

We had medical diagnosis from Primary Health Care clinics from the counties throughout Sweden; Blekinge (2009 - 2016), Dalarna (2005 - 2013), Värmland (2005 - 2015), Kalmar Län (2007 - 2016), Sörmland (1992 - 2017), Uppsala Län (2005 - 2015), Västernorrland (2008 - 2015) Norrbotten Län (2001 - 2014), Gävleborg (2010 - 2017), Gotland (2011 - 2018), Halland (2007 - 2014), Jönköpings Län (2008 - 2014), Kronoberg (2006 - 2016), Skåne (1989 - 2018), Västerbotten (1992- 2018), Östergötland (1990 - 2014), Stockholms Län (2003 - 2016), and Västra Götaland (2000 - 2013).

TABLE S1. Sensitivity model-fitting results in full sample

Model	Description	-2logL	# of Parameters	AIC	Diff in AIC	p-value (LR-test)
1	r_g free, r_c free	734,242.5	14	734,270.5		
2s	r_g free, $r_c = 0$	734,242.5	13	734,268.5	-2	0.999
3s	$r_g = 0$, r_c free	734,258.6	13	734,284.6	14.1	<0.0001
4s	$r_g = 0$, $r_c = 0$	734,948.0	12	734,972.0	701.5	<0.0001

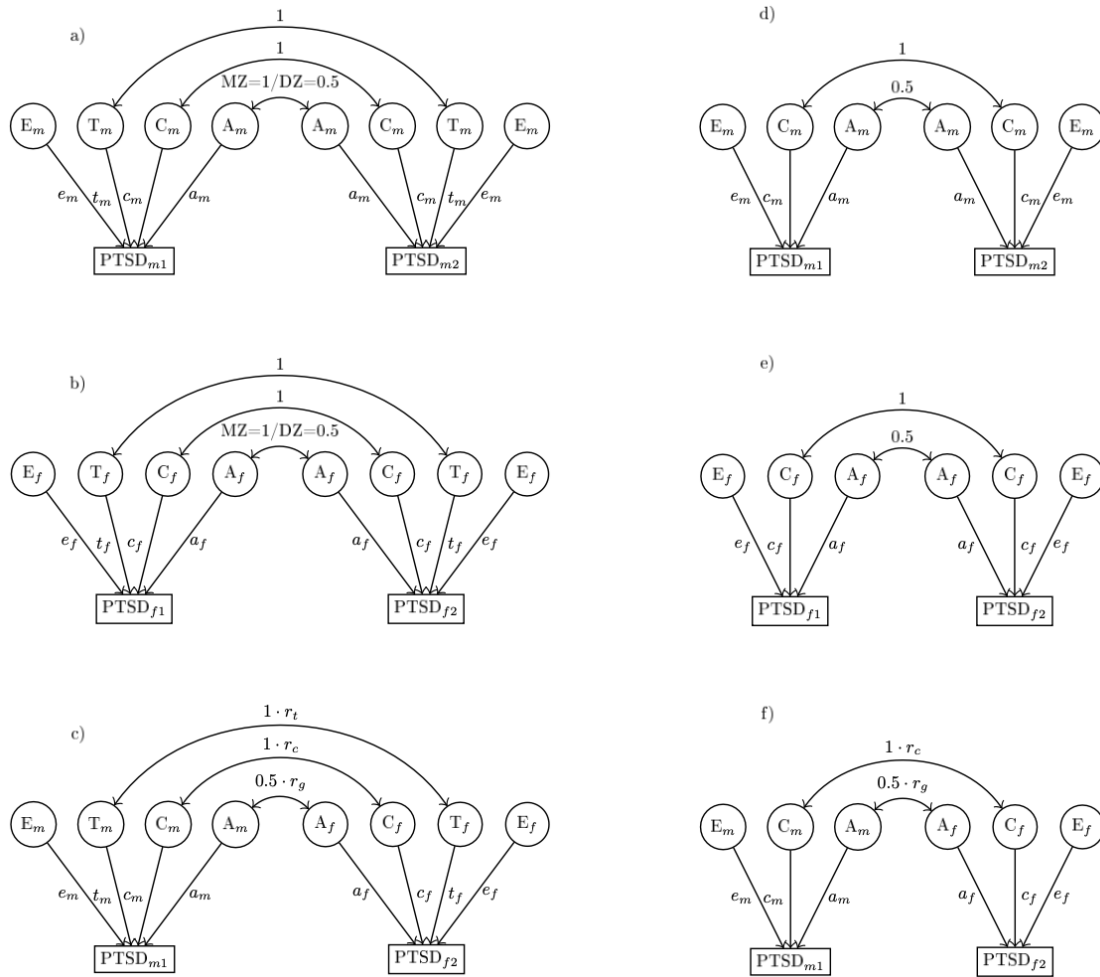
Notes: genetic correlation (r_g), shared environment correlation (r_c), Negative Two Log Likelihood (-2logL), Akaike Information Criterion (AIC), difference in AIC (Diff), likelihood-ratio (LR).

