Lecture B

Exhaustive and non-exhaustive algorithms with resampling

Samuel Müller and Garth Tarr

THE UNIVERSITY OF SYDNEY

Overview

B1. Cross validation

B2. The `mplot` package

- Artificial example: *Information criteria can be blind*
- Variable inclusion plots
- Model stability plots
- Bootstraping the lasso

B3. Subtractive stability measures

B1. Cross-validation for model selection

Resampling procedures

- Cross-validation (CV) and bootstrapping are the two most popular classes of resampling methods in model building
- In model building, resampling is often used to
- assess the stability of a model
- infer on model parameters (tests, confidence intervals, point estimates, bias)
- measure prediction error

Cross-validation algorithms

- Cross-validation schemes can be implemented in most statistical frameworks and for most estimation procedures
- The key principle of CV is to split the data into a training set and a validation set
- Estimators are built on the training set
- Validation set is used to validate/assess the performance of the estimators, e.g. estimating their prediction risk
- This training / validation splitting is repeated several times

10-fold cross validation

Cross-validation algorithms

The most popular cross-validation schemes are,

- Hold-out CV, based on a single split of the data
- k-fold CV: the data is split into k subsamples. Each subsample is successively removed for validation, the remaining data being used for training
- Leave-one-out (LOOCV) which corresponds to n-fold CV
- Leave- q-out every of the $\binom{n}{q}$ possible subsets is removed for validation

CV prediction error

- In k-fold CV the data is split into k subsamples (the k folds)
- Each subsample is successively removed for validation, the remaining data being used for training
- Thus, for each of the k folds $f = 1, \ldots, k$, $\iota_f \subset \{1, \ldots, n\}$ denotes the $n_f = |\iota_f|$ observations in the fth fold and we calculate

$$\mathrm{CV}_{(k)} = \frac{1}{k} \sum_{f=1}^{k} \mathrm{MSE}_f = \frac{1}{k} \sum_{f=1}^{k} \frac{1}{n_f} \sum_{i \in \iota_f} [y_i - \hat{y}_{\alpha i}(-\iota_f)]^2$$

- Similarly, for estimating classification errors

Choice of k affects the quality of the CV error

- If $k = 2$: split-sample CV - CV error estimates biased upwards because only half the data used in the training samples
- If $k = n$: LOOCV - CV estimates have high variance because in the above equation a total of n positively correlated quantities are averaged;
- Standard choices are $k = 10$ (default in `cv.glmnet` through option `nfolds=10`) or $k = 5$: This balances bias and variance
- The k partly overlapping training sets can be used to learn more about the stability of selected models

Case study: selecting λ for Lasso

How to best choose λ?

- Many options!
- Use information criteria along the lasso, ridge, or elastic-net path
- Use cross-validation
- as an alternative to `lambda.min` often `lambda.1se` does give better performance in terms of prediction
- `lambda.1se` is the largest λ at which the MSE is within one standard error of the minimal MSE (at `lambda.min`)

Diabetes example

```
data("diabetes", package = "lars")
library("glmnet")
x = diabetes$x2 # includes squares and interactions
y = diabetes$y
lasso.fit = glmnet(x, y)
length(lasso.fit$lambda)
```

```
## [1] 100
```

```
lasso.predict = predict(lasso.fit, newx = x)
dim(lasso.predict)
```

```
## [1] 442 100
```

Diabetes example: AIC to select λ

```
lasso.aic = rep(0, 100)
sigma.hat = summary(lm(y ~ x))$s
for (m in 1:100) {
  yhat = lasso.predict[, m]
  k = lasso.fit$df[m]
  lasso.aic[m] = sum((y - yhat)^2)/(sigma.hat^2) + 2*k
}
which.min(lasso.aic)
```

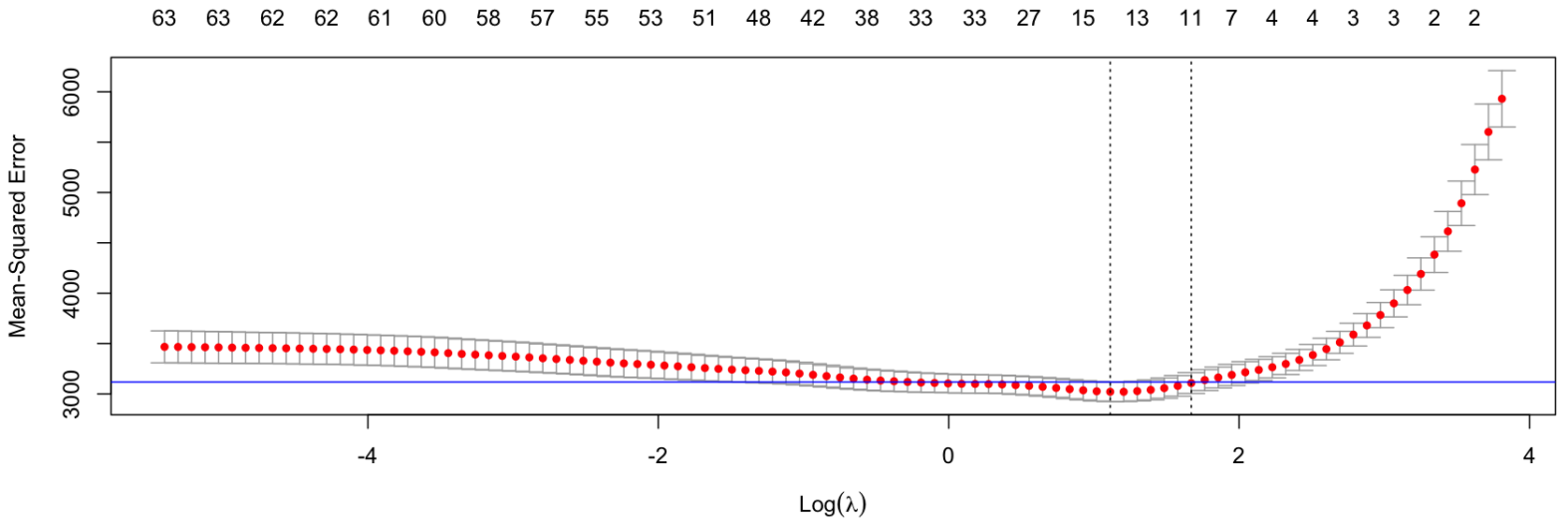
```
## [1] 32
```

```
lasso.fit$lambda[32]
```

```
## [1] 2.524812
```

Diabetes example: CV to select λ

```
set.seed(2020)
lasso.cv = cv.glmnet(x, y)
plot(lasso.cv)
abline(h = min(lasso.cv$cvm) + lasso.cv$cvsd[which.min(lasso.cv$cvm)],
       col = "blue")
```




```
lasso.cv$lambda.1se
```

Diabetes example:

Predictors selected by **AIC**:

```
aic_betas = glmnet(x, y, lambda = lasso.fit$lambda[32])$beta
as.matrix(aic_betas)[as.matrix(aic_betas)>0, ]
```

```
##         bmi         map         ltg         glu      age^2      bmi^2
## 500.775931 262.976223 469.918325  25.416346  17.558198  42.899478
##      glu^2    age:sex    age:map    age:ltg    age:glu    sex:map
##  76.518096 115.463280  30.647942  12.662471   9.365541   7.745166
##    bmi:map
##  90.571069
```

Predictors selected by **CV**:

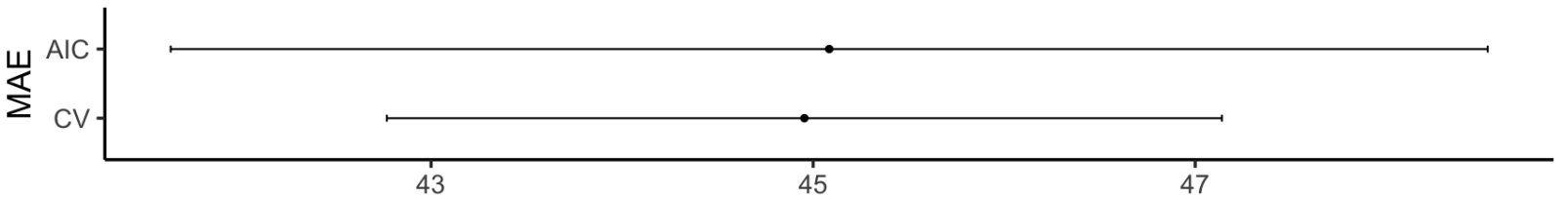
```
cv_betas = glmnet(x, y, lambda = lasso.cv$lambda.1se)$beta
as.matrix(cv_betas)[as.matrix(cv_betas)>0,]
```

```
##         bmi         map         ltg      bmi^2      glu^2    age:sex
## 502.887614 205.892655 453.531965  17.266008  39.776736  60.581213
##    age:map    age:glu    bmi:map
##  14.945884   7.108415  59.023875
```

