BIOS 7720: Applied Functional Data Analysis Lecture 13: Multilevel fPCA

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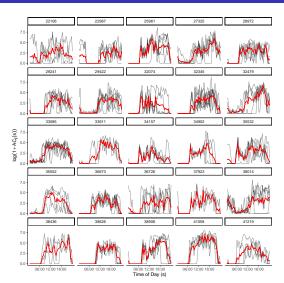
Logistics

- HW 3 due 5/13
- Final group projects
 - Presentations 5/11 and 5/13
 - Write up due 5/20
- Group presentation order

Multilevel Functional Data

```
## change data_path to whereever your NHANES file is located
data_path <- here::here("data","data_processed","NHANES_AC_processed.rds")</pre>
df <- readr::read_rds(data_path)</pre>
df_sub <-
 df %>%
  filter(n_good_days >= 3, good_day == 1, Age <= 25)
uid <- unique(df_sub$SEQN)</pre>
## extract the PA data
1X <- log(1+as.matrix(df_sub[,paste0("MIN",1:1440)]))</pre>
lX[is.na(lX)] <- 0
N < - nrow(1X)
## bin the data into 30 minute intervals
tlen <- 30
nt <- ceiling(1440/tlen)
inx_cols <- split(1:1440, rep(1:nt, each=tlen)[1:1440])
1X_bin <- vapply(inx_cols, function(x) rowMeans(1X[,x], na.rm=TRUE), numeric(N))</pre>
colnames(lX_bin) <- paste0("epoch_",1:nt)</pre>
```

Multilevel Functional Data



Multilevel fPCA

• Multilevel fPCA [Di et al., 2009]

$$egin{aligned} Y_{ij}(s) &= \mu_0(s) + b_i(s) +
u_{ij}(s) + \epsilon_{ij}(s) \ b_i &\stackrel{ ext{iid}}{\sim} GP(0, oldsymbol{\Sigma_b}) \
u_{ij} &\stackrel{ ext{iid}}{\sim} GP(0, oldsymbol{\Sigma_{
u}}) \ \epsilon_{ij}(s) &\stackrel{ ext{iid}}{\sim} N(0, \sigma_{\epsilon}^2) \end{aligned}$$

- \bullet b_i is the participant deviation from the population average
- ν_{ij} is the day deviation from a participants' average $(\mu_0(s) + b_i(s))$

Multilevel Functional Data

```
set.seed(10)
## remove unnecessary columns
df sub <-
 df sub %>%
  dplyr::select(-one_of(paste0("MIN",1:1440)))
## add in the binned data to our data frame
df_sub[["lX_bin"]] <- lX_bin</pre>
## subset to only 100 participants
nsamp <- 100
uid_samp <- sample(uid, size=nsamp, replace=FALSE)</pre>
df_mfpca <-
  filter(df_sub, SEQN %in% uid_samp) %>%
  group_by(SEQN) %>%
 mutate(J = 1:n()) %>%
  ungroup() %>%
  arrange(SEQN, J)
```

Multilevel Functional Data

- Suppose we observe $y_{ij}(s)$ for
 - participant (level 1) i = 1, ..., N
 - visit (level 2) $j = 1, \ldots, J$
- We want to estimate the mfPCA model

$$y_{ij}(s) = \mu(s) + b_i(s) + \nu_{ij}(s) + \epsilon_{ij}(s)$$



- Suppose we observe $y_{ij}(s)$ for
 - participant (level 1) i = 1, ..., N
 - visit (level 2) $j = 1, \dots, J$
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$$y_{ij}(s) = \mu(s) + b_i(s) + \nu_{ij}(s) + \epsilon_{ij}(s)$$

