Predicting County-Level Heart Disease Mortality in the United States

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Introduction

Background

Heart disease remains one of the leading causes of death in adults in the US. Understanding risk factors for diseases of this kind is an important task in working towards reducing the number of lives lost. There is obvious benefit in doing this at an individual level, examining personal lifestyle, genetic profile, and family history. But there may be important environmental components that have predictive value in assessing risk for heart disease. We examine economic, health, and demographic data for thousands of counties across the US. This data is synthesized from several sources, including the USDA Economic Research Service, Bureau of Labor Statistics, US Census, Behavioral Risk Factor Surveillance System, the CDC, and others. Our goal in this project is to most effectively predict the county-level heart disease mortality rate per 100,000 persons. We build 6 predictive models (stepwise linear regression, Lasso, Ridge, PCR, GAM, and MARS), and compare them on their predictive capacity quantified by the root mean squared error (RMSE).

Exploratory Data Analysis (Laura)

Data Methods

**note: transform test data by centering and scaling with TRAINING means and standard deviations. Does predict do this automatically when using `preProcess` in caret? – done

can consider imputation: say 10%, one possible solution. use the training set to build. Look at the preProcess function, can use knn. – done. Still dropped two columns because they had 90% missing data; imputation not reliable

Check/detect near-zero variance predictors: to decrease computational time and complexity. – done. A few of the categories for urban influence came back as having near-zero variance. These were examined as dummy variables; 2000 rows divided across 12 levels means that these are likely to be "rare". We determined that we ought to leave them in the model since they are part of the larger variable "urban_influence".

Linear Models

Stepwise Selection (Alyssa)

We first fit a stepwise linear regression model.

Lasso (Charlotte)

Ridge (Laura)

PCR (Charlotte)

Nonlinear Models

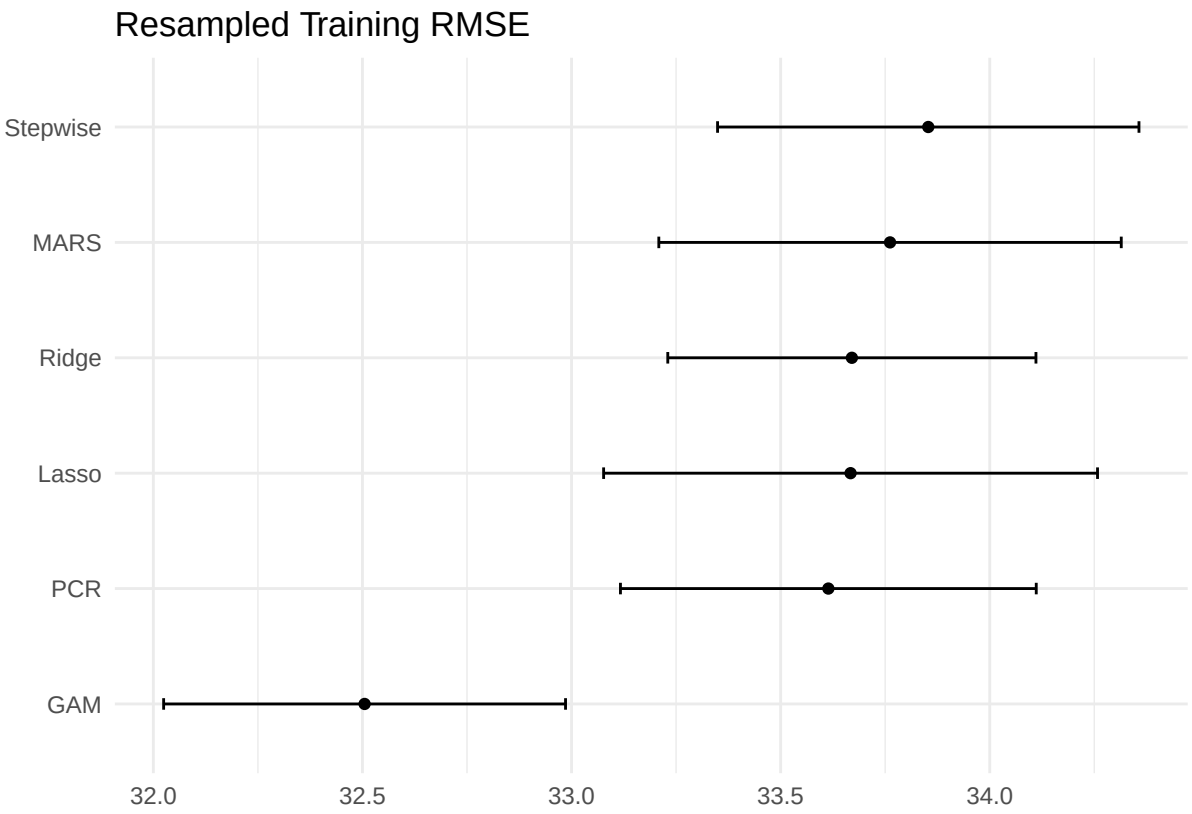
GAM (Alyssa)

