DSSFA Project

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Upload data from 'psych'

This dataset contains 25 self-report personality items from the International Personality Item Pool (ipip.ori.org). It was developed as part of the Personality Assessment Project. The data contains the responses of 2800 people and can be used for demonstration purposes, as well as for the factor analysis that we will use here. We try to reduce the dimension to at least 25-1=24 factors, but we can even be more ambitious and propose directly $k_{max}=15$ for the speed of implementation of the following algorithms. More information here.

```
data(bfi)
bfi = na.omit(bfi)
bfi = bfi[which(bfi$age>50),1:25]
```

A1 A2 A3 A4 A5 C1 C2 C3 C4 C5 E1 E2 E3 E4 E5 N1 N2 N3 N4 N5 O1 O2 ## 61661 -1 -2 -4 -5 -1 -1 -2 61669 -2 -1 -1 -2 -4 2 -3 61782 -1 -5 61813 -1 -2 -4 -1 -3 -5 -4 -4 -2-2-262260 -1 -4 ## 62267 -1 -2 -1 -5 -5 -2 ## 62333 -1 -1 -5 62345 -2 -3 -4 -1 ## 62368 -1 -5 -6 62423 -2 -2 -3 -3 -2 -2 -4 -2 -6 62498 -1 -4 -1 -6 -6 62518 -2 2 -5 ## 62577 -2 -4 -5 -6 -5 -2 -2 62597 - 2-5 -1 -2 62599 -1 -3 -1 -6 -3 62617 -2 -1 -1 -1-4 -1 -1-5 62638 -2 -2 -1 -1 -2 -2 62664 -1 ## 62688 -1 -2 -5 -1 -1 -5 -1 -3 -1 -1 -3 62719 -1 -1 -1 -1 ## 62750 -2 -2 -2 ## 62874 -1 6 -1 -1 -1 -1 5 -2

```
## 66965 -2
## 67026 -5
## 67029 -5
## 67055 -5
## 67098 -1
## 67232 -2
## 67342 -4
## 67388 -3
## 67406 -2
## 67453 -1
```

These data are preprocessed by us. Here, we hide a part of the code if it is not directly related to the subject, for a better readability.

Note: The algorithms called with "source()" are presented in the appendix, to ease the reading.

Gibbs Sampler

```
burn_in = 5000
```

Burn-in for the sampler

```
p = dim(gibbs$y)[2]
```

Number of variables: 25

```
thin = 5
thinning = seq(burn_in+1,gibbs$N_sampl,by=thin)
```

Thinning

```
Omega_post = array(NA,c(p,p,length(thinning)))
```

Posterior sample of the covaraince matrix

Object to build

```
obj = list()
```

```
obj$P = p
```

Number of variables in the sample : 25

```
obj$samp.size = length(thinning)
```

Sample size: 2000

```
obj$post.cov = Omega_post
```

Posterior sample covariance matrix

```
obj$nsim = 2000
obj$thin = 1
```

Posterior sample size: 2000

DSSFA Method applied to our object $(k_max = 15)$:

```
source("DSSFA.R")
obj.bfa.list.CUSP = DSSFA(obj, length.lambda = 2, k.max = 15, print.out = T, tol.em = 0.00001)
## Factor = 1
## Factor = 2
## Factor = 3
## Factor = 4
## Factor = 5
## Factor = 6
## Factor = 7
## Factor = 8
## Factor = 9
## Factor = 10
## Factor = 11
## Factor = 12
## Factor = 13
## Factor = 14
## Factor = 15
```

Creation of the 95% confidence interval:

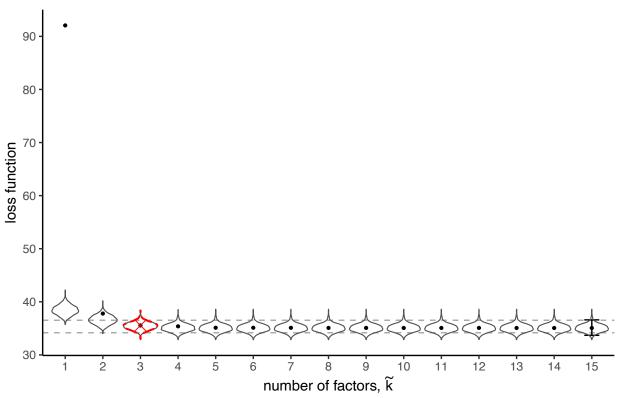
```
CI = list()
CI$CI.85 = list(c("85"),c(0.075,0.925))
CI$CI.90 = list(c("90"),c(0.05,0.95))
CI$CI.95 = list(c("95"),c(0.025,0.975))
CI$CI.99 = list(c("99"),c(0.005,0.995))
```

Plots that summarize the DSSFA method:

```
source("summary_plot.R")
summary.plot(obj.bfa.list.CUSP,CI[[3]],cov.dssfa = T, text_main_prior = "CUSP prior,", col.lambda = 1,1
```

Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0. ## i Please use 'linewidth' instead.

