Genome-wide significance

In genome-wide association studies, **genome-wide significance** (abbreviated **GWS**) is a specific threshold for determining the statistical significance of a reported association between a given single-nucleotide polymorphism (SNP) and a given trait. The most commonly accepted threshold is $p < 5 \times 10^{-8}$, which is based on performing a Bonferroni correction for all the independent common SNPs across the human genome.[1] If a *p*-value is found to be lower than this threshold in a genome-wide association study, the null hypothesis of no true SNP-association will typically be rejected.[2] However, there has been some criticism of this threshold, with a 2012 study suggesting that a significant number of associations with *p*-values just above this threshold are genuine, replicable associations. The authors of this study concluded that their finding "...suggests a possible relaxation in the current GWS threshold."[3] More recently, it has been suggested that the conventional threshold should be modified to take into account the increasing prevalence of low-frequency genetic variants in genome-wide association studies.[4]

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