# **Administration**

- Homework 1 available Thursday
- Discussion of project requirements on Thursday
- NSERC summer undergraduate awards
- Fields-MITACS undergraduate summer research

http://www.fields.utoronto.ca/programs/scientific/10-11/summer-research/

# Geometric view of least squares fitting

$$\hat{\beta} = (X^T X)^{-1} X^T y$$
$$\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1, \dots, \hat{\beta}_p)$$

•  $\hat{\beta}_p$  can be obtained by a series of regressions (projections) as outlined in algorithm 3.1 on p.54

regress  $\mathbf{x}_1$  on 1, get coefficient  $\hat{\gamma}_{01}$ , form residual  $z_1 = \mathbf{x}_1 - \hat{\mathbf{x}}_1$ regress  $\mathbf{x}_2$  on 1,  $z_1$ , get coeffs  $\hat{\gamma}_{02}$ ,  $\hat{\gamma}_{12}$ , form residual  $z_2 = \mathbf{x}_2 - \hat{\gamma}_{02}\mathbf{1} - \hat{\gamma}_{12}z_1$ : regress  $\mathbf{x}_p$  on  $z_{p-1}, z_{p-2}, \dots, z_1, \mathbf{1}$  to get  $z_p = \mathbf{x}_p - \hat{\mathbf{x}}_p$ regress y on  $z_p$  to get  $\hat{\beta}_p$ 

illustration on prostate training data – see prostateRsession.txt

# **QR Decomposition** $X = Z\Gamma$

- matrix representation  $X = Z\Gamma$
- Z has columns z<sub>j</sub>

$$\Gamma = \begin{pmatrix} 0 & \hat{\gamma}_{01} & \hat{\gamma}_{02} & \dots & \hat{\gamma}_{0p} \\ 0 & 0 & \hat{\gamma}_{12} & \dots & \hat{\gamma}_{1p} \\ & & \ddots & & \\ & & & & \hat{\gamma}_{p-1,p} \\ 0 & \dots & & 0 \end{pmatrix}$$

- Let  $D_{jj} = (z_j^T z_j)^{1/2} = ||z_j||$  and  $D = \text{diag}(D_{jj})$  dimension?
- $\bullet X = ZD^{-1}D\Gamma = QR$
- $Q^T Q = I$ , *R* is upper triangular
- $\triangleright \hat{\beta} = R^{-1}Q^T y$
- $\hat{y} = QQ^T y$  check pr.lm\$qr
- Gram-Schmidt

# Singular value decomposition, X = UDV

- X assumed to be centered, so all columns add to zero (p.64, l.-4)
- *U* is  $N \times p$ , *V* is  $p \times p$
- ▶ *D* is diagonal,  $d_1 \ge d_2 \ge \cdots \ge d_p \ge 0$  not the same *D*

$$X^T X = V D^2 V^T$$

eigendecomposition of  $X^T X$  and of  $NS = XX^T$ 

•  $\hat{y} = X\hat{\beta} = UU^T y$ =  $QQ^T y$  different orthogonal bases for ...

define

$$\mathbf{z}_1 = X \mathbf{v}_1 = u_1 \mathbf{d}_1$$

- note that  $var(z_1) = d_1^2/N$
- z<sub>1</sub> is the derived variable with the largest variance: the first principal component of X
- z<sub>2</sub> has the largest variance among linear combinations orthogonal to z<sub>1</sub>



FIGURE 3.9. Principal components of some input data points. The largest principal component is the direction that maximizes the variance of the projected data, and the smallest principal component minimizes that variance. Ridge regression projects y onto these components, and then shrinks the coefficients of the lowvariance components more than the high-variance components.

#### ... singular value decomposition

$$\begin{aligned} X_{N \times p} &= U_{N \times p} D_{p \times p} V_{p \times p}^{T}, \quad U^{T} U = I, \quad V^{T} V = I, \\ D &= \operatorname{diag}(d_{1}, \dots d_{p}) \end{aligned}$$

$$\begin{aligned} X\hat{\beta}_{LS} &= X(X^TX)^{-1}X^Ty \\ &= UDV^T(VDU^TUDV^T)^{-1}VDU^Ty \\ &= UDV^TV^{T-1}D^{-2}V^{-1}VDU^Ty \\ &= UU^Ty = \sum_{j=1}^p u_j u_j^Ty \end{aligned}$$

svd(model.matrix(pr.lm)), for example

# Model selection: subsets (§3.3.1)

 linear regression: forward, backward, stepwise, all possible subsets regression

► 
$$RSS(\hat{\beta}) = (y - X\hat{\beta})^T (y - X\hat{\beta}) = \Sigma (y_i - \hat{y}_i)^2$$
  
