Package 'DiabetesTxPath'

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Type Package

Title Learning Effective Clinical Treatment Pathways for Type-2 Diabetes

Version 0.1.0

Author Rohit Vashisht

Maintainer The package maintainer <rohitv@stanford.edu>

Description
    This package can be used to learn effective clinical treatment pathways for Type-2 diabetes.

License What license is it under?

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

R topics documented:

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drugEfficacyAnalysis   *drugEfficacyAnalysis*

Usage

```
drugEfficacyAnalysis(drugCombName, numThread, outCome, cid2Rm, outComeName)
```

Arguments

drugCombName	Name of the drug combination for which the analysis need to be performed.
numThread	Number of threads to be used for parallel processing. Give it as much as you can :)
outCome	The outcome Id for which the analysis need to be performed.
cid2Rm	List of concept IDs to be removed before patient-level matching.
outComeName	Name of the outcome measure. This will be used for naming the files.

Details

This function can be used to perform the drug efficacy analysis. Very briefly, this function a) obtain treatment and comparator cohorts from target schema b) perform patient-level propensity score matching c) perform cox-proportional hazard modeling of the given outcome. Please note this function can only performe analysis if there are >= 100 patients in both treatment and comparator cohorts. Right now I've hard coded these values. May be in the future we'll see how to generalize this.

Author(s)

Rohit Vashisht

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getCohort   *Get Cohort*

Usage

```
getCohort(connectionDetails, cdmDatabaseSchema, resultsDatabaseSchema,
  sqlFileName, targetDatabaseSchema, targetCohortTable, idOne, idTwo, idThree,
  idFour, idFive, idSix)
```

Arguments

connectionDetails

> The details of database schema.

cdmDatabaseSchema

> The details of CDM schema.

resultsDatabaseSchema

> The details of results schema.

sqlFileName   Name of SQL file that will used to construct the cohort.

targetDatabaseSchema

> Name of target database schema.

targetCohortTable

> Name of target cohort table.

idOne   Numeric value = 1 represents one of the drug combination. This is representative of Treatment Cohort.

idTwo   Numeric value = 2 representing one of the drug combination. This is representative of the Comparator Cohort.

idThree   Numeric value = 3 representing one of the outcome measure. In case of DiabetesTxPathway this represents HbA1c

idFour   Numeric value = 4 representing one of the outcome measure. In case of DiabetesTxPathway this represents Myocardial Infraction

Details

The function get cohort can be used to generate the required cohort for a given drug combination. You can use this function to generate your own cohort based on given SQL query or use one of the SQL query provided. For DiabetesTxPathway it is highly recomended to use the SQLs provided in this package.

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hello   *Hello, World!*

Description

Prints 'Hello, world!'.

Usage

```
hello()
```

Examples

```
hello()
```

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runStudy   *runStudy*

Usage

```
runStudy(connectionDetails, cdm_database_schema, results_database_schema,
  target_database_schema, target_cohort_table, numThread, idOne, idTwo, idThree,
  idFour, idFive, idSix)
```

Arguments

```
connectionDetails
                The connection details of the database.
cdm_database_schema
                The name of your cdm database schema.
results_database_schema
                The name of your results database schema.
```

Details

This function can be used to perform the DiabetesTxPathway analysis end-to-end. Just supply the details and leave it running overnight. Please note the function will perform analysis if there are atleast 100 patients for each of the drug group considered in the study.

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