MARS (Laura)

Note that we chose the most parsimonious model.

Model Comparison

Training RMSE



The more flexible model

Test RMSE (Alyssa)

Table 1: Predictive RMSE on training and test data

	Train RMSE	Test RMSE
Stepwise	33.85305	32.90754

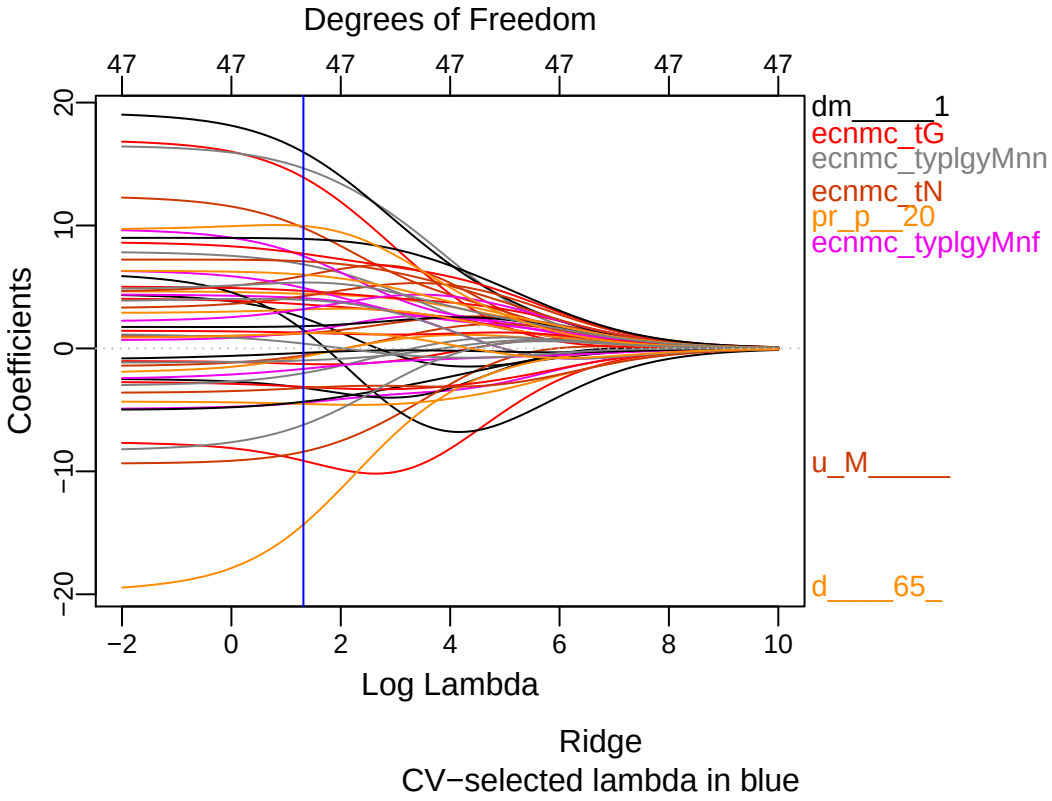
	Train RMSE	Test RMSE
Ridge	33.67035	33.04168
Lasso	33.66725	32.89532
PCR	33.61412	32.86776
GAM	32.50513	30.67289
MARS	33.76163	30.83814

Table 1 presents the RMSE of the predicted heart disease mortality rate for all models on both the training and testing datasets. Although GAM appeared to have the lowest RMSE when using the training data, MARS has similar performance with GAM in the test data.

