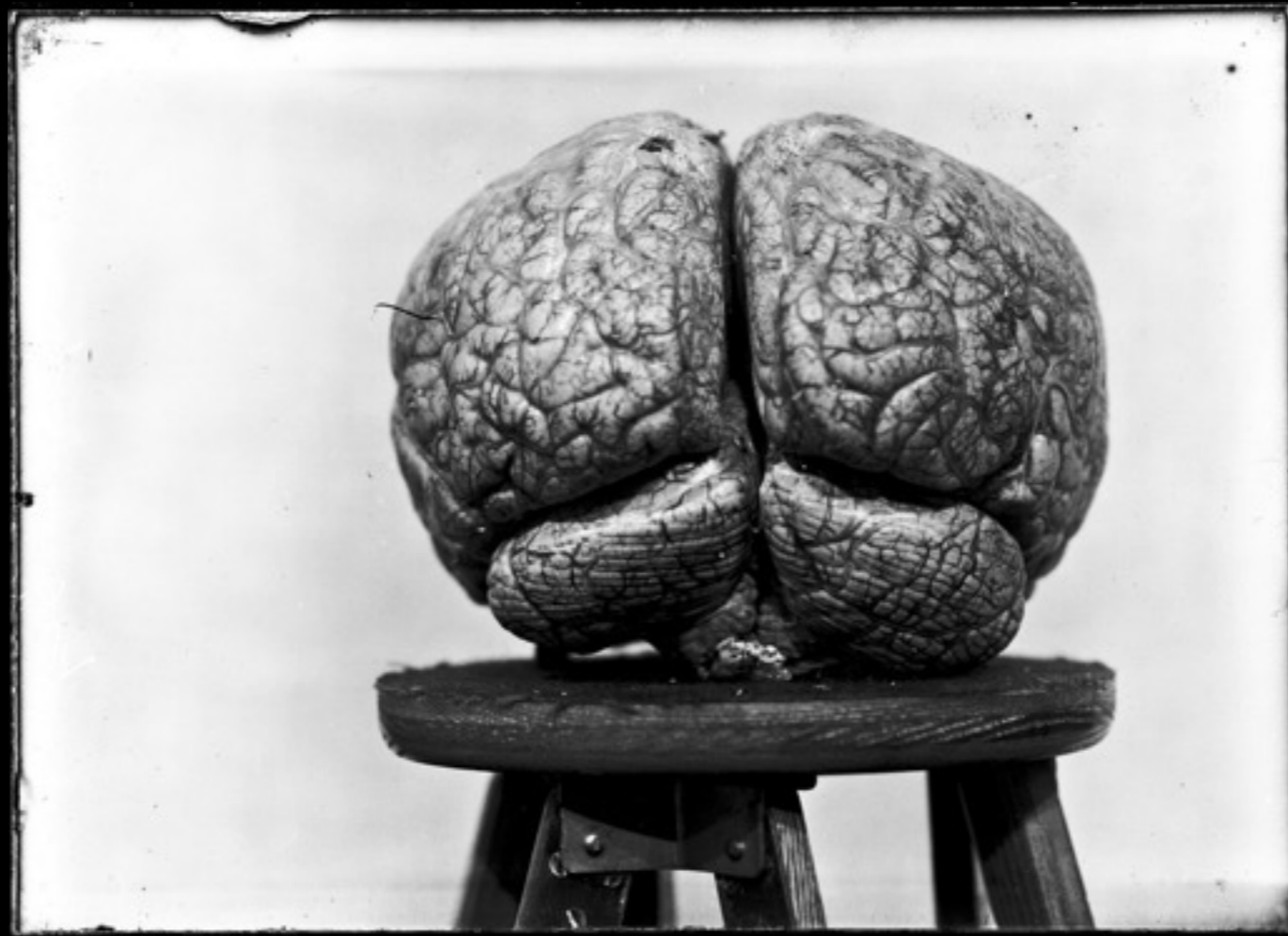
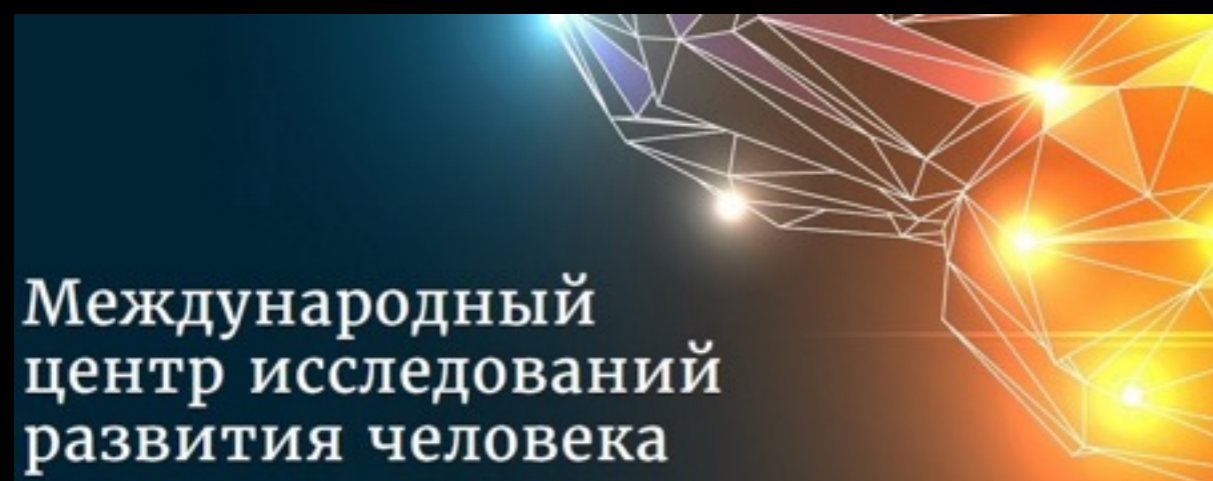


