Resource Summary Report

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Hardy-Weinberg Equilibrium Calculator

RRID:SCR_008371
Type: Tool

Proper Citation

Hardy-Weinberg Equilibrium Calculator (RRID:SCR_008371)

Resource Information

URL: http://www.oege.org/software/hwe-mr-calc.shtml

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Description: This portal leads to the Chi-sq Hardy-Weinberg equilibrium test calculator for biallelic markers (SNPs, indels etc), including analysis for ascertainment bias for dominant/recessive models (due to biological or technical causes.) The purpose of this web program is for estimating possible missingness and an approach to evaluating missingness under different genetic models. Mendelian randomization (MR) permits causal inference between exposures and a disease. It can be compared with randomized controlled trials. Whereas in a randomized controlled trial the randomization occurs at entry into the trial, in MR the randomization occurs during gamete formation and conception. Several factors, including time since conception and sampling variation, are relevant to the interpretation of an MR test. Particularly important is consideration of the missingness of genotypes that can be originated by chance, genotyping errors, or clinical ascertainment. Testing for Hardy-Weinberg equilibrium (HWE) is a genetic approach that permits evaluation of missingness. Through this tool, the authors demonstrate evidence of nonconformity with HWE in real data. They also perform simulations to characterize the sensitivity of HWE tests to missingness. Unresolved missingness could lead to a false rejection of causality in an MR investigation of trait-disease association. These results indicate that large-scale studies, very high quality genotyping data, and detailed knowledge of the life-course genetics of the alleles/genotypes studied will largely mitigate this risk. Sponsors: This resource is supported by an Intermediate Fellowship (grant FS/05/065/19497) from the British Heart Foundation.

Synonyms: HWE Calculator

Resource Type: software resource, software application, simulation software

Keywords: gamete, genetic, allele, analysis, biallelic, biological, caluclator, conception,

disease, dominant, genotype, hardy-weinberg equilibrium, marker, mendelian, model, randomization, recessive, snp, test, trait

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Resource Name: Hardy-Weinberg Equilibrium Calculator

Resource ID: SCR_008371

Alternate IDs: nif-0000-25608

Record Creation Time: 20220129T080247+0000

Record Last Update: 20250513T061001+0000

Ratings and Alerts

No rating or validation information has been found for Hardy-Weinberg Equilibrium Calculator.

No alerts have been found for Hardy-Weinberg Equilibrium Calculator.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 93 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Chatterjee M, et al. (2023) Glutamate receptor genetic variants affected peripheral glutamatergic transmission and treatment induced improvement of Indian ADHD probands. Scientific reports, 13(1), 19922.

Al Ageeli E, et al. (2022) Migration/Differentiation-Associated LncRNA SENCR rs12420823*C/T: A Novel Gene Variant Can Predict Survival and Recurrence in Patients with Breast Cancer. Genes, 13(11).

Ben Salah H, et al. (2021) Rapid high-resolution melting method to identify human leukocyte antigen-G (HLA-G) 3' untranslated region polymorphism +3142C/G (rs1063320). Molecular genetics & genomic medicine, 9(11), e1817.

Benna C, et al. (2021) Gender-specific associations between polymorphisms of the circadian gene RORA and cutaneous melanoma susceptibility. Journal of translational medicine, 19(1), 57.

Ignaszak-Kaus N, et al. (2021) Relationship of Postoperative Pain and PONV after Minimally Invasive Surgery with the Serotonin Concentrations and Receptors' Gene Polymorphisms. Journal of personalized medicine, 11(9).

Mehrzad J, et al. (2020) The independent and combined effects of selected risk factors and Arg399Gln XRCC1 polymorphism in the risk of colorectal cancer among an Iranian population. Medical journal of the Islamic Republic of Iran, 34, 75.

Shan C, et al. (2020) Association of TLR-2 Gene Polymorphisms with the Risk of Periodontitis: A Meta-Analysis. Disease markers, 2020, 9353958.

Sahmoud S, et al. (2020) Association of VDBP rs4701 Variant, but not VDR/RXR-? Over-Expression with Bone Mineral Density in Pediatric Well-Chelated ?-Thalassemia Patients. Mediterranean journal of hematology and infectious diseases, 12(1), e2020037.

Martins JSC, et al. (2020) Investigation of Human IFITM3 Polymorphisms rs34481144A and rs12252C and Risk for Influenza A(H1N1)pdm09 Severity in a Brazilian Cohort. Frontiers in cellular and infection microbiology, 10, 352.

Fawzy MS, et al. (2020) Analysis of microRNA-34a expression profile and rs2666433 variant in colorectal cancer: a pilot study. Scientific reports, 10(1), 16940.

Arayasongsak U, et al. (2020) Genetic association study of interferon lambda 3, CD27, and human leukocyte antigen-DPB1 with dengue severity in Thailand. BMC infectious diseases, 20(1), 948.

Coto E, et al. (2020) IL17RA in early-onset coronary artery disease: Total leukocyte transcript analysis and promoter polymorphism (rs4819554) association. Cytokine, 136, 155285.

Fawzy MS, et al. (2020) Analysis of the autoimmune regulator (AIRE) gene variant rs2075876 (G/A) association with breast cancer susceptibility. Journal of clinical laboratory analysis, 34(9), e23365.

Nathan S, et al. (2020) Functional Haplotypes in the ADIPOQ Gene are Associated with Underweight, Immunosuppression and Viral Suppression in Kenyan HIV-1 Infected Antiretroviral Treatment Naive and Experienced Injection Substance Users. Ethiopian journal of health sciences, 30(4), 489.

Ellwanger JH, et al. (2020) Role of the genetic variant CCR5?32 in HBV infection and HBV/HIV co-infection. Virus research, 277, 197838.

Fawzy MS, et al. (2020) Analysis of microRNA processing machinery gene (DROSHA, DICER1, RAN, and XPO5) variants association with end-stage renal disease. Journal of

clinical laboratory analysis, 34(12), e23520.

Saber-Ayad M, et al. (2019) The FTO genetic variants are associated with dietary intake and body mass index amongst Emirati population. PloS one, 14(10), e0223808.

Ghosh A, et al. (2019) Dopamine ? Hydroxylase (DBH) is a potential modifier gene associated with Parkinson's disease in Eastern India. Neuroscience letters, 706, 75.

Decharatchakul N, et al. (2019) Association of genetic polymorphisms in SOD2, SOD3, GPX3, and GSTT1 with hypertriglyceridemia and low HDL-C level in subjects with high risk of coronary artery disease. PeerJ, 7, e7407.

Filiz B, et al. (2019) Evaluation of interleukin-23 receptor (IL-23R) gene polymorphisms and serum IL-23 levels in patients with psoriasis. Turkish journal of medical sciences, 49(5), 1386.