CLOSER Conference

Education 1

Chair: **Alison Park**

- Changing Inequalities in Teenage Vocabulary: A comparison of cohorts born in 1970 and 2000
  Alice Sullivan

- Examining the genetic influences on educational attainment and the validity of value-added measures of progress in educational research
  Tim Morris

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Institute of Education

Teenage vocabulary: a comparison of cohorts born in 1970 and 2000

Alice Sullivan, Vanessa Moulton, Emla Fitzsimons

CENTRE FOR LONGITUDINAL STUDIES

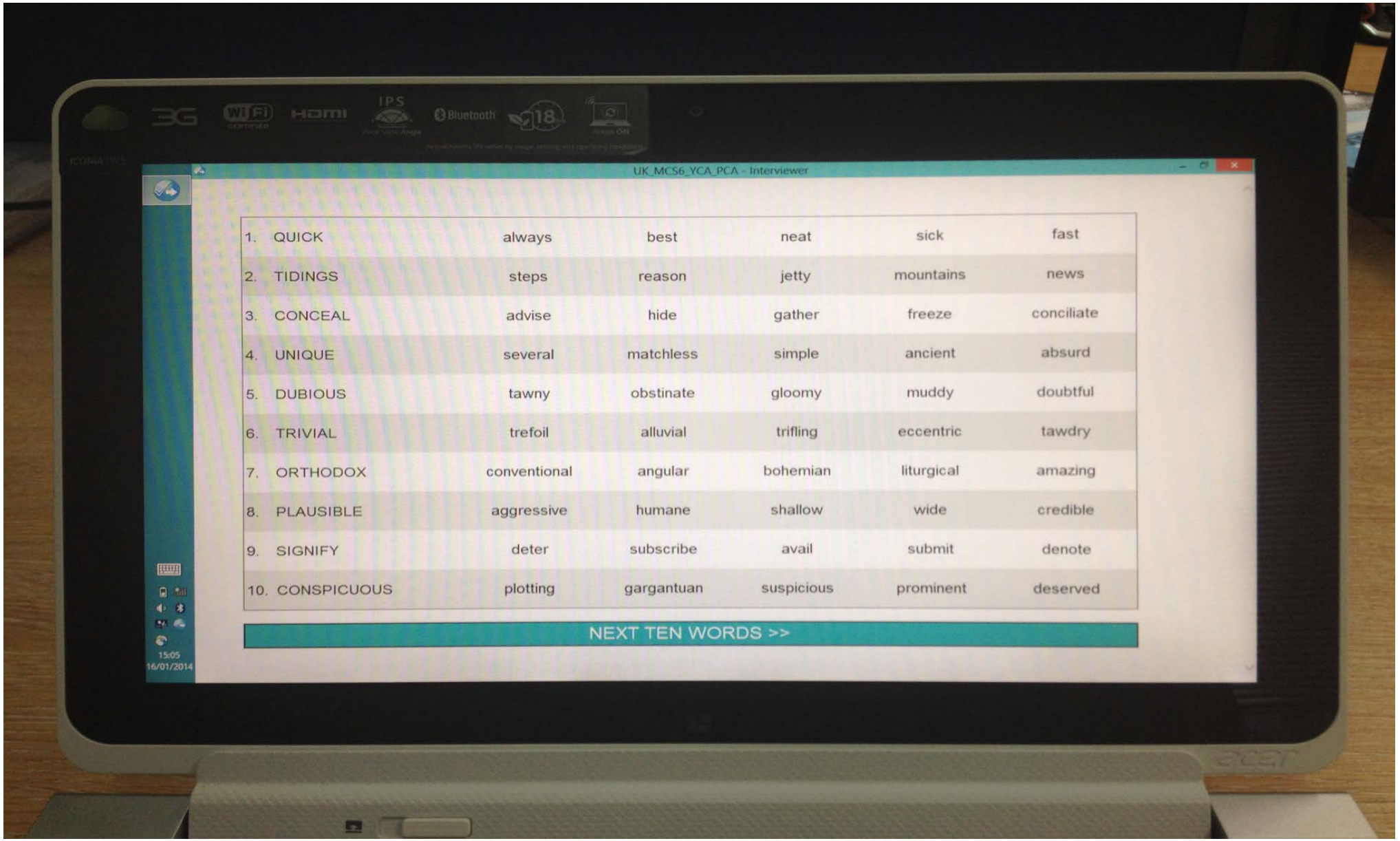
Background

- Importance of language transmission in theories of social stratification in education (Bourdieu, Bernstein)
- Although there is evidence of fluid IQ gains over time (Flynn) there is little evidence on whether language skills are improving
- Are inequalities changing over time?

Aims

- Investigate the inter-generational change in vocabulary attainment in Britain using young people's vocabulary test scores in MCS6 (age 14) and BCS70 (age 16).
- Changes in: distribution of cognitive attainment, socio-economic differentials, other factors (region, sex).
- Can cross cohort differences be explained by changes in: occupational and educational characteristics; family structure and parenting, reading behaviours.

