VarSelLCM

Variable Selection for Model-Based Clustering of Mixed-Type Data Set with Missing Values.

References:

- Marbac, M. and Sedki, M. (2017), Variable selection for model-based clustering using the integrated complete-data likelihood, Statistics and Computing, Volume 27, Issue 4, pp 1049–1063.
- Marbac, M., Patin, E. and Sedki, M. (2018), Variable selection for mixed data clustering: Application in human population genomics, Arxiv 1703.02293.

Introduction

VarSelLCM permits a full model selection (detection of the relevant features for clustering and selection of the number of clusters) in model-based clustering, according to classical information criteria (BIC, MICL or AIC).

Data to analyzed can be composed of continuous, integer and/or categorical features. Moreover, missing values are managed, without any pre-processing, by the model used to cluster with the assumption that values are missing completely at random. Thus, VarSelLCM can also be used for data imputation via mixture models.

An R-Shiny application is implemented to easily interpret the clustering results

Mixed-type data analysis

This section performs the whole analysis of the *Heart* data set. *Warning continuous features must be stored in numeric, integer features must be stored in integer and categorical features must be stored in factor.*

```
library(VarSelLCM)
# Data loading
data("heart")
head(heart)
```

```
  Age Sex ChestPainType RestBloodPressure SerumCholestoral
1  70   1             4               130              322
2  67   0             3               115              564
3  57   1             2               124              261
4  64   1             4               128              263
5  74   0             2               120              269
6  65   1             4               120              177
  FastingBloodSugar ResElectrocardiographic MaxHeartRate ExerciseInduced
1                 0                       2          109               0
2                 0                       2          160               0
3                 0                       0          141               0
4                 0                       0          105               1
5                 0                       2          121               1
6                 0                       0          140               0
  Slope MajorVessels Thal Class
1     2            3    3     2
2     2            0    7     1
3     1            0    7     2
```

```
4     2            1    7     1
5     1            1    3     1
6     1            0    7     1
```

Clustering is performed with variable selection. Model selection is done with BIC because n>>d. The number of components is between 1 and 4. Do not hesitate to use parallelisation (here only two cores are used).

```
# Add a missing value artificially (just to show that it works!)
heart[1,1] <- NA
# Clustering with variable selection and a number of cluster betwee 1 and 4
# Model selection is BIC (to use MICL, the option must be specified)
out <- VarSelCluster(heart[,-13], 1:4, nbcores = 2)
```

Now, all the results can be analyzed by the Shiny application...

```
# Start the shiny application
 VarSelShiny(out)
```

... but this analysis can also be done on R.

To get a summary of the selected model.

```
# Summary of the best model
summary(out)
```

