



# Variance Components Models for Physical Activity With Age as Modifier: A Comparative Twin Study in Seven Countries

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Physical activity is influenced by genetic factors whose expression may change with age. We employed an extension to the classical twin model that allows a modifier variable, age, to interact with the effects of the latent genetic and environmental factors. The model was applied to self-reported data from twins aged 19 to 50 from seven countries that collaborated in the GenomEUtwin project: Australia, Denmark, Finland, Norway, Netherlands, Sweden and United Kingdom. Results confirmed the importance of genetic influences on physical activity in all countries and showed an age-related decrease in heritability for 4 countries. In the other three countries age did not interact with heritability but those samples were smaller or had a more restricted age range. Effects of shared environment were absent, except in older Swedish participants. The study confirms the importance of taking age effects into account when exploring the genetic and environmental contribution to physical activity. It also suggests that the power of genome-wide association studies to identify the genetic variants contributing to physical activity may be larger in young adult cohorts.

■ **Keywords:** genes, environment, physical activity, life span, cross-cultural

Physical activity is influenced by genetic factors, although the estimate of the magnitude varies widely between studies (Beunen & Thomis, 1999; Carlsson et al., 2006; Eriksson et al., 2006; Franks et al., 2005; Lauderdale et al., 1997; Stubbe et al., 2006). Inspection of the existing studies suggests that part of the heterogeneity in these heritability estimates may derive from striking changes in the genetic contribution to this trait across the age range. In childhood, between the ages of 4 to 10 years old, shared environmental factors largely explain the individual differences in physical activity level (Franks et al., 2005). In adolescence, a shift is observed in factors contributing to

exercise participation in a Dutch sample. Between the ages of 13 and 16 years, environmental factors shared by twins largely account for individual difference in exercise participation. At the age of 17–18 years, genetic influences start to appear and the role of common environment decreases. At

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the age of 19–20 years, genes largely explain individual differences in exercise participation and common environmental factors no longer contribute significantly (Stubbe et al., 2005). Genetic contribution remains high after adolescence (Mustelin et al., 2009; Stubbe et al., 2006) but seems to decrease towards middle age (De Geus et al., 2003).

Whereas heritability analyses have tested and found sex differences in heritability of physical activity (Beunen & Thomis, 1999; Stubbe et al., 2005; 2006) the effects of age have not been systematically examined in large samples of adult twins. Purcell suggested extensions to the twin model that allow a modifier variable like age to interact with the effects of the latent factors (Purcell, 2002; 2005). These interaction models were designed for continuous variables. Recently, those models were extended to a dichotomous trait (Medland et al., 2009). We examined whether the magnitude of the genetic and environmental influences on physical activity (yes/no) varies between the age of 19 and 50 years, and whether this is different for males and females. Data on physical activity in seven countries participating in the GenomEUtwin project were used (males and females in six countries, females only in the UK). Because different instruments were used in the seven countries, physical activity was defined as a dichotomy that has a reasonably comparable interpretation across countries. The large datasets allowed the inclusion of age as a modifier variable to examine potential differences in the effects of age and sex on the heritability of physical activity.

## Methods

### Study Samples

This study is based on surveys in twin samples from seven countries participating in the GenomEUtwin project: Australia, Denmark, Finland, the Netherlands, Norway, Sweden, and United Kingdom. The exact descriptions of the twin registries of these countries have been given in detail elsewhere (Boomsma et al., 2002; 2006; Harris et al., 2002; Hopper, 2002; Kaprio et al., 2002; Pedersen et al., 2002; Skytthe et al., 2002; Spector & Williams, 2006). When data on physical activity were available from more than one survey in a country, we used the most recent survey completed by both twins. If only one twin had completed the most recent survey, we searched for the most recent survey that was completed by both members of the pair. If the other member never filled out a survey, the single twin was nonetheless retained in the analysis to improve on the estimation of exercise prevalence and its variance (Stubbe et al., 2006). An overview of the number of participants and the sample sizes are presented in Table 1. Subjects aged between 19 and 50 years old were selected.

### Phenotype: Physical Activity

Different exercise and physical activity questions were asked in each country. We aimed to define a dichotomy

that would be reasonably comparable across countries. Subjects were classified as physically active if they met a predefined criterion that corresponded to about 60 minutes of weekly exercise activities with a minimum intensity of four metabolic equivalents (METs), according to the compendium of Ainsworth (Ainsworth et al., 2000). One MET is the rate of energy expenditure of an individual sitting quietly, which is approximately 1 kcal/kg/h. They were classified as 'not physically active' otherwise.

