# BIOS 7720: Applied Functional Data Analysis

Lecture 8: Scalar on Function Regression (SoFR)

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## Roadmap

- Logistics
- In Class Exercises

### Logistics

- Homework 1
  - Grading
  - Solutions
- Homeworks 2/3
  - Due dates:
    - HW 2: 4/26
    - HW 3: 5/6
    - Lengths
      - 4 (generally shorter) questions each
      - No "extensive" simulation studies

#### In Class Exercises

- Break into 4 groups
- Each group gets a different question (next slide)
- 50 minutes to work together to answer the question
- 20 minutes to present on group solutions
- Use the NHANES physical activity data created by the *R* script "lecture\_8.R"

Consider the numeric approximation approach to fitting GFLM

$$g(E[y_i|x_i, \mathbf{z}_i]) = \alpha_0 + x_i\beta + \int_{\mathcal{S}} z_i(s)\gamma(s)ds$$

$$= \alpha_0 + x_i\beta + \int_{\mathcal{S}} z_i(s)\sum_k \xi_k\phi_k(s)ds$$

$$\approx \alpha_0 + x_i\beta + \sum_{j=1}^J I(s_j)z_i(s_j)\left[\sum_{k=1}^{K_{\gamma}} \xi_k^{\gamma}\phi_k^{\gamma}(s_j)\right]$$

$$= \alpha_0 + x_i\beta + \sum_{k=1}^{K_{\gamma}} \xi_k^{\gamma}\left[\sum_{j=1}^J I(s_j)z_i(s_j)\phi_k^{\gamma}(s_j)\right]$$

• Where  $I(s_j)$  is the quadrature weight associated with the numeric approximation method



- Consider the GFLM from last class fit to the NHANES data (5-year mortality on smoothed PA profiles)
- Do the following:
  - ① Using the formula from the previous slide, fit the **unpenalized** model as a standard GLM using a small number of basis functions (e.g.  $K_{\gamma}=5$ ) using Riemann integration. You can use mgcv to set up the relevant basis, but **don't** use the "by" argument. **Hint**: you will not want to use the matrix smat, you'll need to use another object which is related to smat.
  - ② Compare your results from the previous step to those obtained from the unpenalized fit using mgcv by plotting point estimates with 95% pointwise CIs for  $\hat{\gamma}(s)$ . The mgcv unpenalized fit can be estimated using the syntax:

- Now, we'll incorporate the penalty term
- You can use mgcv to perform custom regularized regression when you have a quadratic penalty
- This is performed using the "paraPen" argument
- Take for example the additive model

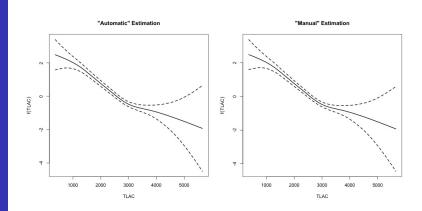
$$g(E[y_i|\mathsf{TLAC}_i]) = \beta_0 + f(\mathsf{TLAC}_i)$$

Where

$$egin{aligned} \mathsf{TLAC}_i &= \sum_{j=1}^J \log(1 + AC_i(s_j)) \ &= \sum_{i=1}^J z_i(s_j) \end{aligned}$$

```
df$TLAC <- rowSums(df$Zraw,na.rm=TRUE) ## calculate TLAC
## let mgcv do everything
fit_TLAC <- gam(mort_5yr ~ s(TLAC, bs="cr",k=30), data=df,
              family=binomial, method="REML")
## do the fitting manually
# set up the smooth
smTLAC <- smoothCon(s(TLAC, bs="cr",k=30), data=df,absorb.cons = TRUE)
# get the basis matrix
Phi TLAC <- smTLAC[[1]]$X
# get the penalty
S_TLAC <- smTLAC[[1]]$S[[1]]
# fit the manual model
fit_TLAC_man <- gam(mort_5yr ~ Phi_TLAC, data=df,
                   paraPen=list(Phi_TLAC=list(S_TLAC)),
              family=binomial, method="REML")
```

```
## get range of TLAC values to predict over
TLAC_pred <- seq(min(df$TLAC), max(df$TLAC), len=100)
## get basis matrix for the TLAC values to predict over
Phi_pred <- PredictMat(smTLAC[[1]], data=data.frame(TLAC=TLAC_pred))
## get point estimates for \hat{f}(TLAC)
fhat_TLAC <- Phi_pred %*% coef(fit_TLAC_man)[-1]
## get the variance/covariance matrix for the spline coefficients
var_xi_TLAC <- vcov(fit_TLAC_man)[-1,-1]
## get se(\hat{f}(TLAC))
se_fhat_TLAC <- sqrt(diag(Phi_pred %*% var_xi_TLAC %*% t(Phi_pred)))</pre>
```



- Do the following:
  - Combine your results from problem 1 with the approach presented above to fit the functional regression model

$$g(E[y_i|z_i]) = \alpha_0 + \int z_i(s)\gamma(s)ds$$

where  $y_i$  is a binary RV for 5-year all cause mortality and  $z_i$  is the smoothed log activity count profile. This model, as given last lecture, is specified by the syntax:

Again, the basis can be constructed using mgcv::smoothCon, but do not us the "by" argument to s().

② Plot  $\hat{\gamma}(s) + / - 2SE\hat{\gamma}(s)$  from your manual fit and from the automatic fits, show they're identical. Do not use *plot.gam()*.

- Do the following:
  - Try adjusting for potential confoudning variables such as age or comorbidities included in the dataset
  - 4 How do the estimates of the association change?