

es2

2024-01-13

Load libraries

```
shhh = function(lib_name){ # It's a library, so shhh!
  suppressWarnings(suppressMessages(require(lib_name, character.only = TRUE)))
}
shhh("tidyverse")
shhh("ACutils")
shhh("mvtnorm")
shhh("salso")
shhh("FGM")
shhh("gmp")
shhh("mcclust")
shhh("mcclust.ext")
shhh("logr")
shhh("tidygraph")
shhh("ggraph")
shhh("igraph")
shhh("Rcpp")
shhh("RcppArmadillo")
shhh("RcppEigen")

## Load custom functions
source("functions/utility_functions.R");
source("bulky_functions_old.R");
source("functions/data_generation.R")
sourceCpp("functions/wade.cpp")
Rcpp::sourceCpp('functions/UpdateParamsGSL.cpp')

library('RcppGSL')
library(fda)
library(tidyverse)
library(coda)
library(lattice)
```

Goal

Stima della partizione dei dati simulati usando bulky functions del vecchio gruppo.

Simulated data

Simuliamo i dati in `sim_data.R` con $p=20$ basi e 3 cluster di dimensioni $[6,6,8]$. Grafo e matrice di precisione sono generati attraverso la funzione `Generate_BlockDiagonal`.

```
# Import simulated data
BaseMat = as.matrix(read_csv('BaseMat.csv'))           # matrix Phi, dim = 200 x 20
y_hat_true = as.matrix(read_csv('y_hat_true.csv'))     # y true, dim = 300 x 200
beta_true = as.matrix(read_csv('beta_true.csv'))       # beta, dim = 300 x 20
mu_true = as.matrix(read_csv('mu_true.csv'))          # mu true, dim = 20 x 1

# object containing the true graph G, the true precision matrix K
simKG <- readRDS("simKG.rds")

n <- dim(y_hat_true)[1] # n=300
r <- dim(y_hat_true)[2] # r=200
p <- dim(BaseMat)[2]    # p=20
```

Initialization

```
# Define the starting Beta matrix
Beta = t(beta_true)

# Define the starting value of mu
mu = as.vector(mu_true)

# Fix tau_eps (squared)
tau_eps = 100

# Define the starting precision matrix K and graph G
K = matrix(0,p,p)
G = matrix(0,p,p)

# Define the starting partition (all in one group)
rho = p
z = rep(1,p)

# Compute quantities for function UpdateParamGSL
tbase_base = t(BaseMat)%*%BaseMat           # p x p (phi_t * phi)
tbase_data = t(BaseMat)%*%t(y_hat_true)     # p x n (phi_t * Y_t)
Sdata = sum(diag(y_hat_true)%*%t(y_hat_true))) # initialize phi*beta = 0

# Set True binary flag used to update values
Update_Beta <- FALSE
Update_Mu <- FALSE
Update_Tau <- FALSE

# Define hyperparameters values
a_tau_eps <- 2000
b_tau_eps <- 2
sigma_mu <- 100
```

```

# Define variance of the Beta
beta_sig2 = 0.2

# Compute graph density
graph_density = sum(simKG$Graph) / (p*(p-1))

# Set the number of iterations and burn-in
niter <- 10000
burn_in <- 1000

# initialization of parameters for set_options
sigma <-0.5 # parameter of the prior of the partition
theta <-1 # parameter of the prior of the partition
weights_a <- rep(1,p-1) # starting weights
weights_d <- rep(1,p-1) # starting weights

```

Gibbs sampler

```

# Set options for Gibbs_sampler
options = set_options(
  sigma_prior_0=sigma,
  sigma_prior_parameters=list("a"=1,"b"=1,"c"=1,"d"=1),
  theta_prior_0=theta,
  theta_prior_parameters=list("c"=1,"d"=1),
  rho0=rho,
  weights_a0=weights_a,
  weights_d0=weights_d,
  alpha_target=0.234,
  beta_mu=graph_density, # expected value beta distr of the graph
  beta_sig2=beta_sig2, # var beta distr del grafo, fra 0 e 0.25
  d=3, # param della G wishart (default 3)
  alpha_add=0.5,
  adaptation_step=1/(p*1000),
  update_sigma_prior=TRUE,
  update_theta_prior=TRUE,
  update_weights=TRUE,
  update_partition=TRUE,
  update_graph=TRUE,
  perform_shuffle=TRUE
)

# Gibbs Sampler
res <- Gibbs_sampler(
  data = t(Beta-mu),
  niter = niter-burn_in, # niter finali, già tolto il burn in
  nburn = burn_in,
  thin = 1,
  options = options,
  seed = 123456,