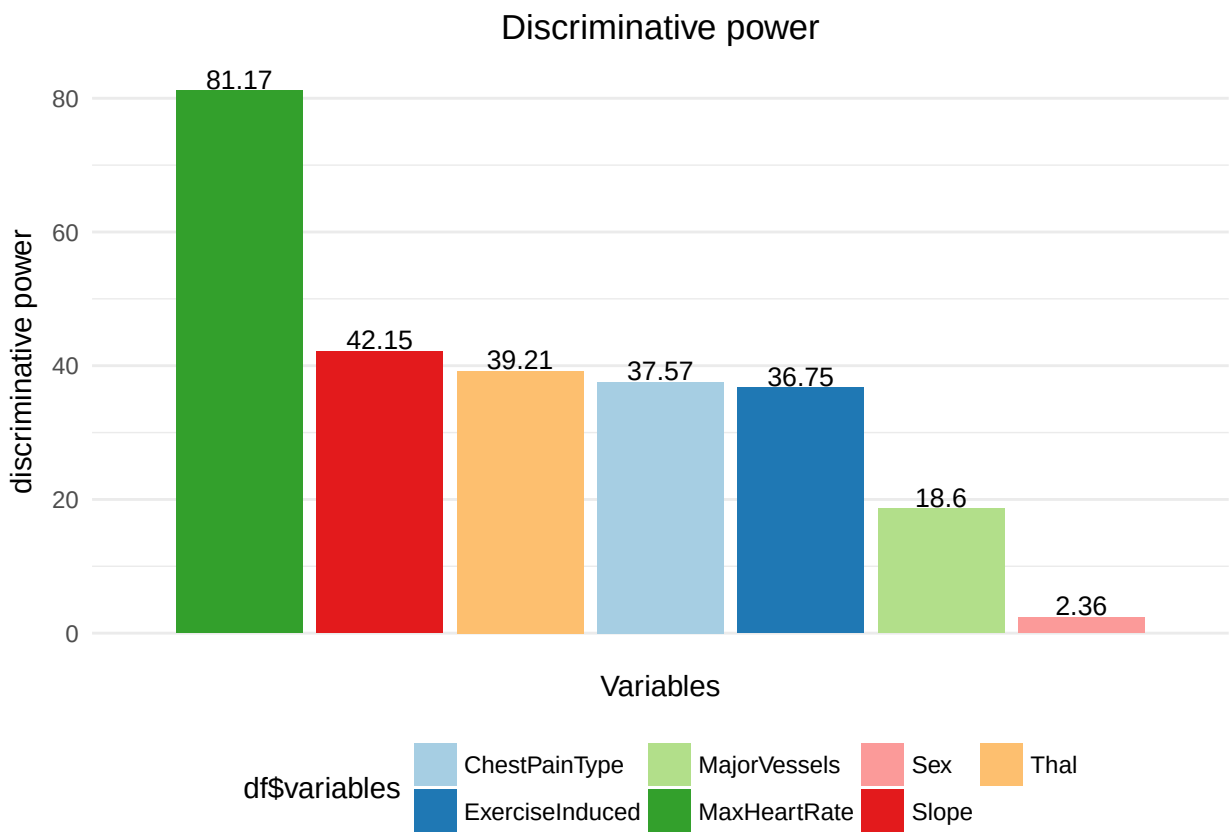
```
Data set:
   Number of individuals: 270
   Number of continuous variables: 3
   Number of count variables: 1
   Percentile of missing values for the integer variables: 0.37
   Number of categorical variables: 8

Model:
   Number of components: 2
   Model selection has been performed according to the BIC  criterion
   Variable selection has been performed, 8  ( 66.67 % ) of the variables are relevant for clustering

Information Criteria:
   loglike: -6403.136
   AIC:     -6441.136
   BIC:     -6509.506
   ICL:     -6638.116
```

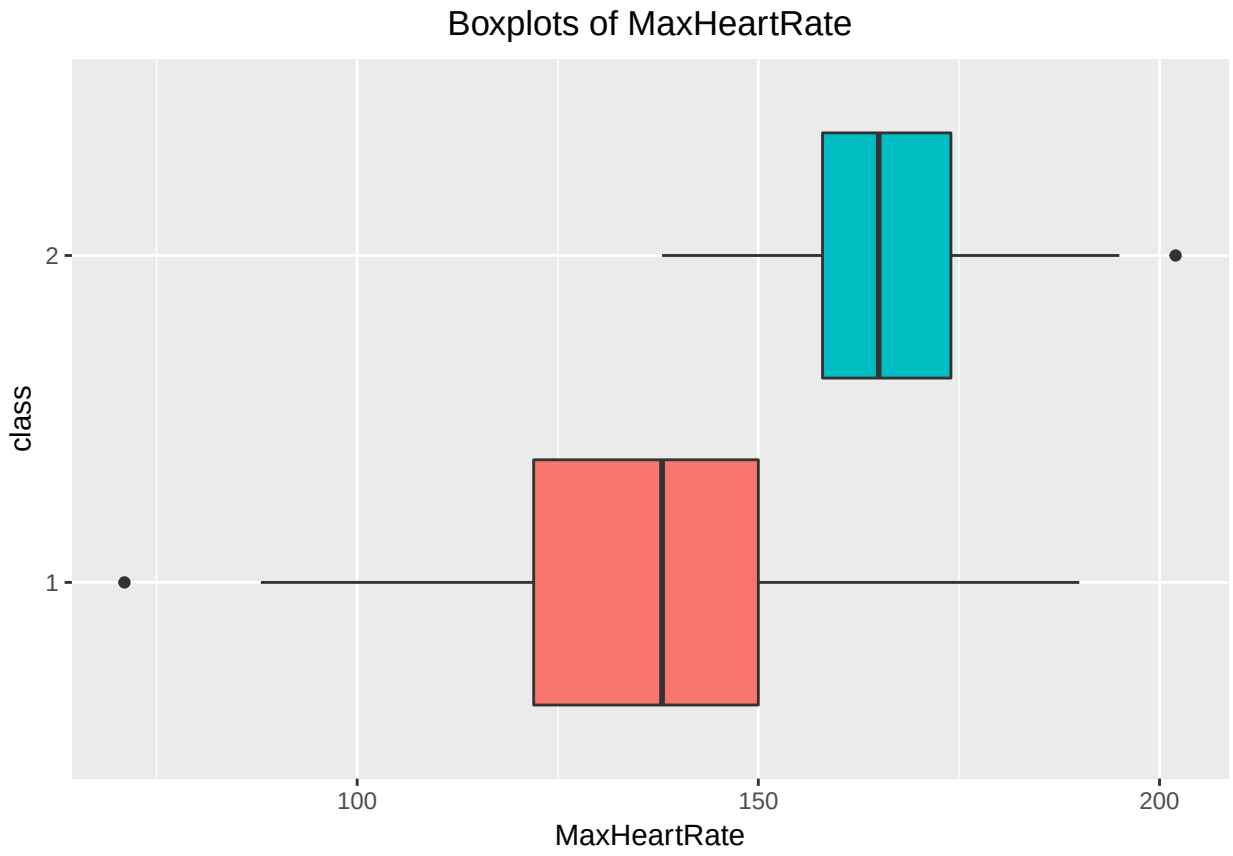
Model interpretation should focus on the most discriminative variables. These variables can be found with the following plot.

```
# Discriminative power of the variables (here, the most discriminative variable is MaxHeartRate)
plot(out, type="bar")
```