In Australia, to meet the criterion, subjects had to exercise in their leisure time once a week with a minimal intensity comparable to moderate activities like gardening; in Denmark, they had to engage in hard physical activity (contrasted with light physical activity) outside their working hours for at least one hour a week; in Finland, they had to engage in leisure time exercise at least once a week with a minimum intensity comparable to light jogging for a duration of at least one hour; in the Netherlands they had to engage in one or more leisure time exercise activities with a minimum intensity of four METs, and the total time spent on all such activities was at least 60 minutes a week; in Norway, they exercised during leisure time between one and two times a week at sufficient intensity to build up a sweat for 30–60 minutes in duration; in Sweden, they had to exercise 'rather a lot', 'a lot' or 'really a lot' (in contrast to 'not very much', 'rather little', 'very little', and 'almost none'); in the UK, they had to be regularly engaged in exercise activities with a minimum intensity of four METs.

### Model Fitting Approach

To investigate the inheritance of physical activity, the phenotype was assumed to have an underlying, continuous liability. The variation of the liability can be both genetic and environmental in origin (Falconer & Mackay, 1996). Thresholds divide this normal liability distribution into discrete categories. In the present study, this underlying normal distribution is separated by one threshold, which is obtained from the observed proportions in the two categories (i.e. individuals who are physically active or not) and can be interpreted as a  $z$  value. Individuals falling below the threshold are not physically active and those exceeding the threshold are physically active.

The modifier variable age was transformed to a  $z$  score (Zage) separately for males and females. To obtain a first description of the data, tetrachoric correlations were estimated for two age groups:  $Zage \leq 0$  and  $Zage > 0$  (except in Norwegian where the age range was limited from 19–31 years). Since the age distribution was not the same in the different countries, the age representing  $Zage = 0$  could differ across the countries. The  $z$  scores for age 20, 30, 40 and 50 are shown in Appendix A.

Next, a threshold model designed to test interactions between latent genetic or environmental effects with a measured modifier variable was fitted to the data (Medland et al., 2009; Purcell, 2002). In this model, the variance in

TABLE 1

Overview of Number of Participants for Each Country

Country	Survey	Complete twin pairs	Incomplete twin pairs	Total N	% females
Australia	1990	2,043	518	4,604	63.9%
Denmark	1995, 1997–2000, 2002	10,538	5,222	26,298	51.3%
Finland	1975, 2000–2004	10,324	2,447	23,095	51.2%
Netherlands	1991, 1993, 1995, 1997, 2000, 2002	2,916	921	6,753	62.3%
Norway <sup>1</sup>	1992–1993, 1998	3,995	1,076	9,066	55.1%
Sweden <sup>2</sup>	1973, 2000–2003	12,409	2,596	27,414	53.0%
United Kingdom <sup>3</sup>	1992, 2000, 2001	1,005	441	2,451	100%

Note: <sup>1</sup>Age range 19–31, <sup>2</sup>No dizygotic opposite sex twins, <sup>3</sup>Female twins only

All subjects are aged between 19 and 50 years old. Survey = year(s) of data collection; Complete pairs = number of complete twin pairs in the analyses;

Incomplete twins = twins included in the analyses, but co-twins did not participate; Total N = total number of subjects included in the analyses; % females = percentage females in total sample.

liability is partitioned into the usual genetic (a), common environmental (c) and nonshared environmental (e) components, but also incorporates the interaction between these components and a measured modifier variable, in this case, Zage.

The model incorporates an effect of Zage on the thresholds:

$$T_{\text{males}} = X_{\text{males}} + \beta_{\text{males}} \text{Zage for man and } T_{\text{females}} = X_{\text{females}} + \beta_{\text{females}} \text{Zage for women,}$$

where X is the z-value of the threshold when Zage=0.

The expected phenotypic variance is:  $(a + \beta_a \text{Zage})^2 + (c + \beta_c \text{Zage})^2 + (e + \beta_e \text{Zage})^2$ , where a, c and e are respectively the genetic, common environmental and nonshared environmental path coefficients,  $\beta_a$  represents the effect of age on a,  $\beta_c$  the effect of age on c,  $\beta_e$  the effect of age on e and Zage the z score of the age of the twin when completing the survey.

