UK Biobank - Neale lab

NEALE LAB



[1ST AUGUST 2018] WE'RE THRILLED TO ANNOUNCE AN UPDATED GWAS ANALYSIS OF THE UK BIOBANK.

LEARN MORE

GWAS RESULTS

Multi-ancestry analysis:

GWAS analysis of 7,221 phenotypes across 6 continental ancestry groups in the UK Biobank. This effort was led by Alicia Martin, Hilary Finucane, Mark Daly and Ben Neale, lead analysts Konrad Karczewski and Elizabeth Atkinson, with contributions from team members at ATGU. The summary statistics have been made available on the **Pan UKBB website.**

GWAS round 2:

Results shared 1st August 2018.

Imputed genotypes from HRC plus UK10K & 1000 Genomes reference panels as released by UK



Got questions about our GWAS of the UK Biobank?

What samples, markers and phenotypes we used? The format of our GWAS results files? Use permissions of the results? How to cite our results? **Read our FAQs**.

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GWAS round 2 results can be found here

GWAS round 2 Github code repository

GWAS round 2 Blog post: Addition of Biomarker GWAS results

GWAS round 2 <u>Blog post: Genotyped SNPs in UK</u> Biobank failing Hardy-Weinberg equilibrium test

GWAS round 2 Blog post: Genetic correlation results for heritable phenotypes in the UK Biobank

GWAS round 2 Blog post: Updating SNP heritability results from 4,236 phenotypes in UK Biobank

GWAS round 1:

The round 1 version of results will be removed from Dropbox on December 15th 2019

Results shared 20th September 2017. Imputed genotypes from HRC as released by UK Biobank in May 2017.

GWAS round 1 **Blog post announcing the release** GWAS round 1 **Blog post describing details of how** we conducted the GWAS GWAS round 1 **GWAS results**

GWAS round 1 Github code repository

I HE TEAM

Core contributors:

Liam Abbott, Sam Bryant, Claire Churchhouse, Andrea Ganna, Daniel Howrigan, Duncan Palmer, Ben Neale, Raymond Walters, Caitlin Carey, The Hail team

Also:

Verneri Anttila, Krishna Aragam, Alex Baumann, Joanne Cole, Mark J. Daly, Rob Damian, Mary Haas, Joel Hirschhorn, Eric Jones, Ruchi Munshi, Manuel Rivas, Sailaja Vedantam

THANK HERITABILIT¥OU

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our heritability estimation and genetic correlation analyses in the UK Biobank: Heritability browser: https://nealelab.github.io/UKBB_ldsc/index.html Genetic correlation browser: https://ukbbrg.hail.is/

Read our series of blog posts on understanding and estimating heritability in complex traits:

Updating SNP heritability results from 4,236 phenotypes in UK Biobank A quick summary of what has changed since the last release.

Insights from estimates of SNP-heritability for >2,000 traits and disorders in UK Biobank We discuss what we have learned so far from the heritability analysis of the UK Biobank phenotypes.

Heritability 501: LDSR-based h2 in UKBB for the technically minded

A technical deep dive in to how we used LD Score regression to estimate heritability in the UK Biobank data set.

Heritability 201: Types of heritability and how we estimate it Learn about the different types of heritability and

how these related to each other.

Heritability 101: What is "heritability"? A layman's explanation of what we mean by "heritability" of a trait.

Heritability of >2,000 traits and disorders in the UK Biobank

extend a huge thank you to the UK Biobank for creating such a rich and unprecedented resource and. furthermore, for making it publicly available to the community. We received continuous administrative support from the UK Biobank **Research Access** Administration team, in particular from Tobietta Rhyman who helped make this process as smooth as possible.

performea on the UK Biobank data.

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