be very strong, implying that the same genes are
essentially affecting both traits although weakly. Alternative models to explore co-
occurring phenotypes are also possible (Neale & Kendler, 1995).
II AIMS OF THE STUDY
The general purpose of this thesis was to investigate the contribution of genetic and environmental factors to i) the stability and change in psychological well-being and distress over time, and to ii) the co-occurrence between indicators of well-being and distress, in a population based sample of young adults twins.

Specifically we aimed to answer the following research questions:

1) How stable are levels of subjective well-being and psychological distress (symptoms of anxiety and depression) during young adulthood? What are the relative contributions of genetic and environmental factors to stability and change during this particular life stage?

2) To what extent are the genetic and environmental factors influencing covariation between i) subjective well being and sleep problems and ii) life satisfaction, symptoms of anxiety and symptoms of depression, common or distinct?

3) Do the genetic and environmental sources of variability differ in males and females?
III MATERIALS & METHODS
The present study was conducted as part of the larger Norwegian Institute of Public Health Twin (NIPH) Study. The NIPH Study is an ongoing longitudinal twin study with a cohort sequential design, aiming to explore genetic and environmental influences on health and development. The database consists of population-based registry data that includes data from all like- and unlike-sexed twins born in Norway between 1967 and 1979. Twins were initially identified through information about plural births in the Medical Birth Registry of Norway (MBRN) which began in 1967 and requires mandatory notification of all pregnancies from 16 weeks gestation and registration of standardized information regarding all births in Norway (Bjerkedal & Bakkeiteig, 1975; Irgens, Bergsjo, & Lie, 2000). Altogether, there were 15,374 twin births in those birth cohorts and the percentage of pairs for which both twins survived to age 3 ranged from 82 to 89%. These twins constituted the recruitment basis for the NIPH Study. The current data material consists of two waves of questionnaire data. Twins born from 1967 through 1974 and who were at least 18 years of age were contacted in 1992 via a mail-out questionnaire (Q1). Of the participating twins, 98% confirmed that they could be contacted for further data collection in the future. These twins were re-contacted in a longitudinal follow-up survey conducted in 1998 (Q2). At this time five younger cohorts (born 1975 to 1979), were also recruited into the register and sent the Q2 questionnaire.

3.1 First data wave

Questionnaire data on symptoms of anxiety and depression, well-being, drug use, and somatic health were first collected in 1992 (Q1) from twins born 1967-1974. In November 1992, a questionnaire was mailed to all twins who had reached the age of 18, from pairs in which both twins survived to age 3, and for whom addresses could be obtained (N=7992). The questionnaire (Q1) included items to assess zygosity, current height/weight, demographic information, physical health history with ages at onset and last episode, subjective well-being (SWB), anxiety and depression symptoms, self-rated health, health behaviour, planned education, occupation, and co-twin contact.

Responses on Q1 were obtained from a total of 2,570 complete pairs and 724 singletons, altogether 5,864 individuals, representing an individual response rate of 74% and a pairwise response rate of 63%.

3.2. Second data wave

In 1998, a second and greatly extended questionnaire (Q2) was sent to all twins born 1967-1979. In addition to repeating all items from the first questionnaire (Q1), this follow-up questionnaire was considerably more comprehensive regarding the measurement of physical and mental health, health-related behaviours and exposures, and included screening items for a number of sub-projects. The questionnaire also
included 91 items essentially related to Axis II disorders that had been validated against interview data (SIDP-R) in an epidemiological study (N=4000).

Altogether, 12,700 twins were sent the Q2 questionnaire and responses were obtained from 8,045 twins including 3,334 complete pairs and 1,377 singletons. The individual and pair-wise response rates were 63% and 53%, respectively.

Data for this dissertation thesis come from both data collections (Q1 and Q2). The combined Q1 and Q2 questionnaire samples include 9478 twins who responded to at least one of the questionnaires. About 80% of the twins participating at Q1 also participated at Q2 and the longitudinal sample consists of 4430 twins who participated at both data collections, including 1725 complete pairs and 980 single responders. The mean ages of the respondents were 21.73 (SD 2.23) and 25.59 (SD 3.67) for Q1 and Q2 respectively.

3.3. Zygosity

As zygosity information is not included in the Norwegian Medical Birth Registry, zygosity assignment was initially based on seven questionnaire items in Q1 and the same seven and two additional items in Q2 previously shown to categorize correctly more than 97% (Harris et al., 2002). Twenty-four micro-satellite markers were then genotyped on a sub-sample of 676 of the like-sexed pairs in the sample. Results from these markers were used as dependent variable in a discriminant analysis with the above mentioned questionnaire items as independent variables. Seventeen of the 676 pairs with DNA information were found to be misclassified by the questionnaire data and were corrected. Thus, the total number of expected misclassified pairs could be estimated as 2.51% of the like sexed pairs with only questionnaire based zygosity. This number corresponds to a misclassification ratio of 1.38% for the total sample, including unlike sexed twins.

3.4. Measures

3.4.1. SWB

SWB was measured by a set of items originally suggested by Mound, Næss, Sørensen, Tambs, & Holmen (1990a; 1990b). The index was constructed using a mean score of four items: (1) “When you think about your life at present, would you say that you are mostly satisfied with your life, or mostly dissatisfied?” (Six response categories, ranging from 1 = ”extremely satisfied” to 6 = ”very dissatisfied”. (2) “Are you usually happy or dejected?” (Five response categories, ranging from 1 = “dejected” to 5 = “happy”. (3) “Do you mostly feel strong and fit, or tired and worn out?” (Five response categories ranging from 1 = “very strong and fit” to 5 = “tired and worn out”. (4) “Over the last
month, have you suffered from nervousness (felt irritable, anxious, tense, or restless)?” (Four response categories ranging from 1 = “almost all the time” to 4 = “never”). Thus, the index comprises a cognitive aspect (life satisfaction), positive affect (happy, strong) and negative affect (worn out, nervous), thereby conforming to the generally accepted operationalisation of SWB. Prior to scale construction all items were rescored such that high scores reflect a high degree of SWB. In paper I all items were transformed to 0-10 scales (transformation algorithm: \( X = \frac{Y - 1}{Z - 1} \times 10 \), in which \( X \) is the new score, \( Y \) the original score, and \( Z \) the number of response categories) to provide a common metric. In paper III the four items were summed without transformation. Cronbach’s \( \alpha \) for the index was estimated to be 0.71 and 0.70 for the Q1 and Q2 data, respectively. The scale has been shown to correlate 0.995 and 0.998 with corresponding indices based on the sum of the same, but standardised items, and a principal component analysis (PCA) yielded a clear unidimensional solution (eigenvalue 2.1) with all items loading above 0.70 on this factor. A multi-sample CFA yielded good overall fit and did not indicate significant sex-differences in the factor structure (Roysamb et al., 2002). A student pilot study at the University of Oslo (n = 99) was conducted to further validate the index, and estimating the correlation between the index and the widely used Satisfaction With Life Scale (Pavot & Diener, 1993) to be 0.73 (\( r = 0.88 \) when modelling latent variables). Further description of the index can be found elsewhere (Roysamb et al., 2002; 2003).

3.4.2. Life satisfaction

Life satisfaction (LS) is generally defined as a global reflection about the quality of a person’s life according to his or her subjective evaluation, rather than an experience of pleasant emotion. LS was thus conceptualised as an overall judgement of the quality of life as a whole, rather than evaluative appraisals of life-domains such as satisfaction with one’s marriage or work. In this study we focussed on satisfaction with present life. Whereas the SWB index contained both cognitive and affective components, the LS measure reflects the basic cognitive evaluation of life. LS was measured by the following single item “When you think about your life at present, would you say that you are mostly satisfied with your life, or mostly dissatisfied?” The participants responded on a scale ranging from 1 = ”extremely satisfied” to 6 = ”very dissatisfied”. Empirical tests have revealed that responses to such questions are quite valid and considerably reliable (e.g. Veenhoven, 1984; Scherpenzeel, 1995). A similar one-item scale developed by Andrews and Withey (1976) showed high reliability with a re-test correlation of 0.77 for two administrations of the item (Andrews & Robinson, 1991).