The expected covariance is:  $(a + \beta_a \text{Zage})^2 + (c + \beta_c \text{Zage})^2$  for MZ twin pairs and  $0.5(a + \beta_a \text{Zage})^2 + (c + \beta_c \text{Zage})^2$  for DZ twin pairs.

The variance of the underlying liability distribution is constrained at 1 for Zage = 0:  $(a + \beta_a \text{Zage})^2 + (c + \beta_c \text{Zage})^2 + (e + \beta_e \text{Zage})^2$ , that is,  $a^2 + c^2 + e^2 = 1$ .

Quantitative sex differences were tested by allowing the magnitude of the genetic and environmental effects to be different in men and women. The correlation between the genetic factors in opposite-sex twin pairs were allowed to be less than 0.5, allowing for qualitative sex difference (i.e., partly different genes expressed in men and women).

The modifier model was applied to raw ordinal data on physical activity of seven different countries: Denmark, Finland, Netherlands, Australia, Sweden (no DOS twins), Norway (age 19–31), and United Kingdom (women only).

Different genetic models were fitted. Under the full model (model 1), all variables were allowed to vary between men and women. In model 2, the components a,  $\beta_a$ , c,  $\beta_c$ , e and  $\beta_e$  were constrained to be equal in men and women. The shared environmental components ( $\beta_c$  and c) were tested in model 3 and the genetic components

( $\beta_a$  and a) in model 4. In model 5, the regression coefficient for the unique environmental influences ( $\beta_e$ ) was fixed to zero.

The fit and parsimony of the various nested models are judged using likelihood ratio tests in which the negative log-likelihood (-2LL) of the model is subtracted from the -2LL of the previous (less restrictive) model. The difference yields a statistic that is asymptotically distributed as  $\chi^2$  with degrees of freedom (df) equal to the difference in the degrees of freedom of the two models. Models with fewer parameters are preferred if they do not give a significant deterioration of the fit. Due to large sample sizes and multiple testing, a significance level of 0.01 was used. Models were fitted using the software package MX (Neale et al., 2006).

## Results

### Analysis of Data of Seven Different countries

The prevalence of physical activity across the age ranges in the 7 different countries is depicted in Table 2. The prevalence decreased with age in most countries, but not in the Netherlands (remained stable) and in Swedish women (increased with age). In general, physical activity was (slightly) higher in men than in women.

To obtain a first impression of twin resemblance, the data were split into 2 age groups for each country and tetrachoric correlations for physical activity were estimated. In general, the MZ correlations were higher than the DZ correlations suggesting genetic influences on physical activity. Twin correlations were higher in the younger age groups compared to the older age groups which indicate that the heritability of physical activity decreases with age (see Table 3).

Next, genetic models were fitted to the data with age as a continuously distributed modifier variable. In the full model, the variance components A, C and E and modifier effects of age were estimated simultaneously. The model fitting results are shown in Table 4. The point estimates for the full model when Zage is zero are shown in Table 5. The

**TABLE 2**

Observed Prevalence of Physical Activity (Proportion of Total Sample) in the Seven Countries for Males and Females in Different Age Groups

		19–24	25–29	30–34	35–39	40–44	45–50
Australia	M	0.73	0.68	0.64	0.63	0.58	0.44
	F	0.63	0.62	0.56	0.54	0.48	0.44
Denmark	M	0.49	0.47	0.40	0.33	0.29	0.19
	F	0.38	0.35	0.30	0.22	0.19	0.15
Finland	M	0.36	0.37	0.34	0.32	0.28	0.24
	F	0.28	0.28	0.22	0.24	0.20	0.15
Netherlands	M	0.59	0.57	0.54	0.53	0.54	0.54
	F	0.52	0.57	0.55	0.60	0.56	0.47
Norway	M	0.57	0.53	0.50	—	—	—
	F	0.53	0.49	0.48	—	—	—
Sweden	M	0.39	0.38	0.35	0.32	0.35	0.40
	F	0.22	0.20	0.24	0.25	0.35	0.44
United Kingdom	F	0.73	0.55	0.47	0.46	0.41	0.39

Note: M = males, F = females.

