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Summary statistics from the publication "Genetic of suicide attempts in individuals with and without mental disorders: a population-based genome-wide association study" by Erlangsen et. al in Molecular Psychiatry, June 2018. (https://doi.org/10.1038/s41380-018-0218-y)

Three summary statistics files:

1. Model1.txt: Corresponds to model 1 from the publication where cases (N = 6024) were individuals over the age of 15 as of December 2012 with at least one incidence of self-harm as per the Danish national health registers, controls (N = 44240) were individuals over the age of 15 as of December 2012 with no incidence of self-harm. Covariates included in the model were gender, age and first ten principal components of genetic ancestry.

2. Model2.txt: Corresponds to model 2 from the publication where cases (N = 6024) were individuals over the age of 15 as of December 2012 with at least one incidence of self-harm as recorded in the Danish national health registers, controls (N = 44240) were individuals over the age of 15 as of December 2012 with no incidence of self-harm. Covariates included in the model were gender, age, first ten principal components of genetic ancestry, a binary covariate indicating diagnostic status for the six major iPSYCH disorders (Schizophrenia, Bipolar disorder, Autism, ADHD, Anorexia and Affective Disorder) and an additional covariate indicating diagnosis for any psychiatric disorder.

3. Model3.txt: Corresponds to model 3 from the publication where cases (N = 4302) were individuals over the age of 15 as of December 2012, who were diagnosed with affective disorder and at least one incidence of self-harm as per the Danish national health registers, controls (N = 13294) were individuals over the age of 15 as of December 2012 with no psychiatric diagnosis. Covariates included in the model were gender, age and first ten principal components of genetic ancestry.

All association analyses were conducted using PLINK.

Columns:

1. SNP: rsId or unique identifier for each genetic marker tested
2. CHR: chromosome
3. POS: Genomic position as per hg19
4. A1: Effect Allele
5. A2: Alternate Allele
6. FRQ: Allele frequency of A1 as calculated by PLINK
7. INFO: Imputation info score as calculated by PLINK
8. BETA: Effect size
9. OR: Odds ratio

10. SE: Standard Error of the Effect
11. P: p-value

Data Use Agreement

1. Investigators acknowledge that these data are provided on an "as-is" basis, without warranty of any type, expressed or implied, including but not limited to any warranty as to their performance, merchantability, or fitness for any particular purpose;
2. Investigators will use these results for scientific research and educational use only.
3. The downloaded results can be shared among collaborators but the reposting or public distribution of the result file is prohibited;
4. Investigators certify that they are in compliance with all applicable local, state, and federal laws or regulations and institutional policies regarding human subjects and genetics research;
5. Investigators will cite the appropriate publication in any communications or publications arising directly or indirectly from these data;
6. Investigators will never attempt to identify any participant who contributed to these data;
7. Investigators may not use these data to develop any type of risk or predictive test for an unborn individual;
8. For any risk or predictive test for a child or adult, investigators must acknowledge that this is an experimental use of these data and that essentially all psychiatric disorders have important non-genetic etiological components;
9. When these data are made available prior to publication, investigators agree to respect and not compete with the scientific priorities of the iPSYCH team according to the Fort Lauderdale principles.

Experience has taught us that the appropriate use of these data requires considerable attention to detail, prior experience, and technical skill. Errors are easy to make. If investigators use these data, any and all consequences are entirely their responsibility.