STK-IN4300
Statistical Learning Methods in Data Science

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Outline of the lecture

- Regularization and Sparsity
  - Boosting and regularization path
  - The "bet on sparsity" principle
- High-Dimensional Problems: $p \gg N$
  - When p is much larger than N
  - Feature Assessment and Multiple Testing Problem
  - The False Discovery Rate
- Stability Selection
  - Selection probability
  - Stability path
  - Choice of regularization

Regularization and Sparsity: ensemble learning

With **ensemble learning** we denote methods which:

- apply base learners to the data;
- combine the results of these learner.

Examples:

- bagging;
- random forests;
- boosting,
  - in boosting the approach is sequential.

Regularization and Sparsity: boosting and regularization path

Consider the following algorithm,

Algorithm 16.1 *Forward Stagewise Linear Regression.*

1. Initialize $\check{\alpha}_k = 0,\ k = 1, \ldots, K$. Set $\varepsilon > 0$ to some small constant, and M large.
2. For $m = 1$ to M:
   (a) $(\beta^*, k^*) = \arg\min_{\beta,k} \sum_{i=1}^{N} \left(y_i - \sum_{l=1}^{K} \check{\alpha}_l T_l(x_i) - \beta T_k(x_i) \right)^2$.
   (b) $\check{\alpha}_{k^*} \leftarrow \check{\alpha}_{k^*} + \varepsilon \cdot \text{sign}(\beta^*)$.
3. Output $f_M(x) = \sum_{k=1}^{K} \check{\alpha}_k T_k(x)$.

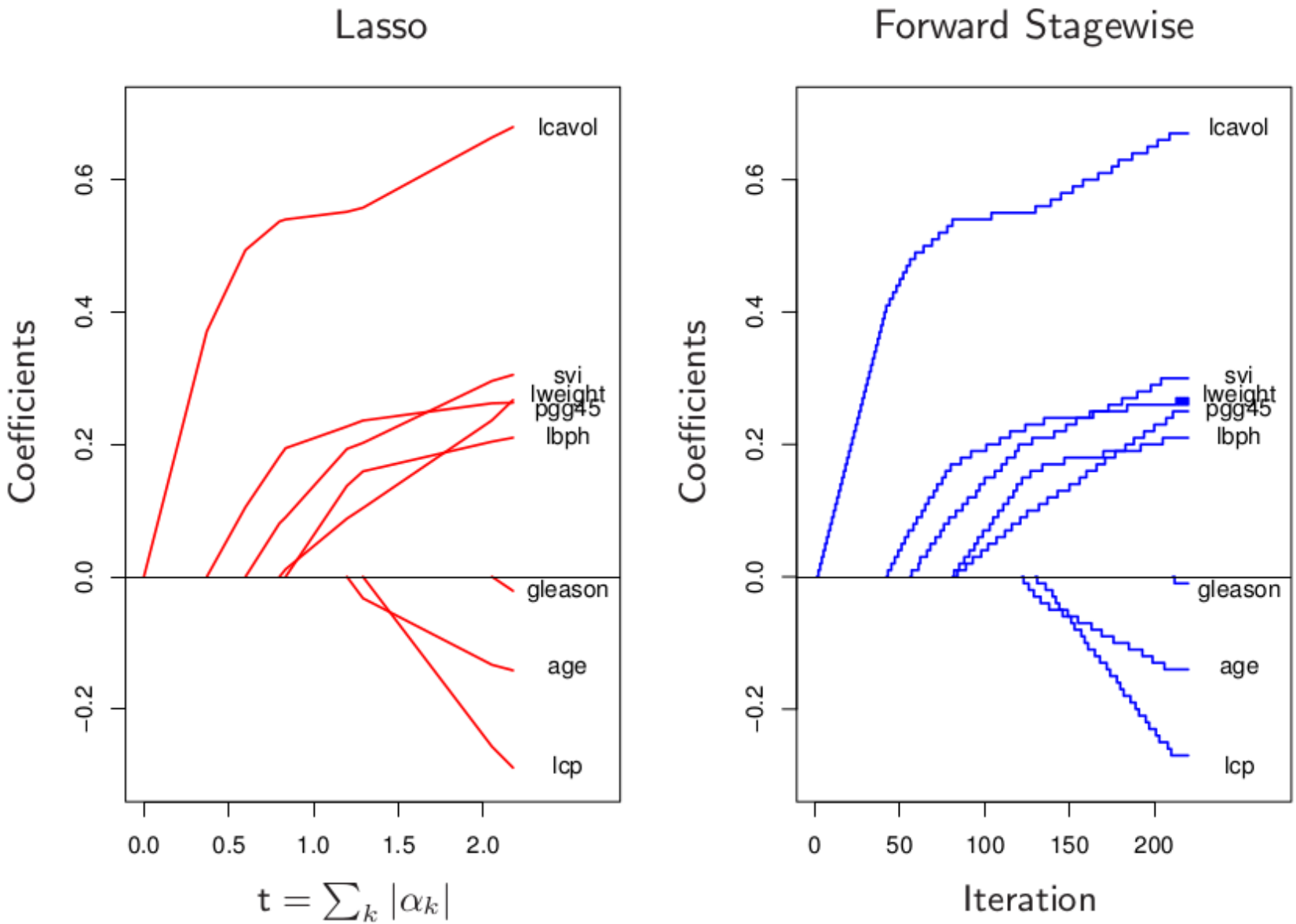
(note its similarities with the boosting algorithm)

Ensemble Learning: boosting and regularization path

In comparison with lasso:

- initialization ($\breve{\alpha}_k = 0, k = 1, \ldots, K$) $\longleftrightarrow$ $\lambda = \infty$;
- for small values of M:
  - some $\breve{\alpha}_k$ are not updated $\longleftrightarrow$ coefficients "forced" to be 0;
  - $\breve{\alpha}_k^{[0]} \leqslant \breve{\alpha}_k^{[M]} \leqslant \breve{\alpha}_k^{[\infty]}$ $\longleftrightarrow$ shrinkage;
  - M inversely related to λ;
- for M large enough ($M = \infty$ in boosting) and $K < N$, $\breve{\alpha}_k^{[M]} = \hat{\alpha}_{LS}$ $\longleftrightarrow$ $\lambda = 0$

Regularization and Sparsity: boosting and regularization path



Regularization and Sparsity: boosting and regularization path

If

- all the basis learners T_K are mutually uncorrelated,

then

- for $\varepsilon \to 0$ and $M \to \infty$, such that $\varepsilon M \to t$,

Algorithm 16.1 gives the lasso solutions with $t = \sum_k |\alpha_k|$.

In general component-wise boosting and lasso do not provide the same solution:

- in practice, often similar in terms of prediction;
- for ε (ν) $\to 0$ boosting (and forward stagewise in general) tends to the path of the least angle regression algorithm;
- lasso can also be seen as a special case of least angle.