TABLE S2. Parameter estimates from the full model

<i>Parameter</i>	<i>Estimate (SE)</i>
Threshold MZ/DZ, same-sex pairs males	1.31 (0.02)
Threshold DZ, opposite-sex pairs males	1.31 (0.02)
Threshold MZ/DZ, same-sex pairs females	0.75 (0.01)
Threshold DZ, opposite-sex pairs females	0.74 (0.02)
Slope (by year) males	0.16 (0.01)
Slope (by year) females	0.24 (0.01)
a_m	0.53 (0.01)
a_f	0.60 (0.01)
r_g	0.81 (0.04)

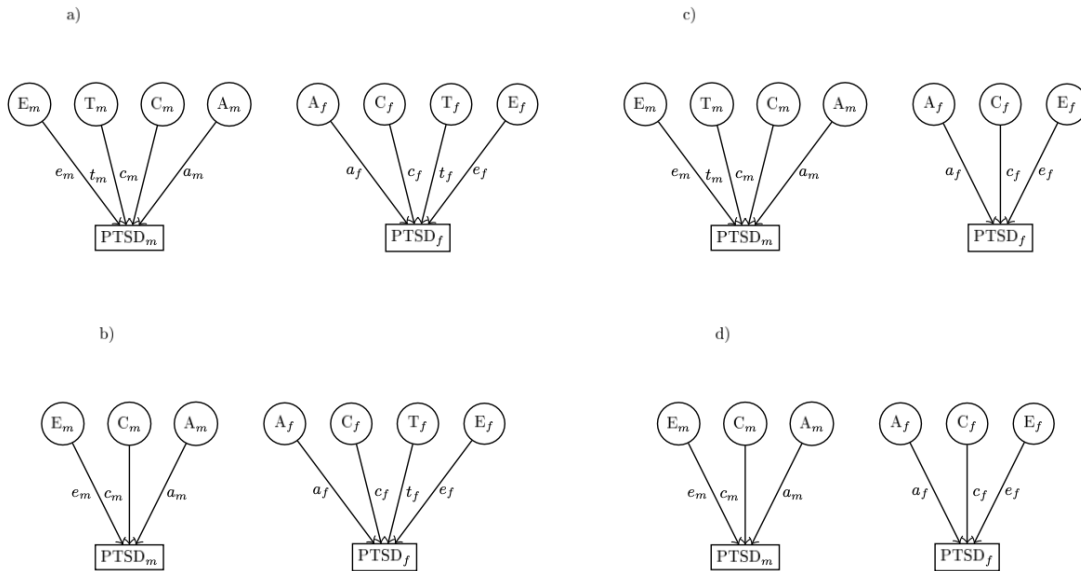
Notes: monozygotic (MZ), dizygotic (DZ), additive genetic male (a_m), additive genetic female (a_f), genetic correlation (r_g).

FIGURE S1. Graphical illustration of the variance components in all twin and full sibling pairs in the full theoretical model



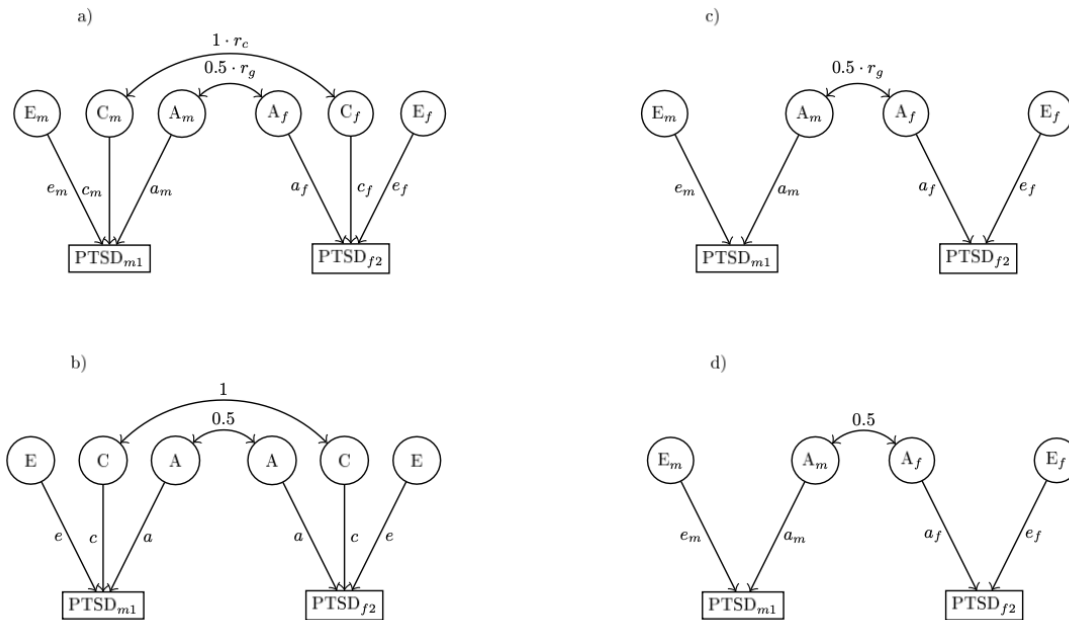
Notes: An ACTE model with qualitative and quantitative gender differences. a) Male-male MZ/DZ pairs. b) Female-female MZ/DZ pairs. c) Male-female DZ pairs. d) Male-male full sibling pairs. e) Female-female full sibling pairs. f) Male-female full sibling pairs. Posttraumatic stress disorder (PTSD), male (m), female (f), unique environment (E), twin specific environment (T), shared environment (C), additive genetic (A), genetic correlation (r_g), shared environment correlation (r_c).

