

Negative Selection in the 20th Century

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April 2020

1 Introduction

Existing work suggests that natural selection is taking place in modern populations, but that effect sizes are small. In this paper we investigate natural selection in the UK over the twentieth century, using data from UK Biobank. We use questions on number of children and number of siblings to reconstruct two generations of family size per respondent. We then relate these to polygenic scores for several different characteristics.

Natural selection is taking place on most polygenic scores, and is broadly “negative” in that characteristics that most people would consider undesirable are being selected for. Effect sizes are larger for number of siblings than for number of children. This is not because the strength of natural selection has changed over time: effect sizes do not differ between early- and late-born respondents, within either children or siblings. Instead, the difference is probably due to ascertainment bias in UK Biobank. Indeed, natural selection is concentrated among population subgroups that are under-represented in the sample, including less-educated people and poorer households. When we weight the sample to correct for ascertainment bias, many effect sizes are considerably larger.

Among mothers who were older at first birth, and among parents with fewer sexual partners, effect signs are reversed so that natural selection is broadly “positive”. The effects of PGS can be decomposed into two channels: an effect on age at first live birth, and an opposite-signed effect on number of children conditional on age at first live birth. This pattern may be explained by economic theories of fertility. In these, higher potential earnings have two opposite effects on fertility: a fertility-increasing income effect (higher income makes children more affordable), and a fertility-lowering substitution effect (time spent on childrearing has a higher cost in foregone earnings). Among couples who can take advantage of coordination in childcare activities, the income effect dominates; among single parents or those in unstable relationships, the substitution effect dominates.

2 Open questions/TODO

- If we weight with the GHS, and plot the means of figure 1 using this w weighting, most things stay the same - but the change in EA is reversed! EA increases over time. Could this be because the sample includes many relatively educated older people? If so, then mean effects are *overestimated* by figure 1.
- Need to make the weighting very watertight.
 - Include income?
 - Interact age and other variables?
 - Investigate “MRP” (Gelman 2005)
 - Understand reweighting on subsets of survey data.
 - Check for existing work
- Reweight other regressions (e.g. the omnibus regression in the appendix)
- Could be useful: f.2139 - age first had sex (includes “never had sex” which may explain some of the many NAs for f.2141, num sex partners)

- Need f.6138 to correctly calculate `age_fulltime_edu` including those who went to college.
- Look at geography, esp. in siblings regressions.
- control for age in `n_partners` regressions.

3 Data

Data is taken from UK Biobank. Polygenic scores were normalized to mean 0, variance 1.

4 Results

Figure 1 plots mean polygenic scores by 5-year birth intervals, for the entire sample. Several scores show consistent increases or declines over this 30-year period, of the order of 5% of a standard deviation.

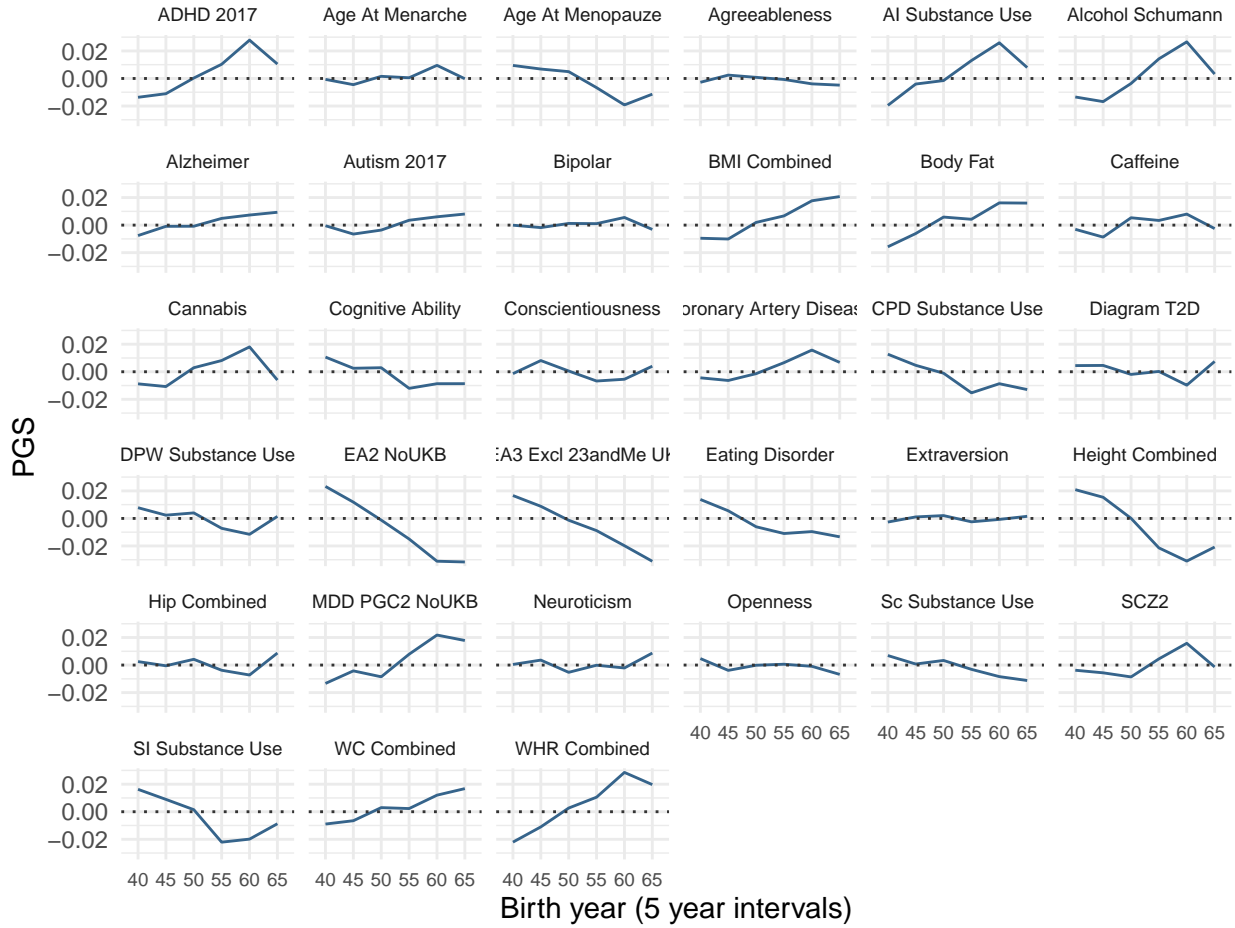


Figure 1: Mean polygenic scores by birth year in UK Biobank. Lines are means for 5-year intervals

We run bivariate regressions on two dependent variables:

- *siblings*, the number of full siblings in the respondent's sib (including himself or herself).
- The number of *children* ever born to/fathered by the respondent.

Figure 2 shows effect sizes of a one-standard deviation shift in each polygenic score.

Estimates are broadly consistent across generations. However, effect sizes are much larger for *siblings* than for *children* regressions. Among consistently-signed estimates, the effect size for siblings is 371.12 per cent at the median.

