



# Sex differences in genetic influences on childlessness

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**ICS**  
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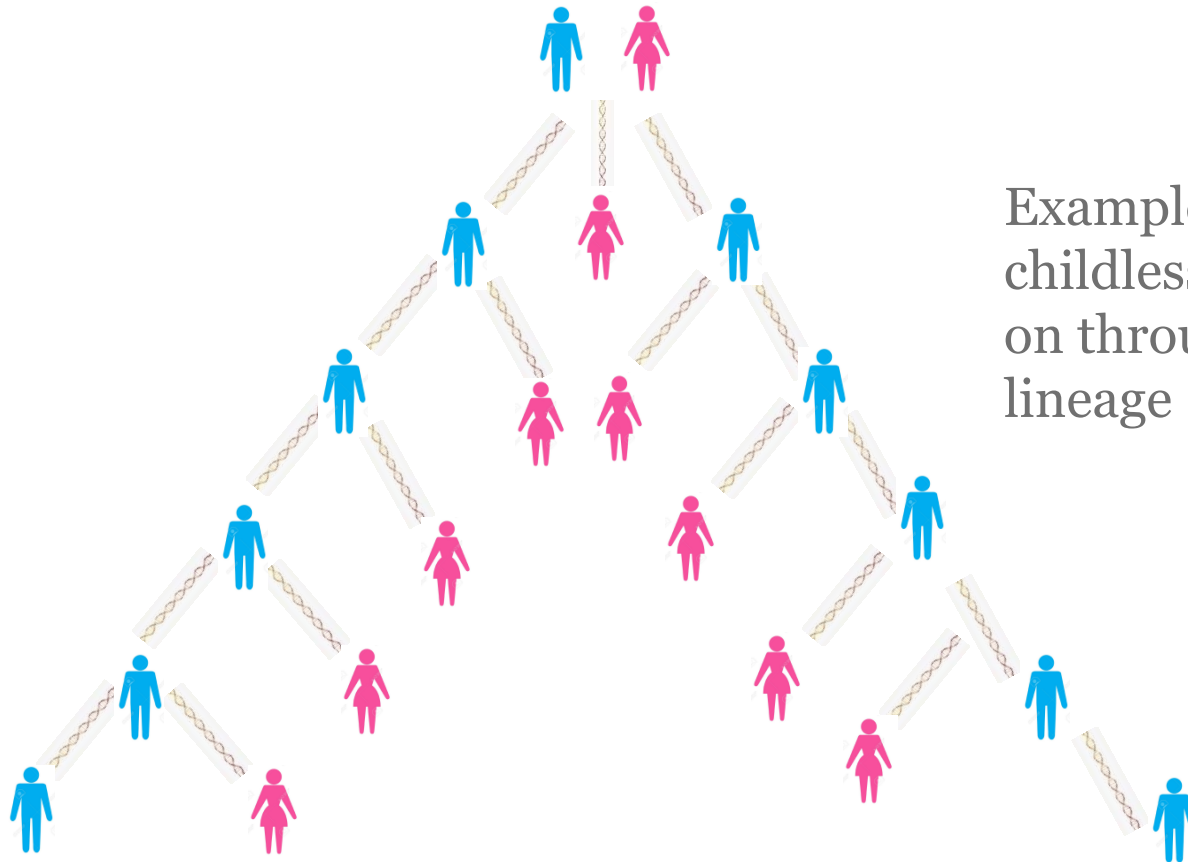


# Background

- › Previous research found:
  - Genetic influence on age at first birth (Nisen et al, 2013; Tropf et al, 2015)
  - Genetic influence on number ever born (Rodgers, Kohler, et al, 2001; Zietsch et al, 2014)
  - Genetic influence on childlessness (Kohler et al, 1999)
- › Evolutionary unlikely (Fisher, 1930)
- › However....
- › Gene environment interactions (Rodgers, Hughes et al, 1999)
  - Fertility norms and genetic influences (Bras, Bavel & Mandemakers, 2013)
  - Genetic influence on early menopause and endometriosis (He et al, 2010)
- › Sex differences (Hughes & Burlleson, 2000; Gershoni & Pietrokovski, 2014)



# Sexual antagonism



Example: female  
childlessness passed  
on through male  
lineage



# Research questions

- › Is there is a genetic influence on childlessness?
- › Do different genes influence childlessness in men and women?



