Recap: the de-biased Lasso

$$\sqrt{n}\left((Z^{(j)})^T X^{(j)}/n\right)\left(\hat{b}_j - \beta_j^0\right)$$

$$= \underbrace{\text{bias estimation error}_j}_{\text{uniformly negligible}} + \underbrace{n^{-1/2}\sum_{i=1}^{n} Z_i^{(j)}\varepsilon_i}_{\sim\mathcal{N}(0,\sigma^2\|Z^{(j)}\|_2^2/n)}$$

$\rightsquigarrow$

$$\frac{\hat{b}_j - \beta_j^0}{\widehat{s.e.}(\hat{b}_j)} \approx \mathcal{N}(0,1),$$

$$\widehat{s.e.}(\hat{b}_j) = n^{-1/2}\frac{\hat{\sigma}\|Z^{(j)}\|_2/\sqrt{n}}{|(Z^{(j)})^T X^{(j)}/n|}$$

can also use the bootstrap...!

Stability Selection (Ch. 10 in Bühlmann and van de Geer (2011))

has been developed before one knew about the de-biased/de-sparsified Lasso

even with new tools such as the de-biased/de-sparsified Lasso estimation of discrete structures ("relevant" variables in a generalized linear model; edges in a graphical model) is notoriously difficult
choice of tuning parameters...?

The generic setup

i.i.d. data $Z_1, \ldots, Z_n$

main example: $Z_i = (X_i, Y_i)$ from regression or classification

$\hat{S}_\lambda$ is a "feature selection" method/algorithm among $\{1, \ldots, p\}$ features

can we assign "relevance" to the selected features in $\hat{S}_\lambda$?

a "natural" approach: resampling!
here: use subsampling:

- I^* random sub-sample of size $\lfloor n/2 \rfloor$ of $\{1, \ldots, n\}$
- compute $\hat{S}_\lambda(I^*)$
- repeat B times to obtain $\hat{S}_\lambda(I^{*1}), \ldots, \hat{S}_\lambda(I^{*B})$
- consider the "overlap" among $\hat{S}_\lambda(I^{*1}), \ldots, since the P - values are set to 1 if \hat{S}_\lambda(I^{*B})$

regarding the latter, for example:

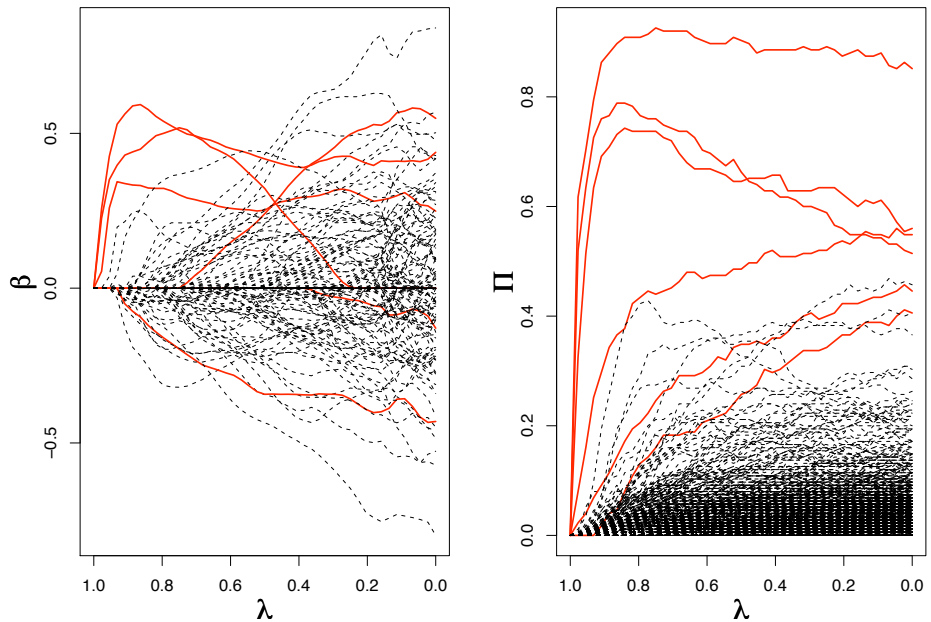
$$\hat{\Pi}_K(\lambda) = \mathbb{P}^*[K \subseteq \hat{S}_\lambda(I^*)] \approx B^{-1} \sum_{b=1}^{B} I(K \subseteq \hat{S}_\lambda(I^{*b}))$$

