

# Package ‘SLModels’

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**Title** Stepwise Linear Models for Binary Classification Problems under Youden Index Optimisation

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**Depends** stats, ROCR

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**Description** Stepwise models for the optimal linear combination of continuous variables in binary classification problems under Youden Index optimisation. Information on the models implemented can be found at Aznar-Gimeno et al. (2021) <[doi:10.3390/math9192497](https://doi.org/10.3390/math9192497)>.

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**Description**

Stepwise models for the optimal linear combination of continuous variables in binary classification problems under Youden Index optimisation. Information on the models implemented can be found at Aznar-Gimeno et al. (2021) <doi:10.3390/math9192497>.

**Usage**

```
SLModels(data, algorithm="stepwise", scaling=FALSE)
```

**Arguments**

data	Data frame containing the input variables and the binary output variable. The last column must be reserved for the output variable.
algorithm	string; Stepwise linear model to be applied. The options are: "stepwise", "min-max", "minmaxmedian", "minmaxiqr"; default value: "stepwise".
scaling	boolean; if TRUE, the Min-Max Scaling is applied; if FALSE, no normalisation is applied to the input variables; default value: FALSE.

**Details**

The "stepwise" algorithm refers to our proposed stepwise algorithm on the original variables which is the adaptation for the maximisation of the Youden index of the one proposed by Esteban et al. (2011) <doi:10.1080/02664761003692373>. The general idea of this approach, as suggested by Pepe and Thompson (2000) <doi:10.1093/biostatistics/1.2.123>, is to follow a step by step algorithm that includes a new variable in each step, selecting the best combination (or combinations) of two variables, in terms of maximising the Youden index.

The "minmax" algorithm refers to the distribution-free min-max approach proposed by Liu et al. (2011) <doi:10.1002/sim.4238>. The idea is to reduce the order of the linear combination beforehand by considering only two markers (maximum and minimum values of all the variables/biomarkers). This algorithm was adapted in order to maximise the Youden index.

The "minmaxmedian" algorithm refers to our proposed algorithm that considers the linear combination of the following three variables: the minimum, maximum and median values of the original variables.

The "minmaxiqr" algorithm refers to our proposed algorithm that considers the linear combination of the following three variables: the minimum, maximum and interquartile range (IQR) values of the original variables.

More information on the implemented algorithms can be found in Aznar-Gimeno et al. (2021) <doi:10.3390/math9192497>.

**Value**

Optimal linear combination that maximises the Youden index. Specifically, the function returns the coefficients for each variable, optimal cut-off point and Youden Index achieved.

**Note**

The "stepwise" algorithm becomes a computationally intensive problem when the number of variables exceeds 4.

**Author(s)**

Rocío Aznar-Gimeno, Luis Mariano Esteban, Gerardo Sanz, Rafael del Hoyo-Alonso

**References**

Aznar-Gimeno, R., Esteban, L. M., Sanz, G., del-Hoyo-Alonso, R., & Savirón-Cornudella, R. (2021). Incorporating a New Summary Statistic into the Min–Max Approach: A Min–Max–Median, Min–Max–IQR Combination of Biomarkers for Maximising the Youden Index. *Mathematics*, 9(19), 2497, doi:10.3390/math9192497.

Esteban, L. M., Sanz, G., & Borque, A. (2011). A step-by-step algorithm for combining diagnostic tests. *Journal of Applied Statistics*, 38(5), 899-911, doi:10.1080/02664761003692373.

Pepe, M. S., & Thompson, M. L. (2000). Combining diagnostic test results to increase accuracy. *Biostatistics*, 1(2), 123-140, doi:10.1093/biostatistics/1.2.123.

Liu, C., Liu, A., & Halabi, S. (2011). A min–max combination of biomarkers to improve diagnostic accuracy. *Statistics in medicine*, 30(16), 2005-2014, doi:10.1002/sim.4238.

**Examples**

```
#Create dataframe
x1<-rnorm(100,sd =1)
x2<-rnorm(100,sd =2)
x3<-rnorm(100,sd =3)
x4<-rnorm(100,sd =4)
z <- rep(c(1,0), c(50,50))
DT<-data.frame(cbind(x1,x2,x3,x4))
data<-cbind(DT,z)

#Example 1#
SLModels(data) #default values: algorithm="stepwise", scaling=FALSE
#Example 2#
SLModels(data, algorithm="minmax") #scaling=FALSE, default value
#Example 3#
SLModels(data, algorithm="minmax", scaling=TRUE)
#Example 4#
SLModels(data, algorithm="minmaxmedian", scaling=TRUE)
#Example 5#
SLModels(data, algorithm="minmaxiqr", scaling=TRUE)
```

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