3.4.3. Symptoms of anxiety and depression

The SCL-25 (Hesbacher, Rickels, Morris, Newman, & Rosenfeld, 1980) is a widely used self-administered screening instrument for detecting psychological problems in non-psychiatric settings. It was specifically designed to measure symptoms of anxiety and depression, and includes highly correlated scales for anxiety (10 items) and depression.
(15 items). The SCL anxiety and depression scales have similar reliability and validity (Koeter, 1992) and figures of sensitivity and specificity (Goldberg, Rickels, & Downing, 1976) as the General Health Questionnaire (GHQ) (Goldberg & Williams, 1988). They were initially designed as “state” measures, but a range of studies have demonstrated that common psychological symptoms display considerable temporal stability, to a large extent reflect stable or “trait”-like aspects (e.g. Foley, Neale, & Kendler, 2001), and strongly predict prospective risk of mental disorder (e.g. anxiety and mood disorders) (Kendler, Walter, Truett, Heath, Neale, Martin, & Eaves, 1994). The SCL-5 used in the present study (papers II and IV) includes five items (two anxiety and three depression items) empirically selected from the SCL-25 that explain the maximally highest proportion of the variance of the two sub-scales and the total scores (Tambs & Moum, 1993). Development of the SCL-5 was based on SCL data from a sample of 5999 subjects (2993 men, 3006 women) participating in a health screening by the government Norwegian Health Screening Service in 1990. Cronbach’s α for the short form questionnaire was 0.85 and the sum of the five selected items has been shown to correlate 0.92 with the global SCL-25 score.

The sum of the two first SCL-5 items that had highest loadings on the anxiety factor (short-form anxiety score, SA) correlated 0.84 with the full scale anxiety score, whereas the sum of the three last items with the highest loadings on the depression factor (short-form depression scale, SD) correlated 0.89 with the full scale depression score. Cronbach’s α for SA, SD, and the full scale were estimated to be 0.69, 0.80, and 0.85, respectively. Corresponding estimates for the full scale values (SCL-25) were 0.81, 0.87, and 0.91. The sum of the five selected items has been shown to correlate 0.92 with the global SCL-25 score, and the correlation between SA and SD has been estimated to 0.69.

Respondents completing the SCL-5 were asked to indicate if he/she during the last 14 days was bothered or distressed at all, was a little bit, quite much, or very much bothered by: 1) “Feeling fearful”, 2) “Nervousness or shakiness inside”, 3) “Feeling hopeless about the future”, 4) “Feeling blue”, and 5) “Worrying too much about things” (scale 1-4). In paper II, responses on the items were summed to make a total index score, constructed as the mean score (1-5) of the five items. Alpha reliabilities for the sample, based on imputed item values (see below), were estimated to 0.82 and 0.84 for Q1 and Q2 respectively. A multi-sample confirmatory factor analysis using the software program Mx (Neale, Boker, Xie, & Maes, 1999) was conducted to further validate the scale and test for cross-sex measurement invariance. Due to the variables being standardised, the invariance of the factor loadings were tested. Minor, but significant sex differences were observed at Q1 (Δχ² = 51.00, p = 0.00, AIC = 41.00). Item loadings ranged from 0.74 - 0.90 for females and 0.78 - 0.92 for males. No significant sex differences were observed at Q2 (Δχ² = 8.22, p = 0.14, AIC = -1.78), and item loadings ranged from 0.72 – 0.89. Further psychometric information of the instrument is described elsewhere (Tambs & Moum, 1993a).

In paper IV, responses on the two first items were summed to make an anxiety index (SA), and the three remaining items summed to make a depression index (SD). Cronbach’s α for the sample was estimated to be 0.62 and 0.81 for SA and SD,
respectively. The correlation between SA and SD was estimated to be 0.65. Polychoric cross-time correlations for the two sub-scales measured 6 years apart were estimated to be 0.51 (n = 3976) for SA, and to be 0.48 (n = 3924) for SD, indicating considerable stability and trait-like aspects. Further psychometric information of the instrument is described elsewhere (Tambs & Moum, 1993a).

3.4.4. Subjective sleep problems

The sleep index used in paper III comprised three items as follows: (1) “Have you, or have you ever had sleep problems?” with two response categories, yes and no, (2) “How often have you used sleep medication (hypnotics) the last month?” with four response categories ranging from 1 = never to 4 = almost every night, and (3) “Over the last month, have you suffered from problems falling asleep or other sleep problems?” with four response categories ranging from 1 = never to 4 = almost every night. The index was constructed as a mean score of items 2 and 3, plus the score (0 or 1) on item 1, thus ranging on a scale from 1 to 5. Cronbach’s α for the index was calculated based on polychoric correlations due to the ordinal and dichotomous nature of the items, and estimated to be 0.86.

3.4.5. Covariance between measures

Table 1 shows the polychoric correlations between all measures (phenotypes) utilised in the present thesis. The correlations are based on Q2 data for 4438 females and 3337 males, and all found to be highly significant.

Table 1.

<table>
<thead>
<tr>
<th></th>
<th>SCL</th>
<th>SA</th>
<th>SD</th>
<th>Sleep</th>
<th>SWB</th>
<th>LS</th>
</tr>
</thead>
<tbody>
<tr>
<td>SCL</td>
<td>0.76*</td>
<td>0.86*</td>
<td>0.41*</td>
<td>-0.68**</td>
<td>-0.53*</td>
<td></td>
</tr>
<tr>
<td>SA</td>
<td>0.81*</td>
<td>0.71</td>
<td>0.43</td>
<td>-0.60*</td>
<td>-0.43</td>
<td></td>
</tr>
<tr>
<td>SD</td>
<td>0.89*</td>
<td>0.71</td>
<td>0.49</td>
<td>-0.70*</td>
<td>-0.62</td>
<td></td>
</tr>
<tr>
<td>Sleep</td>
<td>0.42*</td>
<td>0.44</td>
<td>0.44</td>
<td>-0.44*</td>
<td>-0.36</td>
<td></td>
</tr>
<tr>
<td>SWB</td>
<td>-0.66*</td>
<td>-0.61</td>
<td>-0.71</td>
<td>-0.44</td>
<td>0.84</td>
<td></td>
</tr>
<tr>
<td>LS</td>
<td>-0.55*</td>
<td>-0.45</td>
<td>-0.63</td>
<td>-0.34</td>
<td>0.86</td>
<td></td>
</tr>
</tbody>
</table>

* Polyserial correlation
** Pearson correlation
Female estimates are tabulated below the diagonal
3.5. Statistical analyses

Statistical analyses were conducted using SPSS for Windows, LISREL, and Mx (Neale et al., 1999). Structural equation modelling (SEM) was utilised in all papers, using the software package Mx which is specially designed for analysing biometrically informative data.

As initial estimates of the importance of genetic and environmental influences cross-twin (i.e., correlations between twin1 and twin2 for each time point) and cross-twin cross-time correlations (i.e., correlations between twin1-T2 and twin2-T1) for the five zygosity groups were calculated. Due to the skewed distribution of the data, the scales analysed in papers II-IV were polytomized into four or three categories (three or two thresholds) and model-fitting analyses were conducted on raw ordinalized data using the maximum likelihood (ML) estimation procedure in Mx. As variances cannot be estimated when thresholds are estimated, they are constrained to unity. In paper I, raw continuous data scores were analysed and variances and covariances modelled.

The raw data approach allows for preliminary testing of the basic assumptions concerning the homogeneity of response (thresholds) distributions or variances within pairs, across sex, and zygosity, and between complete and incomplete pairs, thereby reducing the impact of ascertainment bias, and increasing the accuracy.

Tests for various sex-specific effects, which can be either qualitative or quantitative, were conducted. Quantitative sex effects refer to sex differences in the magnitudes of the genetic and environmental path coefficients (a, c, e), whereas qualitative effects refer to sex differences in the sets of genes influencing trait variation, and is expressed as the correlation between genetic effects in males and females (r_g). Models that allow for both quantitative and qualitative sex differences are compared to models in which only the magnitude of the genetic and environmental parameters may vary, and models in which sex-specific effects are removed (Neale & Cardon, 1992).