Diabetes example

We can choose between the two competing models using **cross validation**.

```
library(caret)
control <- trainControl(method = "cv", number = 10)
dat <- cbind(y, x)
aic_cv <- train(y ~ bmi + map + ltg + glu + `age^2` + `bmi^2` +
                  `glu^2` + `age:sex` + `age:map` + `age:ltg` +
                  `age:glu` + `sex:map` + `bmi:map`,
                method = "lm", data = dat, trControl = control)
cv_cv <- train(y ~ bmi + map + ltg + `bmi^2` + `glu^2` +
                 `age:sex` + `age:map` + `age:glu` + `bmi:map`,
               method = "lm", data = dat, trControl = control)
results <- resamples(list(AIC = aic_cv, CV = cv_cv))
ggplot(results) + theme_classic(base_size = 18) +
  labs(x = "MAE")
```



B2. The mplot package

Installing the mplot package

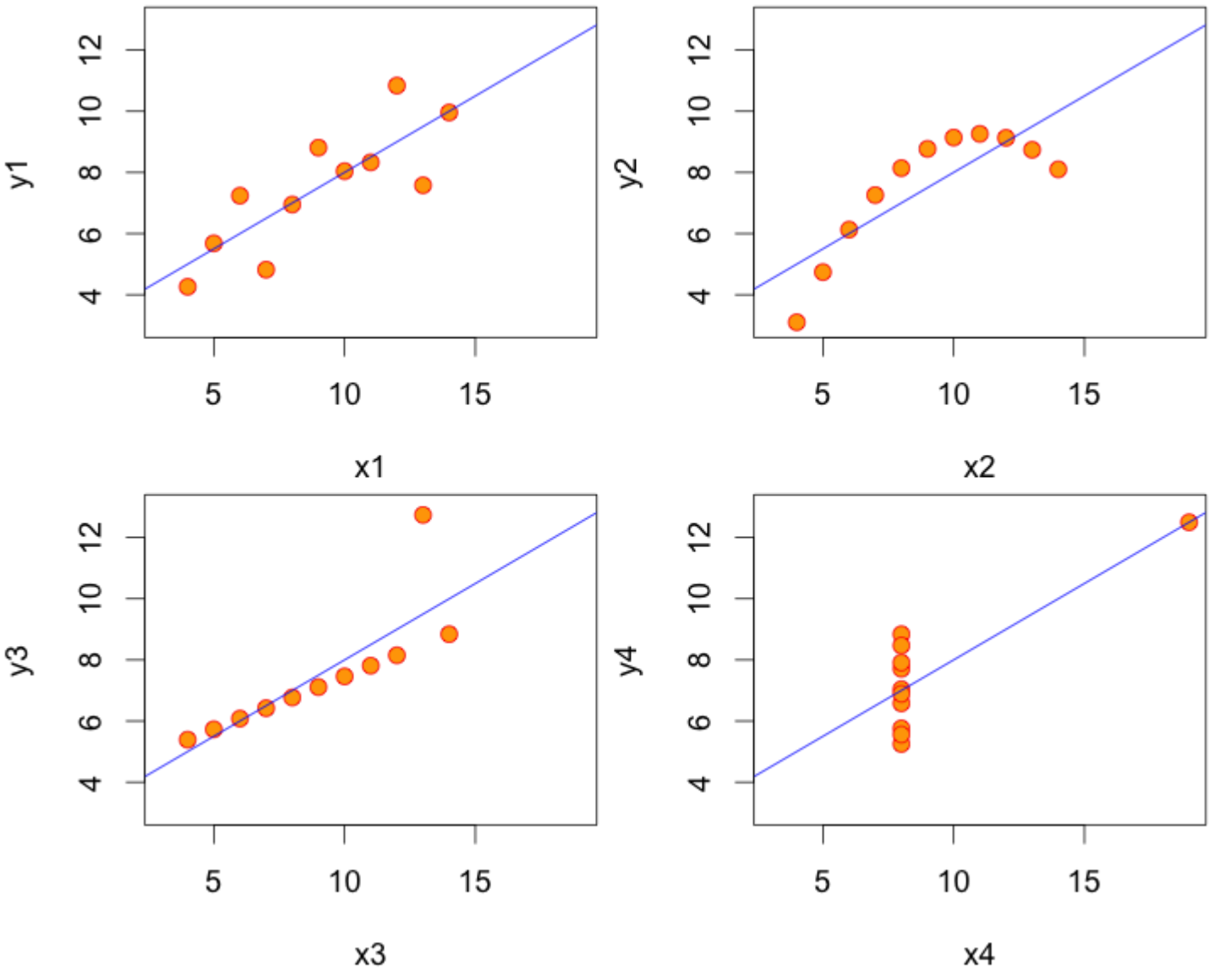
```
# install.packages("devtools")
# devtools::install_github("garthtarr/mplot")
install.packages("mplot")
library(mplot)
```

Website: http://garthtarr.github.io/mplot

Main functions

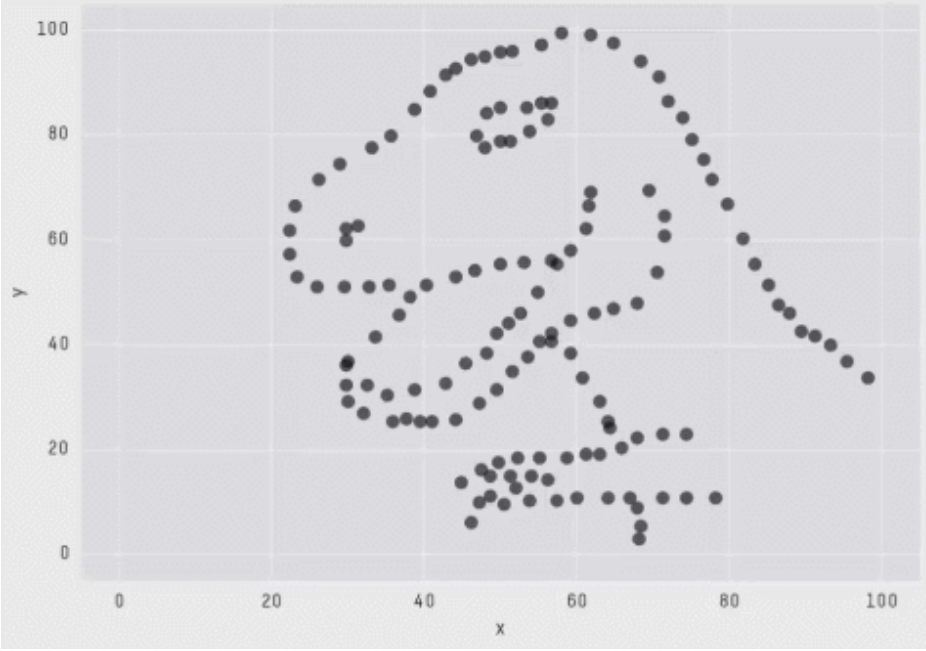
- `af()` for the adaptive fence for `lm()` and `glm()`
- `vis()` for variable importance plots and model stability plots for `lm()` and `glm()`
- `bglmnet()` for bootstrapping `glmnet()` and variable importance and model stability plots
- `mplot()` for an interactive shiny interface

