Week 2, Lecture 3 - Fitting & Regression Redux, Regularization

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Outline

- Administrative Issues
- ► Fitting Regularization
 - Lasso
 - Ridge regression
 - ► Elastic net
- ► Some Examples

Based on slides from Rob Tibshirani.

The Bias-Variance Tradeoff

The Bias-Variance Tradeoff

Estimating β

As usual, we assume the model:

$$y = f(\mathbf{z}) + \epsilon, \epsilon \sim \mathcal{N}(0, \sigma^2)$$

In regression analysis, our major goal is to come up with some good regression function

$$\hat{f}(\mathbf{z}) = \mathbf{z}^{\mathsf{T}} \hat{\beta}$$

- ▶ So far, we've been dealing with $\hat{\beta}^{ls}$, or the least squares solution:
 - $lackbox{}{\hat{eta}^{ls}}$ has well known properties (e.g., Gauss-Markov, ML)
- But can we do better?

Choosing a good regression function

Suppose we have an estimator

$$\hat{f}(\mathbf{z}) = \mathbf{z}^{\mathsf{T}} \hat{\beta}$$

- ► To see if this is a good candidate, we can ask ourselves two questions:
 - 1. Is $\hat{\beta}$ close to the true β ?
 - 2. Will $\hat{f}(\mathbf{z})$ fit future observations well?
- ▶ These might have very different outcomes!!

Is $\hat{\beta}$ close to the true β ?

- To answer this question, we might consider the **mean** squared error of our estimate $\hat{\beta}$:
 - i.e., consider squared distance of $\hat{\beta}$ to the true β :

$$MSE(\hat{\boldsymbol{\beta}}) = \mathbb{E}\left[\left\|\hat{\boldsymbol{\beta}} - \boldsymbol{\beta}\right\|^{2}\right] = \mathbb{E}[(\hat{\boldsymbol{\beta}} - \boldsymbol{\beta})^{\mathsf{T}}(\hat{\boldsymbol{\beta}} - \boldsymbol{\beta})]$$

Example: In least squares (LS), we now that:

$$\mathbb{E}[(\hat{\boldsymbol{\beta}}^{ls} - \boldsymbol{\beta})^{\mathsf{T}}(\hat{\boldsymbol{\beta}}^{ls} - \boldsymbol{\beta})] = \sigma^2 \mathrm{tr}[(\mathbf{Z}^T \mathbf{Z})^{-1}]$$

Will $\hat{f}(z)$ fit future observations well?

- ▶ Just because $\hat{f}(z)$ fits our data well, this doesn't mean that it will be a good fit to new data
- ▶ In fact, suppose that we take new measurements y_i' at the same \mathbf{z}_i 's:

$$(\mathbf{z}_1, \mathbf{y}_1'), (\mathbf{z}_2, \mathbf{y}_2'), ..., (\mathbf{z}_n, \mathbf{y}_n')$$

- ▶ So if $\hat{f}(\cdot)$ is a good model, then $\hat{f}(\mathbf{z}_i)$ should also be close to the new target y_i'
- ▶ This is the notion of **prediction error** (PE)

Prediction error and the bias-variance tradeoff

- So good estimators should, on average have, small prediction errors
- Let's consider the PE at a particular target point z_0 :
 - $PE(\mathbf{z}_0) = \sigma_{\epsilon}^2 + Bias^2(\hat{f}(\mathbf{z}_0)) + Var(\hat{f}(\mathbf{z}_0))$
 - Not going to derive, but comes directly from previous definitions
- Such a decomposition is known as the bias-variance tradeoff
 - As model becomes more complex (more terms included), local structure/curvature can be picked up
 - But coefficient estimates suffer from high variance as more terms are included in the model
- ightharpoonup So introducing a little bias in our estimate for eta might lead to a substantial decrease in variance, and hence to a substantial decrease in PE

Depicting the bias-variance tradeoff

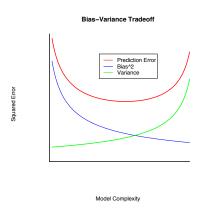


Figure: A graph depicting the bias-variance tradeoff.