DSSFA Posterior Summary, 95% quantile. $\lambda = \lambda_0$, $\widetilde{k} = 3$



"Summary.plot" creates a summary graph for the Bayesian factor analysis model, as above. This function uses a default CI of 95%. It uses the fit values of the model to select the best number of factors and the best lambda value of the loss. Then the function uses the selected loadings and uniquenesses to calculate the Omega matrices. In this case, we can see the selected number of factors: k=3.

Select the right number of factors:

```
source("DSSFA_sel_mat.R")
mat.sel = sel.model.dssfa(obj.bfa.list.CUSP,CI[[3]])
sel = min(which(lapply(mat.sel$mat.sel.ksel,is.null) == F))
cat('The right number of factors is : k =', sel)
```

```
## The right number of factors is : k = 3
```

"Sel.model.dssfa" selects the "best" model from a list of models based on the confidence interval. The function checks if a k-value has been provided (number of factors), otherwise it uses all k-values between 1 and the maximum k-value provided in the input list, here k_max=15. Then, it calculates the quantiles of the credible interval using the fit values of the models and loops over the selected k-values and checks whether the fit value of each model is within the credible interval. If this is the case, the function saves the parameters of the corresponding model, otherwise it saves a null value. It also records uniquenesses and correlation matrices if they have been provided in the input list. Here, the function returns "3": the selected model (ie. the selected number of factors).

Loadings Matrix:

We finally obtain the loadings matrix from the DSSFA method, for k=3 number of factors (F1, F2, and F3). A clear and interpretable pattern is observed in the loadings from the DSSFA method, despite the reduction of the factor dimension.



Appendix

You will find the functions useful for the realization of our code.