Motivation – Recall Anscombe's quartet



Datasaurus

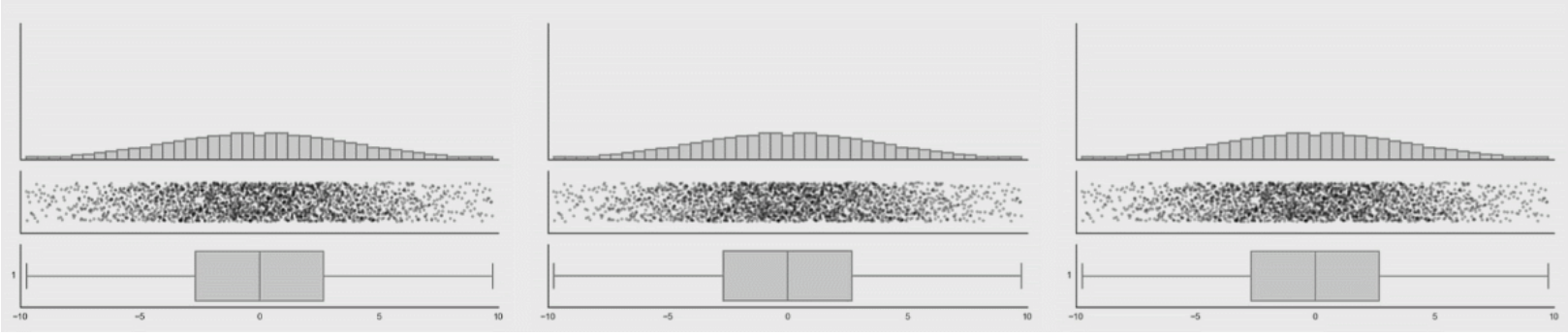
```
library(datasauRus)
```

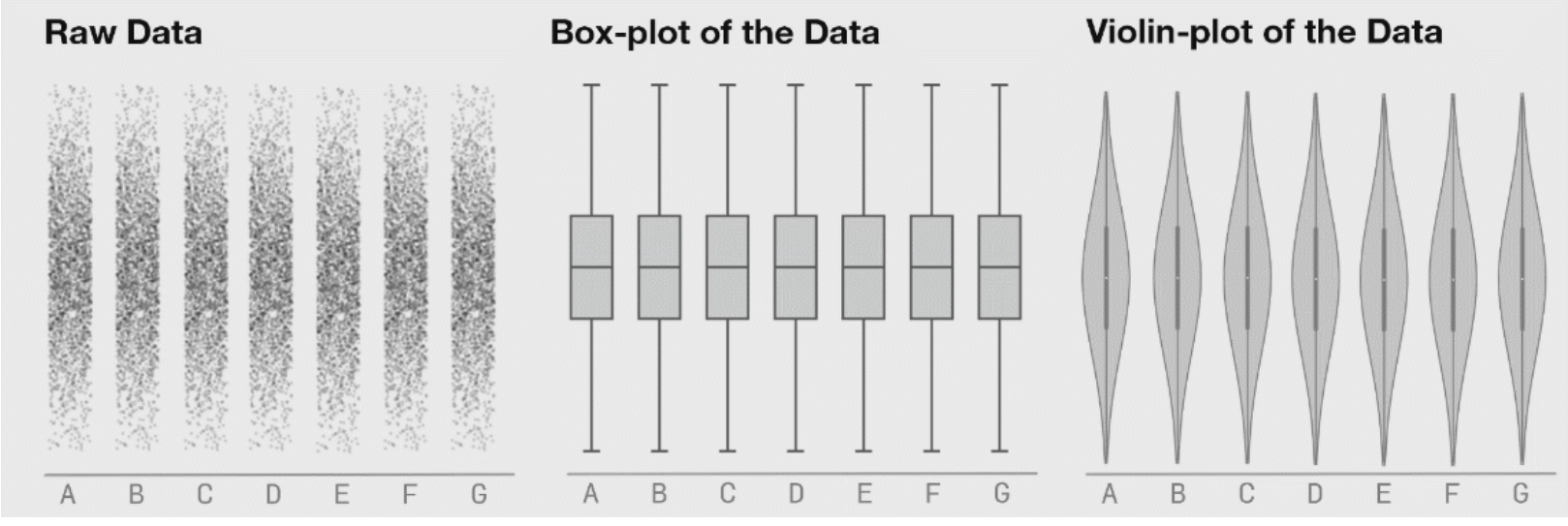


X Mean: 54.2659224
Y Mean: 47.8313999
X SD : 16.7649829
Y SD : 26.9342120
Corr. : -0.0642526

Matejka J and Fitzmaurice G (2017). Same Stats, Different Graphs: Generating Datasets with Varied Appearance and Identical Statistics through Simulated Annealing. Autodesk Research, Toronto Ontario Canada. DOI: 10.1145/3025453.3025912

See also





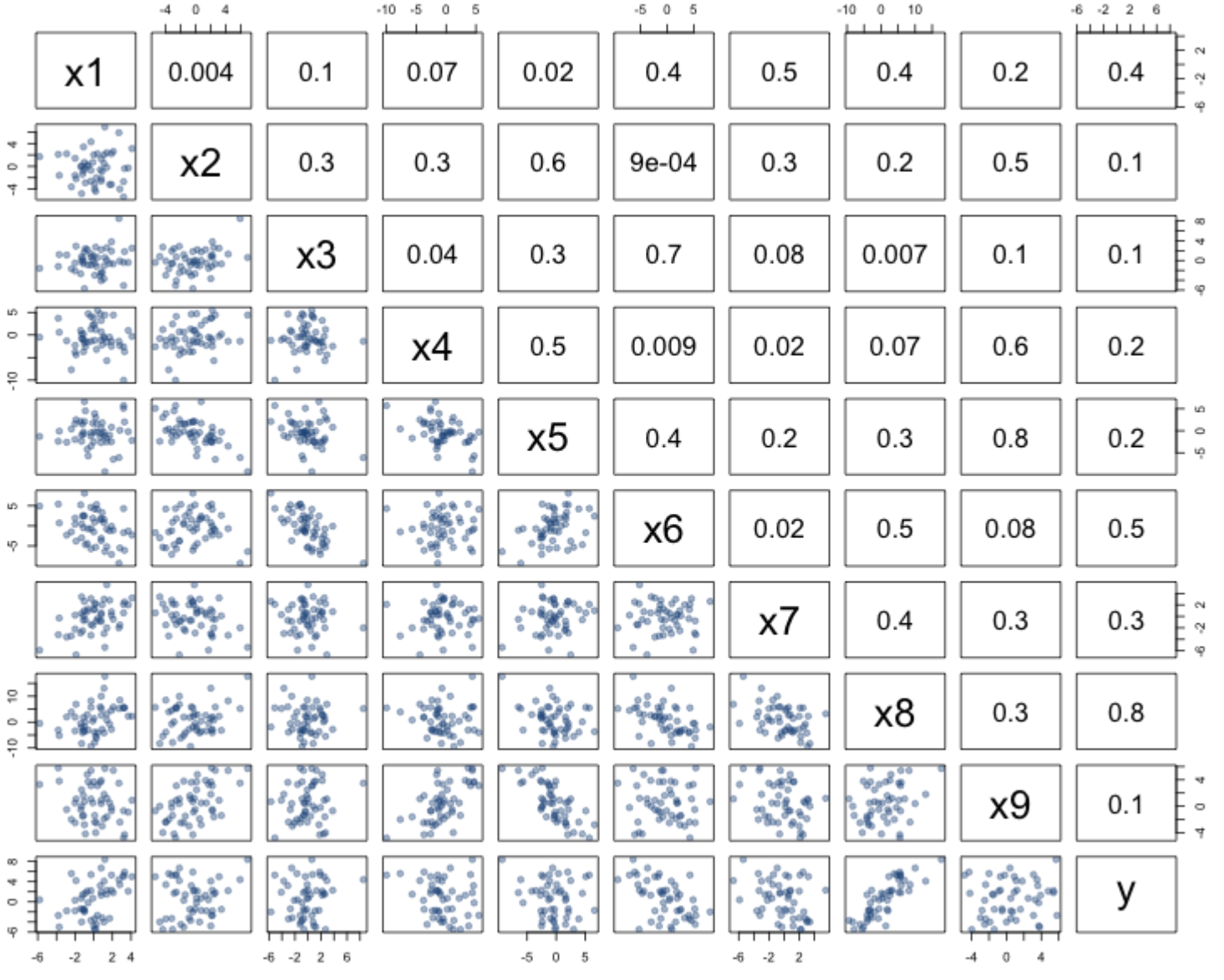
Matejka J and Fitzmaurice G (2017). Same Stats, Different Graphs: Generating Datasets with Varied Appearance and Identical Statistics through Simulated Annealing. Autodesk Research, Toronto Ontario Canada. DOI: 10.1145/3025453.3025912

Graphical tools for model selection

- Underused!
- Fence and its variants (series of papers by Jiang et al, starting with Jiang, Rao, Gu, and Nguyen (2008))
- Stability selection Meinshausen and Bühlmann (2010)
- Model selection curves Müller and Welsh (2010)
- Variable inclusion plots Müller and Welsh (2010) and Murray, Heritier, and Müller (2013)
- Variable selection with `mplot` (this lecture)