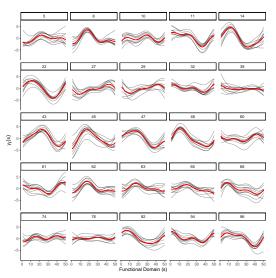
Start with no error present

$$y_{ij}(s) = \mu(s) + b_i(s) + \nu_{ij}(s)$$



```
set.seed(1989)
N <- 100 # number of subjects
J <- 10 # number of visits per subject
nS <- 50 # number of observations of the functional domain
sind <- seq(0.1.len=nS)
# true eigenvalues
K1 <- K2 <- 4
lambda1 <- 0.5^(0:(K1-1)) # for lvl 1
lambda2 <- 0.5^(0:(K2-1)) # for lvl 2
# true Eigenfunctions
Phi1 <- sqrt(2)*cbind(sin(2*pi*sind),cos(2*pi*sind),
                      sin(4*pi*sind),cos(4*pi*sind))
Phi2 <- cbind(rep(1,nS),
              sqrt(3)*(2*sind-1),
              sqrt(5)*(6*sind^2-6*sind+1),
              sqrt(7)*(20*sind^3-30*sind^2+12*sind-1))
```

```
# simulate b_i(s)
xi lvl1 <- matrix(rnorm(N*K1),N.K1);
xi_lvl1 <- xi_lvl1 %*% diag(sqrt(lambda1))</pre>
b_i <- xi_lvl1 %*% t(Phi1);
# simulate nu_ij(s)
xi_lvl2 <- matrix(rnorm(N*J*K2),N*J,K2);</pre>
xi_lvl2 <- xi_lvl2 %*% diag(sqrt(lambda2))</pre>
nu_ij <- xi_lv12 %*% t(Phi2)
# combine to create y_ij(s)
mu_0 <- function(s) sin(2*pi*s)</pre>
b_i_mat <- kronecker(b_i,matrix(1, J, 1))</pre>
v_{ij} < - kronecker(matrix(mu_0(sind), 1, nS), matrix(1, N*J, 1)) +
                 nu_ij +
                 b i mat
df_mfpca_sim <- data.frame("id"=rep(1:N, each=J),</pre>
                         "visit" = rep(1:J, N),
                         "b_i" = I(b_i_mat),
                         "y_i" = I(y_i),
                         "nu_ij" = I(nu_ij)
```



We have three covariances functions of interest

$$K_T(s, u) = Cov(y_{ij}(s), y_{ij}(u))$$

$$K_B(s, u) = Cov(y_{ij}(s), y_{ik}(u))$$

$$K_W(s, u) = K_T(s, u) - K_B(s, u)$$

- Follow a similar estimation procedure as fPCA
- Estimate a mean model, decompose covariance of the residuals (K_T)

$$K_{T}(s, u) = Cov(y_{ij}(s), y_{ij}(u))$$

$$= Cov(\mu(s) + b_{i}(s) + \nu_{ij}(s), \mu(s) + b_{i}(s) + \nu_{ij}(s))$$

$$= Cov(b_{i}(s) + \nu_{ij}(s), b_{i}(u) + \nu_{ij}(u))$$

$$= Cov(b_{i}(s), b_{i}(u)) + Cov(b_{i}(s), \nu_{ij}(u)) + Cov(\nu_{ij}(s), b_{i}(u)) + Cov(\nu_{ij}(s), \nu_{ij}(u))$$

$$= Cov(b_{i}(s), b_{i}(u)) + Cov(\nu_{ij}(s), \nu_{ij}(u))$$

$$= \sum_{b=1}^{\infty} \lambda_{k}^{b} \phi_{k}^{b}(s) \phi_{k}^{b}(u) + \sum_{k=1}^{\infty} \lambda_{k}^{\nu} \phi_{k}^{\nu}(s) \phi_{k}^{\nu}(u)$$

$$\approx \sum_{k=1}^{K_{b}} \lambda_{k}^{b} \phi_{k}^{b}(s) \phi_{k}^{b}(u) + \sum_{k=1}^{K_{\nu}} \lambda_{k}^{\nu} \phi_{k}^{\nu}(s) \phi_{k}^{\nu}(u)$$