```

```

    print = FALSE
  )

```

Useful plots

```

# Before saving, also append true data
res$true_rho = c(6,6,8)
res$true_precision = simKG$Prec
res$true_graph = simKG$Graph
# remove self loops
res$true_graph[col(res$true_graph)==row(res$true_graph)] = 0

# Posterior analysis

## Recomputing the partition in other forms and the number of groups

rho_true = res$true_rho
r_true = rho_to_r(rho_true)
z_true = rho_to_z(rho_true)
p = length(z_true)
num_clusters_true = length(rho_true)
rho = res$rho
r = do.call(rbind, lapply(res$rho, rho_to_r))

## Warning in (function (... , deparse.level = 1) : number of columns of result is
## not a multiple of vector length (arg 13)

z = do.call(rbind, lapply(res$rho, rho_to_z))
num_clusters = do.call(rbind, lapply(res$rho, length))
num_clusters = as.vector(num_clusters)

### Acceptance frequency
mean(res$accepted)    #0.02175

## [1] 0.08944444

### Barplot of changepoints
bar_heights = colSums(r)
cp_true = which(r_true==1)
color <- ifelse(seq_along(bar_heights) %in% c(cp_true), "red", "gray")

barplot(
  bar_heights,
  names = seq_along(bar_heights),
  border = "NA",
  space = 0,

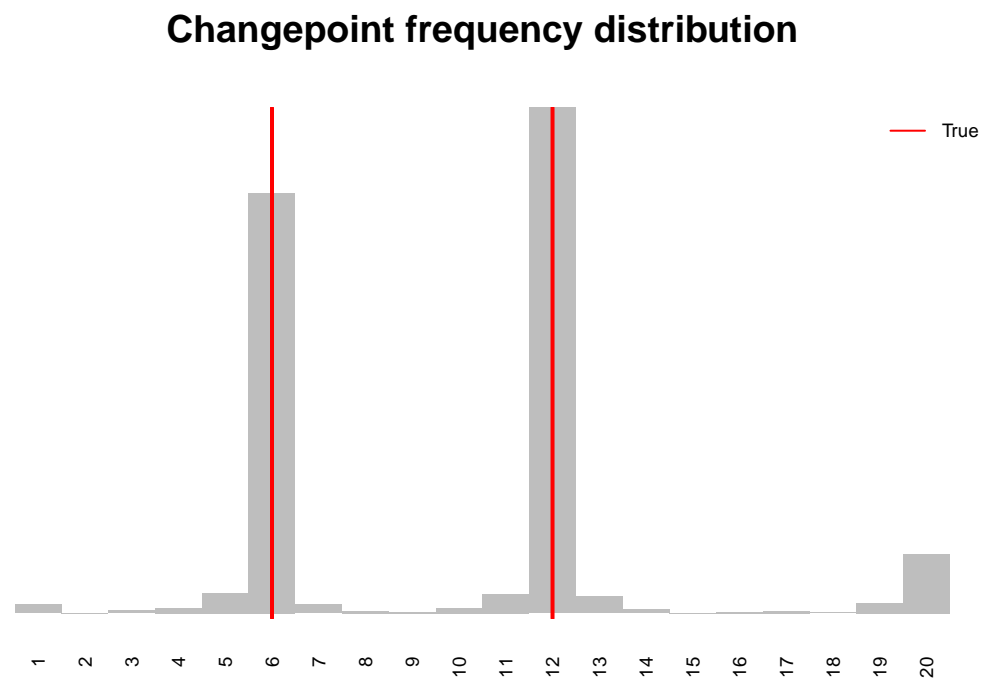
```

```

yaxt = "n",
main="Changepoint frequency distribution",
#col = color,
cex.names=.6,
las=2
)

abline(v=cp_true-0.5, col="red", lwd=2)
legend("topright", legend=c("True"), col=c("red"),
      bty = "n",
      lty = 1,
      cex = 0.6)