Gibbs sampler

```
gibbs_sampler <- function(y,my_seed,N_sampl,alpha,a_sig,b_sig,a_theta,b_theta,
                                                                                            theta_inf,start_adapt,Hmax,alpha0,alpha1){
      set.seed(my_seed)
      n<-dim(y)[1]</pre>
      p<-dim(y)[2]</pre>
      u<-runif(N_sampl)
      H<-rep(NA,N_sampl)</pre>
      Hstar<-rep(NA,N_sampl)</pre>
      Lambda_post<-vector("list", N_sampl)</pre>
      eta_post<-vector("list",N_sampl)</pre>
      theta_inv_post<-vector("list",N_sampl)</pre>
      w_post<-vector("list", N_sampl)</pre>
      z_post<-vector("list", N_sampl)</pre>
      inv_sigma_sq_post<-matrix(NA,p,N_sampl)</pre>
      H[1] \leftarrow p+1
      Hstar[1]<-p</pre>
      Lambda_post[[1]] <-matrix(rnorm(p*H[1]),p,H[1])</pre>
      eta_post[[1]]<-matrix(rnorm(n*H[1]),n,H[1])</pre>
      theta_inv_post[[1]] <-rep(1,H[1])</pre>
      w_post[[1]]<-rep(1/H[1],H[1])</pre>
      z_post[[1]] <-rep(H[1],H[1])
      inv_sigma_sq_post[,1]<-1</pre>
      t0 <- proc.time()
      for (t in 2:N_sampl){
           Lambda_post[[t]] <-matrix(NA,p,H[t-1])</pre>
            eta_post[[t]] <-matrix(NA,n,H[t-1])</pre>
           theta_inv_post[[t]] <-rep(NA,H[t-1])</pre>
            w_post[[t]] \leftarrow rep(NA, H[t-1])
           z_{post}[[t]] \leftarrow rep(NA,H[t-1])
           for (j in 1:p){
                   V_j < -\text{chol2inv(chol(diag(theta_inv_post[[t-1]], nrow=H[t-1])+inv_sigma_sq_post[j,t-1]*(t(eta_post[[t-1]), nrow=H[t-1])+inv_sigma_sq_post[j,t-1]*(t(eta_post[[t-1]), nrow=H[t-1])+inv_sigma_sq_post[j,t-1]) } 
                  mu_j \leftarrow V_j \% * (eta_post[[t-1]]) \% * (y[,j]) * inv_sigma_sq_post[j,t-1]
                  Lambda_post[[t]][j,]<-mvrnorm(1,mu_j,V_j)</pre>
           }
           \label{lem:diff_y<-apply((y-(eta_post[[t-1]])**t(Lambda_post[[t]])))^2,2,sum)} \\
           for (j in 1:p){
                  inv_sigma_sq_post[j,t] <-rgamma(n=1,shape=a_sig+0.5*n,rate=b_sig+0.5*diff_y[j])
            V_{\text{eta}} = \frac{\text{V_eta}}{\text{Chol2inv}} \\ \\ \text{Chol(diag(H[t-1])+t(Lambda_post[[t]])} \\ \\ \text{Miag(inv\_sigma\_sq\_post[,t])} 
           for (i in 1:n){
```

```
mu_eta_i<-V_eta%*%t(Lambda_post[[t]])%*%diag(inv_sigma_sq_post[,t])%*%y[i,]</pre>
  eta_post[[t]][i,]<-mvrnorm(1,mu_eta_i,V_eta)</pre>
lhd_spike<-rep(0,H[t-1])</pre>
lhd slab<-rep(0,H[t-1])
for (h in 1:H[t-1]){
  lhd_spike[h] <-exp(sum(log(dnorm(Lambda_post[[t]][,h], mean = 0, sd = theta_inf^(1/2), log = FALSE
  lhd_slab[h] <-dmvt(x=Lambda_post[[t]][,h], mu=rep(0,p), S=(b_theta/a_theta)*diag(p), df=2*a_theta)
  prob_h < w_post[[t-1]] *c(rep(lhd_spike[h],h),rep(lhd_slab[h],H[t-1]-h))
  if (sum(prob_h)==0){
    prob_h<-c(rep(0,H[t-1]-1),1)
  }
  else{
    prob_h<-prob_h/sum(prob_h)</pre>
  z_post[[t]][h]<-c(1:H[t-1])%*%rmultinom(n=1, size=1, prob=prob_h)</pre>
v \leftarrow rep(NA, H[t-1])
for (h in 1:(H[t-1]-1)){
  v[h]<-rbeta(1, shape1 = 1+sum(z_post[[t]]==h), shape2 = alpha+sum(z_post[[t]]>h))
v[H[t-1]] < -1
w post[[t]][1]<-v[1]</pre>
for (h in 2:H[t-1]){
  w_{post}[[t]][h] < -v[h] * prod(1-v[1:(h-1)])
}
for (h in 1:H[t-1]){
  if (z_post[[t]][h]<=h){</pre>
    theta_inv_post[[t]][h]<-theta_inf^(-1)
  }
  else{
    theta_inv_post[[t]][h] <-rgamma(n=1, shape=a_theta+0.5*p, rate=b_theta+0.5*t(Lambda_post[[t]][,h])
}
active <- which(z_post[[t]]>c(1:H[t-1]))
Hstar[t] <- length(active)</pre>
H[t] \leftarrow H[t-1]
if (t>=start_adapt & u[t] <= exp(alpha0+alpha1*t)){</pre>
  if (Hstar[t]<H[t-1]-1){</pre>
    H[t] \leftarrow Hstar[t] + 1
    eta_post[[t]] <-cbind(eta_post[[t]][,active],rnorm(n))</pre>
    theta_inv_post[[t]]<-c(theta_inv_post[[t]][active],theta_inf^(-1))</pre>
    w_post[[t]] <-c(w_post[[t]][active],1-sum(w_post[[t]][active]))</pre>
    Lambda_post[[t]] <-cbind(Lambda_post[[t]][,active],rnorm(p,mean=0,sd=sqrt(theta_inf)))
  } else if (H[t-1]<Hmax) {</pre>
    H[t] \leftarrow H[t-1] + 1
    eta_post[[t]] <-cbind(eta_post[[t]],rnorm(n))</pre>
    v[H[t-1]]<-rbeta(1,shape1=1,shape2=alpha)</pre>
```

```
v < -c(v, 1)
      w_post[[t]] <-rep(NA,H[t])</pre>
      w_post[[t]][1]<-v[1]</pre>
      for (h in 2:H[t]){
        w_post[[t]][h]<-v[h]*prod(1-v[1:(h-1)])</pre>
      theta_inv_post[[t]]<-c(theta_inv_post[[t]],theta_inf^(-1))</pre>
      Lambda_post[[t]]<-cbind(Lambda_post[[t]],rnorm(p,mean=0,sd=sqrt(theta_inf)))</pre>
    }
  }
}
runtime <- proc.time()-t0</pre>
output<-list("y"=y,"my seed"=my seed,"N sampl"=N sampl,
              "alpha"=alpha, "a_sig"=a_sig, "b_sig"=b_sig, "a_theta"=a_theta, "b_theta"=b_theta,
              "theta_inf"=theta_inf, "start_adapt"=start_adapt, "Hmax"=Hmax,
              "alpha0"=alpha0, "alpha1"=alpha1,
              "H"=H, "Hstar"=Hstar, "Lambda_post"=Lambda_post, "eta_post"=eta_post,
              "theta_inv_post"=theta_inv_post, "w_post"=w_post, "z_post"=z_post,
              "inv_sigma_sq_post"=inv_sigma_sq_post, "runtime"=runtime)
return(output)
```