e.g. $\hat{\Pi}_j(\lambda)$ $(j \in \{1, \ldots, p\})$

the probability $\mathbb{P}^*$ is with respect to subsampling: a sum over $\binom{n}{m}$ terms, $m = \lfloor n/2 \rfloor$, i.e., all possible subsampling combinations
$\rightsquigarrow$ it is approximated by B (≈ 100) times random subsampling

The stability regularization path

Riboflavin data: $n = 115$, $p = 4088$
Y: log-production rat of riboflavin by bacillus subtilis
X: gene expressions of bacillus subtilis
all X-variables permuted except 6 “a-priori relevant” genes



left: Lasso regularization path (red: the 6 non-permuted “relevant” genes)
right: Stability path with $\hat{\Pi}_j$ on y-axis (red: the 6 non-permuted “relevant” variables stick out much more clearly from the noise covariates)

What is a good truncation value (for $\hat{\Pi}$)?

aim: choose π_{thr} such that

$$\hat{S}_{\text{stable}} = \{j; \max_{\lambda \in \Lambda} \hat{\Pi}_j(\lambda) \geq \pi_{\text{thr}}\} \mathit{since the P-values are reset to 1 if}$$

has not too many false positives
Λ can be a singleton or a range of values

as a measure for type I error control (against false positives):

$$V = \text{ number of false positives} = |\hat{S}_{\text{stable}} \cap S_0^c|$$

where S_0 is the set of the true relevant features, e.g.:
– active variables in regression
– true edges in a graphical model

"the miracle":

a simple formula connecting π_{thr} with $\mathbb{E}[V]$

consider a setting with p possible features
$\hat{S}(\lambda)$ is a feature selection algorithm
$\hat{S}_\Lambda = \cup_{\lambda \in \Lambda} \hat{S}(\lambda)$
$q_\Lambda = \mathbb{E}[\hat{S}_\Lambda(\underbrace{\quad I \quad}_{\text{random subsample}})]$

Theorem 10.1
Assume:

- exchangeability condition:
  $\{1(j \in \hat{S}(\lambda)\}), j \in S_0^c\}$ is exchangeable for all $\lambda \in \Lambda$
- $\hat{S}$ is not worse than random guessing

$$\frac{\mathbb{E}|S_0 \cap \hat{S}_\Lambda|)}{\mathbb{E}(|S_0^c \cap \hat{S}_\Lambda|)} \geq \frac{|S_0|}{|S_0^c|}.$$

Then, for $\pi_{\text{thr}} \in (1/2, 1)$:

$$\mathbb{E}[V] \quad \leq \quad \frac{1}{2\pi_{\text{thr}} - 1} \frac{q_\Lambda^2}{p}.$$

suppose we know q_Λ (see later)
strategy: specify $\mathbb{E}[V] = v_0$(e.g. $= 5$)
$\rightsquigarrow$ for $\pi_{\text{thr}} := \frac{1}{2} + \frac{q_\Lambda^2}{2pv_0}$: $\mathbb{E}[V] \leq v_0$

example: regression model with $p = 1000$ variables

$\hat{S}_\lambda =$ the top 10 variables from Lasso (e.g. the different λ from Lasso by CV and choose the top 10 variables with the largest absolute values of the corresponding estimated coefficients; if less than 10 variables are selected, take the selected variables) the value λ corresponds to the "top 10"; Λ is a singleton

we then know that $q_\Lambda = \mathbb{E}[|\hat{S}_\lambda(I)|] \leq 10$

For $\mathbb{E}[V] = v_0 := 5$ we then obtain

$$\pi_{\text{thr}} = \frac{1}{2} + \frac{q_\Lambda^2}{2pv_0} = 0.5 + \frac{10^2}{2 * 1000 * 5} = 0.51$$