Regularization and Sparsity: boosting and regularization path

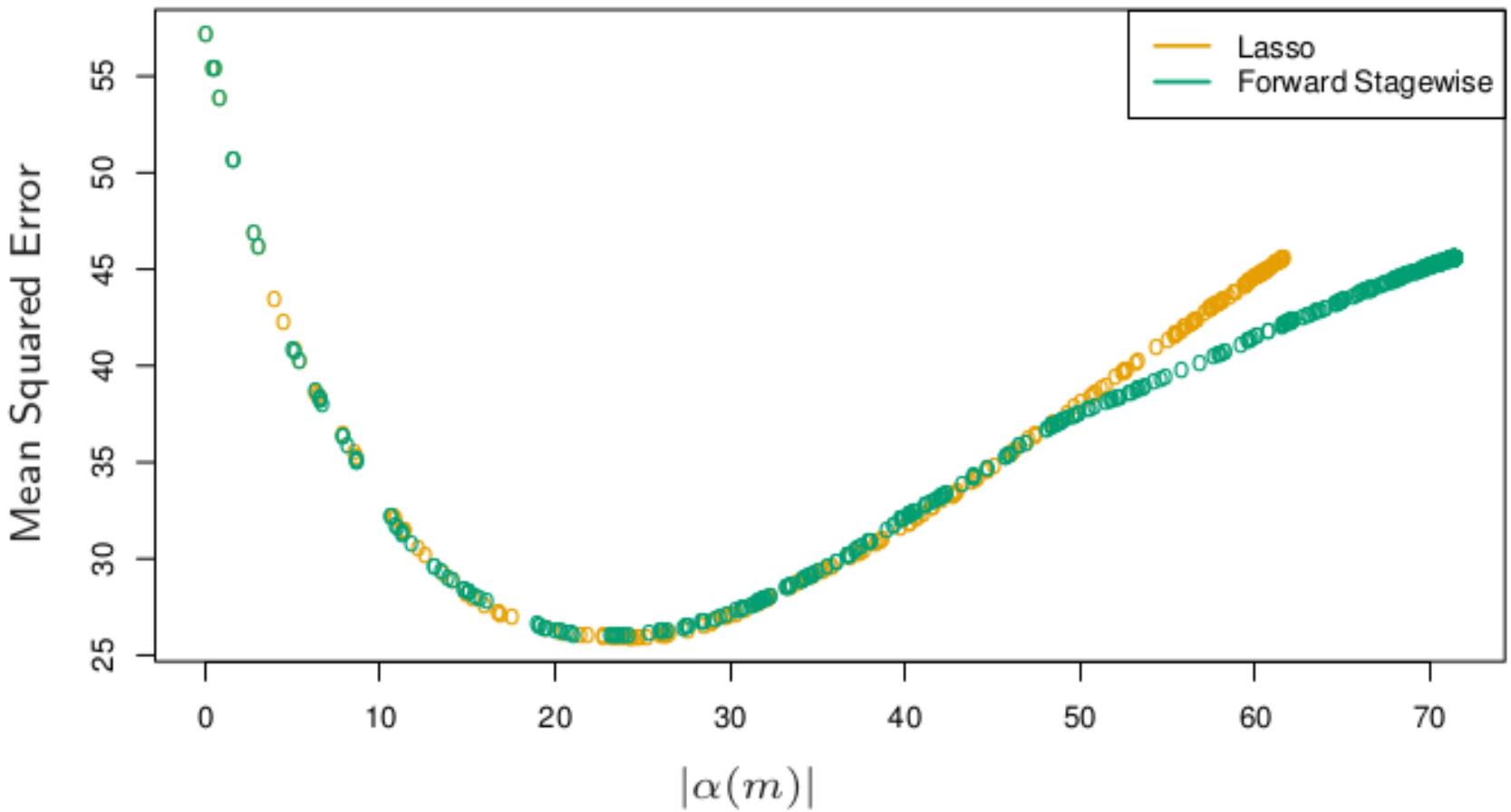
Consider 1000 Gaussian distributed variables:

- strongly correlated ($\rho = 0.95$) in blocks of 20;
- uncorrelated blocks;
- one variable with effect on the outcome for each block;
- effects generated from a standard Gaussian.

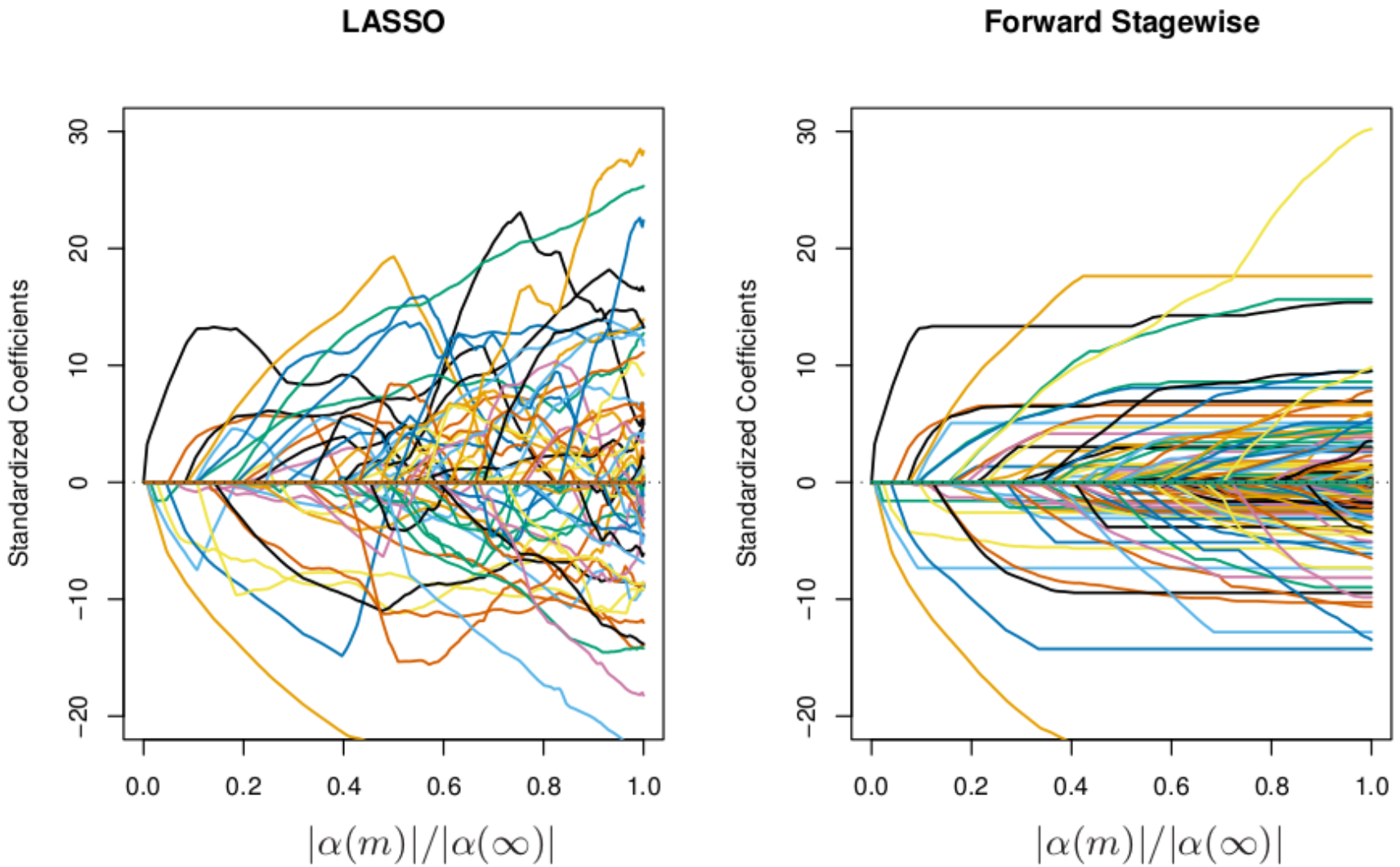
Moreover:

- added Gaussian noise;
- noise-to-signal ratio $= 0.72$.