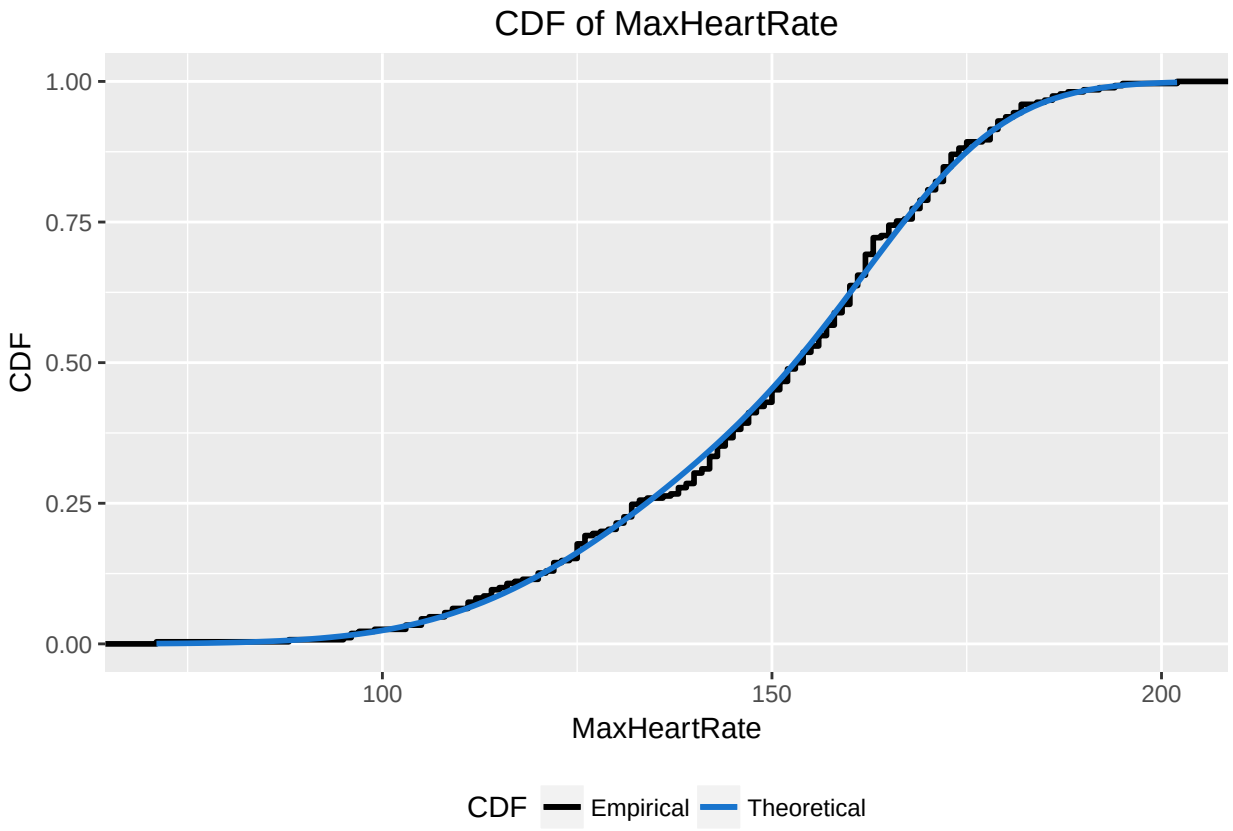
Interpretation of the most discriminative variable is based on its distribution per cluster.

```
# Boxplot for continuous (or interger) variable
plot(out, y="MaxHeartRate", type="boxplot")
```