Artificial example

Artificial example: Correlations



Artificial example: Full model

```
library(mplot)
lm.art = lm(y ~ ., data = artificialeg)
summary(lm.art)
```

```
##
## Call:
## lm(formula = y ~ ., data = artificialeg)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.7254 -1.2126  0.2456  1.3446  3.4808
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.1002     0.3268  -0.307    0.761
## x1            0.6403     0.6924   0.925    0.361
## x2            0.2574     0.6176   0.417    0.679
## x3           -0.5105     1.2391  -0.412    0.683
## x4           -0.2978     0.2515  -1.184    0.243
## x5            0.3551     0.5982   0.594    0.556
## x6           -0.5428     0.9612  -0.565    0.575
## x7           -0.4280     0.6308  -0.678    0.501
## x8            0.1503     0.6175   0.243    0.809
```

Artificial example: Final model

```
step(lm.art)
```

```
## Start:  AIC=79.3
## y ~ x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x9
##
##        Df Sum of Sq    RSS    AIC
## - x8    1    0.2423 163.94 77.374
## - x3    1    0.6946 164.39 77.512
## - x2    1    0.7107 164.41 77.517
## - x6    1    1.3051 165.00 77.698
## - x5    1    1.4425 165.14 77.739
## - x9    1    1.6065 165.31 77.789
## - x7    1    1.8835 165.58 77.873
## - x1    1    3.4999 167.20 78.358
## - x4    1    5.7367 169.44 79.023
## <none>              163.70 79.301
##
## Step:  AIC=77.37
## y ~ x1 + x2 + x3 + x4 + x5 + x6 + x7 + x9
##
##        Df Sum of Sq    RSS     AIC
## <none>              163.94  77.374
## - x2    1    20.359 184.30  81.227
```

Artificial example: Final model

```
lm.fin = lm(y ~ . - x8, data = artificialeg)
summary(lm.fin)
```

```
##
## Call:
## lm(formula = y ~ . - x8, data = artificialeg)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6881 -1.2352  0.2787  1.4102  3.5420
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.1143     0.3179  -0.360 0.720952
## x1            0.8019     0.1941   4.132 0.000173 ***
## x2            0.4011     0.1778   2.256 0.029438 *
## x3           -0.8083     0.1914  -4.223 0.000131 ***
## x4           -0.3514     0.1196  -2.938 0.005408 **
## x5            0.4927     0.1933   2.548 0.014667 *
## x6           -0.7738     0.1490  -5.194    6e-06 ***
## x7           -0.5772     0.1465  -3.941 0.000309 ***
## x9            0.5478     0.1890   2.899 0.005987 **
## ---
```

Artificial example: Data generating model

The true data generating model is: $y = 0.6\, x_8 + \varepsilon$.

```
art.true = lm(y ~ x8, data = artificialeg)
summary(art.true)
```

```
##
## Call:
## lm(formula = y ~ x8, data = artificialeg)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.6013 -1.2985  0.1303  1.4605  3.8056
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.03235    0.29458    0.11    0.913
## x8           0.54928    0.05264   10.43 6.18e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.046 on 48 degrees of freedom
## Multiple R-squared:  0.694,    Adjusted R-squared:  0.6877
## F-statistic: 108.9 on 1 and 48 DF,  p-value: 6.18e-14
```

Information criteria can be blind

Use resampling and graphs to **see** more!

Bootstrapping regression models

The **bootstrap** is a resampling strategy to generate B training sets

Popular implementations

- **Paired bootstrap**: samples (with replacement) rows of $[\boldsymbol{y}, \boldsymbol{X}]$
- **Weighted bootstrap** (used in `vis()` and `bglmnet()`): mimics the paired bootstrap by keeping $[\boldsymbol{y}, \boldsymbol{X}]$ as is but weighs each observation (row) through using a weights vector, where the weights are sampled from a distribution with expectation 1 (e.g. exponential).
- **Parametric bootstrap** (used in `af()`): estimate the (parametric) distribution of $\boldsymbol{y}$ (or $\boldsymbol{\varepsilon}$) and draw new observations from it
- **Residual bootstrap**: baseline model + bootstrapped error

Stability

- In practice it is important that selected models are stable

Key idea: small changes should have small effects

- Example: Information criterion is *unstable* when $\hat{\alpha}(\lambda)$ is selected with dimension $p_{\hat{\alpha}(\lambda)}$ but, for some small $\delta > 0$, $\hat{\alpha}(\lambda + \delta)$ selected with $p_{\hat{\alpha}(\lambda+\delta)} < p_{\hat{\alpha}(\lambda)}$
- Investigate model selection criterion in a neighborhood of λ

Obtaining stability information

Use resampling: repeatedly calculate how well (the best) model(s) perform given λ, summarise performance with statistics and graphs

We will do the following:

- Investigate model detectability as a function of λ
- Estimate probability that model $\alpha \in \mathcal{A}$ is optimal at λ
- Estimate best model(s) within each size/dimension
- Show model selection curves also for models that are never optimal

Variable inclusion plots

Variable inclusion plots

Aim: To visualise inclusion probabilities as a function of the penalty multiplier $\lambda \in [0, 2\log(n)]$

Procedure

1. Calculate (weighted) bootstrap samples $b = 1, \ldots, B$.
2. For each bootstrap sample, at each λ value, find $\hat{\alpha}_\lambda^{(b)} \in \mathcal{A}$ as the model with smallest $\text{GIC}(\alpha; \lambda) = -2 \times \text{LogLik}(\alpha) + \lambda p_\alpha$.
3. The **inclusion probability** for variable x_j is estimated as $\frac{1}{B} \sum_{b=1}^{B} 1\{j \in \hat{\alpha}_\lambda^{(b)}\}$.

The **inclusion probability** for variable x_j is the proportion of times variable x_j is in the best model

- Müller and Welsh (2010) for linear regression models
- Murray, Heritier, and Müller (2013) for generalised linear models

Artificial example: VIP

```
library(mplot)
vis.art = vis(lm.art)
plot(vis.art, which = "vip", interactive = TRUE)
```

Model stability plots

Artificial example: Loss against size

```
plot(vis.art, which="lvk", interactive = TRUE)
```

Artificial example: Loss against size

```
plot(vis.art, which = "lvk", highlight = "x6", interactive = TRUE)
```

Model stability plots

Aim: To add value to the loss against size plots by choosing a symbol size proportional to a measure of stability

