Wave IV BMI Genetic Risk Score

File name: GRS_BMI.xpt

Introduction

This guide describes the BMI genetic risk score for Add Health twin and full sibling respondents who provided saliva samples at Wave IV. This variable is the sum of risk alleles as identified in the Speliotes et al. (2010) genome-wide association study for the respondents of the Add Health Sibling Pairs sample. An overview of the predictive performance of the variable (amongst the black and white respondents) can be found in Domingue et al. (2014).

Construction

The Add Health Sibling Pairs (Harris et al., 2013) data used to construct the BMI risk score consists of 1,595 individuals (58% white, 42% black) from 965 families (564 sibling pairs, 30 sibling trios, 2 sibling quads, and 369 singletons) who were genotyped from samples collected during Wave IV. Genotyping was conducted with the Illumina HumanOmni1-Quad v1 platform using DNA extracted (via Oragene saliva collection) from 1,946 individuals at Wave IV. After quality controls (additional details can be found in McQueen et al., 2014), the genetic database included 1,886 individuals with valid data on 940,862 single nucleotide polymorphisms. The genetic risk score included 31 SNPs discovered in GWAS of adult BMI in European-descent individuals (Speliotes et al., 2010). We summed the BMI-increasing alleles for each SNP and then summed these counts of BMI-increasing alleles across the SNPs. The SNPs included in the genetic risk scores are reported in tables below. The base rates of the risk alleles varied between the white and black samples so the score was standardized with the weighted sums of risk alleles having a mean of 0 and a SD of 1 separately in each of the white and black samples for each genetic risk score.

Add Health single-nucleotide polymorphisms (SNPs) included in the genetic risk score for Europeans.

rs10489741
rs1514175
rs2815752
rs543874
rs1523702
rs2192497
rs2867125
rs713587
rs7635103
rs9852127
rs10938397
rs13107325
rs10057967
rs4836133

rs206936
rs987237
rs10968576
rs11041994
rs7103411
rs7124681
rs7138803
rs9512699
rs17109256
rs2241423
rs12444979
rs1421085
rs3888190
rs571312
rs2287019
rs29942
rs3810291

Add Health single nucleotide polymorphisms (SNPs) included in the African American genetic risk score.

rs543874
rs6752483
rs10938397
rs7719067
rs974417
rs1966841
rs3751812
rs6567160

Special Codes

Due to genotyping errors, some individuals do not have genotypes available for each SNP. These individuals have a missing value of 99 for the sum of the risk alleles.

Data Dictionary

AID   Respondent Identifier

GRS_BMI   Sum of BMI risk alleles for 31 SNPs

References

Domingue, B. W., Belsky, D. W., Harris, K. M., Smolen, A., McQueen, M. B., & Boardman, J. D. (2014). Polygenic Risk Predicts Obesity in Both White and Black Young Adults. PloS one, 9(7), e101596.

Harris KH, Halpern CT, Haberstick BC Smolen A (2013) The National Longitudinal Study of Adolescent Health (Add Health) Sibling Pairs Data. Twin Res Hum Genet 16: 391–398. doi: 10.1017/thg.2012.137

McQueen MB, Boardman JD, Domingue B, Smolen A, Tabor J, Killeya-Jones L,Halpern CT, Whitsel EA, Harris KM. (In Press). The National Longitudinal Studyof Adolescent Health (Add Health) Sibling Pairs Genome-Wide Data. Behavior Genetics.

Speliotes, E. K., Willer, C. J., Berndt, S. I., Monda, K. L., Thorleifsson, G., Jackson, A. U., ... &Hoesel, V. (2010). Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature genetics, 42(11), 937-948.

Wave IV Genetic Risk Score - BMI

Number of observations: 1,886	

AID		Char	RESPONDENT IDENTIFIER NOTE: Smallest 5 and largest 5 values are displayed.
Frequency	Percent	Value	Label
1	0%	10316654	
1	0%	11574211	
1	0%	11718821	
1	0%	12571478	
1	0%	12714332	
1876	99%	Values omitted	
1	0%	99719278	
1	0%	99719934	
1	0%	99719938	
1	0%	99884905	
1	0%	99884906	

GRS_BMI		Num	GENTIC RISK SCORE - BMI NOTE: Smallest 5 and largest 5 values are displayed.
Frequency	Percent	Value	Label
1	0%	17	
11	1%	18	
15	1%	19	
35	2%	20	
39	2%	21	

1606	85%	22-34	NOTE: Range of values omitted from display
11	1%	35	
9	0%	36	
5	0%	37	
1	0%	39	
153	8%	99	Genotypes not available to compute score