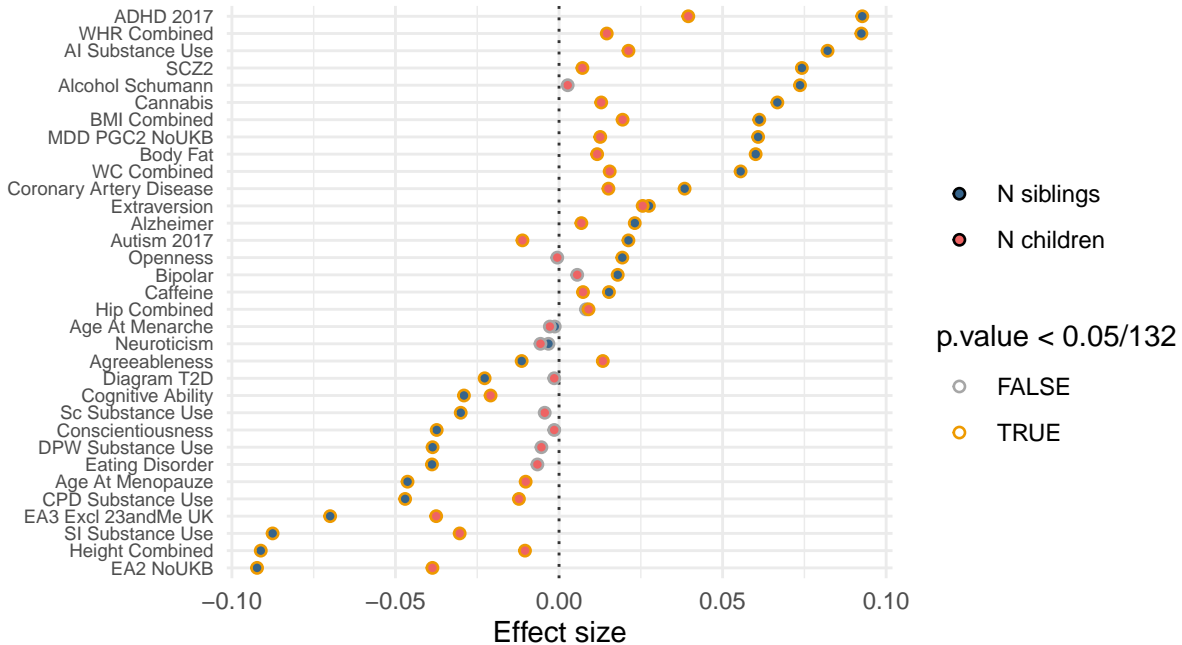


Figure 2: Effects of polygenic scores on number of siblings/children.

5 Subgroups

We next examine how different subgroups of the population contribute to natural selection. These analyses have two goals: to get a sense of how ascertainment bias could affect our basic results, and to learn more about the causes of natural selection in the UK population. Because we have more data on respondents than on their parents, we focus on *children* regressions.

5.1 Sex, income and education

Figure 3 shows effect sizes of PGS on number of children separately for males and females. Differences are particularly large for educational attainment, height and MDD. There is no overall pattern in differences of effect size, however.

Figure 4 splits respondents up by education levels. Selection effects are typically larger and more significant for those who left school before 16. Figure 5 splits respondents by household income category. A very similar pattern holds, with selection effects being larger for those in the poorest income category.

These results could be driven by age, if older respondents are poorer and less educated, and also more subject to selection on polygenic scores. However, if we rerun the regressions, interacting the polygenic score with income category and also with a quadratic in age, the interaction with income remains significant at 0.05/33 for 21 out of 33 regressions. Similarly if we interact the PGS with age of leaving full time education and a quadratic in age, the interaction with age leaving FTE remains significant at 0.05/33 for 12 out of 33 regressions.