In all studies, the data were analysed using correlated factor models (Neale & Cardon, 1992) in which the variance in each variable is decomposed separately into its genetic and environmental components, and the correlations across components are estimated. However, in study IV, we also tested a single factor independent pathway model containing 3 common latent variables (A_C, C_C, and E_C) in addition to 3 specific variables (A_S, C_S, and E_S) for each phenotype. In such models, the degree to which the three phenotypes share common and genetic risk factors will be reflected in the loadings on the common versus specific factors. The independent pathway model was found not to be an optimal model for the purpose, however, and the correlated factor model was eventually applied in the paper (IV).

By means of different fit measures, comparisons between competing models are possible. The fit of the full model is compared to several nested submodels. When using ML analysis of raw data, no overall measure of fit is obtained. However, the difference in -2 log likelihood between the models is distributed as χ², allowing the relative fit of
submodels against the saturated to be tested using the $\chi^2$ difference test ($\Delta\chi^2_{df}$). A non-significant $\chi^2$ difference is regarded as consistent with the data, whereas a significant value ($p < .05$) suggests poor model fit. Models with fewer parameters are preferred if they do not provide a significant deterioration in fit. To select the best fitting model we used the Akaike Information Criterion (AIC). This measure provides a summary index of both parsimony and fit ($\Delta\chi^2 - 2\Delta df$) (Akaike, 1987), and the lowest AIC value indicates the best fitting model.

3.6. Missing data

Due to missing SCL data in the first data collection, the Expectation Maximization (EM) imputation option in SPSS 12.0.1 was used in paper II to impute missing values for each SCL-5 item using the remaining SCL items and 7 selected items as matching variables. Imputation of missing values increased the total effective sample size from 5175 subjects (complete data on all 5 SCL items) to 5834 subjects at Q1, and from 7829 to 8004 at Q2, whereas the longitudinal material increased from 3870 to 4393 twins. The EM procedure is a process of regression imputation based on the observed relationship between variables. Missing values are replaced iteratively until successful iterations are sufficiently similar, and yield a complete set of data. The matching variables were highly associated with the SCL score. Regression analysis using the 7 matching variables as predictors for the total SCL score yielded Multiple R's of 0.73 and of 0.75 for the Q1 and Q2 data, respectively. To avoid the possibility of artefactual inflation of the twin correlations, imputation was carried out on an individual basis, thus ignoring the paired structure of the twin data. Data from respondents with more than 5 values missing on the total 12 selected items were excluded from the analyses. The same procedure was repeated for each measurement occasion.
IV SUMMARY OF PAPERS
4.1. Paper I


**Background:** Substantial stability in well-being levels is well established, and previous cross-sectional studies have indicated considerable genetic influences on individual variation in subjective well-being (SWB). Consequently, SWB has been suggested to be determined by emotional set-points, or equilibrium levels strongly influenced by genetic factors. One twin study has previously reported on the genetic and environmental influences on stability in SWB. However, the results were based on a very small sample and correlation analyses only, and did not permit exploration of sex-specific effects. The genetic and environmental influences on stability and change in SWB are thus largely unexplored.

**Methods:** Two-wave questionnaire data on SWB from a population-based sample of young adult Norwegian twins born 1967 to 1979, initially surveyed in 1992 and resurveyed in 1998, were analysed using structural equation modelling to explore the relative effects of genetic and environmental influences on phenotypic stability and change.

**Results:** Phenotypic cross-time correlations for SWB were estimated to be 0.51 and 0.49 in males and females, respectively, indicating considerable temporal stability in well-being scores. Genetic and environmental effects accounted for roughly 80% and 20% of this phenotypic correlation. Best-fitting longitudinal model specified additive genetic and individual environmental effects only, with both qualitative and quantitative sex-specific genetic influences. In both males and females, the additive genetic factors influencing SWB were largely stable, with cross-time correlations for genetic effects estimated to be 0.85 and 0.78, respectively. Minor time-specific genetic contributions were also indicated. Individual environmental influences were primarily time-specific (80%), although some environmental contributions exerted long-term effects.

**Conclusions:** In both males and females, long-term stability of SWB was mainly attributable to stable additive genetic factors, whereas susceptibility to change was largely related to the non-shared environment. The results support the notion of hedonic adaptation, essentially attributable to a genetically influenced predisposition for SWB, and provide evidence for substantial time-specific influences from the unique environment. Well-being thus changes continuously in response to immediate life events, but in most circumstances return to a set-point level. Some new genetic influences also emerge, suggesting that the effects of current biological and psychosocial circumstances are of sufficient magnitude to elicit different genetic factors for SWB over time, and some life circumstances exert long-term effects, either due to generating lasting effects or due to being persistently or consistently experienced.
4.2. Paper II


**Background:** Accumulating evidence has indicated considerable stability in vulnerability to psychological distress, anxiety, and depression and sex-specific differences in prevalence, incidence, and morbidity risk are well established. However, aetiological factors for stability and change in symptoms of anxiety and depression, including sex-specific effects are largely unexplored in young adults. This paper explored (i) heritabilities of symptoms of anxiety and depression, (ii) effects of genetic and environmental factors on the stability and change of such symptoms, and (iii) sex-specific effects.

**Methods:** Two-wave longitudinal questionnaire data from 4393 Norwegian twins aged 18-31 were analysed using biometric modelling by means of Mx.

**Results:** The best-fitting longitudinal model specified additive genetic and non-shared environmental influences, and emerging effects from the shared environment in females only. For both males and females, long-term stability was mainly attributable to stable additive genetic factors, whereas change was essentially due to the environment. Minor time-specific genetic effects were also indicated, and some stable variance was accounted for by the non-shared environment. Additive genetic risk factors explained 87% and 68% of the phenotypic cross-time correlation for males and females, with the unique environment accounting for the remaining co-variance. Several notable sex differences in the aetiology were indicated. Firstly, the non-shared environment accounted for a larger proportion of the phenotypic cross-time correlation in females than in males. Secondly, environmental risk factors were significantly more stable in females. Finally, there were considerable sex differences in the magnitude of the genetic and environmental influences at the second measurement occasion, suggesting that contributions from the environment exert a stronger impact on liability to symptoms of anxiety and depression in females than in males.

**Conclusion:** The results provide strong evidence for the temporal stability of genetic risk factors for symptoms of anxiety and depression in young adults, and substantial sex-specific influences on heritability, stability and change. The stability of individual differences and the continuity of genetic factors are noteworthy when considering the normative biological, psychological, and social changes occurring during young adulthood. Based on the current and previous findings, liability to symptoms of anxiety and depression in childhood, adolescence, and adult life appears to be primarily characterised by stable genetic influences and transitory environmental effects.

**Background:** Experiencing good quality sleep is an important part of healthy functioning. Yet, subjective sleep problems affect as much as 30% of the population and often remain a chronic complaint. Sleep problems are highly distressing, strongly associated with mental health problems (e.g. mood disorders), and often do not warrant a separate diagnosis. This suggests a common diathesis. The present study aims to delineate the aetiological relationship between SWB (well-being) and self-reported sleep problems (distress) in a cross-sectional twin design by exploring the shared and non-shared genetic and environmental influences.

**Methods:** Subjective well-being (SWB) and sleep problems were investigated in a large population-based cohort of Norwegian twins aged 18 to 31 years. Questionnaire data from 8045 same- and opposite-sexed twins were analyzed using structural equation modeling by means of the software program MX to explore the relative effects of genetic and environmental influences on phenotypic variance and covariance.

**Results:** The phenotypes were substantially negatively correlated (-.43), with genetic and environmental factors accounting for 60% and 40% percent of the correlation, respectively. Univariate analyses indicated considerable genetic influences for both SWB and sleep problems, for males and females alike. Best fitting bivariate model specified additive genetic and individual environmental factors for both phenotypes, non-additive genetic influences on sleep problems, and no sex-specific effects. The additive genetic factors were highly overlapping ($r_g = -.85$), suggesting that a substantial part of the genetic effects that positively influence SWB also protect against problems sleeping. Environmental influences were largely phenotype specific ($r_e = -0.30$), indicating considerable distinct environmental contributions to the association between SWB and subjective sleep problems.