Regularization and Sparsity: boosting and regularization path



Regularization and Sparsity: boosting and regularization path



Regularization and Sparsity: the "bet on sparsity" principle

We consider:

- L_1-type of penalty (shrinkage, variable selection);
- L_2-type of penalty (shrinkage, computationally easy);
- boosting's stagewise forward strategy minimizes something close to a L_1 penalized loss function;
- step-by-step minimization.

Can we characterize situations where one is preferable to the other?

Regularization and Sparsity: the "bet on sparsity" principle

Consider the following framework:

- 50 observations;
- 300 independent Gaussian variables.

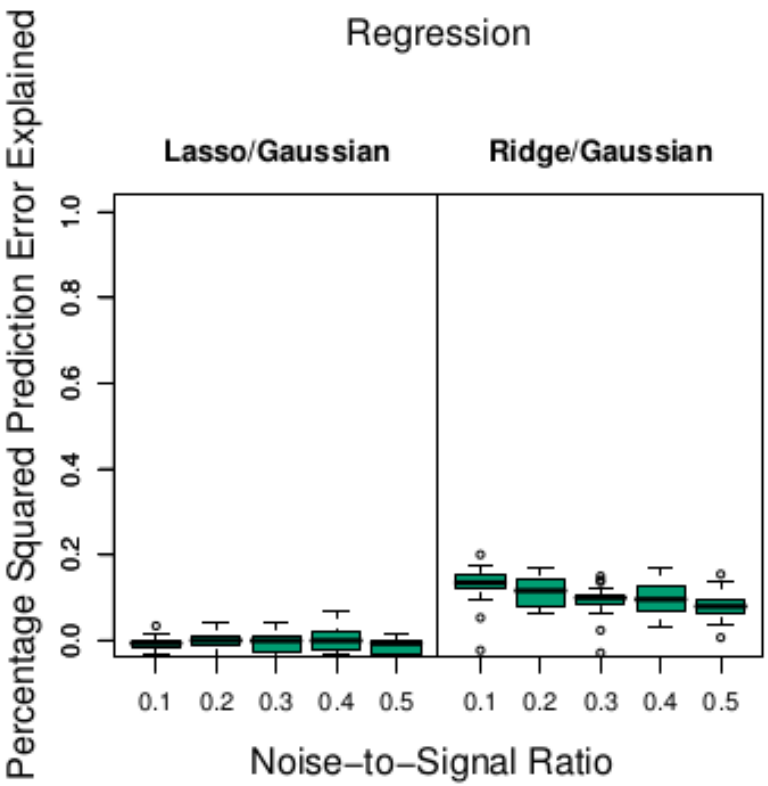
Three scenarios:

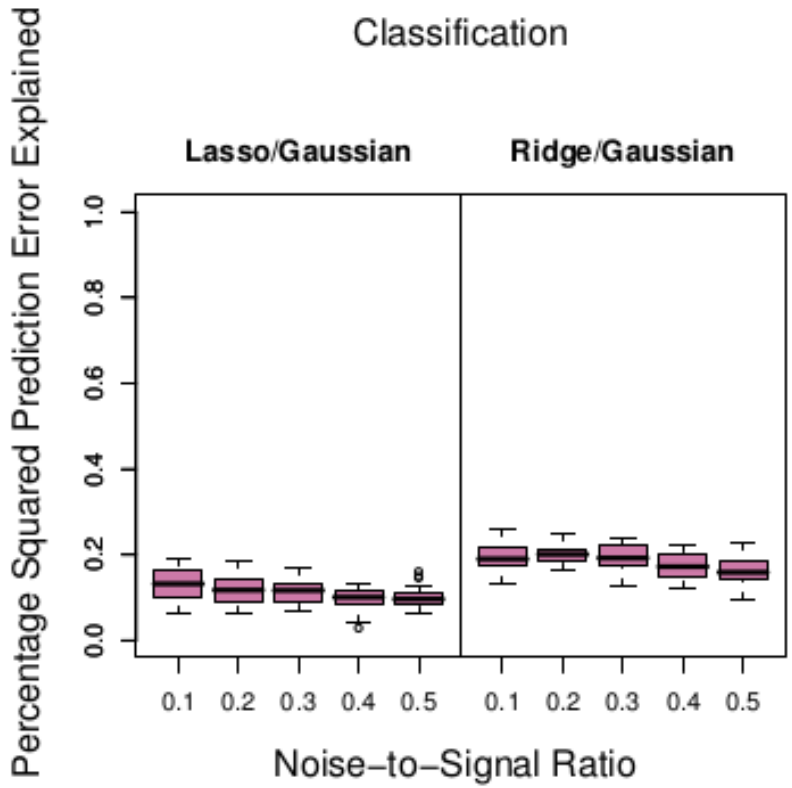
- all 300 variables are relevant;
- only 10 out of 300 variables are relevant;
- 30 out of 300 variables are relevant.

Outcome:

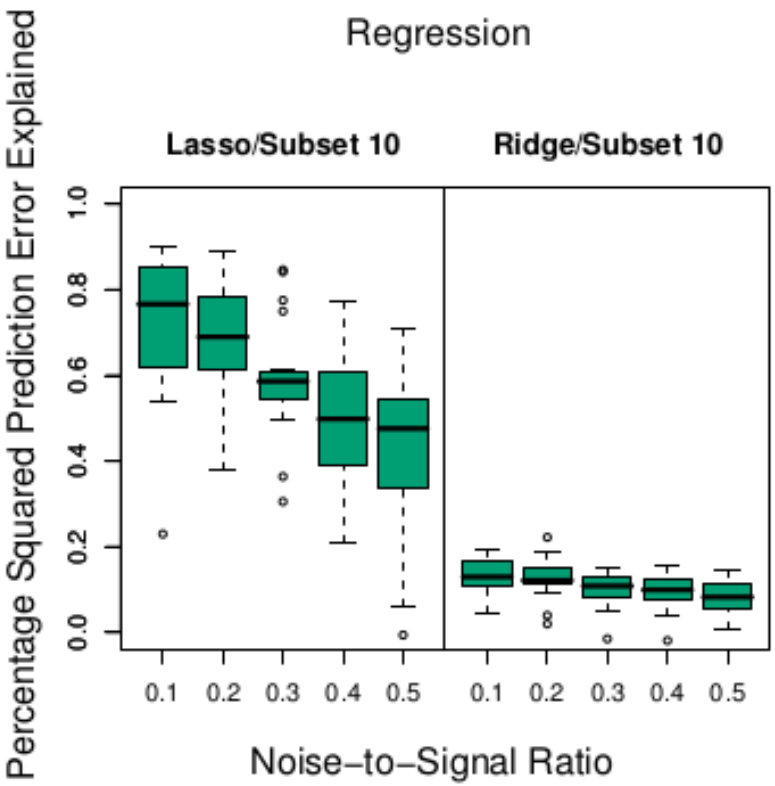
- regression (added standard Gaussian noise);
- classification (from an inverse-logit transformation of the linear predictor)