Figure 3.5 this is called SSE in the 302 text

- ▶ if we add a regressor, say from X<sub>p-1</sub> to X<sub>p</sub>, RSS(β̂) necessarily decreases
- forward (stepwise) selection starts with one predictor (usually the constant term) and stops when no additional predictor is statistically significant step(pr.lm, direction = "forward", ...)
- backward (stepwise) selection starts with all predictors and deletes least significant ... direction = "backward"...
- stepwise selection checks at each stage whether or not to add variables back in direction = "both"

## ... subset selection

- forward stagewise: a "slow" version of forward stepwise, in which coefficients are not re-computed
- all possible subsets regression considers all 2<sup>p</sup> models.
- for p < 30, feasible with the "leaps and bounds" algorithm, implemented in package leaps (See Figure 3.6), also regsubsets
- Figure 3.7
- huh?
- 10-fold cross-validation
- model selection related to expected prediction error: theory to come in Ch. 7

# "Mallows' C<sub>p</sub>"

a common adjustment to measure benefit of adding further parameters:

$$C_{
ho} = rac{RSS_{
ho}}{\sigma^2} + 2
ho - N \;\; ext{ if } \sigma^2 \; ext{is known};$$

- or an estimate of this, if  $\sigma^2$  is unknown
- ▶ rule of thumb: choose *p* so that  $C_p$  is small and  $C_p \simeq p$
- can be shown to be a good choice for prediction (details deferred until Chapter 7)
- a closely related, more general, criterion AIC (Akaike's Information Criterion)
- for our linear model

 $AIC \approx N \log(RSS_p/N) + 2p + constant$ 

stepAIC in MASS library; step in base

#### prostate data: all possible subsets



Figure 3.5

```
step
```

```
> step(pr.lm)
Start: AIC=-37.13
lpsa ~ lcavol + lweight + age + lbph + svi + lcp + gleason +
pgg45
```

		Df	Sum	of	Sq	RSS		AIC	
-	gleason	1		0.0	011	29.437	-39	.103	
<r< td=""><td>none&gt;</td><td></td><td></td><td></td><td></td><td>29.426</td><td>-37</td><td>.128</td><td></td></r<>	none>					29.426	-37	.128	
-	age	1		0.	989	30.415	-36	.914	
-	pgg45	1		1.	532	30.959	-35	.727	
-	lcp	1		1.	768	31.195	-35	.218	
-	lbph	1		2.3	144	31.571	-34	.415	
-	svi	1		3.0	093	32.520	-32	.430	
-	lweight	1		3.	B39	33.265	-30	.912	
-	lcavol	1	1	L4.	610	44.037	-12	.118	

Step: AIC=-39.1
lpsa ~ lcavol + lweight + age + lbph + svi + lcp + pgq45

		Df	Sum	of	Sq	RS	S	AIC
<none></none>						29.43	7 -39	0.103
-	age	1		1.3	102	30.54	0 -38	8.639
-	lcp	1		1.	758	31.19	6 - 37	.216
-	lbph	1		2.3	135	31.57	3 - 36	5.411
-	pgg45	1		2.3	376	31.81	3 - 35	5.903
-	svi	1		3.3	166	32.60	4 - 34	.258
-	lweight	1		4.0	005	33.44	2 - 32	2.557
-	lcavol	1	1	14.8	387	44.32	5 -13	8.681

Call:

lm(formula = lpsa ~ lcavol + lweight + age + lbph + svi + lcp + pgg45, data = train)

# Shrinkage Methods: (§3.4)

Ridge regression

$$\hat{\beta}_{LS} = (X^T X)^{-1} X^T y$$
$$\hat{\beta}_{ridge} = (X^T X + \lambda I)^{-1} X^T y$$

• can show that  $\hat{\beta}_{ridge}$  satisfies

$$\begin{split} \min_{\beta} \left( \Sigma \{ y_i - \beta_0 - \Sigma_{j=1}^{p} x_{ij} \beta_j \}^2 + \lambda \Sigma_{j=1}^{p} \beta_j^2 \right) \\ \min_{\beta} \Sigma \{ y_i - \beta_0 - \Sigma_{j=1}^{p} x_{ij} \beta_j \}^2 \quad \text{s.t. } \Sigma \beta_j^2 \le t \end{split}$$