**Conclusion:** The results indicate a considerable overlap in genetic aetiology for SWB and subjective sleep problems, for males and females alike, and largely non-shared influences from the environment. Genetic factors contributing to enhanced well-being are thus similarly operating to protect against sleep problems.
4.4. Paper IV


Background: Well-being and psychological distress (e.g. anxiety and depression) are not conceptualised as polar opposites, but a number of studies have evidenced strong negative associations. Why is this so? Are well-being and distress manifestations of different or overlapping aetiological factors? This study examines the genetic and environmental relationship between liabilities to anxiety, depression, and satisfaction with life (LS).

Method: Questionnaire data on self-reported symptoms of anxiety (SA), symptoms of depression (SD), and LS from a large population-based sample of Norwegian twins (n = 8045) aged 18-31 were analysed using structural equation modelling. A trivariate correlated factor model was applied to the data using the statistical software program Mx.

Results: All three phenotypes were substantially correlated. Decomposition of the phenotypic correlations revealed that environmental influences explained roughly 75% of the phenotypic correlations in females, and 50% or less in males. Correlations between SA and SD were close to unity ($r_e = .92$) and high for SD and LS ($r_e = .79$) and SA and LS ($r_e = .64$), thus highly overlapping. Contributions from the non-shared environment were to a larger extent phenotype-specific, with correlations between environmental factors ranging between .26 and .56. Best-fitting multivariate model specified sex-specific differences in the magnitude of the latent genetic and environmental influences, implicating higher male heritability estimates, and influences from the shared environment for all phenotypes in females.

Conclusion: Genetic and environmental causes of life satisfaction, symptoms of anxiety, and symptoms of depression are partly shared, partly distinct, and exert differential magnitude of effects in males and females. In both sexes, however, aetiological factors influencing life satisfaction appear to be involved in countervailing feelings of sadness and displeasure, but do not seem similarly engaged in softening the aversive experiences of anxiety and tension. The results complement and refine the research literature by adding information concerning the nature of the associations, and by implicating sex-specific effects.
V DISCUSSION
5.1. Interpretation

The specific findings of each of the empirical studies are discussed in the papers. The main results will therefore be discussed shortly, focusing on the two major objectives outlined in the aims section; namely (i) the genetic and environmental effects on stability and change in psychological well-being and distress during young adulthood, including the stability of such influences, and (ii) the extent to which the genetic and environmental etiology for well-being and distress is overlapping or distinct. Methodological considerations will be addressed more specifically in later sections.

5.1.1. Stability and change

To our knowledge, papers I and II represent the very first attempts to explore the aetiological factors underlying stable and transient levels of SWB (paper I) and psychological distress (paper II) in young adults by means of a large population-based twin sample.

Substantial stability was found for both SWB and psychological distress with cross-time correlations estimated to be approximately 0.50, indicating that roughly 50% of the variance at each specific time-point was due to long-term stability factors. Remaining variance was attributable to time-specific variance including random or stochastic chance effects (change). The relative importance of genes and environment were fairly similar at each assessment, explaining approximately 50% of the variance each, although female heritability estimates were significantly reduced at the second assessment, with complementary increases in environmental influences.

Additive genetic influences were found to largely determine the temporal stability, with approximately 80% of the covariance being due to such factors. Virtually identical genetic estimates have been reported for well-being and distress in previous studies using alternative measures, different statistical methodology, and age heterogeneous samples (e.g. Lykken & Tellegen, 1996; Rijsdijk et al., 2003) as well as for personality (McGue, Bacon, & Lykken, 1993).

In both longitudinal studies, negligible stable effects appeared to be due to being raised in the same family, implying that familial resemblance which is stable over time essentially is due to shared genetic contributions. Such findings fit well with the majority of research on mental health and psychopathology in adult populations which quite consistently suggests that the shared environment generally do not contribute to similarity between co-twins over time (e.g. Lykken & Tellegen, 1996; Gillespie et al., 2004; Rijsdijk et al., 2003; O’Connor, Neiderhiser, Reiss, Hetherington, & Plomin, 1998). Nevertheless, shared environmental contributions are sometimes found to be evident in designs assessing vulnerability factors more directly even when not apparent when treated as unmeasured inferred variance (Kendler, Neale, Prescott, Kessler, Heath, Corey, & Eaves, 1996). The power to detect small effects from shared environmental
influences is also generally low in samples of our size even in multivariate analyses (Schmitz, Cherny, & Fulker, 1998), consequently leaving us unable to entirely dismiss minor stable effects from the common environment.

Non-shared environmental factors constituted the main source of change, accounting for roughly 80% of the time-specific variance. Findings of predominantly transient effects from such influences are consistent with longitudinal research on SWB, anxiety, and depression in both twin and non-twin samples (e.g. Gillespie et al., 2004; Rijsdijk et al., 2003; Lykken & Tellegen, 1996; Diener, Sandvik, Pavot, & Fujita, 1992; Merikangas et al., 2003). Research on personality similarly suggests that environmental influences do not exert long-lasting redirection or enduring changes unless exposure is continuous (e.g. McGue et al., 1993). In addition, alternative new research methods such as the Day Reconstruction Method, which basically utilises experience sampling methodology by means of a daily diary approach, also confirm the limited stable effect of most environmental circumstances on related measures (e.g. life satisfaction levels) (Kahneman et al., 2004). The results thus challenge the acceptance by many clinicians, researchers, and lay people of the long-lasting importance of environmental effects, for example deriving from psychosocial deprivation, stress, and adversity.

Despite environmental factors mainly exerting transient effects, some environmental experiences were shown to exert stable influences throughout the period investigated. These stable effects from past or persistent events appeared to be stronger in females than in males, although differences reached significant levels only for psychological distress. Environmental influences i) explained more of the temporal stability in females than in males, and ii) and the influences themselves were more stable, suggesting a special female susceptibility to long-term effects from environmental risks. Due to our study not measuring environmentally mediated risks stemming from measured risk factors, we were not able to explore whether these effects represent long-term effects from past or persistent events, or consistently occurring factors in the environment. Nor did the design permit identification of any specific experiences accounting for the observed effects. Previous research, however, has documented both differential sex-specific exposure (sexual abuse, crime) and susceptibility to number or severity of risk factors (Rutter, Caspi, & Moffitt, 2003). On average, women are more sensitive to the effects of low levels of social support (Kendler, Myers, & Prescott, 2005), more vulnerable than men to the effects of undesirable events in their proximal social networks and interpersonal relationships (e.g. Maciejewski, Prigerson, & Mazure, 2001), and particularly at risk for crises involving children, housing, and reproductive difficulties (Nazroo, Edwards, & Brown, 1997). We may thus speculate that young adult males and females undergo partly different developmental trajectories due to gender-based experiences and dispositions that are possibly connected to differential social, relational, and family related transactions during this particular life stage.

A second sex-specific effect was also indicated in both longitudinal studies. Whereas male heritability remained largely unchanged, female heritability significantly decreased, being accompanied by either increasing influences from the individual-specific (SWB) or the shared environment (psychological distress). These increasing contributions from the environment may reflect sex-specific experiences faced when establishing separate
lives and adopting adult lifestyles as adult role transitions may involve different changes and challenges (e.g. pregnancies, investments in parenting and work, etc) in males and females. Relationship status has for example been found to entail gender-dependent effects on the stability of personality traits like extraversion and neuroticism (Costa, Herbst, McCrae, & Siegler, 2000).