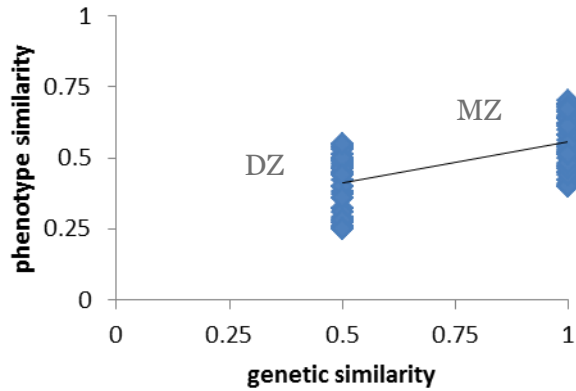
# Data

- › Swedish Twin Register (n=9,942)
- › Same sex and opposite sex twin pairs
- › Individuals with measured genetic information
- › Women over 45 and men over 50 years of age

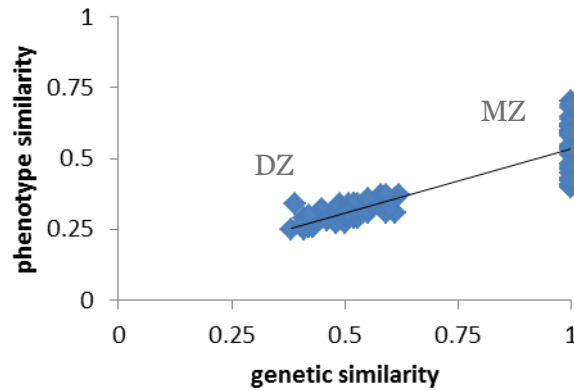


# Twin and GREML method

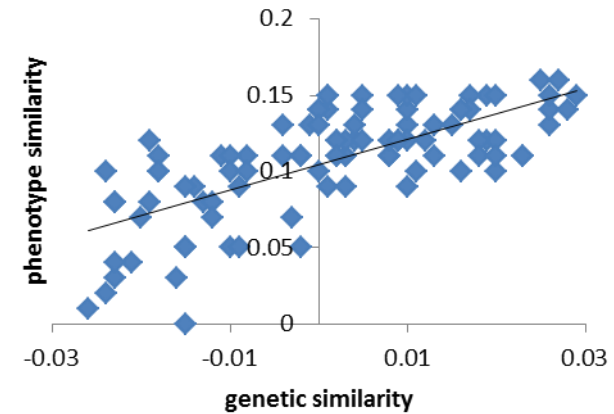
