An Introduction to `islasso`

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Abstract

In this short note we present and briefly discuss the R package islasso dealing with regression models having a large number of covariates. Estimation is carried out by penalizing the coefficients via a quasi-lasso penalty, wherein the nonsmooth lasso penalty is replaced by its smooth counterpart determined iteratively by data according to the induced smoothing idea. The package includes functions to estimate the model and to test for linear hypothesis on linear combinations of relevant coefficients. We illustrate R code throughout a worked example, by avoiding intentionally to report details and extended bibliography.

Introduction

Let $\mathbf{y} = \mathbf{X}\beta + \epsilon$ be the linear model of interest with usual zero-means and homoscedastic errors. As usual, $\mathbf{y} = (y_1, \ldots, y_n)^T$ is the response vector, $\mathbf{X}$ is the $n \times p$ design matrix (having p quite large) with regression coefficients β. When interest lies in selecting the non-noise covariates and estimating the relevant effect, one assumes the lasso penalized objective function (Tibshirani, 1996),

$$\frac{1}{2}||\mathbf{y} - \mathbf{X}\beta||_2^2 + \lambda||\beta||_1$$

The R functions

The main function of the package are *islasso()* where the user supplies the model formula as in the usual *lm* or *glm* functions, i.e.

```
islasso(formula, family = gaussian, lambda, alpha = 1, data, weights, subset, offset,
    unpenalized, contrasts = NULL, control = is.control())
```

and *islasso.path* used to fit the regularization path via the induced smoothed lasso framework, i.e.

```
islasso.path(formula, family = gaussian, lambda = NULL, nlambda = 100, lambda.min.ratio = ifelse(nobs <
    nvars, 0.001, 1e-05), alpha = 1, data, weights, subset, offset, unpenalized,
    contrasts = NULL, control = is.control())
```

family accepts specification of family and link function as in Table 1, *lambda* is the tuning parameter, *alpha* is elastic-net mixing parameter, *nlambda* is the number of lambda values, *lambda.min.ratio* is the smallest value for lambda (as a fraction of lambda.max), and *unpenalized* allows to indicate covariates with unpenalized coefficients.

Table 1. Families and link functions allowed in islasso

family	link
gaussian	identity
binomial	logit, probit
poisson	log
gamma	identity, log, inverse

The fitter functions are `islasso.fit()` and `islasso.path.fit()` which reads as

```
islasso.fit(X, y, family = gaussian(), lambda, alpha = 1, intercept = FALSE, weights = NULL,
    offset = NULL, unpenalized = NULL, control = is.control())
```

and

```
islasso.path.fit(X, y, family = gaussian(), lambda, nlambda, lambda.min.ratio, alpha = 1,
    intercept = FALSE, weights = NULL, offset = NULL, unpenalized = NULL, control = is.control())
```

whose actually implements the estimating algorithm as described in the paper. The *lambda* argument in *islasso.fit* and *islasso* specifies the positive tuning parameter in the penalized objective. Any non-negative value can be provided, but if missing, it is computed via K-fold cross validation by the function *cv.glmnet()* from package **glmnet**. The number of folds being used can be specified via the argument *nfolds* of the auxiliary function *is.control()*. The *lambda* argument in *islasso.path.fit* and *islasso.path* specifies the sequence of positive tuning parameters, user supplied or automatically computed based on *nlambda* and *lambda.min.ratio*.

A worked example: the Diabetes data set

We use the well-known **diabetes** dataset available in the **lars** package. The data refer to $n = 442$ patients enrolled to investigate a measure of disease progression one year after the baseline. There are ten covariates, (age, sex, bmi (body mass index), map (average blood pressure) and several blood serum measurements (tc, ldl, hdl, tch, ltg, glu). The matrix *x2* in the dataframe also includes second-order terms, namely first-order interactions between covariates, and quadratic terms for the continuous variables.

To select the important terms in the regression equation we could simply apply the lasso using the R package **glmnet**

```
library(islasso)

data("diabetes", package = "islasso")

a1 <- with(diabetes, cv.glmnet(x2, y))
n <- nrow(diabetes)
a1$lambda.min * n
```

```
> [1] 1224.772
```

```
b <- drop(coef(a1, "lambda.min", exact = TRUE))
length(b[b != 0])
```

```
> [1] 16
```

Ten-fold cross validation "selects" $\lambda = 1224.772$. corresponding to 16 non null coefficients

```
names(b[b != 0])
```

```
>  [1] "(Intercept)" "sex"         "bmi"         "map"         "hdl"
>  [6] "ltg"         "glu"         "age^2"       "bmi^2"       "glu^2"
> [11] "age:sex"     "age:map"     "age:ltg"     "age:glu"     "sex:map"
> [16] "bmi:map"
```

The last six estimates are

```
tail(b[b != 0])
```

```
>    age:sex    age:map    age:ltg    age:glu    sex:map    bmi:map
> 111.670599  30.380499  10.690284  10.484821   3.963129  88.148806
```