Males and females commonly score equally high on most SWB measures (Diener et al., 1999), and descriptive analyses in this study (paper I) indicated only minor sex differences in mean levels of SWB. Nevertheless, qualitative (non-scalar) sex-specific effects were found, indicating that a partly different set of genes are involved in generating SWB in males and females. Such qualitative sex-specific genetic effects may either represent a direct genetic effect, or an indirect effect in which genetic influences are mediated through environmental circumstances. Biological influences are not likely to operate in ways entirely free of social-contextual pressures, and differentiated social influences in males and females do not commonly arise independently of biological or genetic features (Rutter et al., 2003). SWB is associated with a multitude of positive life outcomes, benefits, and adaptive successes in various life domains such as marriage, friendship, health, and income (Lyubomirsky et al., 2005). As different factors appear to generate success in males and females, differential genetic factors involved in well-being and ill-being is reasonable. Sex-specific genetic effects may therefore be partly dependent on specific life situations or gender cultures influencing young adult males and females, for example associated with work, marriage/partnership, and parenting, which are the three domains undergoing most pronounced changes during young adulthood. Other explanations are also possible, and future challenges involve further disentangling of the specific mechanisms involved in generating these processes.

In paper II, the model specifying qualitative sex-specific effects showed a fit close to the best-fitting model suggesting that qualitative effects may be relevant also for psychological distress. The difference in fit between the two best fitting models in both longitudinal papers was small, consequently leaving us unable to conclude with confidence. Our finding of sex-specific genetic effects, however, fits well with research on related constructs such as major depression (Kendler et al., 2006) and neuroticism (Fanous, Gardner, Prescott, Cancro, & Kendler, 2003).

In both males and females, some new genetic influences were found at the second assessment, implying that genetic factors, although primarily representing a source of continuity, also represent a minor source of change. Genetic effects on change processes are a reminder that although the DNA may not change, different life-situations at different ages might make different genetic factors salient. Findings of some new genetic influences also compares well with recent studies exploring stability of depressive symptoms in young people (e.g. Lau & Eley, 2006), and may represent developmentally sensitive genetic factors that are being activated when facing transitional changes or challenges occurring during young adulthood.

Three features should be kept in mind when interpreting the results. Of primary importance is our use of two-wave data across a span of six years, which allows only linear change trajectories to be estimated. Biometric modelling of data from only two
assessments does not enable separation of short-term shifts from long-term stability that might be hidden by momentary influences. Only overall trajectories are analysed, leaving inter-individual differences largely unexplored. People may vary considerably in their direction and rate of change, as well as in the amount of curvature that defines their trajectories (Mroczek & Spiro, 2005). Developmental research on non-twin samples has indicated that life span development may be characterised by individual differences in intra-individual change (Baltes & Nesselroade, 1973), and inter-individual change trajectories have recently been found for LS (Mroczek & Spiro, 2005). The latter finding was based on a non-twin sample however, that did not enable control of hereditary factors which may be involved in generating and sustaining such individual trajectories.

Important for interpretation of the findings is also the estimation of the non-shared environmental component. The E estimate constitutes the residual variance after the effects of A and C have been accounted for and tends to overestimate the non-shared environmental influences due to confounding with measurement error. Our estimates of transient environmental effects may thus by somewhat attenuated.

Thirdly, the similarity between findings for SWB and psychological distress are not altogether surprising due to some overlap in content between the phenotypes. Results from the two longitudinal studies should therefore not be considered entirely independent. SWB and distress symptoms are conceptually related, with absence of negative affect being one of the three SWB components.

Notwithstanding shortcomings, the collective results indicate considerable top-down as well as bottom-up influences on current well-being and distress in males and females alike. Genetically-based homeostatic dispositions seem to strongly regulate emotional tone over time, whether it is feelings of well-being, happiness and satisfaction or sadness and tension. The results therefore provide considerable support for models assuming individual, affective set-points or equilibrium levels essentially due to stable additive genetic influences. However, at any given moment in time, environmental circumstances are as influential in determining our affective valence as genetically based dispositions. In as much as life consists of ongoing change; the non-shared environment constitutes the main source of such change. Keeping in mind that long-term stability was accounting for only half of the total variance in scores, notions of rigid, genetic predispositions governing our ongoing emotional life therefore appear somewhat exaggerated. Integration of past findings, renders the existence of a “soft baseline” more plausible. For example, reported LS levels have been shown to change for some people over longer periods despite stabilising factors such as heredity (e.g. Lucas et al., 2004; Fujita & Diener, 2005), indicating that adaptations sometimes remain incomplete, and that our well-being or ill-being is not unalterable as if set in concrete. Overall, however, genetic influences place limits on the extent of change that is possible, with ever-increasing happiness or despair highly unlikely. Results from the current dissertation strongly suggest that both genetic and environmental factors are contributing to generate stability and change in SWB and psychological distress. A soft personal baseline or set-point predominantly genetic in origin is suggested however, with environmental factors representing the main source of temporary displacement from
the baseline. Along with the majority of longitudinal behaviour genetic research into personality, psychopathology, and affect, our two longitudinal studies suggest that psychological well-being and distress during young adulthood is characterised by genetic continuity and environmental change.

5.1.2. Is well-being the flip side of ill-being?

An important question in the aetiology of mental health concerns the extent to which risk and protective factors underlying different indicators are common or distinct, and to what extent they are sex-specific. A second major aim to this thesis was therefore to explore whether measures of psychological well-being and distress are subject to differential causal factors. Such questions concerning the specificity and commonality of aetiological contributions are partly related to the broader and still ongoing debate in psychology concerning the structure of emotions. In previous research on circumplex models of emotion, measures of happiness and sadness consistently fall near the poles a bipolar valence dimension, indicating that people seem to treat the two emotions as diametric opposites, or mutually exclusive (Larsen, McGraw, & Cacioppo, 2001). Alternative models (e.g. Cacioppo & Berntson, 1994), conceptualise the affect system in a bivariate space in which positivity and negativity have antagonistic effects, the former fostering approach, the latter avoidance. These affects may be reciprocally activated, but may also be uncoupled, co-activated, or co-inhibited.

Although our measures of positive and negative affectivity, well-being and distress, were crude and must be regarded as specific representations, we aimed to provide a first look into the shared or non-shared aetiology influencing covariation between measures to contribute to a more complete understanding of the aetiological factors involved.

In paper III the correlation between well-being (SWB) and distress (subjective sleep problems) was found to be mediated by both genetic and environmental factors, explaining 60% and 40% of the covariance, respectively. In both males and females the genetic factors were highly correlated ($r_g = -0.85$) and consequently mainly overlapping, indicating a single underlying genetic disposition simultaneously involved in heightening levels of SWB and protecting against sleeping problems. In contrast, contributions from the environment were largely independent ($r_e = -0.30$), either operating to enhance levels of well-being or conferring vulnerability to sleeping problems.

A somewhat similar pattern of overlap and specificity was indicated in paper IV, with overlap in aetiological factors found to be more pronounced for genetic than non-shared environmental factors. Correlational figures of past research on well-being, anxiety, and depression in non-twin samples have indicate that anxiety and depression show differing relationships with measures of well-being (Headey et al., 1993; Schimmack et al., 2004), finding life satisfaction to be closer associated with depression than with anxiety. Our results replicated such findings, and extend the research literature by evidencing that the structure of both genetic and environmental factors reflects the commonly reported phenotypic structure. Associations between both latent genetic and
latent environmental factors influencing life satisfaction and symptoms of depression are considerably closer than corresponding associations between latent factors influencing life satisfaction and symptoms of anxiety. Thus, a common set of genetic and environmental factors appear to simultaneously enhance life satisfaction and protect against symptoms of depression, sadness and displeasure, but to a lesser extent buffer against symptoms of anxiety. This is particularly salient for non-shared environmental influences, which are essentially independent. However, decomposition of the phenotypic correlations revealed that environmental factors (shared and non-shared) explained as much as 75% of the female covariance, thus constituting a larger source of covariance than additive genetic factors, whereas in males, the non-shared factors accounted for 36-50%.

In paper III, significant but modest sex differences in SWB and prevalence of sleep problems were found with male responders reporting to be happier and having less sleep problems than their female counterparts. Polychoric cross-twin correlations did suggest sex-specific effects for SWB, but the bivariate analyses did not show differential aetiological processes influencing the association between SWB and sleep problems in males and females.