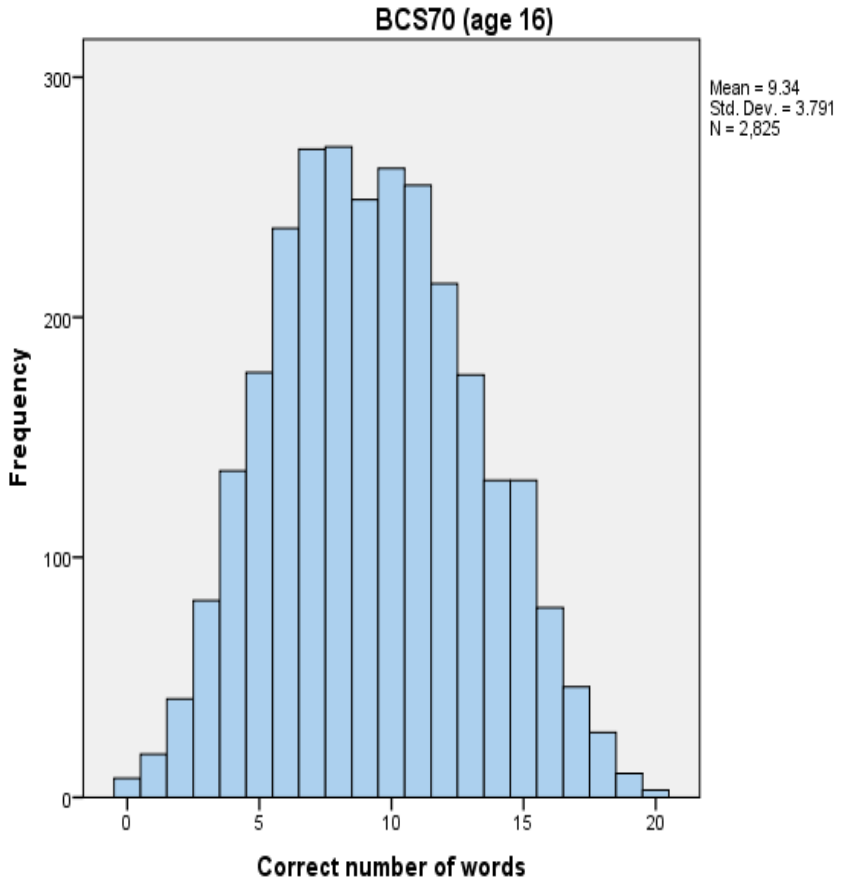
MCS Age 14: Word Activity

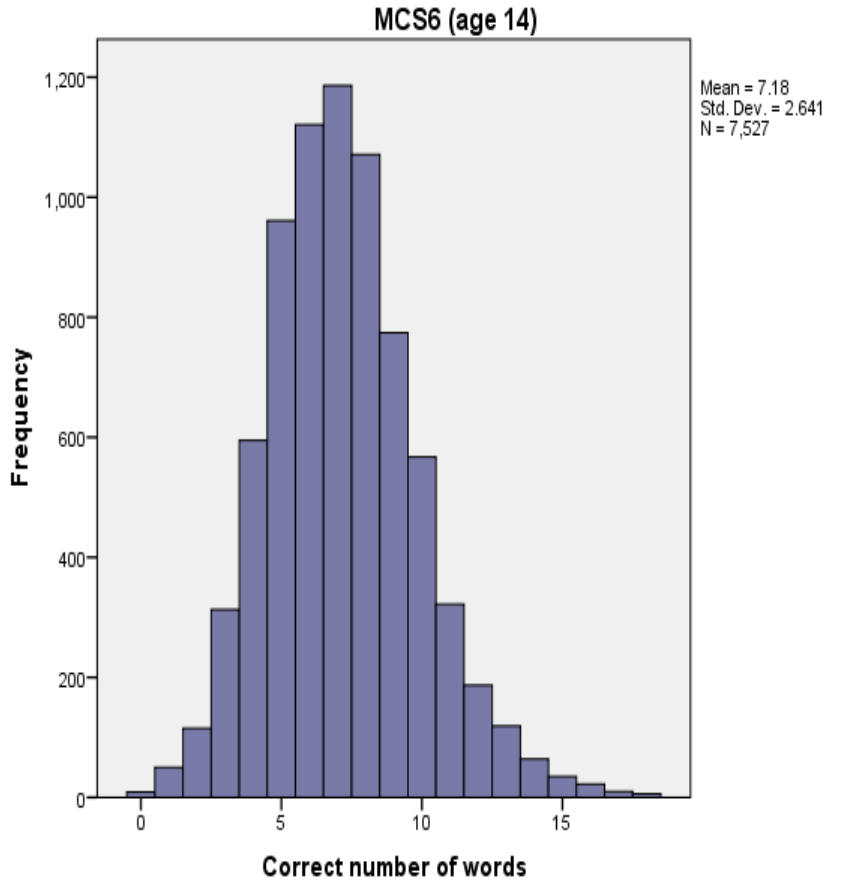


CENTRE FOR LONGITUDINAL STUDIES

MCS and BCS

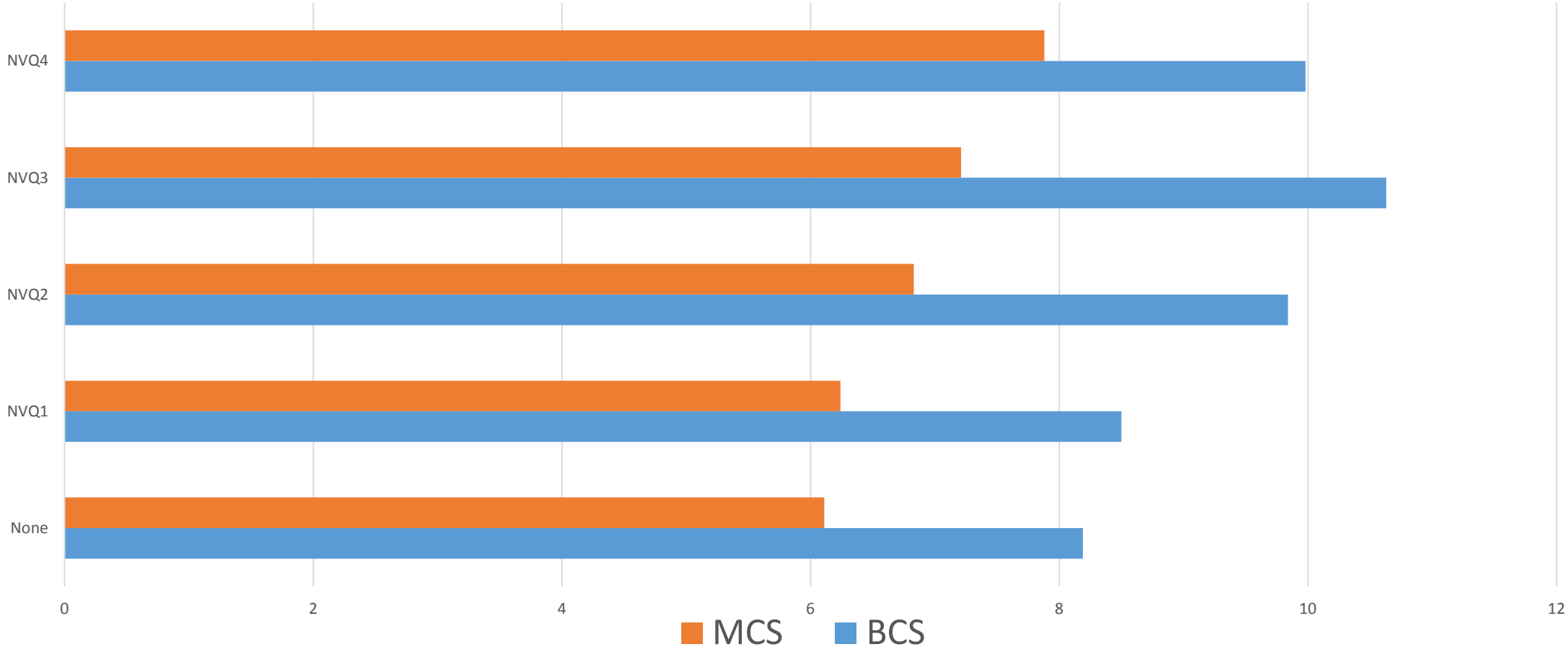
- Distribution of YP vocabulary scores by cohort (All giving vocab score, age and date of test, and white British).
- MCS sample aged from 162-182 months (13 yrs 6 months to 15 yrs 2 months)





CENTRE FOR LONGITUDINAL STUDIES

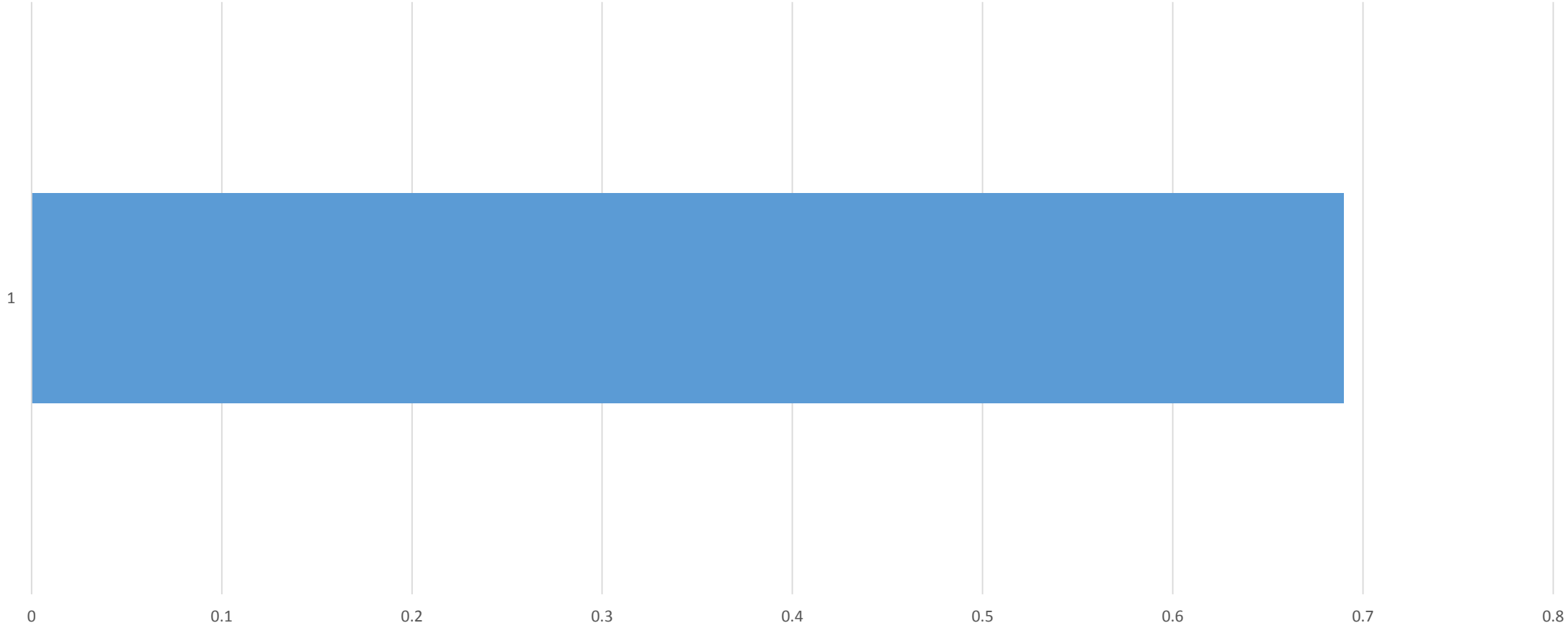
Maternal education and child mean vocab



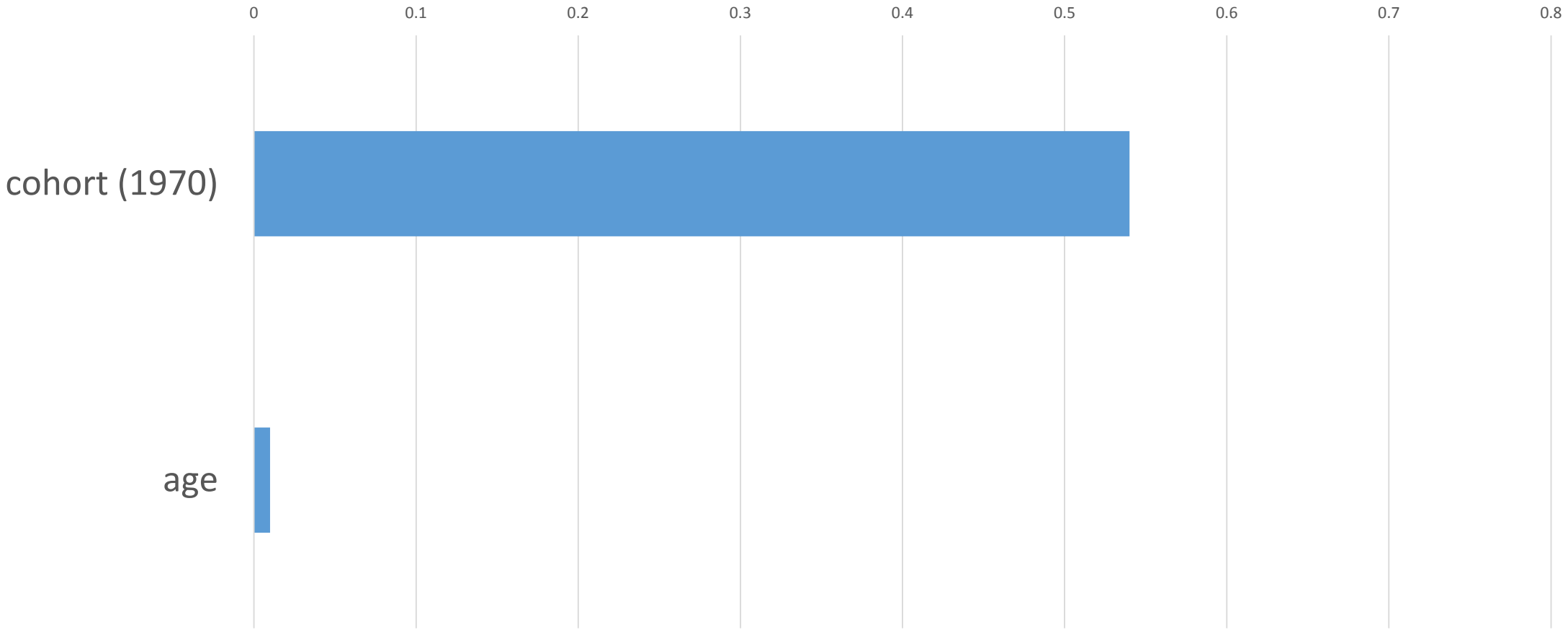
Linear regression: vocabulary scores

- Standardised across cohorts
- Model 0: cohort
- Model 1: cohort + age
- Model 2: model 1+ sex, country, social class, education, home ownership
- Model 3: model 2+ breastfeeding, age of mother at birth, birthweight, single parent, position in the birth order
- Model 4: model 3+ read to at 5, reading at 10/11, library visits at 10/11, reading at 14/16.