Генетика когнитивных функций





Количественная vs. молекулярная генетика

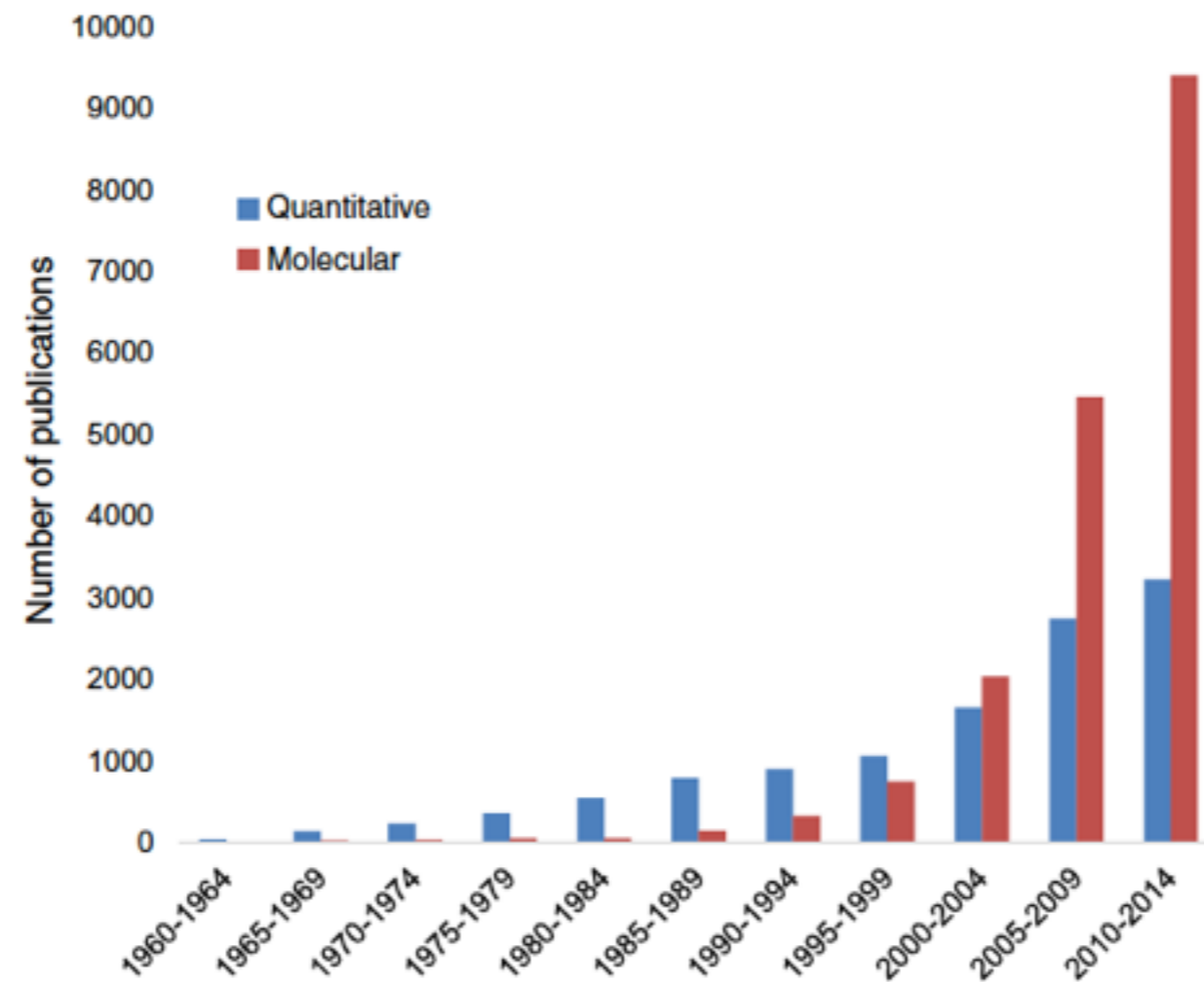


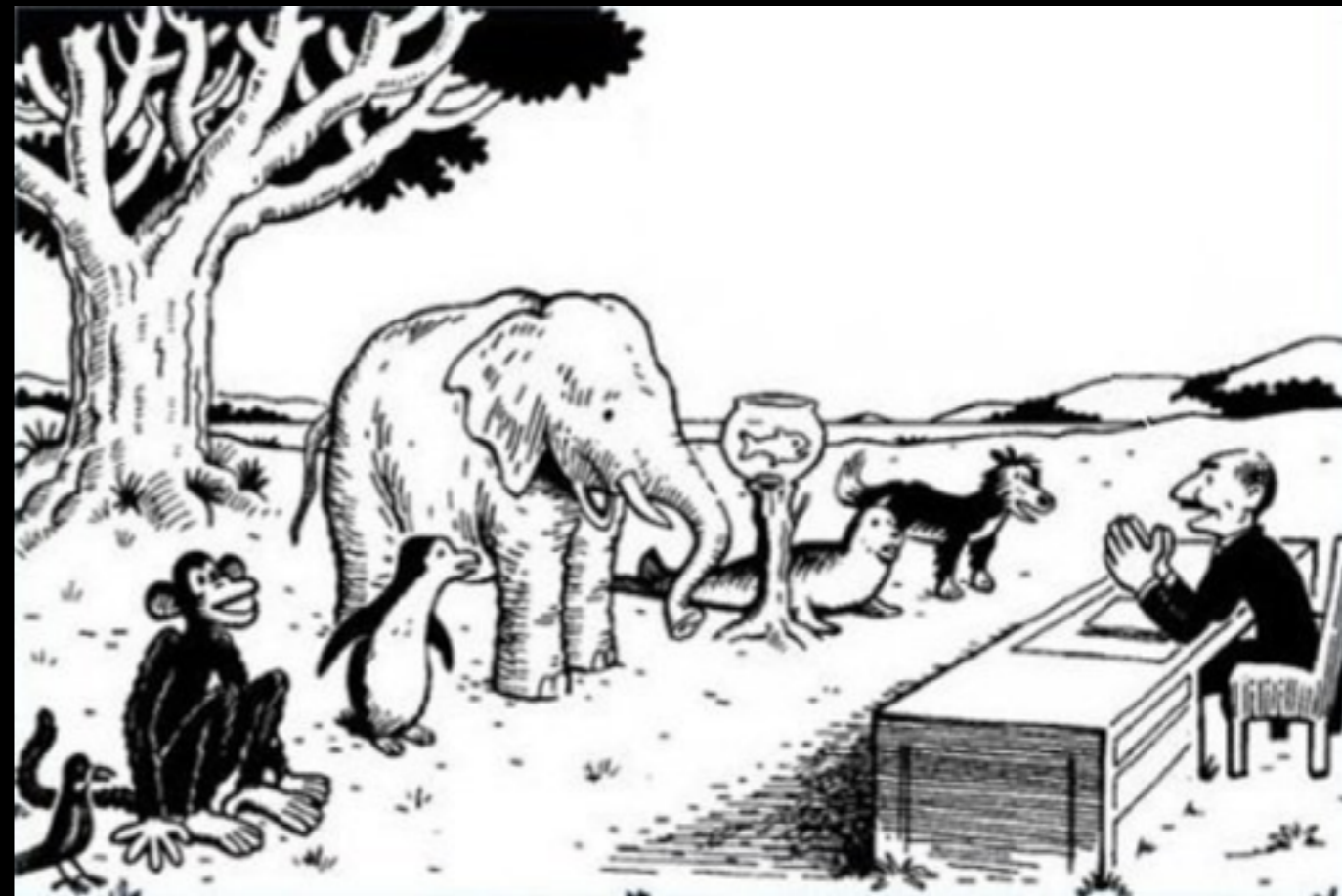
Fig. 2 Number of human behavioral genetic papers by lustrum since 1960, comparing quantitative and molecular genetic research

Спорный термин

Мышление - процесс
решения задач

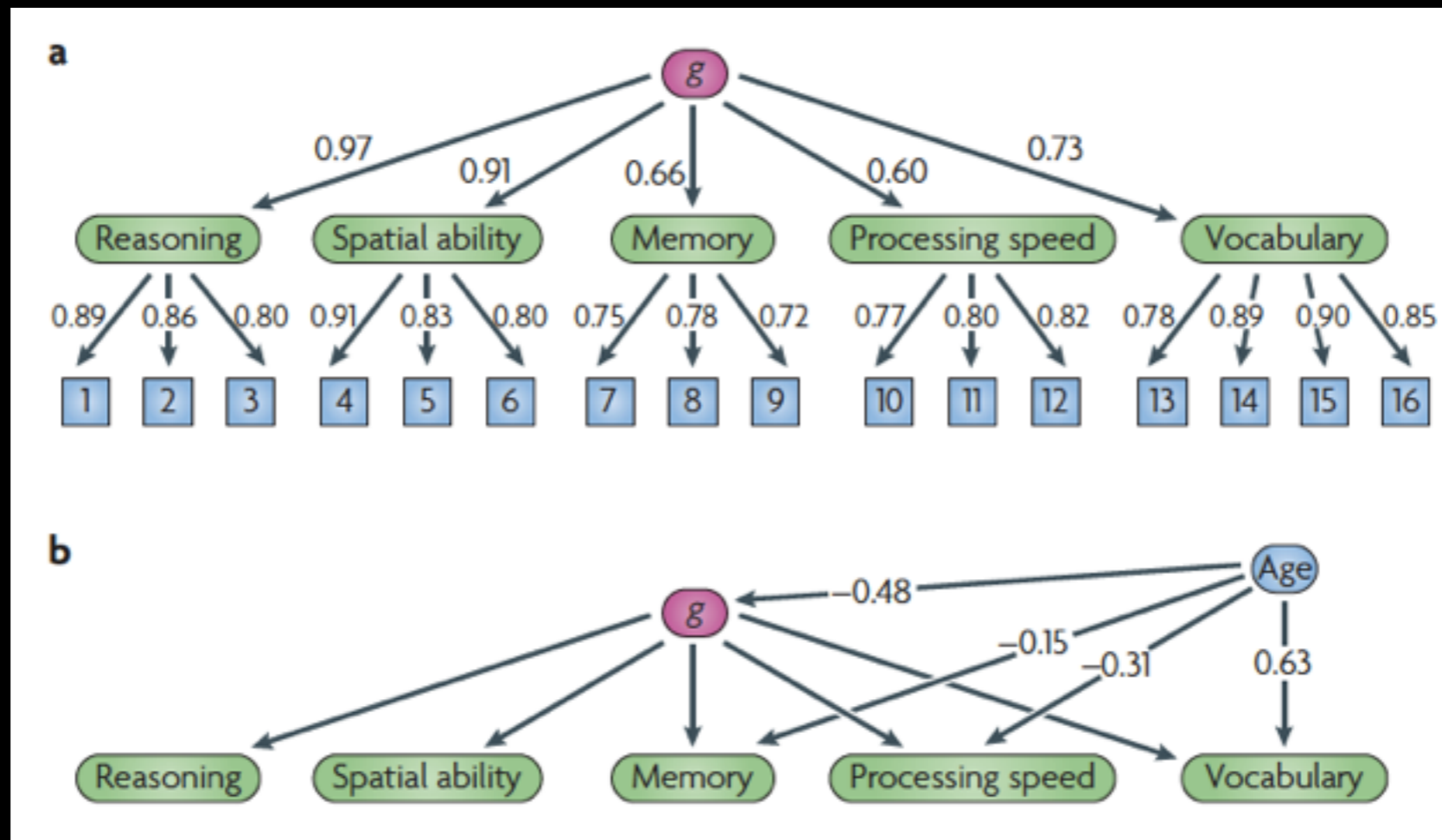
Интеллект - g factor

Коэффициент интеллекта
- то, что меряют тесты
интеллекта



У меня нет предвзятости ни к одному из вас, поэтому для всех будет
одинаковое задание. Вам нужно залезть на дерево

g factor - общие и когнитивные способности

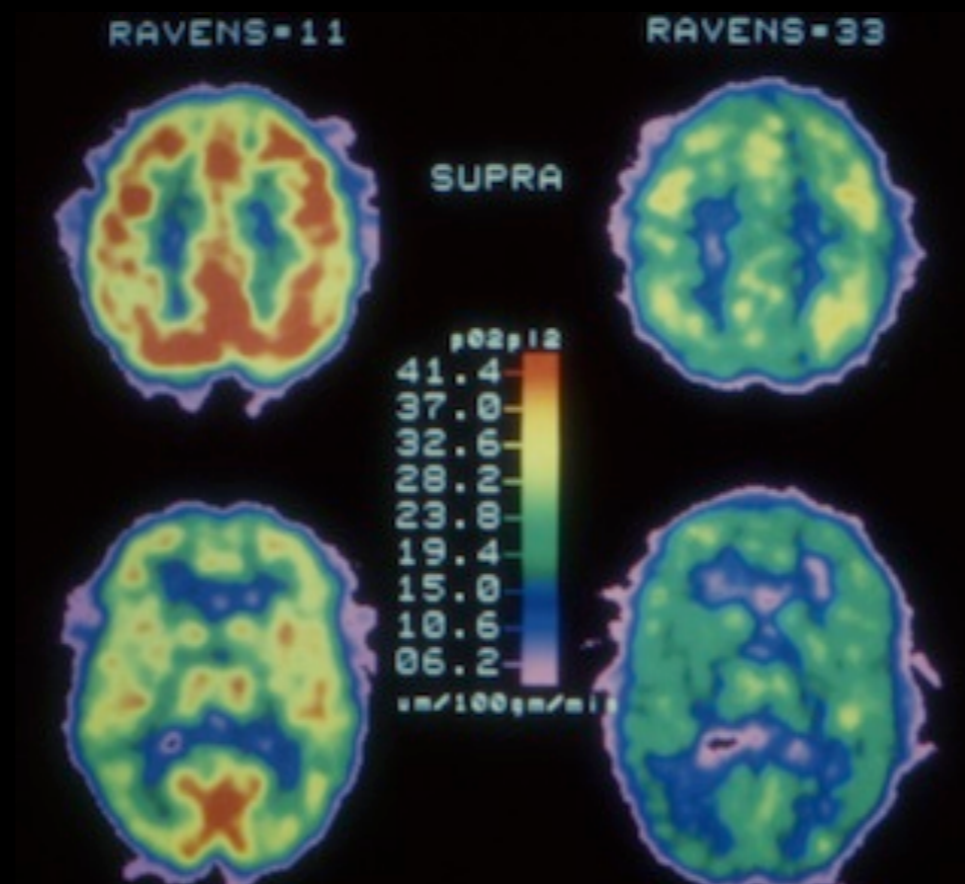


Intelligence - the ability to reason, plan, solve problems, think abstractly, comprehend complex ideas, learn quickly, and learn from experience'