```



```

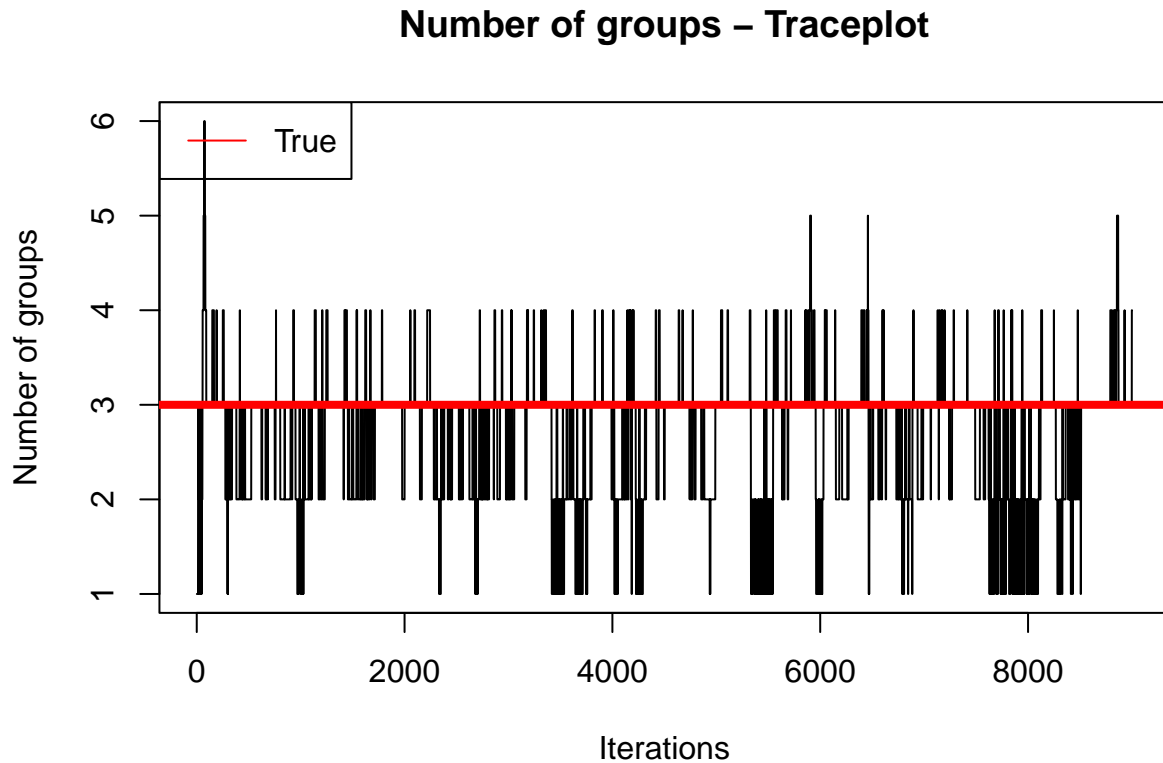
### Evolution of the number of clusters
plot(
  x = seq_along(num_clusters),
  y = num_clusters,
  type = "n",
  xlab = "Iterations",
  ylab = "Number of groups",
  main = "Number of groups - Traceplot"
)
lines(x = seq_along(num_clusters), y = num_clusters)
abline(h = length(z_to_rho(z_true)),
      col = "red",