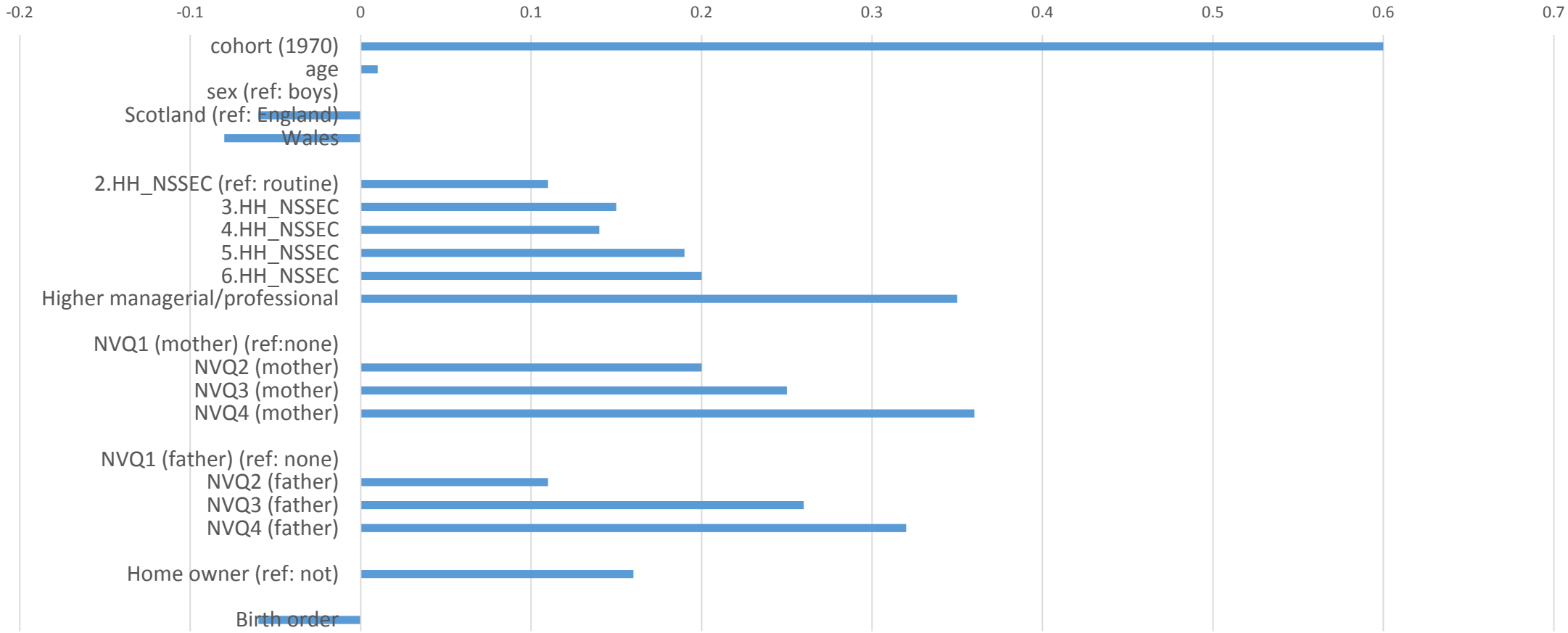
Model 0: raw cohort difference



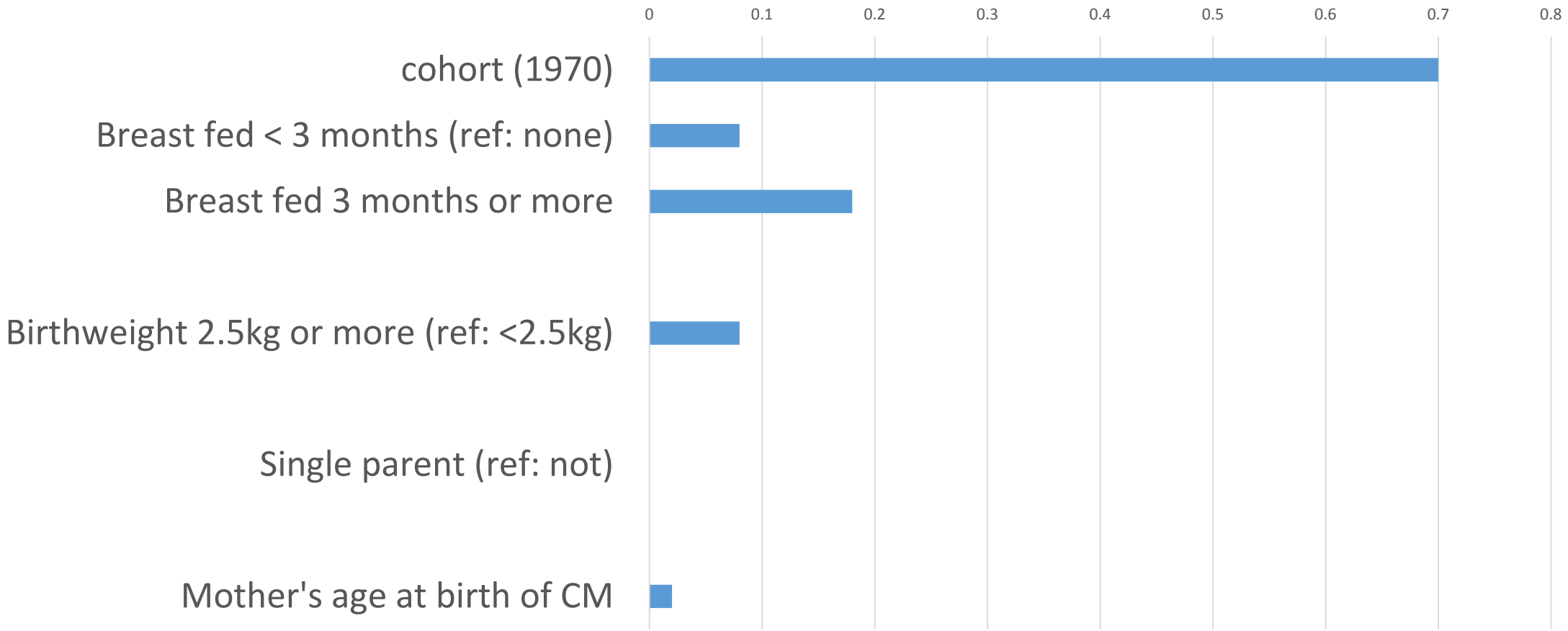
Model 1: cohort + age in months



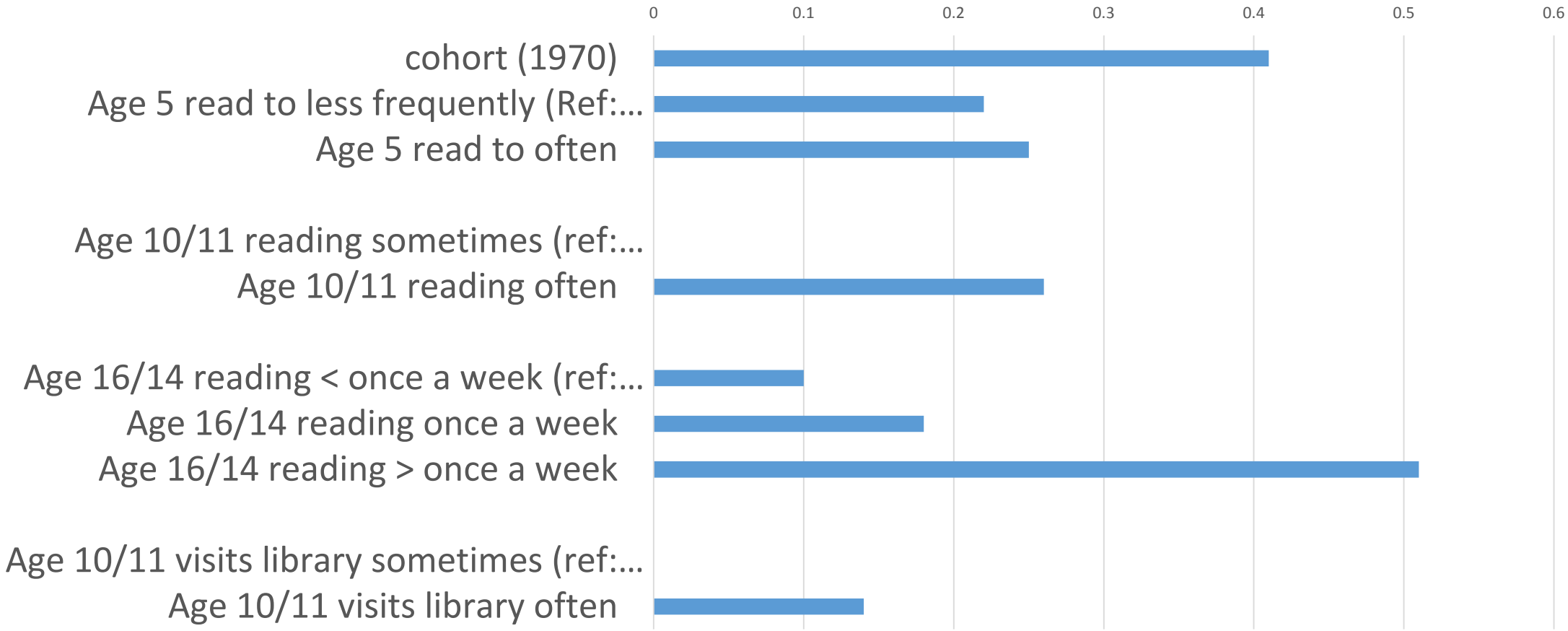
Model 2: socio-economic and demographic controls