In paper IV, smaller heritability estimates and essentially overlapping effects from shared environmental factors were found for all three phenotypes in females. Support for the aetiologcal significance of shared environmental factors on well-being and psychopathology in adult populations has been scarce, but the power to detect small effects from shared environmental factors is generally low in samples even of our size, possibly leading to dismissal of minor effects in many studies. In paper II, emerging effects from shared environmental influences on psychological distress was found in females. Collectively, results from papers II and IV therefore suggest that sex-differential contributions from shared environmental influences emerge as the co-twins are establishing separate lives and adopting adult lifestyles. Although contributions from the shared environment commonly are found to be larger when co-twins are younger and still share the same household, the results suggest that life situations and challenges occurring during young adulthood may activate or re-activate shared environmental influences. Heritability estimates are contingent on the immediate social, demographic and socioeconomic context, and C effects may diminish or increase when social norms and economic conditions allow a broader or narrower range of life alternatives. Young adulthood is transitional and involves many biological, psychological, and social changes. Most young adults leave their childhood home, complete their education, establish a career, and many take on family responsibilities and nurse small children. Adult role transitions in many females may involve different challenges than for their male counterparts and be subject to different social norms, possibly allowing a smaller range of behaviour alternatives. Comparatively stronger female vulnerability towards risks such as crises involving children, relationship status, and housing, and (Nazroo, Edwards, & Brown, 1997) are closely related to the three domains undergoing most pronounced changes during young adulthood, namely work, marriage/partnership, and parenting. Different contributions from genes and environments in males and females may thus be partly dependent on gender-based norms and challenges associated with such developmental transitions.
Some general caveats should be kept in mind when interpreting the results. Relevant for both of the cross-sectional studies are limitations involved in the estimation of the environmental correlations. Although measurement error does not contribute to the phenotypic covariance, the correlation between E factors may be biased by random error and unreliability and consequently produce deflated correlations between environmental factors. The estimated commonality of environmental factors may thus be biased somewhat downward. Secondly, the power to detect sex-specific effects with confidence is limited in samples of our size even in multivariate studies, and the results need further replication.

Nevertheless, the collective results in papers III and IV suggest, that indicators of psychological well-being and distress appear to share a common genetic and environmental aetiology, with construct specific aspects mostly being due to differing environmental factors operating.

5.2. Methodological considerations

5.2.1. Validity

Construct validity refers to links between the psychometric and theoretical notions of a test (i.e. the substantive meaning of a given measure), thus reflecting whether a given scale measures what it is intended to measure (Kerlinger, 1986). Convergent and discriminant validity are considered subcategories of construct validity (Cook & Campbell, 1979), and refers to whether different measures of constructs that theoretically should be related are, in fact, related to each other (convergence) and whether measures of constructs that theoretically should not be related, in fact, are observed not to be related. Below, construct validity features of the different phenotypes and some general validity concerns are discussed briefly.

The SWB index (papers I and III) has generally been found to have good psychometric properties, and conforms well to accepted operationalisations of global subjective well-being (e.g. Diener et al., 1999) in which SWB consists of a tripartite structure. This three-dimensional structure of SWB has been confirmed both at the item and scale level in previous studies (Arthaud-Day, Rode, Mooney, & Near, 2005).

Validity of the SCL-5, the SA, and the SD depends on the validity of the SCL-25. The SCL-25 has been proved to have satisfactory validity as a measure of psychological distress (Derogatis, Lipman, Rickels, Uhlenhut, & Covi, 1974), with highly correlated subscales for anxiety and depression, partly because these conditions are, in fact, highly interrelated in both clinical and normal populations (Tambs & Moum, 1993a). High correlations may in part result from over-inclusion of non-specific symptoms shared by
anxiety and depression as compared to items loading on relatively specific symptoms (e.g. panic attacks and feelings of worthlessness). Discriminative validity for anxiety and depression states appears to be more evident in clinical samples (perhaps partly due to greater variance with increased number of severe cases) and when measured by a clinician. Whether this latter finding reflects i) a sensitivity to cues that the patients neglects or is unaware of, or ii) biased ratings by the clinician due to over-differentiation within the diagnostic tradition, is not yet clear (Mineka et al., 1998).

Agreement between dimensional measures and clinical diagnoses based on structured interviews is usually only moderate. A comparison of the SCL-25 and the Composite International Diagnostic Interview (CIDI) (Wittchen, 1994), revealed that the two instruments to some extent identified different cases. The tetrachoric correlation between SCL and depressive disorders, anxiety disorders, and somatoform disorders could be estimated to be 0.48, suggesting that the SCL may not be a very good indicator of CIDI diagnoses, or that the mental health dimensions assessed by the two instruments are different (Sandanger, Moum, Ingebrigtsen, Dalgard, Sørensen, & Bruusgaard, 1998).

Notwithstanding potential validity concerns, the SCL-5 utilised here conform well to key characteristics of anxiety and depression separately, with anxiety items focussing on fearfulness, nervousness, and shakiness inside, and depression items reflecting feelings of hopeless about the future, feeling blue, and worrying to much about things. Anxiety disorders subsume a diverse array of symptoms, however, and the SCL-5 items may be more related to GAD which is more closely linked to major depression than to other anxiety disorders containing less general distress variance (Mineka et al., 1998).

The SCL and SWB indices were strongly negatively correlated, and SWB items were used as predictor variables when imputing missing values on the SCL index (paper II). A key component of SWB is the relative absence of negative affects, such that high correlations between SWB and SCL are to be expected. Due to this overlap in meaning between the SWB and SCL, we used a single item life satisfaction measure in paper IV when exploring the genetic and environmental influences on associations between well-being and distress. Single item measures are commonly considered a threat to validity concerns. However, the item was seemingly relevant (i.e. face valid) to the construct investigated (global life satisfaction), and an almost identical single item measure have been used previously with empirical tests indicating that responses to such questions are quite valid (e.g. Veenhoven, 1984; Scherpenzeel, 1995).

The sleep index (paper III) showed adequate psychometric properties as a measure of global subjective sleep dissatisfaction, and a confirmatory multi-sample two-factor analysis of the SWB and sleep items indicated divergent validity. Additional validation against other scales or indices would have been useful, however.

Epidemiological surveys often employ self-report ratings consisting of a limited number of items due to cost-efficiency or because better measures are difficult, or impossible to include in large scale surveys (Diener et al., 2003). Twins represent a limited resource, and a lot of research groups usually compete to take part in national twin studies. All
data analysed in the current thesis were from self-report, and the latent constructs measured by small number of items (1-5). In addition, the well-being measures used were global questions referring to somewhat different time frames. Answering such questions, require the responder to evaluate, integrate, and retrieve experiences and memories (Kahneman & Riis, 2005). To some extent, “evaluated” and “experienced” indicators are different. Nevertheless, they do not represent independent phenomena, and are usually highly correlated (Kahneman & Riis, 2005).

Questionnaire data are sometimes suggested to reflect the reporting behaviour of symptoms rather than the actual occurrence of symptoms, and genetic effects on reporting behaviour have been suggested (Kendler & Karkowski-Shuman, 1997). In general however, response styles do not seem to have a strong effect on affect ratings (Schimmack, Bökenholt, & Reisenzein, 2002).

Concerning the convergence of different methods and sources, the results must be compared and validated against other studies using different measures and methodology. With regard to some of our salient findings, such as the limited stability of environmental effects, our results are highly consistent with longitudinal research using non-twin samples and various statistical methods (e.g. Diener et al., 1992), behavioural genetic research on personality (e.g. McGue et al., 1993; Loehlin, 1992), and results obtained through alternative research methods such as the DRM (Kahneman et al., 2004). Heritability estimated for the various measures and the sex-specific effects indicated by our results, also fit well with previous estimates of highly related phenotypes using different statistical techniques and modelling approaches (e.g. Lykken & Tellegen, 1996; Kendler et al., 2006; Roysamb et al., 2002; 2003).

