Using the SuperLearner R Package

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Outline

1. SuperLearner
2. Boston Housing
3. ALL data
4. van’t Veer data
The package is available at:
https://github.com/ecpolley/SuperLearner

These slides are available in the package and at:
https://github.com/ecpolley/

Need to install R packages `nnls` and `quadprog` before installing SuperLearner.
Table: Main functions in the SuperLearner package

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
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<tr>
<td>SuperLearner</td>
<td>fits super learner</td>
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<td>CV.SuperLearner</td>
<td>cross-validate in super learner</td>
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<td>listWrappers</td>
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<td>write.SL.template</td>
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<td>write.screen.template</td>
<td>screening wrapper template</td>
</tr>
<tr>
<td>write.method.template</td>
<td>method wrapper template</td>
</tr>
</tbody>
</table>
SuperLearner

```r
fitSL <- SuperLearner(Y = Y,
                      X = X,
                      SL.library = c('SL.glm'),
                      family = gaussian(),
                      method = 'method.NNLS',
                      verbose = TRUE,
                      cvControl = list(V = 10))
```
## SuperLearner

**Table:** Main arguments for SuperLearner

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
<th>Req.</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y</td>
<td>outcome</td>
<td>Y</td>
<td>–</td>
</tr>
<tr>
<td>X</td>
<td>data.frame for fit</td>
<td>Y</td>
<td>–</td>
</tr>
<tr>
<td>newX</td>
<td>data.frame for predict</td>
<td>N</td>
<td>X</td>
</tr>
<tr>
<td>SL.library</td>
<td>library of algorithms</td>
<td>Y</td>
<td>–</td>
</tr>
<tr>
<td>cvControl</td>
<td>list for CV control</td>
<td>N</td>
<td>–</td>
</tr>
<tr>
<td>control</td>
<td>optional controls</td>
<td>N</td>
<td>–</td>
</tr>
<tr>
<td>verbose</td>
<td>detailed report</td>
<td>N</td>
<td>FALSE</td>
</tr>
<tr>
<td>family</td>
<td>error distribution</td>
<td>N</td>
<td>gaussian</td>
</tr>
<tr>
<td>method</td>
<td>loss function &amp; model</td>
<td>N</td>
<td>NNLS</td>
</tr>
<tr>
<td>id</td>
<td>cluster id</td>
<td>N</td>
<td>–</td>
</tr>
<tr>
<td>obsWeights</td>
<td>observations weights</td>
<td>N</td>
<td>–</td>
</tr>
</tbody>
</table>
SuperLearner

- $Y$ and $X$ are the data used to fit each algorithm (the learning data)
- $\text{new}X$ is not required but can be a helpful shortcut. $\text{new}X$ will **not** be used to fit the models.

Example with $X$ and $\text{new}X$:

```r
fit <- glm(Y ~ ., data = X)
out <- predict(fit, newdata = newX)
```

The formula $Y \sim \cdot$ means an additive linear model using all columns of $X$.
newX might be a test set, the interesting values of X for prediction, a stacked data.frame with exposure levels set to be used with for G-computation, etc

Example setting exposure level for newX

```r
newData <- rbind(
  cbind(A = 0, subset(X, select = -A)),
  cbind(A = 1, subset(X, select = -A))
)
```
SuperLearner

- **family**: currently either `gaussian()` or `binomial()`.
- **method**: either `method.NNLS`, `method.NNloglik`, or your own method (see `create.method.template()`).
- **verbose**: helpful to set this to `TRUE` to see the progress of the estimation.
The ensemble model for “NNLS” is:

$$\Psi_{SL}(W) = \sum_{j=1}^{K} \alpha_j \Psi_j(W), \quad \alpha_j \geq 0, \sum \alpha_j = 1$$

The ensemble model for “NNloglik” is:

$$\Psi_{SL}(W) = \frac{1}{1 + \exp \left\{ - \sum_{j=1}^{K} \alpha_j \logit_{\gamma} (\Psi_j(W)) \right\}}, \quad \alpha_j \geq 0, \sum \alpha_j = 1$$

where \(\logit_{\gamma}\) is the trimmed logit function to control when \(\Psi_j(W)\) is near 0 or 1.
There are two types of algorithms that can be used in \texttt{SL.library}:

1. **Prediction algorithms.** Algorithms that take as input $X$ and $Y$ and return a predicted $Y$ value.

