Package 'MHTrajectoryR'

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Type Package

Title Bayesian Model Selection in Logistic Regression for the
Detection of Adverse Drug Reactions

Version 1.0.1

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Author Matthieu Marbac and Mohammed Sedki

Maintainer Mohammed Sedki <Mohammed.sedki@u-psud.fr>

Description Spontaneous adverse event reports have a high potential for detecting adverse drug reactions. However, due to their dimension, the analysis of such databases requires statistical methods. We propose to use a logistic regression whose sparsity is viewed as a model selection challenge. Since the model space is huge, a Metropolis-Hastings algorithm carries out the model selection by maximizing the BIC criterion.

License GPL (>= 2)

Imports parallel, mgcv

Depends R (>= 2.10)

Repository CRAN

NeedsCompilation no

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R topics documented:

MHTrajectoryR-package   *Detection of adverse drug events by analyzing Metropolis-Hastings Markov chain trajectory.*

Description

Spontaneous adverse event reports have a high potential for detecting adverse drug reactions. However, due to their dimension, the analysis of such databases requires statistical methods. The MH-TrajectoryR package propose to use a logistic regression whose sparsity is viewed as a model selection challenge. Since the model space is huge, a Metropolis-Hastings algorithm carries out the model selection by maximizing the BIC criterion through Markov chain trajectory.

Details

Package:	MHTrajectoryR
Type:	Package
Version:	1.0
Date:	2016-02-07
License:	GPL (>= 2)

The main function is Analyze_oneAE.

Author(s)

Matthieu Marbac and Mohammed Sedki Maintainer: Mohammed Sedki <mohammed.sedki@u-psud.fr>

References

Matthieu Marbac, Pascale Tubert-Bitter, Mohammed Sedki: Bayesian model selection in logistic regression for the detection of adverse drug reactions. (http://arxiv.org/abs/1505.03366) (accepted for publication in Biometrical Journal).

Examples

```
## Not run:
  data(exampleAE)
  data(exampleDrugs)
  res <- Analyze_oneAE(exampleAE[,1], exampleDrugs, 10, 1, 10)
  # print signals (drugs relied to the adverse event)
  print(res$signal)

## End(Not run)
```

Analyze_oneAE	*Signal detection using via variable selection in logistic regression. The Bayesian Information Criterion maximization is assessed using Metropolis-Hastings algorithm.*

Description

Spontaneous adverse event reports have a high potential for detecting adverse drug reactions. However, due to their dimension, the analysis of such databases requires statistical methods. The MH-TrajectoryR package propose to use a logistic regression whose sparsity is viewed as a model selection challenge. Since the model space is huge, a Metropolis-Hastings algorithm carries out the model selection by maximizing the BIC criterion.

Usage

```
Analyze_oneAE(ae, drug, maxit, alpha, nbinit)
```

Arguments

ae	The response binary vector which indicates if the adverse event is observed (value 1) and (value 0) otherwise. It must have the sime length with the number of rows of matrix of drugs consumption.
drug	The matrix of drugs consumption or the matrix of binary covariates. Each row corresponds to one individual drugs consumption. Each column corresponds to one drug.
maxit	Number of iteration of the Metropolis-Hastings algorithm. In other words, the length of one trajectory of the Metropolis-Hastings Markov Chain.
alpha	The parameter that define the neighbordhood.
nbinit	The number of random initialisations.

Value

list of (best) the best model that maximize the BIC. (all) all explored models through the trajectory. (signals) the detected signals (positive, negative or unknown) in OMOP reference set.

Author(s)

Mohammed Sedki and Matthieu Marbac

References

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Examples

```
## Not run:
  data(exampleAE)
  data(exampleDrugs)
  res <- Analyze_oneAE(exampleAE[,1], exampleDrugs, 10, 1, 10)
  # print signals (drugs relied to the adverse event)
  print(res$signal)

## End(Not run)
```

---

exampleAE   *A simulated data*

Description

This simulated data indicates the adverse events of 100 individuals about 5 events (0: absence, 1: presence)

Examples

```
data(exampleAE)
```

---

exampleDrugs   *A simulated data*

Description

This simulated data indicates the drugs consumption of 100 individuals about 100 drugs (0: absence, 1: presence)

Examples

```
data(exampleDrugs)
```

`OmopReference`	*The OMOP reference set*

Description

The OMOP Ryan et al.(2013) reference set of test cases that contains both positive and negative controls.

Usage

```
data(OmopReference)
```

Format

A set of 399 negative and positive controls or couples of adverse event and drug.

AE a character vector indicating adverse events

ATC The Anatomical Therapeutic Chemical (ATC) code

statu a numeric vector indicating if positive (1) or negative (0) control

Details

To evaluate and compare the performances of the competing methods, we use the OMOP Ryan et al.(2013) reference set of test cases that contains both positive and negative controls. Four adverse events (i.e. $d = 4$) were studied in this reference set : acute myocardial infarction (AMI), acute kidney injury (AKI), acute liver injury (ALI), and upper gastro-intestinal bleeding (GIB). There are three-hundred and ninety-nine test cases where 165 positive controls and 234 negative controls were identified across the four adverse events of interest. More details are given by Table 1. Ryan et al. (2013) indicate that the majority of positive controls for AKI and GIB were supported by randomized clinical trial evidence, while the majority of positive controls for ALI and AMI were only based on published case reports. Then a positive control is a pair (drug and adverse event) which is supported by randomized clinical trial evidence or based on published case reports whereas a negative control is not met by neither of the these methods.

Source

Ryan, P., Schuemie, M., Welebob, E., Duke, J., Valentine, S., and Hartzema, A. (2013). Defining a reference set to support methodological research in drug safety. Drug safety, 36(1), 33-47.

References

Ryan, P., Schuemie, M., Welebob, E., Duke, J., Valentine, S., and Hartzema, A. (2013). Defining a reference set to support methodological research in drug safety. Drug safety, 36(1), 33-47.

Examples

```
data(OmopReference)
```

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