Interpretations (Laura)

Coefficient Shrinkage: Lasso and Ridge

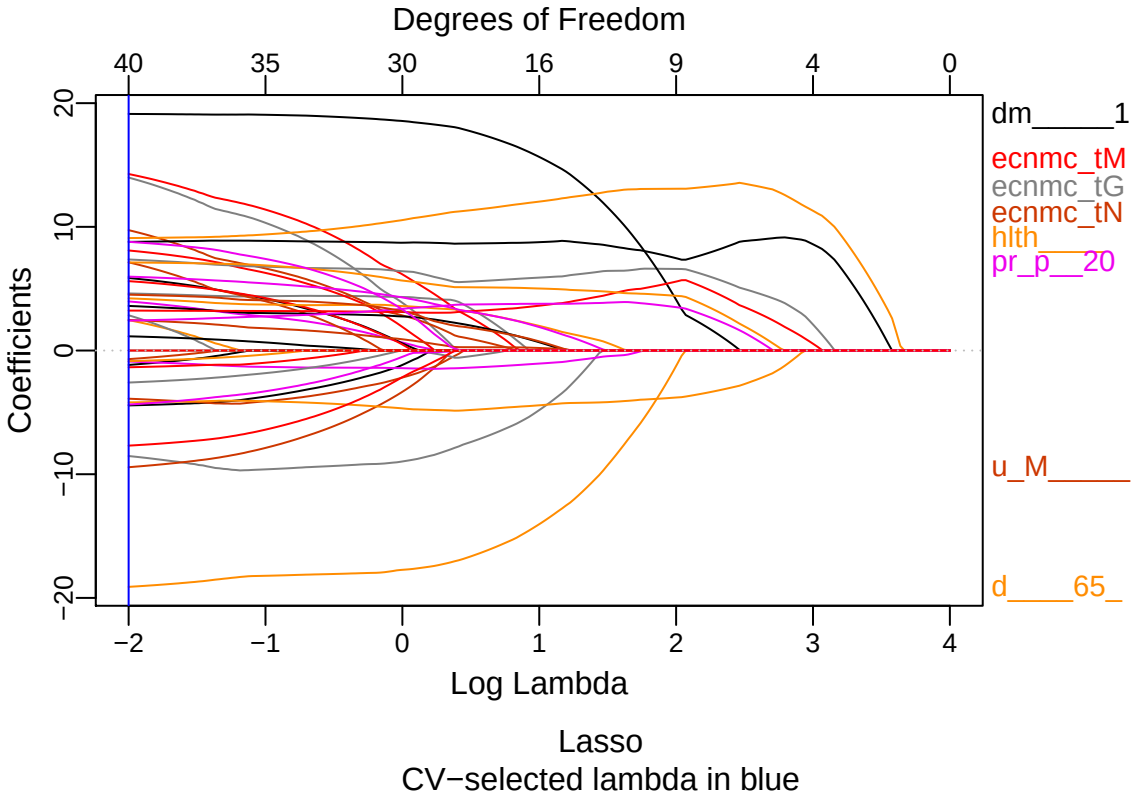
```
## [1] 48  1
```




```
## integer(0)
```

Table 2: Top Absolute-Values Coefficients, Ridge

row	column	value
(Intercept)	1	268.695291
demo___death_rate_per_1k	1	15.898754
economic_typologyMining	1	14.612043
economic_typologyGovernment	1	13.841795
pure_populationmore_than_20k	1	9.947095
economic_typologyNonspecialized	1	9.753701
health___pct_physical_inacticity	1	8.899230
health___pct_diabetes	1	7.686107
economic_typologyManufacturing	1	7.460263
health___pct_low_birthweight	1	7.079183




```
## integer(0)
```

```
## Selecting by value
```

```
## Selecting by value
```

For better visualization, a `glmnet` model was fit and the lambda value selected by `caret` was plotted.