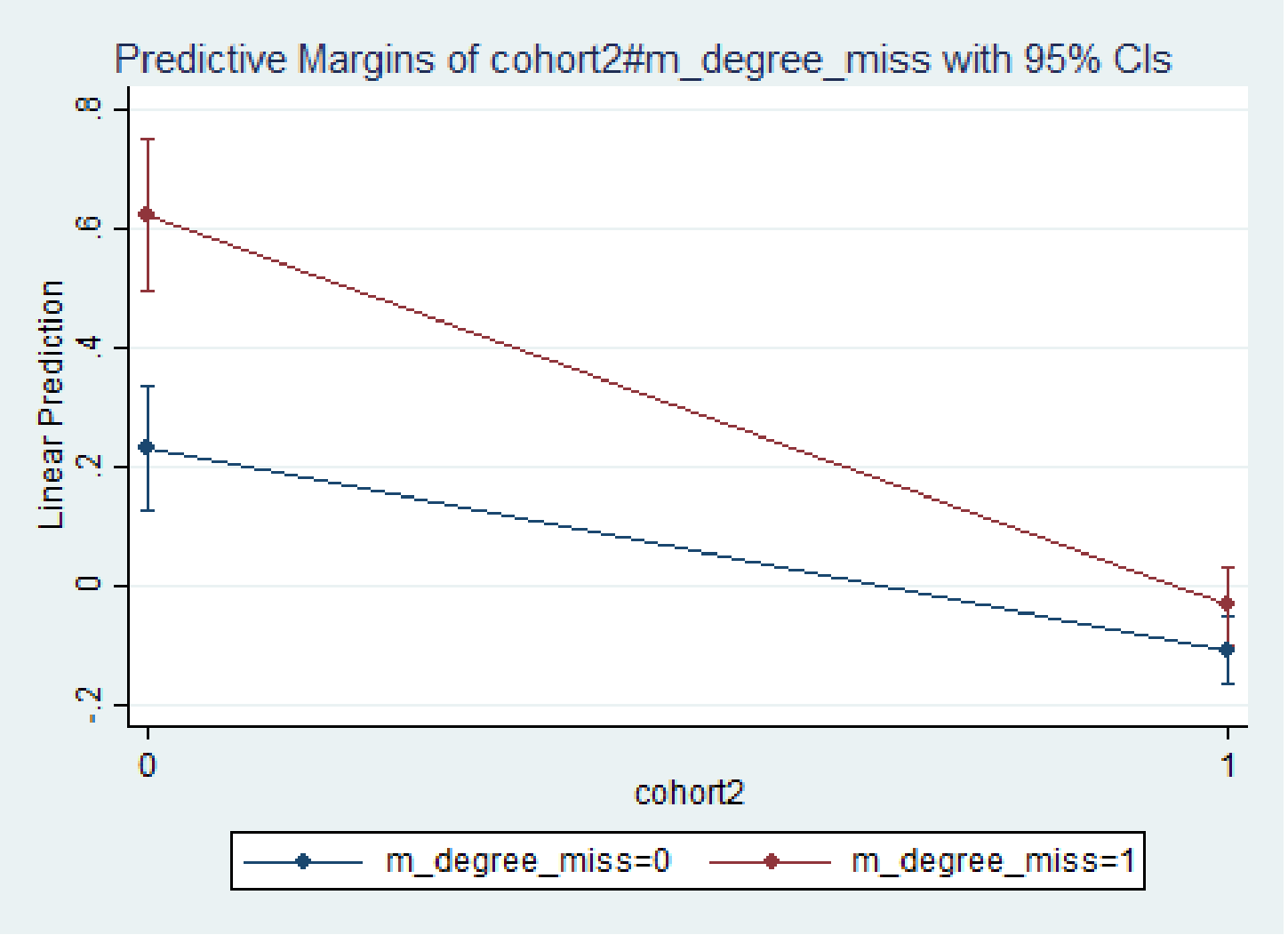
Model 3: 1+ other childhood circumstances



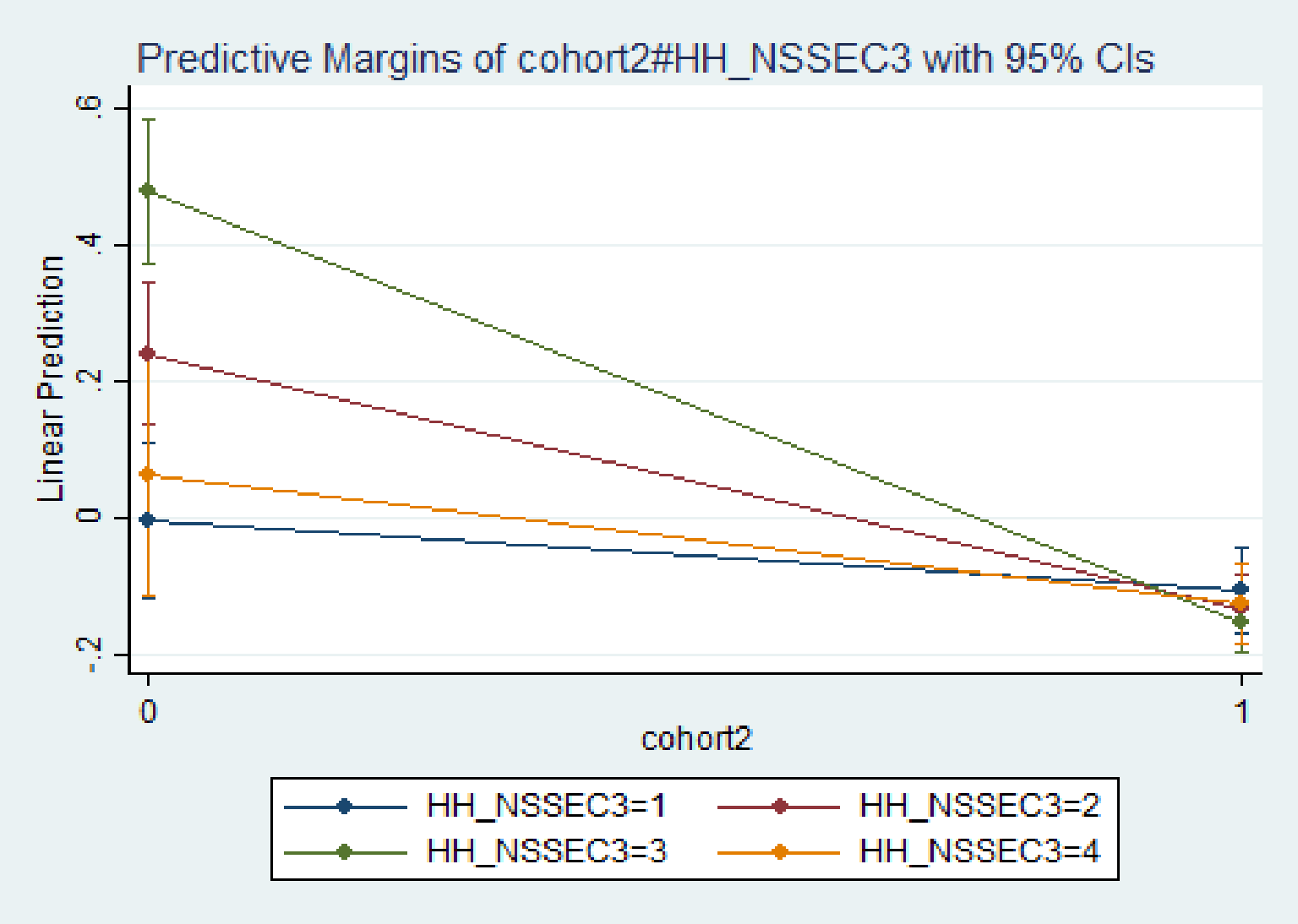
Model 4: model 3 + reading



Education x cohort



Class x cohort



Discussion

- Results are preliminary and issues in x-cohort comparison need more attention.
- Apparent lower scores for younger cohort
- Class/education inequalities appear reduced
- X-cohort difference is amplified when controlling for factors such as breastfeeding and maternal age
- X-cohort difference is somewhat explained by reading behaviour

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Examining genetic influences of educational attainment and the validity of value-added measures of progress in educational research

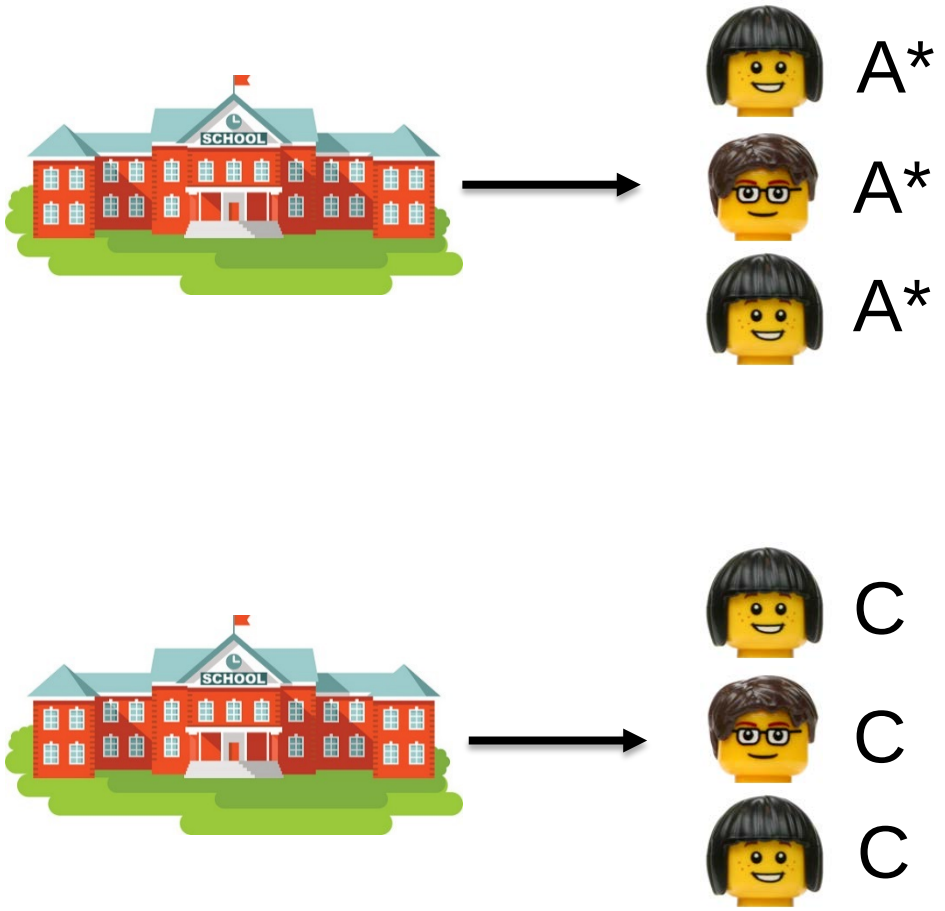
Tim Morris, Neil Davies, Danny Dorling, George Davey Smith