Ridge Regression

Ridge Regression

Ridge regression as regularization

- ▶ If the β_i 's are unconstrained...
 - ► They can explode
 - And hence are susceptible to very high variance
- ► To control variance, we might **regularize** the coefficients
 - ▶ i.e., Might control how large the coefficients grow
- ▶ Might impose the ridge constraint (both equivalent):
 - ightharpoonup minimize $\sum_{i=1}^n (y_i \boldsymbol{\beta}^{\mathsf{T}} \mathbf{z}_i)^2$ s.t. $\sum_{i=1}^p \beta_i^2 \leq t$
 - ightharpoonup minimize $(y \mathbf{Z}\beta)^\intercal (y \mathbf{Z}\beta)$ s.t. $\sum_{j=1}^p \beta_j^2 \leq t$
- By convention (very important!):
 - **Z** is assumed to be standardized (mean 0, unit variance)
 - **y** is assumed to be centered

Ridge regression: l_2 -penalty

Can write the ridge constraint as the following **penalized** residual sum of squares (PRSS):

$$PRSS(\boldsymbol{\beta})_{\ell_2} = \sum_{i=1}^{n} (y_i - \mathbf{z}_i^{\top} \boldsymbol{\beta})^2 + \lambda \sum_{j=1}^{p} \beta_j^2$$
$$= (\mathbf{y} - \mathbf{Z}\boldsymbol{\beta})^{\top} (\mathbf{y} - \mathbf{Z}\boldsymbol{\beta}) + \lambda ||\boldsymbol{\beta}||_2^2$$

- lacksquare Its solution may have smaller average PE than $\hat{oldsymbol{eta}}^{ls}$
- ▶ $PRSS(\beta)_{l_2}$ is convex, and hence has a unique solution
- ► Taking derivatives, we obtain:

$$\frac{\delta PRSS(\beta)_{l_2}}{\delta \beta} = -2\mathbf{Z}^T(y - \mathbf{Z}\beta) + 2\lambda\beta$$

The ridge solutions

▶ The solution to $PRSS(\hat{\beta})_{l2}$ is now seen to be:

$$\hat{\beta}_{\lambda}^{ridge} = (\mathbf{Z}^{\intercal}\mathbf{Z} + \lambda\mathbf{I}_p)^{-1}\mathbf{Z}^{\intercal}\mathbf{y}$$

- Remember that Z is standardized
- y is centered
- Solution is indexed by the tuning parameter λ (more on this later)
- Inclusion of λ makes problem non-singular even if $\mathbf{Z}^{\mathsf{T}}\mathbf{Z}$ is not invertible
 - ► This was the original motivation for ridge regression (Hoerl and Kennard, 1970)

Tuning parameter λ

- lacktriangle Notice that the solution is indexed by the parameter λ
 - \triangleright So for each λ , we have a solution
 - Hence, the λ 's trace out a path of solutions (see next page)
- $\triangleright \lambda$ is the shrinkage parameter
 - \triangleright λ controls the size of the coefficients
 - \triangleright λ controls amount of **regularization**
 - lacktriangle As λ decreases, we obtain the least squares solutions
 - \blacktriangleright As λ increases, we have $\hat{\beta}_{\lambda=0}^{ridge}=0$ (intercept-only model)

Ridge coefficient paths

▶ The λ 's trace out a set of ridge solutions, as illustrated below

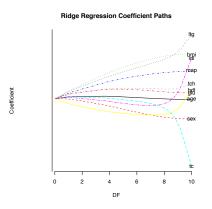


Figure: Ridge coefficient path for the diabetes data set found in the lars library in R.

Choosing λ

- Need disciplined way of selecting \(\lambda \)
- ▶ That is, we need to "tune" the value of λ
- In their original paper, Hoerl and Kennard introduced ridge traces:
 - lacksquare Plot the components of $\hat{eta}_{\lambda}^{ridge}$ against λ
 - Choose λ for which the coefficients are not rapidly changing and have "sensible" signs
 - No objective basis; heavily criticized by many
- Standard practice now is to use cross-validation (next lecture!)