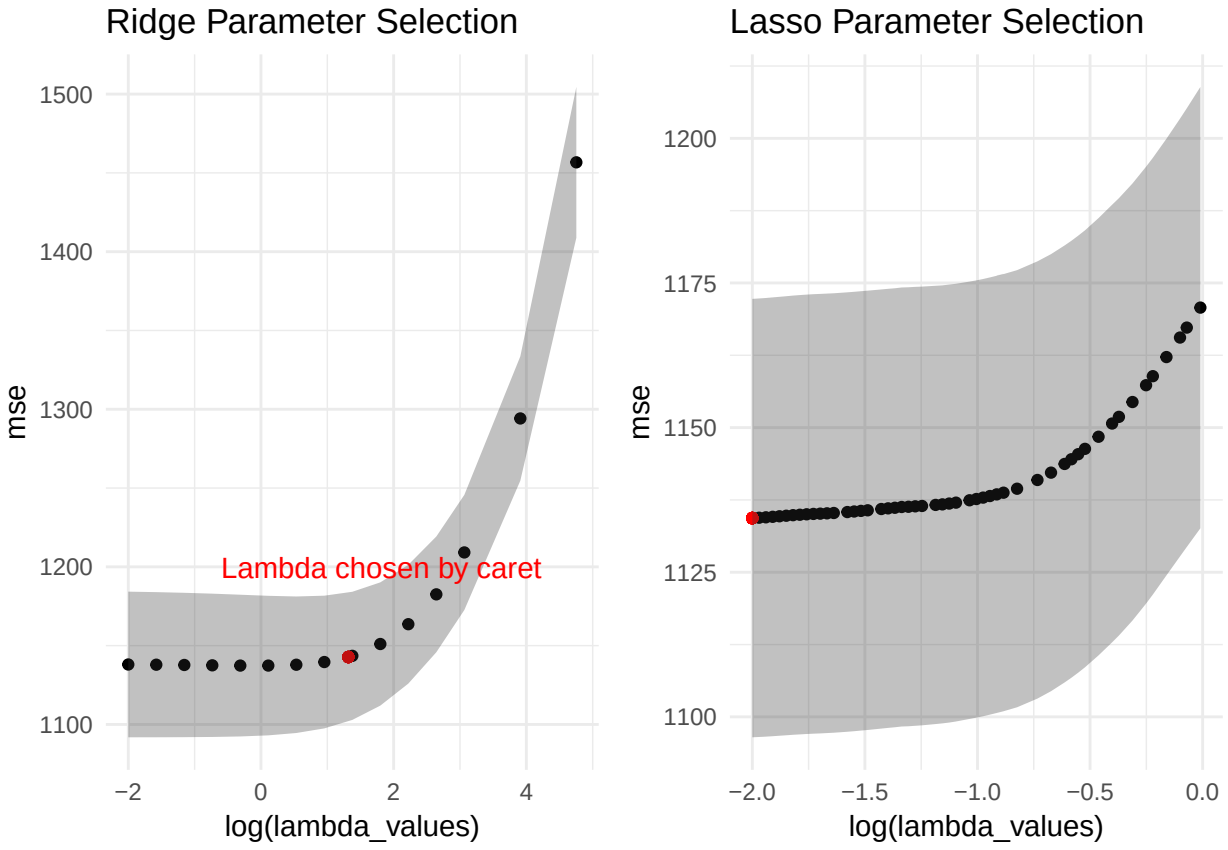
Overall, this modeling problem was perhaps not the best fit for lasso and ridge. Neither of the methods shrunk many coefficients in such a way that completely removed them from the model and improved the RMSE. The best visualization of the effect of shrinkage can be seen in the ridge coefficient plot, where it can be seen that the vast majority of coefficients shrunk equally. Lasso's more stringent shrinking power did not improve MSE for this problem.

