

2018 SISG Practical

Pleiotropy / LD Score

1. Log into the LD Hub website: <http://ldsc.broadinstitute.org/>. This site allows you to calculate the (co-) heritability between different traits using summary statistics. From the site:

“LD Hub is a centralized database of summary-level GWAS results for diseases/traits from different publicly available resources/consortia and a web interface that automates the LD score regression analysis pipeline. LD score regression is a reliable and efficient method of using genome-wide association study (GWAS) summary-level results data to estimate the SNP heritability of complex traits and diseases, partition this heritability into functional categories, and estimate the genetic correlation between different phenotypes.”

2. Go to the “Look up Center”.
3. Select two traits and interpret the heritability results. Is the inflation factor (λ) due to population stratification or polygenic effects?
4. Look at the correlation between these two traits. Are they correlated? In what direction? Interpret this correlation. What does it imply about potential pleiotropy?