**TABLE 3**

Twin Correlations in Two Age-Groups — All Samples Were Split in Half Based on the Age Distribution (Zage ≤ 0 and Zage &gt; 0)

	Australia	Den-mark	Finland	Netherlands	Norway	Sweden	United Kingdom
Zage ≤ 0							
Age range	22–36	19–33	19–27	19–25	19–31	19–35	19–40
MZM	0.27 (.00–.51)	0.54 (.45–.54)	0.65 (.57–.74)	0.72 (.59–.81)	0.65 (.56–.72)	0.66 (.59–.71)	—
DZM	0.4 (.12–.64)	0.3 (.20–.39)	0.34 (.27–.42)	0.38 (.317–.56)	0.48 (.36–.58)	0.32 (.25–.38)	—
MZF	0.5 (.35–.63)	0.59 (.51–.66)	0.66 (.59–.72)	0.73 (.64–.81)	0.58 (.50–.65)	0.6 (.53–.67)	0.66 (.49–.79)
DZF	0.29 (.08–.49)	0.32 (.29–.42)	0.34 (.34–.42)	0.47 (.26–.61)	0.24 (.13–.34)	0.3 (.22–.38)	0.43 (.26–.57)
DOS	0.12 (-.08–.31)	0.06 (-.01–.14)	0.2 (.08–.31)	0.14 (-.01–.28)	0.17 (.09–.26)	—	—
Zage > 0							
Age range	37–50	34–50	28–50	26–50	32–50	36–50	41–50
MZM	0.49 (.26–.68)	0.43 (.30–.53)	0.53 (.43–.63)	0.59 (.39–.74)	—	0.44 (.35–.52)	—
DZM	0.37 (.01–.65)	0.18 (.08–.29)	0.28 (.20–.36)	0.36 (.07–.60)	—	0.22 (.14–.30)	—
MZF	0.34 (.18–.49)	0.32 (.16–.46)	0.48 (.36–.58)	0.49 (.38–.60)	—	0.46 (.38–.53)	0.55 (.36–.71)
DZF	0.25 (.04–.45)	0.26 (.15–.37)	0.19 (.09–.28)	0.27 (.08–.45)	—	0.26 (.26–.33)	0.39 (.23–.53)
DOS	0.16 (-.06–.37)	0.05 (.02–.13)	—	0.03 (-.16–.22)	—	—	—

estimates for A, C and E in the best fitting models are shown in Figure 1.

None of the datasets showed quantitative sex differences (model 2, Table 4) so the estimates were constrained to be equal for males and females. For all countries, except Sweden, dropping the shared environmental influences did not significantly worsen the fit of the model. In Sweden the shared environmental factors are low or zero for Zage < 1 and increases if Zage > 1 indicating that those

factors only plays a role in older subjects (Figure 1A). Based on the standardized estimates, heritability gradually decreased between age 19 and 50 in Denmark, Finland, the Netherlands and Sweden. The unstandardized estimates (Figure 1B) show a decrease of genetic influences for Denmark, Finland and Sweden. In the Netherlands the genetic variance did not vary with age but the unique environmental variance increased with age. The heritability was not influenced by age in Norway (age range

