lecture_8_answer_key.R

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```
rm(list=ls())
library("tidyr"); library("here"); library("readr"); library("dplyr"); library("refund"); library("mgcv")
## Warning: package 'tidyr' was built under R version 4.0.4
## here() starts at C:/Users/Goodgolden5/Desktop/BIOS7720/bios7720_functional
## Warning: package 'dplyr' was built under R version 4.0.4
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
## Warning: package 'refund' was built under R version 4.0.4
## Loading required package: nlme
##
## Attaching package: 'nlme'
## The following object is masked from 'package:dplyr':
##
##
       collapse
## This is mgcv 1.8-33. For overview type 'help("mgcv-package")'.
#####################
## Data processing ##
#####################
## change data_path to where you have your data downloaded
         <- read_rds(here("NHANES_AC_processed.rds"))</pre>
data_mort <- read_rds(here("data_mort.rds"))</pre>
## subset the data
data <-
    ## only consider good days of data and individuals age 50 or over
   filter(good_day %in% 1, Age > 50)
## get mortality data from the rnhanesdata package
```

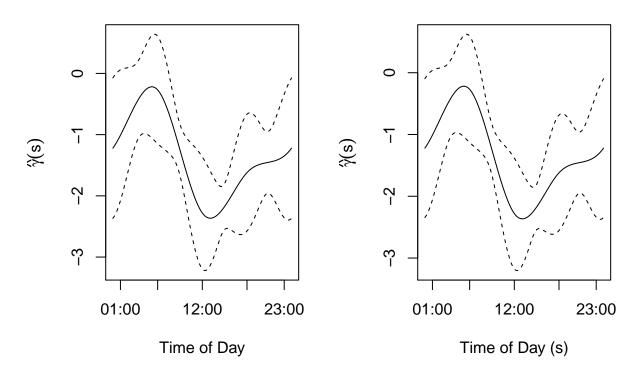
```
## merge with our data and derive 5-year mortality indicator
data <-
    left_join(data, data_mort, by="SEQN") %>%
    mutate(mort 5yr = as.numeric(permth exm/12 <= 5 & mortstat %in% 1),</pre>
           ## replace accidental deaths within 5 years as NA
           mort_5yr = ifelse(mort_5yr == 1 & ucod_leading %in% "004", NA, mort_5yr)) %>%
    ## drop anyone missing mortality data or who had accidental deaths within 5 years
    filter(!is.na(mort_5yr))
## extract just the activity count data
Z <- log(as.matrix(data[,paste0("MIN",1:1440)])+1)</pre>
Z[is.na(Z)] \leftarrow 0
## average across days within participants (SEQN)
uid <- unique(data$SEQN)</pre>
                              # unique subject identifiers
nid <- length(uid)</pre>
                               # number of participants
Zmat <- matrix(NA, nid, 1440) # empty container to store average profiles
inx_ls <- lapply(uid, function(x) which(data$SEQN %in% x)) # list of indices
for(i in seq_along(uid)){
    Zmat[i,] <- colMeans(Z[inx_ls[[i]],,drop=FALSE])</pre>
}
## do fpca on the log(1+AC)
fpca_Z <- fpca.face(Y=Zmat, knots=50)</pre>
Zsm <- fpca_Z$Yhat
## Get a data frame for analysis which contains one row per participant
df <- data[!duplicated(data$SEQN), ]</pre>
## drop the activity count columns
df <-
    df %>%
    dplyr::select(-one_of(paste0("MIN",1:1440)))
## add in the activity count matrix using the AsIs class via I()
## note!! be careful when working with dataframes which contain matrixes
df$Zsm <- I(Zsm)</pre>
df$Zraw <- I(Zmat)</pre>
## clean up the workspace a bit
rm(Zsm);rm(Zmat);rm(Z)
## set up the functional domain matrix
## mgcv will use this to construct the basis \phi_k^\gamma(s)
sind < seq(0,1,len=1440)
smat <- matrix(sind, nrow(df), 1440, byrow=TRUE)</pre>
df$smat <- I(smat)</pre>
## set up the matrix of integration weights
df$lmat <- I(matrix(1/1440, nrow(df), 1440))</pre>
## multiply integration weights by the functional predictor
df$zlmat <- I(df$lmat*df$Zsm)</pre>
fit_fglm_ps <- gam(mort_5yr ~ s(smat, by=zlmat, bs="cc",k=30), data=df,</pre>
                     method="REML", family=binomial)
```