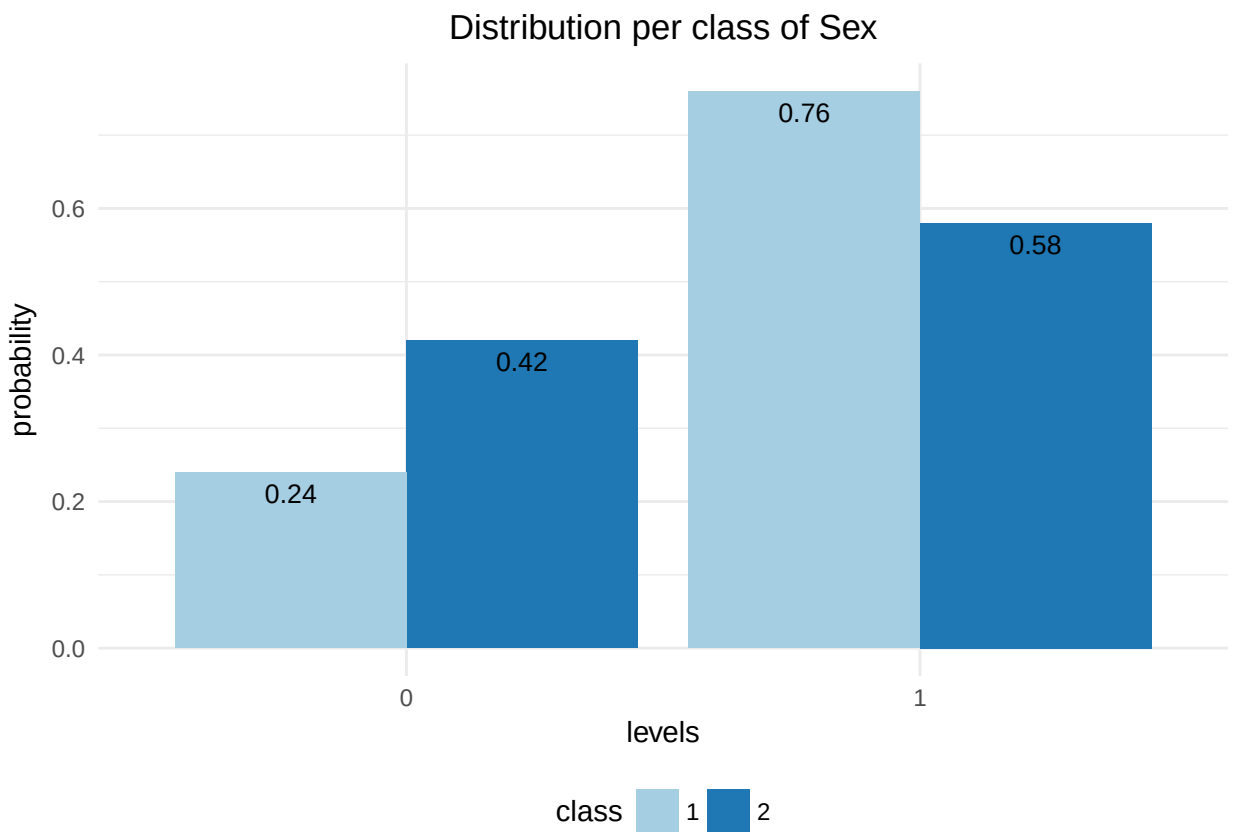
We can check that the distribution used to cluster is relevant.

```
# Empirical and theoretical distributions (to check that clustering is pertinent)
plot(out, y="MaxHeartRate", type="cdf")
```



