



Technical details on linear regression for proteomics

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Statistical Genomics

##1. Linear Regression

- Consider a vector of predictors $\mathbf{x} = (x_1, \dots, x_{p-1})$ and
- \bullet a real-valued response Y
- then the linear regression model can be written as

$$Y = f(\mathbf{x}) + \epsilon = \beta_0 + \sum_{j=1}^{p-1} x_j \beta + \epsilon$$

with i.i.d. $\epsilon \sim N(0, \sigma^2)$

- n observations $(\mathbf{x}_1, y_1) \dots (\mathbf{x}_n, y_n)$
- Regression in matrix notation

$$\mathbf{Y} = \mathbf{X}oldsymbol{eta} + oldsymbol{\epsilon}$$

with
$$\mathbf{Y} = \begin{bmatrix} y_1 \\ \vdots \\ y_n \end{bmatrix}$$
, $\mathbf{X} = \begin{bmatrix} 1 & x_{11} & \dots & x_{1p-1} \\ \vdots & \vdots & & \vdots \\ 1 & x_{n1} & \dots & x_{np-1} \end{bmatrix}$, $\boldsymbol{\beta} = \begin{bmatrix} \beta_0 \\ \vdots \\ \beta_{p-1} \end{bmatrix}$ and $\boldsymbol{\epsilon} = \begin{bmatrix} \epsilon_1 \\ \vdots \\ \end{bmatrix}$

1.1 Least Squares (LS)

• Minimize the residual sum of squares

$$RSS(\beta) = \sum_{i=1}^{n} e_i^2$$
$$= \sum_{i=1}^{n} \left(y_i - \beta_0 - \sum_{j=1}^{p} x_{ij} \beta_j \right)^2$$

or in matrix notation

$$RSS(\beta) = (\mathbf{Y} - \mathbf{X}\beta)^{T} (\mathbf{Y} - \mathbf{X}\beta)$$
$$= \|\mathbf{Y} - \mathbf{X}\beta\|^{2}$$

with the L_2 -norm of a p-dim. vector $v \| \mathbf{v} \| = \sqrt{v_1^2 + \ldots + v_p^2}$

$$\rightarrow \hat{\boldsymbol{\beta}} = \operatorname{argmin}_{\boldsymbol{\beta}} \|\mathbf{Y} - \mathbf{X}\boldsymbol{\beta}\|^2$$

Minimize RSS

$$\frac{\partial RSS}{\partial \beta} = \mathbf{0}$$

$$\frac{(\mathbf{Y} - \mathbf{X}\beta)^T (\mathbf{Y} - \mathbf{X}\beta)}{\partial \beta} = \mathbf{0}$$

$$-2\mathbf{X}^T (\mathbf{Y} - \mathbf{X}\beta) = \mathbf{0}$$

$$\mathbf{X}^T \mathbf{X}\beta = \mathbf{X}^T \mathbf{Y}$$

$$\hat{\boldsymbol{\beta}} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{Y}$$

```
data<-readRDS("heartProtQ92736.rds")
fit <- lm(exprs~location+patient,data,x=TRUE)
head(fit$x,4)</pre>
```

##	(Intercept)	locationLV	${\tt locationRA}$	${\tt locationRV}$	patient4	pat
## LA3	1	0	0	0	0	
## LA4	. 1	0	0	0	1	
## LA8	1	0	0	0	0	
## T.V.3	1	1	0	0	0	

The model matrix can also be obtained without fitting the model:

```
X<-model.matrix(~location+patient,data)
head(X,4)</pre>
```

##		(Intercept)	${\tt locationLV}$	${\tt locationRA}$	${\tt locationRV}$	patient4	pat
##	LA3	1	0	0	0	0	
##	LA4	1	0	0	0	1	
##	LA8	1	0	0	0	0	
##	I.V.3	1	1	0	0	0	

```
fit$coefficient

## (Intercept) locationLV locationRA locationRV patient4
## 27.50063357 -3.40997017 0.36748910 1.44473120 0.08573147 -
sigma(fit)
```

[1] 0.7812888

Variance Estimator?

