Package ‘accept’

October 12, 2022

Title The Acute COPD Exacerbation Prediction Tool (ACCEPT)

Version 0.9.1

Description Allows clinicians to predict the rate and severity of future acute exacerbation in Chronic Obstructive Pulmonary Disease (COPD) patients, based on the clinical prediction model published in Adibi et al. (2020) <doi:10.1016/S2213-2600(19)30397-2>.

Depends R (>= 3.6.0)

License GPL-3

Encoding UTF-8

LazyData true

Imports stats, dplyr, reldist, splines

Suggests plotly

RoxygenNote 7.2.0

NeedsCompilation no

Author Amin Adibi [aut, cre],
Mohsen Sadatsafavi [aut, cph],
Abdollah Safari [aut],
Ainsleigh Hill [aut]

Maintainer Amin Adibi <`adibi@alumni.ubc.ca`>

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R topics documented:

`accept` *Predicts COPD exacerbation rate by severity level based on Acute COPD Exacerbation Tool (ACCEPT)*

Description

Predicts COPD exacerbation rate by severity level based on Acute COPD Exacerbation Tool (ACCEPT)

Usage

```
accept(
  patientData,
  random_sampling_N = 100,
  lastYrExacCol = "LastYrExacCount",
  lastYrSevExacCol = "LastYrSevExacCount",
  ...
)
```

Arguments

`patientData`	patient data matrix. Can have one or many patients in it
`random_sampling_N`	number of random sampling. Default is 100.
`lastYrExacCol`	the column specifying last year all exacerbation count
`lastYrSevExacCol`	the column specifying last year severe exacerbation count
`...`	for backward compatibility

Value

patientData with prediction

Examples

```
results <- accept(samplePatients)
```

`accept2` *Predicts COPD exacerbation rate by severity level based on the updated accept2 model, which improves accuracy in patients without an exacerbation history.*

Description

Predicts COPD exacerbation rate by severity level based on the updated accept2 model, which improves accuracy in patients without an exacerbation history.

Usage

```
accept2(
  patientData,
  random_sampling_N = 100,
  lastYrExacCol = "LastYrExacCount",
  lastYrSevExacCol = "LastYrSevExacCount",
  KeepSGRQ = TRUE,
  KeepMeds = TRUE,
  ...
)
```

Arguments

`patientData`	patient data matrix. Can have one or many patients in it
`random_sampling_N`	number of random sampling. Default is 100.
`lastYrExacCol`	the column specifying last year all exacerbation count
`lastYrSevExacCol`	the column specifying last year severe exacerbation count
`KeepSGRQ`	default is TRUE. If set to false, the reduced model without SGRQ will be used.
`KeepMeds`	default is TRUE. If set to false, the reduced model without medication predictors will be used.
`...`	for backward compatibility

Value

patientData with prediction

Examples

```
results <- accept2(samplePatients)
```

`plotExacerbations` *Creates bar graph comparing no treatment with azithromycin treatment*

Description

Creates bar graph comparing no treatment with azithromycin treatment

Usage

```
plotExacerbations(
  patientResults,
  type = "rate",
  interval = "PI",
  colors = c("#007bff", "rgb(204,204,204)")
)
```

Arguments

`patientResults`	patient results vector, produced by accept.
`type`	string: either "probability" or "rate"
`interval`	string: either "CI" or "PI" PI = Predicted Interval CI = Confidence Interval
`colors`	vector: a vector of colors to be used in the graph must be length 2 can use hexadecimal, rgb, or R color codes

Value

a bar graph

Examples

```
results <- accept(samplePatients[1,])
plotExacerbations(results)
```

`plotHeatMap` *Creates heatmap of number of exacerbations*

Description

Creates heatmap of number of exacerbations

Usage

```
plotHeatMap(patientResults, n = 10, shortened = TRUE)
```

Arguments

`patientResults`	patient results vector, produced by accept.
`n`	how many exacerbations to consider
`shortened`	boolean

Value

a heatmap

Examples

```
results <- accept(samplePatients[1,])
plotHeatMap(results)
```

`predictCountProb` *Predicts probability of observing n exacerbations in the next year*

Description

Predicts probability of observing n exacerbations in the next year

Usage

```
predictCountProb(patientResults, n = 10, shortened = TRUE)
```

Arguments

`patientResults`	patient results vector, produced by accept.
`n`	how many exacerbations
`shortened`	boolean: Shortened results groups into 0, 1, 2, and 3 or more exacerbations

Value

a matrix of probabilities with the number of exacerbations as rows and number of severe exacerbations as columns

Examples

```
results <- accept(samplePatients[1,])
predictCountProb (results)
```

`samplePatients` *Sample Patient Characteristics Inputs*

Description

A dataset containing sample patient characteristics to run the prediction model variables are as follows:

Format

A data frame with 2 rows and 19 variables

Details

- ID. A unique character string identifying a patients
- male. whether the patient is male (0,1)
- age. the age of the patient (40–90)
- smoker. whether the patient is currently a smoker (0,1)
- oxygen. whether the patient has had supplemental oxygen therapy within the past year (0,1)
- FEV1. forced expiratory volume in 1 second in L (0–5)
- BMI. body mass index (10–60)
- SGRQ. St. George's Respiratory Questionnaire score (0–100)
- statin. whether the patient is taking statins due to cardiovascular conditions (0,1)
- LAMA. whether the patient is on long acting muscarinic antagonist (0,1)
- LABA. whether the patient is on long acting beta agonist (0,1)
- ICS. whether the patient is on inhaled corticosteroids (0,1)
- randomizedLAMA. whether the patient was randomized to receivelong acting muscarinic antagonist. Should be 0 for prediction.(0,1)
- randomizedLABA. whether the patient was randomized to receive on long acting beta agonist. Should be 0 for prediction (0,1)
- randomizedICS. whether the patient was randomized to receive on inhaled corticosteroids. Should be 0 for prediction (0,1)
- randomizedAzithromycin. whether the patient was was randomized to receive long-term azithromycin therapy. Should be 0 for prediction (0,1)

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