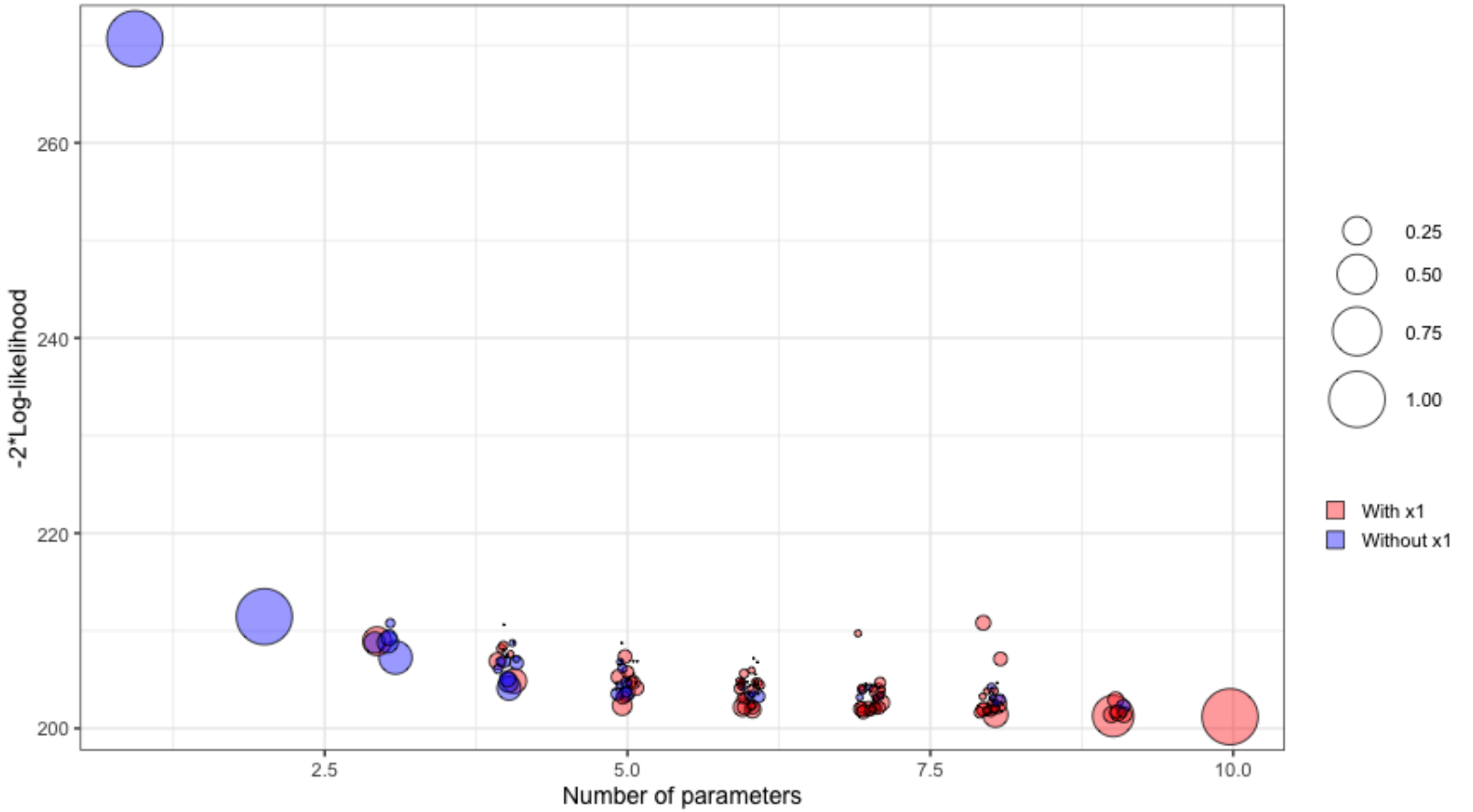
Procedure

1. Calculate (weighted) bootstrap samples $b = 1, \ldots, B$
2. For each bootstrap sample, identify the *best* model at each dimension
3. Add this information to the loss against size plot using model identifiers that are proportional to the frequency with which a model was identified as being *best* at each model size

Murray, Heritier, and Müller (2013) for generalised linear models

Artificial example: Model stability plot

```
plot(vis.art, which = "boot", interactive = FALSE)
```



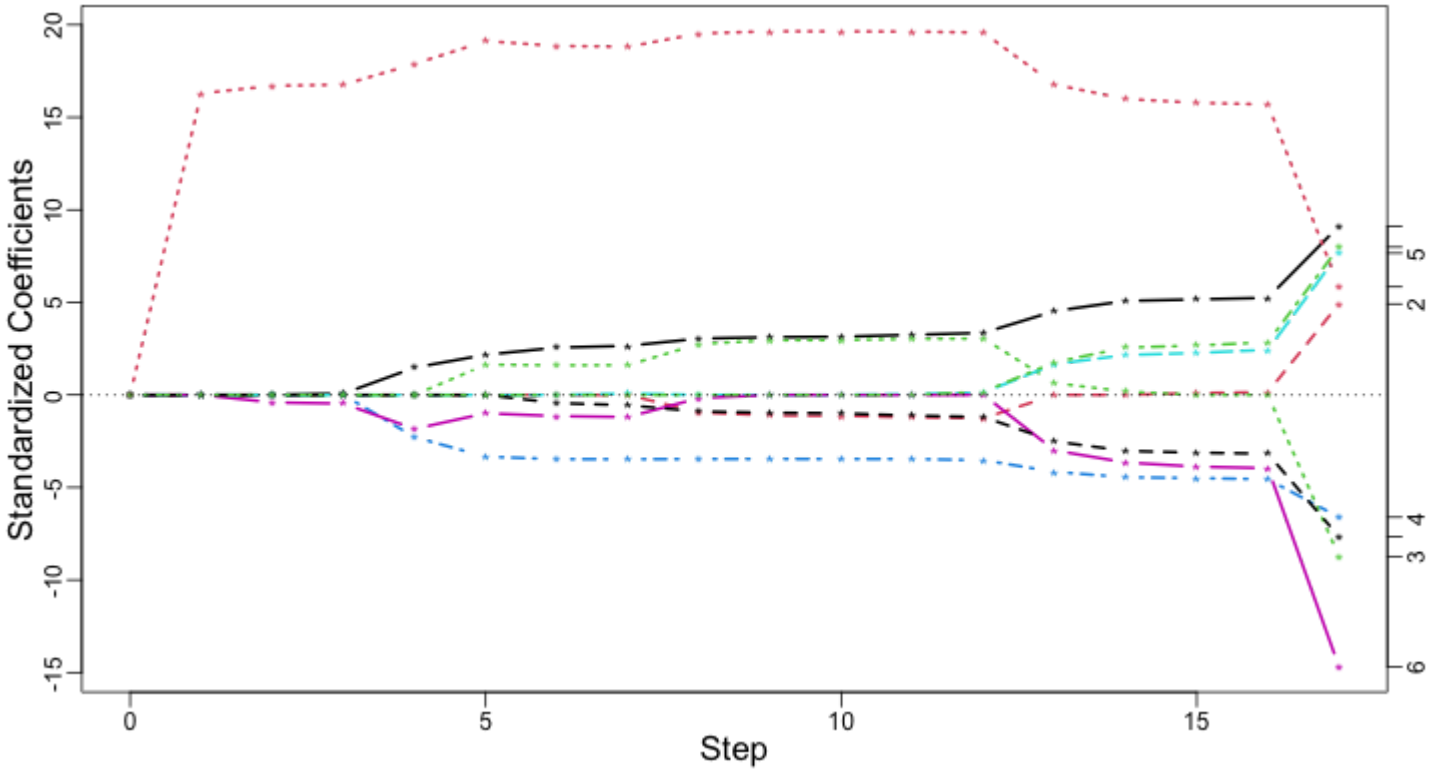
Artificial example: Model stability plot

```
plot(vis.art, which = "boot", interactive = TRUE)
```

Bootstrapping the lasso

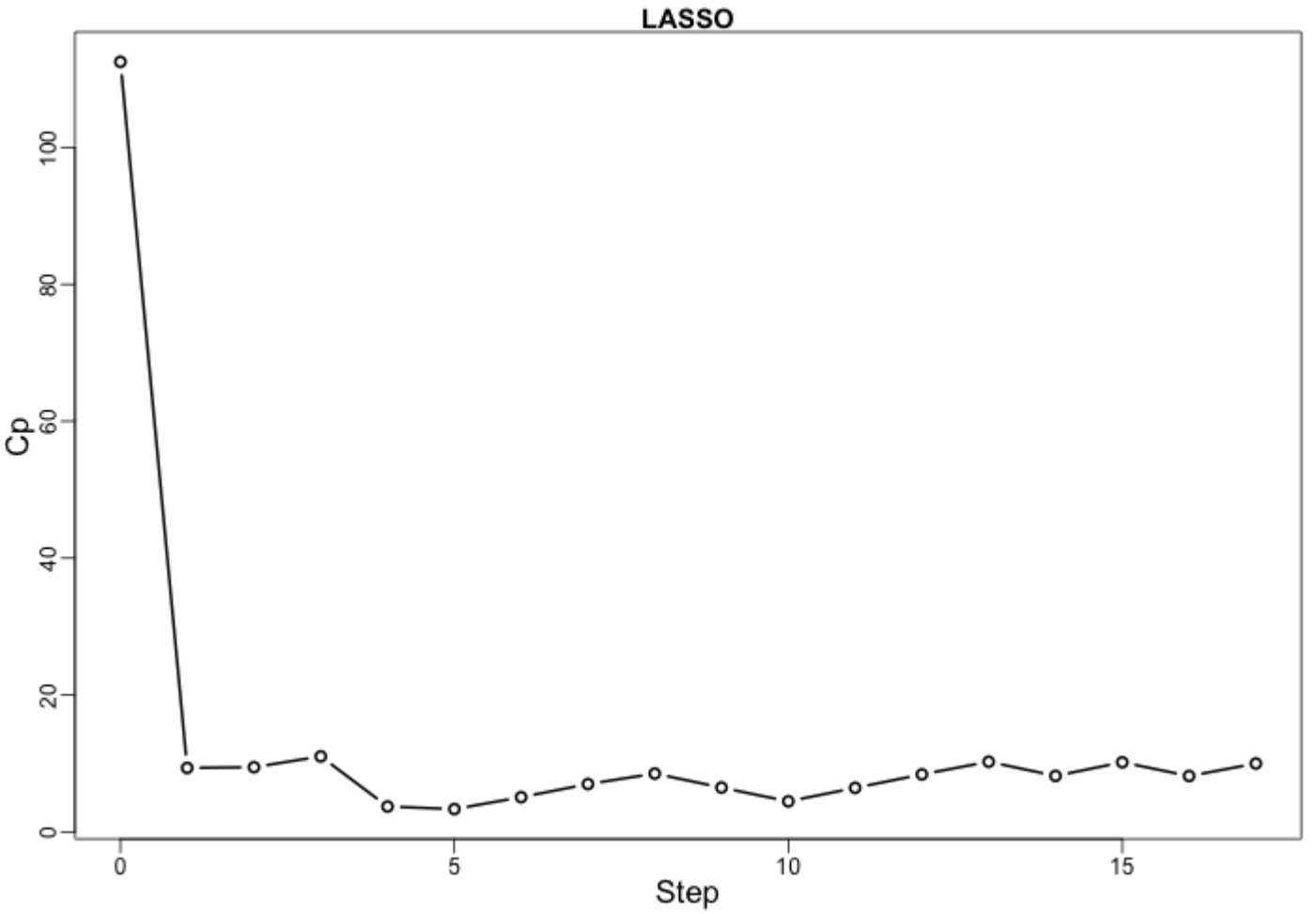
Artificial example: Lasso

```
library(lars)
x = as.matrix(subset(artificialeg, select = -y))
y = as.matrix(subset(artificialeg, select = y))
art.lars=lars(x, y)
plot(art.lars, xvar = "step", breaks = FALSE, lwd = 2, cex.lab = 1.4)
```