MRC Integrative Epidemiology Unit, University of Bristol

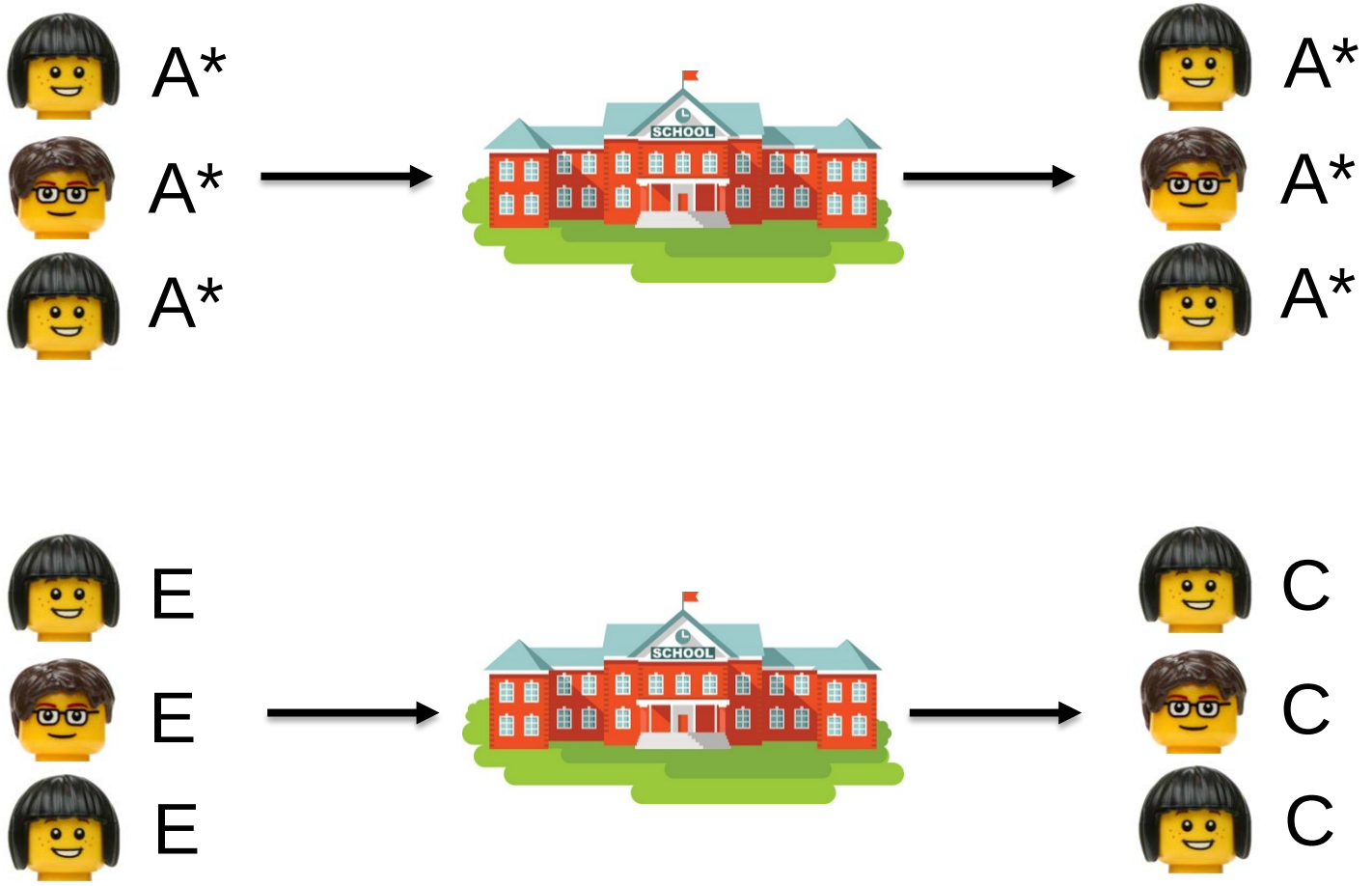
Value added measures

- Used to rank UK schools and feed into school league tables (Leckie & Goldstein, 2016)
- Permits estimation of knowledge gained, or value added by a teacher/school (Taylor & Nguyen. 2006)
- Used and discussed extensively in educational research
- Designed to overcome issues of intake bias when using raw attainment (Goldstein & Thomas, 1996)

Intake bias



Intake bias



Raw or contextual VA?

- Raw VA measures adjust only for *prior* attainment
- Regardless, should account for background confounders through their association with the baseline measure of attainment
- Contextual VA measures additionally adjust for 9 socioeconomic and demographic characteristics
- Contextual VA measures also modelled in a multilevel framework

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Influences of EA

Parental involvement

Genetics

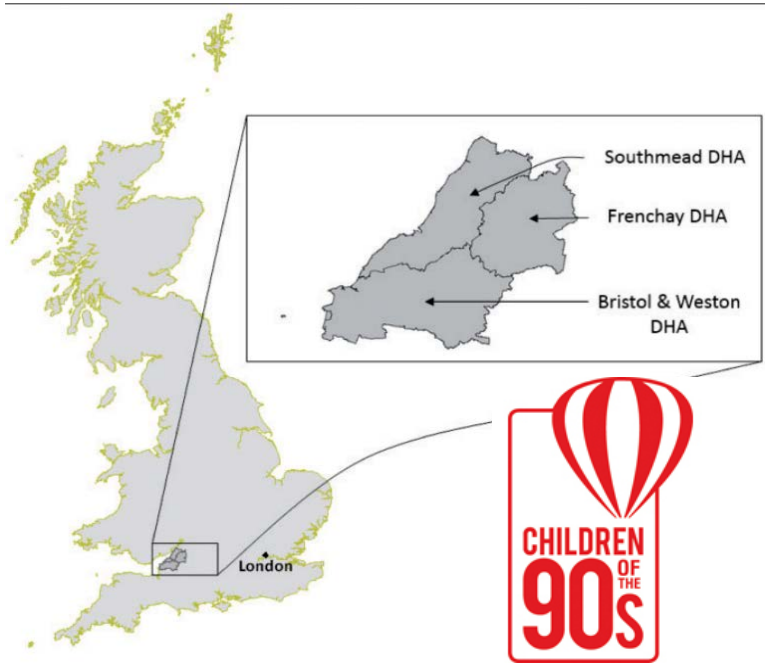
Personality

Genetics and VA

- VA measures SHOULD control for any genetic influences on educational attainment, and therefore demonstrate zero heritability
- But… Previous study estimated heritability at 52%! (Haworth et al, 2011)
- Findings seemed to be missed (ignored?) by educational researchers, but represents a potential problem with VA
- *Our aim*: to estimate heritability in VA scores built from rich point score data

Data source

- Data from the Avon Longitudinal Study of Parents and Children (ALSPAC)
- Recruited in 1991 & 1992
- Representative of UK population
- 14 775 children in full sample



- 7 988 children with data on 1+ outcome measure and genetic data
- Data linked to the UK National Pupil Database (NPD)

Outcomes

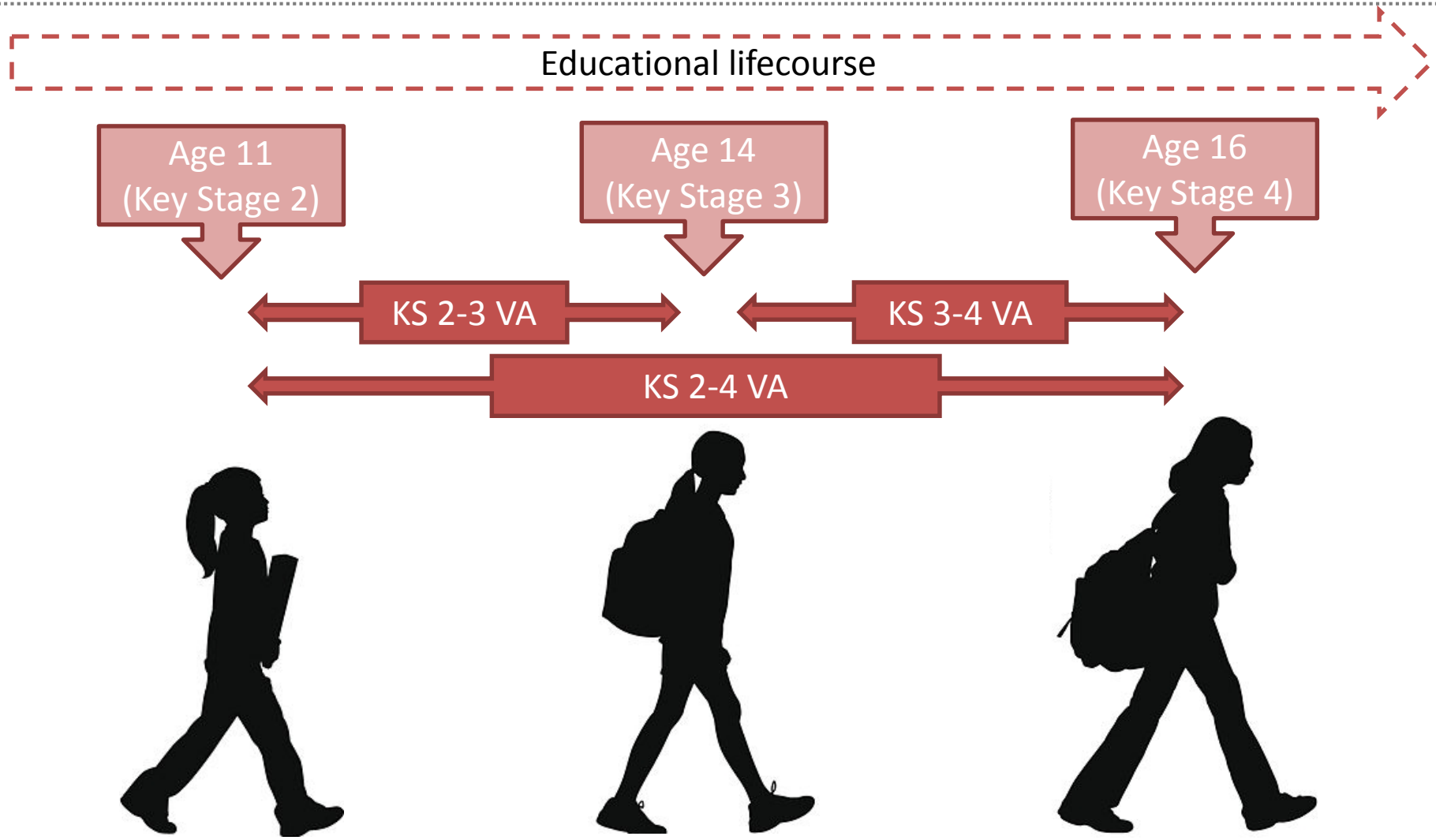
Educational lifecourse

Age 11
(Key Stage 2)