$$K_{B}(s, u) = \operatorname{Cov}(y_{ij}(s), y_{ik}(u))$$

$$= \operatorname{Cov}(\mu(s) + b_{i}(s) + \nu_{ij}(s), \mu(s) + b_{i}(s) + \nu_{ik}(s))$$

$$= \operatorname{Cov}(b_{i}(s) + \nu_{ij}(s), b_{i}(u) + \nu_{ik}(u))$$

$$= \operatorname{Cov}(b_{i}(s), b_{i}(u)) + \operatorname{Cov}(b_{i}(s), \nu_{ik}(u)) + \operatorname{Cov}(\nu_{ij}(s), b_{i}(u)) + \operatorname{Cov}(\nu_{ik}(s), \nu_{ij}(u))$$

$$= \operatorname{Cov}(b_{i}(s), b_{i}(u))$$

$$= \sum_{k=1}^{\infty} \lambda_{k}^{b} \phi_{k}^{b}(s) \phi_{k}^{b}(u)$$

$$\approx \sum_{k=1}^{K_{b}} \lambda_{k}^{b} \phi_{k}^{b}(s) \phi_{k}^{b}(u)$$

$$\begin{split} \hat{K}_{T}(s,u) &= \frac{\sum_{i=1}^{N} \sum_{j=1}^{J} (y_{ij}(s) - \hat{\mu}_{0}(s))(y_{ij}(u) - \hat{\mu}_{0}(u))}{(N \times J)} \\ \hat{K}_{B}(s,u) &= \frac{\sum_{i=1}^{N} \sum_{j_{1} \neq j_{2}} (y_{ij_{1}}(s) - \hat{\mu}_{0}(s))(y_{ij_{2}}(u) - \hat{\mu}_{0}(u))}{(N \times J \times (J-1))} \\ \hat{K}_{W}(s,u) &= \hat{K}_{T}(s,u) - \hat{K}_{B}(s,u) \end{split}$$

```
# library("mqcv")
## set up the long data frame for estimating mean function
## (could also use empirical mean here since data are measured without error)
# df_mfpca_long <-
    data.frame("id" = rep(df_mfpca$id, each=nS),
               "visit" = rep(df_mfpca$visit, each=nS),
               "u" = as.vector(t(df mfpca$u ii)).
               "sind" = rep(sind, N*J))
# fit_naive <- qam(y ~ s(sind, bs="cr",k=30), method="REML", data=df_mfpca_long)
# resid_mat <- matrix(fit_naive$residuals, N*J, nS, byrow=TRUE)</pre>
resid_mat <- y_ij - kronecker(matrix(colMeans(y_ij),1,nS), matrix(1, N*J, 1))
KT hat <- KB hat <- matrix(0, nS, nS)
## estimate K_{-}T
inx <- 1
for(i in 1:N){
for(j in 1:J){
   KT hat <- KT hat + tcrossprod(resid mat[inx.])</pre>
   inx <- inx+1
```

```
matrixcalc::is.positive.semi.definite(KT_hat)

## [1] TRUE

matrixcalc::is.positive.semi.definite(KB_hat)

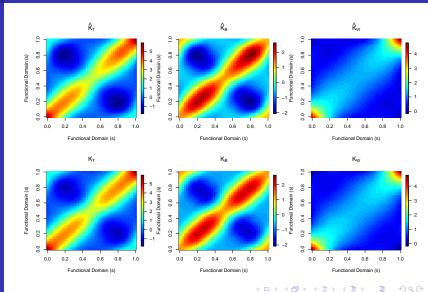
## Error in matrixcalc::is.positive.semi.definite(KB_hat): argument x is not a symmetric matrix

matrixcalc::is.positive.semi.definite(KW_hat)

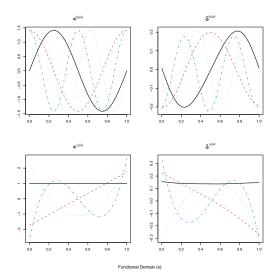
## Error in matrixcalc::is.positive.semi.definite(KW_hat): argument x is not a symmetric matrix
```

```
KB_hat[1:5,1:5]
          [,1] [,2] [,3] [,4] [,5]