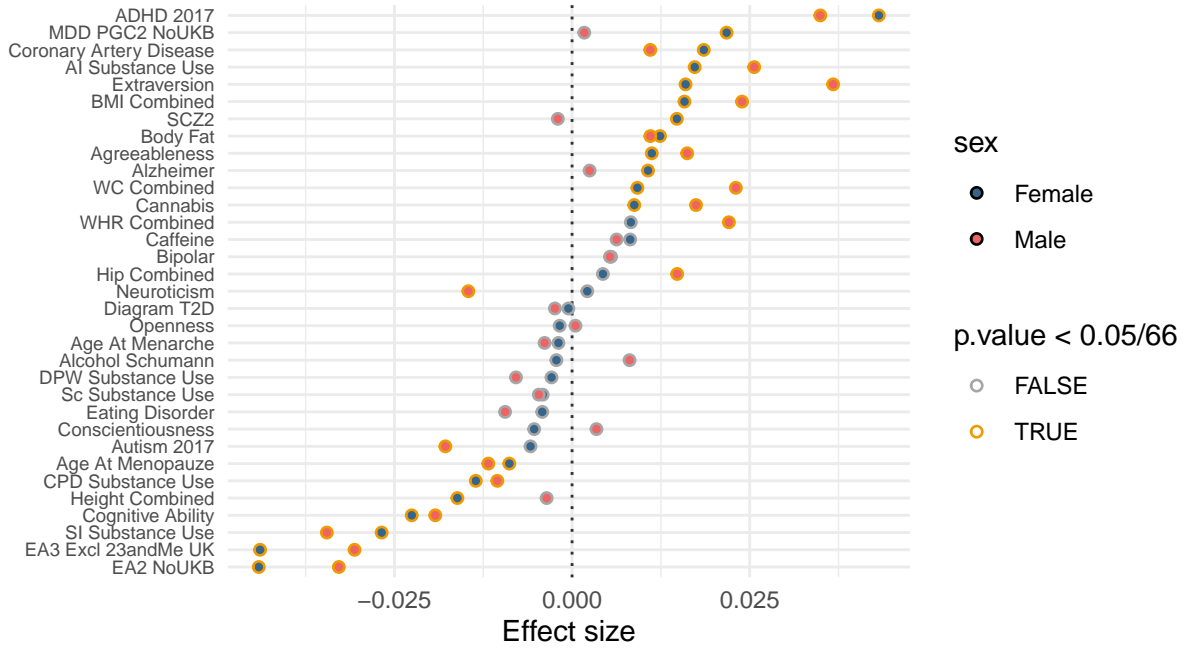


Figure 3: Effect sizes on number of children by sex

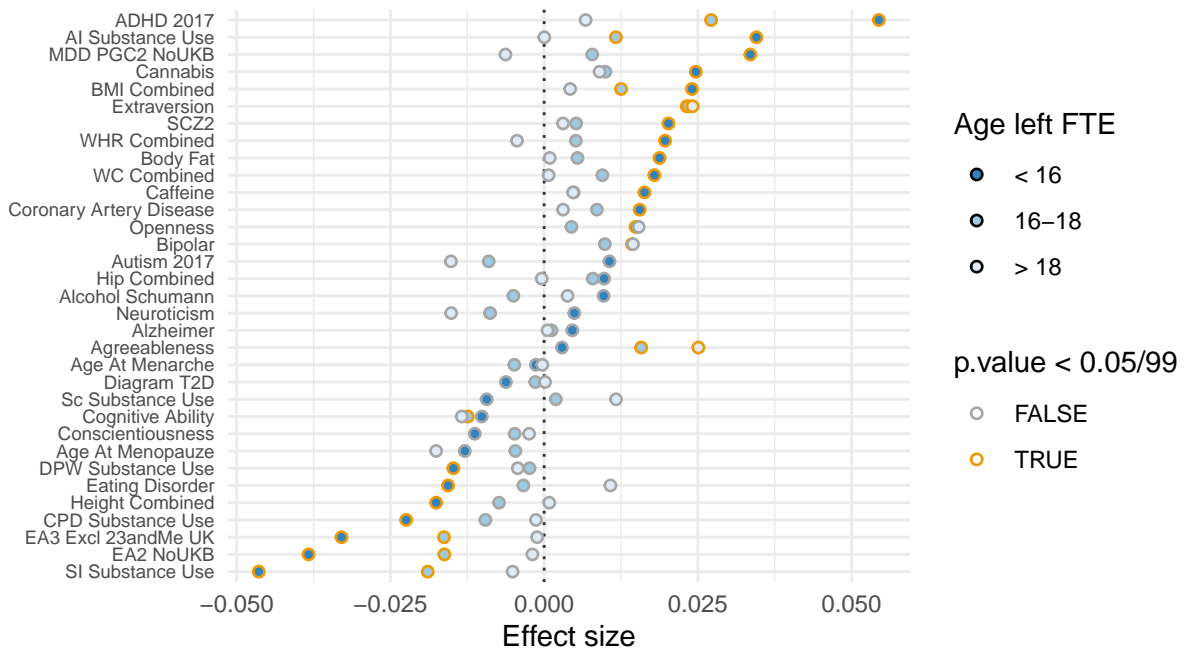


Figure 4: Effect sizes on number of children by age left full-time education

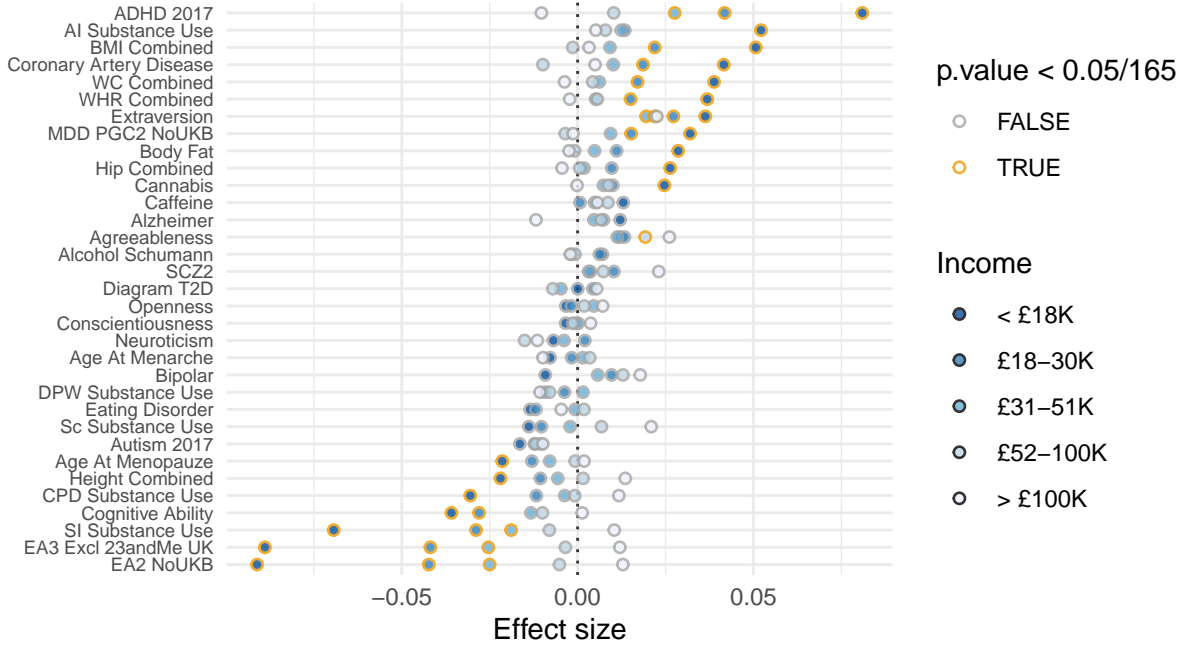


Figure 5: Effect sizes on number of children by household income

The UK Biobank sample overrepresents highly educated people and high-income households. This suggests that statistics from the sample may underestimate the level of natural selection in the population.

5.2 Age at first live birth

Age at first live birth correlates with number of children ever born. Figure 6 shows *children* regressions estimated separately for each tercile of age at first live birth. Several effects are strikingly different across terciles. ADHD and MDD are selected for amongst the youngest third of mothers, but selected against among the oldest two-thirds. Educational attainment is selected for among the oldest two-thirds of mothers, but is not significantly selected among the youngest third. Similarly, several PGS of body measurements are selected against only among older mothers. The correlation between effect sizes for the youngest and oldest terciles is -0.54. This is the first sign that selection may work in different directions across different subgroups.

Figure 7 splits males and females by lifetime number of sexual partners, at the median value of 3. Again, selection effects are reversed across the groups. Among men and women with more than 3 sexual partners, for example, EA is selected against; among those with 3 or fewer sexual partners, it is selected for. Selection is broadly negative (positive) among those with more (less) partners.

Lastly Figure 8 splits respondents up by whether they were living with a spouse or partner at the time of interview. Effects are generally the same sign in both groups, but are much larger among those not living with a spouse or partner.

6 Accounting for ascertainment bias

Our results are subject to two kinds of ascertainment bias. First, Biobank is not a random sample of the UK population: for example, it overrepresents educated people and high income households. Second, sampling parents of respondents inherently overweights parents who have many children. For instance, parents of

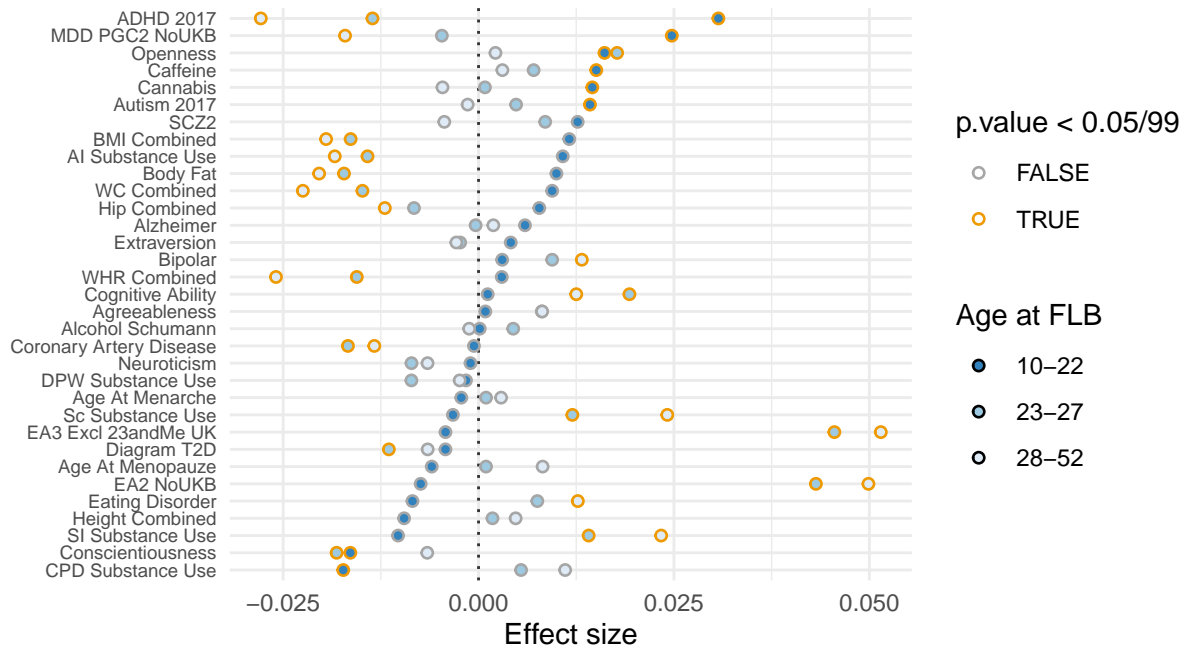


Figure 6: Effect sizes on number of children, by age at first live birth terciles