Orthonormal **Z** in ridge regression

- ▶ If **Z** is orthonormal, then $\mathbf{Z}^T\mathbf{Z} = \mathbf{I}_p$, then a couple of closed form properties exist
- $lackbox{ Let } \hat{eta}^{ls}$ denote the LS solution for our orthonormal ${f Z};$ then

$$\hat{\boldsymbol{\beta}}_{\lambda}^{ridge} = \frac{1}{1+\lambda} \hat{\boldsymbol{\beta}}^{ls}$$

The optimal choice of λ minimizing the expected prediction error is:

$$\lambda^* = \frac{p\sigma^2}{\sum_{j=1} p\beta_j^2},$$

where $\boldsymbol{\beta} = (\beta_1, \beta_2, \dots, \beta_p)$ is the true coefficient vector

Smoother matrices and effective degrees of freedom

▶ A **smoother matrix S** is a linear operator satisfying:

$$\hat{\mathbf{y}} = \mathbf{S}\mathbf{y}$$

- ► Smoothers put the "hats" on y
- ▶ So the fits are a linear combination of the y_i 's, i = 1, ..., n
- **Example:** In ordinary least squares, recall the hat matrix

$$\mathbf{H} = \mathbf{Z}(\mathbf{Z}^T \mathbf{Z})^{-1} \mathbf{Z}^T$$

- For rank(\mathbf{Z}) = p, we know that tr(\mathbf{Z}) = p, which is how many degrees of freedom are used in the model
- By analogy, define the effective degrees of freedom (or effective number of parameters) for a smoother to be:

$$df(\mathbf{S}) = tr(\mathbf{S})$$

Degrees of freedom for ridge regression

In ridge regression, the fits are given by:

$$\hat{\mathbf{y}} = \mathbf{Z}(\mathbf{Z}^{\mathsf{T}}\mathbf{Z} + \lambda \mathbf{I}_p)^{-1}\mathbf{Z}^T\mathbf{y}$$

▶ So the smoother or "hat" matrix in ridge takes the form:

$$\mathbf{S}_{\lambda} = \mathbf{Z}(\mathbf{Z}^{\mathsf{T}}\mathbf{Z} + \lambda \mathbf{I}_{p})^{-1}\mathbf{Z}^{T}$$

➤ So the effective degrees of freedom in ridge regression are given by:

$$df(\lambda) = tr(S_{\lambda}) = tr[\mathbf{Z}(\mathbf{Z}^{\mathsf{T}}\mathbf{Z} + \lambda \mathbf{I}_{p})^{-1}\mathbf{Z}^{T}] = \sum_{j=1}^{p} \frac{d_{j}^{2}}{d_{j}^{2} + \lambda}$$

- Note that $df(\lambda)$ is monotone decreasing in λ
- ▶ Question: What happens when $\lambda = 0$?

How do we choose λ ?

- lacktriangle We need a disciplined way of choosing λ
- lackbox Obviously want to choose λ that minimizes the mean squared error
- Issue is part of the bigger problem of model selection

K-Fold Cross-Validation

- \blacktriangleright A common method to determine λ is K-fold cross-validation.
- We will discuss this next lecture.

Plot of CV errors and standard error bands

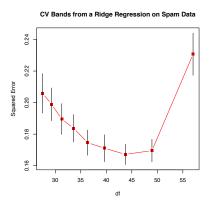


Figure: Cross validation errors from a ridge regression example on spam data.