since the P-values are set to 1 if

there is room to play around
recommendation: take $|\hat{S}(\lambda)|$ rather large and stability selection will reduce again to reasonable size

when taking the "top 30", the threshold becomes

$$\pi_{\text{thr}} = \frac{1}{2} + \frac{q_\Lambda^2}{2pv_0} = 0.5 + \frac{30^2}{2 * 1000 * 5} = 0.59$$

adding noise...
can always add (e.g. independent $\mathcal{N}(0,1)$) noise covariates
enlarged dimension p_{enlarged}

error control becomes better (for the same threshold)

$$\mathbb{E}[V] \quad \leq \quad \frac{1}{2\pi_{\text{thr}} - 1} \, \frac{q_\Lambda^2}{p_{\text{enlarged}}}$$

this sometimes helps indeed in practice – at the cost of loss in power

The assumptions for mathematical guarantees

not worse than random guessing

$$\frac{\mathbb{E}|S_0 \cap \hat{S}_\lambda|)}{\mathbb{E}(|S_0^c \cap \hat{S}_\lambda|)} \geq \frac{|S_0|}{|S_0^c|}$$

perhaps hard to check but very reasonable...
for Lasso in linear models it holds assuming the variable screening property
asymptotically: if beta-min and compatibility condition hold

exchangeability condition $\{1(j \in \hat{S}(\lambda)\}), j \in S_0^c\}$ is exchangeable for all $\lambda \in \Lambda$
a very special case:
random equi-correlation design linear model

$$Y = X\beta^0 + \varepsilon,\ \mathrm{Cov}(X)_{i,j} \equiv \rho\ (i \neq j),\ \mathrm{Var}(X_j) \equiv 1 \forall j$$

distributions of $(Y, X^{(S_0)}, \{X^{(j)};\ j \in S_0^c\})$ and of $(Y, X^{(S_0)}, \{X^{(\pi(j))};\ j \in S_0^c\})$ are the same for any permutation $\pi : S_0^c \to S_0^c$

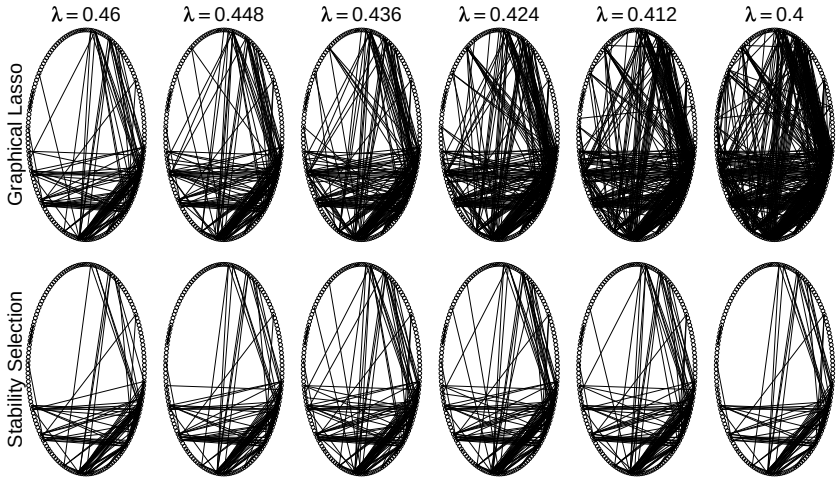
- distribution of $X^{(S_0)}, \{X^{(\pi(j))};\ j \in S_0^c\}$ is the same for all π (because of equi-correlation)
- distribution of $Y|X^{(S_0)}, \{X^{(\pi(j))};\ j \in S_0^c\}$ is the same for all π (because it depends only on $X^{(S_0)}$
- therefore: distribution of $Y, X^{(S_0)}, \{X^{(\pi(j))};\ j \in S_0^c\}$ is the same for all π
  and hence exchangeability condition holds for any (measurable) function $\hat{S}(\lambda)$