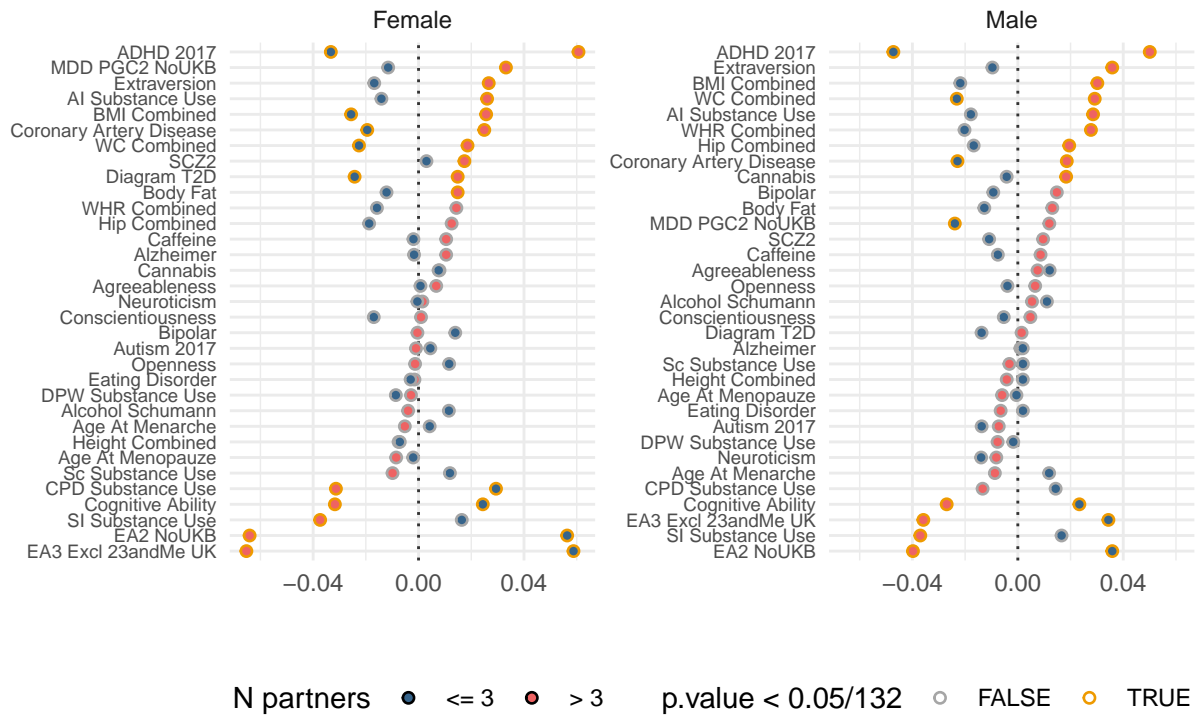


Figure 7: Effect sizes on number of children by number of sexual partners

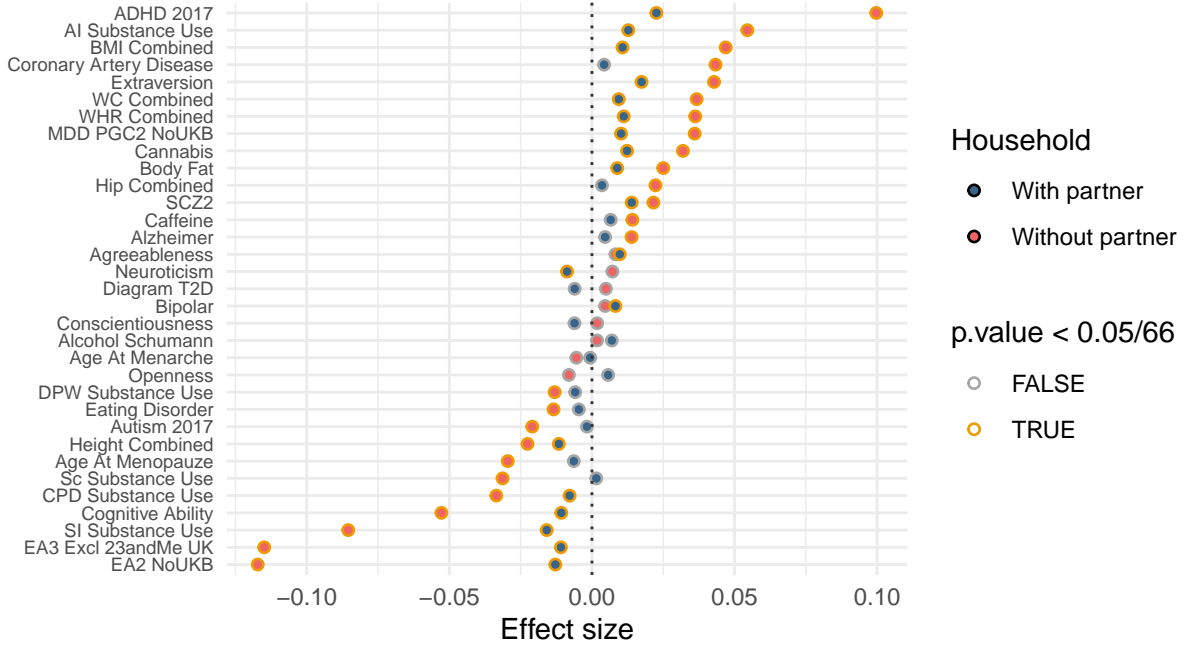


Figure 8: Effect sizes on number of children by household type

three children will have three times more children as respondents in UK Biobank than parents of one child, on average. Parents of no children will, by definition, not be represented at all.

To compensate for ascertainment bias in the UK Biobank sample, we weight participants by sex, age (within the 40-71 age group), and education. Our sample weights are calibrated based on the 2006 General Household Survey. We then calculate the proportions of respondents within each sibling group size, based on the respondent weights, and use this to create weights for the sibling regressions.

We rerun the basic regressions for both children and siblings, using the new weights. Figure 9 shows the results. The weightings are fairly successful at reconciling the overall size of effects from siblings and children regressions. Among weighted scores that are significant (at $p < 0.05/33$) in either regression, 16 estimates are higher for children and 15 are lower. However, some estimates differ widely or change sign across the generations.

We also weighted data for women with children only, by age, education and age at first live birth. Figure 10 shows the results. There are large changes for some variables, including EA3 (103.77 per cent), cognitive ability (102.98 per cent) and waist-hip ratio (WHR; 146.76 percent).

Overall, these results suggest that previous work may have underestimated the level of selection occurring in the population. [TODO: who?]

6.1 Mechanisms behind natural selection

Why are selection effects *oppositely* signed in certain subgroups – for example, in older and younger mothers (by age at first live birth) or in those with more and fewer lifetime sexual partners? A possible answer is given by the economic theory of fertility [TODO cite Becker 1960]. According to this, increases in potential earned income affect fertility via two opposing channels. There is an “income effect” by which children become more affordable, like any other good. Since childrearing has a cost in time, there is also a substitution effect: the opportunity cost of childrearing increases if one’s market wage is higher. The income effect would lead higher earners to have more children. The substitution effect would lead higher earners to have fewer children. It is often assumed that the substitution effect will dominate for lone parents, since they have less opportunity

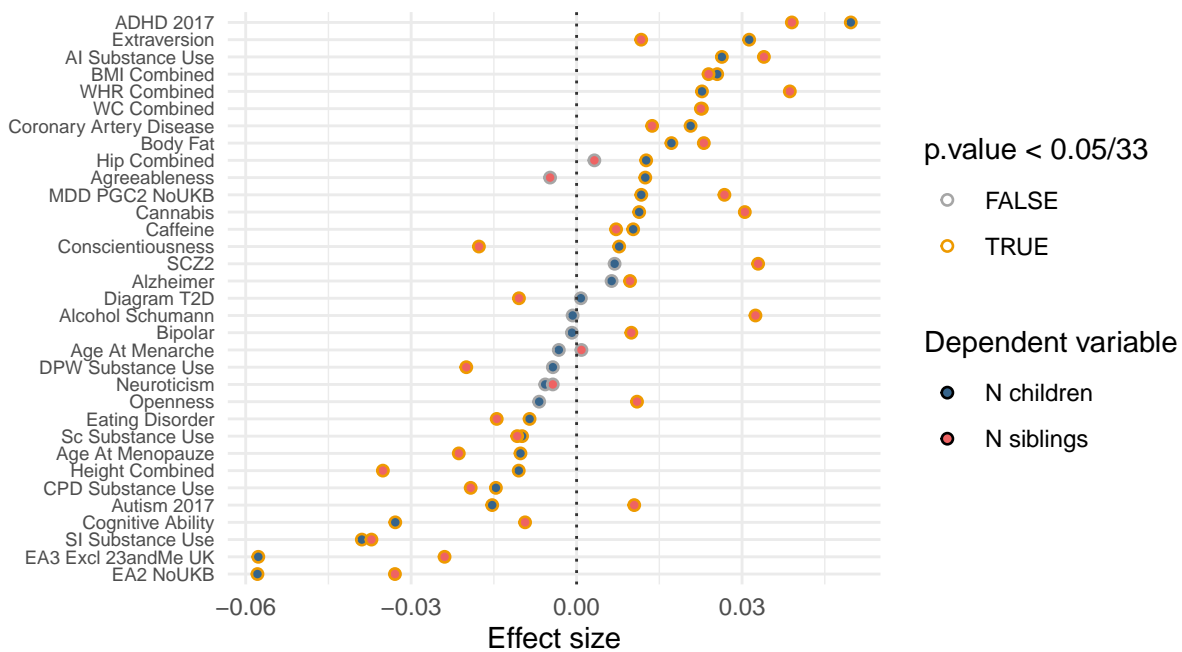


Figure 9: Effects of polygenic scores on number of children/siblings. Regressions weighted by sex, age and education.