The LASSO

The LASSO

The LASSO: l_1 penalty

- ► Tibshirani (*J of the Royal Stat Soc* 1996) introduced the LASSO: least absolute shrinkage and selection operator
- ▶ LASSO coefficients are the solutions to the l_1 optimization problem:

minimize
$$(\mathbf{y} - \mathbf{Z}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{Z}\boldsymbol{\beta})$$
 s.t. $\sum_{j=1}^p \|\beta_j\| \le t$

► This is equivalent to loss function:

$$PRSS(\boldsymbol{\beta})_{l_1} = \sum_{i=1}^{n} (y_i - \mathbf{z}_i^T \boldsymbol{\beta})^2 + \lambda \sum_{j=1}^{p} \|\beta_j\|$$
$$= (\mathbf{y} - \mathbf{Z}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{Z}\boldsymbol{\beta}) + \lambda \|\boldsymbol{\beta}\|_1$$

λ (or t) as a tuning parameter

- Again, we have a tuning parameter λ that controls the amount of regularization
- One-to-one correspondence with the threshhold t:
 - recall the constraint:

$$\sum_{j=1}^{p} = \|\beta_j\| \le t$$

- ▶ Hence, have a "path" of solutions indexed by t
- If $t_0 = \sum_{j=1}^p \left\| \hat{\beta}_j^{ls} \right\|$ (equivalently, $\lambda = 0$), we obtain no shrinkage (and hence obtain the LS solutions as our solution)
- lackbox Often, the path of solutions is indexed by a fraction of shrinkage factor of t_0

Sparsity and exact zeros

- ▶ Often, we believe that many of the β_j 's should be 0
- Hence, we seek a set of sparse solutions
- ▶ Large enough λ (or small enough t) will set some coefficients exactly equal to 0!
 - So the LASSO will perform model selection for us!

Computing the LASSO solution

- Unlike ridge regression, $\hat{eta}_{\lambda}^{lasso}$ has no closed form λ
- Original implementation involves quadratic programming techniques from convex optimization
- But Efron et al. (Annals of Statistics 2004) proposed LARS (least angle regression), which computes the LASSO path efficiently
 - ▶ Interesting modification called is called forward stagewise
 - In many cases it is the same as the LASSO solution
 - ► Forward stagewise is easy to implement: http://www-stat.stanford.edu/~hastie/TALKS/nips2005.pdf

Forward stagewise algorithm

- ► As usual, assume **Z** is standardized and **y** is centered
- ▶ Choose a small ϵ . The forward-stagewise algorithm then proceeds as follows:
 - 1. Start with initial residual $\mathbf{r} = \mathbf{y}$, and $\beta_1 = \beta_2 = \ldots = \beta_p = 0$
 - 2. Find the predictor $\mathbf{Z}_j (j=1,\ldots,p)$ most correlated with \mathbf{r}
 - 3. Update $\beta_j = \beta_j + \delta_j$, where $\delta_j = \epsilon \cdot \operatorname{sign}\langle \mathbf{r}, \mathbf{Z}_j \rangle = \epsilon \cdot \operatorname{sign}(\mathbf{Z}_j^T \mathbf{r})$
 - 4. Set $\mathbf{r} = \mathbf{r} \delta_j \mathbf{Z}_j$
 - 5. Repeat from step 2 many times

The LASSO, LARS, and Forward Stagewise paths

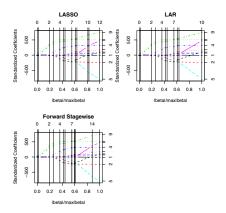


Figure: Comparison of the LASSO, LARS, and Forward Stagewise coefficient paths for the diabetes data set.

Comparing LS, Ridge, and the LASSO

- ightharpoonup Even though $\mathbf{Z}^T\mathbf{Z}$ may not be of full rank, both ridge regression and the LASSO admit solutions
- We have a problem when $p\gg n$ (more predictor variables than observations)
 - ▶ But both ridge regression and the LASSO have solutions
 - Regularization tends to reduce prediction error

More comments on variable selection

- Now suppose $p \gg n$
- Of course, we would like a parsimonious model (Occam's Razor)
- Ridge regression produces coefficient values for each of the p-variables
- ▶ But because of its l_1 penalty, the LASSO will set many of the variables exactly equal to 0!
 - ► That is, the LASSO produces sparse solutions
- So LASSO takes care of model selection for us
 - And we can even see when variables jump into the model by looking at the LASSO path

