

Package ‘vici’

August 21, 2019

Title Vaccine Induced Cellular Immunogenicity with Bivariate Modeling

Version 0.5.2

Date 2019-08-20

Description A shiny app for accurate estimation of vaccine induced immunogenicity with bivariate linear modeling. Method is detailed in: Lhomme E, Hejblum BP, Lacabaratz C, Wiedemann A, Lelièvre J-D, Levy Y, Thiebaut R & Richert L (2019). Submitted.

BugReports <https://github.com/borishejblum/vici/issues>

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Encoding UTF-8

LazyData true

Imports cowplot, DT, ggplot2, grDevices, ggpubr, nlme, shiny, stats, tidy, utils

RoxygenNote 6.1.1

NeedsCompilation no

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ICS_ex

*Toy data to upload in the app.***Description**

Toy data to upload in the app.

Usage

```
data(ICS_ex)
```

Format

A tab-separated .txt file

Examples

```
if(interactive()){
  set.seed(1382019)
  nsubj <- 20
  ntp <- 3
  nstim <- 3
  narm <- 3
  subj <- rep(rep(rep(1:nsubj, each = ntp), times = nstim), times = narm)
  stim <- rep(rep(c("NS", "S1", "S2"), each = nsubj*ntp), times = narm)
  tp <- rep(rep(c("D0", "D1", "D3"), times=nsubj*nstim), times = narm)
  a <- rep(c("Placebo", "A2", "A3"), each = nsubj*nstim*ntp)
  y1 <- round(abs(rnorm(n=nsubj*nstim*ntp*narm,m = 0.03, sd=0.06)) +
    (stim=="S2" & a == "A2" & tp == "D1")*abs(rnorm(n=nsubj*nstim*ntp*narm, m = 0.05, sd=0.01)), 4)
  y2 <- round(abs(rnorm(n=nsubj*nstim*ntp*narm,m = 0.03, sd=0.06)) +
    (stim=="S1" & a == "A3" & tp == "D3")*abs(rnorm(n=nsubj*nstim*ntp*narm, m = 0.1, sd=0.02)), 4)
  ICS_ex <- cbind.data.frame("Subject" = subj, "StimulationPool" = stim, "TimePoint" = tp,
    "Arm" = a, "Response1" = y1, "Response2" = y2)

  #View(ICS_ex)
  write.table(ICS_ex, file="Documents/GitHub/vici/data/ICS_ex.txt", sep="\t",
    row.names = FALSE, quote = FALSE)
}
```

run_app

*Launch VICI Shiny App***Description**

Launch VICI Shiny App

run_app

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Usage

```
run_app(...)
```

Arguments

... additional arguments to be passed to the [runApp](#) function.

Examples

```
if(interactive()){  
  vici::run_app()  
}
```

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