DSSFA function

Here are some intermediate functions that we had to set up to use our objects.

```
require(fanc)
fitcpp.post.fanc.cov <- function(Mat1, Mat2) {</pre>
  OmegaSamp <- array(Mat1, dim = c(dim(Mat1)[-3], dim(Mat1)[3]))</pre>
  OmegaBar <- as.matrix(Mat2)</pre>
  M <- dim(OmegaSamp)[2]</pre>
  fit <- numeric(M)</pre>
  for (i in 1:M) {
    fit[i] <- log(det(OmegaBar)) + sum(solve(OmegaBar) * OmegaSamp[,,i])</pre>
  }
  return(fit)
fitcpp.fanc <- function(Mat1, Mat2, Mat3) {</pre>
  c1 \leftarrow array(Mat1, dim = c(dim(Mat1)[-3], dim(Mat1)[3]))
  m2 <- as.matrix(Mat2)</pre>
  OmegaBar <- as.matrix(Mat3)</pre>
  lambda <- dim(c1)[3]</pre>
  fit <- numeric(lambda)</pre>
  for (i in 1:lambda) {
    if(all(dim(c1[,,i]) == dim(m2[i,]))){
      fit[i] <- log(det(c1[,,i] + diag(m2[i,]))) + sum(OmegaBar %*% solve(c1[,,i] + diag(m2[i,])))
      stop("Input matrices have different dimensions.")
```

```
}
return(fit)
}

fit.fanc.post.cov = function(list.bfa){

list.bfa$fit.post.fanc.cov = fitcpp.post.fanc.cov(list.bfa$post.cov,list.bfa$0mega.kmax)
return(list.bfa)
}

fit.fanc = function(list.bfa){

list.bfa$fit.fanc = fitcpp.fanc(list.bfa$betas.prod.fanc,list.bfa$fanc.sigma,list.bfa$0mega.bar)
return(list.bfa)
}
```