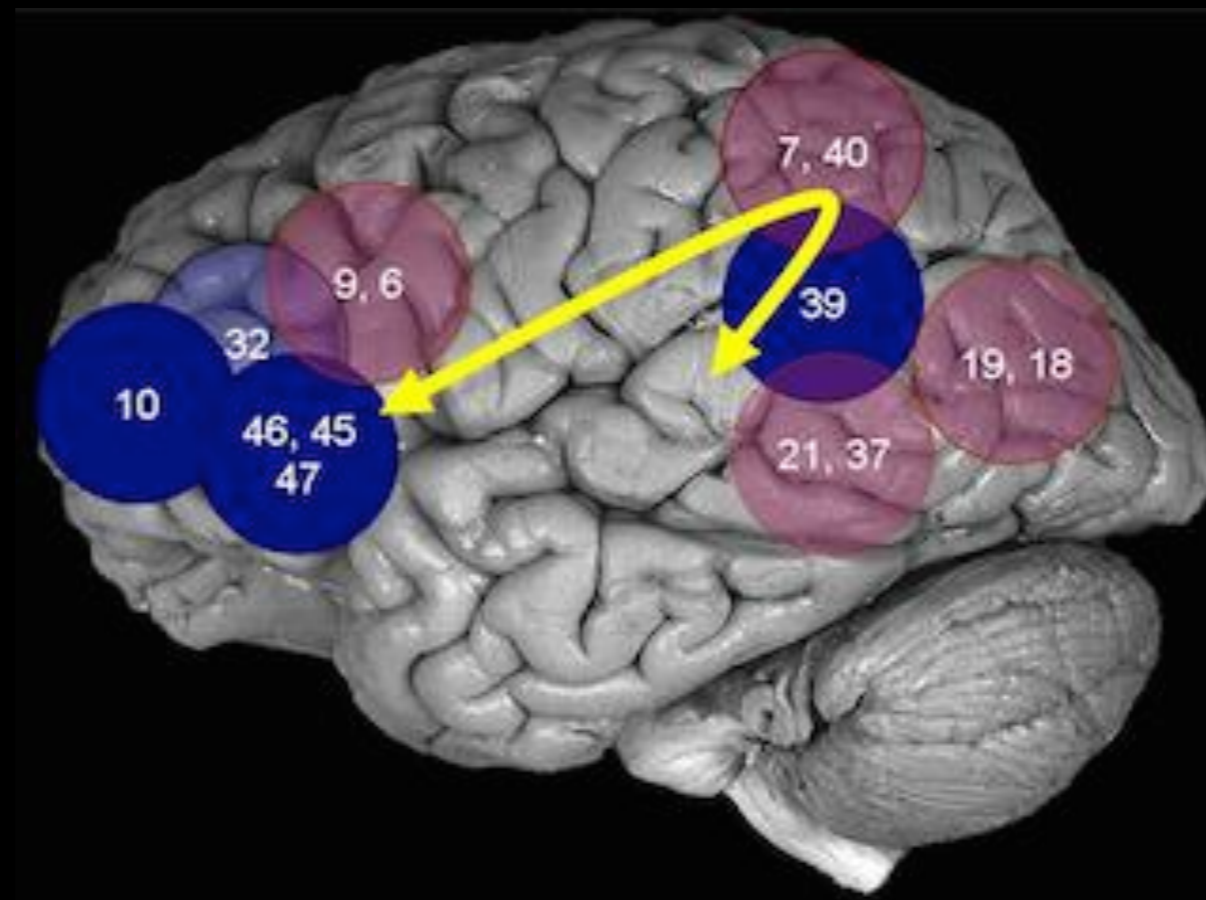
«IQ can reliably predict all kinds of success – academic, professional, social, marital, income, and even physical longevity (it turns out that people with higher IQs live longer). It is not overstating the case to say that IQ is the best single behavioral predictor of future success that we currently have.»

Robert Plomin, King's College, London

Интеллект и мозг: гипотеза эффективности нейронных связей

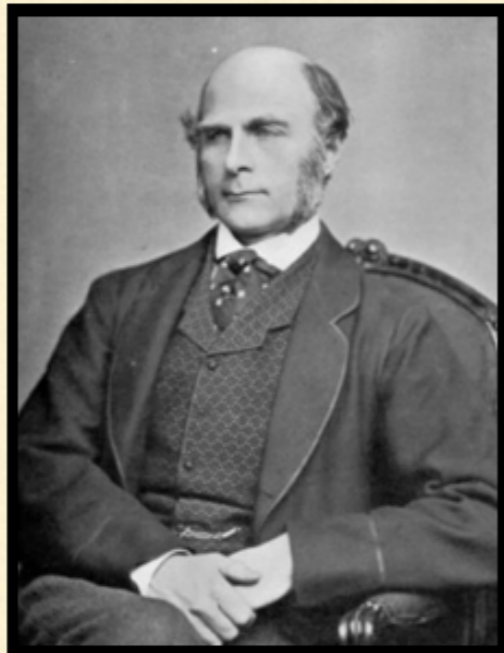


Интеллект и мозг: гипотеза теменной-фронтальной интеграции



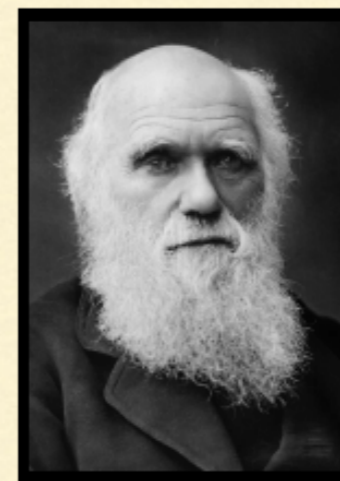
Сложные признаки и количественная генетика

НЕМНОГО ИСТОРИИ



Френсис Гальтон
1822-1911

- Генеалогический метод (изучение родословных) и гениальность
- Основы поведенческой генетики
- Статистические процедуры
- Евгеника



Его не менее знаменитый родственник

Сложные признаки и количественная генетика

Сын	Ты	Отец	Дед	Прадед
50%	Гений	30%	15%	3%

Близнецовый метод



Близнецовый метод

Мз



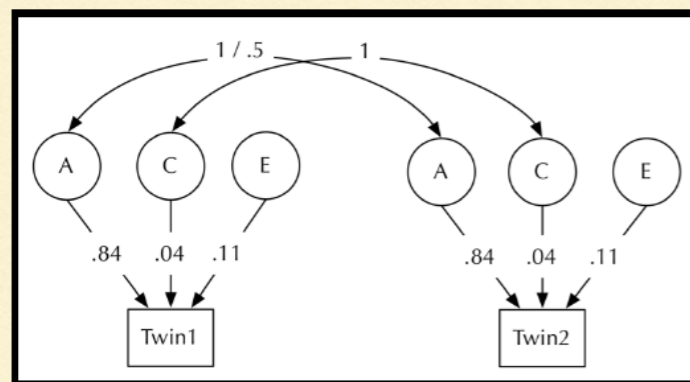
Дз



Первый тест на определение
зиготности - 20-е года XX века

Близнецовый метод

Близнецовые исследования



Общая среда
Индивидуальная среда
Общие гены

МЗ vs. ДЗ

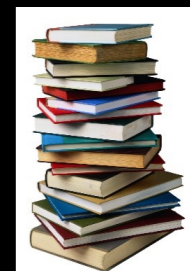
- В каждой популяции существует определённая фенотипическая дисперсия признака.
- Мы можем условно разделить её на три компонента:
 - h – наследуемость. Разница в генотипах.
 - c – общая среда. Разница в семейной среде.
 - e – индивидуальная среда + ошибка измерения.