**TABLE 4**  
Model Fitting Results for Physical Activity for the Seven Countries

	Model	-2LL	Df	Vs	$\Delta df$	$\Delta\chi^2$	<i>p</i>
Australia (age range 22–50)							
1	Full	5127.792	3916				
2	ACE M = f	5131.926	3922	1	6	4.135	0.658
3a	Drop $\beta_c$	5132.293	3923	2	1	0.367	0.5446
3b	Drop C	5134.276	3924	3a	1	1.983	0.159
4a	Drop $\beta_a$	5135.124	3925	3b	1	0.848	0.3571
4b	Drop A	5225.447	3926	4a	1	90.323	0.000
5	Drop $\beta_e$	5136.776	3926	4a	1	1.652	
Denmark							
1	Full	31193.874	26283				
2	ACE M = f	31205.109	26289	1	6	11.235	0.081
3a	Drop $\beta_c$	31205.744	26290	2	1	0.635	0.426
3b	Drop C	31206.24	26291	3a	1	0.496	0.481
4a	Drop $\beta_a$	31231.186	26292	3b	1	24.946	0.000
4b	Drop A	31648.55	26293	3b	2	442.31	0.000
5	Drop $\beta_e$	31206.409	26292	3b	1	0.169	0.681
Finland							
1	Full	27312.892	23080				
2	ACE M = f	27313.199	23086	1	6	0.307	0.999
3a	Drop $\beta_c$	27317.932	23087	2	1	4.733	0.0295
3b	Drop C	27319.243	23088	3a	1	1.311	0.2522
4a	Drop $\beta_a$	27354.73	23089	3b	1	35.487	0.000
4b	Drop A	28050.253	23090	3b	2	731.01	0.000
5	Drop $\beta_e$	27326.634	23089	3b	1	7.391	0.0065
Netherlands							
1	Full	8923.872	6739				
2	ACE M = f	8927.552	6744	1	6	3.68	0.720
3a	Drop $\beta_c$	8930.716	6745	2	1	3.164	0.0752
3b	Drop C	8931.151	6746	3a	1	0.435	0.5095
4a	Drop $\beta_a$	8932.837	6747	3b	1	1.686	0.1941
4b	Drop A	8932.837	6748	4a	1	334.309	0.000
5	Drop $\beta_e$	8954.575	6748	4a	1	21.738	0.000
Norway (age range 19–31)							
1	Full	12148.985	9051				
2	ACE M = f	12157.473	9057	1	6	8.488	0.205
3a	Drop $\beta_c$	12159.06	9058	2	1	1.587	0.2077
3b	Drop C	12162.066	9059	3a	1	3.006	0.0829
4a	Drop $\beta_a$	12162.134	9060	3b	1	0.068	0.7942
4b	Drop A	12509.552	9061	4a	1	347.418	0.000
5	Drop $\beta_e$	12166.048	9061	4a	1	3.914	0.0478
Sweden (no DOS twins)							
1	Full	32995.613	27399				
2	ACE M = f	33006.25	27405	1	6	10.636	0.100
3a	Drop $\beta_c$	33015.554	27406	2	1	9.304	0.002
3b	Drop C	33022.522	27407	2	1	16.272	0.000
4a	Drop $\beta_a$	33056.271	27406	2	1	50.021	0.000
4b	Drop A	33239.182	27407	2	2	232.932	0.000
5	Drop $\beta_e$	33023.891	27406	2	1	17.641	0.000
United Kingdom (female twins only)							
1	Full	3251.24	2444				
3a	Drop $\beta_c$	3252.702	2445	1	1	1.462	0.227
3b	Drop C	3255.093	2446	3a	1	2.391	0.122
4a	Drop $\beta_a$	3256.599	2447	3b	1	1.506	0.220
4b	Drop A	3365.009	2448	4a	1	108.41	0.000
5	Drop $\beta_e$	3258.168	2448	4a	1	0.569	0.210

Note: -2LL = -2 times log likelihood, *df* = degrees of freedom, *vs* = versus, indicates to which model the submodel is compared,  $\Delta df$  = difference in degrees of freedom,  $\Delta\chi^2$  = chi square difference, *p* = *p* value, Full = full model including sex differences for A, C, E,  $\beta_a$ ,  $\beta_c$ ,  $\beta_e$ , T and  $\beta_T + R_{\text{gDOS}}$  free  $\beta$  = regression coefficient, T = threshold, M = males, f = females,  $R_{\text{gDOS}}$  = genetic correlation in opposite sex twins, A = genetic influence, C = shared environmental influence, E = unique environmental influence.

**TABLE 5**  
Point Estimates for A, C and E in the Full Model When Modifier = 0

		Age at Zage = 0	$a^2_0$	$c^2_0$	$e^2_0$	$\beta_a$	$\beta_c$	$\beta_e$	Rgdos
Australia	M	36	.13	.27	.60	.31	.25	.43	.00
	F	37	.37	.06	.57	-.05	-.03	.04	
Denmark	M	34	.47	.01	.52	-.18	-.11	-.04	.23
	F	34	.27	.15	.58	-.48	.04	-.10	
Finland	M	30	.57	.03	.40	-.22	-.15	-.11	.50
	F	29	.56	.03	.42	-.28	.16	-.15	
Netherlands	M	26	.64	.03	.32	-.18	.19	-.01	.25
	F	28	.28	.23	.48	.06	.39	.47	
Norway	M	24	.35	.29	.36	.12	.003	.09	.21
	F	25	.54	.03	.44	-.13	-.13	-.05	
Sweden	M	34	.53	.00	.46	-.41	.28	-.11	NA
	F	35	.54	.00	.46	-.32	-.10	-.19	
United Kingdom	F	40	.57	.09	.42	-.12	.44	-.03	NA

Note: Model includes separate estimates for males and females for: A, C, E, threshold, regression of Zage on A, C, E and regression of Zage on threshold).  $a^2_0$  = estimated genetic influences when Zage = 0,  $c^2_0$  = estimated shared environmental influences when Zage = 0,  $e^2_0$  = estimated unique environmental influences when Zage = 0.  $\beta_a$  = regression coefficient genetic influences,  $\beta_c$  = regression coefficient shared environmental influences,  $\beta_e$  = regression coefficient unique environmental influences.

