

largest genome-wide association study (GWAS) of EA to date (EA3, discovery sample) and estimate polygenic scores (PGS) in two independent target samples of young adults with neuroimaging data from Australia (N = 1165) and the USA (N = 723), to examine how the genetic factors underlying educational attainment and cognitive ability relate to brain structure. Higher EA-PGS significantly predicted larger global brain morphometry measures, such as intracranial volume and total surface area ($R^2 = 0.006$ and 0.016 respectively, $p < 0.001$) in both independent samples. Remarkably, EA-PGS also predicted cortical surface area of three frontal and three temporal regions in both target samples (over and above total surface area). The identified regions have been robustly implicated in language, memory, visual recognition and cognitive processing. Additionally, individuals with higher EA-PGS achieved higher scores in cognitive tests and we demonstrate that these identified brain regions partly mediate the association between EA-PGS and cognitive test performance, accounting for approximately 20% of the variance explained in IQ scores. Altogether, these findings advance our understanding of the neurobiology that underpins educational attainment and cognitive ability and provide focus points for future research.

Update on Australian genetics of depression study

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More than 20,000 depression cases have been enrolled at DNA and GWAS have been obtained on > 16,000 of these. Early results will be presented with a focus on response to anti-depressant medication.

Five ways to analyze 50,000 pairs of related persons in the National Longitudinal Survey of Youth

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With the rise of molecular genetics methodologies like genome-wide complex trait analysis (GCTA), it becomes critical to viscerally understand how these newer methods relate to the older twin and family methods. Such an understanding informs what novel findings may result from the new methods. This presentation uses the National Longitudinal Survey of Youth (NLSY) to exemplify the techniques. The NLSY is an excellent test-bed for a wide array of biometric analysis methods due to its (a) large, representative sample from the United States, (b) copious number of diverse outcomes, (c) longitudinal data collection, and (d) burgeoning cross-generational structure. We analyze both standard and unconventional outcomes from the NLSY in five related ways. First, we analyze outcomes in the standard form of a structural equation model (SEM). Second, the identical analyses are conducted as a multilevel SEM. Third, multiple large blocks of pedigrees are used to include extended relationships such as cousins. Fourth, the entire data are analyzed as a single genetically-related family using the conventional GCTA software. Fifth, multivariate outcomes are studied for the entire data using the OpenMx software. Each of these ways of structuring the analysis for the NLSY allows certain questions to be answered while forcing the researcher to omit or make assumptions about others.

GWAS on the Internet: systematic review of online news and blog articles about GWAS publications from 2005 to 2018

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In this study, we present a systematic review of news and blog articles on GWAS since its inception, combining statistical analysis with text mining techniques. GWAS publications were identified via the NHGRI-EBI GWAS Catalogue and classified into phenotype categories using the ICD-10. Blog and news articles about these studies were identified using the Altmetric database.

As of 19/09/18, there were 3557 GWAS studies on 1945 different traits. We found 5349 different English language websites that mentioned these publications. Only 41.4% of those websites offered original content (not copied from another website). The most researched areas were non-disease traits (e.g., body mass index, educational attainment, metabolic traits, etc.; N = 1197), neoplasms (N = 462), and mental and behavioral disorders (N = 371). However, only 20.1%, 21.4%, and 15.9% of scientific papers in these areas were mentioned in two or more websites, respectively. Year of publication, number of hits, impact factor, and sample size, were positively and significantly associated with number of online mentions. Non-disease traits generated 2.5 times more mentions than predicted by those variables, while behavioral disorders generated 2 times less, suggesting different patterns in public interest. The Top 5 topics in the news were genetics of Alzheimer's disease, depression, breast cancer, intelligence, and asthma. Finally, readability analysis revealed that more than 95% of all online articles required at least university-level reading skills to understand them. Implications for science communication and genetic literacy campaigns will be discussed.

A cross-country, cross-reporter twin study of oppositional defiant disorder

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Oppositional defiant disorder (ODD) is characterized by a persistent pattern of anger, defiance, or vindictiveness that impairs social functioning. Often beginning during preschool years, temporally it precedes most comorbid disorders. Genetics contributes to the etiology of ODD but research that associates parenting practices with ODD has not been conducted in a genetically sensitive design. We examined the heritability of ODD symptoms in two twin cohorts, one Australian and one Dutch. In Australia, mothers (N = 1281) reported ODD for twins at age ~ 14.3 using the SWAN, and twins self-reported (N = 2210) lifetime incidence of ODD at age ~ 27. An overlapping sample on both measures was available on 246 individuals (110 complete pairs). In the Netherlands, mothers (N = 16,584) and fathers (N = 11,676) reported ODD at age ~ 12.2 using the CBCL12, and twins self-reported (N = 4841) ODD at age ~ 16.9 using the YRS. An overlapping sample on parental and self-report was available for 904 monozygotic and 1138 dizygotic complete