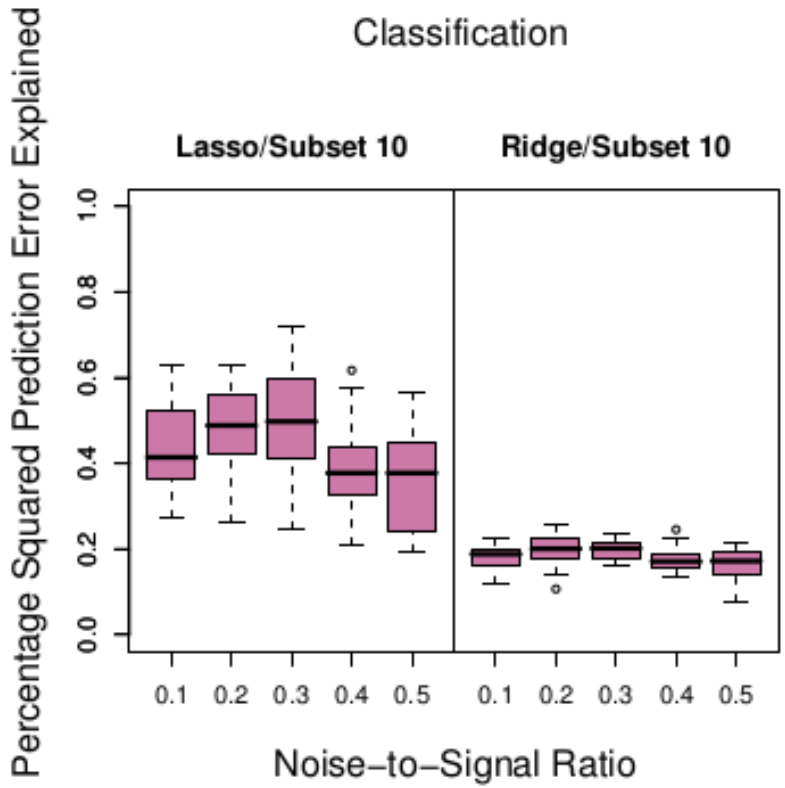
Regularization and Sparsity: the "bet on sparsity" principle



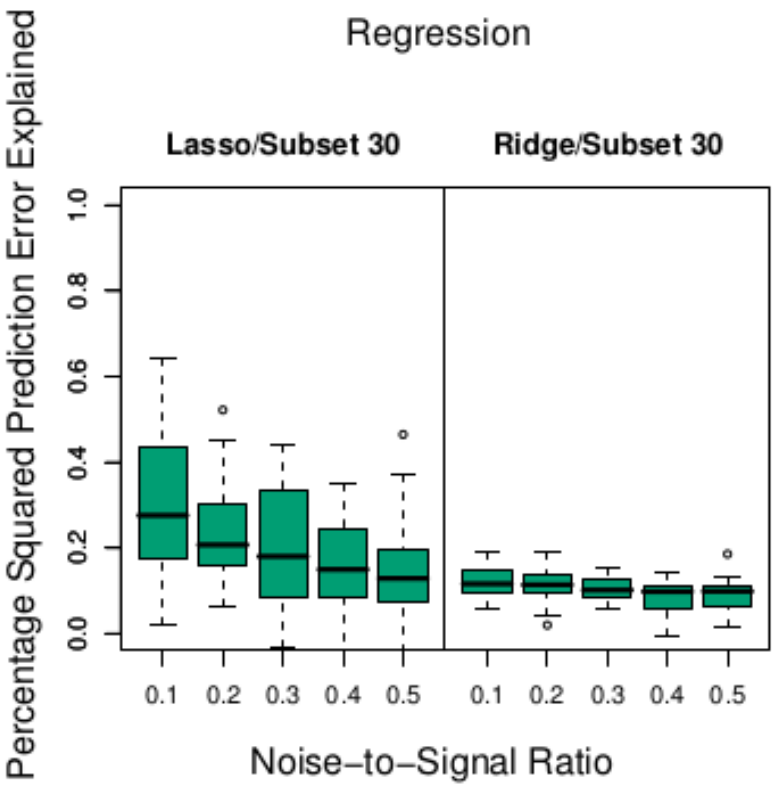


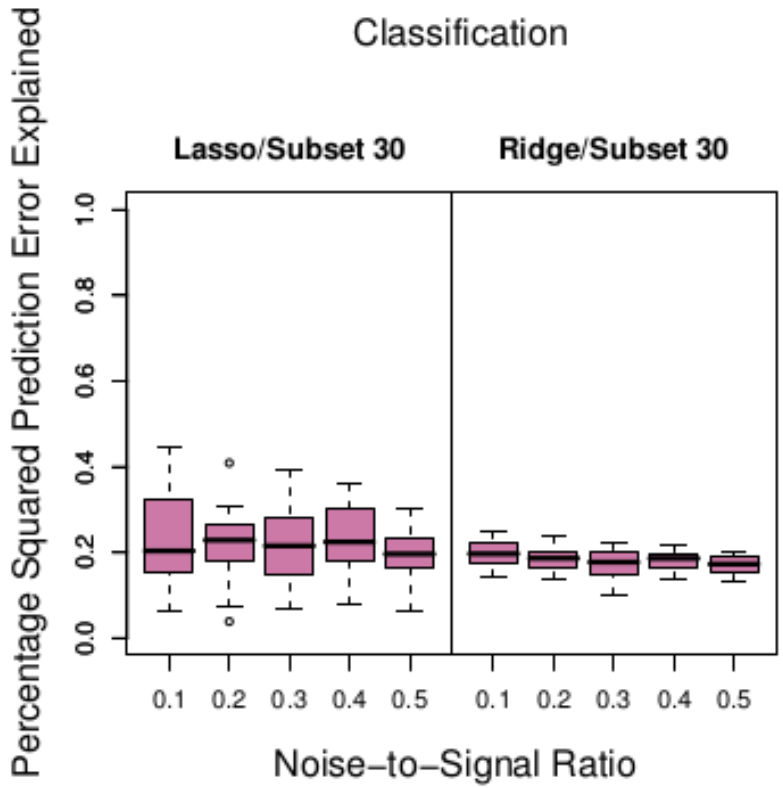
Regularization and Sparsity: the "bet on sparsity" principle





Regularization and Sparsity: the "bet on sparsity" principle





Regularization and Sparsity: the "bet on sparsity" principle

This means that:

- lasso performs better than ridge in sparse contexts;
- ridge gives better results if there are several relevant variables with small effects;
- anyway, in the dense case, the model does not explain a lot,
  - not enough data to estimate correctly several coefficients;

$$\downarrow$$

"bet on sparsity"

$$=$$

"use a procedure that does well in sparse problems, since no procedure does well in dense problems"

Regularization and Sparsity: the "bet on sparsity" principle

The degree of sparseness depends on:

- the unknown mechanism generating the data;
  - it depends on the number of relevant variables;
- size of the training set;
  - larger sizes allow estimating denser models;
- noise-to-signal ratio;
  - smaller NSR $\rightarrow$ denser models (same as before);
- size of the dictionary;
  - more base learners, potentially sparser models.

High-Dimensional Problems: when p is much larger than N

The case $p \gg N$ (number of variable much larger than the number of observations):

- very important in current applications,
  - e.g., in a common genetic study, $p \approx 23000$, $N \approx 100$;
- concerns about high variance and overfitting;
- highly regularized approaches are common:
  - lasso;
  - ridge;
  - boosting;
  - elastic-net;
  - ...