An illustration for graphical modeling

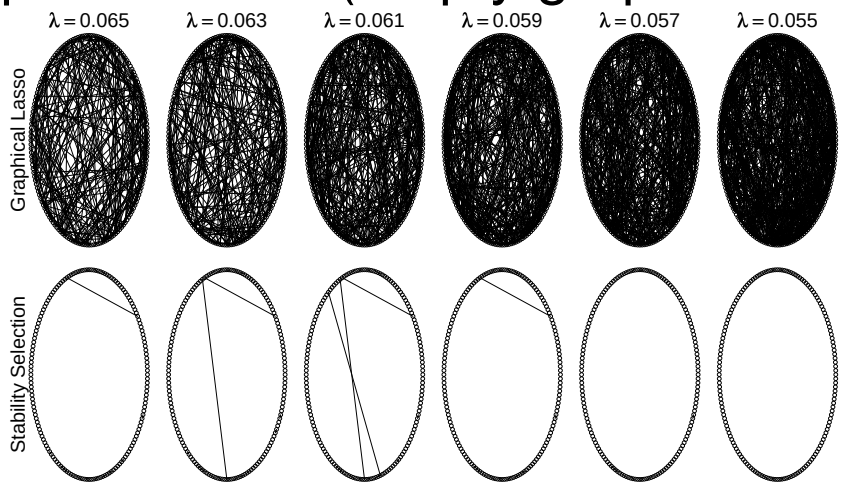
$p = 160$ gene expressions, $n = 115$

GLasso estimator, selecting among the $\binom{p}{2} = 12'720$ features

stability selection with $\mathbb{E}[V] \leq v_0 = 30$



with permutation (empty graph is correct)



Stability Selection is extremely easy to use
and super-generic

the sufficient assumption (far from necessary) for mathematical guarantees are restrictive
but the method seems to work well in practice

P-values based on multi sample splitting

(Ch. 11 in Bühlmann and van de Geer (2011))

Stability Selection

- uses subsampling many times – a good thing!
- provides control of the expected number of false positives rather than e.g. the familywise error rate $\rightsquigarrow$ we will "address" this with
  multi sample splitting and aggregation of P-values

Fixed design linear model

$$Y = X\beta^0 + \varepsilon$$

instead of de-biased/de-sparsified method, consider the "older" technique (which is not statistically optimal but more generic and more in the spirit of stability selection)

split the sample into two parts I_1 and I_2 of equal size $\lfloor n/2 \rfloor$

- use (e.g.) Lasso to select variables based on I_1: $\hat{S}(I_1)$
- perform low-dimensional statistical inference on I_2 based on data $(x_{I_2}^{(\hat{S}(I_1))}, Y_{I_2})$;
  for example using the t-test for single coefficients β_j^0
  (if $j \notin \hat{S}(I_1)$, assign the p-value 1 to the hypothesis $H_{0,j} : \beta_j^0 = 0$(,

  due to independence of I_1 and I_2, this is a "valid" strategy (see later)

