

# Package ‘accept’

July 15, 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](https://doi.org/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

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## R topics documented:

accept	2
accept2	3
plotExacerbations	4
plotHeatMap	4
predictCountProb	5
samplePatients	6
<b>Index</b>	<b>7</b>

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accept	<i>Predicts COPD exacerbation rate by severity level based on Acute COPD Exacerbation Tool (ACCEPT)</i>
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### 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)
```

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accept2	<i>Predicts COPD exacerbation rate by severity level based on the updated accept2 model, which improves accuracy in patients without an exacerbation history.</i>
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### 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)
```

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plotExacerbations	<i>Creates bar graph comparing no treatment with azithromycin treatment</i>
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**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)
```

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plotHeatMap	<i>Creates heatmap of number of exacerbations</i>
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**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*

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**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*

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### **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 receive long 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)

# Index

## \* datasets

samplePatients, 6

accept, 2

accept2, 3

plotExacerbations, 4

plotHeatMap, 4

predictCountProb, 5

samplePatients, 6