```

```

lwd = 4)
legend("topleft", legend=c("True"), col=c("red"),
      lty = 1,
      cex = 1)

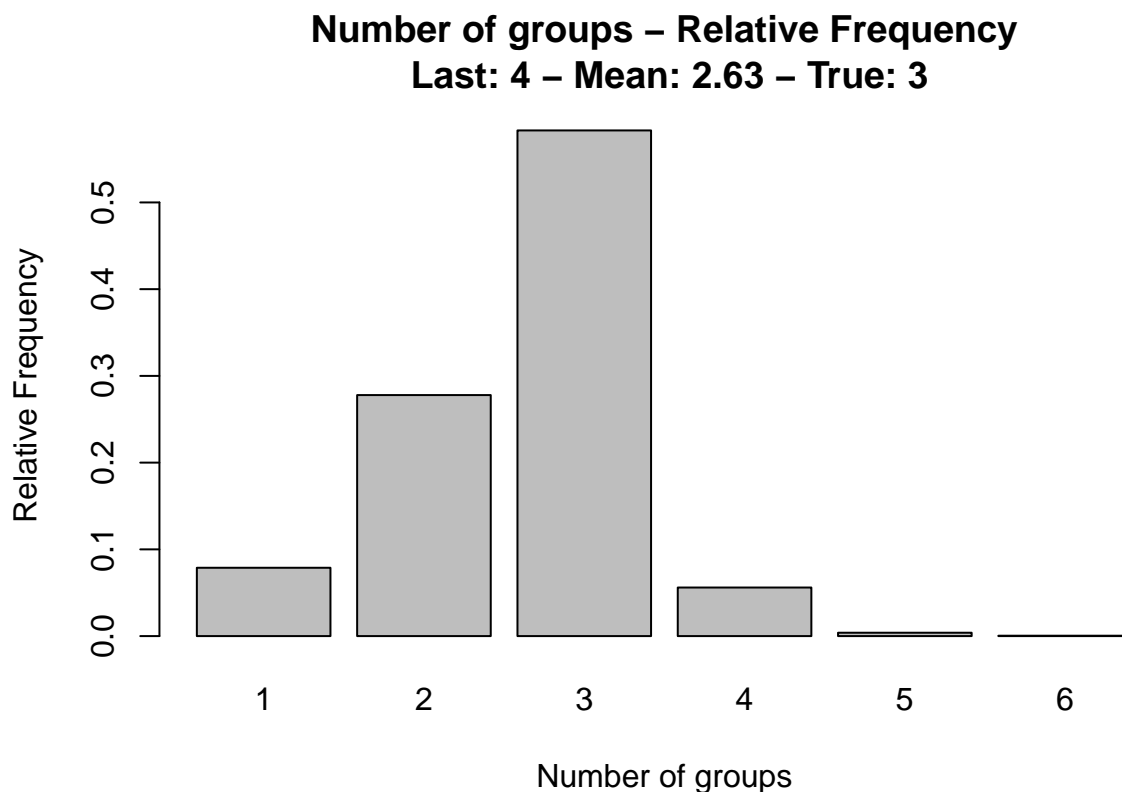
```



```

barplot(
  prop.table(table(num_clusters)),
  xlab = "Number of groups",
  ylab = "Relative Frequency",
  main = paste(
    "Number of groups - Relative Frequency\n",
    "Last:",
    tail(num_clusters, n = 1),
    "- Mean:",
    round(mean(num_clusters), 2),
    "- True:",
    num_clusters_true
  )
)

```



```

### Evolution of the Rand Index

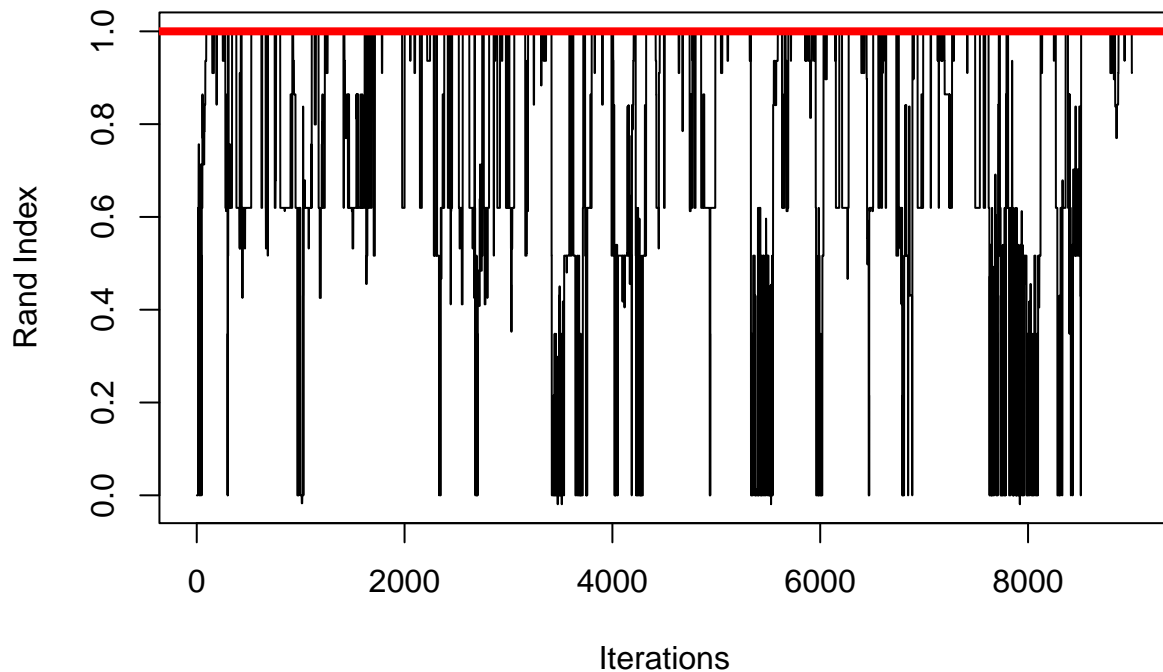
# computing rand index for each iteration
rand_index = apply(z, 1, mcclust::arandi, z_true)

# plotting the traceplot of the index
plot(
  x = seq_along(rand_index),
  y = rand_index,
  type = "n",
  xlab = "Iterations",
  ylab = "Rand Index",
  main = paste(
    "Rand Index - Traceplot\n",
    "Last:",
    round(tail(rand_index, n=1), 3),
    "- Mean:",
    round(mean(rand_index), 2)
  )
)
lines(x = seq_along(rand_index), y = rand_index)
abline(h = 1, col = "red", lwd = 4)