**twin method**



**twins in GREML**



**Unrelated GREML**



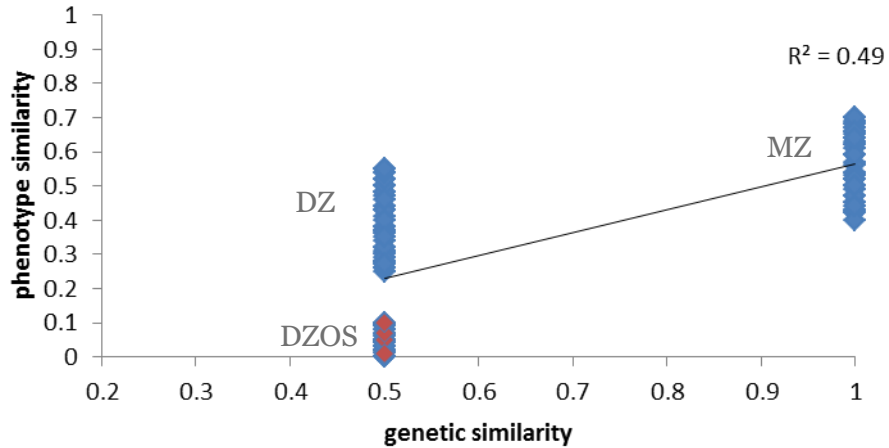




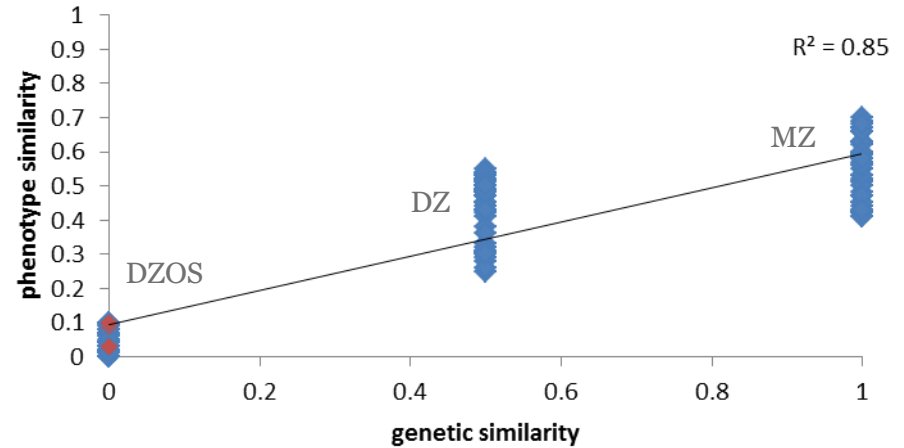
# Sex differences

## Sex-limitation model

opposite sex = 0.5



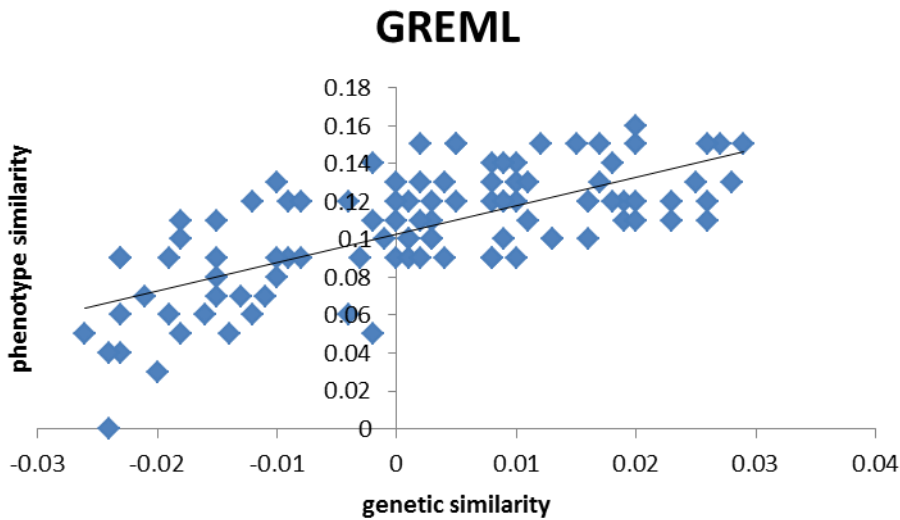
opposite sex = 0