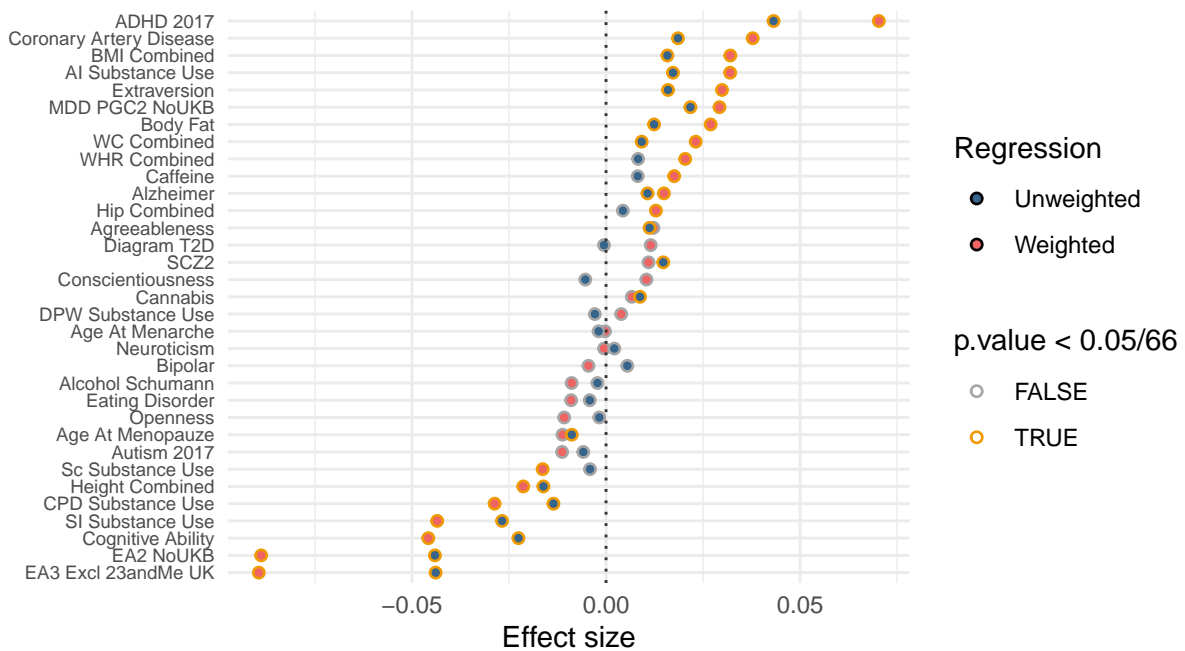


Figure 10: Effect sizes on number of children, female respondents weighted by age at first live birth

to share childcare responsibilities, while the income effect will dominate for couples who are able to reap the gains from specialization.

If so, then genetic characteristics which affect one's earnings potential in the labour market may lead to opposing effects on fertility. Genetic variants which improve one's earnings may increase fertility among couples, but decrease fertility among single parents.

This explanation predicts that the strength of polygenic scores' effects on fertility will correlate with the strength of their relationship with earnings. We measure the correlation of each PGS with household income, as well as with education level, a phenotypic variable which is likely to predict earnings. We then relate these measurements to effect sizes on number of children. Across scores, there is a clear negative relationship between effect on fertility, and the correlation with income and/or education (Figure 11).

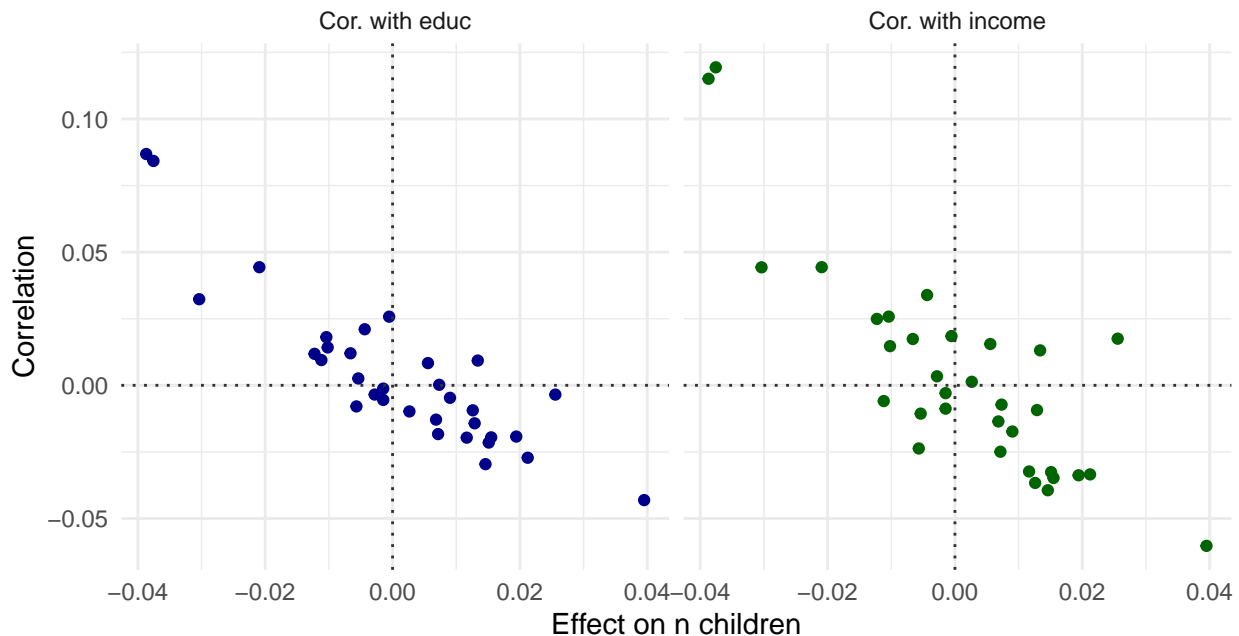


Figure 11: Effect sizes on number of children and correlations with income and education

7 Bits to integrate

Figure 12 shows the results of *children* regressions for women only, controlling for age at first live birth. Effect sizes are greatly reduced. Partly, this is because the regressions exclude childless women. However, in 24 out of 33 cases, effect sizes actually change sign with the controls. The correlation between effect sizes controlling for age at first live birth, and raw effect sizes, is -0.75.

We can run similar regressions for the parents' generation, using the subsets of respondents who reported their mother's or father's age and who had no elder siblings. We run *sibling* regressions on these subsets, controlling for either parent's age at their birth. Figure 13 shows the results. Effect sizes are very similar, whether controlling for father's or mother's age at respondent's birth or mother's age at respondent's birth. Unlike for the respondents' generation, effect sizes are positively correlated with the effect sizes from bivariate regressions (father's age at birth: ρ 0.51; mother's age at birth: ρ 0.57).

These results suggest that polygenic scores may directly correlate with age at first live birth. Figure 14 plots estimated effect sizes from bivariate regressions for respondents, and Figure 15 does the same for their parents. Effect sizes are reasonably large. They are also very highly correlated across generations. Effect