```

Rand Index – Traceplot

Last: 0.91 – Mean: 0.77



```
### Retrieving best partition using VI on visited ones (order is guaranteed here)
```

```
# Here we are satisfied with finding the optimal partition only in the set of those visited, not in all  
# I would say that it is the implementation of formula (13) of the Corradin-Danese paper (https://doi.org/10.1016/j.jml.2016.03.001)
```

```
# compute VI
```

```
sim_matrix <- salso::psm(z)
```

```
dists <- VI_LB(z, psm_mat = sim_matrix)
```

```
# select best partition (among the visited ones)
```

```
best_partition_index = which.min(dists)
```

```
rho_est = rho[[best_partition_index]]
```

```
z_est = z[best_partition_index,]
```

```
# VI loss
```

```
dists[best_partition_index]
```

```
## [1] 0.47101
```

```
# select best partition
```

```
unnname(z_est)
```

```
## [1] 1 1 1 1 1 1 2 2 2 2 2 2 3 3 3 3 3 3 3 3
```



```
# compute Rand Index
mcclust::arandi(z_est, z_true)
```

```
## [1] 1
```

```
## Graph
```

```
# Extract last plinks
last_plinks = tail(res$G, n=1)[[1]]

# Criterion 1 to select the threshold (should not work very well) and assign final graph
threshold = 0.5
G_est <- matrix(0,p,p)
G_est[which(last_plinks>threshold)] = 1

#Criterion 2 to select the threshold
bfdr_select = BFDR_selection(last_plinks, tol = seq(0.1, 1, by = 0.001))

# Inspect the threshold and assign final graph
bfdr_select$best_treshold
```

```
## [1] 0.754
```

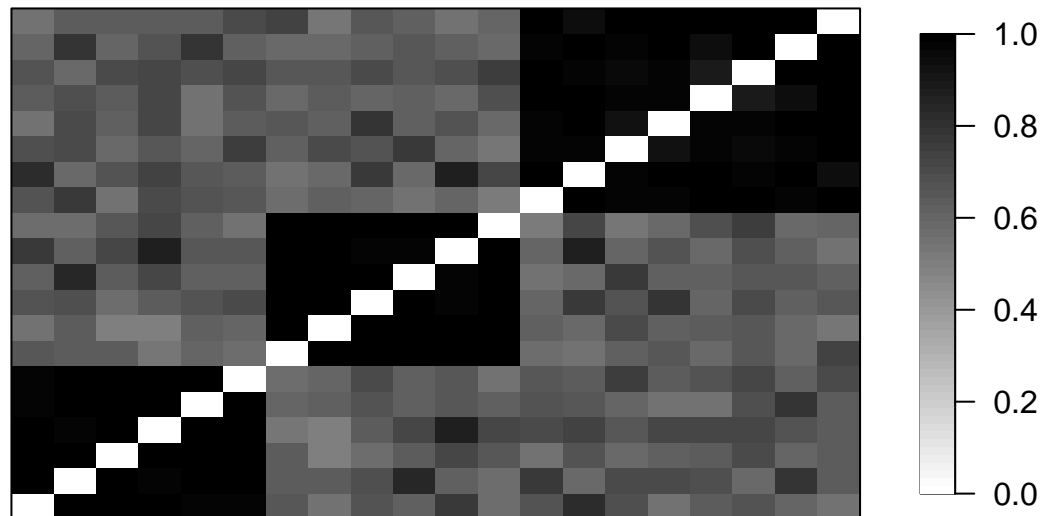
```
G_est = bfdr_select$best_truncated_graph
```

```
### Standardized Hamming distance
SHD = sum(abs(simKG$true_graph - G_est)) / (p^2 - p)
SHD
```

```
## [1] 0
```