=

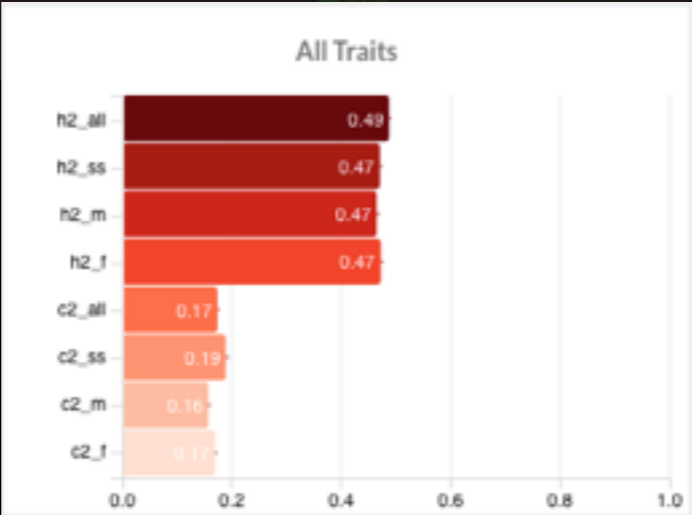
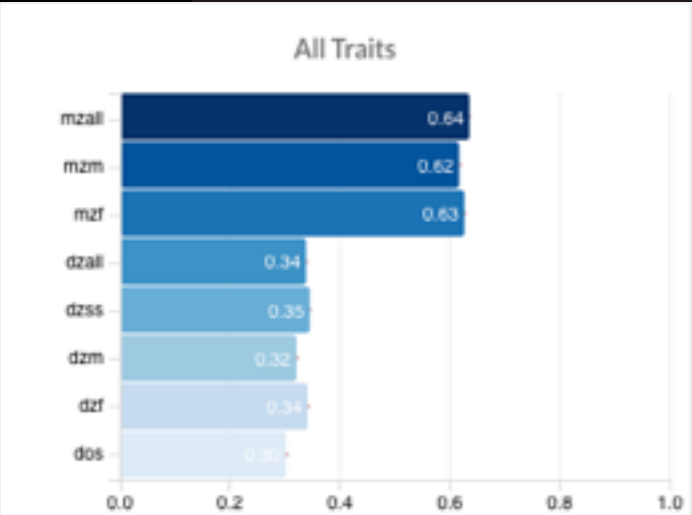
h

(



)

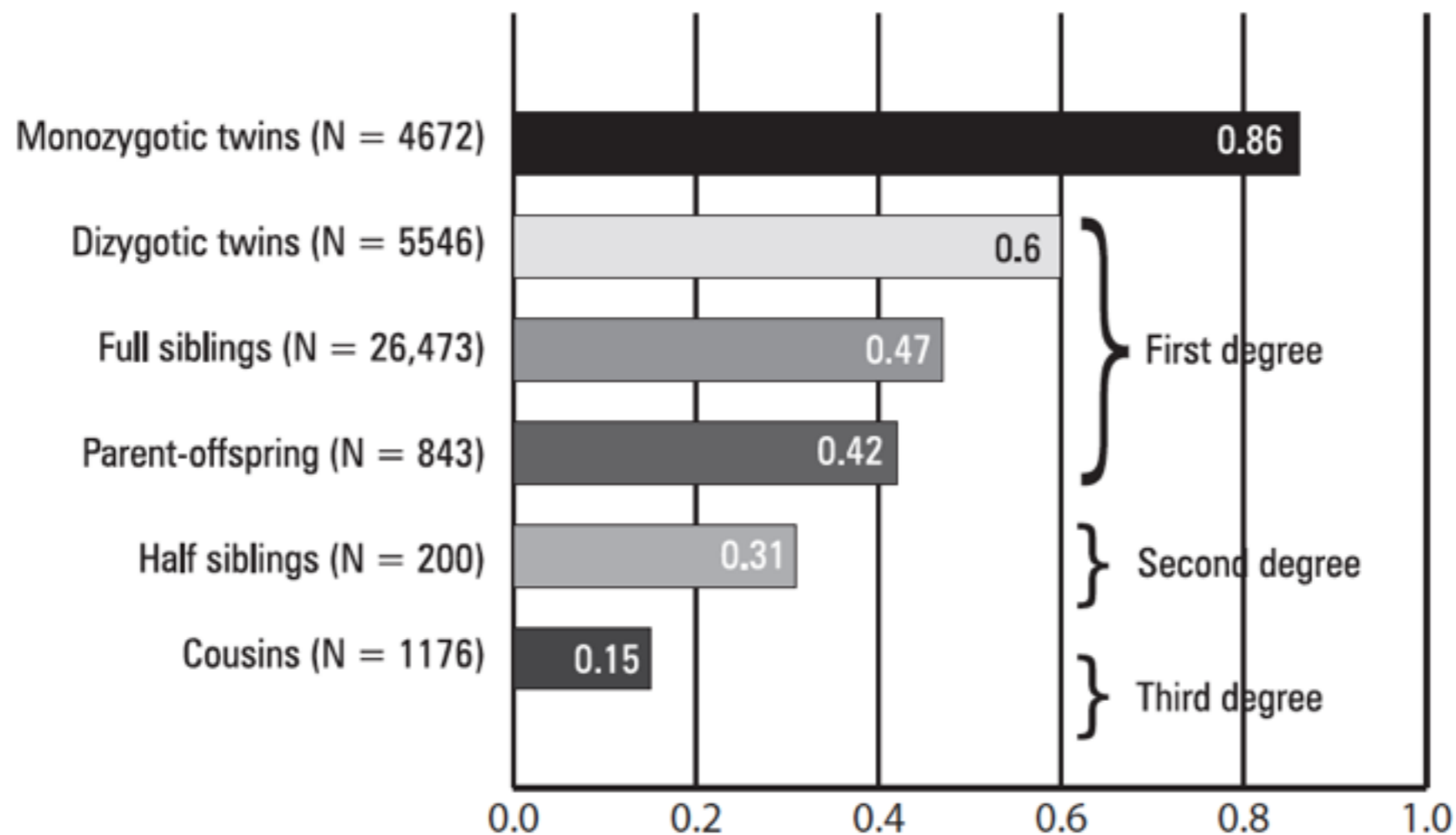
Близнецовый метод



Генетика интеллекта: наследуемость

Figure 2.

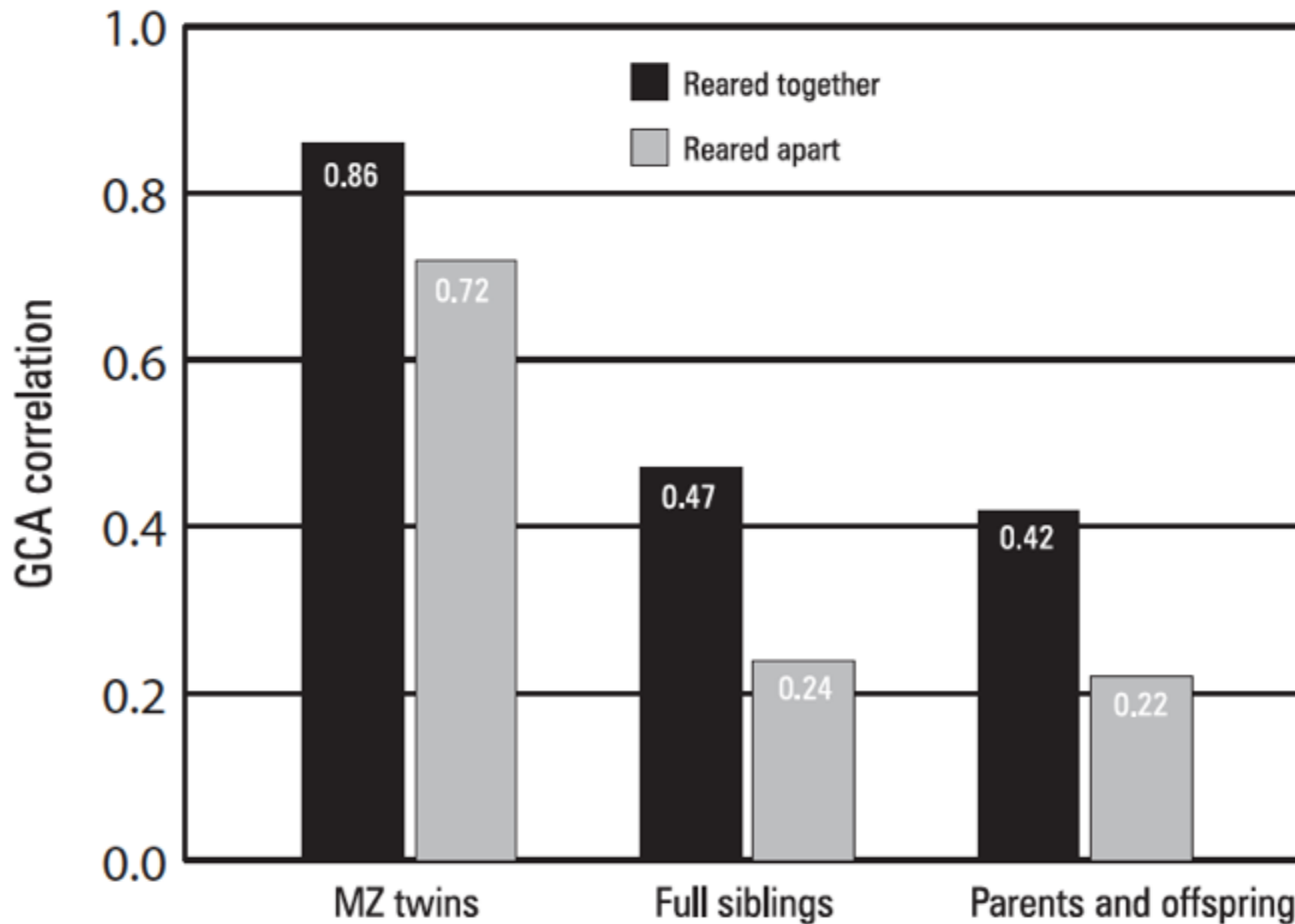
Average correlation for general cognitive ability among reared-together relatives as a function of degree of genetic relatedness



(T. Bouchard and M. McGue, "Familial Studies of Intelligence: A Review," *Science* 212 [1981]: 1055-59).