Assume x<sub>j</sub>'s are centered and put these in matrix X (with no column of 1's:

$$\min_{\beta} (y - X\beta)^{T} (y - X\beta) \qquad \text{s.t. } ||\beta||^{2} \leq t$$

# ... ridge regression

- $\min_{\beta} \{ (y X\beta)^T (y X\beta) + \lambda ||\beta||^2 \}$
- ▶  $\lambda$  is a tuning parameter:  $\lambda = 0$  gives  $\hat{\beta}_{LS}, \lambda \to \infty$

```
Figure 3.8
```

- in R the library MASS library (MASS ) has a ridge regression version of lm called lm.ridge
- if columns of X are nearly linearly dependent (multicollinearity), β̂'s for these columns should be shrunk towards 0.
- essential that the predictors are all scaled to the same units
- this is difficult for interpretation of the coefficients

$$\begin{aligned} X\hat{\beta}_{ridge} &= X(X^TX + \lambda I)^{-1}X^Ty \\ &= UDV^T(VD^2V^T + \lambda I)^{-1}VDU^Ty \\ &= UDV^T(VD^2V^T + \lambda VV^T)^{-1}VDU^Ty \\ &= UD(D^2 + \lambda I)^{-1}DU^Ty \\ &= \sum_{j=1}^p u_j(\frac{d_j^2}{d_j^2 + \lambda})u_j^Ty \end{aligned}$$

$$df(\lambda) = \operatorname{tr}[X(X^TX + \lambda I)^{-1}X^T] = \sum_{j=1}^p \frac{d_j^2}{d_j^2 + \lambda}$$

Figure 3.7

 $df(\lambda)$  called effective number of parameters in Ch. 7



FIGURE 3.8. Profiles of ridge coefficients for the prostate cancer example, as the tuning parameter  $\lambda$  is varied. Coefficients are plotted versus df( $\lambda$ ), the effective degrees of freedom. A vertical line is drawn at df = 5.0, the value chosen by cross-validation.

►

#### Lasso

$$\min_{\beta} \left( \Sigma \{ y_i - \beta_0 - \Sigma_{j=1}^{p} x_{ij} \beta_j \}^2 + \lambda \Sigma_{j=1}^{p} |\beta_j| \right)$$

$$\min_{\beta} \Sigma \{ y_i - \beta_0 - \Sigma_{j=1}^{p} x_{ij} \beta_j \}^2 \quad \text{s.t. } \Sigma |\beta_j| \le t$$

- quadratic programming problem
- $\hat{\beta}^{lasso}$  is nonlinear function of y
- ► Figure 3.10
- Table 3.3



**FIGURE 3.10.** Profiles of lasso coefficients, as the tuning parameter t is varied. Coefficients are plotted versus  $s = t/\sum_{1}^{p} |\hat{\beta}_{j}|$ . A vertical line is drawn at s = 0.36, the value chosen by cross-validation. Compare Figure 3.8 on page 65; the lasso

**TABLE 3.3.** Estimated coefficients and test error results, for different subset and shrinkage methods applied to the prostate data. The blank entries correspond to variables omitted.

Term	LS	Best Subset	Ridge	Lasso	PCR	PLS
Intercept	2.465	2.477	2.452	2.468	2.497	2.452
lcavol	0.680	0.740	0.420	0.533	0.543	0.419
lweight	0.263	0.316	0.238	0.169	0.289	0.344
age	-0.141		-0.046		-0.152	-0.026
lbph	0.210		0.162	0.002	0.214	0.220
svi	0.305		0.227	0.094	0.315	0.243
lcp	-0.288		0.000		-0.051	0.079
gleason	-0.021		0.040		0.232	0.011
pgg45	0.267		0.133		-0.056	0.084
Test Error	0.521	0.492	0.492	0.479	0.449	0.528
Std Error	0.179	0.143	0.165	0.164	0.105	0.152

### ...Lasso

- in Table 3.3 each method had a tuning parameter to choose; they used cross-validation within the training data
- in lm.ridge you can extract a component called \$GCV
- ► the quantity Σd<sup>2</sup><sub>j</sub>/(d<sup>2</sup><sub>j</sub> + λ) has an interpretation as the number of 'degrees of freedom' or number of 'parameters' used by the ridge regression fit
- book says that the best value is 4.16, which corresponds to quite a large λ (39); the GCV criterion chooses λ = 5
- ► analysis of lasso more difficult; note Figure 3.10 plotted against t/Σ|β̂<sub>j</sub>|