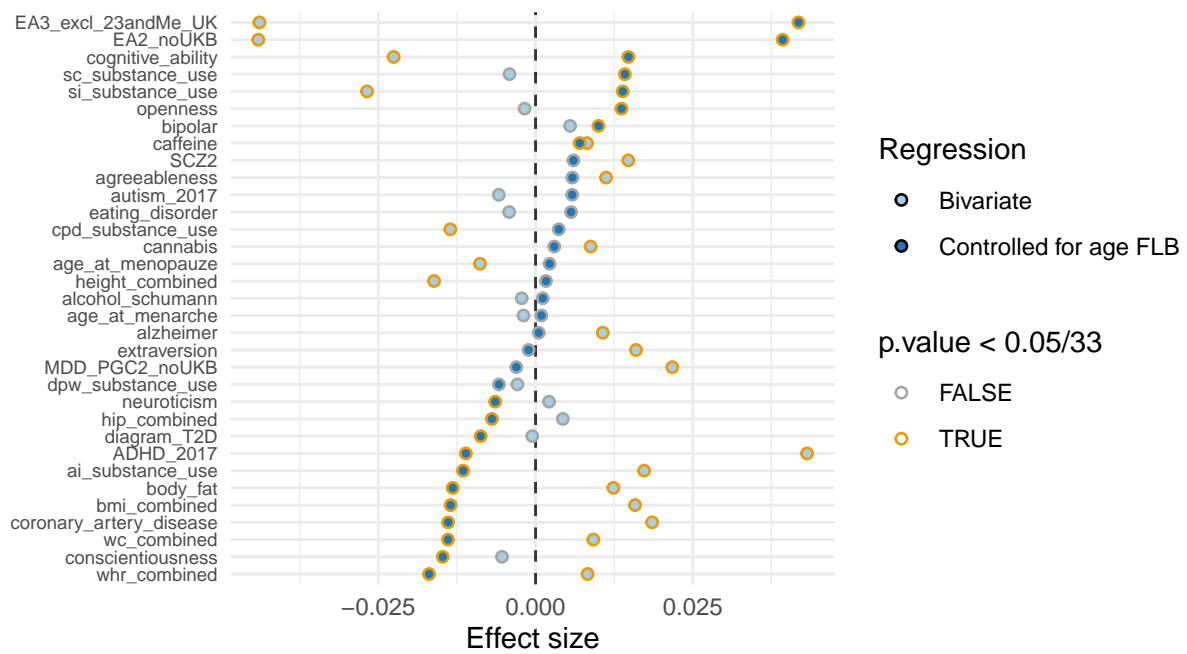


Figure 12: Effect sizes on number of children, controlling for age at first live birth (women only). Effect sizes for women without controls are shown for comparison

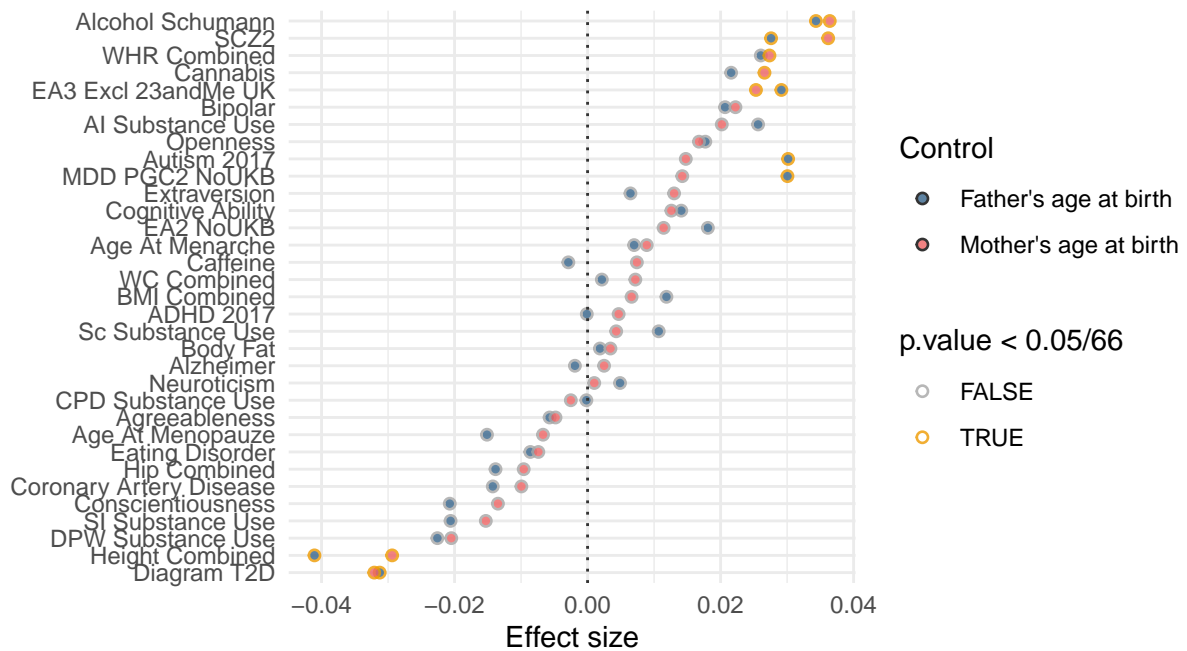


Figure 13: Effect sizes on number of siblings controlling for parents' age at birth, eldest siblings

sizes of PGS on father’s age at own birth, and on own age at first live birth, have a correlation of 0.98; for mother’s age and own age it is 0.98

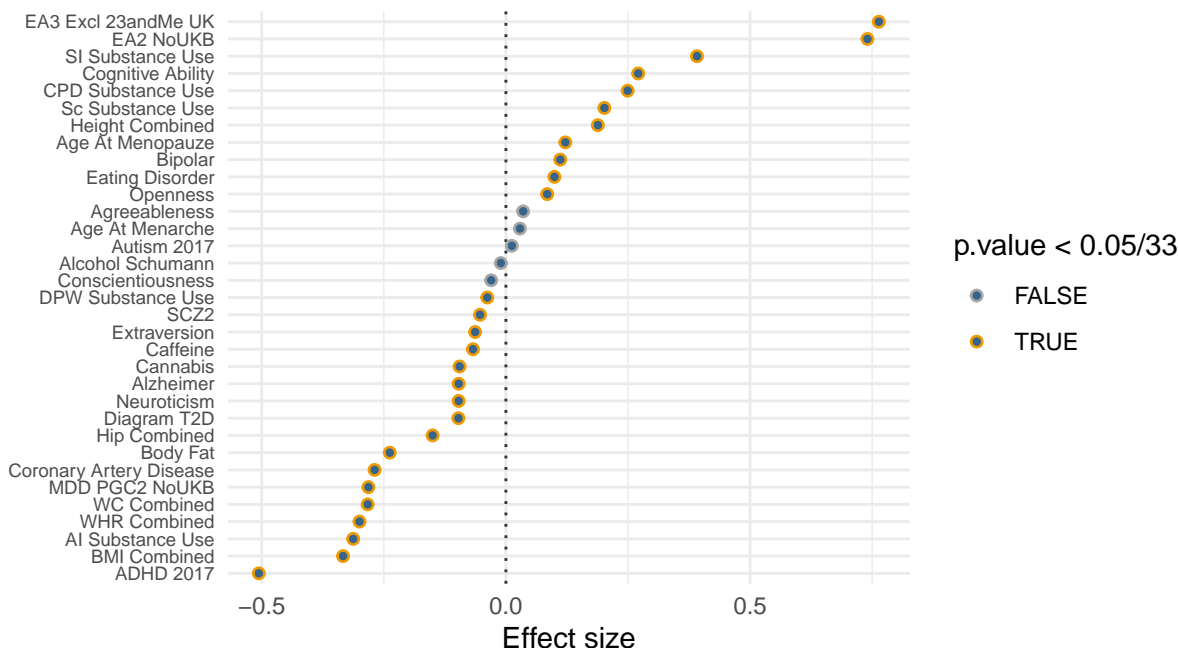


Figure 14: Effects of polygenic scores on age at first live birth

8 Appendix

8.1 Controlling for principal components

Polygenic scores could capture effects that are really due to population stratification, although would not change our results for natural selection of the scores. In 16 we show results for selection on polygenic scores residualized for the top 100 principal components of the genetic data, calculated within the UK Biobank population. (TODO Abdel details.)

In siblings regressions, effect sizes are smaller when residualizing for principal components – sometimes much smaller, as in the case of height. 25 out of 33 “controlled” effect sizes have a smaller absolute value than the corresponding “raw” effect size. The median proportion between raw and controlled effect sizes is 0.89. Among the children regressions, this no longer holds. Effect sizes are barely affected by controlling for principal components.

Overall, 78.79 per cent of effect sizes are consistently signed across all four regressions (on children and siblings, and with and without residualization).

To get a further insight into this we regress *siblings* and *children* on individual principal components. As Figure 17 shows, effects are larger and more significant in siblings regressions. 29 principal components significantly predicted number of siblings, while only 10 significantly predicted number of children.