Variants

- ➤ Zou and Hastie (2005) propose the **elastic net**, which is a convex combination of ridge and the LASSO
 - Paper asserts that the elastic net can improve error over LASSO
 - ► Still produces sparse solutions

High-dimensional data and underdetermined systems

- ▶ In many modern data analysis problems, we have $p \gg n$ ▶ These comprise "high-dimensional" problems
- ▶ When fitting the model $y = \mathbf{z}^{\mathsf{T}}\beta$, we can have many solutions ▶ i.e., our system is *underdetermined*
- Reasonable to suppose that most of the coefficients are exactly equal to 0

S-sparsity and Oracles

- lacktriangle Suppose that only S elements of eta are non-zero
 - Candès and Tao call this S-sparsity
- Now suppose we had an "Oracle" that told us which components of the $\beta = (\beta_1, \beta_2, \dots, \beta_p)$ are truly non-zero
- Let β^* be the least squares estimate of this "ideal" estimator:
 - ▶ So β^* is 0 in every component that β is 0
 - \blacktriangleright The non-zero elements of β^* are computed by regressing ${\bf y}$ on only the S important covariates

The Danzig Selector

lacktriangle Candès and Tao developed the Dantzig selector $\hat{eta}^{Dantzig}$:

$$\min \|\beta\|_{l_1} \text{ s.t. } \|\mathbf{Z}_j^\mathsf{T} \mathbf{r}\|_{l_\infty} \le (1 + t^{-1}) \sqrt{2 \log p} \cdot \sigma$$

- ightharpoonup Here, ${f r}$ is the residual vector and t>0 is a scalar
- They showed that with high probability,

$$\left\|\hat{\beta}^{Dantzig} - \beta\right\|^2 = O(\log p) \,\mathbb{E}(\|\beta^* - \beta\|^2)$$

lackbox So the Dantzig selector does comparably well as someone who was told which S variables to regress on

LETTER

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The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity

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The systematic translation of cancer genomic data into knowledge of tumour biology and therapeutic possibilities remains challenging. Such efforts should be greatly aided by robust preclinical model systems that reflect the genomic diversity of human cancers and for which detailed genetic and pharmacological annotation is available. Here we describe the Cancer Cell Line Encyclopedia (CCLE): a compilation of gene expression, chromosomal copy number and massively parallel sequencing data from 947 human cancer cell lines. When coupled with pharmacological profiles for 24 anticancer drugs across 479 of the cell lines, this collection allowed identification of genetic, lineage, and gene-expression-based predictors of drug sensitivity. In addition to known predictors, we found that plasma cell lineage correlated with sensitivity to IGF1 receptor inhibitors; AHR expression was associated with MEK inhibitor efficacy in NRAS-mutant lines; and SLFN11 expression predicted sensitivity to topoisomerase inhibitors. Together, our results indicate that large, annotated cell-line collections may help to enable preclinical stratification schemata for anticancer agents. The generation of genetic predictions of drug response in the preclinical setting and their incorporation into cancer clinical trial design could speed the emergence of 'personalized' therapeutic regimens2.

Human cancer cell lines represent a mainstay of tumour biology and drug discovery through facile experimental manipulation, global and

known cancer genes were assessed by mass spectrometric genotyping.³ (Supplementary Fig. 1) DNA copy number (Supplementary Fig. 1) DNA copy number was measured using high-density single nucleotide polymorphism arrays (Affymetrix SNP 6.0. Supplementary Methods). Finally, messenger RNA expression levels were obtained for each of the lines using Affymetrix U133 plus 20 arrays. These data were also used to confirm cell line identities (Supplementary Methods and Supplementary Figs 2-4).

