Package 'gaawr2'

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Title Genetic Association Analysis

Version 0.0.9

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Description This is a companion to Henry-Stewart talk by Zhao (2026, <doi: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>) provides a 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

VignetteBuilder knitr, rmarkdown, bookdown

LazyData Yes

LazyLoad Yes

LazyDataCompression xz

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

Config/roxygen2/version 8.0.0

NeedsCompilation no

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Repository CRAN

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Contents

welcome 2

Index **3**

`welcome` *An enhanced welcome*

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)
```

Index

welcome, 2