```
################
## Problem 1 ##
##
#################
## Here we re-formulate the unpenalized GFLM as a linear regression problem
## Step 1: create basis functions and penalty matrix for
           \gamma(s) using a small number (K=5) basis functions
## basis functions for the unpenalized fit
K_up <- 5
## create our matrix of basis functions on the functional domain S
## \phi k(s)
smZ_up <- smoothCon(s(sind, bs="cc",k=K_up), data=data.frame(sind=sind))</pre>
## corresponding penalty matrix
# SZ <- smZ_v1[[1]]$S[[1]]
## extract basis matrix on functional domain s
PhiS_up <- smZ_up[[1]]$X</pre>
## The integral term can be expressed as
## zlmat * Phi
## Denote this quantity syntactically as "bigZ_up"
## where zlmat containes the elementwise product of the functional
## predictor and the quadrature weight at each observed point, assuming
## the functions are observed on the same grid (which we have here)
## create the integral term two ways
## 1) do the multiplication
## 2) loop over each subject
## first way
bigZ_up_v1 <- df$zlmat %*% PhiS_up</pre>
## second ("enefficient") way: looping over each individual
N <- nrow(df)
bigZ up v2 <- matrix(NA, N, K up-1)
quad_vec \leftarrow rep(1/1440,1440)
tPhiS_up <- t(PhiS_up)</pre>
for(i in 1:N){
    bigZ_up_v2[i,] <- tPhiS_up %*% (df$Zsm[i,] * quad_vec)</pre>
}
## check to see they're the same by comparing MSE
## good!
mean((bigZ_up_v1 - bigZ_up_v2)^2)
## [1] 0
## get the unpenalized model using our design matrix
gflm_fit_up_manual <- glm(mort_5yr~ bigZ_up_v1,family=binomial,data=df)</pre>
## get the unpenalized model using mgcv::gam
gflm_fit_up_mgcv <- gam(mort_5yr~ s(smat, by=zlmat, bs="cc",k=5,fx=TRUE),family=binomial,data=df)
```

```
## get the estimated coefficients on a new grid of s values
sind_pred \leftarrow seq(0,1,len=100)
## get the basis matrix evaluated on the new s values
PhiS_up_pred <- PredictMat(smZ_up[[1]], data=data.frame(sind=sind_pred))</pre>
## evaluate \hat{gamma}(s) = Phi * \hat{xi}
## note that we exclude the first coefficient which is associated with the global
## intercept (\alpha_0)
fhat_up <- PhiS_up_pred %*% coef(gflm_fit_up_manual)[-1]</pre>
## get the standard errors using the formulat
## var(\hat{xi}) = var(Phi * \hat{xi}) = Phi var(\hat{xi}) Phi^t
## again we exclude the first row and column of the variance/covariance matrix
## because it's associated with the global intercept
se_fhat_up <- sqrt(diag(PhiS_up_pred %*% vcov(gflm_fit_up_manual)[-1,-1] %*% t(PhiS_up_pred)))</pre>
## plot the results
# x-axis ticks/labels
xinx \leftarrow (c(1,6,12,18,23)*60+1)/1440
xinx_lab \leftarrow c("01:00","06:00","12:00","18:00",'23:00')
\# plot with two panels, 1 row and 2 columns
par(mfrow=c(1,2))
## plot the fit from mgcv::gam
plot(gflm_fit_up_mgcv, xlab="Time of Day", xaxt='n',
     ylab=expression(hat(gamma)(s)),main="Unpenalized: mgcv")
axis(1,at=xinx, xinx_lab)
## plot the fit usin our manual glm approach
matplot(sind_pred, cbind(fhat_up, fhat_up-1.96*se_fhat_up, fhat_up + 1.96*se_fhat_up), type='l',
        lty=c(1,2,2),col='black',xaxt='n',xlab="Time of Day (s)",main="Unpenalized: Manual",ylab=expres
axis(1,at=xinx, xinx_lab)
```

Unpenalized: mgcv

Unpenalized: Manual



```
################
##
   Problem 2
################
# here we do the same thing only we use a greater number of basis functions
# since we'll be adding the penalization component which we specify using the "paraPen" argument
# as seen in the lecture slides
## basis functions for the penalized fit
K_pen <- 30
## create our matrix of basis functions on the functional domain S
smZ_pen <- smoothCon(s(sind, bs="cc",k=K_pen), data=data.frame(sind=sind))</pre>
         <- smZ_pen[[1]]$S[[1]]
                                      # penalty matrix
PhiS_pen <- smZ_pen[[1]]$X
                                      # basis matrix
bigZ_pen_v1 <- df$zlmat %*% PhiS_pen # integral term
## fit the manual penalized model
fit_pen_manual <- gam(mort_5yr ~ bigZ_pen_v1,</pre>
                      paraPen = list(bigZ_pen_v1=list(SZ)),
                      family=binomial,method="REML", data=df)
## fit the penalized model automatically
fit_pen_gam <- gam(mort_5yr ~ s(smat, by=zlmat, bs="cc",k=30),</pre>
                   data=df, method="REML", family=binomial)
## new grid of points to obtain estimates of \hat{f}(x) on
```

Automatic Method

Manual Method

