

Package: MRchecks (via r-universe)

October 5, 2024

Title Tools for detecting genetic variants whose effect changes with age and associated bias

Version 0.0.0.9000

Description This package is a collection of tools to detect SNPs whose effect varies with age whose. owoeosds sd sd. sdsfw. sdfsers ses .

License `use_mit_license()`, `use_gpl3_license()` or friends to pick a license

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Imports mgcv, magrittr, dplyr, itsadug, AER, plotfunctions

Depends R (>= 2.10)

Repository <https://mrcieu.r-universe.dev>

RemoteUrl <https://github.com/jalabrecque/MRchecks>

RemoteRef HEAD

RemoteSha 344ae2f7bbc03106c4a8bf9e50999b2e159d0d42

Contents

SNPxAGE_bias	2
SNPxAGE_effect	2
SNPxAGE_model	3
SNPxAGE_plot	4
Index	5

SNPxAGE_bias	<i>Estimate bias from age-varying genetic effects in Mendelian randomization</i>
--------------	--

Description

Takes output from `SNPxAGE_model` and estimates the bias due to age-varying genetic effects under different exposure windows and at two different ages

Usage

```
SNPxAGE_bias(SNPxAGE_model_output, rep = 2, age_set = 65)
```

Arguments

SNPxAGE_model_output	Output from <code>SNPxAGE_model</code>
rep	Numerical value of the number of iterations to run the simulations

Value

A list of results

SNPxAGE_effect	<i>Function to estimate the per-allele effect at each age</i>
----------------	---

Description

Function to estimate the per-allele effect at each age

Usage

```
SNPxAGE_effect(SNPxAGE_output, reps = 10, ages = 40:70)
```

`SNPxAGE_model`*Flexibly modeling the age/phenotype association by genetic variant*

Description

Takes a genetic variant or single nucleotide polymorphism (SNP) and a phenotype it's associated with and estimates how the relationship between the two varies with age using splines.

Usage

```
SNPxAGE_model(data, SNP, phenotype, age, covars, k = 3, pred_ages, type = "cr")
```

Arguments

<code>data</code>	A data frame containing the SNP, age and phenotype variables
<code>SNP</code>	A character string with the name of the SNP variable in the data frame. This variable itself must be a factor variable containing at most 3 unique values indicating the number of copies
<code>phenotype</code>	A character string with the name of the phenotype variable in the data frame
<code>age</code>	A character string with the name of the age variable in the data frame
<code>covars</code>	A character vector with the names of the variables to be adjusted for (e.g. principal components)
<code>type</code>	A character string with the type splines to be used (see <code>mgcv</code> function)
<code>knots</code>	A numeric value indicating the number of internal knots (default 3)

Value

A list including the model and parameters used. If `pred_ages` is supplied then the predictions for those ages is also returned.

Author(s)

Jeremy A Labrecque, <j.labrecque@erasmusmc.nl>

References

TBA

`SNPxAGE_plot`*Function to plot absolute value of pheontype for each genotype*

Description

Function to plot absolute value of pheontype for each genotype

Usage

```
SNPxAGE_plot(SNPxAGE_model_output)
```

Index

SNPxAGE_bias, [2](#)
SNPxAGE_effect, [2](#)
SNPxAGE_model, [3](#)
SNPxAGE_plot, [4](#)