We next measured the genomic similarities by lineage between CCLE lines and primary tumours from Tumorscape14, expO. MILE and COSMIC data sets (Fig. 1b-d and Supplementary Methods). For most lineages, a strong positive correlation was observed in both chromosomal copy number and gene expression patterns (median correlation coefficients of 0.77, range = 0.52-0.94, $P < 10^{-15}$, for copy number, and 0.60, range = 0.29-0.77, P < 10⁻¹⁵, for expression, respectively; Fig. 1b. c and Supplementary Tables 3 and 4), as has been described previously3-5,15. A positive correlation was also observed for point mutation frequencies (median correlation coefficient = 0.71, range = -0.06-0.97, P < 10⁻² for all but 3 lineages; Supplementary Fig. 5), even when TP53 was removed from the data set (median correlation coefficient = 0.64, range = -0.31-0.97, $P < 10^{-2}$ for all but 3 lineages; Fig. 1d and Supplementary Table 5). Thus, with relatively few exceptions (Supplementary Information), the CCLE may provide representative genetic proxies for primary tumours in many cancer types.

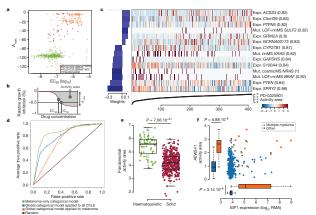


Figure 2.] Predictive modelling of pharmacological sensitivity using CCLE genomic data. An Drug repense for presidential (green) and BVMT20 (orange)rupic) represented by the high-concentration effect level $\{d_{m,k}\}$ and matsitional concentration (EC, g for a signoidal fit to the response curve (b). c. Blatic net regression modelling of genomic features that predict sensitivity to PD-03590. The bottom curve indicates drug reponse, measured as the area over the dose-response curve (activity area), for each cell in. The certal heart map shows the CCLE features in the model (continuous z-acce for expression and contynumber, dark red for discrete mutation calls). Secondary of the contraction of the contract

4. Specificity and sensitivity (receive operating characteristic curves) of cross-valudated categorists models predicting the response to a MRK inhibitor, PD-0325901 (activity area). Mean true positive rate and standard deviation (n = 3) are shown when models are bull using all lines (global categorical model, in blue and orange), or within only melanoma lines (green), e. Activity area values for pandohonate between cell lines derived from harmatopoteic (n = 61) and sold tumour (n = 387). The middle bar, mediane hos, inter-quartile range; but needed to 1875 the inter-quartile range. G. Distribution of activity area values for ANIVS41 relative to IGT mRAN expression. Orange does, multiple are values for ANIVS41 relative to IGT mRAN expression distributions relative to each cell line type (line, mediane, box, inter-quartile range), with have acteming to 1.5 % the inter-quartile range), with have acteming to 1.5 % the inter-quartile range), with have acteming to 1.5 % the inter-quartile range).

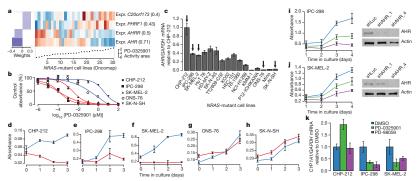


Figure 3. | AHR expression may denote a tumour dependency targeted by MEK inhibitors in NRAS-mutant cell lines. a, Predictive features for PD-0325901 sensitivity (using the 'varying baseline' activity area) in validated NRAS-mutant cell lines. b, Growth inhibition curves for NRAS-mutant cell lines expressing high (red) or low (blue) levels of AHR mRNA in the presence of the MEK inhibitor PD-0325901. c, Relative AHR mRNA expression across a panel of NRAS-mutant cell lines (arrows indicate cell lines where AHR dependency was analysed). d-b, Proliferation of NRAS-mutant cell lines displaying high (d-f) and low (g, b) AHR mRNA expression, after introduction of shRNAs against.

AHR (red lines) or luciferase (blue lines), i, Left; proliferation of IPC-298 cells (high AHR) after introduction of additional shRNAs against AHR (shAHR_1) and shAHR_4; green and purple lines, respectively) or luciferase (control shLuc; blue line). Right: corresponding immunololot analysis of AHR protein by Equivalent studies as in 1 using SK-MEL-2 cells (high AHR). Is, Endogenous CYPIAI mRNA expression in the neuroblastoma line CHP-212 or the melanoma lines IPC-298 and SK-MEL-2 after exposure to vehicle (blue) or MEK inhibitors (PD-0325901, green or PD-98059, purple). Error bars indicate standard deviation between replicates, with n = 12 (b), n = 3 (d, n = 6 (d+N)).