And the main function (from here, partly modified)

```
DSSFA = function(obj,length.lambda = 1, k.max = 1, print.out = F, plot.summary = F, cor.factor = F, tol
  if(cor.factor){
    cat("Oblique - Sparse")
    cat("\n")
  list.bfa = list()
  list.bfa$prior.bfa = obj$prior.bfa
  list.bfa$k.max = k.max
  list.bfa$M = obj$samp.size
  list.bfa$p = obj$P
  list.bfa$length.lambda = length.lambda
  list.bfa$cor.factor = cor.factor
  list.bfa$post.cov = obj$post.cov
  list.bfa$Omega.bar = apply(obj$post.cov,c(1,2),mean)
  fit.fanc.mat = matrix(0,length.lambda,list.bfa$k.max)
  num.zero.mat = matrix(0,length.lambda,list.bfa$k.max)
               = matrix(0,length.lambda,list.bfa$k.max)
  lambda.mat
  fit.sel
              = vector("list",list.bfa$k.max)
  num.zero.list = vector("list",list.bfa$k.max)
  list.sel
              = vector("list", list.bfa$k.max)
  list.full
               = vector("list",list.bfa$k.max)
  uniq.full
              = list()
  if(list.bfa$cor.factor == T){
              = list()
    phi.full
    phi.list = vector("list", list.bfa$k.max)
  for(k.temp in 1:list.bfa$k.max){
    if(length.lambda >= 2){
      fanc.bfa = fanc(covmat = list.bfa$Omega.bar, factors = k.temp,
                      gamma = Inf, control = list(start = "warm", min.rhozero = T, cor.factor = cor.fac
    }else{
      fanc.bfa = fanc(covmat = list.bfa$Omega.bar, factors = k.temp, rho = 0,
                      gamma = Inf, control = list(start = "warm", min.rhozero = T, cor.factor = cor.fac
```

```
list.bfa$lambda = fanc.bfa$rho
lambda.mat[,k.temp] = fanc.bfa$rho
list.bfa$loadings.fanc.bfa = as.array(fanc.bfa$loadings$gamma1)
list.bfa$fanc.sigma.bfa = fanc.bfa$uniquenesses[,,1]
if(length.lambda < 2){</pre>
  list.bfa$fanc.sigma.bfa = matrix(list.bfa$fanc.sigma.bfa,nrow = 1)
fanc.matrix.bfa = matrix(0,length(list.bfa$lambda),list.bfa$p*k.temp)
for(i in 1:length(list.bfa$lambda)){
  fanc.matrix.bfa[i,] = as.numeric(list.bfa$loadings.fanc.bfa[[i]])
}
list.bfa$fanc.matrix.bfa = fanc.matrix.bfa
betas.bfa.fanc.full = replicate(length(list.bfa$lambda),matrix(0,list.bfa$p,k.temp))
for(i in 1:length(list.bfa$lambda)){
  betas.bfa.fanc.full[,,i] = as.matrix(list.bfa$loadings.fanc.bfa[[i]])
}
list.bfa$fanc.matrix.sel = betas.bfa.fanc.full
mat_dif_zero = which(apply(betas.bfa.fanc.full,3,function(x) sum(colSums(x) == 0)) != 0)
if(length(mat_dif_zero) == length.lambda){
  cat("Zeroed Columns")
  fanc.bfa = fanc(covmat = list.bfa$Omega.bar, factors = k.temp, gamma = Inf, control = list(start
  list.bfa$lambda = fanc.bfa$rho
  lambda.mat[,k.temp] = fanc.bfa$rho
  list.bfa$loadings.fanc.bfa = as.array(fanc.bfa$loadings$gamma1)
  list.bfa$fanc.sigma.bfa = t(as.matrix(fanc.bfa$uniquenesses[,,1]))
  if(length.lambda < 2){</pre>
    list.bfa$fanc.sigma.bfa = matrix(list.bfa$fanc.sigma.bfa,nrow = 1)
  fanc.matrix.bfa = matrix(0,length(list.bfa$lambda),list.bfa$p*k.temp)
  for(i in 1:length(list.bfa$lambda)){