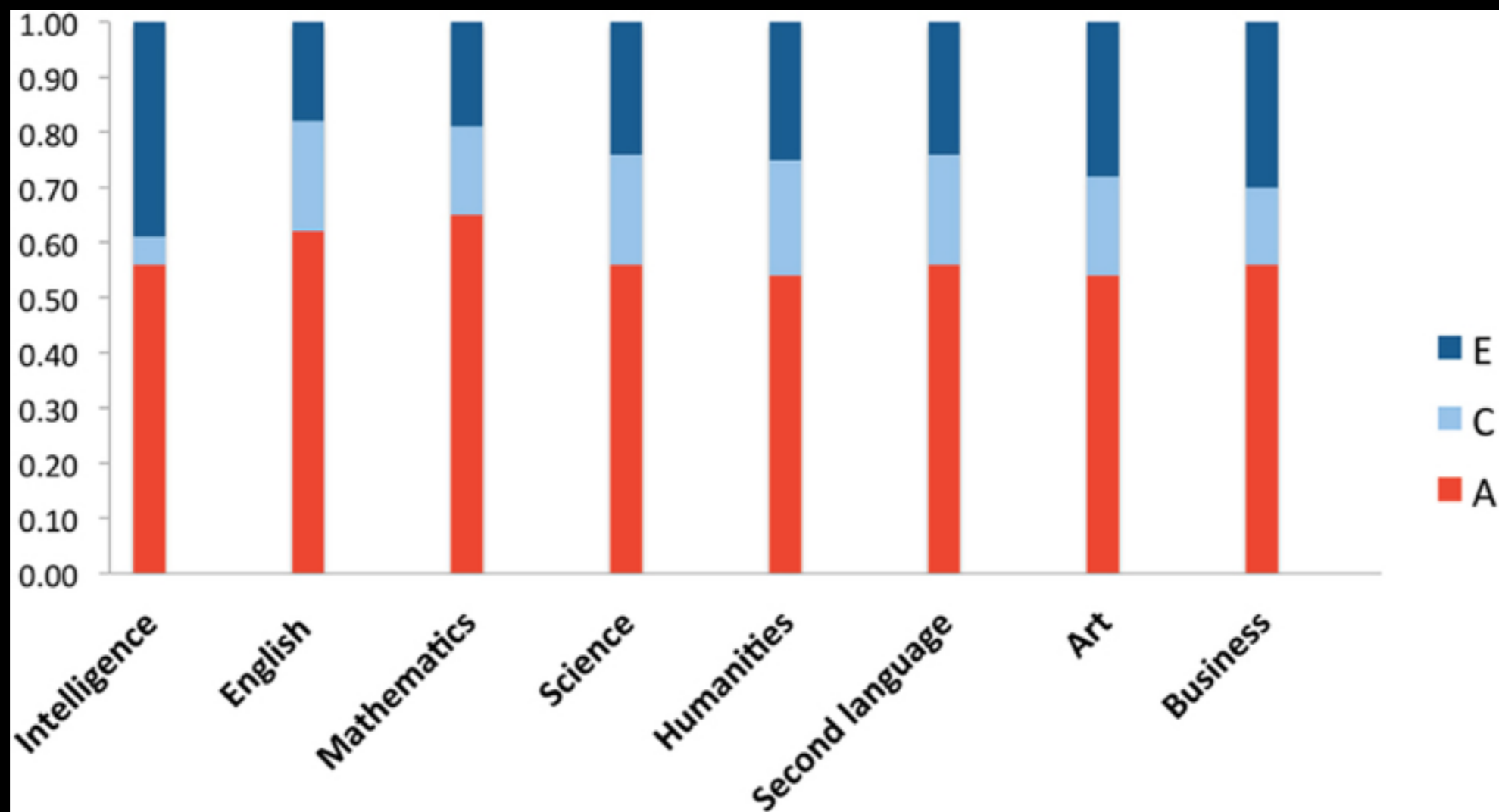
Генетика интеллекта: наследуемость

Average correlation for general cognitive ability among reared-together versus reared-apart relatives

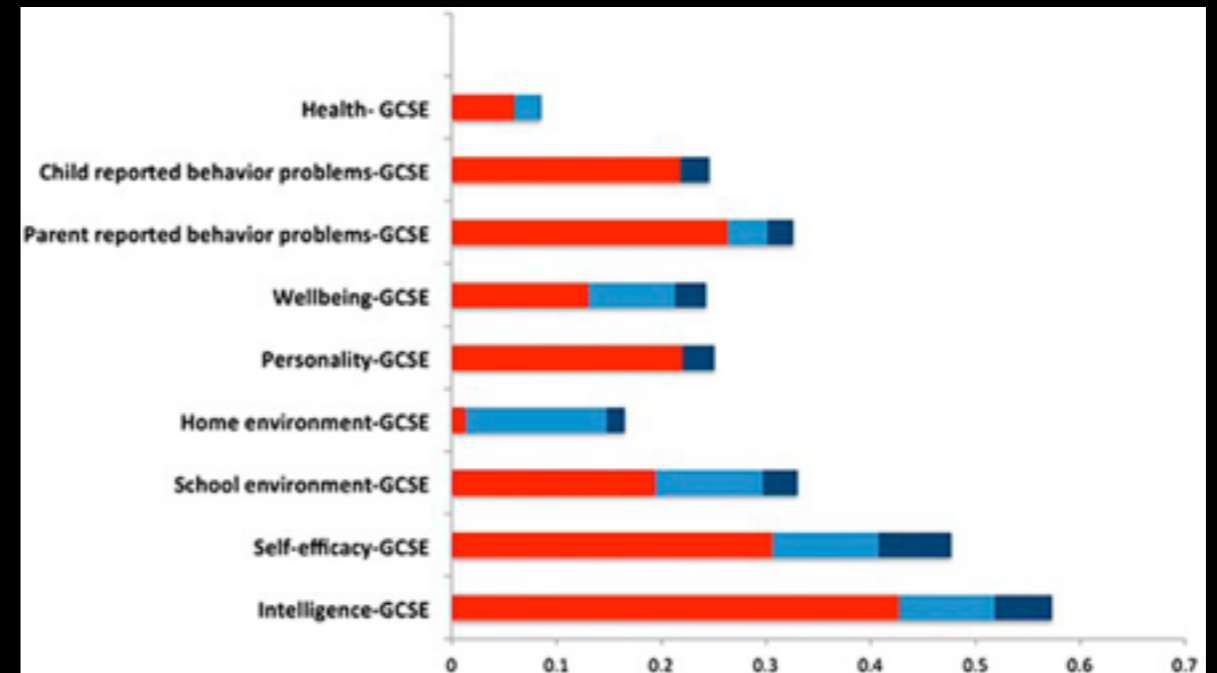
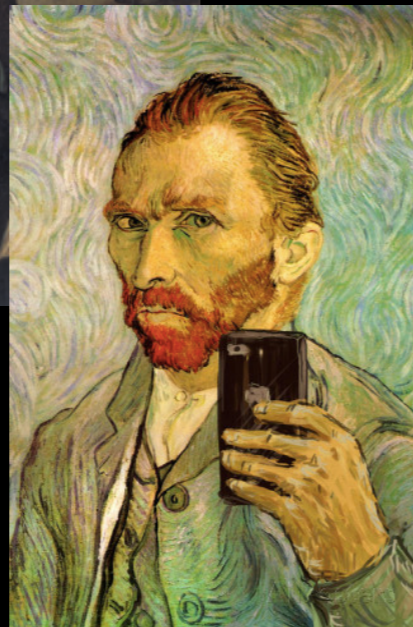
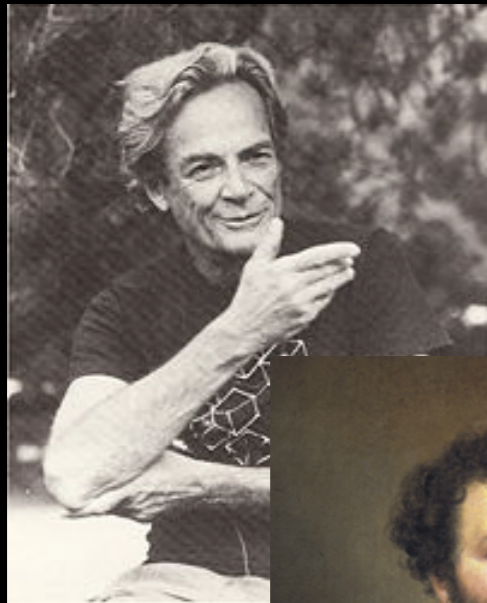


(T. Bouchard and M. McGue, "Familial Studies of Intelligence: A Review," *Science* 212 [1981]: 1055-59).