If lasso and ridge were more appropriate for the problem, parameter selection might have been more obvious.

Table 3: Top Absolute-Valued Coefficients, Lasso

row	column	value
(Intercept)	1	269.100366
demo___death_rate_per_1k	1	19.125559
economic_typologyMining	1	14.248826
economic_typologyGovernment	1	13.960475
economic_typologyNonspecialized	1	9.716805
health___pct_physical_inacticity	1	9.097034
pure_populationmore_than_20k	1	8.797225
health___pct_diabetes	1	8.781068
urban_influenceLarge_in_a_metro_area_with_at_least_1_million_residents_or_more	1	8.028903
demo___pct_adults_less_than_a_high_school_diploma	1	7.367846

As it is, as shown below, the standard error of the mean cross-validated error is quite wide.



Investigation of MARS

The minimum generalized cross-validation error was achieved for

Investigation of GAM

Discussion

Appendix

Data prep

```
## Data import
predictors <- read_csv("./data/Training_values.csv")
response <- read_csv("./data/Training_labels.csv")


## Manipulation
data <- response %>%
  full_join(predictors, by = "row_id") %>%
  separate(col = area__rucc, into = c('metro', 'population'), sep = ' - ') %>%
  rename(urban_influence = area__urban_influence,
         economic_typology = econ__economic_typology) %>%
  mutate(pure_population = fct_collapse(as.factor(population),
                                        "more_than_1mil" = "Counties in metro areas of 1 million popula
                                        "250k_to_1mil" = "Counties in metro areas of 250,000 to 1 milli
                                        "less_than_250k" = "Counties in metro areas of fewer than 250,0
                                        "more_than_20k" = c("Urban population of 20,000 or more, adjace
                                                            "Urban population of 20,000 or more, not
                                        "2500_to_20k" = c("Urban population of 2,500 to 19,999, adjacen
                                                          "Urban population of 2,500 to 19,999, not a
                                        "less_than_2500" = c("Completely rural or less than 2,500 urban
                                                             "Completely rural or less than 2,500 urban popul
         economic_typology = as.factor(recode(economic_typology,
                                              "Nonspecialized" = "Nonspecialized",
                                              "Manufacturing-dependent" = "Manufacturing",
                                              "Farm-dependent" = "Farming",
                                              "Federal/State government-dependent" = "Government",
                                              "Mining-dependent" = "Mining",
                                              "Recreation" = "Recreation")),
         metro = factor(metro,
                        levels = c("Metro", "Nonmetro")),
         urban_influence = str_replace_all(urban_influence, " |/|-", "_"), # replace problematic charact
         urban_influence = str_replace_all(urban_influence, ",", ""), # replace problematic characters
         demo__pct_nonwhite = demo__pct_hispanic + demo__pct_asian + demo__pct_american_indian_or_alaskan
         urban_influence = fct_rev(urban_influence),
         metro_adjacency = fct_collapse(population,
                                        metro = c("Counties in metro areas of 1 million population or mo
                                                  "Counties in metro areas of 250,000 to 1 million popula
                                                  "Counties in metro areas of fewer than 250,000 populati
                                        adjacent = c("Urban population of 20,000 or more, adjacent to a
                                                     "Urban population of 2,500 to 19,999, adjacent to a
                                                     "Completely rural or less than 2,500 urban populatio
                                        nonadjacent = c("Urban population of 20,000 or more, not adjacen
                                                        "Urban population of 2,500 to 19,999, not adjacen
                                                        "Completely rural or less than 2,500 urban popula
  dplyr::select(-demo__pct_hispanic,
                -demo__pct_asian,
                -demo__pct_american_indian_or_alaskan_native,
                -demo__pct_non_hispanic_african_american,
                -demo__pct_non_hispanic_white,
```

```
                -health__homicides_per_100k, # >90% missing
                -health__pct_excessive_drinking, # >90% missing
                -yr,
                -population,
                -row_id)
```