A reasonable question is if all the "selected" coefficients are significant in the model. Unfortunately lasso regression does not return standard errors due to nonsmoothness of objective, and some alternative approaches have been proposed., including the (Lockhart et al., 2013). Among the (few) strategies, including the 'covariance test', the 'post-selection inference' and the '(modified) residual bootstrap', here we illustrate the R package **islasso** implementing the recent 'quasi' lasso approach based on the induced smoothing idea (Brown and Wang, 2005) as discussed in Cilluffo et al. (2019)

While the optimal lambda could be selected (without supplying any value to *lambda*), we use optimal value minimizing a specific criterion chosen between AIC, BIC, AICc, BIC, GCV or GIC. From version 1.4.0 of the R package **islasso** optimal strategy is to built the regularization path

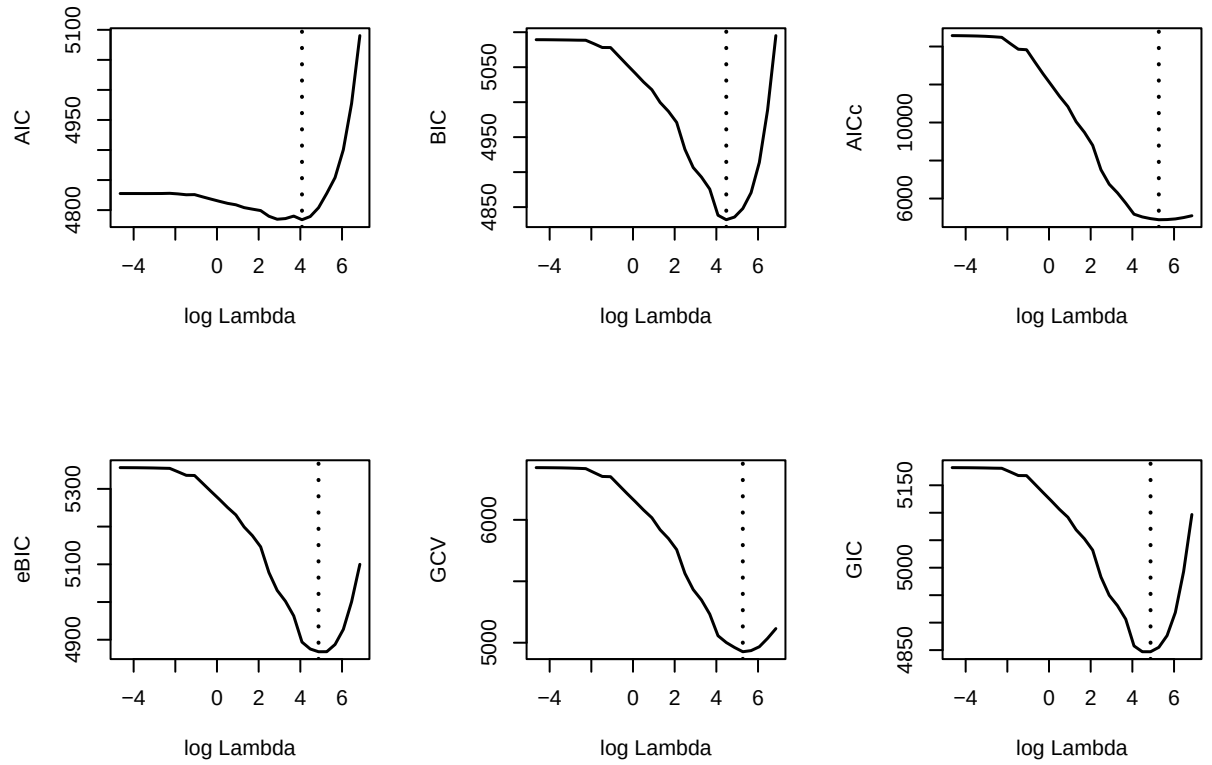
```
out <- islasso.path(y ~ x2, data = diabetes, nlambda = 30L)
out
```

```
>
> Call:
> islasso.path(formula = y ~ x2, nlambda = 30L, data = diabetes)
>
> Coefficients:
>      lambda      df       phi     deviance     logLik
```

```
> 1    0.0096 63.9746 2825.8687 1068250.0676 -2349.8100
> 2    0.0143 63.9617 2825.8380 1068275.0565 -2349.8152
> 3    0.0212 63.9418 2825.8335 1068329.5460 -2349.8265
> 4    0.0315 63.9110 2825.9155 1068447.6038 -2349.8509
> 5    0.0469 63.8632 2826.2291 1068701.1497 -2349.9033
> 6    0.0697 63.7908 2827.1134 1069240.3444 -2350.0148
> 7    0.1036 63.6954 2829.4514 1070394.4412 -2350.2532
> 8    0.1540 62.7071 2828.4990 1072829.4824 -2350.7554
> 9    0.2290 61.7457 2824.6327 1074078.8282 -2351.0126
> 10   0.3405 61.6677 2826.6303 1075058.7383 -2351.2141
> 11   0.5063 59.5786 2813.3243 1075875.5020 -2351.3820
> 12   0.7528 57.4605 2801.1740 1077161.9236 -2351.6461
> 13   1.1193 55.3737 2789.7922 1078607.0325 -2351.9423
> 14   1.6643 53.1677 2780.2609 1081055.1025 -2352.4434
> 15   2.4745 51.0710 2776.5738 1085443.3550 -2353.3386
> 16   3.6792 47.7771 2765.0426 1090043.1190 -2354.2732
> 17   5.4705 45.2957 2763.1675 1096160.3554 -2355.5100
> 18   8.1337 42.0030 2766.2650 1106497.7198 -2357.5843
> 19  12.0935 34.8969 2747.4251 1118485.1931 -2359.9657
> 20  17.9812 29.7707 2745.9953 1131979.8455 -2362.6161
> 21  26.7351 26.1570 2773.8497 1153485.9030 -2366.7755
> 22  39.7509 20.9631 2831.1191 1192005.6370 -2374.0350
> 23  59.1033 13.2863 2839.7888 1217456.3617 -2378.7040
> 24  87.8773 10.4271 2892.3612 1248264.6517 -2384.2269
> 25 130.6596  7.7723 3007.4993 1305939.6066 -2394.2091
> 26 194.2702  4.8935 3195.3473 1396706.9730 -2409.0591
> 27 288.8491  4.0324 3396.8386 1487705.1863 -2423.0081
> 28 429.4729  3.2662 3779.3045 1658108.6614 -2446.9739
> 29 638.5583  2.8155 4502.7361 1977531.9986 -2485.9079
> 30 949.4353  1.1610 5835.2820 2572420.1596 -2544.0304
```