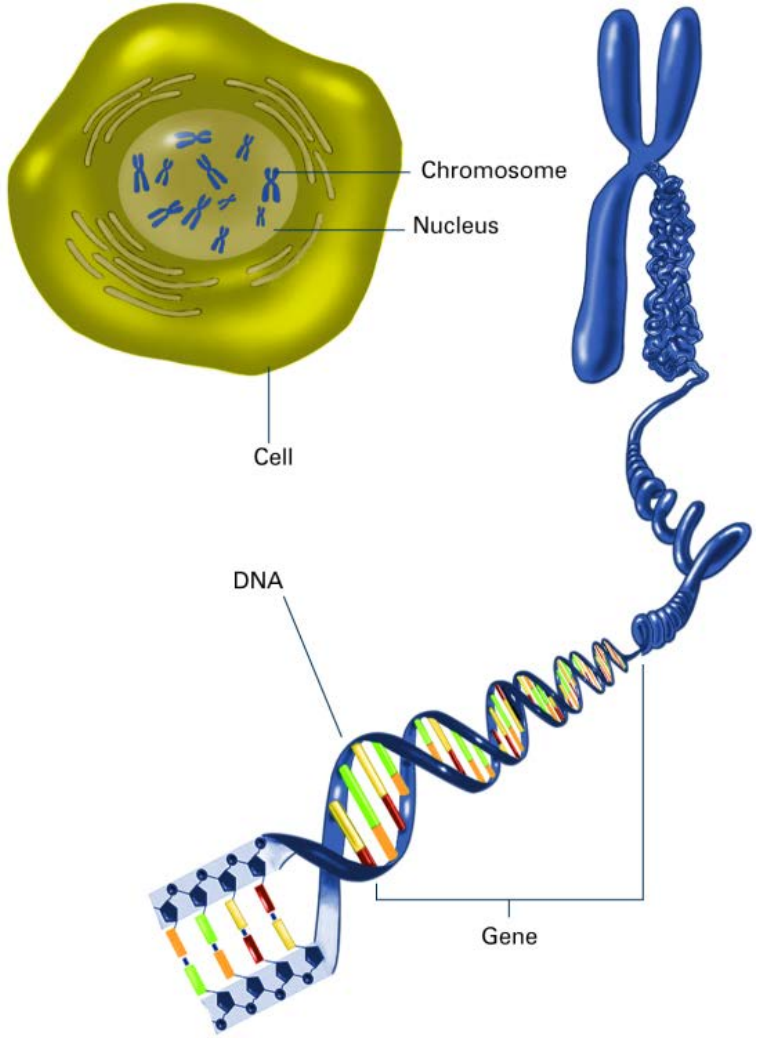
Age 14
(Key Stage 3)

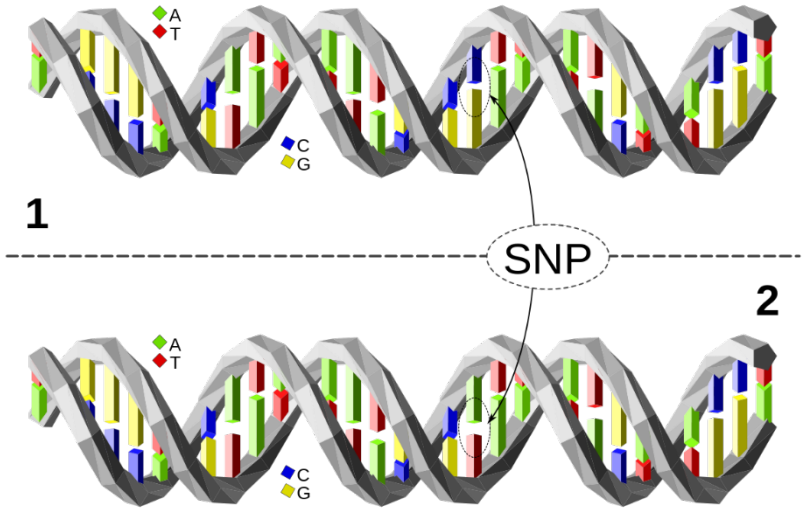
Age 16
(Key Stage 4)

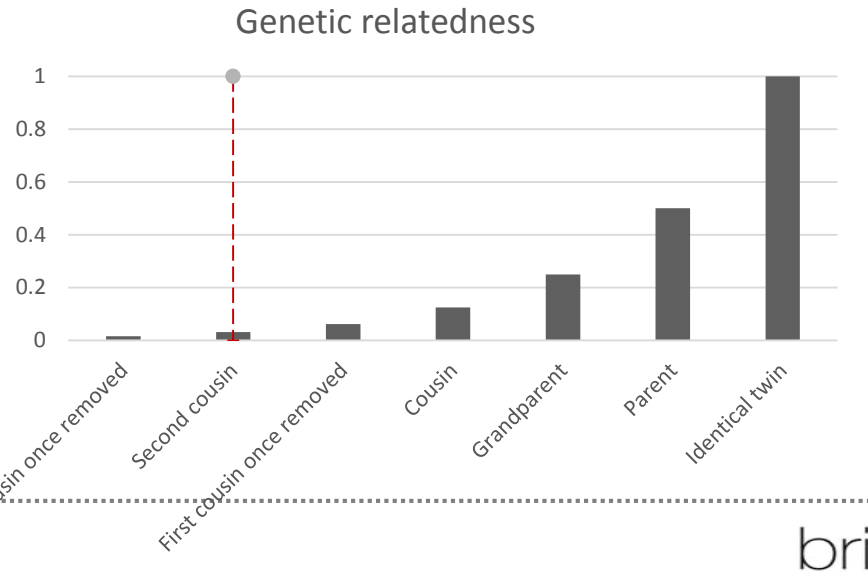
Outcomes


Educational lifecourse
Age 11
(Key Stage 2)
Age 14
(Key Stage 3)
Age 16
(Key Stage 4)
KS 2-3 VA
KS 3-4 VA
KS 2-4 VA

How do we measure genetics?





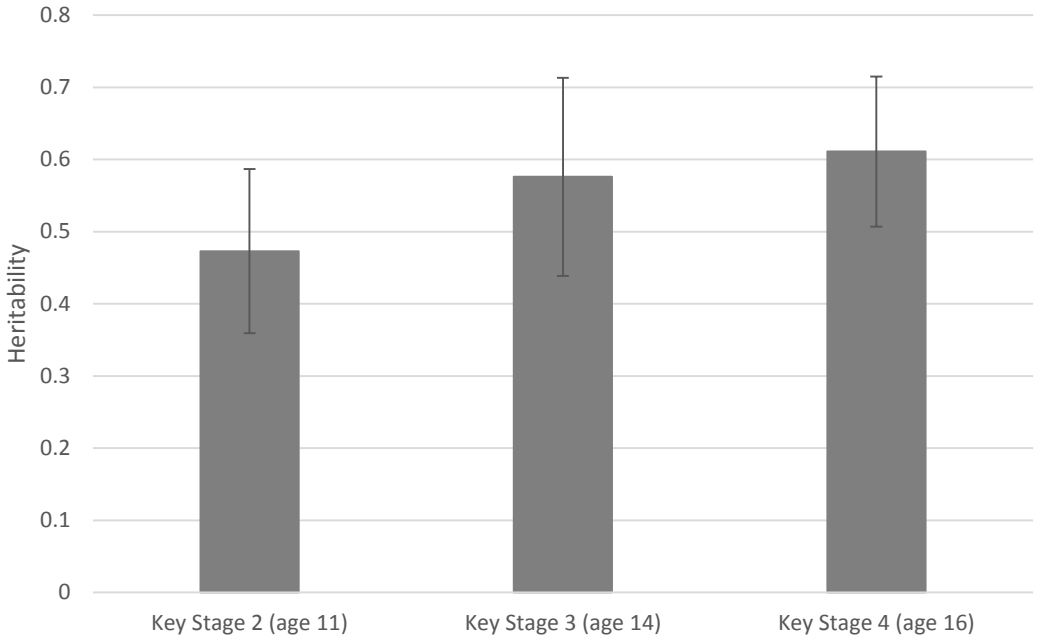


Analyses

- We use genome-wide complex trait analysis (GCTA) to estimate the heritability of EA and VA measures
- GCTA uses measured SNP level variation to compare genetic and phenotypic similarity between all pairs of unrelated individuals
- Where genetically similar pairs are more phenotypically similar than genetically dissimilar pairs then heritability estimates are higher
- The proportion of total variance in EA/VA that can be attributed to common genetic variation tells us the heritability