    fanc.matrix.bfa[i,] = as.numeric(list.bfa$loadings.fanc.bfa[[i]])
  }
  list.bfa$fanc.matrix.bfa = fanc.matrix.bfa
  betas.bfa.fanc.full = replicate(length(list.bfa$lambda),matrix(0,list.bfa$p,k.temp))
  for(i in 1:length(list.bfa$lambda)){
    betas.bfa.fanc.full[,,i] = as.matrix(list.bfa$loadings.fanc.bfa[[i]])
  list.bfa$fanc.matrix.sel = betas.bfa.fanc.full
  if(apply(betas.bfa.fanc.full,3,function(x) sum(colSums(x) == 0)) == 0) cat(" - FULL Matrix") else
  mat_dif_zero = length.lambda-1
num.zero.mat[,k.temp] = apply(fanc.matrix.bfa, 1, function(x) sum(x != 0))
list.sel[[k.temp]] = betas.bfa.fanc.full
list.full[[k.temp]] = betas.bfa.fanc.full
if(list.bfa$cor.factor){
  phi.full[[k.temp]] = fanc.bfa$Phi[,,,1]
betas.prod.bfa.fanc = replicate(length(list.bfa$lambda),matrix(0,list.bfa$p,list.bfa$p))
if(cor.factor == T & k.temp > 1){
```

```
for(i in 1:length(list.bfa$lambda)){
      betas.prod.bfa.fanc[,,i] = betas.bfa.fanc.full[,,i]%*%fanc.bfa$Phi[,,i,1]%*%t(betas.bfa.fanc.fu
    list.bfa$betas.prod.fanc = betas.prod.bfa.fanc
  }else{
    for(i in 1:length(list.bfa$lambda)){
      betas.prod.bfa.fanc[,,i] = betas.bfa.fanc.full[,,i]%*%t(betas.bfa.fanc.full[,,i])
   list.bfa$betas.prod.fanc = betas.prod.bfa.fanc
  if(k.temp == list.bfa$k.max){
    Omega.kmax = list.bfa$betas.prod.fanc[,,length(list.bfa$lambda)]+diag(fanc.bfa$uniquenesses[lengt
    list.bfa$Omega.kmax = Omega.kmax
   list.bfa = fit.fanc.post.cov(list.bfa)
 }
 list.bfa = fit.fanc(list.bfa)
  fit.fanc.mat[,k.temp] = list.bfa$fit.fanc
  if(length(mat_dif_zero) == 0){
    fit.sel[[k.temp]] = list.bfa$fit.fanc
    num.zero.list[[k.temp]] = apply(fanc.matrix.bfa, 1, function(x) sum(x == 0))
    uniq.full[[k.temp]] = fanc.bfa$uniquenesses[,,1]
    if(length.lambda < 2){</pre>
      uniq.full[[k.temp]] = matrix(fanc.bfa$uniquenesses[,,1],nrow = 1)
    if(list.bfa$cor.factor == T){
      phi.list[[k.temp]] = fanc.bfa$Phi[,,,1]
 }else{
   fit.sel[[k.temp]] = list.bfa$fit.fanc[-mat_dif_zero]
   num.zero.list[[k.temp]] = apply(fanc.matrix.bfa, 1, function(x) sum(x == 0))[-mat_dif_zero]
    if(k.temp == 1){
      dim.array = dim(list.sel[[k.temp]][,,-mat_dif_zero])[2]
      list.sel[[k.temp]] = array(list.sel[[k.temp]][,,-mat_dif_zero], dim = c(list.bfa$p,k.temp,dim.ar.
      list.sel[[k.temp]] = list.sel[[k.temp]][,,-mat_dif_zero]
    uniq.full[[k.temp]] = fanc.bfa$uniquenesses[-mat_dif_zero,,1]
    if(length.lambda < 2){</pre>
      uniq.full[[k.temp]] = matrix(fanc.bfa$uniquenesses[,,1],nrow = 1)
    if(list.bfa$cor.factor == T){
      phi.list[[k.temp]] = fanc.bfa$Phi[,,-mat_dif_zero,1]
   }
  if(print.out == T){
    cat("Factor = ",k.temp)
    cat("\n")
 }
}
if(list.bfa$cor.factor){
 list.bfa$phi.list = phi.list
  list.bfa$phi.full = phi.full
```

```
}
list.bfa$uniq.full = uniq.full
list.bfa$fit.sel = fit.sel
list.bfa$num.zero.list = num.zero.list
list.bfa$list.sel = list.sel
list.bfa$list.full = list.full
list.bfa$rho.mat = lambda.mat
return(list.bfa)
}
```