2. **Screening algorithms.** Algorithms designed to reduce the dimension of $X$. They take as input $X$ and $Y$ and return a logical vector indicating the columns in $X$ passing the screening. Screening algorithms can be coupled with prediction algorithms to form new prediction algorithms.
listWrappers()
SuperLearner

There are two ways to specify the algorithms in SL.library:

1. A character vector:
   - `c('SL.glm', 'SL.glmnet', 'SL.gam')`

2. A list of character vectors:
   - `list(c('SL.glm', 'screen.corP'), 'SL.gam')`

If only using prediction algorithms, easier to use the first method.

If using screening algorithms, the list is required. The syntax for the elements in the list is the prediction algorithm is first, followed by the screening algorithms. Multiple screening algorithms can be used. If a singleton, the default is to apply to all variables.
see the help documents for SuperLearner for more examples of SL.library
Creating Wrappers

Many algorithms are included in the package (use listWrappers() for a list of included functions), but these are just enough to get you started.

A few reasons to build your own wrappers:

- Want to use an algorithm not currently included
- Problem suggests different values for the tuning parameters
- Want to include a range of tuning parameters, not just the default
- Want to select tuning parameters in a different way (e.g. SL.glmnet selecting $\lambda$)
- Force variables to be used in step-wise methods
The **SuperLearner** vignette contains a table of tuning parameters for the algorithms in the package.

```r
vignette("SuperLearner")
```
Creating wrappers

Example: Creating new prediction algorithm wrapper
Creating wrappers

Consider the polymars algorithm in the polspline package.

- continuous outcome Y
- data.frame of covariates X
- data.frame of covariates newX

```r
fit.mars <- polymars(Y, X)
out <- predict.polymars(fit.mars,
  x = as.matrix(newX))
```

Now we know how to fit the model and return predicted values, next we check out write.SL.template for integrating the code above into the correct syntax for SuperLearner
Creating wrappers

SL.template <- function(Y, X, newX, family, obsWeights, id, ...) {
  # require('pkg')
  if(family$family == 'gaussian') { }
  if(family$family == 'binomial') { }
  # pred is the predicted responses for newX
  pred <- numeric()
  # fit returns all objects needed for predict.SL.*
  fit <- list(object = )
  # declare class of fit for predict.SL.template
  class(fit) <- 'SL.template'
  # return a list with pred and fit
  out <- list(pred = pred, fit = fit)
  return(out)
}
}
write.SL.template()
## Creating wrappers

Table: The arguments passed to a prediction algorithm in SuperLearner

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y</td>
<td>the outcome variable</td>
</tr>
<tr>
<td>X</td>
<td>the training data set</td>
</tr>
<tr>
<td></td>
<td>(the observations used to fit the model)</td>
</tr>
<tr>
<td>newX</td>
<td>the validation data set</td>
</tr>
<tr>
<td></td>
<td>(the observations to return predictions for)</td>
</tr>
<tr>
<td>family</td>
<td>a description of the error distribution</td>
</tr>
<tr>
<td>id</td>
<td>a cluster identification</td>
</tr>
<tr>
<td>obsWeights</td>
<td>observation weights</td>
</tr>
</tbody>
</table>

You do not need to use all these arguments, but if you use any of them, the name must match exactly.
Creating wrappers

My.SL.polymars <- function (Y, X, newX, family, ...) {
  if (family$family == "gaussian") {
    fit.mars <- polymars(Y, X)
    out <- predict.polymars(fit.mars, x = as.matrix(newX))
  }
  if (family$family == "binomial") {
    # insert estimation function
  }
  ... # next slide
}

SL.polymars
Creating wrappers

What about `family = binomial()`?