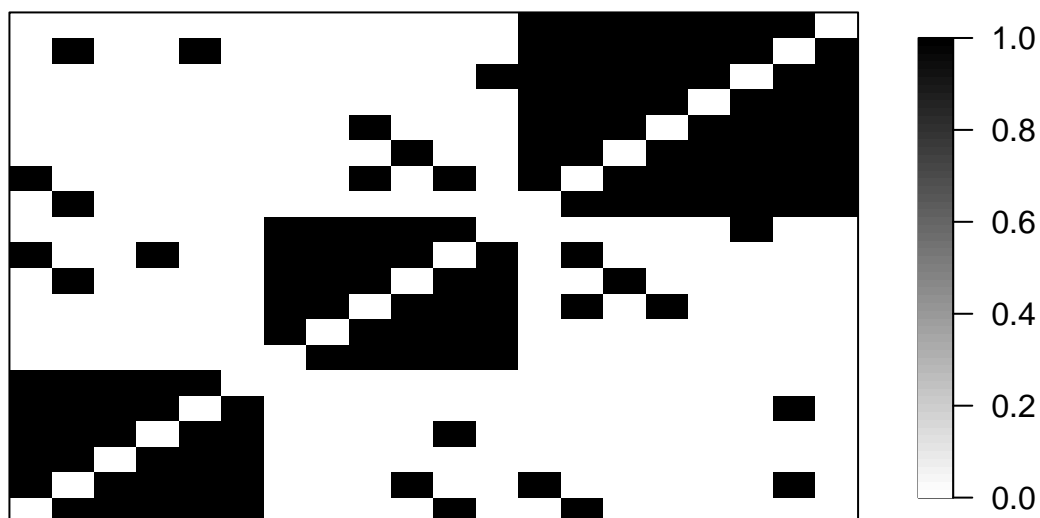
```
### Plot estimated matrices
ACutils::ACheatmap(
  last_plinks,
  use_x11_device = F,
  horizontal = F,
  main = "Estimated plinks matrix",
  center_value = NULL,
  col.upper = "black",
  col.center = "grey50",
  col.lower = "white"
)
```

Estimated plinks matrix



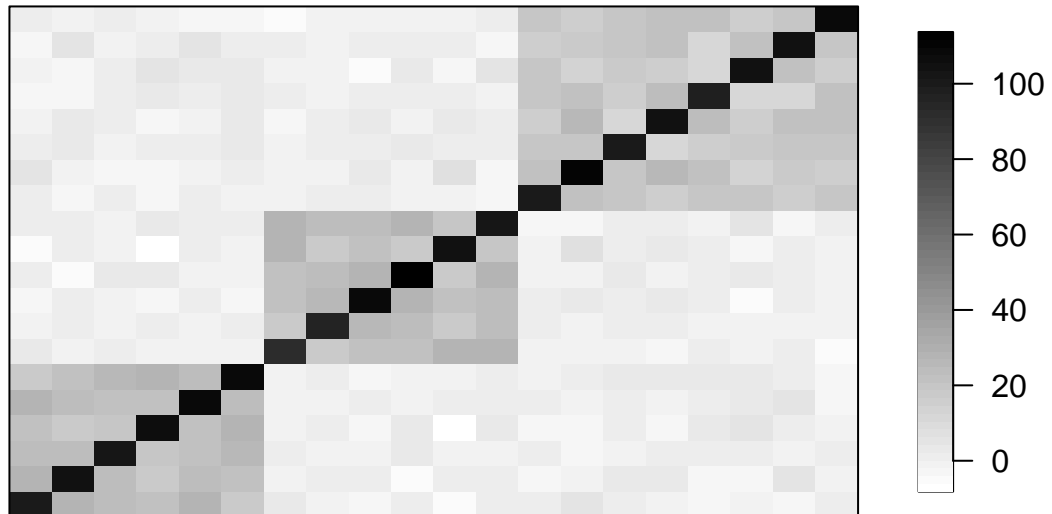
```
ACutils::ACheatmap(  
  G_est,  
  use_x11_device = F,  
  horizontal = F,  
  main = "Estimated Graph",  
  center_value = NULL,  
  col.upper = "black",  
  col.center = "grey50",  
  col.lower = "white"  
)
```