## [1,] 1.370842 1.337534 1.271967 1.175052 1.049277
## [2.] 1.337534 1.376581 1.381063 1.349283 1.281382
## [3,] 1.271967 1.381063 1.454678 1.488579 1.480541
## [4,] 1.175052 1.349283 1.488579 1.586367 1.638159
## [5.] 1.049277 1.281382 1.480541 1.638159 1.747694
matrixcalc::is.symmetric.matrix(round(KB hat.12))
## [1] TRUE
matrixcalc::is.symmetric.matrix(round(KB_hat,13))
## [1] FALSE
matrixcalc::is.positive.semi.definite(round(KB_hat,12))
## [1] FALSE
```

```
## make K_B positive-semidefinite
eigen_KB <- eigen(KB_hat)
inx_rm_1 <- which(eigen_KB$values < 0)
if(length(inx rm 1) > 0){
  eigen_KB$values[inx_rm_1] <- 0
  eigen_KB$vectors[,inx_rm_1] <- 0
KB_hat_trim <- eigen_KB$vectors %*% diag(eigen_KB$values) %*% t(eigen_KB$vectors)
## make K_W positive-semidefinite
KW_hat <- KT_hat-KB_hat_trim</pre>
eigen KW <- eigen(KW hat)
(inx_rm_2 <- which(eigen_KW$values < 0))
## [1] 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43
## [26] 44 45 46 47 48 49 50
if(length(inx_rm_1) > 0){
  eigen_KW$values[inx_rm_2] <- 0
  eigen_KW$vectors[,inx_rm_2] <- 0
KW_hat_trim <- eigen_KW$vectors %*% diag(eigen_KW$values) %*% t(eigen_KW$vectors)</pre>
```



```
## choose the number of eigenvalues
thresh <- 0.95
(pve_lvl1 <- cumsum(eigen_KB$values)/sum(eigen_KB$values))[1:5]
## [1] 0.5527630 0.7905170 0.9242457 0.9970893 0.9999664
(pve_lvl2 <- cumsum(eigen_KW$values)/sum(eigen_KW$values))[1:5]
## [1] 0.5099347 0.7835731 0.9304907 1.0000000 1.0000000
K1 <- min(which(pve_lvl1 >= thresh))
K2 <- min(which(pve_lvl2 >= thresh))
## get the eigenvectors
Phi1_hat <- eigen_KB$vectors[,1:K1]
Phi2_hat <- eigen_KW$vectors[,1:K2]
## get the eigenvalues
lambda1_hat <- eigen_KB$values[1:K1]</pre>
lambda2_hat <- eigen_KW$values[1:K2]</pre>
```

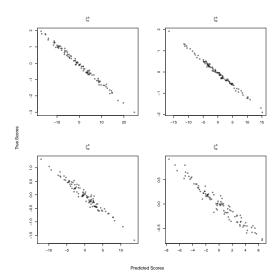


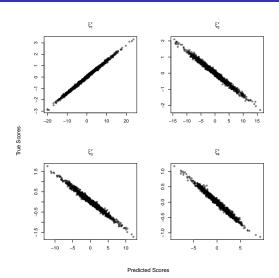
$$egin{aligned} \left[egin{aligned} oldsymbol{\xi}^b \ oldsymbol{\xi}^
u \end{aligned}
ight] = \left[egin{aligned} oldsymbol{A_i} \ oldsymbol{B_i} \end{aligned}
ight] oldsymbol{\Sigma}_i^{-1}(oldsymbol{y}_i - \hat{oldsymbol{\mu}}_i) \ oldsymbol{A}_i = \mathbf{1}_J \otimes (oldsymbol{\Lambda}^b oldsymbol{\Phi}^{b,t}) \ oldsymbol{\Sigma}_i = \mathsf{Cov}(oldsymbol{y}_i, oldsymbol{y}_i) \end{aligned}$$