Summary plot function

Intermediate function:

```
fitcpp.post.plot.cov <- function(Mat1, Mat2) {
   Omegacov <- array(Mat1, dim = c(dim(Mat1)[-3], dim(Mat1)[3]))
   Omegakmax <- array(Mat2, dim = c(dim(Mat2)[-3], dim(Mat2)[3]))

M <- dim(Omegacov)[3]
   kmax <- dim(Omegakmax)[3]
   Omega_lamb <- matrix(nrow = M, ncol = kmax)

for (i in 1:kmax) {
   val <- log(det(Omegakmax[,,i]))
   for (j in 1:M) {
      Omega_lamb[j,i] <- val+sum(solve(Omegakmax[,,i]) * Omegacov[,,j])
   }
   return(Omega_lamb)
}</pre>
```

Main function (from here, partly modified):

```
summary.plot = function(list.bfa,CI = NULL, cov.dssfa = F, reg = T, text_main_prior = "", col.lambda =

if(is.null(CI)){
    ic.1 = 0.025
    ic.2 = 0.975
    CI.text = "95"
}else{
    ic.1 = CI[[2]][1]
    ic.2 = CI[[2]][2]
    CI.text = CI[[1]]
}

q1 = quantile(list.bfa$fit.post.fanc,probs = c(ic.1,ic.2))[1]
    q2 = quantile(list.bfa$fit.post.fanc,probs = c(ic.1,ic.2))[2]

k.sel = min(which(lapply(list.bfa$fit.sel, function(x) length(which(x < q2))) != 0))
lamb.sel = lapply(list.bfa$fit.sel, function(x) list.bfa$length.lambda-length(which(x < q2))+1)
lamb.sel = lamb.sel[[k.sel]]</pre>
```

```
fit.list.plot = list()
for(i in 1:list.bfa$k.max){
  if(length(dim(list.bfa$list.sel[[i]])) == 3){
    dim.size = dim(list.bfa$list.sel[[i]])[3]
    Omega.temp = array(0,dim = c(list.bfa$p,list.bfa$p,dim.size))
    for(j in 1:dim.size){
     beta.max = as.matrix(list.bfa$list.sel[[i]][,,j])
     uniq.sel = list.bfa$uniq.full[[i]][j,]
     Omega.temp[,,j] = beta.max%*%t(beta.max)+diag(uniq.sel)
 }else if(length(dim(list.bfa$list.sel[[i]])) != 3){
    dim.size = 1
    Omega.temp = array(0,dim = c(list.bfa$p,list.bfa$p,1))
    beta.max = as.matrix(list.bfa$list.sel[[i]])
    uniq.sel = list.bfa$uniq.full[[i]]
   Omega.temp[,,1] = beta.max%*%t(beta.max)+diag(uniq.sel)
 }
  if(cov.dssfa == T){
   fit.list.plot[[i]] = as.matrix(fitcpp.post.plot.cov(list.bfa$post.cov,Omega.temp))
 }
  colnames(fit.list.plot[[i]]) = ((list.bfa$length.lambda-dim.size)+1):list.bfa$length.lambda
temp.melt = lapply(fit.list.plot, melt)
for(i in 1:list.bfa$k.max){
 temp.melt[[i]]$kmax = as.numeric(i)
temp = bind_rows(temp.melt)
temp = data.frame(temp)
max.lamb = max(temp$Var2)
temp$Var2 = factor(temp$Var2,levels = 1:max.lamb,ordered = T)
temp.melt2 = lapply(list.bfa$fit.sel,melt)
for(i in 1:list.bfa$k.max){
 temp.melt2[[i]]$kmax = as.numeric(i)
 dim.size = dim(temp.melt2[[i]])[1]
  temp.melt2[[i]]$lamb = ((list.bfa$length.lambda-dim.size)+1):list.bfa$length.lambda
}
temp2 = bind_rows(temp.melt2)
mygreys = colorRampPalette(brewer.pal(9, "Greys"))(max.lamb + 7)
mygreys = mygreys[-((max.lamb+6):(max.lamb+7))]
mygreys = mygreys[-(1:5)]
min = min(temp2$lamb)
g = ggplot() + geom_point(data = temp2, aes(factor(kmax),value, col = factor(lamb, labels = (max.lamb
  scale_color_manual(values = mygreys, aesthetics = c("col")) + theme(legend.position = legend.pos) +
  guides(colour = guide_legend(ncol = col.lambda))
```

```
temp.data.reg = temp[which(temp$kmax == k.sel & temp$Var2 == lamb.sel),]
  temp.point.reg = temp2[which(temp2$kmax == k.sel & temp2$lamb == lamb.sel),]
  g = g + geom_hline(yintercept = q2, lty = "dashed", col = "darkgrey") + geom_hline(yintercept = q1, l
  for(i in 1:max.lamb){
   temp.data = temp[which(temp$Var2 == i),]
   temp.point = temp2[which(temp2$lamb == i),]
   if(i == max.lamb){
      df.summary <- temp.data %>% group_by(kmax) %>%
        summarize(mid = mean(value),
                 lo = quantile(value, ic.1),
                 hi = quantile(value, ic.2))
     g = g + geom_errorbar(data = df.summary[list.bfa$k.max,],aes(factor(max(kmax)),ymin = lo, ymax = 1
   g = g + geom_violin(data = temp.data,aes(factor(kmax), value), alpha = 0, size = 0.4, col = mygrey
   if(i == max.lamb){
     g = g + geom_point(data = temp.point, aes(kmax,value,col = factor(lamb)), col = "#000000", size =
   }else{
     g = g + geom_point(data = temp.point, aes(kmax,value,col = factor(lamb)), col = mygreys[i], size
   if(reg == T & i == lamb.sel){
     g = g + geom_violin(data = temp.data.reg, aes(factor(kmax),value),col = "red", lty = "twodash", a
  g = g + geom_point(data = temp.point.reg, aes(kmax,value), col = "red", size = 4, shape = 4)
  if(reg == T){
   lamb.sel = max.lamb-lamb.sel
   text.lambda = paste("$\\lambda = \\lambda_{",lamb.sel,"}$", sep = "")
   text.main = paste("DSSFA Posterior Summary, ", CI.text, "% quantile. ",text.lambda,", $\\tilde{k} =
 }else{
   text.main = paste("DSSFA Posterior Summary, ", CI.text, "% quantile. ", sep = "")
 g = g + labs(title = TeX(text.main), x = TeX("number of factors, $\\tilde{k}\$"), y = TeX("loss funct
  g
}
```