$$\hat{\Sigma}_{\hat{\beta}} = \operatorname{var}\left[(\mathbf{X}^{T}\mathbf{X})^{-1}\mathbf{X}^{T}\mathbf{Y} \right]
= (\mathbf{X}^{T}\mathbf{X})^{-1}\mathbf{X}^{T}\operatorname{var}\left[\mathbf{Y}\right]\mathbf{X}(\mathbf{X}^{T}\mathbf{X})^{-1}
= (\mathbf{X}^{T}\mathbf{X})^{-1}\mathbf{X}^{T}(\mathbf{I}\sigma^{2})\mathbf{X}(\mathbf{X}^{T}\mathbf{X})^{-1}
= (\mathbf{X}^{T}\mathbf{X})^{-1}\mathbf{X}^{T}\mathbf{I} \quad \mathbf{X}(\mathbf{X}^{T}\mathbf{X})^{-1}\sigma^{2}
= (\mathbf{X}^{T}\mathbf{X})^{-1}\mathbf{X}^{T}\mathbf{X}(\mathbf{X}^{T}\mathbf{X})^{-1}\sigma^{2}
= (\mathbf{X}^{T}\mathbf{X})^{-1}\sigma^{2}$$

1.2 Contrasts

When we assess a contrast we assess a linear combination of model parameters:

$$H_0: \mathbf{L}^{\mathsf{T}} \boldsymbol{\beta} = 0 \text{ vs } H_1: \mathbf{L}^{\mathsf{T}} \boldsymbol{\beta} \neq 0$$

Estimator of Contrast?

$$\mathbf{L}^{T}\hat{\boldsymbol{\beta}}$$

Variance?

$$\mathbf{\Sigma}_{\mathbf{L}\hat{\boldsymbol{\beta}}} = \mathbf{L}^T \mathbf{\Sigma}_{\hat{\boldsymbol{\beta}}} \mathbf{L}$$

1.3 Inference

• When the assumptions of the linear model hold

$$\hat{\boldsymbol{\beta}} \sim \textit{MVN}\left[\boldsymbol{\beta}, \left(\mathbf{X}^T\mathbf{X}\right)^{-1}\sigma^2\right]$$

Hence,

$$\mathbf{L}^T \hat{\boldsymbol{\beta}} \sim \textit{MVN} \left[\mathbf{L}^T \boldsymbol{\beta}, \mathbf{L}^T \left[\left(\mathbf{X}^T \mathbf{X} \right)^{-1} \sigma^2 \right] \mathbf{L} \right]$$

• We estimate σ^2 by MSE

$$\hat{\sigma}^2 = \frac{\mathbf{e}^T \mathbf{e}}{n-p} \to \hat{\mathbf{\Sigma}}_{\hat{\boldsymbol{\beta}}} = \left(\mathbf{X}^T \mathbf{X}\right)^{-1} \hat{\sigma}^2$$

Statistic

$$\mathbf{F} = \hat{\boldsymbol{\beta}}^T \mathbf{L} \left(\mathbf{L}^T \hat{\boldsymbol{\Sigma}}_{\hat{\boldsymbol{\beta}}} \mathbf{L} \right)^{-1} \mathbf{L}^T \hat{\boldsymbol{\beta}} \underset{H_0}{\sim} F_{r,n-p}$$

follows an F distribution with r and n-p degrees of freedom under H_0 : $\mathbf{L}^T \hat{\boldsymbol{\beta}} = \mathbf{0}$

 Note, that r equals the number of contrasts or the rank of the contrast matrix When we test one contrast at the time (e.g. the k^{th} contrast) the statistic reduces to

$$\mathcal{T} = rac{\mathbf{L}_k^T \hat{oldsymbol{eta}}}{\sqrt{\left(\mathbf{L}_k^T \hat{oldsymbol{\Sigma}}_{\hat{oldsymbol{eta}}} \mathbf{L}_k
ight)}} \overset{\sim}{\sim} t_{n-p}$$

follows a t distribution with n-p degrees of freedom under $H_0: \mathbf{L}_k^T \hat{\boldsymbol{\beta}} = 0$