Генетика интеллекта: наследуемость



Гены гениальности и плеiotропия



Генетические корреляции

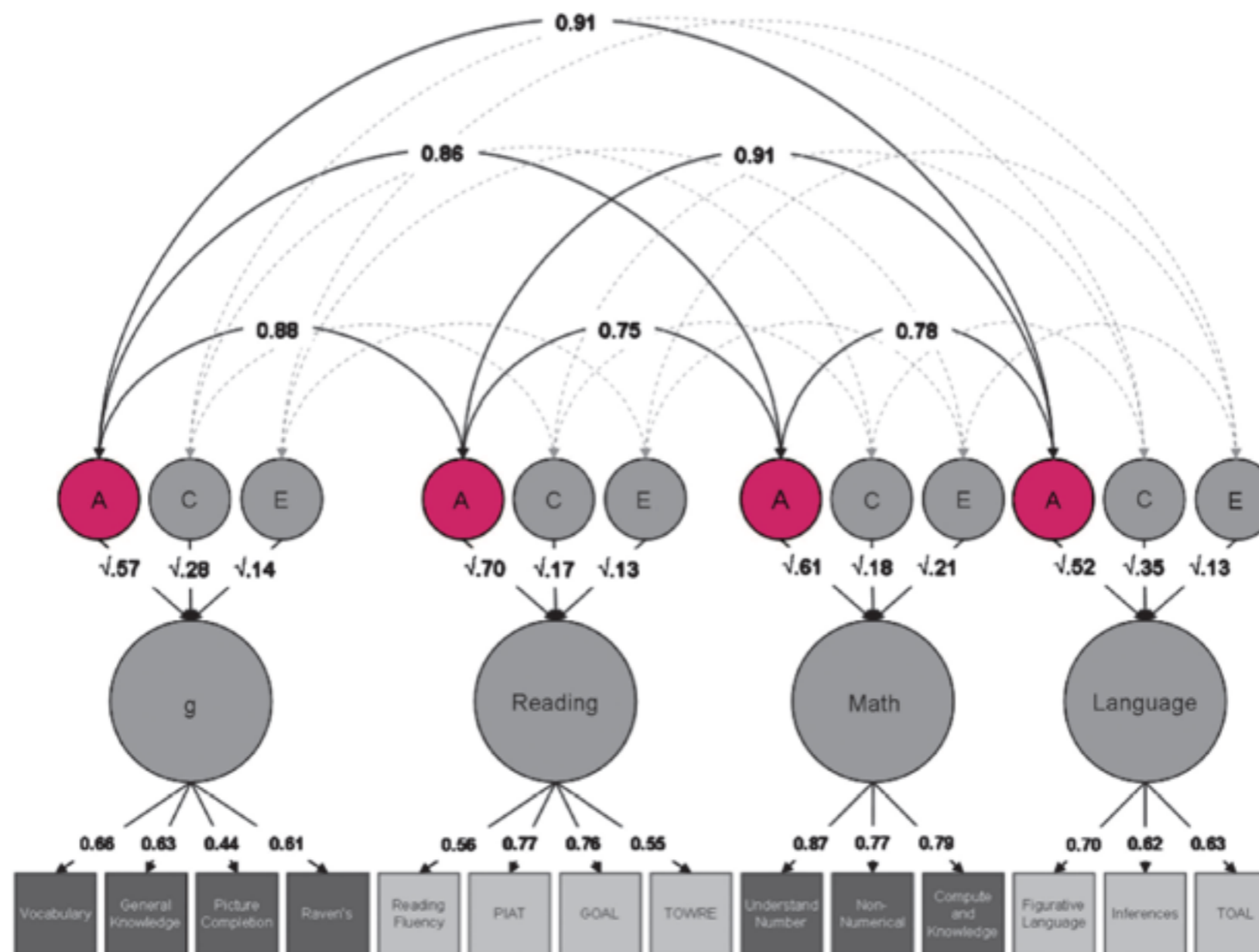
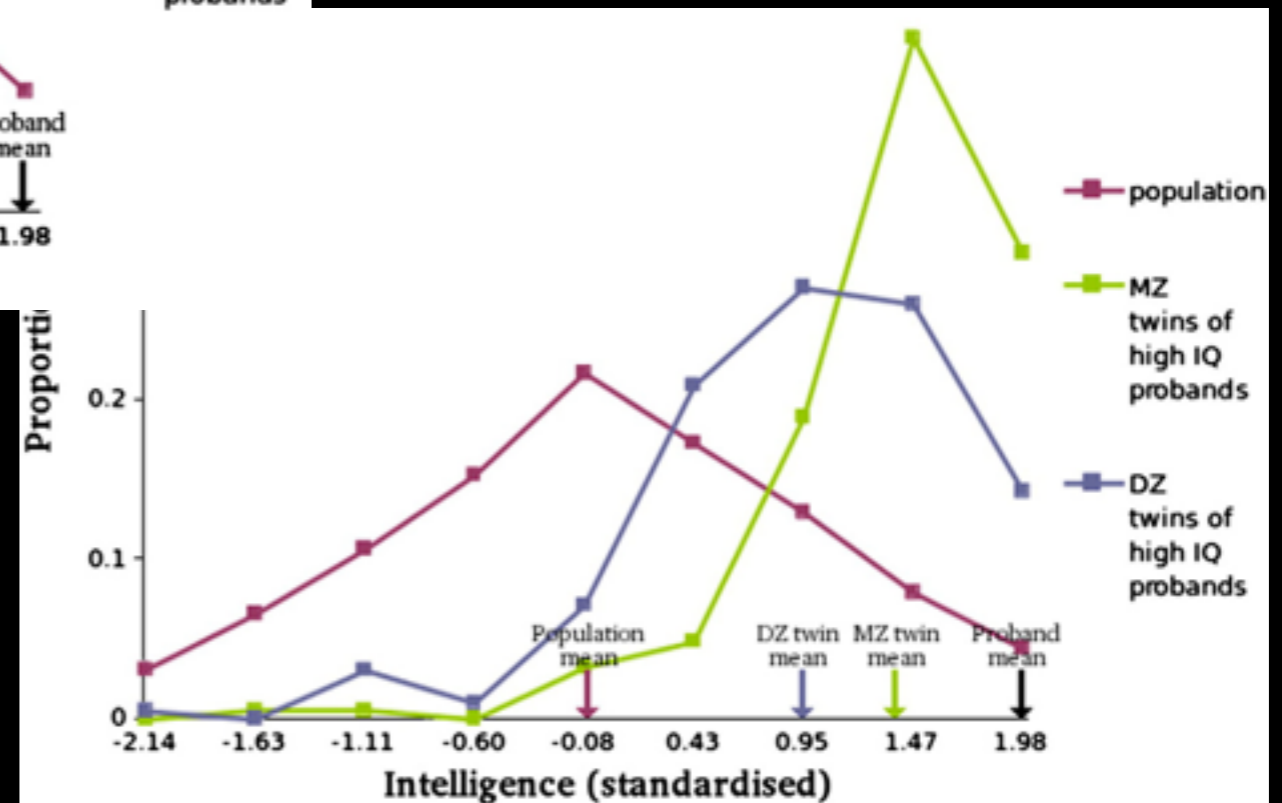
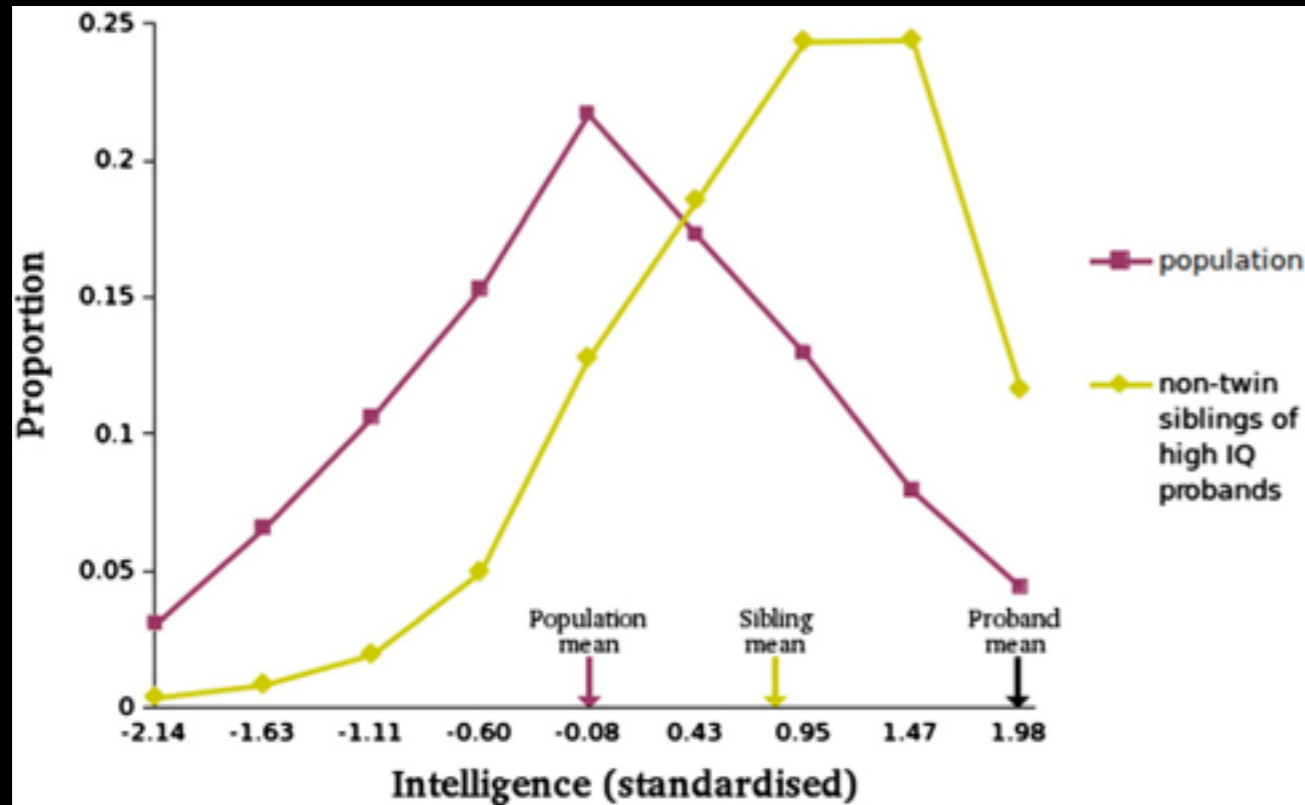


Figure 2. Multivariate (common pathway) genetic analysis in which each latent variable is indexed by three or four tests and the twin method is used to estimate additive genetic (A), shared (common) environmental (C) and nonshared environmental (E) contributions to the variance and covariance among the latent variables. Squares represent measured traits; circles represent latent factors. The lower tier of arrows represents factor loadings; the second tier represents genetic and environmental path coefficients. The curved arrows at the top represent correlations between genetic and environmental latent factors, although only the genetic correlations are shown here. (From Davis *et al.*⁶²).

