# Package: BIGDAWG (via r-universe)

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**Type** Package

**Title** Case-Cotrol Analysis of Multi-Allelic Loci

**Version** 3.0.8

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**URL** `http://tools.immunogenomics.org/`, `https://github.com/IgDAWG/BIGDAWG`

**BugReports** `https://github.com/IgDAWG/BIGDAWG/issues`

**Description** Data sets and functions for chi-squared Hardy-Weinberg and case-control association tests of highly polymorphic genetic data [e.g., human leukocyte antigen (HLA) data]. Performs association tests at multiple levels of polymorphism (haplotype, locus and HLA amino-acids) as described in Pappas DJ, Marin W, Hollenbach JA, Mack SJ (2016) <doi:10.1016/j.humimm.2015.12.006>. Combines rare variants to a common class to account for sparse cells in tables as described by Hollenbach JA, Mack SJ, Thomson G, Gourraud PA (2012) <doi:10.1007/978-1-61779-842-9_14>.

**License** GPL (>= 3)

**LazyData** True

**Depends** R (>= 4.0.0)

**Imports** XML, httr, haplo.stats, parallel

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

**Encoding** UTF-8

**Repository** https://igdawg.r-universe.dev

**RemoteUrl** https://github.com/igdawg/bigdawg

**RemoteRef** HEAD

**RemoteSha** 518e3b38057c10fad314455883e6d8a1843d9431