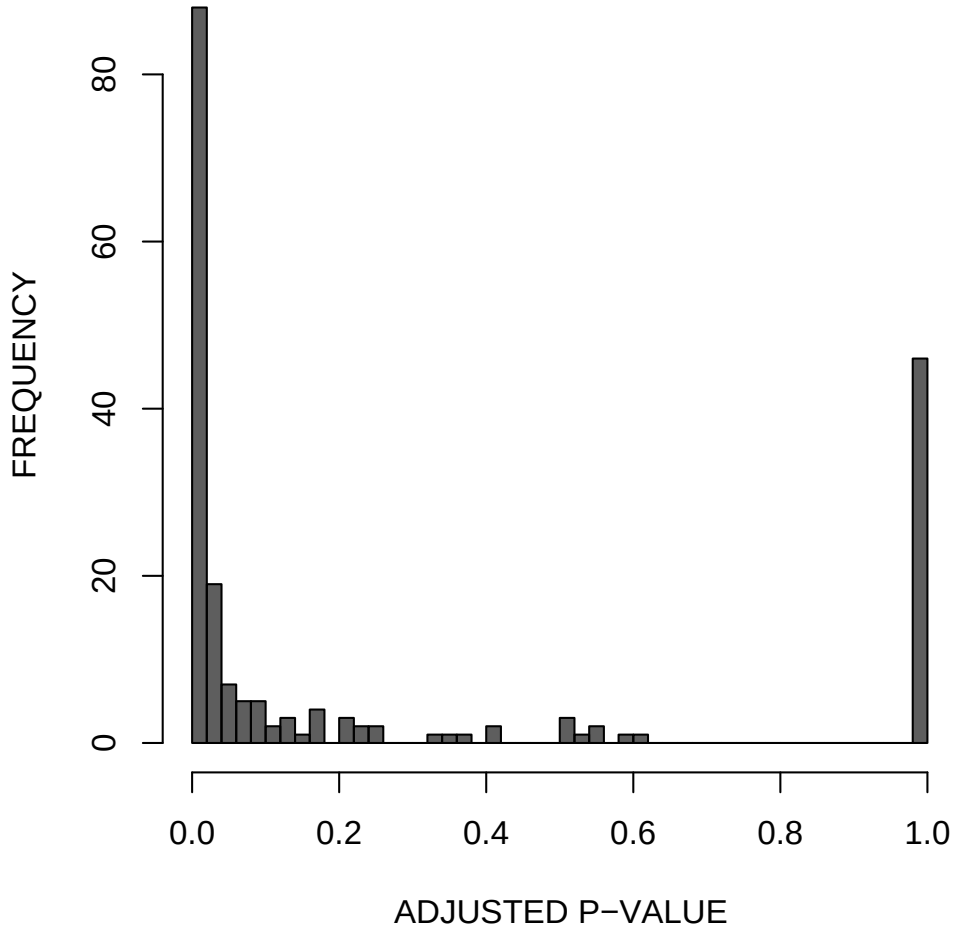
validity of the (single) data splitting procedure
consider testing $H_{0,j}: \ \beta_j^0 = 0$ versus $H_{A,j}: \ \beta_j^0 \neq 0$
assume Gaussian errors for the fixed design linear model :
thus, use the t-test on the second half of the sample I_2 to get a p-value

$$P_{\text{raw},j} \text{ from } t\text{-test based on } X_{I_2,\hat{S}(I_1)}, Y_{I_2}$$

$P_{\text{raw},j}$ is a valid p-value (controlling type I error) for testing $H_{0,j}$ is $\hat{S}(I_1) \supseteq S_0$ (i.e., the screening property holds)
if the screening property does not hold: $P_{\text{raw},j}$ is still valid for $H_{0,j}(M) : \beta_j(M) = 0$ where $M = \hat{S}(I_1)$ is a selected sub-model and $\beta(M) = (X_M^T X_M)^{-1} X_M^T \mathbb{E}[Y]$

a p-value lottery depending on the random split of the data

motif regression $n = 287$, $p = 195$



$\rightsquigarrow$ should aggregate/average over multiple splits!

Multiple testing and aggregation of p-values

the issue of multiple testing:

$$\tilde{P}_j = \begin{cases} P_{\text{raw},j} \text{ based on } \mathbf{Y}_{I_2}, \mathbf{X}_{I_2,\hat{S}(I_1)} & \text{, if } j \in \hat{S}(I_1), \\ 1 & \text{, if } j \notin \hat{S}(I_1) \end{cases}$$

thus, we can have at most $|\hat{S}(I_1)|$ false positives
$\rightsquigarrow$ can correct with Bonferroni with factor $|\hat{S}(I_1)|$ (instead of factor p) to control the familywise error rate

$$\tilde{P}_{\text{corr},j} = \min(\tilde{P}_j \cdot |\hat{S}(I_1)|, 1) \ (j = 1, \ldots, p)$$

decision rule: reject $H_{0,j}$ if and only if $\tilde{P}_{\text{corr},j} \leq \alpha$
$\rightsquigarrow$ FWER $\leq \alpha$

the issue with P-value aggregation:

if we run sample splitting B times, we obtain P-values

$$\tilde{P}^{[1]}_{\text{corr},j}, \ldots, \tilde{P}^{[B]}_{\text{corr},j}$$

how to aggregate these dependent p-values to a single one?