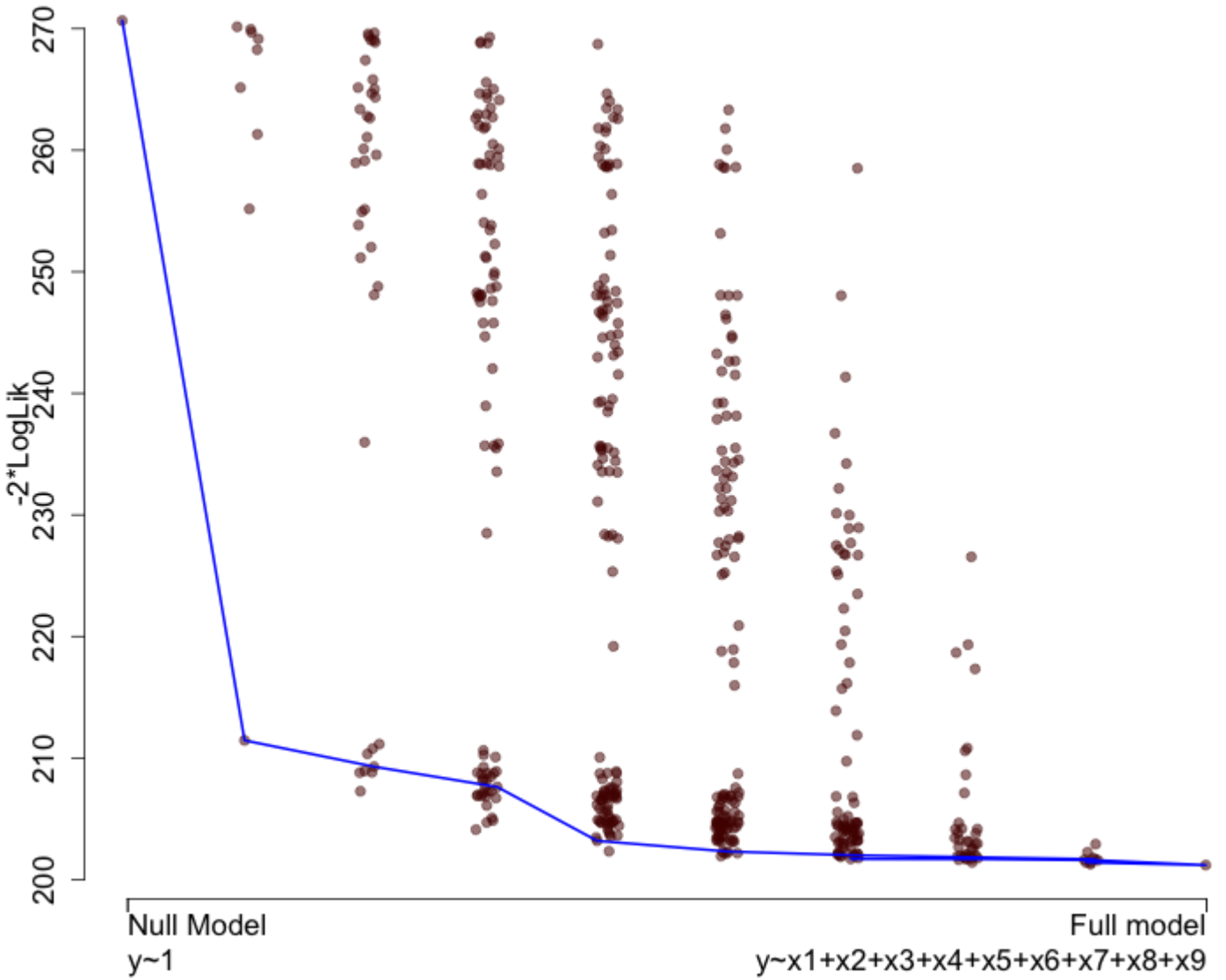


Artificial example: Lasso

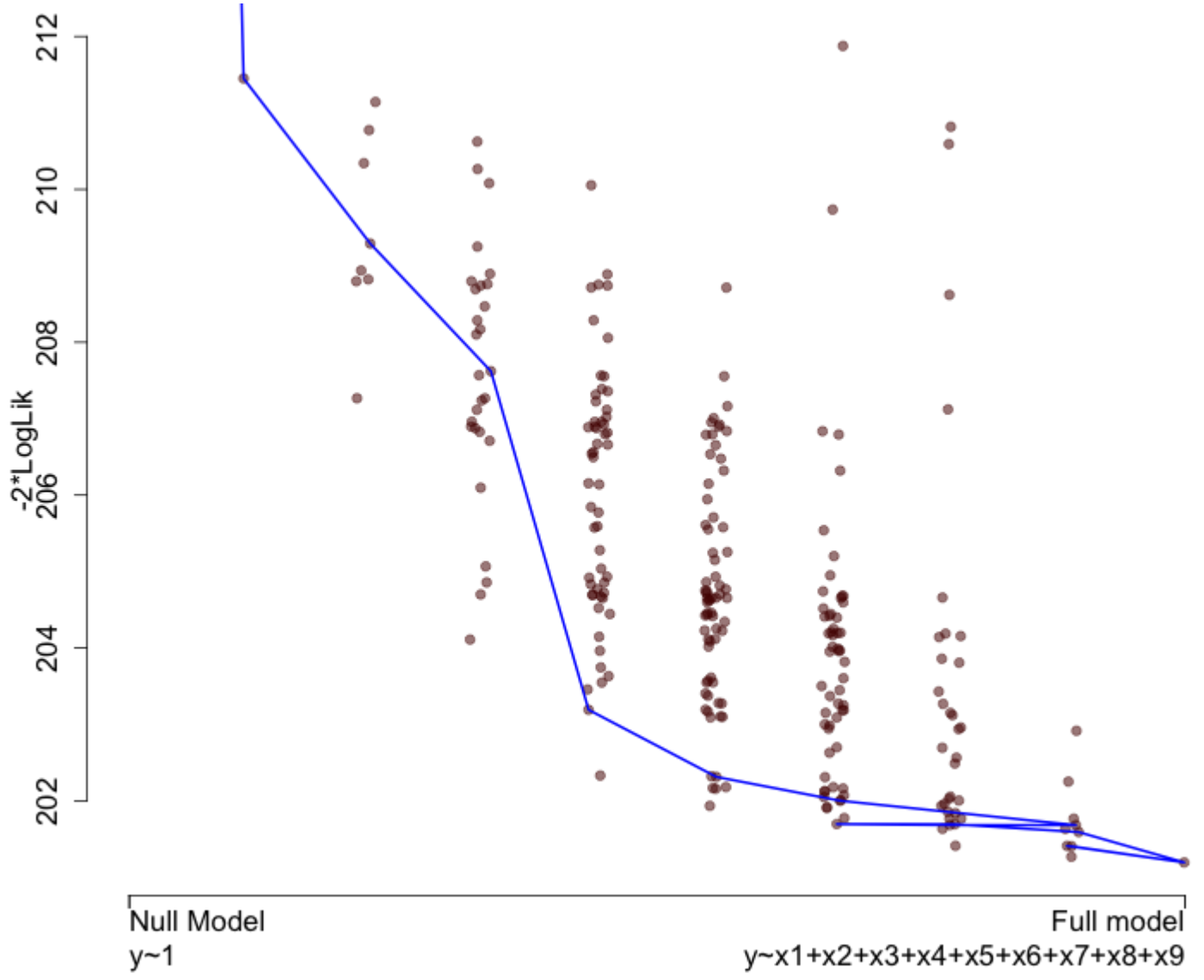
```
plot(art.lars, xvar = "step", plottype = "Cp", lwd = 2, cex.lab = 1.4)
```



