project model 3 model based clustering and model comparison

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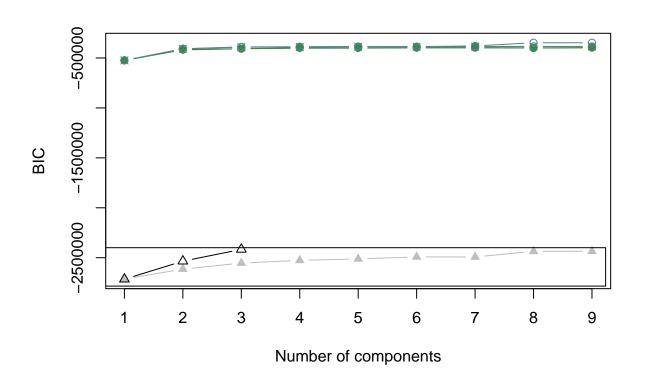
I have trouble plot figures on model density, uncertainty, classification The error message is "figure margin too large" I tried the following methods: dev.off() par(mar=c(1,1,1,1)) drag the plot area bigger I also tried just load a part of the dataset however, these method did not work

Helper packages

```
library(tidyverse)
## -- Attaching packages -----
                                                ----- tidyverse 1.3.2 --
## v ggplot2 3.4.0
                               0.3.4
                      v purrr
## v tibble 3.1.7
                      v dplyr
                              1.0.10
## v tidyr
          1.2.1
                      v stringr 1.4.1
          2.1.2
## v readr
                      v forcats 0.5.2
## -- Conflicts -----
                                        ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                   masks stats::lag()
library(dplyr)
library(stringr)
library(gridExtra)
##
## Attaching package: 'gridExtra'
## The following object is masked from 'package:dplyr':
##
##
      combine
library(cluster)
library(factoextra)
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
library(mclust)
## Package 'mclust' version 6.0.0
## Type 'citation("mclust")' for citing this R package in publications.
## Attaching package: 'mclust'
```

```
##
## The following object is masked from 'package:purrr':
##
##
       map
process the data
df <-read.csv("radiomics_completedata.csv")</pre>
df <- na.omit(df)</pre>
df<-select(df,-c(Institution, Failure.binary))</pre>
set.seed(123)
model based clustering
mdf<- Mclust(df, G = 3)</pre>
a<-summary(mdf) #if print a, too many pages</pre>
plot(mdf, what = "density")
## Error in plot.new(): figure margins too large
plot(mdf, what = "uncertainty")
## Error in plot.new(): figure margins too large
sort(mdf$uncertainty, decreasing = TRUE) %>% head()
                          93
                                        48
## 3.485515e-07 5.757084e-11 5.693224e-13 8.881784e-16 0.000000e+00 0.000000e+00
mdf_mc <- Mclust(df)</pre>
summary(mdf_mc)
## Gaussian finite mixture model fitted by EM algorithm
## Mclust VVI (diagonal, varying volume and shape) model with 9 components:
##
## log-likelihood n
                         df
                                   BIC
         -153331.3 197 7730 -347501.7 -347501.7
##
##
## Clustering table:
## 1 2 3 4 5 6 7 8 9
## 94 38 3 2 10 8 15 9 18
```

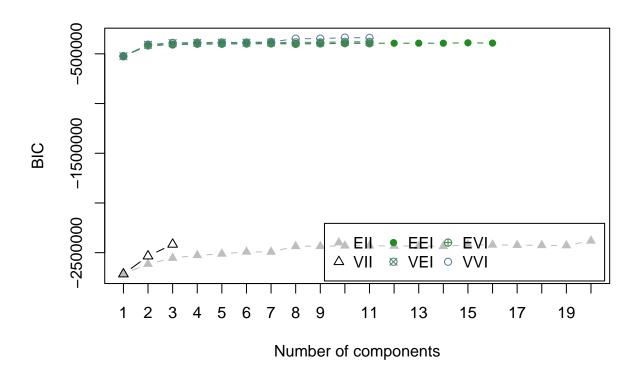
```
legend_args <- list(x = "bottomright", ncol = 427)
plot(mdf_mc, what = 'BIC', legendArgs = legend_args)</pre>
```



```
plot(mdf_mc, what = 'classification')
## Error in plot.new(): figure margins too large
plot(mdf_mc, what = 'uncertainty')
## Error in plot.new(): figure margins too large
df_mc <- Mclust(df, 1:20)</pre>
summary(df_mc)
\hbox{\tt \#\# Gaussian finite mixture model fitted by EM algorithm}
##
## Mclust VVI (diagonal, varying volume and shape) model with 10 components:
##
##
   log-likelihood n
                          df
                                   BIC
         -145818.9 197 8589 -337015.1 -337015.1
##
```

```
##
## Clustering table:
## 1 2 3 4 5 6 7 8 9 10
## 56 39 37 3 2 10 8 15 9 18

plot(df_mc, what = 'BIC',
    legendArgs = list(x = "bottomright", ncol = 5))
```