Can leave this blank (or add `stop('only gaussian')`) if only for a specific example with continuous outcome.

To be complete, we could look up the code for a binary outcome and add this case:

```r
fit.mars <- polyclas(Y, X, cv = 5)
out <- ppolyclas(cov = newX,
    fit = fit.mars)[, 2]
```
Creating wrappers

```
My.SL.polymars <- function(Y, X, newX, family, ...) {
  if(family$family=="gaussian") {
    fit.mars <- polymars(Y, X)
    out <- predict.polymars(fit.mars,
                           x = as.matrix(newX))
  }
  if(family$family=="binomial") {
    fit.mars <- polyclass(Y, X, cv = 5)
    out <- ppolyclass(cov = newX,
                      fit = fit.mars)[, 2]
  }
  ...
}
```
Creating wrappers

Wrappers need to return 2 values:

1. **pred**: predicted $Y$ values for rows in `newX`
2. **fit**: a list with everything needed to use `predict` method

In the `polymars` example: For the gaussian case, `predict()` needs:
- `object = fit.mars`

For the binomial case, `predict()` needs:
- `fit = fit.mars`

**Note**: `SuperLearner` does not use the `fit` list. If you do not plan to use the function `predict.SuperLearner` you can leave the `fit` object as:
- `fit <- vector("list", length = 0)`
My.SL.polymars <- function(Y, X, newX, family, ...) {
  if(family$family=="gaussian") {
    fit.mars <- polymars(Y, X)
    out <- predict.polymars(fit.mars, x = as.matrix(newX))
    fit <- list(object = fit.mars)
  }
  if(family$family=="binomial") {
    fit.mars <- polyclass(Y, X, cv = 5)
    out <- ppolyclass(cov = newX, fit = fit.mars)[, 2]
    fit <- list(fit = fit.mars)
  }
  ...
... # next slide
Final step is putting everything together into a list object. The list must have 2 elements and the names **must** be `pred` and `fit`.

Can also assign a class to the `fit` list. This will be used to look up the correct `predict` method. I’m using S3 methods here. This is only important if using `predict.SuperLearner` afterwards.

Creating wrappers

My.SL.polymars <- function (Y, X, newX, family, ...) {
  ... # previous slides
  out <- list (pred = pred, fit = fit)
  class(out$fit) <- c("SL.polymars")
  return(out)
}

Note: out is just a temporary variable name here.

The function should match SL.polymars in the SuperLearner package.
Important notes for creating wrappers

- Input must following naming syntax: $Y$, $X$, …
- Name of new function must be different than one already in the package
- Must return a list with 2 elements named `pred` and `fit`
- `pred` must be a vector with the predicted $Y$ values for the rows in `newX`
- `fit` can be anything if not using predict method, otherwise is a list with elements needed for `predict`
Creating wrappers

predict.SL.template <- function (object,
   newdata, family, X = NULL, Y = NULL, ...)
{
   pred <- numeric()
   return(pred)
}

Creating wrappers

```r
predict.SL.polymars <- function (object, newdata, family, ...) {
  if (family$family == "gaussian") {
    pred <- predict.polymars(object = object$object, 
                            x = as.matrix(newdata))
  }
  if (family$family == "binomial") {
    pred <- ppolyclass(cov = newdata, 
                        fit = object$fit)[, 2]
  }
  return(pred)
}
```
Example: creating screening algorithm
screening template

```r
screen.template <- function (Y, X, family, obsWeights, id, ...) {
  # require ('pkg ')
  if (family$family == "gaussian") {
  }
  if (family$family == "binomial") {
  }
  # whichVariable is a logical vector,
  # TRUE indicates variable will be used
  whichVariable <- rep(TRUE, ncol(X))
  return (whichVariable)
}
```
Creating wrappers