and then to choose the best tuning parameter through the one of the criteria listed above using the function *GoF.islasso.path*, e.g.,

```
lmb.best <- GoF.islasso.path(out)
```

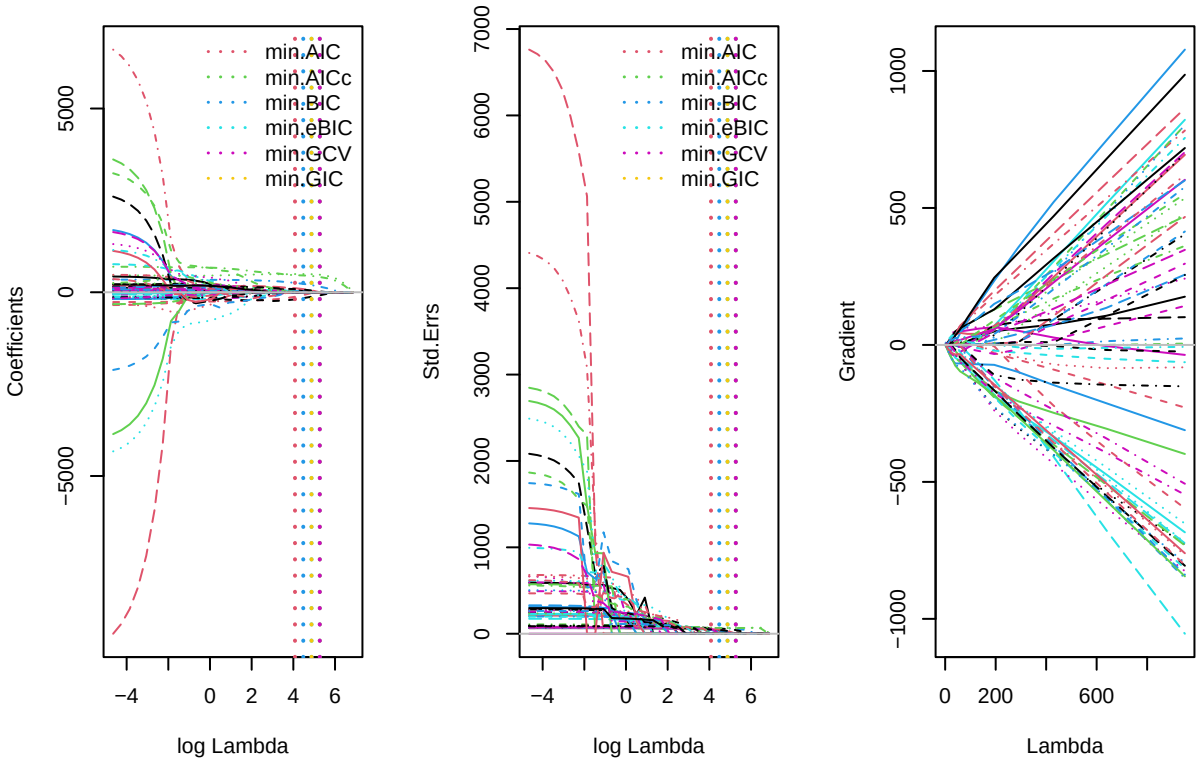



```
lmb.best$lambda.min
```

```
>       AIC       BIC      AICc      eBIC       GCV       GIC
>  59.10332  87.87729 194.27022 130.65964 194.27022 130.65964
```