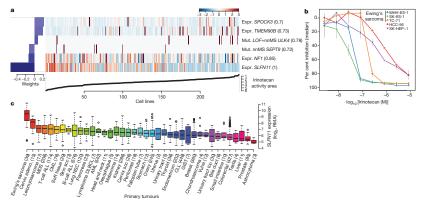


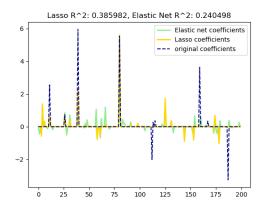
Figure 4 | Predicting sensitivity to topoisomerase I inhibitors. a, Elastic net regression analysis of genomic correlates of irinotecan sensitivity is shown for 250 cell lines b, Dose-response curves for three Ewing's sarcoma cell lines (MSS-ES-1, SK-ES-1 and TC-71) and two control cell lines with low SLFN11 expression (HCC-56 and SK-HEP-1). Grev vertical bars. standard deviation of

the mean growth inhibition (n=2), c_sIENI1 expression across 4,103 primary tumours. Box-and-whisker plots show the distribution of mRNA expression for each subtype, ordered by the median SLENI1 expression level (line), the interquartile range (box) and up to $1.5\times$ the inter-quartile range (bars). Sample numbers (n) are indicated in parentheses.

```
import numpy as np, matplotlib.pyplot as plt
from sklearn.metrics import r2_score
from sklearn.linear_model import Lasso, ElasticNet
# Generate some sparse data to play with
n_samples, n_features = 50, 200
X = np.random.randn(n_samples, n_features)
coef = 3 * np.random.randn(n_features)
inds = np.arange(n_features)
np.random.shuffle(inds)
coef[inds[10:]] = 0 # sparsify coef
y = np.dot(X, coef)
# add noise
y += 0.01 * np.random.normal(size=n_samples)
# Split data in train set and test set
n samples = X.shape[0]
X train, y train = X[:n \text{ samples } // 2], y[:n samples // 2]
X test, y test = X[n \text{ samples } // 2:], y[n \text{ samples } // 2:]
```

```
#...
# Split data in train set and test set
n samples = X.shape[0]
X_{\text{train}}, y_{\text{train}} = X[:n_{\text{samples}} // 2], y[:n_{\text{samples}} // 2]
X_{\text{test}}, y_{\text{test}} = X[n_{\text{samples}} // 2:], y[n_{\text{samples}} // 2:]
# Lasso
alpha = 0.1
lasso = Lasso(alpha=alpha)
y_pred_lasso = lasso.fit(X_train, y_train).predict(X_test)
r2_score_lasso = r2_score(y_test, y_pred_lasso)
# ElasticNet
enet = ElasticNet(alpha=alpha, 11 ratio=0.7)
y pred enet = enet.fit(X train, y train).predict(X test)
r2 score enet = r2 score(y test, y pred enet)
#...
```

```
#...
# ElasticNet
enet = ElasticNet(alpha=alpha, l1_ratio=0.7)
y_pred_enet = enet.fit(X_train, y_train).predict(X_test)
r2_score_enet = r2_score(y_test, y_pred_enet)
plt.plot(enet.coef_, color='lightgreen', linewidth=2,
         label='Elastic net coefficients')
plt.plot(lasso.coef_, color='gold', linewidth=2,
         label='Lasso coefficients')
plt.plot(coef, '--', color='navy', label='original coefficients'
plt.legend(loc='best')
plt.title("Lasso R^2: %f, Elastic Net R^2: %f"
          % (r2 score lasso, r2 score enet))
plt.show()
```



Further Reading

- Computer Age Statistical Inference, Chapter 16
- sklearn: Generalized Linear Models
- ► Candès E. and Tao T. The Dantzig selector: statistical estimation when p is much larger than n.