18–35), United Kingdom (females only) and Australia (age range 22–50).

## Discussion

We used an interaction model approach to explore whether the magnitude of the genetic and environmental influences on physical activity varied with age. The model was applied to the data obtained in twin samples from seven countries participating in the GenomEUtwin project. In most countries, the prevalence of physical activity was seen to decrease with age which is in line with other studies (Haase et al., 2004; Telama & Yang, 2000; Van Mechelen et al., 2000; West et al., 2002). Because the data were cross-sectional, the decrease in physical activity with age may reflect a true ageing effect or it may reflect an increase in leisure time exercise participation in younger birth cohorts.

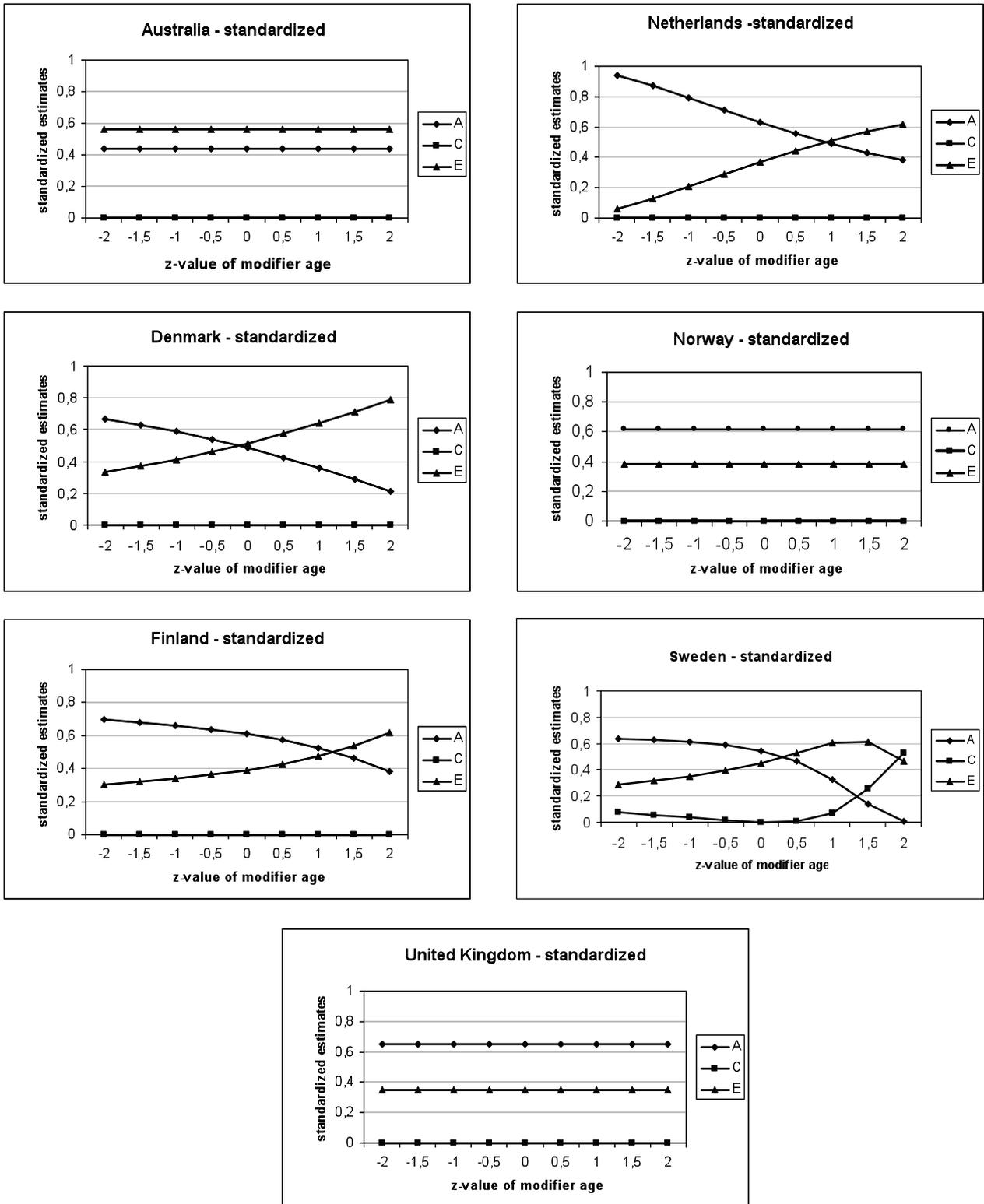
Genetic modeling confirmed the importance of genetic influences on physical activity as previously reported (Aarnio et al., 1997; Beunen & Thomis, 1999; Carlsson et al., 2006; Eriksson et al., 2006; Kaprio et al., 1981; Stubbe et al., 2005; 2006). The twin correlations in two age groups suggested a potential effect of age on the heritability of physical activity. Therefore, a modifier model was used to test whether the magnitude of the genetic and environmental influences on physical activity varies between the age of 19 and 50 years.