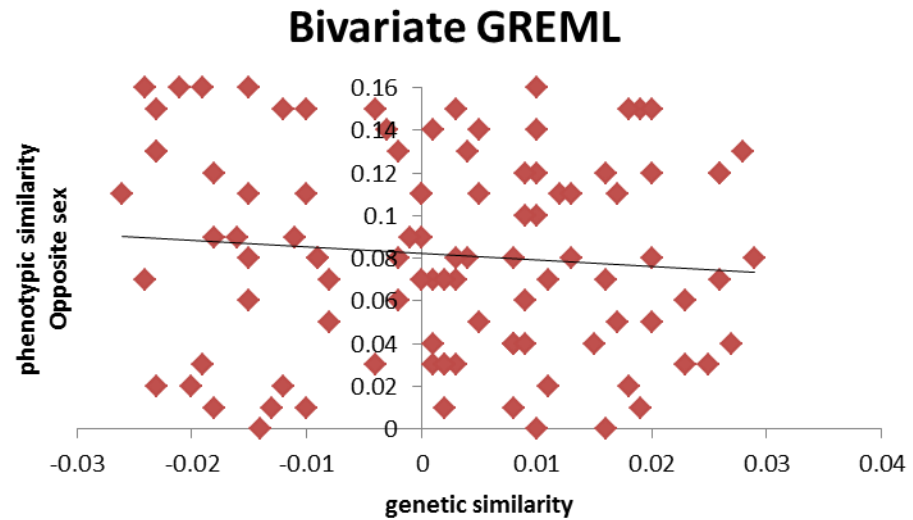


# Sex differences

## Bivariate GREML



Same sex pairs

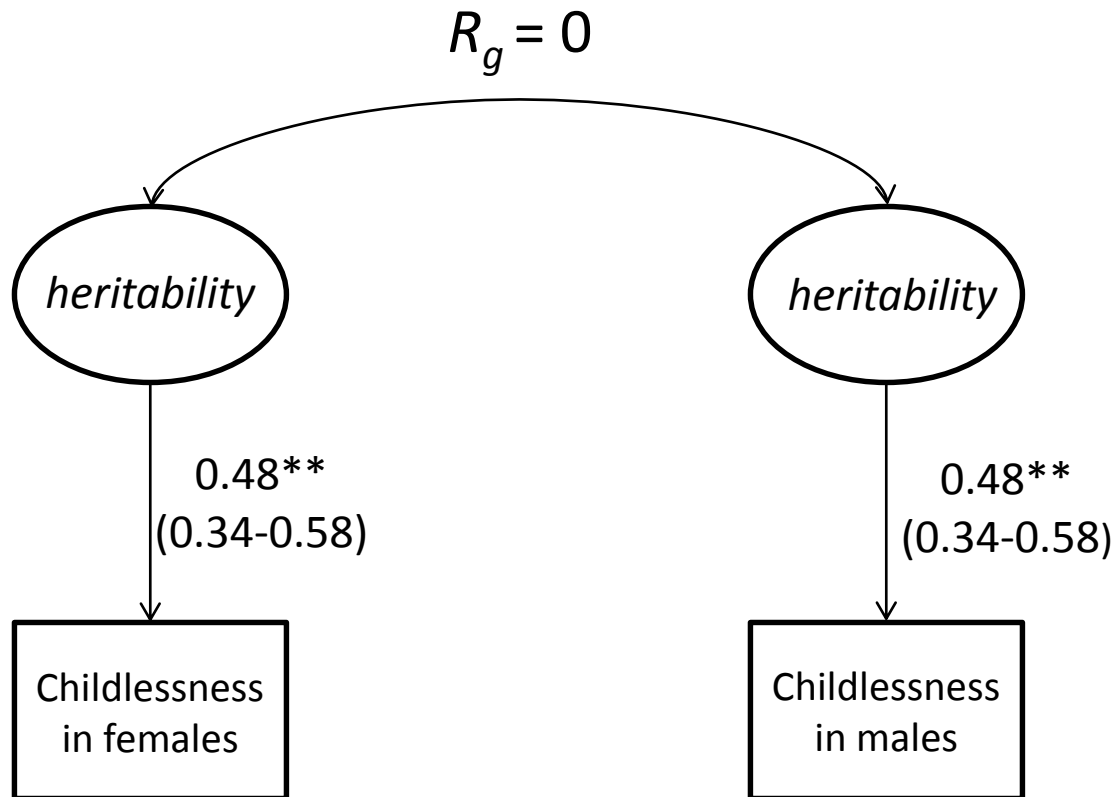


Opposite sex pairs





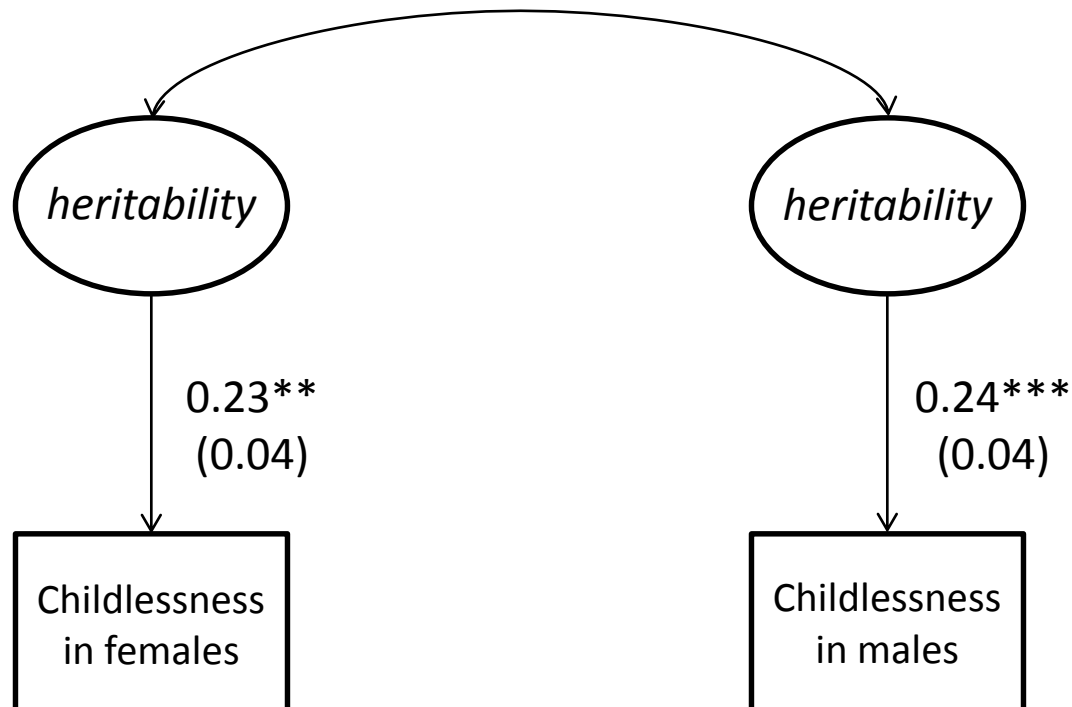
# Results twin method





## Results twins in GREML

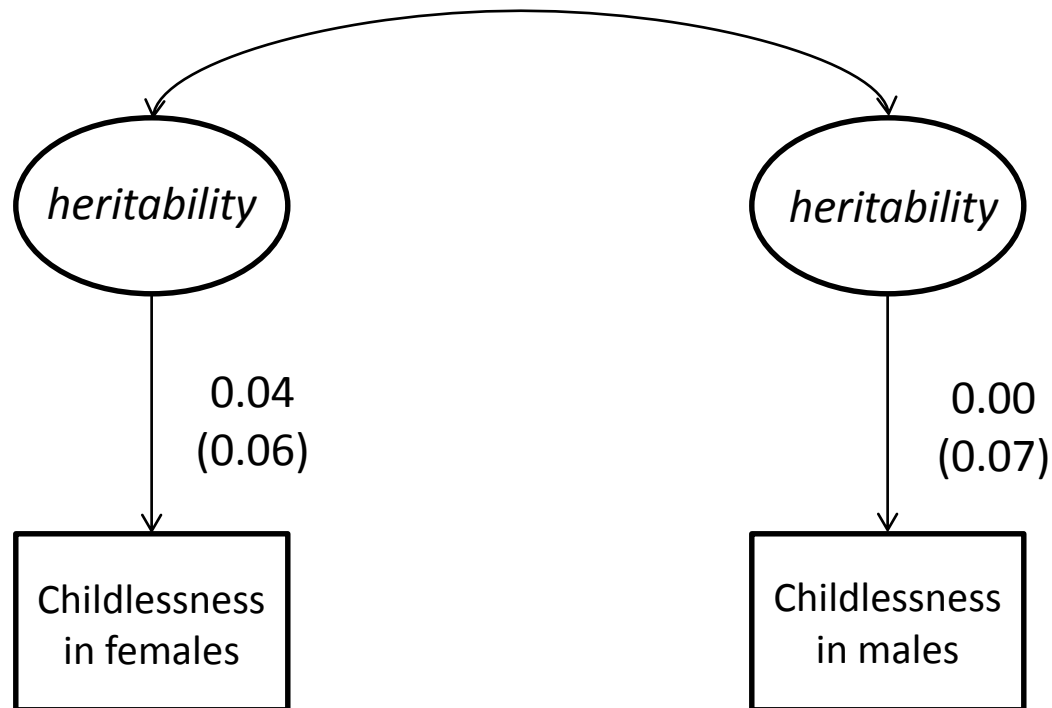
$$R_g = -0.22 (0.34)$$





# Results GREML method on unrelated individuals

$$R_g = 1 (20.67)$$





## Conclusions

- › Moderate levels of heritability of childlessness
- › Different genes involved in childlessness in men and women
- › Higher heritability from the twin study than from the GREML method