Table: The arguments passed to a screening algorithm in SuperLearner

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$Y$</td>
<td>the outcome variable</td>
</tr>
<tr>
<td>$X$</td>
<td>the training data set (the observations used to fit the model)</td>
</tr>
<tr>
<td>family</td>
<td>a description of the error distribution</td>
</tr>
<tr>
<td>id</td>
<td>a cluster identification</td>
</tr>
<tr>
<td>obsWeights</td>
<td>observation weights</td>
</tr>
</tbody>
</table>

You do not need to use all these arguments, but if you use any of them, the name must match exactly.
screen.randomForest <- function (Y, X, family, nVar = 10, ntree = 1000, ...) {
  if (family$family == "gaussian") {
    rank.rf.fit <- randomForest(Y ~ ., data = X, ntree = ntree)
  }
  if (family$family == "binomial") {
    rank.rf.fit <- randomForest(y = as.factor(Y), x = X, ntree = ntree)
  }
  whichVariable <- as.logical(rank(-rank.rf.fit$importance) <= nVar)
  return(whichVariable)
}
Boston Housing example

The outcome variable is the median home value (cmedv) for the 506 census tracts of Boston from the 1970 census.

The covariates are a mix of geographical and socioeconomic variables, like per capita crime rate (crim), average number of rooms per house (rm), distance to Boston employment centres (dis), indicator of tract being on the Charles river (chas), etc.
The Boston Housing data can be found in the `mlbench` package.

```r
library(mlbench)
data(BostonHousing2)
# convert factors to numeric
BostonHousing2$chas <- as.numeric(BostonHousing2$chas == "1")
# select subset of variables
DATA <- BostonHousing2[, c("cmedv", "crim", "zn", "indus", "chas", "nox", "rm", "age", "dis", "rad", "tax", "ptratio", "b", "lstat")]
```
First need to decide which prediction algorithms to include in the library
# Boston Housing

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>Description</th>
<th>Package</th>
</tr>
</thead>
<tbody>
<tr>
<td>glm</td>
<td>linear model</td>
<td>stats</td>
</tr>
<tr>
<td>randomForest</td>
<td>random Forest</td>
<td>randomForest</td>
</tr>
<tr>
<td>bagging</td>
<td>bootstrap aggregation of trees</td>
<td>ipred</td>
</tr>
<tr>
<td>gam</td>
<td>generalized additive models</td>
<td>gam</td>
</tr>
<tr>
<td>gbm</td>
<td>gradient boosting</td>
<td>gbm</td>
</tr>
<tr>
<td>nnet</td>
<td>neural network</td>
<td>nnet</td>
</tr>
<tr>
<td>polymars</td>
<td>polynomial spline regr.</td>
<td>polsplline</td>
</tr>
<tr>
<td>bart</td>
<td>Bayesian additive regr. trees</td>
<td>BayesTree</td>
</tr>
<tr>
<td>glmnet</td>
<td>elastic net</td>
<td>glmnet</td>
</tr>
<tr>
<td>svm</td>
<td>support vector machine</td>
<td>e1071</td>
</tr>
<tr>
<td>bayesglm</td>
<td>Bayesian glm</td>
<td>arm</td>
</tr>
<tr>
<td>step</td>
<td>stepwise glm</td>
<td>stats</td>
</tr>
</tbody>
</table>
One algorithm to consider is the generalized additive model algorithm. This algorithm has a tuning parameter for the degrees of freedom in the smoother. I have set this to be 2 in SL.gam but we might want to consider larger values.

We could create an entirely new wrapper for gam and df = 3, or we can write a wrapper for the wrapper and only change the degrees of freedom value.
look at SL.gam to see how the degrees of freedom parameter is specified:
SL.gam <- function(Y, X, newX,
    family, obsWeights, deg.gam = 2, ...)
{
    ...  # model: Y ~ s(X, deg.gam)
    # see full functions for details
    fit.gam <- gam::gam(gam.model, data = X,
        family = family,
        control = gam.control(maxit = 50, bf.maxit = 50),
        weights = obsWeights)
    pred <- predict(fit.gam, newdata = newX, 
        type = "response")
    ...  # returns list here
}
The \texttt{SL.gam} function contains the argument \texttt{deg.gam = 2}.