Function that selects the right model

This one is from this repo.

```
sel.model.dssfa = function(list.bfa,CI = NULL, k.sel = NULL, fast = F){
  if(length(CI) == 0){
```

```
ic.1 = 0.025
  ic.2 = 0.975
}else{
  ic.1 = CI[[2]][1]
  ic.2 = CI[[2]][2]
if(is.null(k.sel)){
 k.sel = 1:list.bfa$k.max
q1 = quantile(list.bfa$fit.post.fanc,probs = c(ic.1,ic.2))[1]
q2 = quantile(list.bfa$fit.post.fanc,probs = c(ic.1,ic.2))[2]
sel.model
              = list()
mat.sel.ksel = vector("list",length(k.sel))
uniq.sel.ksel = vector("list",length(k.sel))
phi.sel.ksel = vector("list",length(k.sel))
mat.sel.CI = vector("list",list.bfa$k.max)
uniq.sel.CI = vector("list", list.bfa$k.max)
phi.sel.CI = vector("list", list.bfa$k.max)
1 = 1 # count the number of select factors
if(fast){
  for(i in k.sel){
    if(sum(which(list.bfa$fit.sel[[i]] < q2)) == 0){</pre>
      # cat("aqui11")
      mat.sel.ksel[[1]] = NULL
      uniq.sel.ksel[[1]] = NULL
      if(list.bfa$cor.factor){
        phi.sel.ksel[[1]] = NULL
      1 = 1+1
    }else{
      # cat("aqui12")
      min.sel = min(which(list.bfa$fit.sel[[i]] < q2))</pre>
      mat.sel.ksel[[1]] = list.bfa$betas.full[[i]]
      uniq.sel.ksel[[1]] = list.bfa$list.uniqueness[[i]]
      if(list.bfa$cor.factor){
        phi.sel.ksel[[1]] = list.bfa$phi.full[[i]]
      1 = 1 + 1
    }
  }
}else{
  for(i in k.sel){
    if(sum(which(list.bfa$fit.sel[[i]] < q2)) == 0){</pre>
      # cat("aqui11")
      mat.sel.ksel[[1]] = NULL
      uniq.sel.ksel[[1]] = NULL
      if(list.bfa$cor.factor){
        phi.sel.ksel[[1]] = NULL
      1 = 1+1
    }else{
```

```
if(length(dim(list.bfa$list.sel[[i]])) != 3){
          # cat("aqui12")
          min.sel = min(which(list.bfa$fit.sel[[i]] < q2))</pre>
          mat.sel.ksel[[1]] = list.bfa$list.sel[[i]]
          uniq.sel.ksel[[1]] = list.bfa$uniq.full[[i]]
          if(list.bfa$cor.factor){
            phi.sel.ksel[[1]] = list.bfa$list.bfa$phi.list[[i]]
          }
          1 = 1+1
        }else{
          # cat("aqui13")
          min.sel = min(which(list.bfa$fit.sel[[i]] < q2))</pre>
          mat.sel.ksel[[1]] = list.bfa$list.sel[[i]][,,min.sel]
          if(list.bfa$length.lambda < 2){</pre>
            uniq.sel.ksel[[1]] = list.bfa$uniq.full[[i]]
          }else{
            uniq.sel.ksel[[1]] = list.bfa$uniq.full[[i]][min.sel,]
          if(list.bfa$cor.factor){
            if(i == 1){
              phi.sel.ksel[[1]] = 1
            }else{
              phi.sel.ksel[[1]] = list.bfa$phi.list[[i]][,,min.sel]
          }
          1 = 1 + 1
       }
      }
   }
  }
  sel.model$mat.sel.ksel = mat.sel.ksel
  sel.model$uniq.sel.ksel = uniq.sel.ksel
  if(list.bfa$cor.factor){
    sel.model$phi.sel.ksel = phi.sel.ksel
 }
 return(sel.model)
make.plot.mat = function(mat,col.names,fact.name){
  rownames(mat) = col.names
  colnames(mat) = fact.name
 mat = apply(mat, 2, rev)
  longmat = melt(mat)
 names(longmat)[2] = "factors"
  names(longmat)[1] = "variable"
  g1 = ggplot(longmat, aes(x = factors, y = variable)) + geom_tile(aes(fill = value),colour = "grey20")
  g2 = g1 + scale_fill_gradient2(low = "#800000", high = "#191970", mid = "white")+ theme(
   axis.title.x = element_blank(),
   axis.title.y = element_blank(),
    # panel.grid.major = element_blank(),
   text = element_text(size = 12),
```

```
panel.border = element_blank(),
  panel.background = element_blank(),
  axis.ticks = element_blank(),
  # axis.text = element_blank(),
  legend.title = element_text(),
  plot.title = element_text(hjust = 0.5)) + labs(fill = " ")
  g2
}
```