FIGURE S2. Graphical illustration of the variance components in the same-sex model



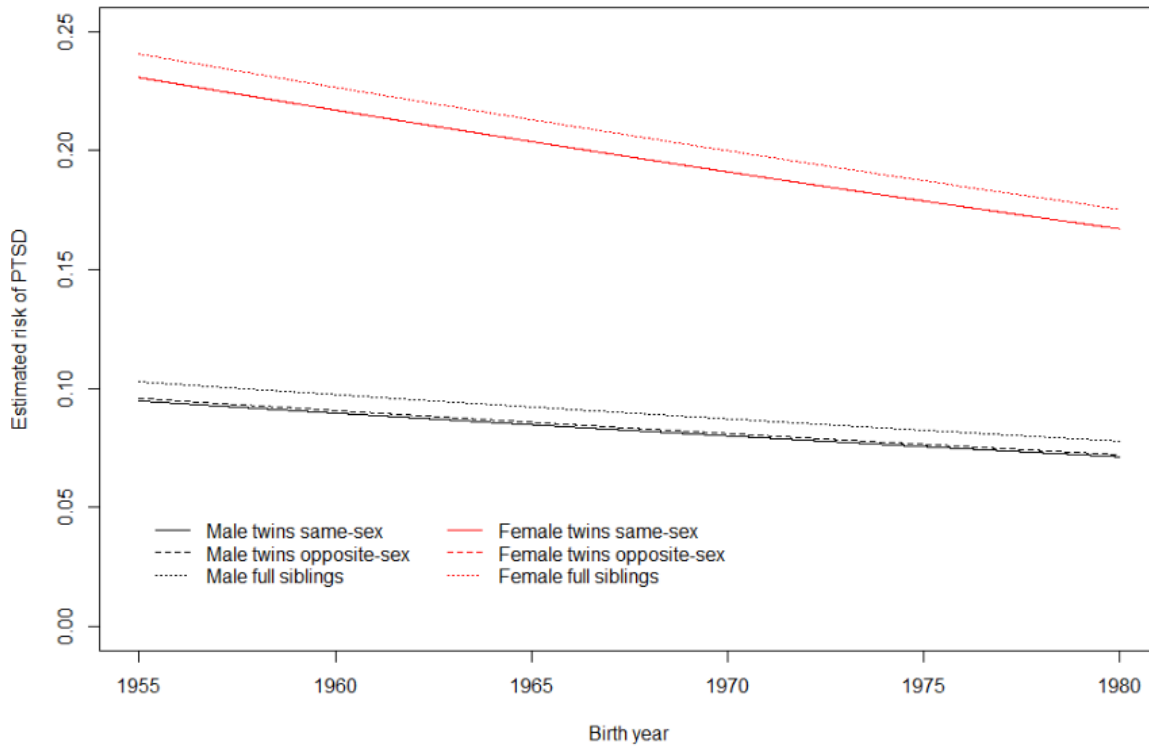
Notes: a) All variance components (ACTE model) b) Dropping T_m. c) Dropping T_f. d) Dropping T_m and T_f. Posttraumatic stress disorder (PTSD), male (m), female (f), unique environment (E), twin specific environment (T), shared environment (C), additive genetic (A).

FIGURE S3. Graphical illustration of the variance components in selected opposite-sex pairs



Notes: a) Qualitative and qualitative genetic and home environment differences, both r_g and r_c free (ACE model). b) No qualitative genetic nor home environment differences, both r_g and r_c are equated to unity, no quantitative gender differences (ACE model). c) Dropping C_m and C_f and allowing for qualitative genetic differences, r_g free (AE model). d) Dropping C_m and C_f , no qualitative genetic differences, equating r_g to unity (AE model). Posttraumatic stress disorder (PTSD), male (m), female (f), unique environment (E), shared environment (C), additive genetic (A), genetic correlation (r_g), shared environment correlation (r_c).

FIGURE S4. Estimated risk of PTSD by group and birth year for the best-fit model



Note: Posttraumatic stress disorder (PTSD).