Artificial example: Lasso



Artificial example: Lasso (zoomed)



Bootstrapping the lasso

```
bgn.art = bglmnet(lm.art, lambda = seq(0.05, 2.75, 0.1))
plot(bgn.art, which = "boot", interactive = TRUE)
```

Bootstrapping the lasso

```
bgn.art = bglmnet(lm.art)
plot(bgn.art, which = "vip", interactive = TRUE)
```

B3. Subtractive stability measures

$$\hat{Q}(M) = \boldsymbol{s} - \sum_{j \in M} \boldsymbol{s}_j$$

Stability measures

- Use resampling, say B resamples (100, 1000 or more)
- Consider baseline models (e.g. all models on a solution path), say K such models
- Learn from an array of $K \times p \times B$ regression coefficients
- Calculate for each feature $j = 1, \ldots, p$
- Inclusion frequency
- Exclusion frequency
- **Other variable importance measure**

What is a subtractive measure?

Ingenious idea by Jiang, Nguyen and Rao (2011, Statistics and Its Interface)

A **subtractive measure** $\hat{Q}$ satisfies

$$\hat{Q}(M_K) = s - \sum_{j \in M_K} s_j$$

with $s_j \geq 0, k = 1, \ldots, K$.

Think **"lack-of-fit"** measure (like a log-likelihood) with **"benefits"** (something additional to a log-likelihood).

Toy example

- Let the full model be $\{1, 2, 3, 4, 5, 6, 7, 8, 9, 10\}$, i.e. $p = 10$
- Let's assume that $s_1 = |-0.05|$, $s_2 = |-0.19|$, with remaining s_j's being 0.34, 0.21, 0.30, 0.19, 0.02, 0.09, **0.42** and 0.03
- Note: all s_j values are non-negative
- Let $s = \sum s_j = 1.84$
- That model minimizing $\hat{Q}$ over all models with one variable is $\{9\}$
- The best model with two variables is $\{3, 9\}$
- $\hat{Q} \geq 0$ by construction, with equality for the full model

What are the benefits?

Magic in s_j and constructing $\hat{Q}$

- Fast access to identify best model of size d
- Remains fast when bootstrapping

Full model fit sufficient to get well performing s_j's

- $s_j = |\hat{\beta}_j|$ (robust, penalised)
- $s_j = |t_j|$ (standardised coefficients)
- Robust quasi-deviance statistics (differences to full/large baseline model)

Coming soon to the mplot package

- Resample $\{y, \mathbf{X}\}$, e.g. through weighted bootstrap
- Use OLS (LIMMA), Ridge, Lasso, Elastic-net, etc
- Observe $s_j^{(b)}$, $b = 1, \ldots, B$, $j = 1, \ldots, p$
- Find the empirical probability that $s_j > s_k$
- Derive new indices
- Mean bootstrapped rank of $s_j^{(b)}$
- Standard deviation of $\mathrm{rank}(s_j^{(b)})$
- Devise new visualisations
- Preprints: Smith, Günnewig, and Müller (2020) and Smith, Müller, and Günnewig (2020)

A function to bootstrap the full model

```
sstab = function(mf, B = 100) {
  full_coeff = coefficients(mf)
  kf = length(full_coeff)
  coef.res = matrix(ncol = kf, nrow = B)
  colnames(coef.res) = names(full_coeff)
  formula = stats::formula(mf)
  data = model.frame(mf)
  for(i in 1:B){
    wts = stats::rexp(n = length(resid(mf)), rate = 1)
    data$wts = wts
    mod = stats::lm(formula = formula,
                    data = data,
                    weights = wts)
    coef.res[i, ] = coefficients(mod)
  }
  return(coef.res)
}
```

Diabetes example

```
data("diabetes", package = "lars")
x = diabetes$x
y = diabetes$y
df = data.frame(scale(cbind(y, x)))
lm1 = lm(y ~ ., data = df)
sj = sstab(lm1)
round(head(sj[, -1], n = 10), 2)
```

```
##          age   sex  bmi  map    tc   ldl   hdl  tch  ltg   glu
##  [1,] -0.05 -0.19 0.34 0.21 -0.30  0.19 -0.02 0.09 0.42  0.03
##  [2,]  0.02 -0.16 0.29 0.23 -0.21 -0.04  0.08 0.29 0.29  0.02
##  [3,]  0.02 -0.04 0.26 0.17 -0.37  0.20  0.05 0.20 0.43  0.06
##  [4,]  0.00 -0.15 0.32 0.26 -0.39  0.11  0.04 0.16 0.40  0.01
##  [5,] -0.04 -0.17 0.34 0.21 -0.56  0.30  0.10 0.15 0.50  0.06
##  [6,] -0.05 -0.11 0.29 0.18 -0.64  0.47  0.11 0.06 0.50  0.08
##  [7,]  0.01 -0.17 0.28 0.23 -0.31  0.03 -0.05 0.14 0.41  0.08
##  [8,]  0.00 -0.12 0.37 0.15 -0.24  0.06 -0.09 0.06 0.34  0.07
##  [9,]  0.00 -0.04 0.33 0.14 -0.40  0.20  0.11 0.08 0.50  0.08
## [10,]  0.01 -0.17 0.34 0.24 -0.76  0.48  0.17 0.15 0.56 -0.01
```

Diabetes example

```
sj = abs(sj[, -1])
sj_ranks = apply(sj, 1, rank)
head(t(sj_ranks), n = 10)
```

```
##       age sex bmi map tc ldl hdl tch ltg glu
##  [1,]   3   6   9   7  8   5   1   4  10   2
##  [2,]   2   5   9   7  6   3   4   8  10   1
##  [3,]   1   2   8   5  9   7   3   6  10   4
##  [4,]   1   5   8   7  9   4   3   6  10   2
##  [5,]   1   5   8   6 10   7   3   4   9   2
##  [6,]   1   5   7   6 10   8   4   2   9   3
##  [7,]   1   6   8   7  9   2   3   5  10   4
##  [8,]   1   6  10   7  8   2   5   3   9   4
##  [9,]   1   2   8   6  9   7   5   3  10   4
## [10,]   1   4   7   6 10   8   5   3   9   2
```

Diabetes example

```
sj_rank_mean = sort(apply(sj_ranks, 1, mean), decreasing = TRUE)
sj_rank_mean
```

```
##  ltg   tc  bmi  map  ldl  sex  tch  hdl  glu  age
## 9.33 8.81 8.06 6.21 6.21 4.67 4.33 3.40 2.38 1.60
```

```
# tc
table(sj_ranks[5, ])/100
```

```
##
##    1    3    4    5    6    7    8    9   10
## 0.02 0.01 0.02 0.02 0.02 0.02 0.18 0.22 0.49
```

```
# ltg
table(sj_ranks[9, ])/100
```

```
##
##    6    8    9   10
## 0.01 0.03 0.57 0.39
```

References

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Smith, C, S. Müller, and B. Günnewig (2020). "Visualization of variable importance differences". In: *Preprint*, pp. 1-8.