Estimated Graph



```
ACutils::ACheatmap(  
  tail(res$K,n=1)[[1]],  
  use_x11_device = F,  
  horizontal = F,  
  main = "Estimated Precision matrix",  
  center_value = NULL,  
  col.upper = "black",  
  col.center = "grey50",  
  col.lower = "white"  
)
```

Estimated Precision matrix

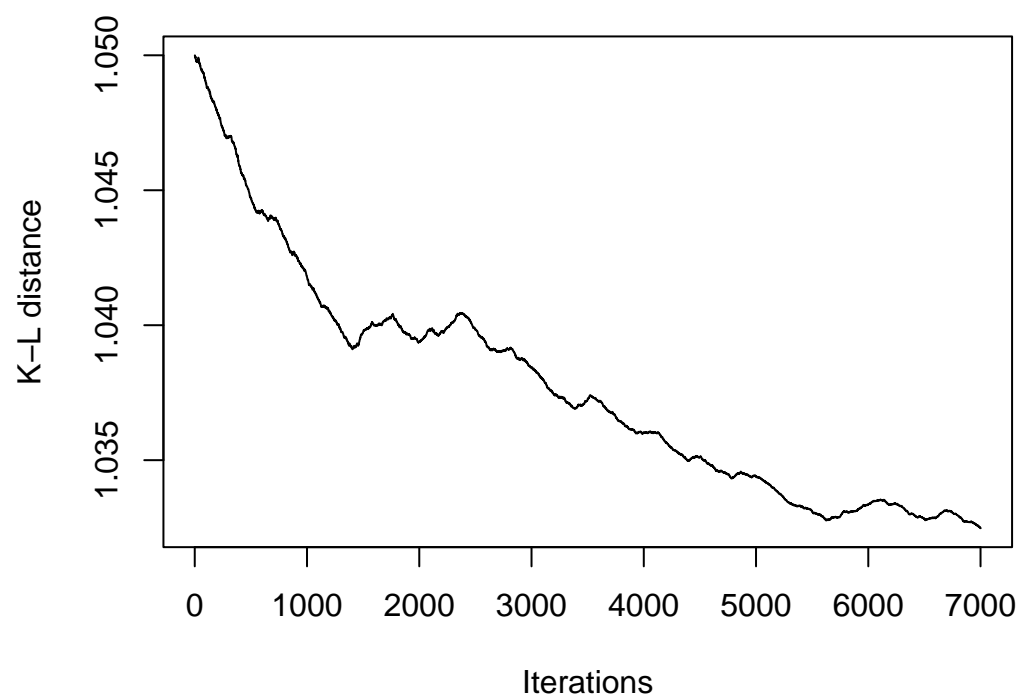


```
### Evolution of the Kullback-Leibler
kl_dist = do.call(rbind, lapply(res$K, function(k) {
  ACutils::KL_dist(res$true_precision, k)
}))

last = round(tail(kl_dist, n=1), 3)
plot(
  x = seq_along(kl_dist[2000:length(kl_dist)]),
  y = kl_dist[2000:length(kl_dist)],
  type = "n",
  xlab = "Iterations",
  ylab = "K-L distance",
  main = paste("Kullback-Leibler distance\nLast value:", last)
)
lines(x = seq_along(kl_dist[2000:length(kl_dist)]), y = kl_dist[2000:length(kl_dist)])
```

Kullback–Leibler distance

Last value: 1.032



non c'è burn in !!!!