Using also the regularization path is very usefull to have more insights about coefficients, standard errors and gradient profile

```
par(mfrow = c(1, 3))
plot(out, yvar = "coefficients")
plot(out, yvar = "se")
plot(out, yvar = "gradient")
```



Once selected the best lambda value minimizing for example the BIC criterion, the last step of the strategy consists on fitting a new islasso model.

```
lambda.bic <- lmb.best$lambda.min["BIC"]
out2 <- islasso(y ~ x2, data = diabetes, lambda = lambda.bic)
out2
```

```
>
> Call:
> islasso(formula = y ~ x2, lambda = lambda.bic, data = diabetes)
>
> Coefficients:
> (Intercept)        x2age        x2sex        x2bmi        x2map         x2tc
>   1.521e+02    0.000e+00   -7.608e+01    4.947e+02    2.283e+02    0.000e+00
>       x2ldl        x2hdl        x2tch        x2ltg        x2glu      x2age^2
>   0.000e+00   -1.603e+02    0.000e+00    4.571e+02    2.346e+01    0.000e+00
>     x2bmi^2      x2map^2      x2tc^2      x2ldl^2      x2hdl^2      x2tch^2
>   4.060e+01    0.000e+00    0.000e+00    0.000e+00    0.000e+00    0.000e+00
>     x2ltg^2      x2glu^2    x2age:sex    x2age:bmi    x2age:map     x2age:tc
>   0.000e+00    5.616e+01    8.551e+01    0.000e+00    3.307e+01    0.000e+00
>   x2age:ldl    x2age:hdl    x2age:tch    x2age:ltg    x2age:glu    x2sex:bmi
>   0.000e+00    0.000e+00    0.000e+00    1.870e-04    1.936e+01    0.000e+00
>   x2sex:map     x2sex:tc    x2sex:ldl    x2sex:hdl    x2sex:tch    x2sex:ltg
>   0.000e+00    0.000e+00    0.000e+00    0.000e+00    0.000e+00    0.000e+00
>   x2sex:glu    x2bmi:map     x2bmi:tc    x2bmi:ldl    x2bmi:hdl    x2bmi:tch
>   0.000e+00    7.162e+01    0.000e+00    0.000e+00    0.000e+00    0.000e+00
>   x2bmi:ltg    x2bmi:glu     x2map:tc    x2map:ldl    x2map:hdl    x2map:tch
>   0.000e+00    0.000e+00    0.000e+00    0.000e+00    0.000e+00    0.000e+00
>   x2map:ltg    x2map:glu     x2tc:ldl     x2tc:hdl     x2tc:tch     x2tc:ltg
```

```
>   0.000e+00    0.000e+00    0.000e+00    0.000e+00    0.000e+00    0.000e+00
>    x2tc:glu    x2ldl:hdl    x2ldl:tch    x2ldl:ltg    x2ldl:glu    x2hdl:tch
>   0.000e+00    0.000e+00    0.000e+00    0.000e+00    0.000e+00    0.000e+00
>   x2hdl:ltg    x2hdl:glu    x2tch:ltg    x2tch:glu    x2ltg:glu
>   0.000e+00    0.000e+00    0.000e+00    1.100e-05    0.000e+00
>
> Degrees of Freedom: 441 Total (i.e. Null);  431.6 Residual
> Null Deviance: 2621000
> Residual Deviance: 1248000
> AIC: 4789
> Lambda: 87.88
```

The **summary** method quickly returns the main output of the fitted model, including point estimates, standard errors and p-values. Visualizing estimates for all covariates could be somewhat inconvenient, especially when the number of covariates is large, thus we decide to print estimates only if the pvalue is less than a threshold value. We use *0.10*

```
summary(out2, pval = 0.1)
```

```
>
> Call:
> islasso(formula = y ~ x2, lambda = lambda.bic, data = diabetes)
>
> Residuals:
>      Min       1Q   Median       3Q      Max
> -136.951  -40.268   -4.936   36.309  144.918
>
>             Estimate Std. Error     Df z value Pr(>|z|)
> (Intercept)  152.133      2.558  1.000  59.471  < 2e-16 ***
> x2sex        -76.084     45.237  0.754  -1.682 0.092588 .
> x2bmi        494.728     67.802  1.000   7.297 2.95e-13 ***
> x2map        228.283     62.556  0.998   3.649 0.000263 ***
> x2hdl       -160.329     60.827  0.957  -2.636 0.008394 **
> x2ltg        457.115     66.245  1.000   6.900 5.19e-12 ***
> x2age:sex     85.505     45.665  0.828   1.872 0.061147 .
> x2bmi:map     71.618     42.849  0.754   1.671 0.094639 .
> ---
> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> (Dispersion parameter for gaussian family taken to be 2892.374)
>
>     Null deviance: 2621009  on 441.0  degrees of freedom
> Residual deviance: 1248265  on 431.6  degrees of freedom
> AIC: 4789.3
> Lambda: 87.877
>
> Number of Newton-Raphson iterations: 1000
```

