

Package ‘gaawr2’

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Title Genetic Association Analysis

Version 0.0.5

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Description This is a companion to Henry-Stewart talk by Zhao (2026, <[doi:10.69645/FRFQ9519](https://doi.org/10.69645/FRFQ9519)>), which gathers information, metadata and scripts to showcase modern genetic analysis -- ranging from testing of polymorphic variant(s) for Hardy-Weinberg equilibrium, association with traits using genetic and statistical models, Bayesian implementation, power calculation in study design, and genetic annotation. It also covers R integration with the Linux environment, GitHub, package creation and web applications. The earlier version by Zhao (2009, <[doi:10.69645/DCRY5578](https://doi.org/10.69645/DCRY5578)>) provides an brief introduction to these topics.

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URL <https://jinghuazhao.github.io/gaawr2/>,
<https://github.com/jinghuazhao/gaawr2>

BugReports <https://github.com/jinghuazhao/gaawr2/issues>

Encoding UTF-8

Depends R (>= 3.5.0)

Imports dplyr, gap, gap.datasets, ggplot2, survival, Rdpack

RdMacros Rdpack

LazyData Yes

LazyLoad Yes

LazyDataCompression xz

VignetteBuilder knitr

Suggests BLR, BGLR, biomaRt, bookdown, Cairo, EnsDb.Hsapiens.v75, ensemblldb, GMMAT, HardyWeinberg, haplo.stats, httr, httpuv, jsonlite, kableExtra, knitr, MCMCglmm, plumber, powerEQTL, R2jags, regress, Rsamtools, SNPAssoc, testthat, tidyr

RoxygenNote 7.3.3
NeedsCompilation no
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welcome	<i>An enhanced welcome</i>
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Description

It prints a welcome message, saying number of times.

Usage

welcome(n)

Arguments

n The number of times (>1 integer) to welcome the user.

Value

Prints a welcome message to the console.

Examples

welcome(3)

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