Wrappers can have additional arguments, but they must have default values.
For the new wrapper, only need to change the value of deg.gam. Use \ldots to pass everything else between SL.gam.3 and SL.gam.

```
SL.gam.3 <- function(..., deg.gam = 3) {
  SL.gam(..., deg.gam = deg.gam)
}
```

Easy to create new wrappers by changing tuning parameter values. Check the code for the wrappers by typing the name of the function without parentheses to see what tuning parameter values are in the arguments.
Similar to the \texttt{SL.gam} example above, the function \texttt{create.SL.glmnet} in the \texttt{SuperLearnerExtra} package can be used to create new \texttt{SL.glmnet} wrappers:

```r
create.SL.glmnet(alpha = c(0.25, 0.50, 0.75))
# and set gbm to no interactions:
SL.gbm.1 <- function(...) {
  SL.gbm(..., interaction.depth = 1)
}
```

Additional wrappers are available at: https://github.com/ecpolley/SuperLearnerExtra
Boston Housing example

```r
SL.library <- c("SL.gam",
"SL.gam.3", "SL.gam.4",
"SL.gam.5", "SL.gbm.1",
"SL.gbm", "SL.glm",
"SL.glmnet", "SL.glmnet.0.25",
"SL.glmnet.alpha.0.5", "SL.glmnet.0.75",
"SL.polymars", "SL.randomForest",
"SL.ridge", "SL.svm",
"SL.bayesglm", "SL.step",
"SL.step.interaction",
"SL.bart")
```
Boston Housing example

```r
fitSL <- SuperLearner(Y = log(DATA$cmedv),
                      X = subset(DATA, select = -c(cmedv)),
                      SL.library = SL.library,
                      family = gaussian())
```

<table>
<thead>
<tr>
<th>Model</th>
<th>Risk</th>
<th>Coef</th>
</tr>
</thead>
<tbody>
<tr>
<td>SL.gam_All</td>
<td>0.03834031</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.gam.3_All</td>
<td>0.03666449</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.gam.4_All</td>
<td>0.03589859</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.gam.5_All</td>
<td>0.03529692</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.gbm.1_All</td>
<td>0.03040543</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.gbm.2_All</td>
<td>0.02501729</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.glm_All</td>
<td>0.03754472</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.glmnet_All</td>
<td>0.03765112</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.glmnet.alpha25_All</td>
<td>0.03754278</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.glmnet.alpha50_All</td>
<td>0.03758802</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.glmnet.alpha75_All</td>
<td>0.03763085</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.polymars_All</td>
<td>0.04587432</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.randomForest_All</td>
<td>0.02105987</td>
<td>0.2956277</td>
</tr>
<tr>
<td>SL.ridge_All</td>
<td>0.03753661</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.svm_All</td>
<td>0.02678290</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.bayesglm_All</td>
<td>0.03754318</td>
<td>0.00000000</td>
</tr>
<tr>
<td>SL.step_All</td>
<td>0.03753337</td>
<td>0.00000000</td>
</tr>
</tbody>
</table>
Table: Elements of the output from SuperLearner

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SL.predict</td>
<td>super learner predicted values for newX</td>
</tr>
<tr>
<td>coef</td>
<td>coefficient for each algorithm</td>
</tr>
<tr>
<td>libraryNames</td>
<td>names of algorithms in library</td>
</tr>
<tr>
<td>library.predict</td>
<td>matrix of predicted values for newX from each algorithm in the library</td>
</tr>
<tr>
<td>cvRisk</td>
<td>V-fold cross-validated risk for each algorithm in the library</td>
</tr>
</tbody>
</table>
The final super learner prediction model is the weighted combination of the library algorithms where the estimates of the weights can be found with `coef(fitSL)`.