In addition to the usual information printed by the summary method, the output also includes the column *Df* representing the degrees of freedom of each coefficient. Their sum is used to quantify the model complexity

```
sum(out2$internal$hi)
```

```
> [1] 10.42884
```

and the corresponding residual degrees of freedom () as reported above. The Wald test (column *z value*) and p-values can be used to assess important or significant covariates. Results suggest that variables bmi, map, hdl and ltg to predict the measure of diabetes progression, while sex and two interactions age:sex and bmi:map are borderline informative. Just to be clear, another way to obtain a similar result without computing the regularization path, is to use the function *aic.islasso* which requires a preliminary islasso fit object and a specification of the criterion to be used. Hence

```
lambda.bic2 <- aic.islasso(out2, method = "BIC", interval = c(1, 100))
```

```
>
> Optimization through BIC
>
> lambda =   38.8146 BIC =  4878.46285
> lambda =   62.1854 BIC =  4833.27143
> lambda =   76.6293 BIC =  4829.91482
> lambda =   71.9900 BIC =  4829.24032
> lambda =   72.4230 BIC =  4829.30009
> lambda =   68.2450 BIC =  4828.75161
> lambda =   65.9304 BIC =  4834.31100
> lambda =   69.6754 BIC =  4828.93141
> lambda =   67.3609 BIC =  4828.65226
> lambda =   66.8145 BIC =  4834.53781
> lambda =   67.6986 BIC =  4828.70500
> lambda =   67.1522 BIC =  4834.63262
> lambda =   67.4899 BIC =  4828.65488
> lambda =   67.4097 BIC =  4828.65199
> lambda =   67.3936 BIC =  4828.71979
> lambda =   67.4403 BIC =  4828.75227
> lambda =   67.4214 BIC =  4828.80288
> lambda =   67.4036 BIC =  4828.65164
> lambda =   67.3998 BIC =  4828.65073
> lambda =   67.3974 BIC =  4828.64370
> lambda =   67.3960 BIC =  4828.64366
> lambda =   67.3967 BIC =  4828.65205
> lambda =   67.3951 BIC =  4828.71997
> lambda =   67.3956 BIC =  4828.65192
> lambda =   67.3962 BIC =  4828.64369
> lambda =   67.3958 BIC =  4828.65195
> lambda =   67.3961 BIC =  4828.65197
> lambda =   67.3959 BIC =  4828.64365
> lambda =   67.3959 BIC =  4828.64365
```

```
out3 <- update(out2, lambda = lambda.bic2)
summary(out3, pval = 0.1)
```

```
>
> Call:
> islasso(formula = y ~ x2, lambda = lambda.bic2, data = diabetes)
```

```
>
> Residuals:
>     Min      1Q  Median      3Q     Max
> -138.64  -40.41   -4.44   34.85  144.27
>
>             Estimate Std. Error     Df z value Pr(>|z|)
> (Intercept)  152.133      2.538  1.000  59.934  < 2e-16 ***
> x2sex       -107.726     53.134  0.888  -2.027  0.04262 *
> x2bmi        495.528     68.679  1.000   7.215 5.39e-13 ***
> x2map        246.388     62.757  0.999   3.926 8.63e-05 ***
> x2hdl       -182.339     63.090  0.983  -2.890  0.00385 **
> x2ltg        463.155     66.163  1.000   7.000 2.56e-12 ***
> x2age:sex    104.159     49.878  0.907   2.088  0.03677 *
> x2bmi:map     82.898     47.324  0.828   1.752  0.07982 .
> ---
> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> (Dispersion parameter for gaussian family taken to be 2847.905)
>
>     Null deviance: 2621009  on 441.0  degrees of freedom
> Residual deviance: 1227099  on 430.9  degrees of freedom
> AIC: 4783.1
> Lambda: 67.396
>
> Number of Newton-Raphson iterations: 1000
```

Comparisons between methods to select the tuning parameter and further discussions are out of the scope of this short note. We conclude this note by emphasizing that **islasso** also accepts the so-called elastic-net penalty, such that

$$\frac{1}{2}||\mathbf{y}-\mathbf{X}\beta||_2^2+\lambda\{\alpha||\beta||_1+\frac{1}{2}(1-\alpha)||\beta||_2^2\}$$