8.2 Selection over time

To check whether effect sizes were changing over time, we ran regressions interacting PGS with birth year, median split at 1950. Tables 1 and 2 summarize the results. Very few scores are significantly different. Only

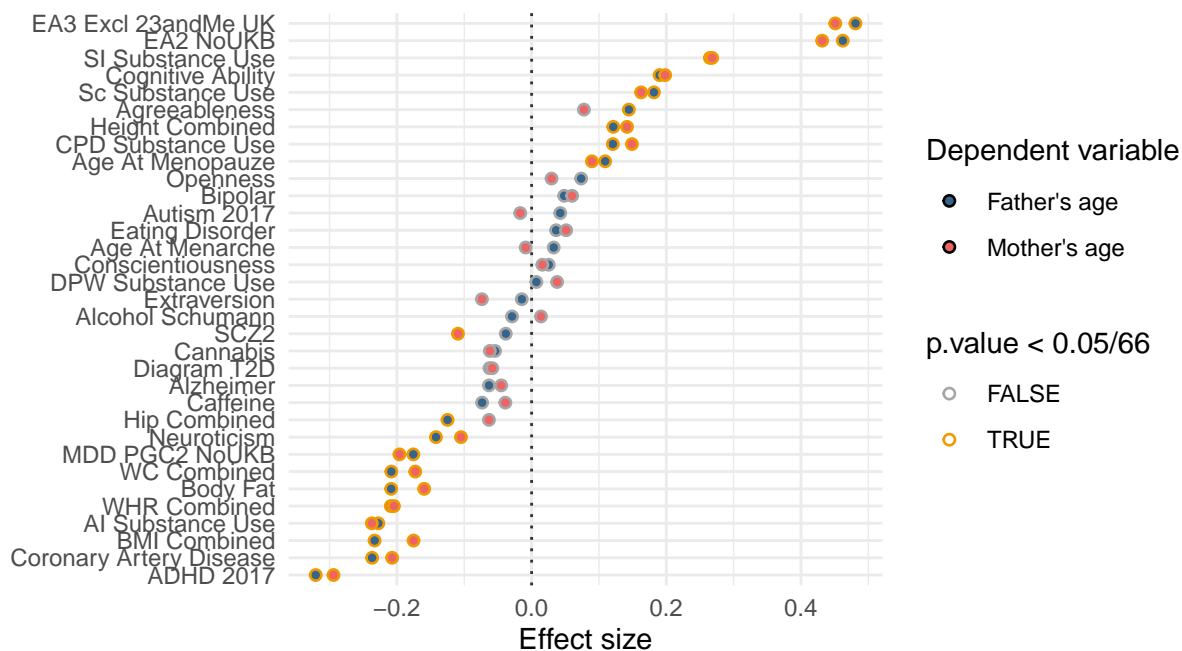


Figure 15: Effects of polygenic scores on parents' age at own birth, eldest siblings

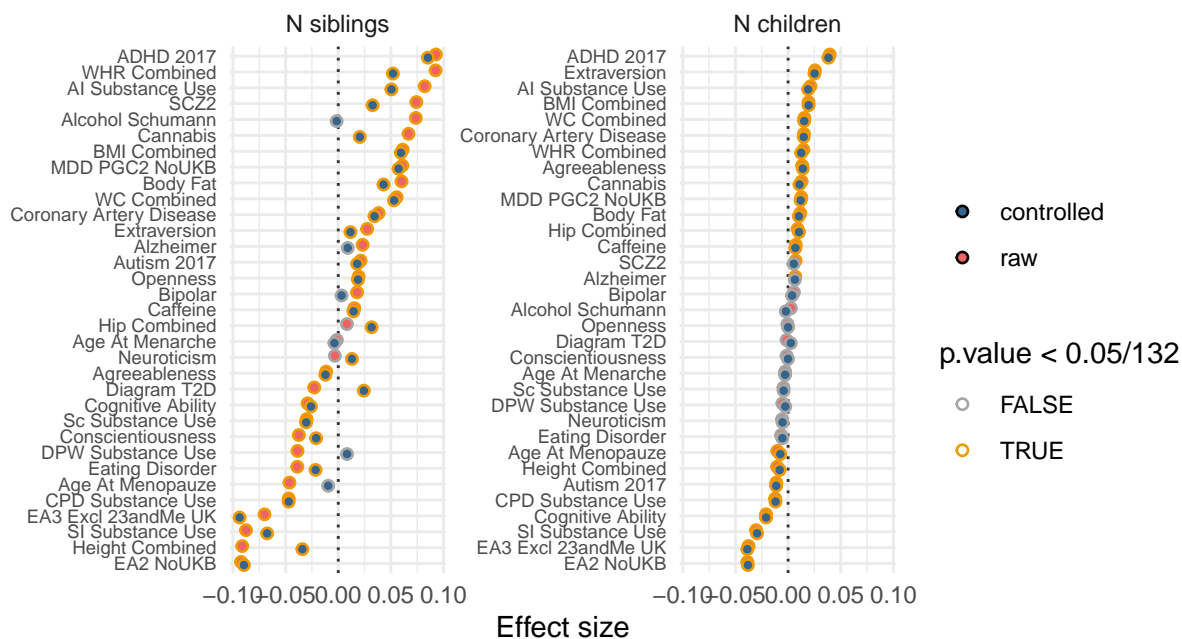


Figure 16: Effects of residualized polygenic scores on number of siblings/children.

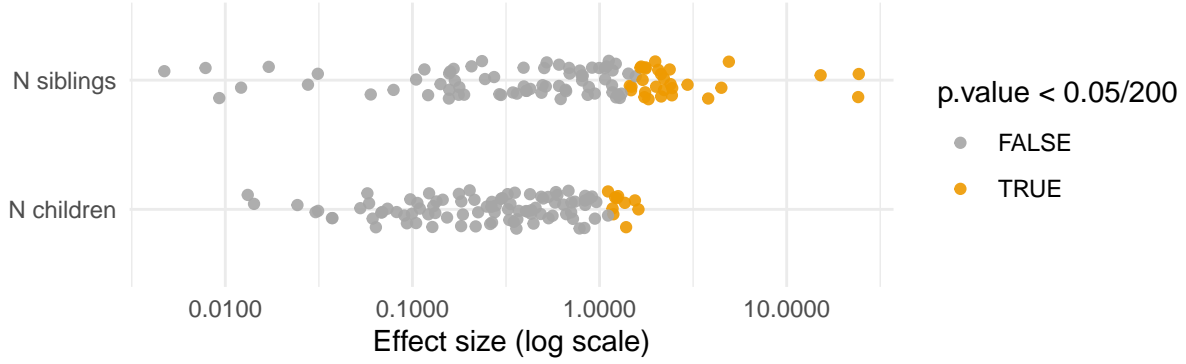


Figure 17: Effect of principal components of genetic data on number of siblings/children. Absolute effect sizes are plotted. Each dot represents one bivariate regression. Points are jittered on the Y axis.

one score, EA3, changes significantly across time in both generations: the absolute size of the (negative) effect significantly increases in sibling regressions, and significantly decreases in children regressions.

Table 1: Change in effect sizes between early and late born parents, 'sibling' regressions

Change	Number of scores
Insignificant	31
Size decreasing	2

Significance is measured at $p < 0.05/66$

Table 2: Change in effect sizes between early and late born respondents, 'children' regressions

Change	Number of scores
Change sign	2
Insignificant	29
Size increasing	2

Significance is measured at $p < 0.05/66$

8.3 Genetic correlations with EA3

Another way to examine the “earnings” theory of natural selection is to compare effect sizes of PGS with their genetic correlation with educational attainment (EA3). Since EA3 strongly predicts earnings, if earnings drives differences in fertility, we’d expect a correlation between the two sets of results. Figure 18 shows this is so.

TODO: ref source of data.

8.4 Number of children

Figure 19 shows the full distribution of number of children born for different ventiles of the EA3 polygenic score. The strongest relationship seems to be for having 0 children versus 1 or more.