Four countries showed a decrease of heritability with age. Age did not interact with heritability in United Kingdom, Norway and Australia. It should be noted that the sample of the United Kingdom consisted of women only and was the smallest of the seven samples. The distribution of age is skewed: about 73% of the sample is aged above 35 years so maybe the sample size at the low end of

the age range ( $\leq 35$  years) is too small to detect a significant interaction with age. The same might be true for the Australian sample: it was the smallest sample after United Kingdom and age range was limited to 22 to 50 years with only 17% of the sample younger than 30 years. In addition, the questionnaire used in Australia deliberately used gardening as an example of regular leisure time activities to be reported as physical activity. This is an activity that older people might engage in. In other countries the type of physical activity queried might have been less salient for older people. The Norwegian sample was limited to 31 years instead of 50 years, which can explain that age did not significantly influence the heritability estimates.

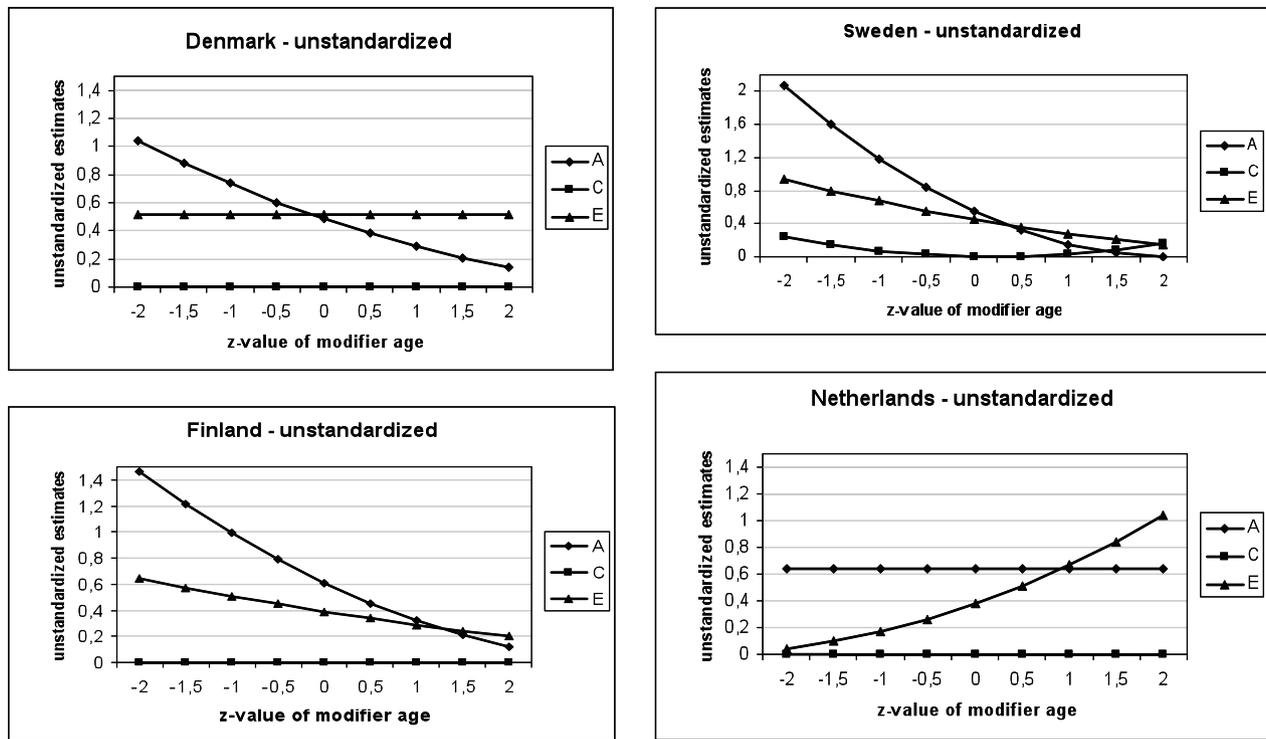
Very little support was found for a role of shared environmental factors in adult physical activity. This is in keeping with previous studies investigating the heritability of exercise or physical activity also report no significant role of common environmental factors (Carlsson et al., 2006; Eriksson et al., 2006; Stubbe et al., 2006).