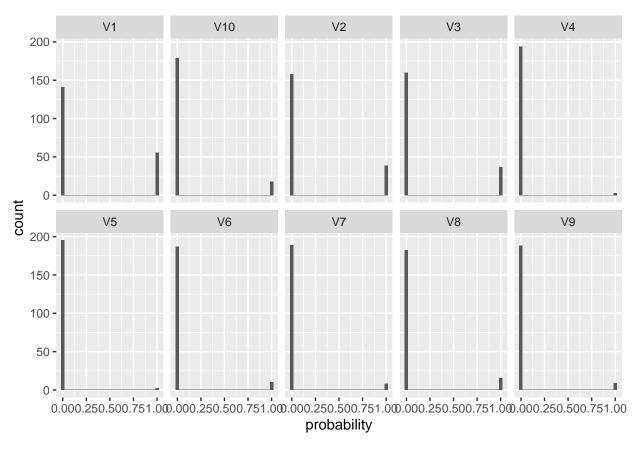


```
probabilities <- df_mc$z

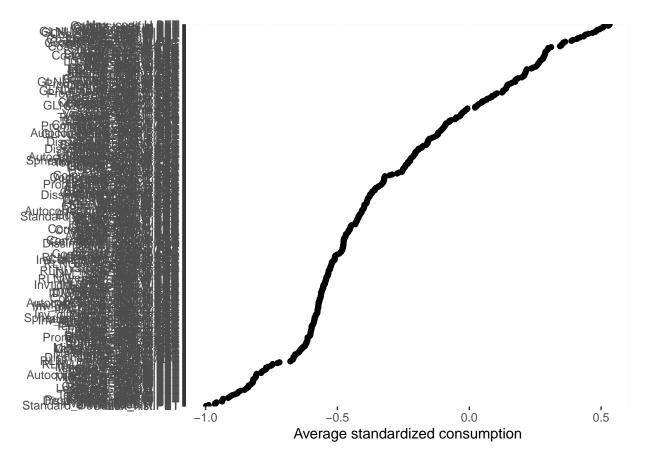
probabilities <- probabilities %>%
   as.data.frame() %>%
   mutate(id = row_number()) %>%
   tidyr::gather(cluster, probability, -id)

ggplot(probabilities, aes(probability)) +
   geom_histogram() +
   facet_wrap(~ cluster, nrow = 2)
```

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



```
uncertainty <- data.frame(</pre>
  id = 1:nrow(df),
  cluster = df_mc$classification,
  uncertainty = df_mc$uncertainty
cluster2 <- df %>%
  scale() %>%
  as.data.frame() %>%
  mutate(cluster = df_mc$classification) %>%
  filter(cluster == 2) %>%
  select(-cluster)
cluster2 %>%
  tidyr::gather(product, std_count) %>%
  group_by(product) %>%
  summarize(avg = mean(std_count)) %>%
  ggplot(aes(avg, reorder(product, avg))) +
  geom_point() +
  labs(x = "Average standardized consumption", y = NULL)
```



compare 3 models In K-mean cluster, the number of clusters is predefined or defined with the elbow method. Since k-mean uses the mean, it is not sensitive to outliers. K-mean also requires more computational power. Hierarchical clustering will create hierarchy of clusters and does not require to pre-specify the number of clusters. Compared to K-mean, hierarchical clustering use dendrogram, so the results can be visualized. k-means and hierarchical clustering are heuristic based methods that generate clusters directly based on the data. Model-based clustering automatically identifying the optimal number of clusters.