for $\gamma \in (0, 1)$ define

$$Q_j(\gamma) = \min \left\{ q_\gamma \left(\{ \tilde{P}^{[b]}_{\text{corr},j} / \gamma;\ b = 1, \ldots, B \} \right), 1 \right\},$$

where $q_\gamma(\cdot)$ is the (empirical) γ-quantile function

Proposition 11.1 (Bühlmann and van de Geer, 2011)
For any $\gamma \in (0, 1)$, $Q_j(\gamma)$ are P-values which control the FWER

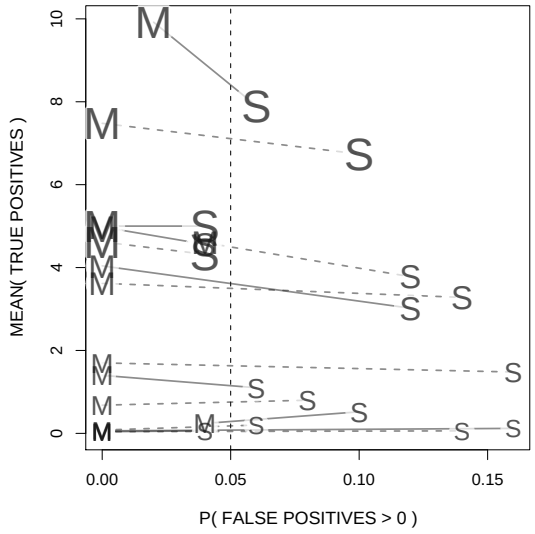
example: $\gamma = 1/2$
aggregate the p-values with the sample median and multiply by the factor 2

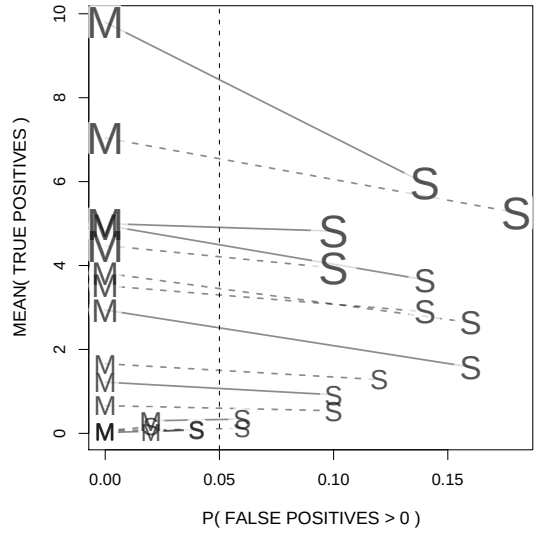
avoid choosing γ:

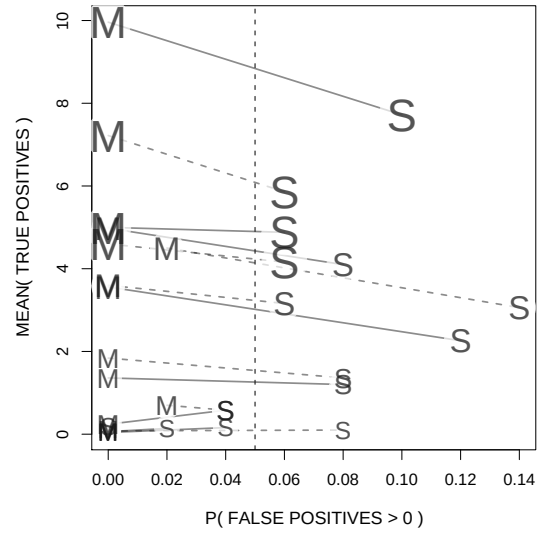
$$P_j = \min \left\{ \underbrace{\left(1 - \log \gamma_{\min}\right)}_{\text{price to optimize over } \gamma} \quad \inf_{\gamma \in (\gamma_{\min}, 1)} Q_j(\gamma), 1 \right\} \ (j = 1, \ldots, p).$$