5.2.2. Reliability

Reliability refers to the degree of accuracy and stability of a given measuring instrument (e.g. Kerlinger, 1986; Kerlinger & Lee, 2000). In twin studies, the non-shared environment effect (e) also subsumes measurement error, and estimates of familial resemblance are therefore proportionally deflated by decreasing reliability. Systematic biases may also inflate test-retest reliability while diminish validity due to all reliable variance not being valid variance.

The most commonly used reliability measure (internal consistency) is the Cronbach’s α (Cronbach, 1951). In this study, the alphas reported for each of the sum-score indices ranged from moderate to high, all but one (SA) exceeding 0.70 indicating a satisfactory or sufficient level of internal consistency (Nunnally, 1978).

The LS measure (paper IV) consisted of only one-item and did not permit estimation of the alpha. It is generally argued that one item measures have limited reliability. An almost identical the LS item developed by Andrews & Withey (1976), has been shown to correlate 0.77 over two administrations of the item. Random error variance in LS judgments is also commonly low (Schimmack & Oishi, 2005; Eid & Diener, 2004). The
data material available for the present study did allow cross-time correlations between two assessments of the item, but the measurement occasions were 6 years apart. Test-retest correlations were consequently rather moderate, being estimated to be 0.37 and 0.34, for males and females respectively. The respective retest correlations for SWB, SCL-5, SA, and SD indicated considerable temporal stability and trait-like aspects with estimates of approximately 0.50 across the 6 year span.

All studies in this thesis were based on analysing covariances or correlations and contributions from genetic and environmental factors to phenotypic correlations are not affected unless the measurement errors are correlated. In addition, all measures were mean score indices, except from the single-item measure of LS, and to some extent random errors of single items are removed by index construction leading to more reliable phenotypes (Kerlinger & Lee, 2000). However, correlations between E factors will be deflated by measurement error, such that the commonality of environmental factors estimated over time (Papers I and II) or across phenotypes (papers III and IV) may be biased somewhat downward.

5.2.3. Stability

Estimates of stability and change based on two-wave studies may have limited reliability as observations over alternative time periods might yield different results, and only linear change trajectories can be measured. Our approach offers a broad understanding of the aetiological processes underlying stability of SWB and psychological distress in young adults, but raises a need for more detailed investigation of individual change processes. Average stable levels of well-being or ill-being may hide substantial individual-level instability. More complex models such as latent growth curve models (LGCM) have great potential for understanding individual differences in change. LGCM enables prediction of more complex patterns of relationship between mean, variance and covariance. Such models may also be empirically tested against simpler models.

5.2.4. Correlated factor models

Although different models were tested, correlated liability models were used in all papers. Our results consequently reflect the limitations specified in these particular models, and do not rule out the possibility of other causal relationships. Co-occurrence in the same individual of symptoms, traits, or disorders may arise from various mechanisms, such as direct phenotypic causation (e.g., reduced SWB causing sleep problems), or reciprocally interacting phenotypes (Neale & Kendler, 1995). Alternative models of co-occurring phenotypes are possible, also in cross-sectional data sets, but the statistical power to detect differences in these models are usually very low with samples of our size (Neale & Kendler, 1995).
5.2.5. Attrition and missingness

Differential attrition and non-response may potentially lead to biased estimates of genetic and environmental parameters (Heath et al., 1998). Longitudinal studies are subject to ascertainment bias and inevitable dropout, and twin studies are particularly vulnerable as cooperation is ideally required from pairs. In this study, the individual response rates (74% and 63%) were lower than optimal and particularly low amongst the youngest cohorts who participated in Q2 only (born 1975 to 1979). The modest response rate may partly result from rules for mailed questionnaire studies decided by Norwegian authorities prohibiting more than one mailed reminder as well as the length of the Q2 questionnaire.

In paper I, significant mean differences in SWB were found between pairs and single responders. Standard problems of small and self-selected samples are usually ruled out when the sample is being derived from a population-based twin register, however, and attrition analyses have not shown substantial recruitment bias on mental health in our sample (Harris et al., in preparation). In paper III, SWB thresholds were not significantly different for twins responding at both data collections (Q1 and Q2) and twins responding only at Q2. Neither were there significant differences in co-twin correlations for SWB observed at Q1 for non-responders and responders at Q2. Testing the homogeneity of thresholds in papers II - IV did not reveal significant differences between pairs and single responders for any of the phenotypes modelled. If participants and non-participants differ phenotypically, single responders who probably resemble their non-responding co-twins to some extent are expected to depart from pair-wise responders in the same direction as do non-participants. Thus, absence of phenotypic differences between single and pair-wise responders indicates no substantial recruitment bias.

There was a fairly high number of missing responses on SCL items at Q1, possibly due to layout aspects of the questionnaire. In paper II, missing data was therefore imputed by means of the EM single imputation procedure in SPSS for Windows. All missing values were imputed, but respondents with more than 5 values missing on a total of 12 selected items (5 SCL items, 7 matching items) were entirely excluded from the analyses. The matching variables were strongly associated with the SCL score and regression analysis using the 7 matching variables as predictors for the total SCL score yielded Multiple R’s of 0.73 and of 0.75 for the Q1 and Q2 data, respectively. Single imputation may provide more apparent power than is justified by the data, however, and tend to underestimate standard errors and overestimate the precision level (Acock, 2005). To avoid the possibility of artefactual inflation of the twin correlations, imputation was carried out on an individual basis, thus ignoring the paired structure of the twin data. Furthermore, multi-sample CFAs of imputed and unimputed SCL items were compared. No significant differences were indicated however, and modelling yielded consistent results.
5.2.6. Twin assumptions and biometric modelling

The advanced behavioural genetic methods utilised in the present dissertation extend the descriptive approach characteristic of basic designs that primarily investigates heritability, to explore the action of genetic risk and protective factors (Kendler, 2005). However, these analyses are subject to many of the same limitations as more basic designs. Some of the most critical assumptions and common criticisms are discussed below.

The validity of the results from the twin method depends on several important assumptions being met. A major assumption is the “Equal Environment Assumption” (EEA). EEA holds that monozygotic (MZ) and dizygotic (DZ) co-twins are equally correlated in their exposure to environmental factors of aetiological importance for the trait under study. Evidence has indicated that the EEA sometimes is violated (e.g. Kendler et al., 1986), leading to inflated heritability estimates. Usually, such violation only represents a problem if the similarity affects the trait that heritability is being estimated for. Research on psychiatric illnesses in general has indicated that differential parental treatment of MZ and DZ twins is unlikely to represent a significant bias in twin studies of the major psychiatric disorders (Kendler, Neale, Kessler, Heath, & Eaves, 1994). A previous study of symptoms of anxiety and depression using the present sample did show violation of the EEA, but the resulting bias effects on the parameter estimates were only minor or trivial (Tambs et al., 1995). More similar treatments of MZ than DZ twins are also likely to result from the fact that genetic resemblance tends to trigger more similar reactions from the environment. Since such excessive equality result from segregating genes, it should not be considered a method artefact.

Assortative mating refers to non-random or selective mating in sexually reproducing organisms that are either genetically similar (positive phenotypic assortment) or very dissimilar (negative phenotypic assortment). When assorting is cued on heritable traits, these two types of assortative mating have the effect of reducing and expanding the range of variation. Positive assortative mating cause transmission of similar genes from both parents, increasing the genetic correlation beyond 0.5 in DZ twins, whereas the MZ correlations is left unaffected. The inflated DZ correlation will produce deflated heritability estimates and inflated effects from the shared environment. In cases with strong transmission of C effects, the co-twin correlation between the latent variables C will increase somewhat as well. However, this extent of inflation will usually be moderate compared to the inflation of the genetic correlation. In the current thesis, no observed spouse correlation was available for any of the phenotypes investigated. However, a spouse correlation of .27 was observed in a Norwegian sample for a measure highly related to the SCL-5 used here (Tambs & Moum, 1993b), and a spouse correlation of 0.35 was observed in the same sample for a SWB index almost identical to ours (paper I and III) (Tambs & Moum, 1992). While these correlations are clearly different from zero, they are not expected to substantially affect the parameter values from our twin studies.