Results: heritability of attainment

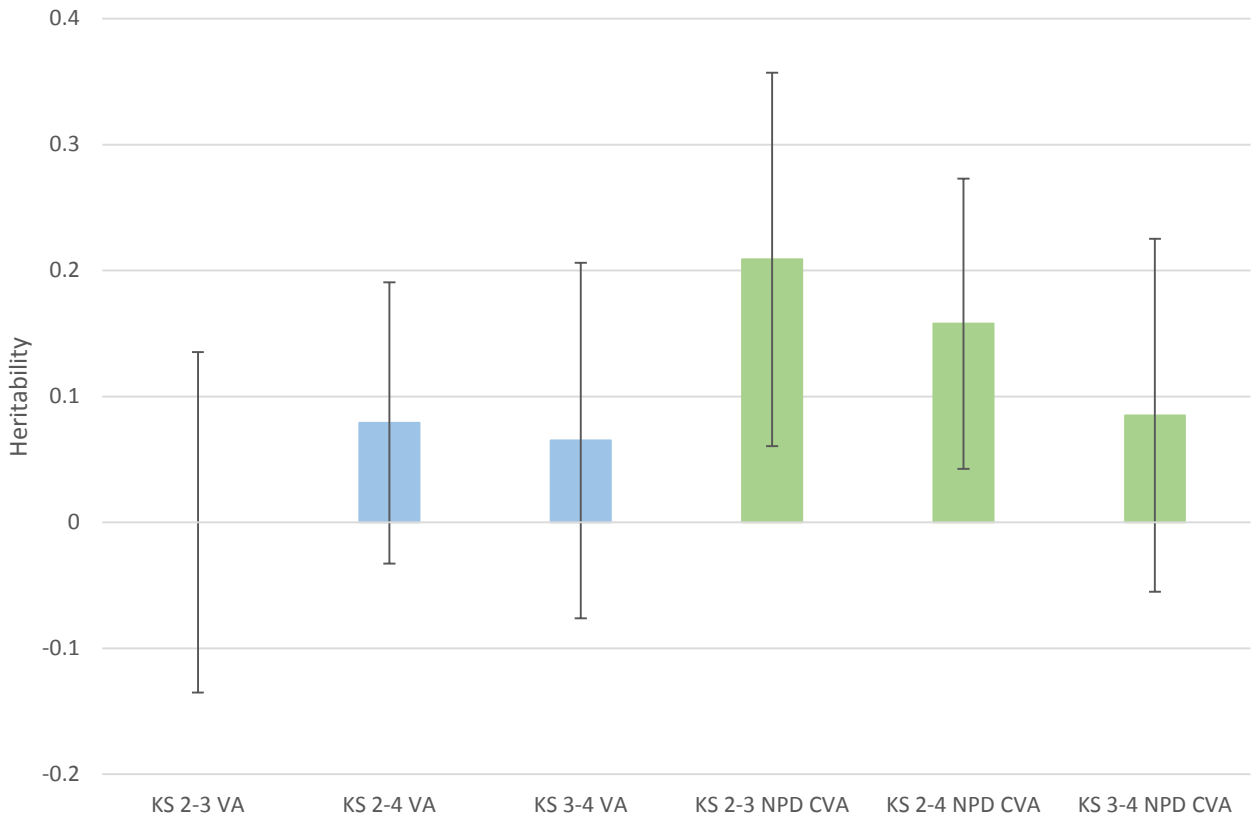
- First step was to estimate heritability of educational attainment:



- Fairly consistent with prior findings (Branigan et al., 2013)

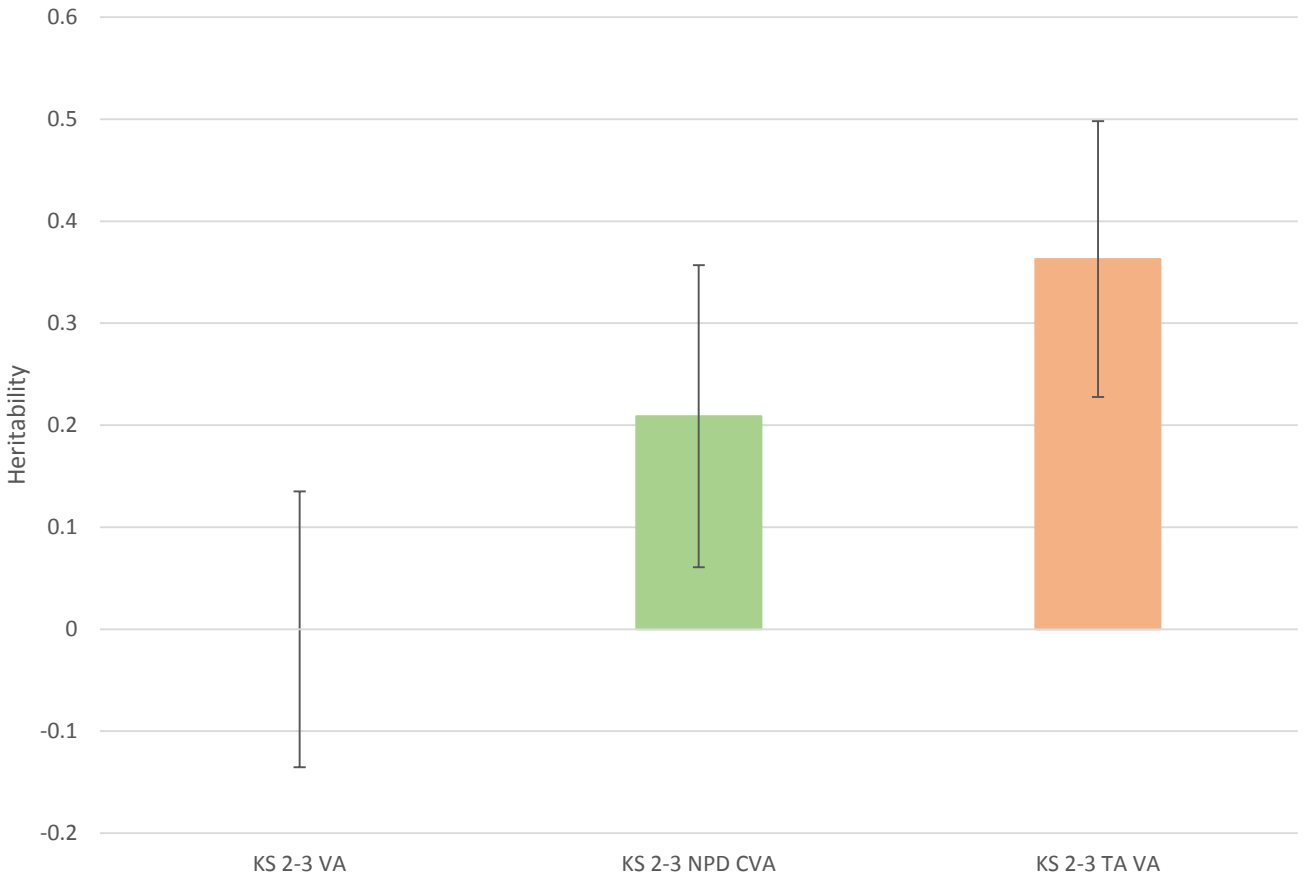
Results: heritability of VA

- Second step was to estimate heritability of VA:



Results: heritability of VA

- Third step was to estimate heritability of teacher assessed VA:



Conclusions

- Mixed evidence that VA measures control for genetic influences on educational attainment
- Raw VA measures have lower heritability than contextual VA measures
- May be due to measurement error, which supports high heritability of teacher assessed VA
- Demonstrates the use of genetic data to social scientists and social science research questions

Thank you for your attention

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References

Leckie G, Goldstein H. 2016. The evolution of school league tables in England 1992-2016: 'contextual value-added', 'expected progress' and 'progress 8'. Bristol Working Papers in Education #02/2016.

Goldstein H, Thomas S (1996) Using examination results as indicators of school and college performance. J Roy Stat Soc A Sta 159: 149–163.

Taylor J, Nguyen AN (2006) An analysis of the value added by secondary schools in England: Is the value added indicator of any value? Oxford B Econ Stat 68: 203–224.J.

Haworth, C.M.A., Asbury, K., Dale, P.S., Plomin, R., 2011. Added value measures in education show genetic as well as environmental influence. PLoS One 6. doi:10.1371/journal.pone.0016006.

Branigan, A.R., Mccallum, K.J., Freese, J., 2013. Variation in the heritability of educational attainment: An international meta-analysis. Soc. Forces 92, 109–140. doi:10.1093/sf/sot076.

Analyses

- We run a series of univariate analyses as follows:

$$y = X\beta + g + \epsilon$$

- where y is the heritability of a phenotype, X is a series of covariates, g is a normally distributed random effect with variance σ_g^2, and ϵ is residual error with variance σ_ϵ^2

- The proportion of total phenotypic variance (genetic variance plus residual variance) that can be attributed to common genetic variation is the heritability of the trait:

$$\frac{\sigma_g^2}{\sigma_g^2 + \sigma_\epsilon^2}$$

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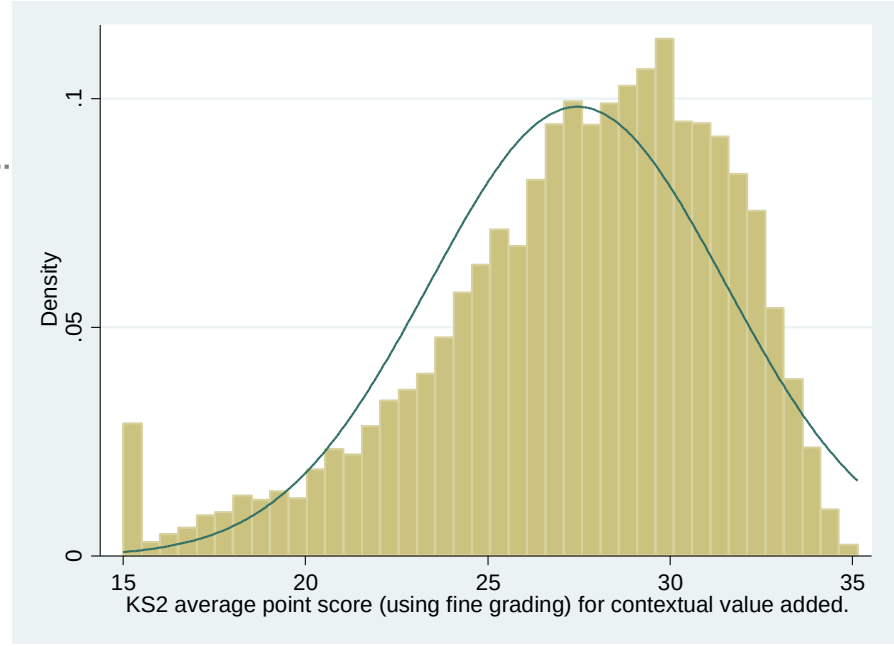
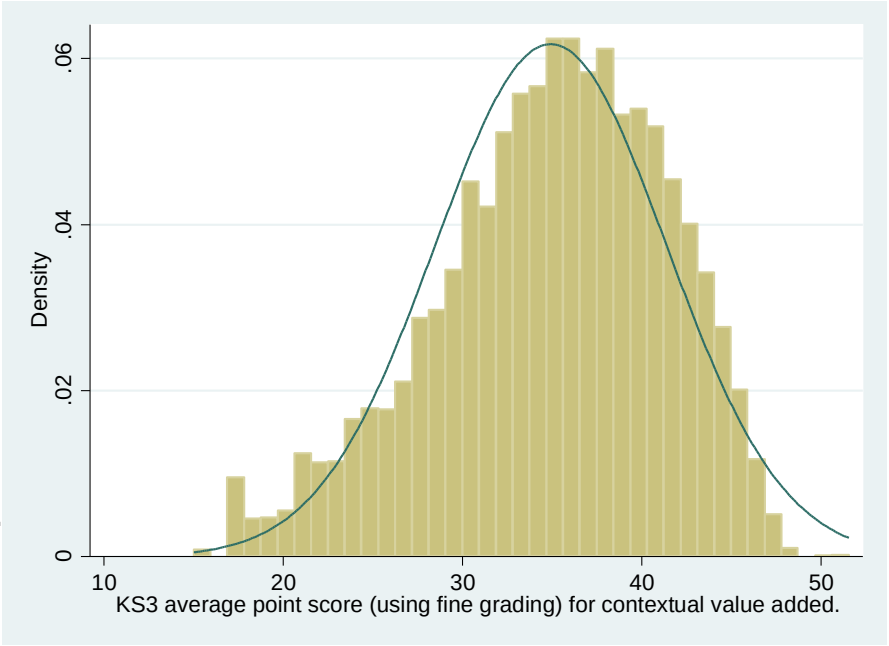
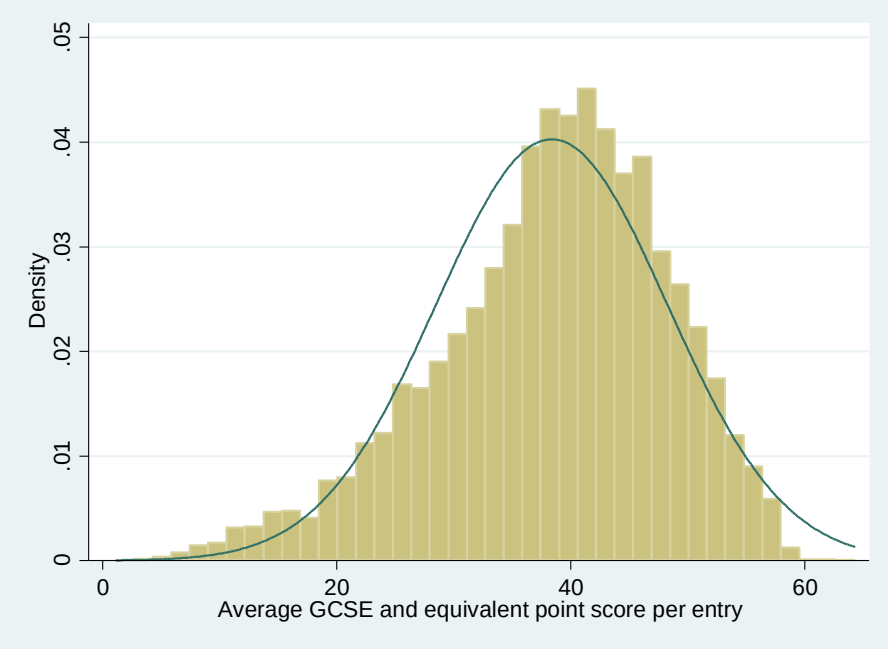
	n	mean	SD	Minimum	Maximum
KS2	6,070	806.875	194.138	245.860	1234.820
KS3	4,971	1338.527	417.615	308.000	2363.900
KS4	6,518	39.894	9.484	4.000	64.269







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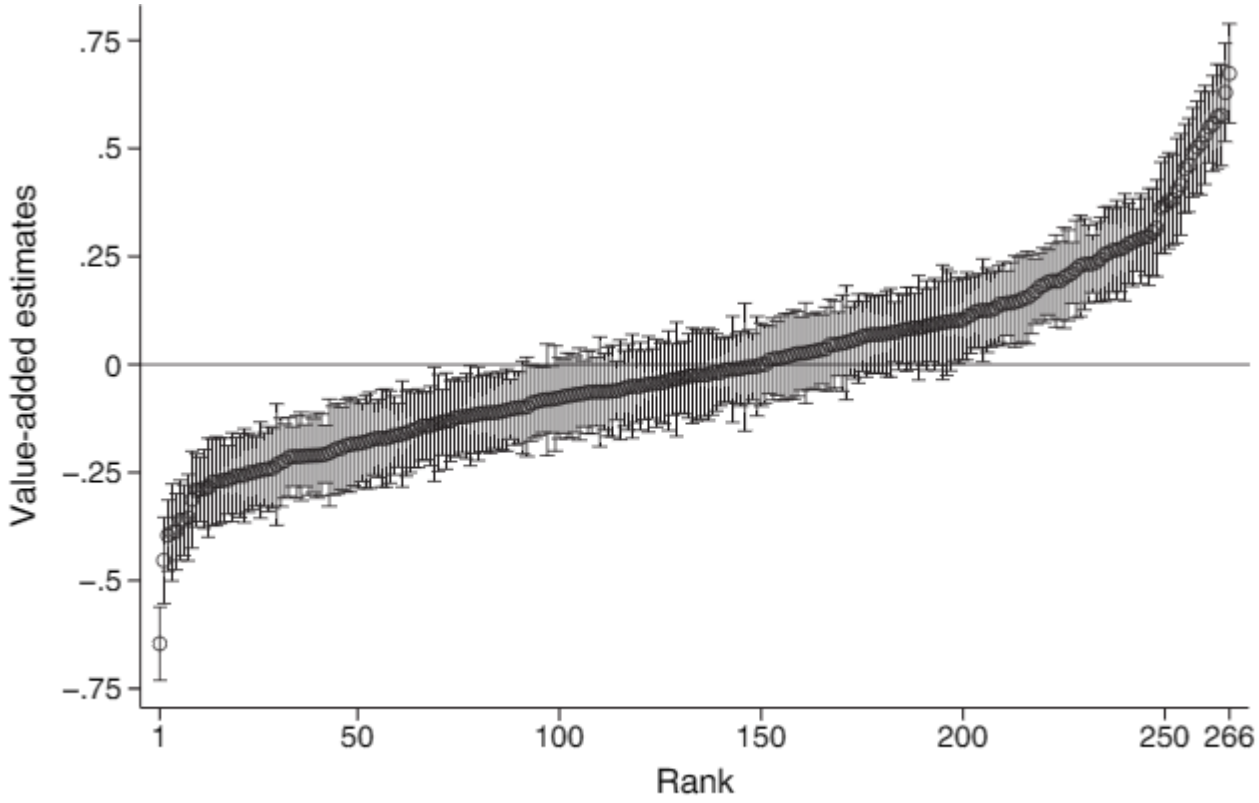

School effects for the 2007 cohort with 95% confidence intervals

Leckie, G., Goldstein, H., 2009. The limitations of using school league tables to inform school choice. J. R. Stat. Soc. Ser. A Stat. Soc. 172, 835–851. doi:10.1111/j.1467-985X.2009.00597.x

Results from population stratification adjusted univariate analyses of attainment

	KS2 points		KS3 points		KS4 points	
	Estimate	SE	Variance	SE	Variance	SE
Genetic variance V(G)	0.452	0.057	0.553	0.070	0.586	0.054
Residual variance	0.504	0.054	0.407	0.067	0.373	0.050
Phenotypic variance V(P)	0.956	0.017	0.960	0.020	0.959	0.017
Heritability (ratio of V(G) to V(P)	0.473	0.058	0.576	0.070	0.611	0.053
Log Likelihood	-2884.42		-2333.41		-3051.38	
	-2920.09		-2368.02		-3122.41	
Likelihood ratio test	71.336		69.226		142.069	
p value	<0.001		<0.001		<0.001	
Sample size	6132		4960		6518	

Results from population stratification adjusted univariate analyses of VA measures

	KS 2-3 value-added		KS 2-4 value-added		KS 3-4 value-added	
	Estimate	SE	Variance	SE	Variance	SE
Genetic variance V(G)	<0.001	0.064	0.071	0.052	0.059	0.066
Residual variance	0.931	0.067	0.835	0.053	0.851	0.067
Phenotypic variance V(P)	0.931	0.019	0.907	0.016	0.909	0.018
Heritability (ratio of V(G) to V(P)	<0.001	0.069	0.079	0.057	0.065	0.072
Log Likelihood	-2265.67		-2736.71		-2217.51	
	-2265.67		-2737.69		-2217.9	
Likelihood ratio test	0		1.979		0.776	
p value	0.500		0.080		0.189	
Sample size	4904		6088		4924	

Results from population stratification adjusted univariate analyses of CVA measures

	KS 2-3 contextual value-added		KS 2-4 contextual value-added		KS 3-4 contextual value-added	
	Estimate	SE	Variance	SE	Variance	SE
Genetic variance V(G)	0.200	0.073	0.143	0.053	0.075	0.063
Residual variance	0.757	0.073	0.762	0.054	0.810	0.065
Phenotypic variance V(P)	0.957	0.020	0.905	0.017	0.885	0.018
Heritability (ratio of V(G) to V(P)	0.209	0.076	0.158	0.059	0.085	0.072
Log Likelihood	-2182.178		-2700.32		-2147.2	
	-2186.222		-2704.01		-2147.91	
Likelihood ratio test	8.087		7.368		1.403	
p value	0.002		0.003		0.118	
Sample size	4600		6028		4914	

Results from population stratification adjusted univariate analyses of teacher assessed VA measures

	KS 2-3 teacher assessed value-added	
	Estimate	SE
Genetic variance V(G)	0.351	0.068
Residual variance	0.616	0.066
Phenotypic variance V(P)	0.967	0.019
Heritability (ratio of V(G) to V(P)	0.363	0.069
Log Likelihood	-2425.38	
	-2440.34	
Likelihood ratio test	29.926	
p value	2.24E-08	
Sample size	5070	