High-Dimensional Problems: when p is much larger than N

Consider the following example:

- $N = 100$;
- p variables from standard Gaussians with $\rho = 0.2$,

  (i) $p = 20$ (ii) $p = 100$ (iii) $p = 1000$.
- response from

$$Y = \sum_{j=1}^{p} X_j \beta_j + \sigma\epsilon;$$

- signal to noise ratio $\text{Var}[E(Y|X)]/\sigma^2 = 2$;
- true β from a standard Gaussian;

High-Dimensional Problems: when p is much larger than N

As a consequence, averaging over 100 replications:

- p_0, the number of significant β (i.e., $\beta : |\hat{\beta}/\hat{\text{se}}| > 2$)

  (i) $p_0 = 9$ (ii) $p_0 = 33$ (iii) $p_0 = 331$.

Consider 3 values of the penalty λ:

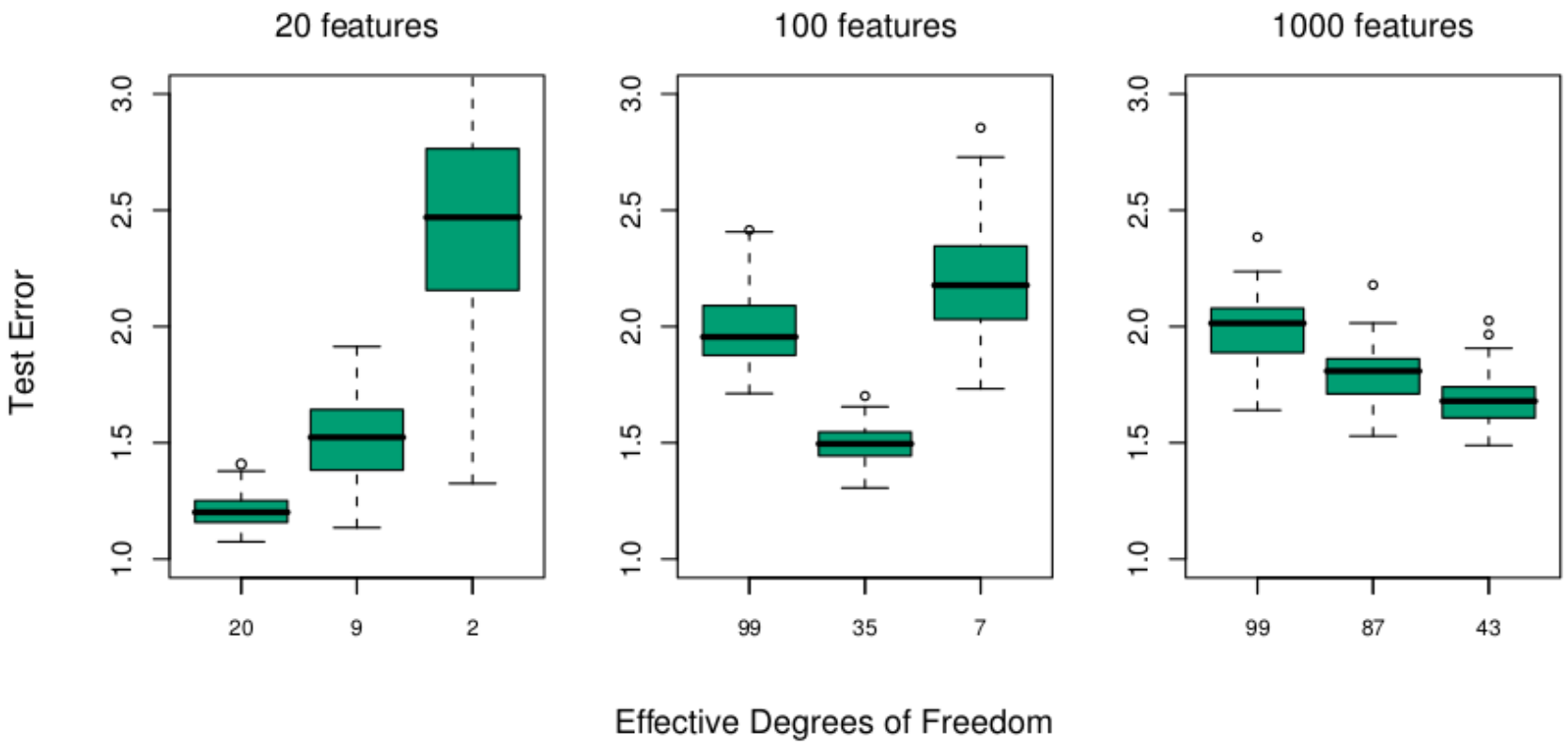
- $\lambda = 0.001$, which corresponds to

  (i) d.o.f. $= 20$ (ii) d.o.f. $= 99$ (iii) d.o.f. $= 99$;
- $\lambda = 100$, which corresponds to

  (i) d.o.f. $= 9$ (ii) d.o.f. $= 35$ (iii) d.o.f. $= 87$;
- $\lambda = 1000$, which corresponds to

  (i) d.o.f. $= 2$ (ii) d.o.f. $= 7$ (iii) d.o.f. $= 43$.

High-Dimensional Problems: when p is much larger than N



High-Dimensional Problems: when p is much larger than N

Remarks:

- with $p = 20$, ridge regression can find the relevant variables;
  - the covariance matrix can be estimated;
- moderate shrinkage works better in the middle case, in which we can find some non-zero effects;
- with $p = 1000$, there is no hope to find the relevant variables, and it is better to shrink down everything;
  - no possibility to estimate the covariance matrix.

Feature Assessment when $p \gg N$: multiple testing problem

Consider now a different issue:

- assess the significance of M variables ...
- ... in a $M \gg N$ framework;
  - in this lecture M is the number of variables (as in the book);

Possible use:

- identify variables related to the outcome,
  - e.g., identify the genes most related to cancer;
- reduce noise,
  - penalised regression methods require standardization;
  - standardization may increase false positive,
  - e.g., variables with almost no variation may become relevant;
- identify group structures.

Feature Assessment when $p \gg N$: multiple testing problem

Assessing the significance of a variable can be done:

- as a by-product of a multivariate model,
  - selection by a procedure with variable selection property;
  - absolute value of a regression coefficient in lasso;
  - variable importance plots (boosting, random forests, . . .);
- evaluating the variables one-by-one:
  - univariate tests;

$$\downarrow$$

multiple hypothesis testing

Feature Assessment when $p \gg N$: multiple testing problem

Consider the data from Rieger et al. (2004):

- study on the sensitivity of cancer patients to ionizing radiation treatment;
- oligo-nucleotide microarray data ($M = 12625$);
- $N = 58$:
  - 44 patients with normal reaction;
  - 14 patients who had a severe reaction.

Feature Assessment when $p \gg N$: multiple testing problem

TABLE 18.4. *Subset of the 12,625 genes from microarray study of radiation sensitivity. There are a total of 44 samples in the normal group and 14 in the radiation sensitive group; we only show three samples from each group.*

	Normal				Radiation Sensitive			
Gene 1	7.85	29.74	29.50	...	17.20	-50.75	-18.89	...
Gene 2	15.44	2.70	19.37	...	6.57	-7.41	79.18	...
Gene 3	-1.79	15.52	-3.13	...	-8.32	12.64	4.75	...
Gene 4	-11.74	22.35	-36.11	...	-52.17	7.24	-2.32	...
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
Gene 12,625	-14.09	32.77	57.78	...	-32.84	24.09	-101.44	...