Tarr, G, S. Müller, and A. H. Welsh (2018). "mplot: An R Package for Graphical Model Stability and Variable Selection Procedures". In: *Journal of Statistical Software* 83.9, pp. 1-28. DOI: 10.18637/jss.v083.i09.

```
devtools::session_info(include_base = FALSE)
```

```
## ─ Session info ──────────────────────────────────────────────────────────────
##  setting  value
##  version  R version 4.0.0 (2020-04-24)
##  os       macOS Catalina 10.15.5
##  system   x86_64, darwin17.0
##  ui       X11
##  language (EN)
##  collate  en_AU.UTF-8
##  ctype    en_AU.UTF-8
##  tz       Australia/Sydney
##  date     2020-07-16
##
## ─ Packages ──────────────────────────────────────────────────────────────────
##  package        * version    date       lib source
##  assertthat       0.2.1      2019-03-21 [1] CRAN (R 4.0.0)
##  backports        1.1.8      2020-06-17 [1] CRAN (R 4.0.0)
##  bibtex           0.4.2.2    2020-01-02 [1] CRAN (R 4.0.0)
##  callr            3.4.3      2020-03-28 [1] CRAN (R 4.0.0)
##  caret          * 6.0-86     2020-03-20 [1] CRAN (R 4.0.0)
##  class            7.3-17     2020-04-26 [1] CRAN (R 4.0.0)
##  cli              2.0.2      2020-02-28 [1] CRAN (R 4.0.0)
##  codetools        0.2-16     2018-12-24 [1] CRAN (R 4.0.0)
##  colorspace       1.4-1      2019-03-18 [1] CRAN (R 4.0.0)
##  crayon           1.3.4      2017-09-16 [1] CRAN (R 4.0.0)
##  data.table       1.12.8     2019-12-09 [1] CRAN (R 4.0.0)
##  datasauRus     * 0.1.4      2018-09-20 [1] CRAN (R 4.0.0)
##  desc             1.2.0      2018-05-01 [1] CRAN (R 4.0.0)
##  devtools         2.3.0      2020-04-10 [1] CRAN (R 4.0.0)
##  digest           0.6.25     2020-02-23 [1] CRAN (R 4.0.0)
##  doParallel       1.0.15     2019-08-02 [1] CRAN (R 4.0.0)
##  doRNG            1.8.2      2020-01-27 [1] CRAN (R 4.0.0)
##  dplyr            1.0.0      2020-05-29 [1] CRAN (R 4.0.0)
##  ellipsis         0.3.1      2020-05-15 [1] CRAN (R 4.0.0)
##  evaluate         0.14       2019-05-28 [1] CRAN (R 4.0.0)
##  fansi            0.4.1      2020-01-08 [1] CRAN (R 4.0.0)
##  farver           2.0.3      2020-01-16 [1] CRAN (R 4.0.0)
##  fastmap          1.0.1      2019-10-08 [1] CRAN (R 4.0.0)
##  foreach          1.5.0      2020-03-30 [1] CRAN (R 4.0.0)
##  fs               1.4.1      2020-04-04 [1] CRAN (R 4.0.0)
##  generics         0.0.2      2018-11-29 [1] CRAN (R 4.0.0)
##  ggplot2        * 3.3.2      2020-06-19 [1] CRAN (R 4.0.0)
##  glmnet         * 4.0-2      2020-06-16 [1] CRAN (R 4.0.0)
##  glue             1.4.1      2020-05-13 [1] CRAN (R 4.0.0)
##  googleVis        0.6.5      2020-06-08 [1] CRAN (R 4.0.0)
##  gower            0.2.2      2020-06-23 [1] CRAN (R 4.0.0)
##  gtable           0.3.0      2019-03-25 [1] CRAN (R 4.0.0)
##  htmltools        0.5.0      2020-06-16 [1] CRAN (R 4.0.0)
##  httpuv           1.5.4      2020-06-06 [1] CRAN (R 4.0.0)
##  httr             1.4.1      2019-08-05 [1] CRAN (R 4.0.0)
##  ipred            0.9-9      2019-04-28 [1] CRAN (R 4.0.0)
##  iterators        1.0.12     2019-07-26 [1] CRAN (R 4.0.0)
##  jsonlite         1.7.0      2020-06-25 [1] CRAN (R 4.0.0)
##  knitcitations  * 1.0.10     2019-09-15 [1] CRAN (R 4.0.0)
##  knitr            1.29       2020-06-23 [1] CRAN (R 4.0.0)
##  labeling         0.3        2014-08-23 [1] CRAN (R 4.0.0)
##  lars           * 1.2        2013-04-24 [1] CRAN (R 4.0.0)
##  later            1.1.0.1    2020-06-05 [1] CRAN (R 4.0.0)
##  lattice        * 0.20-41    2020-04-02 [1] CRAN (R 4.0.0)
##  lava             1.6.7      2020-03-05 [1] CRAN (R 4.0.0)
##  leaps            3.1        2020-01-16 [1] CRAN (R 4.0.0)
##  lifecycle        0.2.0      2020-03-06 [1] CRAN (R 4.0.0)
##  lubridate        1.7.9      2020-06-08 [1] CRAN (R 4.0.0)
##  magrittr         1.5        2014-11-22 [1] CRAN (R 4.0.0)
##  MASS             7.3-51.6   2020-04-26 [1] CRAN (R 4.0.0)
##  Matrix         * 1.2-18     2019-11-27 [1] CRAN (R 4.0.0)
##  memoise          1.1.0      2017-04-21 [1] CRAN (R 4.0.0)
##  mime             0.9        2020-02-04 [1] CRAN (R 4.0.0)
##  ModelMetrics     1.2.2.2    2020-03-17 [1] CRAN (R 4.0.0)
##  mplot          * 1.0.4      2020-02-15 [1] CRAN (R 4.0.0)
##  munsell          0.5.0      2018-06-12 [1] CRAN (R 4.0.0)
##  nlme             3.1-148    2020-05-24 [1] CRAN (R 4.0.0)
##  nnet             7.3-14     2020-04-26 [1] CRAN (R 4.0.0)
##  pillar           1.4.4      2020-05-05 [1] CRAN (R 4.0.0)
##  pkgbuild         1.0.8      2020-05-07 [1] CRAN (R 4.0.0)
##  pkgconfig        2.0.3      2019-09-22 [1] CRAN (R 4.0.0)
##  pkgload          1.1.0      2020-05-29 [1] CRAN (R 4.0.0)
##  plyr             1.8.6      2020-03-03 [1] CRAN (R 4.0.0)
##  prettyunits      1.1.1      2020-01-24 [1] CRAN (R 4.0.0)
##  pROC             1.16.2     2020-03-19 [1] CRAN (R 4.0.0)
##  processx         3.4.2      2020-02-09 [1] CRAN (R 4.0.0)
##  prodlim          2019.11.13 2019-11-17 [1] CRAN (R 4.0.0)
##  promises         1.1.1      2020-06-09 [1] CRAN (R 4.0.0)
##  ps               1.3.3      2020-05-08 [1] CRAN (R 4.0.0)
##  purrr            0.3.4      2020-04-17 [1] CRAN (R 4.0.0)
##  R6               2.4.1      2019-11-12 [1] CRAN (R 4.0.0)
##  Rcpp             1.0.4.6    2020-04-09 [1] CRAN (R 4.0.0)
##  recipes          0.1.13     2020-06-23 [1] CRAN (R 4.0.0)
##  RefManageR       1.2.12     2019-04-03 [1] CRAN (R 4.0.0)
##  remotes          2.1.1      2020-02-15 [1] CRAN (R 4.0.0)
##  reshape2         1.4.4      2020-04-09 [1] CRAN (R 4.0.0)
##  rlang            0.4.6      2020-05-02 [1] CRAN (R 4.0.0)
##  rmarkdown        2.3        2020-06-18 [1] CRAN (R 4.0.0)
##  rngtools         1.5        2020-01-23 [1] CRAN (R 4.0.0)
##  rpart            4.1-15     2019-04-12 [1] CRAN (R 4.0.0)
##  rprojroot        1.3-2      2018-01-03 [1] CRAN (R 4.0.0)
##  scales           1.1.1      2020-05-11 [1] CRAN (R 4.0.0)
##  sessioninfo      1.1.1      2018-11-05 [1] CRAN (R 4.0.0)
##  shape            1.4.4      2018-02-07 [1] CRAN (R 4.0.0)
##  shiny            1.5.0      2020-06-23 [1] CRAN (R 4.0.0)
##  shinydashboard   0.7.1      2018-10-17 [1] CRAN (R 4.0.0)
##  stringi          1.4.6      2020-02-17 [1] CRAN (R 4.0.0)
##  stringr          1.4.0      2019-02-10 [1] CRAN (R 4.0.0)
```