The decrease of genetic influences with age as observed in Denmark, Finland, the Netherlands and Sweden might reflect either an effect of different gene expression in older people or an effect of birth cohort. For example, by the decreased physical activity requirements at work over the last five decades, attitudes on the necessity of leisure time exercise may have changed. This cohort-specific early attitude formation may contribute to birth cohort effects on physical activity. Three generation family data showed smaller parent–offspring correlations than within-generation (siblings, DZ or MZ twin-pairs) correlations (Aarnio et al., 1997). This could both be explained by an effect of birth cohort or by differential expression of genes with age. Possible changes in gene expression with ageing are supported by a study in a cohort of Swedish male twins



**FIGURE 1A**

Best fitting model to explain variance in physical activity for the seven countries.  $A = (a + \beta a * zage)^2 / ((a + \beta a * zage)^2 + (c + \beta c * zage)^2 + (e + \beta e * zage)^2)$ ;  $C = (c + \beta c * zage)^2 / ((a + \beta a * zage)^2 + (c + \beta c * zage)^2 + (e + \beta e * zage)^2)$ ;  $E = (e + \beta e * zage)^2 / ((a + \beta a * zage)^2 + (c + \beta c * zage)^2 + (e + \beta e * zage)^2)$



**FIGURE 1B**

Unstandardized estimates for the best fitting models. Only the countries where the unstandardized estimates are not the same as the standardized estimates are shown.

Note:  $A = (a + \beta a * zage)^2$   
 $C = (c + \beta c * zage)^2$   
 $E = (e + \beta e * zage)^2$

born between 1973 and 1979 where the heritability of occupational physical activity and leisure time physical activity decreased over the 4-year interval from 1998 to 2002 (Eriksson et al., 2006). Prolonged follow-up of physical activity in longitudinal samples is clearly needed to resolve this issue further.

Although several studies, including the present study, have shown that unique environmental factors are important for physical activity, it is currently poorly understood what these factors are. Eriksson et al. suggested that the influence of unshared environmental factors may increase with age when young adult individuals complete their education, marry, and settle down (Eriksson et al., 2006). Numerous studies investigated determinants of physical activity like education, smoking, alcohol use, marital status, having children, job strain or having health problems, but the explained variance by these factors has been modest (Dishman et al., 1985; Seefeldt et al., 2002; Simonen et al., 2003). However, none of these studies took a possible age-dependency of the impact of these environmental factors into account whereas our analyses hint at the possibility that, at least in the Netherlands, the genetic drive to engage in leisure time exercise is increasingly constrained by environmental factors when people

get older. The results can also reflect a genotype–environment interaction.

In conclusion, application of the modifier model to data on physical activity of seven different countries showed an age-related decrease in heritability for the four countries that had the largest number of twins across the 18 to 50 year age range. This confirms the importance of taking age effects into account when exploring the genetic and environmental contribution to adult physical activity in twin family studies. It also suggests that the power of genome-wide association studies to identify the genetic variants contributing to physical activity may be larger in young adult cohorts.

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## Appendix A

Z-scores for Age 20, 30, 40 and 50 Years in Men and Women in the Seven Countries.

		20	30	40	50
Denmark	Men	-1.58	-0.43	0.72	1.86
	Women	-1.60	-0.42	0.76	1.93
Finland	Men	-1.18	-0.00	1.18	2.37
	Women	-1.12	0.08	1.27	2.47
Netherlands	Men	-0.85	0.49	1.83	3.17
	Women	-1.01	0.25	1.50	2.75
Sweden	Men	-1.68	-0.56	0.56	1.69
	Women	-1.75	-0.60	0.54	1.69
Australia	Men	NA	-1.01	0.47	2.19
	Women	NA	-0.94	0.52	2.05
Norway	Men	-1.24	1.96	NA	NA
	Women	-1.27	1.41	NA	NA
United Kingdom	Women	-2.51	-1.26	-0.01	1.23