summary(fit)

```
##
## Call:
## lm(formula = exprs ~ location + patient, data = data, x = TRU
##
## Residuals:
##
     Min 1Q Median 3Q
                                 Max
## -0.8118 -0.3572 -0.1021 0.2641 1.0142
##
## Coefficients:
##
            Estimate Std. Error t value Pr(>|t|)
## locationLV -3.40997 0.63792 -5.345 0.00175 **
## locationRA 0.36749 0.63792 0.576 0.58551
## locationRV 1.44473 0.63792 2.265 0.06413 .
## patient4 0.08573 0.55245 0.155 0.88177
## patient8 -0.31303 0.55245 -0.567 0.59152
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ''
##
## Residual standard error: 0.7813 on 6 degrees of freedom 12/43
```

```
library(multcomp)
L<-matrix(0,nrow=length(fit$coefficient),ncol=2)
rownames(L)<-names(fit$coefficient)
L[2,1]<-1
L[3:4,2]<-c(-1,1)
L</pre>
```

##		[,1]	[,2]
##	(Intercept)	0	0
##	locationLV	1	0
##	locationRA	0	-1
##	locationRV	0	1
##	patient4	0	0
##	patient8	0	0

```
fit %>% glht(linfct=t(L)) %>% summary
##
##
    Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = exprs ~ location + patient, data = data, x
##
## Linear Hypotheses:
        Estimate Std. Error t value Pr(>|t|)
##
## 2 == 0 1.0772 0.6379 1.689 0.25064
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ''
```

(Adjusted p values reported -- single-step method)

2. Robust regression

- No normality assumption needed
- Robust fit minimises the maximal bias of the estimators
- CI and statistical tests are based on asymptotic theory
- ullet If ϵ is normal, the M-estimators have a high efficiency!
- ordinary least squares (OLS): minimize loss function

$$\sum_{i=1}^{n} (y_i - \mathbf{x}_i^T \boldsymbol{\beta})^2$$

M-estimation: minimize loss function

$$\sum_{i=1}^{n} \rho \left(y_i - \mathbf{x}_i^T \boldsymbol{\beta} \right)$$

with

- ρ is symmetric, i.e. $\rho(z) = \rho(-z)$
- ρ has a minimum at $\rho(0) = 0$, is positive for all $z \neq 0$
- $\rho(z)$ increases as |z| increases

The estimator $\hat{\mu}$ is also the solution to the equation

$$\sum_{i=1}^n \Psi(y_i - \mathbf{x}_i \boldsymbol{\beta}) = 0,$$

where Ψ is the derivative of ρ . For $\hat{\beta}$ possessing the robustness property, Ψ should be bounded.

Example: least squares

$$ho(z)=z^2$$
, and thus $\Psi(z)=2z$ (unbounded!). $\hat{oldsymbol{eta}}$ is the solution of

$$\sum_{i=1}^{n} 2\mathbf{x}_{i}(y_{i} - \mathbf{x}_{i}^{T}\boldsymbol{\beta}) = 0 \text{ or } \hat{\boldsymbol{\beta}} = (\mathbf{X}^{T}\mathbf{X})^{-1}\mathbf{X}\mathbf{y}$$

with
$$\mathbf{X} = [\mathbf{x}_1 \dots \mathbf{x}_G]^T$$

When a location and a scale parameter, say σ , have to be estimated simultaneously, we write

$$(\hat{\beta}, \hat{\sigma}) = \operatorname{ArgMin}_{\beta, \sigma} \sum_{i=1}^{n} \rho \left(\frac{y_i - \mathbf{x}_i^T \beta}{\sigma} \right) \text{ and } \sum_{i=1}^{n} \Psi \left(\frac{y_i - \mathbf{x}_i^T \beta}{\sigma} \right) = 0.$$

Define $u_i = \frac{y_i - \mathbf{x}_i^T \boldsymbol{\beta}}{\sigma}$. The last estimation equation is equivalent to

$$\sum_{i=1}^n w(u_i)u_i=0,$$

with weight function $w(u) = \Psi(u)/u$. This is the typical form that appears when solving the *iteratively reweighted least squares problem*,

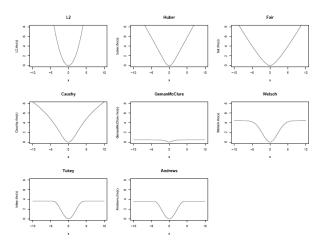
$$(\hat{\beta}, \hat{\sigma}) = \operatorname{ArgMin}_{\mu, \sigma} \sum_{i=1}^{n} w(u_i^{(k-1)}) \left(u_i^{(k)}\right)^2,$$

where k represents the iteration number.