Continuity Hypothesis



Низкий интеллект

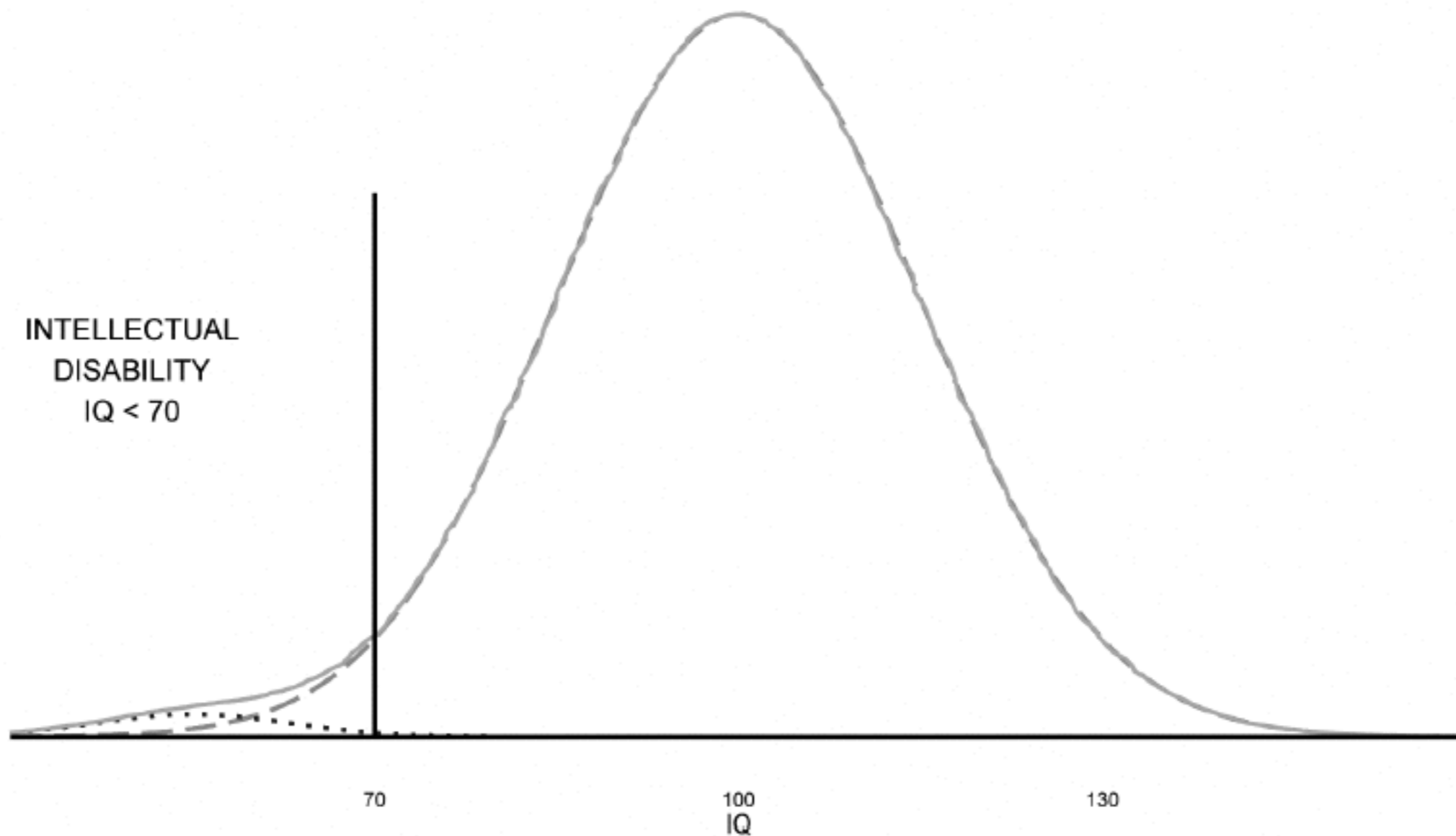


Figure 1.
Two-group model of intellectual disability

Молекулярные исследования

Looking at genes – ~95% of heritability is missing

NEWS FEATURE PERSONAL GENOMES

NATURE | Vol 456 | November 2008



The case of the missing heritability

When scientists opened up the human genome, they expected to find the genetic components of common traits and diseases. But they were nowhere to be seen. **Brendan Maher** shines a light on six places where the missing loot could be stashed away.

Полигенный индекс

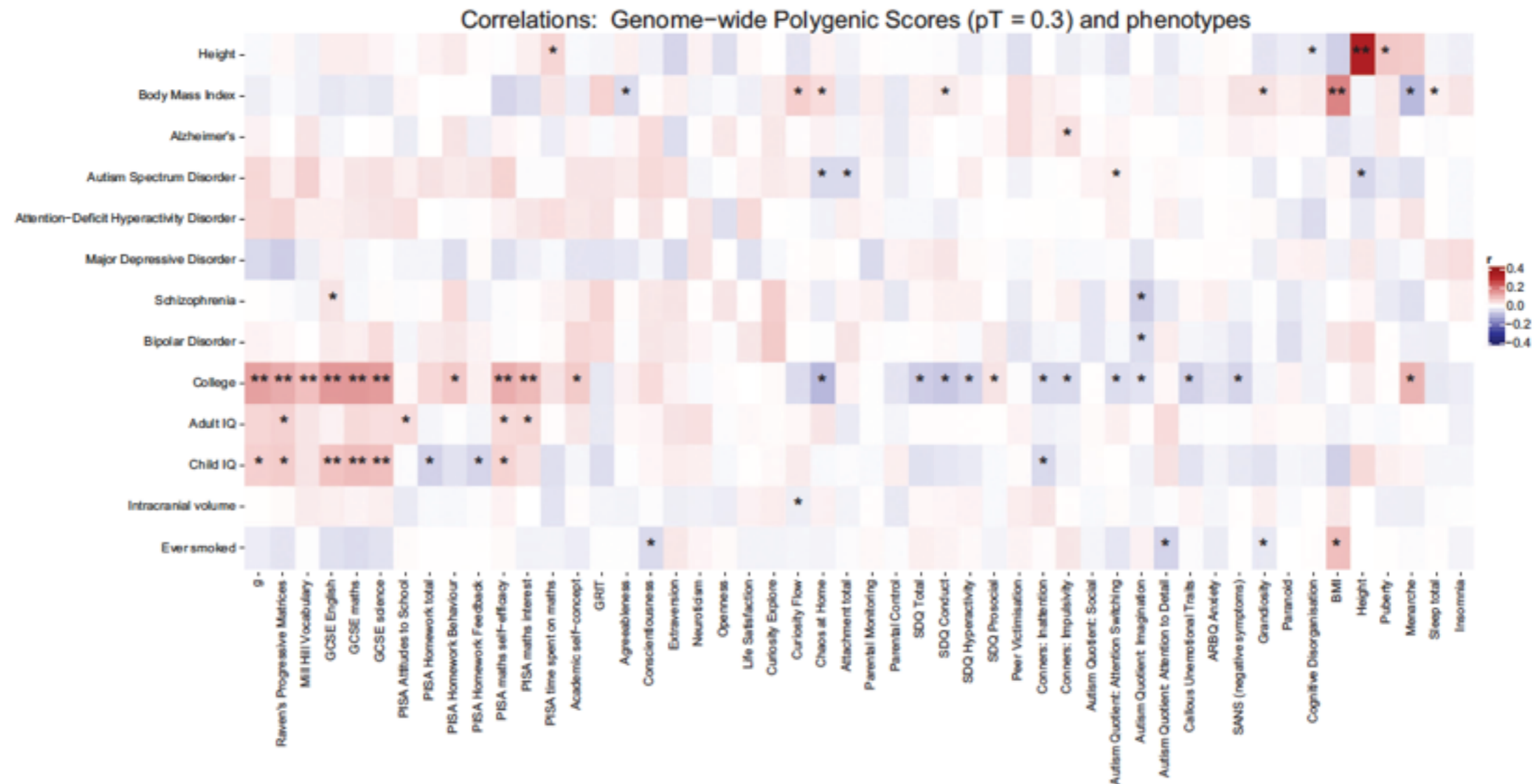


Figure 1. Correlations between 13 genome-wide polygenic scores and 50 traits from the behavioral phenome. These results are based on GPS constructed using a GWAS P -value threshold (P_T) = 0.30; results for P_T = 0.10 and 0.05 (Supplementary Figures 1a and b and Supplementary Table 3). P -values that pass Nyholt-Sidak correction (see Supplementary Methods 1) are indicated with two asterisks, whereas those reaching nominal significance (thus suggestive evidence) are shown with a single asterisk.