Theorem 11.1 (Bühlmann and van de Geer (2011))
For any $\gamma_{\min} \in (0, 1)$, P_j are P-values which control the FWER

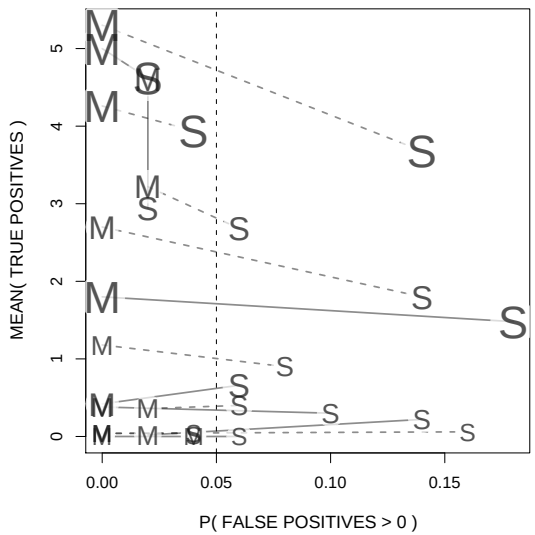
$n = 100, p = 100$

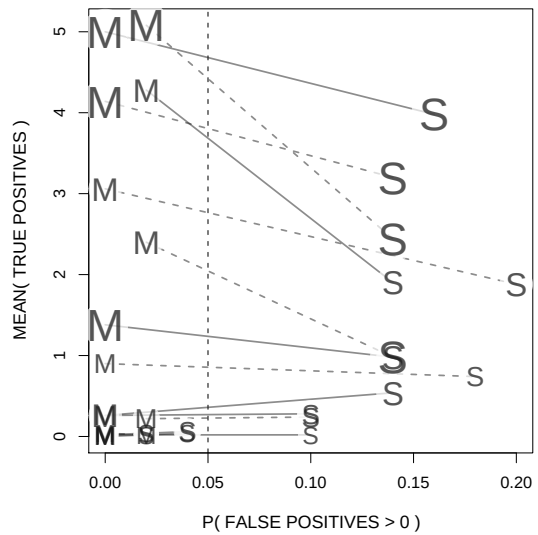


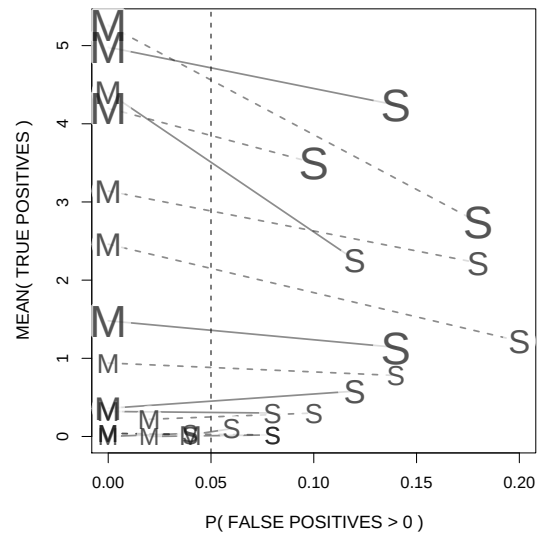




$n = 100, p = 1000$







one can also adapt =the method to control the False Discovery Rate (FDR)

multi sample splitting and p-value construction:

- is very generic, also for “any other” model class
- is powerful in terms of multiple testing correction: we only correct for multiplicity from $|\hat{S}(I_1)|$ variables
- it relies in theory on the screening property of the selector in practice: it is a quite competitive method!

current MSc thesis of Christoph Schultheiss: can improve multi sample splitting by multi carve methods, based on “technology” from selected inference