Some Examples of Robust Functions

Name	$\rho(x)$	$\psi(x)$	w(x)
Huber $\begin{cases} \text{if } x \le k \\ \text{if } x > k \end{cases}$	$\begin{cases} x^2/2 \\ k(x -k/2) \end{cases}$	$\begin{cases} x \\ k \operatorname{sgn}(x) \end{cases}$	$\begin{cases} 1 \\ \frac{k}{ x } \end{cases}$
'Fair''	$c^{2}\left(\frac{ x }{c} - \log\left(1 + \frac{ x }{c}\right)\right)$ $\frac{c^{2}}{2}\log\left(1 + (x/c)^{2}\right)$	$\frac{x}{1+\frac{ x }{c}}$	$\frac{1}{1+\frac{ x }{c}}$
Cauchy		$\frac{x}{1+(x/c)^2}$	$\frac{1}{1+(x/c)^2}$
Geman-McClure	$\frac{x^2/2}{1+x^2}$	$\frac{x}{(1+x^2)^2}$	$\frac{1}{(1+x^2)^2}$
Welsch	$\frac{c^2}{2} \left(1 - \exp \left(- \left(\frac{x}{c} \right)^2 \right) \right)$	$x \exp\left(-(x/c)^2\right)$	$\exp\left(-(x/c)^2\right)$
Tukey $\begin{cases} \text{if } x \le c \\ \text{if } x > c \end{cases}$	$\frac{c^2}{2} \left(1 - \exp\left(-\left(\frac{x}{c}\right)^2\right) \right)$ $\left\{ \frac{c^2}{6} \left(1 - \left(1 - (x/c)^2\right)^3 \right)$ $\frac{c^2}{6}$	$\begin{cases} x \left(1 - (x/c)^2\right)^2 \\ 0 \end{cases}$	$\begin{cases} \left(1 - (x/c)^2\right)^2 \\ 0 \end{cases}$
Andrews $\begin{cases} \text{if } x \le k\pi \\ \text{if } x > k\pi \end{cases}$	$\begin{cases} k^2(1-\cos(x/k))\\ 2k^2 \end{cases}$	$\begin{cases} k\sin(x/k) \\ 0 \end{cases}$	$\begin{cases} \frac{\sin(x/k)}{x/k} \\ 0 \end{cases}$

The ρ functions



Common Ψ-Functions

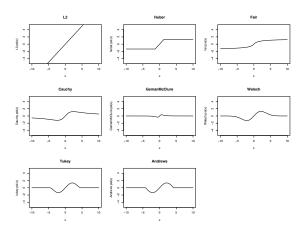


Figure 4.2: The ψ functions for some common M-estimators.

Corresponding Weight Functions

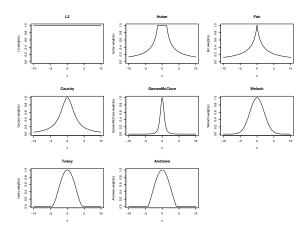
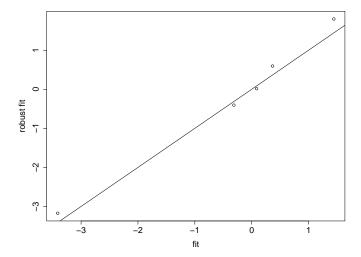


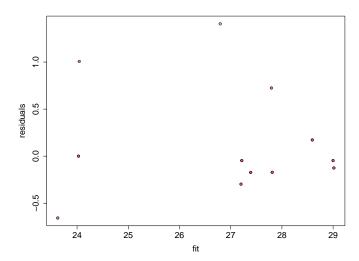
Figure 4.3: The weight functions for some common M-estimators.

```
library("MASS")
rfit <- rlm(exprs-location*patient,data,maxit=500)
plot(fit$coefficient[-1],rfit$coefficient[-1],xlab="fit",ylab="robust fit",cex.axis=1.5,cex.lab=1.5)
abline(0,1)</pre>
```



```
## [1] 1.0000000 1.0000000 0.2448895 1.0000000 0.3418904 0.5239307 0.4754051
```

plot(rfit\$fitted,rfit\$res,cex=rfit\$w,pch=19,col=2,cex.lab=1.5,cex.axis=1.5,ylab="residuals",xlab="fit")
points(rfit\$fitted,rfit\$res)