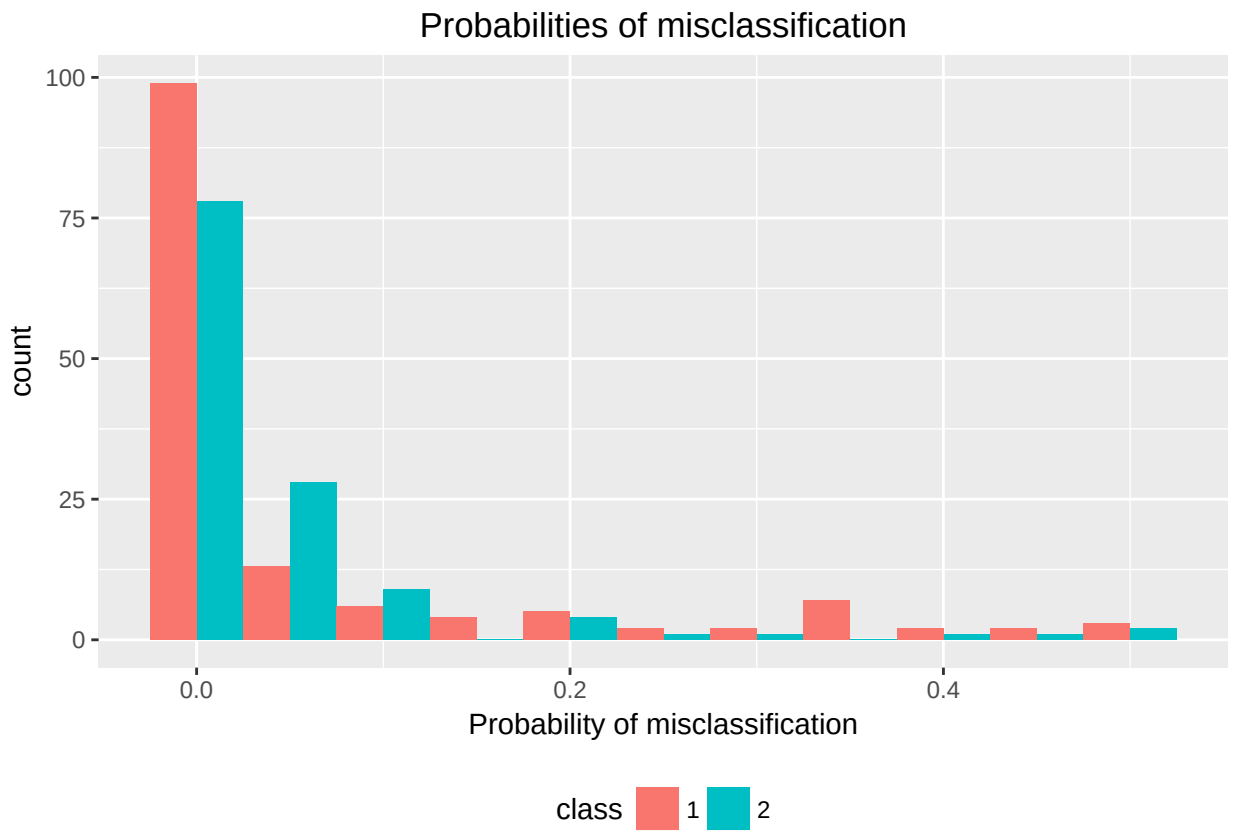
Interpretation of a categorical variable is based on its distribution per cluster.

```
# Summary of categorical variable
plot(out, y="Sex")
```



Interpretation of the cluster overlaps by using the probabilities of missclassification.

```
# Summary of the probabilities of missclassification
plot(out, type="probs-class")
```



Missing values can be imputed.

```
# Imputation by posterior mean for the first observation
not.imputed <- heart[1,-13]
imputed <- VarSelImputation(out)[1,]
rbind(not.imputed, imputed)
```

```
       Age Sex ChestPainType RestBloodPressure SerumCholestoral
1       NA   1             4               130              322
2 58.11329   1             4               130              322
  FastingBloodSugar ResElectrocardiographic MaxHeartRate ExerciseInduced
1                 0                       2          109               0
2                 0                       2          109               0
  Slope MajorVessels Thal
1     2            3    3
2     2            3    3
```