Полигенный индекс

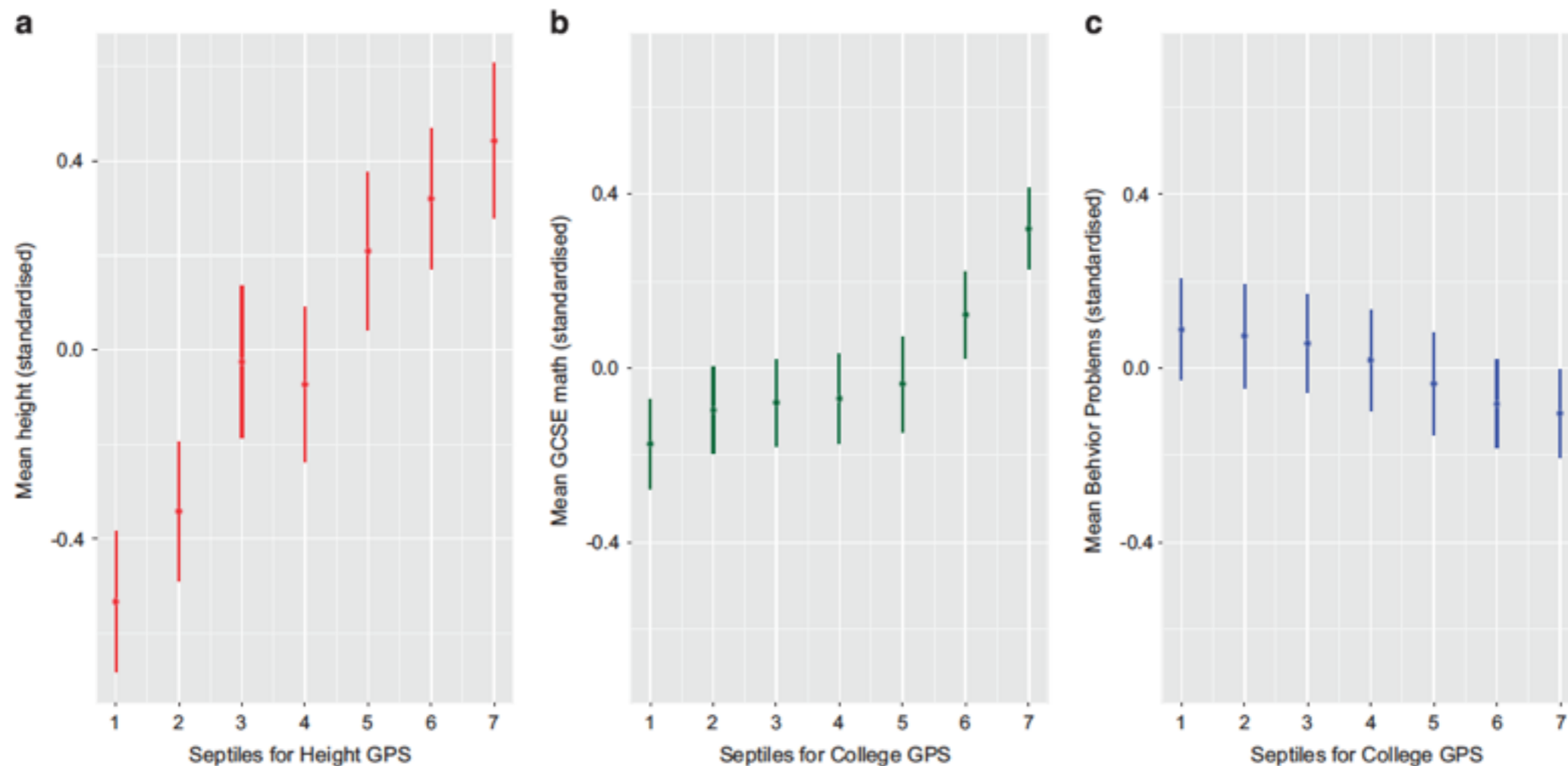
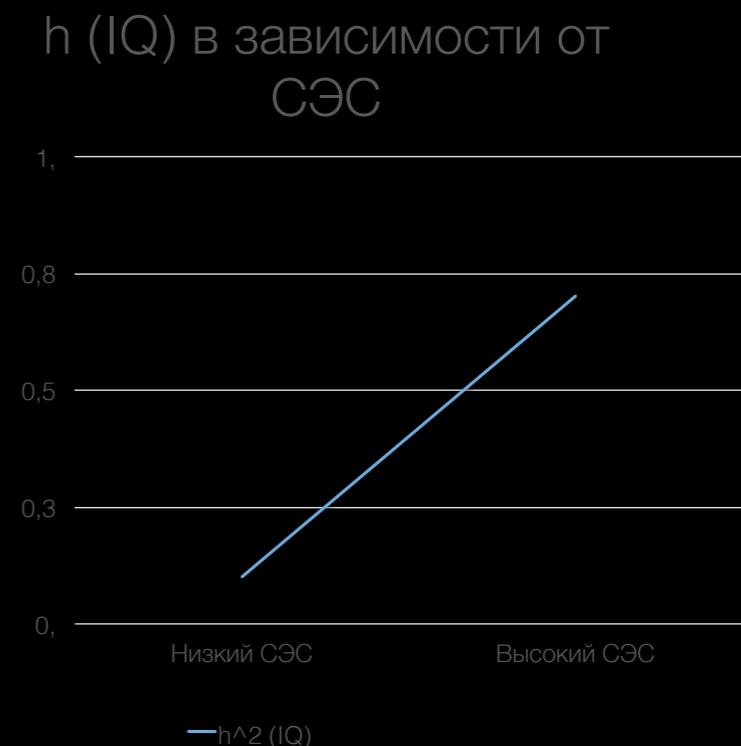


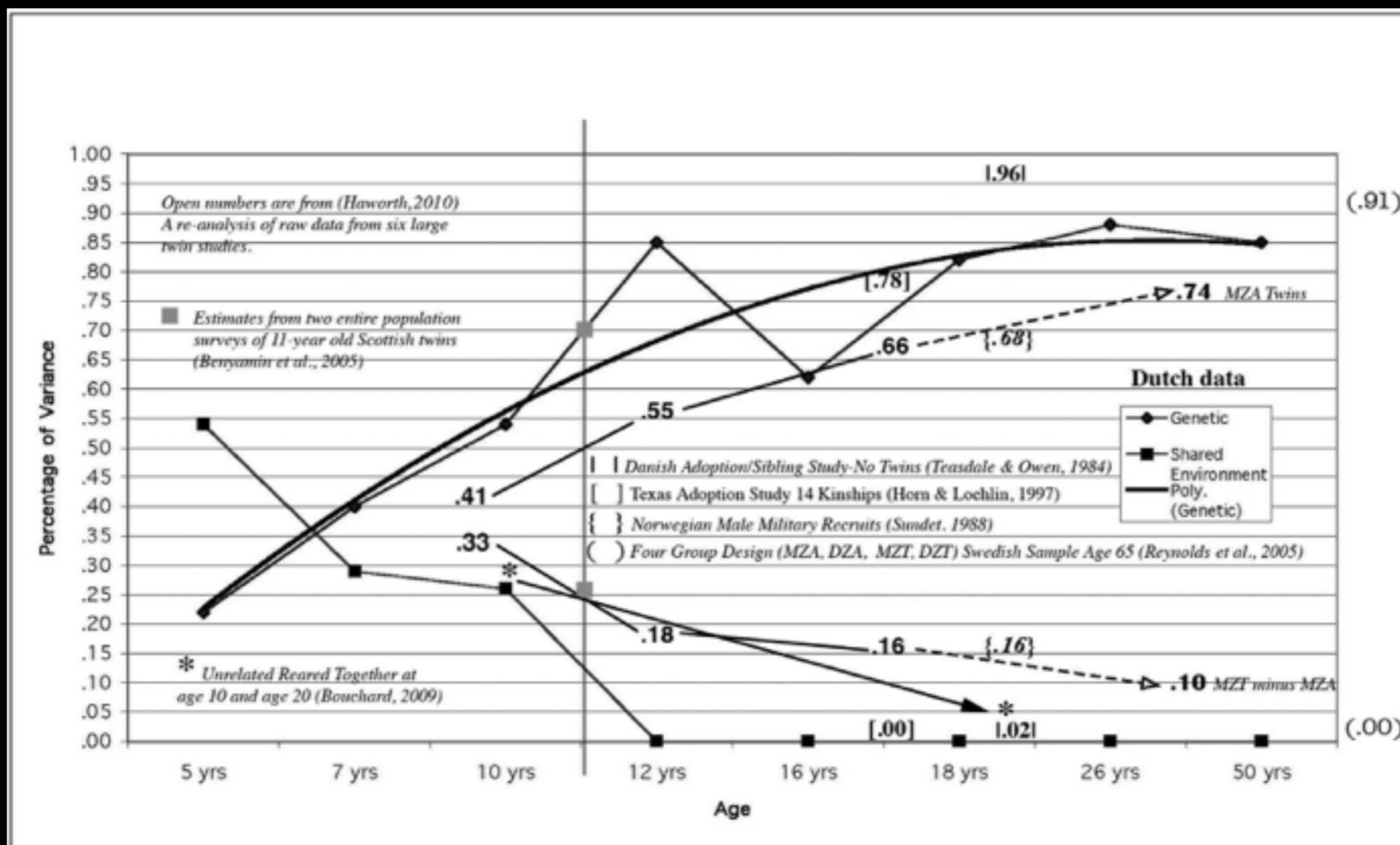
Figure 2. (a) Mean for height at age 16 by adult Height genome-wide polygenic score (GPS) septicile. The threshold for selecting trait-associated alleles was $P_T < 0.30$. The GPS were converted to quantiles (1 = lowest, 7 = highest GPS). Mean phenotypic values and 95% confidence intervals (CIs) for the quantile groups (bars) were estimated using general linear regression with ancestrally informative principal components, sex and age of measurement as covariates. (b) Mean for children's mathematics educational achievement at age 16 (compulsory subject on the General Certificate of Secondary Examination (GCSE), see Materials and Methods for details) by College GPS septicile. The threshold for selecting trait-associated alleles was $P_T < 0.30$. The GPS were converted to quantiles (1 = lowest, 7 = highest GPS). Mean phenotypic values and 95% CI for the quantile groups (bars) were estimated using general linear regression with ancestrally informative principal components, sex and age of measurement as covariates. (c) Mean for total parent-reported behavior problems at age 16 by adult College GPS septicile. The threshold for selecting trait-associated alleles was $P_T < 0.30$ (the best-fit GPS as estimated by PRSice software, see Materials and Methods). The GPS were converted to quantiles (1 = lowest, 7 = highest GPS). Mean phenotypic values and 95% CI for the quantile groups (bars) were estimated using general linear regression with ancestrally informative principal components, sex and age of measurement as covariates.

Генетика интеллекта: влияние

- Вариабельность факторов среды, влияющих на IQ в семьях с низким СЭС, примерно в 5 раз выше, чем в семьях с высоким СЭС.
- Иначе говоря, семьи с низким СЭС отличаются между собой в 5 раз больше, чем семьи с высоким.



Генетика интеллекта: изменения с возрастом



Зачем психологам поведенческая генетика?

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PMCID: PMC2899491

NIHMSID: NIHMS216251

Beyond Heritability: Twin Studies in Behavioral Research

[Wendy Johnson](#),^{1,2} [Eric Turkheimer](#),³ [Irving I. Gottesman](#),^{2,3,4} and [Thomas J. Bouchard, Jr.](#)²

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Спасибо за внимание!