^{# [8] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000}

summary(fit)

Call:

##

```
## Residuals:
##
     Min 1Q Median 3Q
                                Max
## -0.8118 -0.3572 -0.1021 0.2641 1.0142
##
## Coefficients:
##
            Estimate Std. Error t value Pr(>|t|)
## locationLV -3.40997 0.63792 -5.345 0.00175 **
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## patient4 0.08573 0.55245 0.155 0.88177
## patient8 -0.31303 0.55245 -0.567 0.59152
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ''
##
## Residual standard error: 0.7813 on 6 degrees of freedom
```

lm(formula = exprs ~ location + patient, data = data, x = TRU

summary(rfit)

```
##
## Call: rlm(formula = exprs ~ location + patient, data = data,
## Residuals:
             10 Median
                                30
                                       Max
##
       Min
## -0.65730 -0.17198 -0.04697 0.31060 1.40606
##
## Coefficients:
##
             Value Std. Error t value
## (Intercept) 27.2010 0.4518 60.2081
## locationLV -3.1727 0.5217 -6.0817
## locationRA 0.5947 0.5217 1.1400
## locationRV 1.7986 0.5217 3.4478
## patient4 0.0150 0.4518 0.0333
## patient8 -0.4052 0.4518 -0.8970
##
## Residual standard error: 0.256 on 6 degrees of freedom
```

Illustration of implementation of robust regression: https://statomics.github.io/SGA2020/assets/rmarkdownExamples/robustRegression.html

3. Empirical Bayes/Moderated *t*-test.

A general class of moderated test statistics is given by

$$T_g^{mod} = rac{ar{Y}_{g1} - ar{Y}_{g2}}{c ilde{\mathcal{S}}_g},$$

where \tilde{S}_g is a moderated variance estimate. Simple approach: set $\tilde{S}_g = S_g + S_0/c$: simply add a small positive constant to the denominator of the t-statistic **empirical Bayes** theory provides formal framework for borrowing strength across genes, e.g. popular bioconductor package **limma**

$$\tilde{S}_{g} = \sqrt{\frac{d_{g}S_{g}^{2} + d_{0}S_{0}^{2}}{d_{g} + d_{0}}},$$

and the moderated t-statistic is t-distributed with d_0+d_g degrees of freedom. Note that the degrees of freedom increase by borrowing strength across genes.

Intermezzo: Bayesian Methods

- Frequentists consider data as random and population parameters as fixed but unknown
- In Bayesian viewpoint a person has prior beliefs about the population parameters and the uncertainty on this prior beliefs are represented by a probability distribution placed on this parameter. This distribution reflects the person's subjective prior opinion about plausible values of the parameter. And is referred to as the prior $g(\theta)$.
- Bayesian thinking will update the prior information on the population parameters by confronting the model to data (Y).
- By using Bayes Theorem this results in a posterior distribution on the model parameters.

$$g(\theta|\mathbf{Y}) = \frac{g(\theta)f(Y|\theta)}{\int g(\theta)f(Y|\theta)d\theta}$$
 (posterior = $\frac{\text{prior} \times \text{likelihood}}{\text{Marginal distribution}}$)

Limma approach

$$P\{\beta_{gk} \neq 0\} = p_k$$

Prior

$$\beta_{gk}|\sigma_g^2, \beta_{gk} \neq 0 \sim N(0, v_{0k}\sigma_g^2)$$

$$\frac{1}{\sigma_g^2}\sim s_0^2 rac{\chi_{d_0}^2}{d_0}$$

$$\hat{eta}_{gk}|eta_{gk},\sigma_g^2 \sim N(eta_{gk},v_{gk}\sigma_g^2)$$

Distributional assumptions

$$s_g^2 \sim \sigma_g^2 rac{\chi_{dg}^2}{d_g}$$

Limma approach

Under this assumption, it can be shown

• Posterior Mean for inverse of the variance parameter:

$$\mathsf{E}\left[\frac{1}{\sigma_g^2}|S_g^2\right] = \frac{d_0 + d_g}{d_0 s_0^2 + d_g s_g^2}$$

and
$$ilde{t}=rac{\hat{eta}_{gk}}{ ilde{oldsymbol{arsigma}_{g}}\sqrt{v_{gj}}}$$
 is

$$\tilde{t}|eta_{gk}=0\sim t_{d_0+d_g}$$

with
$$ilde{s}_g = \sqrt{rac{d_0 s_0^2 + d_g s_g^2}{d_0 + d_g}}$$

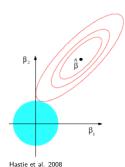
Empirical Bayes

- A fully Bayesian would define the prior distribution by carefully choosing the prior parameters
- In an empirical Bayesian approach one estimates the prior parameters based on the data
- In Limma moment estimators for s_0 and d_0 are derived.