Note that the math is a bit more complicated if not all participants are fully observed on the same grid

```
Lambda_b <- diag(lambda1_hat)</pre>
Lambda_nu <- diag(lambda2_hat)</pre>
A_i <- kronecker(matrix(1, 1, J), Lambda_b%*% t(Phi1_hat))
B_i <- kronecker(diag(1, J), Lambda_nu %*%t(Phi2_hat))
Sigma_ii <- KW_hat_trim + KB_hat_trim
Sigma ii <- KB hat trim
Sigma_i <- as.matrix(Matrix::bdiag(lapply(1:J, function(x) Sigma_ii)))</pre>
inx_j1 <- 1:nS
for(j1 in 1:J){
 if(j1 < J-1){
    for(j2 in (j1+1):(J-1)){
      inx_j2 \leftarrow 1:nS + nS*j2
      Sigma_i[inx_j1,inx_j2] <- Sigma_ij
      Sigma i[inx i2.inx i1] <- t(Sigma ii)
  inx_j1 \leftarrow inx_j1 + nS
```

```
Sigma_i_inv <- MASS::ginv(Sigma_i)
inx_i <- 1:J
xi_hat_lvl1 <- matrix(NA, N, K1)
xi_hat_lvl2 <- matrix(NA, N*J, K2)
for(i in 1:N){
    r_i <- as.vector(t(resid_mat[inx_i,]))
    scores_i <- rbind(A_i, B_i) %*% Sigma_i_inv %*% r_i
    xi_hat_lvl1[i,] <- scores_i[1:K1]
    xi_hat_lvl2[inx_i,] <- matrix(scores_i[-c(1:K1)], J, K2, byrow=TRUE)
    inx_i <- inx_i + J
}</pre>
```

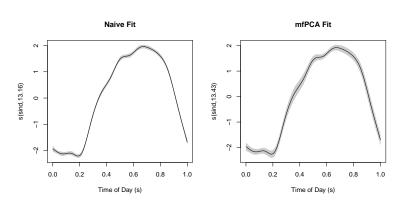




Multilevel Functional Data: mgcv

```
library("mgcv")
sind \leftarrow seq(0,1,len=nt)
N <- nrow(df mfpca)
df_mfpca_long <-
  data.frame("id" = factor(rep(df_mfpca$SEQN, each=nt)),
             "day" = rep(df mfpca$J, each=nt).
             "sind" = rep(sind, N),
             "y" = as.vector(t(df_mfpca$1X_bin)))
df_mfpca_long$id_day = factor(paste0(df_mfpca_long$id,"_",df_mfpca_long$day))
K1 <- K2 <- 2
for(k in 1:K1){
  df_mfpca_long[[paste0("phi_b_",k)]] <-</pre>
   rep(mfpca_fit$efunctions$level1[,k],N)
for(k in 1:K2){
  df_mfpca_long[[paste0("phi_nu_",k)]] <-</pre>
    rep(mfpca_fit$efunctions$level2[,k],N)
fit_naive <- bam(y ~ s(sind, bs="cr", k=15),
                data=df_mfpca_long, method="fREML", discrete=TRUE)
fit_mgcv <- bam(y ~ s(sind, bs="cr", k=15) +
                  s(id, by=phi_b_1, bs="re") + s(id, by=phi_b_2, bs="re") +
                  s(id_day, by=phi_nu_1, bs="re") + s(id_day, by=phi_nu_2, bs="re"
                data=df_mfpca_long, method="fREML", discrete=TRUE)
                                                イロン イ御 とくきと くきと こまし
```

Multilevel Functional Data: mgcv



References I



Di, C., Crainiceanu, C. M., Caffo, B. S., and Punjabi, N. M. (2009). Multilevel functional principial component analysis.

Annals of Applied Statistics, 3(1):458-488.