Feature Assessment when $p \gg N$: multiple testing problem

The simplest way to identify significative genes:

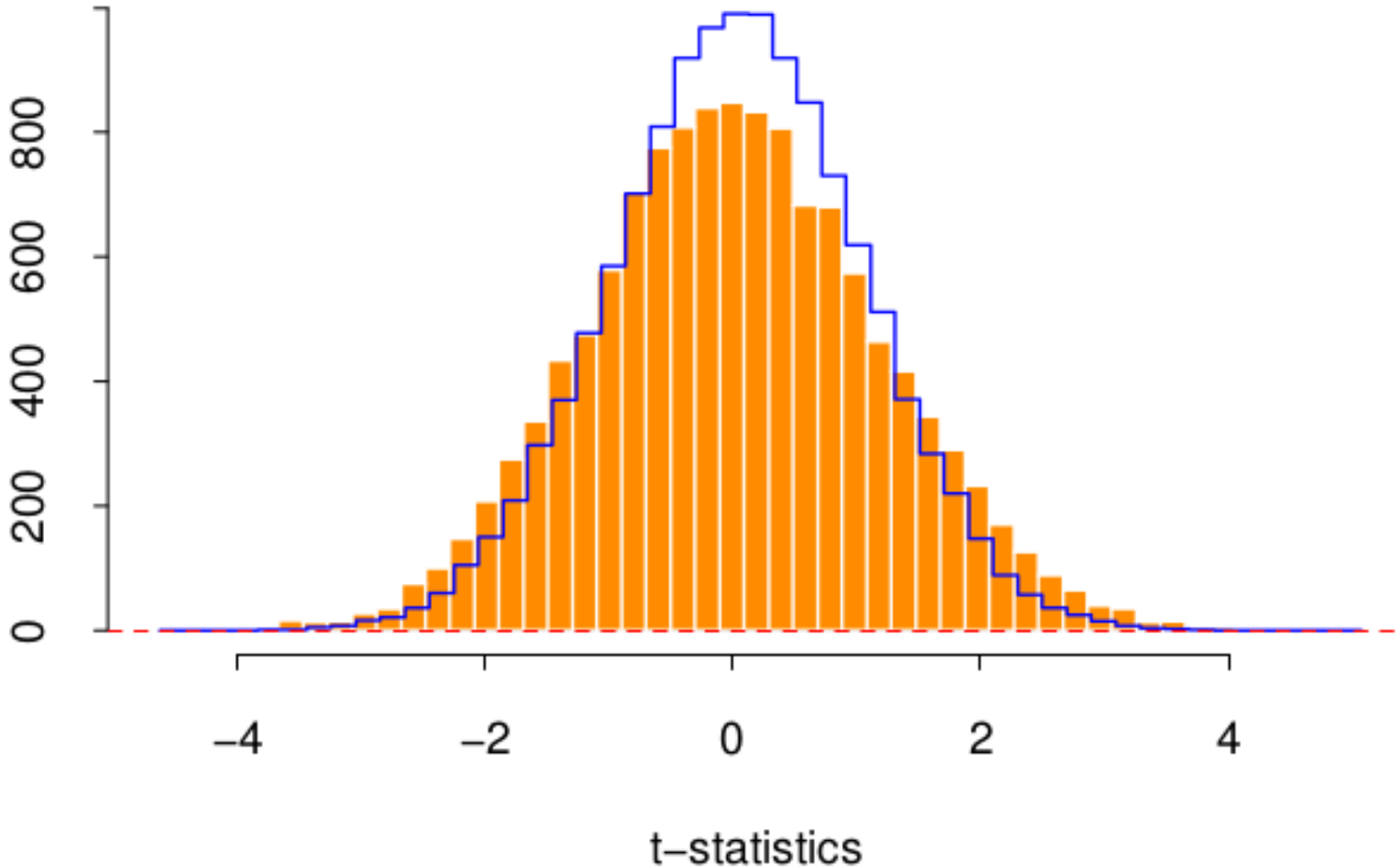
- two-sample t-statistic for each gene,

$$t_j = \frac{\bar{x}_{2j} - \bar{x}_{1j}}{se_j}$$

where

- $\bar{x}_{kj} = \sum_{i \in C_k} x_{kj}/N_k$;
- C_k are the indexes of the N_k observations of group k;
- $se_j = \hat{\sigma}_j \sqrt{\frac{1}{N_1} + \frac{1}{N_2}}$;
- $\hat{\sigma}_j^2 = \frac{1}{N_1+N_2-2} \left(\sum_{i \in C_1} (x_{ij} - \bar{x}_{1j})^2 + \sum_{i \in C_2} (x_{ij} - \bar{x}_{2j})^2 \right)$.

Feature Assessment when $p \gg N$: multiple testing problem



Feature Assessment when $p \gg N$: multiple testing problem

From the histogram (12625 t-statistics):

- the values range from -4.7 to 5.0;
- assuming $t_j \sim N(0,1)$, significance at 5% when $|t_j| \geqslant 2$;
- in the example, 1189 genes with $|t_j| \geqslant 2$.

However:

- out of 12625 genes, many are significant by chance;
- supposing (it is not true) independence:
  - expected falsely significant genes, $12625 \cdot 0.05 = 631.25$;
  - standard deviation, $\sqrt{12625 \cdot 0.05 \cdot (1 - 0.05)} \approx 24.5$;
- the actual 1189 is way out of range.

Feature Assessment when $p \gg N$: multiple testing problem

Without assuming normality, permutation test:

- perform $K = \binom{58}{14}$ permutations of the sample labels;
- compute the statistic $t_j^{[k]}$ for each permutation k;
- the p-value for the gene j is

$$p_j = \frac{1}{K} \sum_{k=1}^{K} \mathbb{1}(|t_j^{[k]}| > |t_j|)$$

($\binom{58}{14}$ not all are needed, random sample of $K = 1000$)

Feature Assessment when $p \gg N$: multiple testing problem

For $j \in 1, \ldots, M$ test the hypotheses:

H_{0j}: treatment has no effect on gene j

H_{1j}: treatment has an effect on gene j

H_{0j} is rejected at level α if $p_j < \alpha$:

- α is the type-I error;
- we expect a probability of falsely rejecting H_{0j} of α.

Feature Assessment when $p \gg N$: family-wise error rate

Define $A_j = \{H_{0j} \text{ is falsely rejected}\} \longrightarrow Pr(A_j) = \alpha$.

The **family-wise error rate** (FWER) is the probability of at least one false rejection,

$$Pr(A) = Pr(\bigcup_{j=1}^{M} A_j)$$

- for p large, $Pr(A) \gg \alpha$;
- it depends on the correlation between the test;
- if tests independent, $Pr(A) = 1 - (1 - \alpha)^M$;
- test with positive dependence, $Pr(A) < 1 - (1 - \alpha)^M$;
  - positive dependence is typical in genomic studies.

Feature Assessment when $p \gg N$: family-wise error rate

The simplest approach to correct the p-value for the multiplicity of the tests is the **Bonferroni method**:

- reject H_{0j} if $p_j < \alpha/M$;
- it makes the individual test more stringent;
- controls the FWER
  - it is easy to show that FWER $\leqslant \alpha$;
- it is very (too) conservative.

In the example:

- with $\alpha = 0.05$, $\alpha/M = 0.05/12635 \approx 3.9 \times 10^{-6}$;
- no gene has a p-value so small.

Feature Assessment when $p \gg N$: the false discovery rate

Instead of FWER, we can control the **false discovery rate** (FDR):

- expected proportion of genes incorrectly defined significant among those selected as significant,

	Called Not Significant	Called Significant	Total
H_0 True	U	V	M_0
H_0 False	T	S	M_1
Total	$M - R$	R	M

- in formula, FDR $= E[V/R]$;
- procedure to have the FDR smaller than an user-defined α.