4. Penalized regression: ridge

- Ridge penalty
- Parameter estimation of ridge regression
- Link between ridge regression and mixed models

4.1. Ridge Penalty

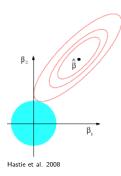


Add a ridge penalty

$$\hat{\boldsymbol{\beta}} = \operatorname{argmin}_{\boldsymbol{\beta}} \left\{ \| \mathbf{Y} - \mathbf{X} \boldsymbol{\beta} \|^2 + \lambda \| \boldsymbol{\beta} \|^2 \right\}$$

 λ: penalty parameter that controls the amount of penalisation

4.1. Ridge Penalty



Add a ridge penalty

$$\hat{\boldsymbol{\beta}} = \operatorname{argmin}_{\boldsymbol{\beta}} \left\{ \| \mathbf{Y} - \mathbf{X} \boldsymbol{\beta} \|^2 + \lambda \| \boldsymbol{\beta} \|^2 \right\}$$

- λ: penalty parameter that controls the amount of penalisation
- Equivalent to

$$\hat{\beta} = \operatorname{argmin}_{\beta} \|\mathbf{Y} - \mathbf{X}\boldsymbol{\beta}\|^2$$
 subject to $\|\boldsymbol{\beta}\|^2 \leq s$

 \bullet Note, that s has a one-to-one correspondence with λ

4.2. Closed form solution

$$\hat{\boldsymbol{\beta}}^{\mathsf{ridge}} = \mathsf{argmin}_{\boldsymbol{\beta}} \left\{ \|\mathbf{Y} - \mathbf{X}\boldsymbol{\beta}\|^2 + \lambda \|\boldsymbol{\beta}\|^2 \right\}$$

Matrix form

• Let $\mathbf{D} = \begin{bmatrix} \mathbf{0} & \mathbf{0}_{1 \times p} \\ \mathbf{0}_{p \times 1} & \mathbf{I}_{p \times p} \end{bmatrix}$, which allows the criterion to be written in matrix form and to leave the intercept β_0 unpenalized.

$$\hat{\boldsymbol{\beta}}^{\mathsf{ridge}} = \mathsf{argmin}_{\boldsymbol{\beta}} \left\{ \| \mathbf{Y} - \mathbf{X} \boldsymbol{\beta} \|^2 + \lambda \boldsymbol{\beta}^{\mathsf{T}} \mathbf{D} \boldsymbol{\beta} \right\}$$

Minimization:

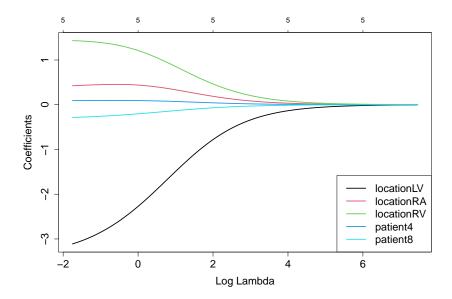
$$\frac{d\left\{\|\mathbf{Y} - \mathbf{X}\boldsymbol{\beta}\|^2 + \lambda\boldsymbol{\beta}^T\mathbf{D}\boldsymbol{\beta}\right\}}{d\boldsymbol{\beta}} = 0$$

$$\Leftrightarrow -\mathbf{X}^{\mathsf{T}}\mathbf{Y} + \mathbf{X}^{\mathsf{T}}\mathbf{X}\boldsymbol{\beta} + \lambda\mathbf{D}\boldsymbol{\beta} = 0$$

$$\Leftrightarrow (\mathbf{X}^T\mathbf{X} + \lambda \mathbf{D})\beta = \mathbf{X}^T\mathbf{Y}$$

$$\Leftrightarrow \hat{\boldsymbol{\beta}} = (\mathbf{X}^T \mathbf{X} + \lambda \mathbf{D})^{-1} \mathbf{X}^T \mathbf{Y}$$

```
library(glmnet)
ridgeFit<-glmnet(fit$x[,-1],data$exprs,family="gaussian", alpha=
plot(ridgeFit,xvar="lambda")
legend("bottomright",legend=colnames(fit$x)[-1],col=1:5,lty=1,cel=1:5]</pre>
```