## Limitations

- › Heritability estimates and sex differences based on related individuals
- › Inflation due to environmental influences



university of  
 groningen



10/28/2015 | 13

Thank you for your attention



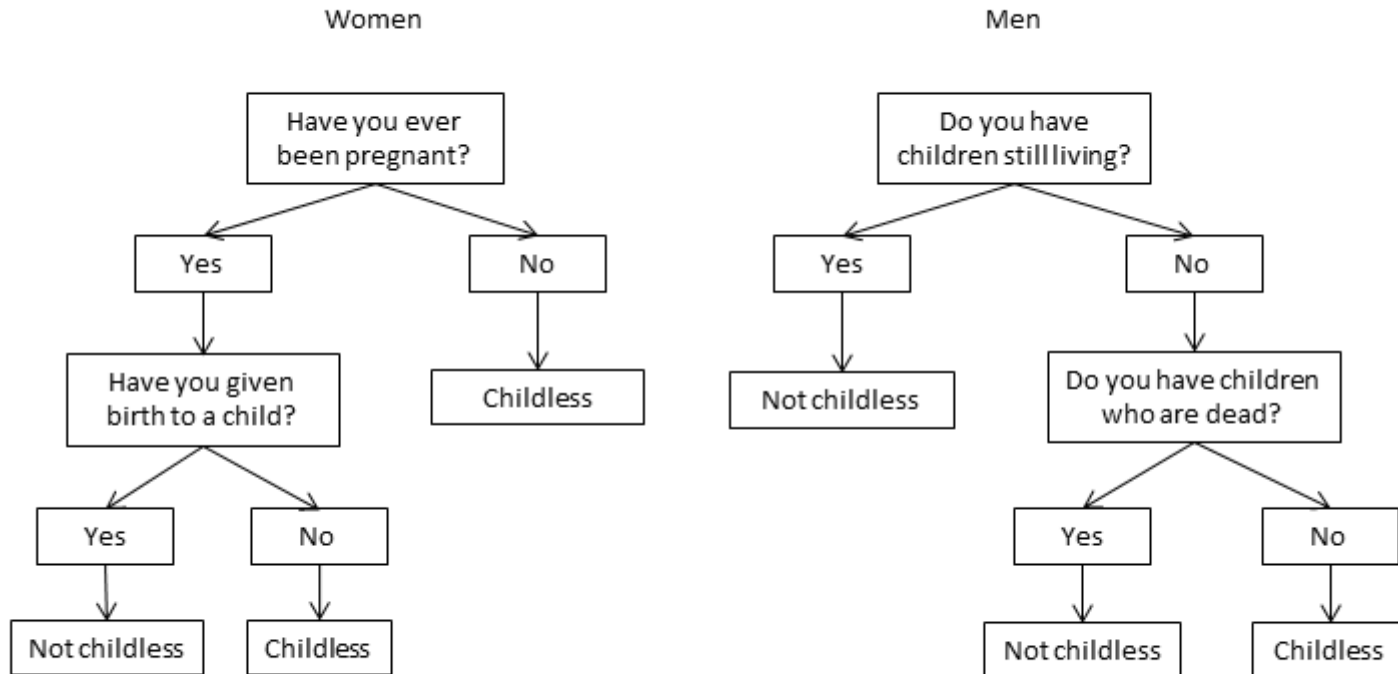
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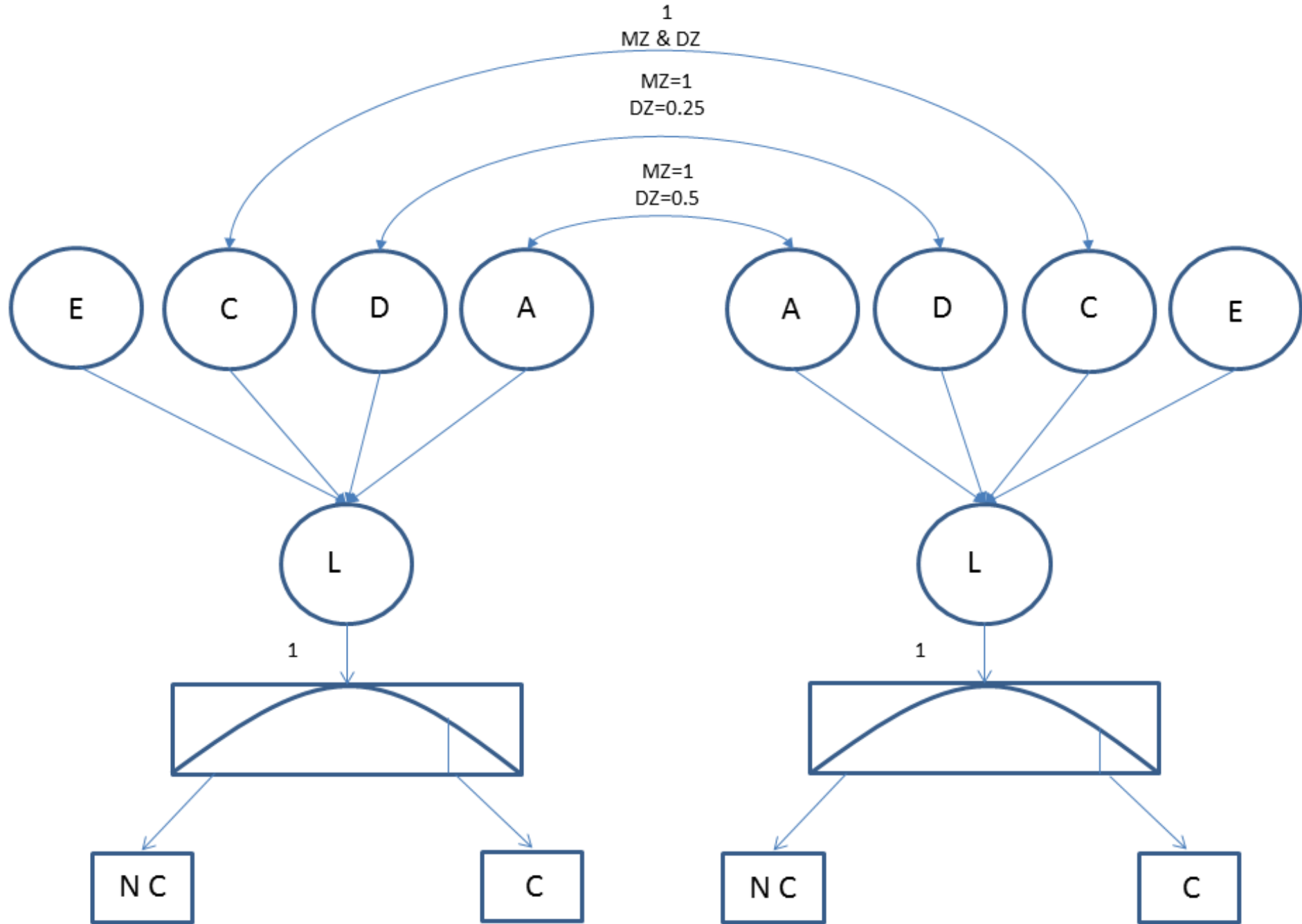
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# Extra information







# Genotyping

- › Genotyping with Illumina OmniExpress 700K chip
- › Imputed according to the 1000 genome imputation panel
- › Selected SNPs from the HapMap3 panel
- › SNPs with MAF 1%, missing rate 3% and who failed the Hardy-Weinberg equilibrium for a threshold of  $10^{-6}$  are removed



# Sample sizes

Sample		N	N complete pairs
Female	MZ	1158	513
	DZ	2254	814
Male	MZ	1167	513
	DZ	1612	549
Opposite sex		3751	1223
Total		9942	3612