To attain predictions on new observations (not in `newX`), the `predict` function will usually work. If you created new wrappers, you also need to create `predict` S3 methods for those new wrappers.
SuperLearner is a model selection algorithm. It does not contain a good estimate for model assessment (you could use the re-substitution method to estimate the risk but this is optimistic).

Our suggestion to assess the performance of the super learner is to run CV.SuperLearner (example in the next case study).
- The outcome variable is an indicator of the molecular biology of the cancer tissue, either Negative or BCR/ABL.
- The sample consists of 79 individuals (42 Neg, 37 BCR/ABL).
- The data contain 2200 features (X) to be used after the filtering steps.
- Need to select algorithms appropriate for a binary outcome and a large number of covariates.
The next 2 slides are the processing steps following in Gentleman, Huber and Carey (2008) “Supervised Machine Learning” in Bioconductor Case Studies.

```
# source("http://bioconductor.org/biocLite.R")
# biocLite()
# biocLite("ALL")
library(ALL)
library(genefilter)
data(ALL)
```
# restrict to only the NEG and BCR/ABL outcomes

```r
bcell <- grep("^B", as.character(ALL$BT))
moltyp <- which(as.character(ALL$mol.biol) %in% c("NEG", "BCR/ABL"))
ALL_bcrneg <- ALL[, intersect(bcell, moltyp)]
# drops unused levels
ALL_bcrneg$mol.biol <- factor(ALL_bcrneg$mol.biol)
```

# filter features

```r
ALLfilt_bcrneg <- nsFilter(ALL_bcrneg, var.cutoff = 0.75)$eset
```
# standardize the features
rowIQRs <- function(eSet) {
    numSamp <- ncol(eSet)
    lowQ <- rowQ(eSet, floor(0.25 * numSamp))
    upQ <- rowQ(eSet, ceiling(0.75 * numSamp))
    upQ - lowQ
}
standardize <- function(x) {
    (x - rowMedians(x)) / rowIQRs(x)
}
exprs(ALLfilt_bcrneg) <- standardize(
    exprs(ALLfilt_bcrneg))

# convert to numeric matrix for the SuperLearner
Y <- as.numeric(
    ALLfilt_bcrneg$mol.biol == "BCR/ABL")
X <- t(exprs(ALLfilt_bcrneg))
Possible prediction algorithms include:

- k-nearest neighbors
- elastic net (penalized regression)
- random forest

These algorithms have tuning parameters:

- knn: \( k \)
- glmnet: \( \alpha \)
- randomForest: mtry and nodesize
tuneGrid <- expand.grid(mtry = c(500, 1000, 2200),
           nodesize = c(1, 5, 10))

for (mm in seq(nrow(tuneGrid))) {
    eval(parse(file = "", text =
       paste("SL.randomForest.", mm,
           "<- function(..., mtry = ", tuneGrid[mm, 1],
           ", nodesize = ", tuneGrid[mm, 2], ") {
       SL.randomForest(..., mtry = mtry,
           nodesize = nodesize) }", sep = ""))))
}
The code above is hard to follow, but I’m doing the same thing we did with SL.gam.3 just in a for loop.

```r
> SL.randomForest.1
function(..., mtry = 500, nodesize = 1) {
  SL.randomForest(..., mtry = mtry, nodesize = nodesize) }

> SL.randomForest.2
function(..., mtry = 1000, nodesize = 1) {
  SL.randomForest(..., mtry = mtry, nodesize = nodesize) }

> SL.randomForest.9
function(..., mtry = 2200, nodesize = 10) {
  SL.randomForest(..., mtry = mtry, nodesize = nodesize) }
```
Add additional \texttt{knn} wrappers using functions in \texttt{SuperLearnerExtra}