## ... smoothing

- ridge regression gives "proportional shrinkage"
- ▶ subset selection gives "hard thresholding" (some  $\beta_i \rightarrow 0$ )
- lasso gives "soft thresholding": blend of shrinkage and zeroing (Figure 3.10 and Figure 3.11)
- Least Angle Regression (LAR): combine forward stagewise regression with the lasso
- related to the Dantzig selector (Candes and Tao, AS 2007)

## Mean squared error of prediction in linear models

Let  $\tilde{\beta} = \tilde{\beta}(y)$  be a competing estimator of  $\beta$  (not  $\hat{\beta}$ , the LS estimator). Using  $\tilde{\beta}$  for prediction would give  $\tilde{y}_0 = x_0^T \tilde{\beta}$ , where  $x_0^T = (1, x_{01}, \ldots, x_{0\rho})$  is the new value of the inputs. The expected prediction error is

$$E(\tilde{y}_0 - y_0)^2 = E(x_0^T \tilde{\beta} - y_0)^2 \text{ (by definition)}$$
  

$$= E(y_0 - x_0^T \beta + x_0^T \beta - x_0^T \tilde{\beta})^2$$
  

$$= \operatorname{var}(y_0) + E(x_0^T \tilde{\beta} - x_0^T \beta)^2 \text{ (why is cross prod 0?)}$$
  

$$= \sigma^2 + E\{x_0^T (\tilde{\beta} - \beta)(\tilde{\beta} - \beta)^T x_0\}$$
  

$$= \sigma^2 + x_0^T E\{(\tilde{\beta} - \beta)(\tilde{\beta} - \beta)^T\} x_0$$
  

$$= \sigma^2 + x_0^T E\{(\tilde{\beta} - E\tilde{\beta} + E\tilde{\beta} - \beta)(\tilde{\beta} - E\tilde{\beta} + E\tilde{\beta} - \beta)x_0$$
  

$$= \sigma^2 + x_0^T [E\{(\tilde{\beta} - E\tilde{\beta})(\tilde{\beta} - E\tilde{\beta})^T\} + (E\tilde{\beta} - \beta)(E\tilde{\beta} - \beta)^T] x_0$$
  

$$= \sigma^2 + x_0^T [E\{(\tilde{\beta} - E\tilde{\beta})(\tilde{\beta} - E\tilde{\beta})^T\} + (E\tilde{\beta} - \beta)(E\tilde{\beta} - \beta)^T] x_0$$

The first term,  $\sigma^2$ , is unavoidable. The next two terms together are the Mean Squared Error (MSE) of the prediction  $\tilde{y}_0$ , and are shown here to be a function of  $x_0$  and the MSE of  $\tilde{\beta}$ . If  $\tilde{\beta}$  is unbiased, i.e.  $E\tilde{\beta} = \beta$ , then we only need to worry about the covariance terms. Estimates of  $\beta$  obtained by ridge regression, Lasso, and LARS are all biased. This could be useful if the variance is decreased enough to give smaller MSE.

►

# Derived features §3.5

- replace x<sub>1</sub>,...x<sub>p</sub> with linear combinations of columns
- principal components from SVD are natural candidates

$$\blacktriangleright \mathbf{z}_m = X \mathbf{v}_m, \quad m = 1, \dots, M < p$$

z<sub>m</sub> are orthogonal by construction

$$\hat{y}_{(M)}^{pcr} = \bar{y}\mathbf{1} + \sum_{m=1}^{M} \hat{\theta}_m \mathbf{z}_m$$

$$\hat{\theta}_m = \frac{\langle \mathbf{z}_m, \mathbf{y} \rangle}{\langle \mathbf{z}_m, \mathbf{z}_m \rangle}$$

inputs should be scaled first (mean 0, variance 1)

► Figure 3.17

# ... derived features

- closely related method Partial least squares
- also constructs derived variables
- ▶ widely used in chemometrics, where often p > N
- see §3.6 for discussion





# Thursday and next week

- more on ridge regression and lasso in R
- construction of Table 3.3 in R test set error
- discussion of project
- HW 1 will be available
- Next week Chapter 4: §4.1 to §4.4