Testing prer and tidymixmod

Joshua Rosenberg 10/11/2017

Loading, setting up

First, run these three lines of code in order to install prcr (for cluster analysis-based profile analysis) and tidymixmod (for model-based profile analysis, or Latent Profile Analysis):

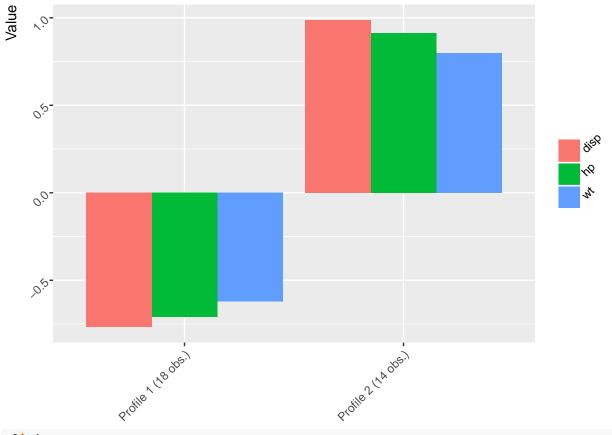
```
install.packages("prcr")
install.packages("devtools")
devtools::install_github("jrosen48/tidymixmod)
Next, load the packages:
library(tidymixmod)
library(prcr)
```

Getting started with prcr

plot(m2)

```
Now, we'll start with prcr. Run this line of code:
```

```
?create_profiles
This should give us an idea of how to use the function create_profiles(). Here's an example:
m2 <- create_profiles(mtcars, disp, hp, wt, n_profiles = 2, to_scale = TRUE, to_center = TRUE)
## Prepared data: Removed 0 incomplete cases
## Hierarchical clustering carried out on: 32 cases
## K-means algorithm converged: 1 iteration
## Clustered data: Using a 2 cluster solution
## Calculated statistics: R-squared = 0.654
summary(m2)
## 2 cluster solution (R-squared = 0.654)
##
## Profile n and means:
##
## # A tibble: 2 x 4
##
                 Cluster
                                                        wt.
                                disp
                                             hp
                               <dbl>
                                          <dbl>
## 1 Profile 1 (18 obs.) -0.7679844 -0.7093044 -0.6215850
## 2 Profile 2 (14 obs.) 0.9874085 0.9119628 0.7991807
```



m2\$.data

```
## # A tibble: 32 x 12
##
                   disp
              cyl
                            hp
                                drat
                                                                 gear
        mpg
                                         wt
                                             qsec
                                                      ٧S
                                                            am
##
      <dbl> <
                                                         <dbl>
                                                                <dbl>
                 6 160.0
                                3.90 2.620 16.46
##
    1 21.0
                           110
                                                       0
                                                              1
                                                                    4
                                                                           4
##
    2
       21.0
                 6 160.0
                           110
                                3.90 2.875 17.02
                                                       0
                                                              1
                                                                           4
       22.8
                 4 108.0
                                3.85 2.320 18.61
                                                                    4
##
    3
                            93
                                                       1
                                                              1
                                                                          1
##
       21.4
                6 258.0
                           110
                                3.08 3.215 19.44
                                                              0
                                                                    3
                                                                          1
                                                       1
                                                                          2
##
    5 18.7
                8 360.0
                                3.15 3.440 17.02
                                                              0
                                                                    3
                           175
                                                       0
      18.1
                 6 225.0
                           105
                                2.76 3.460 20.22
                                                              0
                                                                    3
                                                                          1
    6
                                                       1
                                                                    3
##
    7
       14.3
                 8 360.0
                           245
                                3.21 3.570 15.84
                                                       0
                                                              0
                                                                          4
       24.4
                 4 146.7
                                3.69 3.190 20.00
                                                              0
                                                                    4
                                                                          2
##
    8
                            62
                                                       1
##
   9 22.8
                 4 140.8
                            95
                                3.92 3.150 22.90
                                                              0
                                                                    4
                                                                          2
## 10 19.2
                 6 167.6
                           123 3.92 3.440 18.30
## # ... with 22 more rows, and 1 more variables: cluster <int>
```

Getting started with tidymixmod

We'll do the same thing with tidymixmod that we did with prcr, starting with the help file:

```
?create_profiles_mclust
```

Here's some example code:

```
m3 <- create_profiles_mclust(iris, Sepal.Length, Sepal.Width, Petal.Length, n_profiles = 3, model = 1,
```

```
## [[1]]
## <quosure: global>
## ~Sepal.Length
##
## [[2]]
## <quosure: global>
## ~Sepal.Width
##
## [[3]]
## <quosure: global>
## ~Petal.Length
##
## attr(,"class")
## [1] "quosures"
## Fit model with 3 profiles using the 'constrained variance' model.
## Model BIC is 807.309
calculate_centroids_mclust(m3)
         Variable Profile1 Profile2 Profile3
## 1 Sepal.Length 5.006056 5.879192 6.845031
## 2 Sepal.Width 3.427429 2.740044 3.072953
## 3 Petal.Length 1.462947 4.398460 5.679276
plot_mclust(m3)
  6 -
                                                                            Variable
  4 -
                                                                                Petal.Length
<u>Val</u>
                                                                                Sepal.Length
                                                                                Sepal.Width
  2 -
```

Profile3

Profile2

key

0 -

Profile1

Determining the number of clusters (for prcr) or mixture components (for tidymixmod)

In prcr, we can use the $plot_r_squared()$ function

```
?plot_r_squared
```

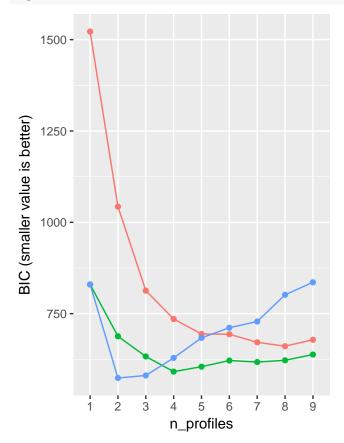
Here's an example:

```
##
     cluster r_squared_value
## 1
            2
                         0.654
## 2
            3
                         0.750
            4
                         0.833
## 3
            5
                            NA
## 4
## 5
            6
                            NA
## 6
            7
                            NA
```

There is also a very powerful function for performing cross-validation, cross_validate().

In tidymixmod, we can use the explore_models_mclust() function:

```
df <- dplyr::select(iris, -Species)
explore_models_mclust(df)</pre>
```



Covariance matrix structure

- Constrained variance, fixed covariance
- Constrained variance, constrained covariance
- Freed variance, freed covariance

Future directions

We are actively working to combine prcr and tidymixmod and to improve the user interface for the combined package. We are also working to add additional functionality.