\begin{verbatim}
create.SL.knn(k = c(k = 20, 30, 40, 50))
\end{verbatim}

available at: https://github.com/ecpolley/SuperLearnerExtra
SL.library <- c("SL.knn",
    "SL.knn.20",
    "SL.knn.30",
    "SL.knn.40",
    "SL.knn.50",
    "SL.randomForest",
    "SL.glmnet",
    "SL.glmnet.0.25",
    "SL.glmnet.0.5",
    "SL.glmnet.0.75",
    "SL.mean",
paste("SL.randomForest.",
    seq(nrow(tuneGrid)), sep = ""))
fitSL <- SuperLearner(Y = Y, X = X, 
SL.library = SL.library, family = binomial(), 
method = "NNLS",
cvControl = list(stratifyCV = TRUE))

fitSL
<table>
<thead>
<tr>
<th>Model</th>
<th>Risk</th>
<th>Coef</th>
</tr>
</thead>
<tbody>
<tr>
<td>SL.knn_All</td>
<td>0.20658228</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.knn20_All</td>
<td>0.22423347</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.knn30_All</td>
<td>0.2229664</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.knn40_All</td>
<td>0.2345986</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.knn50_All</td>
<td>0.2392321</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.randomForest_All</td>
<td>0.1241809</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.glmnet_All</td>
<td>0.0843063</td>
<td>0.98039534</td>
</tr>
<tr>
<td>SL.glmnet.alpha25_All</td>
<td>0.1048793</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.glmnet.alpha50_All</td>
<td>0.0933153</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.glmnet.alpha75_All</td>
<td>0.0868151</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.randomForest.1_All</td>
<td>0.1310352</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.randomForest.2_All</td>
<td>0.1226909</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.randomForest.3_All</td>
<td>0.1191843</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.randomForest.4_All</td>
<td>0.1302410</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.randomForest.5_All</td>
<td>0.1235104</td>
<td>0.000000000</td>
</tr>
<tr>
<td>SL.randomForest.6_All</td>
<td>0.1175273</td>
<td>0.01960466</td>
</tr>
<tr>
<td>SL.randomForest.7_All</td>
<td>0.1287138</td>
<td>0.000000000</td>
</tr>
</tbody>
</table>
```r
fitSL.CV <- CV.SuperLearner(Y = Y, X = X, 
    SL.library = SL.library, 
    V = 2/zero.noslash, family = binomial(),
    method = "method.NNLS",
    cvControl = list(stratifyCV = TRUE))

summary(fitSL.CV)

# can also print the LaTeX table
# requires Hmisc package
# latex(summary(fitSL.CV))
```
<table>
<thead>
<tr>
<th>Algorithm</th>
<th>subset</th>
<th>Risk</th>
<th>SE</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>SuperLearner</td>
<td>–</td>
<td>0.101</td>
<td>0.020</td>
<td>0.003</td>
<td>0.382</td>
</tr>
<tr>
<td>Discrete SL</td>
<td>–</td>
<td>0.095</td>
<td>0.021</td>
<td>0.004</td>
<td>0.347</td>
</tr>
<tr>
<td>SL.knn(10)</td>
<td>All</td>
<td>0.212</td>
<td>0.018</td>
<td>0.070</td>
<td>0.460</td>
</tr>
<tr>
<td>SL.knn(20)</td>
<td>All</td>
<td>0.220</td>
<td>0.011</td>
<td>0.152</td>
<td>0.322</td>
</tr>
<tr>
<td>SL.knn(30)</td>