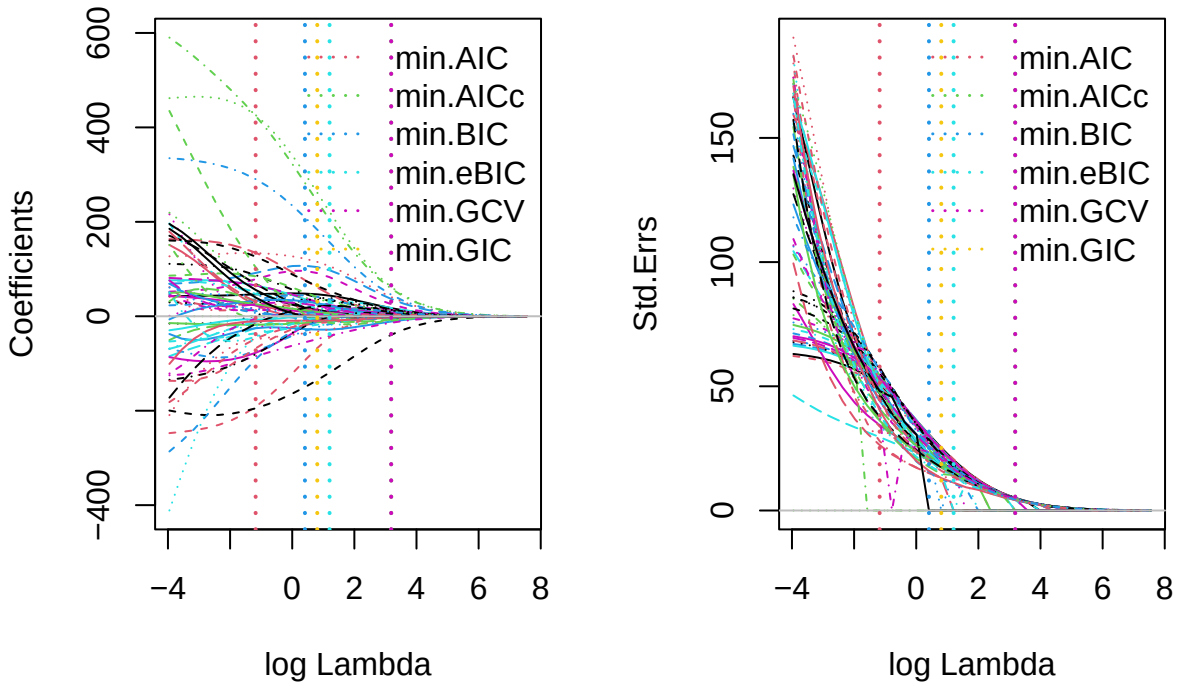
where $0 \leq \alpha \leq 1$ is the mixing parameter to be specified in *islasso()* and *islasso.path()* via the argument *alpha*, e.g.

```
# update the islasso path to fit an elastic-net model
out4 <- update(out, alpha = 0.5)
out4
```