Training and testing data split. Imputation on missing data.

```
## training/test data
set.seed(1)
train_ind <- sample(seq_len(nrow(data)), size = 2/3*nrow(data)) # select rows in 2:1 ratio

train <- data[train_ind, ] # training dataset
test <- data[-train_ind, ] # testing dataset

# Imputation for missing values with caret, based on training data
training_preproc = caret::preProcess(train[,-1],
                                     method = "knnImpute", # automatically centers and scales data
                                     pcaComp = 10,
                                     na.remove = TRUE,
                                     k = 5,
                                     knnSummary = mean,
                                     outcome = NULL,
                                     fudge = .2,
                                     numUnique = 3,
                                     verbose = TRUE)

# Impute training imputation on both training and testing datasets
train_imputed = predict(training_preproc, train)
test_imputed = predict(training_preproc, test)

#save files to Rdata: was not saving the factor structure in read from csv
saveRDS(train_imputed, file = './data/train_imputed.Rdata')
saveRDS(train_imputed, file = './data/test_imputed.Rdata')
```

Linear Models

Set up `caret` training control. We will use this for all models.

```
set.seed(100)
ctrl <- trainControl(method = "repeatedcv", number = 10, repeats = 5)
```

Stepwise regression:

```
set.seed(2)
step.fit = caret::train(x, y,
                        method = 'glmStepAIC',
                        metric = "RMSE",
                        trControl = ctrl)
saveRDS(step.fit, "lm_step_imputed.rds")
```

Lasso:

```
set.seed(2)
lasso_fit <- caret::train(x, y,
                          method = "glmnet",
                          metric = "RMSE",
```

```
                          tuneGrid = expand.grid(alpha = 1,
                                                 lambda = exp(seq(-2, 4, length = 200))),
                          trControl = ctrl)
plot(lasso_fit, xTrans = function(x) log(x)) #in correct range

saveRDS(lasso_fit, "lasso_imputed.rds")
```

Ridge:

```
set.seed(100)

ridge_fit <- caret::train(x, y,
                      method = "glmnet",
                      tuneGrid = expand.grid(alpha = 0,
                                             lambda = exp(seq(-2, 10, length = 200))),
                     trControl = ctrl1)


plot(ridge_fit, xTrans = function(x) log(x)) #in correct range

best_lambda_ridge = ridge_fit$bestTune$lambda

saveRDS(ridge_fit, "ridge.rds")
```

PCR:

```
set.seed(2)
pcr_fit <- caret::train(x, y,
                        method = "pcr",
                        trControl = ctrl,
                        metric = "RMSE",
                        tuneLength = 200)
saveRDS(pcr_fit, "pcr_imputed.rds")
```

Non-linear models

GAM:

```
set.seed(2)
gam_fit <- caret::train(x, y,
                        method = "gam",
                        metric = 'RMSE',
                        tuneGrid = data.frame(method = "GCV.Cp", select = c(TRUE, FALSE)),
                        trControl = ctrl)
summary(gam_fit)
saveRDS(gam_fit, "gam_fit_imputed.rds")
```

MARS:

```
mars_grid <- expand.grid(degree = 1:3, # degree: 1 vs 2 vs 3, no interaction vs. interaction;
                         nprune = 10:40) # nprune is number of coef

set.seed(2)

mars_fit <- caret::train(x, y,
                         method = "earth",
                         tuneGrid = mars_grid,
```

```
                          trControl = ctrl)

saveRDS(mars_fit, "mars.rds")

#based on initial results, choose parsimonious version
mars_grid_refined <- expand.grid(degree = 2, nprune = 25:40)

mars_fit_refined <- caret::train(x, y,
                                 method = "earth",
                                 tuneGrid = mars_grid_refined,
                                 trControl = ctrl)
saveRDS(mars_fit_refined, "mars2.rds")
```