Gene-environment correlations (CorGE) refer to genetic factors influencing exposure to a non-random sample of environments. People are active agents in selecting and shaping
their surrounding environments (active CorGE), and in turn, these environments respond to their behaviour (evocative CorGE), amplifying or strengthening genetically based dispositions. Whereas the latter simply reflects “the way genes act”, passive covariation is clearly conceptually different from genetic effects. Passive CorGE arise due to correlations between the individual’s genotype and the environment provided by their biological relatives. Cross-sectional twin studies do not allow for separation between the effect of such CorGE and the other estimates. Such bias only reach non-trivial values when both genetic and environmental transmission from parents are substantial, and low shared environmental effects in our results in the first place seems to exclude strong environmental parental transmission.

*Gene-environment interactions* (GxE) refers to genetic control of the sensitivity to different environments, and generally, an interaction between A and E will act like E (Purcell, 2002). Analysis of such mechanisms is complicated due to most samples not being large enough to secure sufficient power to detect effects that may be minor compared to the main effects of genes and environment (Neale & Cardon, 1992). Genetically informative designs have previously evidenced mediated effects from particular risk environments for anxiety and depression (Rutter, 2005; Caspi et al., 2003). Such findings underscore the importance of investigating the transactional processes of genes and environments more explicitly in future studies.

The proper understanding of biological phenomena is an ongoing debate, and many biologists criticise the mathematical, quantitative genetic approach for oversimplifying the factors that enter their formulas for producing unrealistic results and ignoring the uniqueness of biological individuals (Morrison, 2002). Specifically, the foundation of quantitative behavioural genetics has been criticised for not being grounded in empirical genetics and resulting in a misleading impression of the potential relationship between genetic functioning and the development of complex behaviours. The research field is likewise attacked for acknowledging environmental contributions in a limited way due to generally regarding the environment as an error variance around the genotypic “true-score” (Partridge, 2005). Partridge underscores that the behavioural genetic approach neither measure environmental nor genetic variance as the only variance being explicitly measured is that of the dependent variable. Hence, genetic variability is inferred from the relative degree of phenotypic similarity in MZ and DZ twins, which is not identical to the observed genetic variability. As proportions of genetic variance not necessarily are meaningfully related to actual genetic variability, many biologists therefore question what can be inferred from the statistical estimates obtained through quantitative genetic analyses. There seems to be an impressive context-dependency of the gene effects that underpin essentially all traits, and estimates of heritability or risk ratios may not necessarily provide information on the relative contributions of specific genes or of the number of genes influencing susceptibility (Ober et al., 2001). Heritability estimates may also not reflect the underlying genetic models and should be used with caution when selecting phenotypes for mapping studies.

Still, a major aim in genetic epidemiology is to be able to disentangle these complex and intricate relationships. Genetic risk and protective factors reflect statistical signals from susceptibility genes, and inability to trace the specific genes which are operating, do not
disconfirm evidence for genetic factors (Kendler, 2005). The general criticisms presented above may be perceived as motivators and challenges to develop more integrated approaches to the testing of specific aetiological hypotheses. A similarly important question as “which genes and environmental factors are involved?” is “how are those genes and environments acting together?” With well-planned data collection, psychometrically sound instruments, and continued expansion of computing capabilities, the quantitative behavioural genetic research field might come closer in providing answers to the important questions of specific mechanisms. Specifically, increased power to improve opportunities for more complex and realistic modelling framework is highly promising. Research materials and methods available may often not enable researchers to analyse complexities such as secular trends, GxE interaction, time-trend effects, genetic heterogeneity, leading researchers to ignore these processes – not because they are unimportant, but because the research tool are still limited (Rao & Province, 2000).
VI IMPLICATIONS AND FUTURE DIRECTIONS
“Although it is disappointing to recognize that there is no formula for happiness, at least not one that applies to everyone, it is reassuring to understand the origins of the emotions in whose loops we dance. It may be so hard to control our emotions, so difficult to foster happiness, and to damp down sadness and envy, because those who could do that were deprived of crucial tools for adaptation, while those whose emotional experiences mapped accurately to the situation in which they were useful had a selective advantage” (Nesse, 2004, p. 1344).

Although the findings presented are subject to caveats and shortcomings, they do offer a first look at the aetiological processes involved in stability and change in mental health during young adulthood, and provide new insight into the relationship between well-being and distress.

Two salient findings from the longitudinal studies concerns i) the importance of genetic factors in generating stability, and ii) the importance of the environment in generating change. The limited stability of most environmental influences indicates that circumstantial boosts in well-being usually are short-lived. Most people adapt to new circumstances and cease to derive positive experiences from them. However, environmental contributions are substantial and our current affective state continuously influenced by new environmental influences causing temporary displacement from affective baselines. Recent research underscores the importance of intentional activities in generating varied experiences and new opportunities for sustained positive effects which directly counteract genetic dispositions. By integrating such findings, the situation appears far more optimistic than suggested by theories proclaiming rigid genetic set-points. Although not everything is possible in ontogenetic development, some changes are. There is considerable evidence for success, albeit short-term, in using interventions to enhance well-being such as practicing certain virtues (e.g. gratitude, mindfulness, self-reflection) and choosing particular goals, as well as cognitive factors amenable to volitional control (Sheldon & Lyubomirsky, 2006). Kahneman has underscored the importance of time use in generating positive mental health. Time is a scare resource, and the allocation of time and attention present difficult choices that greatly influence the content and quality of our lives. By spending more time doing pleasurable and varied activities, higher levels of well-being may be possible. Given that research has evidenced that continual efforts and engagements in intentional processes provides longer lasting boosts in well-being than circumstantial changes, intentional activity may provide a useful means to counteracting the tendency towards affective adaptation (Sheldon & Lyubomirsky, 2006). Happiness or well-being may largely be a state emerging as an individual is making progress towards his or her individual life goals.

While such approaches have a sound empirical basis, they are individual-level interventions, highlighting the need and potential for people to take responsibility for their own mental health. Knowledge on change processes and whether certain changes represent long-term trajectories or short-term fluctuations in mental health is essential also from a public health perspective. People are tremendously influenced by the wider social and political context in which they live. While positive states are related to numerous beneficial gains and desirable outcomes, negative emotion states, particularly when prolonged and
intense, may produce serious problems for the individual as well as the society at large. Commonly, population strategies are targeted at high-risk groups or sub-populations with particular disorders, whereas health promotion and population interventions are less directed at specific sub-groups. However, the population prevalence of many common disorders has been shown to be directly related to the population mean of underlying risk and protective factors (Huppert, 2005), leading researchers to propose that by shifting the population mean in a beneficial direction, many more will flourish. As a consequence of well-being promotion in the general population, the prevalence of both mental disorders and sub-threshold conditions may thus be reduced (Figure 3). Prevalence of the common mental health problems investigated in this thesis (psychological distress) has been shown to meet the criteria for population prevention due to continuous distribution in both symptoms and diverse risk factors (e.g., stress). In addition, the specific results indicate that psychological distress may be reduced by improving levels of well-being and satisfaction. Both common genetic and common environmental risk and protective factors are influencing well-being and psychological distress, indicating that specific factors residing in the environment which simultaneously operate to foster positive mental health and protect against negative health, may be targeted for intervention and prevention purposes.

Figure 3.

As environmental factors constitute the main source of change, future research should focus on further identification of such common environmental influences. Many environmental factors are also specific to well-being and distress, and refined understanding of the commonality as well as the heterogeneity and specificity in individual responses to environmental factors are important for our understanding of how specific influences are related to mental health, well-being and distress, and for future efforts aiming to design intervention, promotion, and treatment programs.

The results highlight a need for methodologically advanced studies which optimize the opportunities for causal inferences. Designs not permitting control for genetic factors may reach erroneous conclusions concerning the effect from specific life events and causal factors residing in the environment. More advanced behavioral genetic research may provide a useful means for detangling of the specific causal pathways. Such designs
may also provide a potential for further exploration and clarification of the sex-specific mechanisms indicated by the current research.

To be continued
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