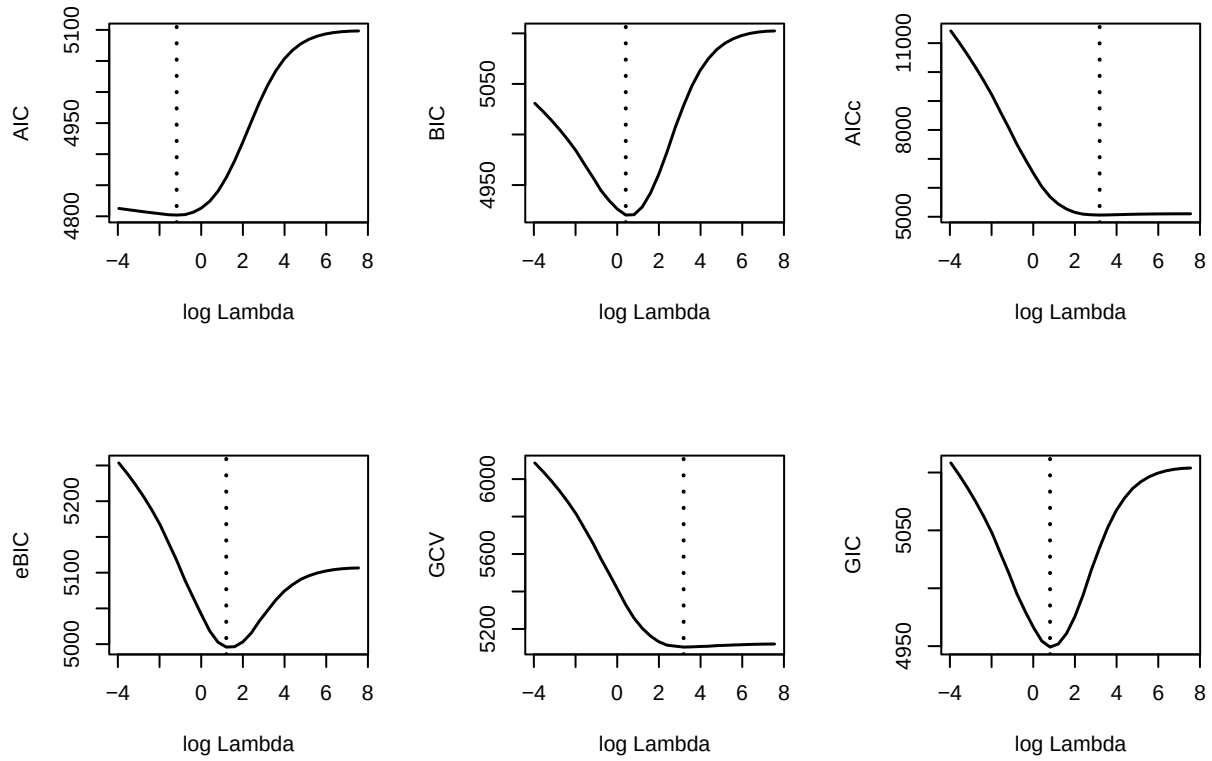
```
>
> Call:
> islasso.path(formula = y ~ x2, nlambda = 30L, alpha = 0.5, data = diabetes)
>
> Coefficients:
>       lambda      df       phi     deviance     logLik
> 1     0.0192 53.3378 2788.1530 1083649.6469 -2352.9731
> 2     0.0285 51.8074 2785.2072 1086767.2213 -2353.6080
> 3     0.0424 50.1275 2783.2995 1090698.4552 -2354.4060
> 4     0.0630 48.2721 2782.6748 1095616.6721 -2355.4003
> 5     0.0937 46.2059 2783.6291 1101743.9506 -2356.6328
> 6     0.1394 43.8866 2786.8431 1109479.6886 -2358.1791
> 7     0.2072 41.0769 2792.4528 1119558.9740 -2360.1778
> 8     0.3081 38.1354 2806.0099 1133248.0879 -2362.8636
> 9     0.4581 34.7083 2830.2195 1152724.9908 -2366.6296
```

```
> 10    0.6811 31.3060 2874.6662 1180608.0556 -2371.9117
> 11    1.0127 27.5587 2943.2851 1219818.8439 -2379.1324
> 12    1.5057 23.4888 3042.6670 1273390.0639 -2388.6311
> 13    2.2387 19.6313 3182.1778 1344052.3655 -2400.5665
> 14    3.3286 16.1734 3368.4809 1434388.7081 -2414.9424
> 15    4.9491 13.0060 3603.1211 1545717.4335 -2431.4621
> 16    7.3585 10.1515 3882.8559 1676805.5672 -2449.4520
> 17   10.9409  7.7452 4196.5842 1822386.8243 -2467.8517
> 18   16.2674  5.9856 4524.5562 1972771.5581 -2485.3753
> 19   24.1870  4.4169 4836.4617 2116353.6704 -2500.9017
> 20   35.9623  3.3391 5114.5917 2243571.5288 -2513.8024
> 21   53.4703  2.5363 5345.3425 2349083.7275 -2523.9588
> 22   79.5018  1.9372 5525.9084 2431746.5982 -2531.6019
> 23  118.2066  1.5835 5662.1775 2493716.6510 -2537.1633
> 24  175.7546  1.3146 5760.5054 2538570.5856 -2541.1030
> 25  261.3193  1.1559 5829.6730 2569977.0284 -2543.8204
> 26  388.5404  1.0666 5877.0083 2591369.2249 -2545.6524
> 27  577.6982  1.0271 5907.8717 2605211.2844 -2546.8297
> 28  858.9459  1.0138 5926.8651 2613665.6463 -2547.5457
> 29 1277.1167  1.0051 5938.4931 2618845.1503 -2547.9833
> 30 1898.8705  1.0002 5943.1748 2620938.7814 -2548.1599
```

```r
# some diagnostic plot
par(mfrow = c(1, 2))
plot(out4, yvar = "coefficients")
plot(out4, yvar = "se")
```




```r
# select the best tuning parameter
lmb.best2 <- GoF.islasso.path(out4)
```




```
lmb.best2$lambda.min
```

```
>        AIC        BIC       AICc       eBIC        GCV        GIC
>  0.3080847  1.5056683 24.1870426  3.3285790 24.1870426  2.2386907
```

```
# fit a new islasso model with elastic-net penalty
lambda.bic3 <- lmb.best2$lambda.min["BIC"]
out5 <- update(out2, alpha = 0.5, lambda = lambda.bic3)
summary(out5, pval = 0.1)
```

```
>
> Call:
> islasso(formula = y ~ x2, lambda = lambda.bic3, alpha = 0.5,
>     data = diabetes)
>
> Residuals:
>      Min       1Q   Median       3Q      Max
> -120.696  -40.098   -5.179   39.143  154.979
>
>             Estimate Std. Error     Df z value Pr(>|z|)
> (Intercept)  152.133      2.623  1.000  58.009  < 2e-16 ***
> x2sex        -92.139     30.576  0.524  -3.013 0.002583 **
> x2bmi        300.885     28.831  0.443  10.436  < 2e-16 ***
> x2map        209.877     30.044  0.484   6.986 2.84e-12 ***
> x2hdl       -148.335     23.292  0.365  -6.369 1.91e-10 ***
> x2tch        121.563     19.401  0.280   6.266 3.71e-10 ***
> x2ltg        281.328     27.947  0.417  10.066  < 2e-16 ***
> x2glu        106.431     30.327  0.481   3.509 0.000449 ***
```

```
> x2bmi^2       95.651     28.761  0.455   3.326 0.000882 ***
> x2glu^2       45.792     27.564  0.396   1.661 0.096655 .
> x2age:sex     75.138     29.930  0.495   2.510 0.012058 *
> x2age:ldl    -54.473     22.136  0.336  -2.461 0.013861 *
> x2age:ltg     48.020     27.292  0.395   1.760 0.078491 .
> x2sex:hdl     46.184     25.423  0.404   1.817 0.069278 .
> x2bmi:map     76.316     28.571  0.434   2.671 0.007559 **
> x2tch:glu     38.543     20.768  0.273   1.856 0.063466 .
> ---
> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> (Dispersion parameter for gaussian family taken to be 3040.087)
>
>     Null deviance: 2621009  on 441  degrees of freedom
> Residual deviance: 1270727  on 418  degrees of freedom
> AIC: 4824.4
> Lambda: 1.5057
>
> Number of Newton-Raphson iterations: 154
```

```r
# or select the best tuning parameter using BIC with an islasso object
lambda.bic4 <- aic.islasso(out5, method = "BIC", interval = c(1, 100))
```

```
>
> Optimization through BIC
>
> lambda =   38.8146 BIC =  5051.72582
> lambda =   62.1854 BIC =  5068.72021
> lambda =   24.3707 BIC =  5029.72592
> lambda =   15.4439 BIC =  5005.53468
> lambda =    9.9268 BIC =  4979.49142
> lambda =    6.5171 BIC =  4956.70746
> lambda =    4.4097 BIC =  4937.73402
> lambda =    3.1073 BIC =  4929.13054
> lambda =    2.3024 BIC =  4924.94408
> lambda =    1.8049 BIC =  4923.41105
> lambda =    1.4975 BIC =  4922.61320
> lambda =    1.3075 BIC =  4923.73094
> lambda =    1.5751 BIC =  4922.40274
> lambda =    1.5950 BIC =  4923.47355
> lambda =    1.5454 BIC =  4922.47125
> lambda =    1.5637 BIC =  4922.42724
> lambda =    1.5827 BIC =  4922.38740
> lambda =    1.5874 BIC =  4922.37837
> lambda =    1.5903 BIC =  4922.37296
> lambda =    1.5921 BIC =  4922.36974
> lambda =    1.5932 BIC =  4922.36785
> lambda =    1.5939 BIC =  4922.36681
> lambda =    1.5943 BIC =  4922.36734
> lambda =    1.5939 BIC =  4922.36686
> lambda =    1.5940 BIC =  4922.36669
> lambda =    1.5941 BIC =  4922.36664
> lambda =    1.5942 BIC =  4922.36654
> lambda =    1.5942 BIC =  4922.36650
```

```
> lambda =    1.5943 BIC =  4922.36649
> lambda =    1.5943 BIC =  4922.36649
```

```
out6 <- update(out5, lambda = lambda.bic4)
summary(out6, pval = 0.1)
```

```
>
> Call:
> islasso(formula = y ~ x2, lambda = lambda.bic4, alpha = 0.5,
>     data = diabetes)
>
> Residuals:
>      Min       1Q   Median       3Q      Max
> -120.008  -40.854   -5.302   39.039  155.229
>
>             Estimate Std. Error     Df z value Pr(>|z|)
> (Intercept)   152.13       2.63  1.000  57.842  < 2e-16 ***
> x2sex         -88.30      29.83  0.511  -2.960 0.003074 **
> x2bmi         295.19      27.99  0.431  10.546  < 2e-16 ***
> x2map         206.12      29.23  0.472   7.052 1.76e-12 ***
> x2hdl        -146.33      22.71  0.357  -6.442 1.18e-10 ***
> x2tch         120.71      18.90  0.275   6.388 1.68e-10 ***
> x2ltg         275.65      27.13  0.406  10.160  < 2e-16 ***
> x2glu         106.26      29.49  0.468   3.603 0.000315 ***
> x2bmi^2        95.31      27.95  0.443   3.410 0.000650 ***
> x2glu^2        44.65      26.69  0.385   1.673 0.094325 .
> x2age:sex      72.88      29.15  0.482   2.500 0.012406 *
> x2age:ldl     -53.54      21.61  0.329  -2.478 0.013228 *
> x2age:ltg      46.70      26.46  0.385   1.765 0.077604 .
> x2sex:hdl      45.20      24.78  0.395   1.824 0.068123 .
> x2bmi:map      74.55      27.73  0.423   2.688 0.007181 **
> x2tch:glu      37.90      20.16  0.266   1.880 0.060064 .
> ---
> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> (Dispersion parameter for gaussian family taken to be 3057.643)
>
>     Null deviance: 2621009  on 441.0  degrees of freedom
> Residual deviance: 1279745  on 418.5  degrees of freedom
> AIC: 4826.4
> Lambda: 1.5943
>
> Number of Newton-Raphson iterations: 974
```

References

- Tibshirani R. *Regression shrinkage and selection via the lasso.* J R Stat Soc: Series B 1996; 58: 267–288
- Cilluffo, G, Sottile, G, La Grutta, S and Muggeo, VMR (2019) *The Induced Smoothed lasso: A practical framework for hypothesis testing in high dimensional regression.* Statistical Methods in Medical Research, online doi: 10.1177/0962280219842890.
- Brown B and Wang Y. *Standard errors and covariance matrices for smoothed rank estimators.* Biometrika 2005; 92: 149–158.