# MATH 567: Mathematical Techniques in Data Science Lab 3

Dominique Guillot

Departments of Mathematical Sciences University of Delaware

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## Exercise 1

- Install the package glmnet (if not already installed).
- Standard Examine the documentation of the glmnet function (?glmnet)
- Generate random data:

```
n <- 100 # Sample size
p <- 500 # Nb. of variables
true_p <- 10
X <- matrix(rnorm(n*p), nrow=n, ncol=p)</pre>
true_beta = matrix(rep(0,p), nrow=p)
true beta[1:10] = 1
SNR <- 1 # Signal-to-noise ratio
          # = ratio of variances
noise <- matrix(rnorm(n, sd=1/sqrt(SNR)),nrow=n)</pre>
y <- X %*% true_beta + noise
```

Note: y depends only on the first 10 predictors.

## Exercise 1 (cont.)

- Fit a ridge regression model to the data (use the options family="gaussian", alpha=0 in glmnet).
- What does the \$beta variable of your ridge model contain? What about \$lambda?
- Use the command matplot to plot the regression coefficients as a function of λ for the first 10 estimated coefficients. (Note: matplot plots the *columns* of a matrix). Use the option type="l".
- $\bigcirc$  Plot the coefficients 11:100 as a function of  $\lambda$ .
- **③** Repeat steps 4–7 for a lasso model instead of ridge (i.e., use  $\alpha = 1$  in glmnet).
- Repeat the previous steps with a lasso model, but with smaller values of SNR (e.g. SNR = 0.5, 0.25, 0.1). What do you observe?

### Exercise 2: Cross-validation

- Generate data as in the previous exercise with SNR = 1.0.
- Q Run ?cv.glmnet to see what cv.glmnet returns.
- Fit a lasso model using cross-validation:

- Ipot the mean cross-validated error as a function of lambda.
- Sun plot(cvlasso) to plot the cross-validated error and its standard error.
- Fit a lasso model (no cross-validation) with parameter  $\lambda = cvlasso$  lambda.min. Examine the coefficients.

- What does the variable cvlasso\$lambda.1se contain?
- Get the non-zero coefficients in the previous model: which(best\_lasso\$beta != 0).
- Fit a linear model (1m) using only the lasso selected variables.

#### Exercise 3: Breast cancer tumors

The file Westbc.rda (available on Sakai) contains gene expression data (p = 7, 129 genes) for n = 49 breast cancer tumor samples (West et al., 2001).

- Load the data using load("path-to-file/Westbc.rda"). (You should have two new variables: Westbc\$assay and Westbc\$pheno).
- Convert the variables Westbc\$pheno to binary (0/1) values: pheno <- matrix(rep(0,49), nrow=49) pheno[Westbc\$pheno == 'positive'] = 1
- Split the data into a training set (2/3) and a test set (1/3) randomly.
- Fit a lasso model on the training set using cross-validation.
- In the resulting cross-validation error (plot(cvlasso)).
- Compute the prediction error on the test set using the optimal model.
- Repeat the previous experiment with 100 random train/test sets and compute the average test error.