Feature Assessment when $p \gg N$: the false discovery rate

Algorithm 18.2 *Benjamini–Hochberg (BH) Method.*

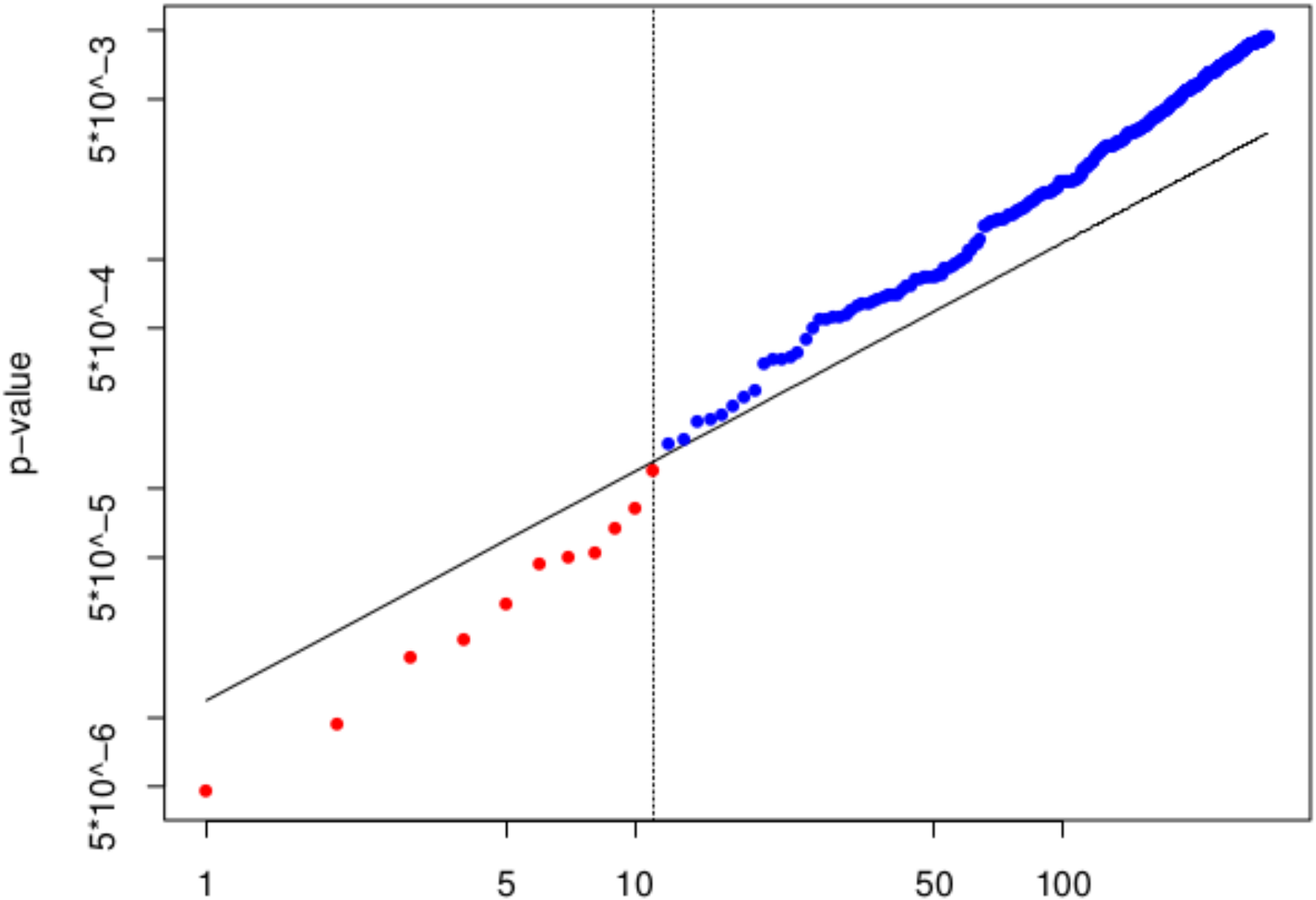
1. Fix the false discovery rate α and let $p_{(1)} \leq p_{(2)} \leq \cdots \leq p_{(M)}$ denote the ordered p-values

2. Define

$$L = \max\left\{j : p_{(j)} < \alpha \cdot \frac{j}{M}\right\}. \tag{18.44}$$

3. Reject all hypotheses H_{0j} for which $p_j \leq p_{(L)}$, the BH rejection threshold.

Feature Assessment when $p \gg N$: the false discovery rate



Feature Assessment when $p \gg N$: the false discovery rate

In the example:

- $\alpha = 0.15$;
- the last p_j under the line $\alpha \cdot (j/M)$ occurs at $j = 11$;
- the smallest 11 p-values are considered significative;
- in the example, $p_{(11)} = 0.00012$;
- the corresponding t-statistic is $|t_{(11)}| = 4.101$;
- a gene is relevant if the corresponding t-statistics is in absolute value larger than 4.101.

Feature Assessment when $p \gg N$: the false discovery rate

It can be proved (Benjamini & Hochberg, 1995) that

$$\text{FDR} \leqslant \frac{M_0}{M}\alpha \leqslant \alpha$$

- regardless the number of true null hypotheses;
- regardless the distribution of the p-values under H_1;
- suppose independent test statistics;
- in case of dependence, see Benjamini & Yekutieli (2001).

Stability Selection: introduction

In general:

- the L_1-penalty is often use to perform model selection;
- no oracle property (strict conditions to have it);
- issues with selecting the proper amount of regularization;

Meinshausen & Bühlmann (2010) suggested a procedure:

- based on subsampling (could work with bootstrapping as well);
- determines the amount of regularization to control the FWER;
- new structure estimation or variable selection scheme;
- here presented with L_1-penalty, works in general.

Stability Selection: introduction

Setting:

- β is a p-dimensional vector of coefficients;
- $S = \{j : \beta_j \neq 0\}$, $|S| < p$;
- $S^C = \{j : \beta_j = 0\}$;
- $Z^{[i]} = (X^{[i]}, Y^{[i]})$, $i = 1, \ldots, N$, are the i.i.d. data,
  - univariate response Y;
  - $N \times p$ covariate matrix X.
- consider a linear model

$$Y = X\beta + \epsilon$$

with $\epsilon = (\epsilon_1, \ldots, \epsilon_N)$ with i.i.d. components.

Stability Selection: introduction

The goal is to infer S from the data. We saw that lasso,

$$\hat{\beta}^{\lambda} = \text{argmin}_{\beta \in \mathbb{R}^p} \left(||Y - X\beta||_2^2 + \lambda \sum_{j=1}^{p} |\beta_j| \right)$$

provides an estimate of S, $S^{\lambda} = \{j : \hat{\beta}_j \neq 0\} \subseteq \{1, \ldots, p\}$.

