Package: gaawr2 (via r-universe)

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Title Genetic Association Analysis

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Description It gathers information, meta-data and scripts in a two-part Henry-Stewart talk by Zhao (2009, <doi:10.69645/DCRY5578>), which showcases analysis in aspects such as testing of polymorphic variant(s) for Hardy-Weinberg equilibrium, association with trait using genetic and statistical models as well as 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.

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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, EnsDb.Hsapiens.v75, ensembldb, GMMAT, HardyWeinberg, haplo.stats, httr, httpuv, jsonlite, kableExtra, knitr, MCMCglmm, plumber, powerEQTL, R2jags, regress, seqminer, SNPassoc, testthat, tidyr

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Config/pak/sysreqs make libicu-dev libssl-dev

Repository https://jinghuazhao.r-universe.dev

RemoteUrl https://github.com/jinghuazhao/gaawr2

RemoteRef HEAD

RemoteSha eb933c0283de9d4e84173b723d853c0a86edf27e

Contents

`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)
```

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