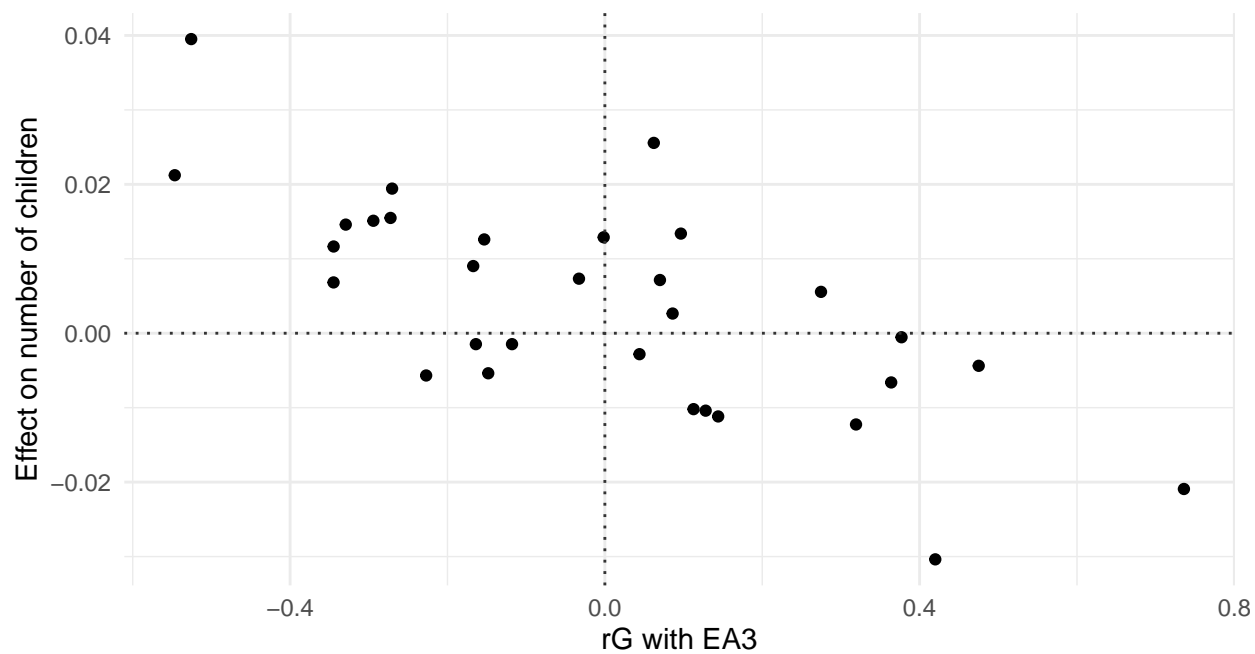


Figure 18: Effect size on n siblings by genetic correlation with EA3

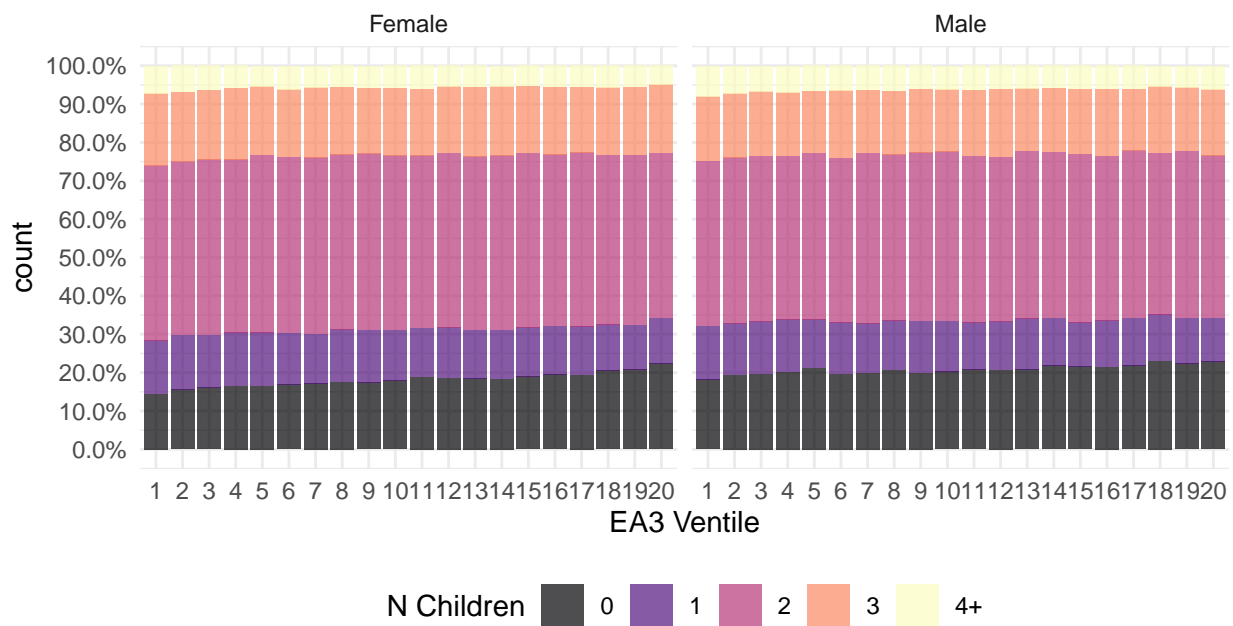


Figure 19: Number of children by ventiles of EA3 PGS

8.5 Causality

Different polygenic scores are correlated. Table 3 shows the top correlations in the sample. Because of this, bivariate correlations between PGS and number of children might be driven by other genetic scores. To explore which polygenic scores are driving negative selection, we run a single omnibus regression of *number of children* on all the PGS. We exclude EA2, waist-hip ratio, waist-circumference, and “Hip combined” since they are highly correlated with other scores, which could make our estimates unstable. Figure 20 shows the results. Interestingly, several PGS remain independently significant, although effect sizes are reduced.

Table 3: Top 10 correlations between polygenic scores

PGS	PGS	Correlation
EA2 NoUKB	EA3 Excl 23andMe UK	0.89
Hip Combined	WC Combined	0.807
BMI Combined	WC Combined	0.753
WC Combined	WHR Combined	0.711
BMI Combined	Hip Combined	0.697
Body Fat	WC Combined	0.435
BMI Combined	Body Fat	0.425
BMI Combined	WHR Combined	0.425
Body Fat	Hip Combined	0.385
ADHD 2017	Autism 2017	0.328

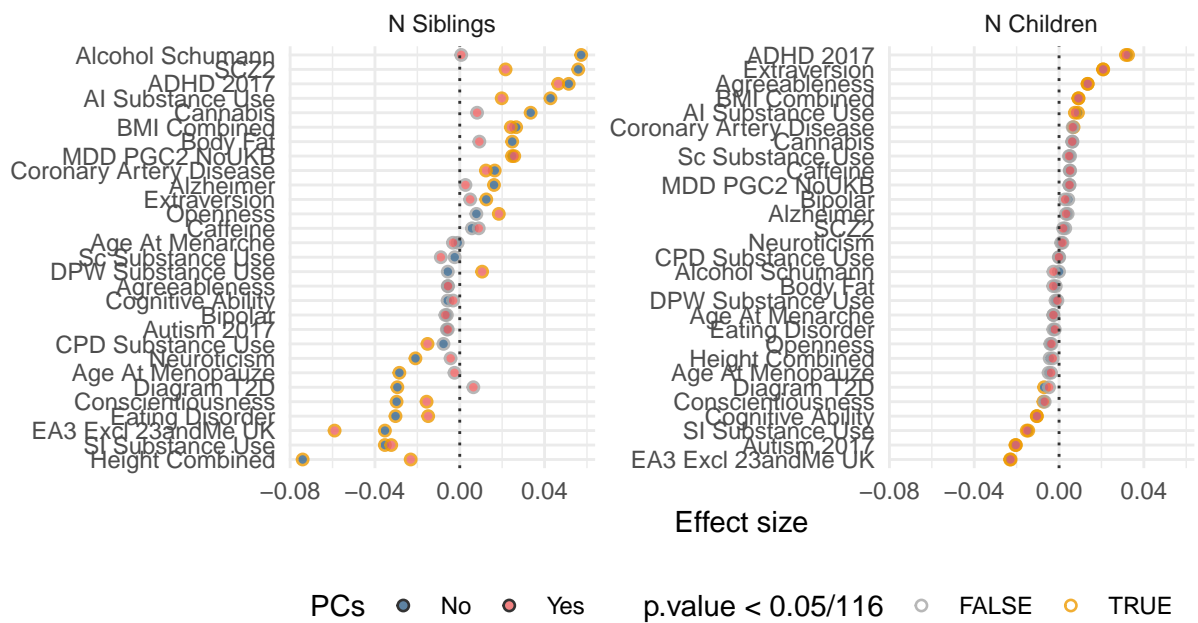


Figure 20: Partial correlations with number of children