Remember:

- $\lambda \in \mathbb{R}^+$ is the regularization factor;
- $||X_j||_2^2 = \sum_{i=1}^{N} (x_j^{[i]})^2 = 1$;

Stability Selection: selection probability

Stability selection is built on the concept of **selection probability**,

Definition 1: Let I be a random subsample of $\{1, \ldots, N\}$ of size $\lfloor N/2 \rfloor$ drawn without replacement. We define selection probability the probability for a variable X_j of being in $S^\lambda(I)$,

$$\hat{\Pi}_j^\lambda = Pr^*[j \subseteq S^\lambda(I)]$$

Note:

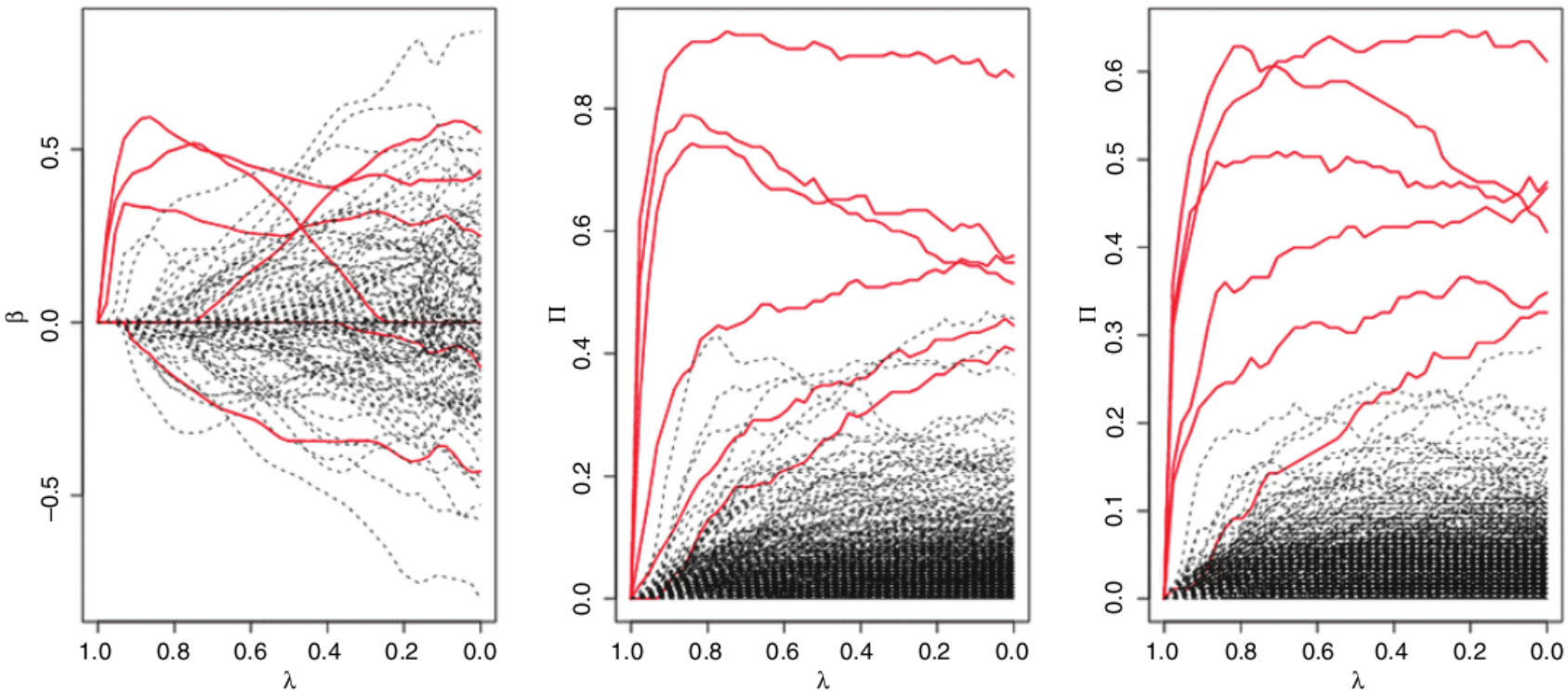
- Pr^* is with respect of both the random subsampling and other sources of randomness if S^λ is not deterministic;
- $\lfloor N/2 \rfloor$ is chosen for computational efficiency.

Stability Selection: stability path

Once we have the selection probability, we can define the **stability path**, as the evolution of $\hat{\Pi}_j^{\lambda}$ when $\lambda \in \Lambda$ varies,

- similar to the learning path plot of lasso;
- it shows the selection probabilities for all variables;
- it is very useful in high-dimensional settings.

Stability Selection: stability path



- left: lasso learning path;
- center: stability path of the lasso;
- right: stability path of the randomized lasso.

Stability Selection: stability path

Normally we would choose a specific λ:

- it is a single element of the set $\hat{S}^{\lambda}, \lambda \in \Lambda$;
- S might not be a member of the set;
- even if it is, it is hard to find the right λ high-dimensions.

With **stability selection**:

- we do not simply select one model in $\hat{S}^{\lambda}, \lambda \in \Lambda$;
- the data are perturbed (e.g. by subsampling) many times;
- we choose all variables that occur in a large fraction of the resulting selection sets.

Stability Selection: stability selection

Definition 2: For a cut-off π_{thr}, with $0 < \pi_{thr} < 1$, and a set of regularization parameters Λ, the set of stable variables is defined as

$$\hat{S}^{\text{stable}} = \left\{ j : \max_{\lambda \in \Lambda} (\Pi_j^{\lambda}) \geqslant \pi_{\text{thr}} \right\}.$$

In this way:

- we keep variables with a high selection probability;
- we disregard those with low selection probabilities;
- the exact cut-off π_{thr} is a tuning parameter;
- the results vary surprisingly little for sensible choices of π_{thr};
- results do not strongly depend on the choice of λ or Λ.

Stability Selection: choice of regularization

Let:

- $S^{\Lambda} = \bigcup_{\lambda \in \Lambda} \hat{S}^{\lambda}$ be the set of selected variables $\forall \lambda \in \Lambda$;
- $q_{\Lambda} = E[|\hat{S}^{\Lambda}(I)|]$ be the average number of selected variables;
- $V = |S^C \bigcap \hat{S}^{\text{stable}}|$ the number of falsely selected variables with stability selection.

Theorem (Meinshausen & Bühlmann, 2010): *Assuming that the distribution of* $\{\mathbb{1}_{j \in \hat{S}^{\lambda}}\}$ *is exchangeable* $\forall \lambda \in \Lambda$ *and the procedure is not worse than a random guess, then*

$$E[V] \leqslant \frac{1}{2\pi_{\text{thr}} - 1} \frac{q_{\Lambda}^2}{p}$$

Stability Selection: choice of regularization

Therefore:

- π_{thr} is a tuning parameter whose influence is very small;
  - sensible values are in $(0.6, 0.9)$;
- once decided π_{thr}, Λ is determined by the error control desired;
- specifically for $\pi_{\text{thr}} = 0.9$,
  - $\Lambda : q_\Lambda = \sqrt{0.8p} \quad \longrightarrow \quad E[V] \leqslant 1$;
  - $\Lambda : q_\Lambda = \sqrt{0.8\alpha p} \quad \longrightarrow \quad Pr[V > 0] \leqslant \alpha$;
- i.e., we need to find Λ that gives a specific q_Λ,
  - q is given by the number of variables which enter in the model;
  - for lasso, find $\lambda_{\text{min}} : |\bigcup_{\lambda_{\text{max}} \geqslant \lambda \geqslant \lambda_{\text{min}}} \hat{S}^\lambda| \leqslant q$

Stability Selection: choice of regularization

Final remarks:

- without stability selection, λ depends on the unknown noise level of the observations;
- the advantages of stability selection are:
  - exact error control is possible;
  - the method works fine even though the noise level is unknown;
- real advantage when $p \geqslant N$ (hard to estimate the noise level);

- consistency can be proved (see Meinshausen & Bühlmann, 2010, for the proof for randomized lasso);
- exchangeability in Theorem 1 is only need for the proof.

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