4.3 Tune ridge penalties

Tune the ridge penalties by exploiting the link between ridge regression and Mixed Models:

$$y_i = \mathbf{X}_i^T \boldsymbol{\beta} + \epsilon_i$$

with

- ullet $eta_j \sim N\left(0, rac{\sigma^2}{\lambda}
 ight)$
- $\epsilon_i \sim N(0, \sigma^2)$
- ullet Variance components can be estimated using Ime4 mixed model software and the predictions of the random effects eta_j coincide with solution of ridge estimator.

Best linear unbiased predictor: BLUP

Optimize the joint log-likelihood $L(\mathbf{Y}, \beta)$ towards β

$$L(\mathbf{Y}, \boldsymbol{\beta}) = \prod_{i=1}^{n} f(y_i|\boldsymbol{\beta}) f(\boldsymbol{\beta})$$

Best linear unbiased predictor: BLUP

Optimize the joint log-likelihood $L(\mathbf{Y}, \beta)$ towards β

$$L(\mathbf{Y}, \boldsymbol{\beta}) = \prod_{i=1}^{n} f(y_i|\boldsymbol{\beta}) f(\boldsymbol{\beta})$$

$$-2I(\mathbf{Y}, \boldsymbol{\beta}) \propto n \log(\sigma^2) + \frac{(\mathbf{Y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{Y} - \mathbf{X}\boldsymbol{\beta})}{\sigma^2} + p \log \frac{\sigma^2}{\lambda} + \frac{\lambda}{\sigma^2} \boldsymbol{\beta}^T \boldsymbol{\beta}$$

$$\begin{split} \hat{\boldsymbol{\beta}} &= & \operatorname{argmin}_{\boldsymbol{\beta}} \left\{ I(\mathbf{Y}, \boldsymbol{\beta}) \right\} \\ &= & \operatorname{argmin}_{\boldsymbol{\beta}} \left\{ ||\mathbf{Y} - \boldsymbol{\beta}||_2^2 + \lambda \boldsymbol{\beta}^T \boldsymbol{\beta} \right\} \end{split}$$

```
library(lme4)
ridgeFit<-lmer(exprs~(1|location)+(1|patient),data)
## boundary (singular) fit: see ?isSingular
summary(ridgeFit)
## Linear mixed model fit by REML ['lmerMod']
## Formula: exprs ~ (1 | location) + (1 | patient)
##
     Data: data
##
## REML criterion at convergence: 35.9
##
## Scaled residuals:
##
       Min 1Q Median
                                  3Q
                                          Max
## -1.64229 -0.43326 -0.09407 0.42918 1.30037
##
## Random effects:
##
   Groups Name Variance Std.Dev.
   location (Intercept) 4.2367 2.0583
##
   patient (Intercept) 0.0000 0.0000
##
   Residual
                       0.5019 0.7084
##
```

ranef(ridgeFit)

```
## $location
      (Intercept)
##
## I.A 0.3842645
## LV -2.8961753
## RA 0.7377943
## RV 1.7741165
##
## $patient
##
     (Intercept)
## 3
## 4
## 8
##
## with conditional variances for "location" "patient"
```

```
LG<-matrix(0,nrow=length(fit$coefficient),ncol=4)
rownames(LG)<-names(fit$coefficient)</pre>
LG[1,1]<-1
LG[c(1,2),2]<-1
LG[c(1,3),3]<-1
LG[c(1,4),4]<-1
sd(unlist(fit$coef%*%LG))
## [1] 2.09857
sd(unlist(fixef(ridgeFit)+ranef(ridgeFit)$location))
## [1] 2.018854
```

plot(unlist(fit\$coef%*%LG),unlist(fixef(ridgeFit)+ranef(ridgeFit
abline(0,1)