<td>All</td>
<td>0.223</td>
<td>0.008</td>
<td>0.192</td>
<td>0.274</td>
</tr>
<tr>
<td>SL.knn(40)</td>
<td>All</td>
<td>0.232</td>
<td>0.006</td>
<td>0.187</td>
<td>0.268</td>
</tr>
<tr>
<td>SL.knn(50)</td>
<td>All</td>
<td>0.238</td>
<td>0.004</td>
<td>0.218</td>
<td>0.260</td>
</tr>
<tr>
<td>SL.randomForest</td>
<td>All</td>
<td>0.120</td>
<td>0.014</td>
<td>0.026</td>
<td>0.256</td>
</tr>
<tr>
<td>SL.glmnet((\alpha = 1.0))</td>
<td>All</td>
<td>0.088</td>
<td>0.022</td>
<td>0.002</td>
<td>0.395</td>
</tr>
<tr>
<td>SL.glmnet((\alpha = 0.25))</td>
<td>All</td>
<td>0.113</td>
<td>0.022</td>
<td>0.007</td>
<td>0.451</td>
</tr>
<tr>
<td>SL.glmnet((\alpha = 0.50))</td>
<td>All</td>
<td>0.106</td>
<td>0.023</td>
<td>0.004</td>
<td>0.447</td>
</tr>
<tr>
<td>SL.glmnet((\alpha = 0.75))</td>
<td>All</td>
<td>0.093</td>
<td>0.021</td>
<td>0.004</td>
<td>0.347</td>
</tr>
<tr>
<td>SL.mean</td>
<td>All</td>
<td>0.249</td>
<td>0.004</td>
<td>0.242</td>
<td>0.251</td>
</tr>
<tr>
<td>SL.randomForest.1</td>
<td>All</td>
<td>0.125</td>
<td>0.014</td>
<td>0.034</td>
<td>0.269</td>
</tr>
<tr>
<td>SL.randomForest.2</td>
<td>All</td>
<td>0.114</td>
<td>0.014</td>
<td>0.023</td>
<td>0.250</td>
</tr>
<tr>
<td>SL.randomForest.3</td>
<td>All</td>
<td>0.111</td>
<td>0.015</td>
<td>0.016</td>
<td>0.238</td>
</tr>
<tr>
<td>SL.randomForest.4</td>
<td>All</td>
<td>0.123</td>
<td>0.014</td>
<td>0.036</td>
<td>0.264</td>
</tr>
<tr>
<td>SL.randomForest.5</td>
<td>All</td>
<td>0.117</td>
<td>0.014</td>
<td>0.023</td>
<td>0.262</td>
</tr>
<tr>
<td>SL.randomForest.6</td>
<td>All</td>
<td>0.110</td>
<td>0.015</td>
<td>0.015</td>
<td>0.252</td>
</tr>
<tr>
<td>SL.randomForest.7</td>
<td>All</td>
<td>0.126</td>
<td>0.014</td>
<td>0.034</td>
<td>0.266</td>
</tr>
<tr>
<td>SL.randomForest.8</td>
<td>All</td>
<td>0.117</td>
<td>0.014</td>
<td>0.023</td>
<td>0.259</td>
</tr>
<tr>
<td>SL.randomForest.9</td>
<td>All</td>
<td>0.110</td>
<td>0.015</td>
<td>0.013</td>
<td>0.245</td>
</tr>
</tbody>
</table>
van’t Veer example

- 97 breast cancer patients followed for 5 years.
- Outcome is binary yes/no recur in 5 years (we do not have the date of recurrence)
- 7 clinical variables are available (age, tumor grade, etc.)
- 4348 gene expression values post-filtering
The original data is available at:
One interesting “screening” is to consider the prediction algorithms on only the clinical variables or on only the gene expression variables.

```r
screen.clinical <- function(...){
  return(c(rep(TRUE, 7), rep(FALSE, 4348)))
}

screen.array <- function(...){
  return(c(rep(FALSE, 7), rep(TRUE, 4348)))
}
```
SL.library <- list(
  c("SL.knn", "All", "screen.clinical",
    "screen.corP", "screen.corP.01", "screen.glmnet"),
  c("SL.knn.20", "All", "screen.clinical",
    "screen.corP", "screen.corP.01", "screen.glmnet"),
  c("SL.glmnet", "screen.corRank.50",
    "screen.corRank.20"),
  c("SL.glmnet.0.75", "screen.corRank.50",
    "screen.corRank.20"),
  c("SL.glmnet.0.5", "screen.corRank.50",
    "screen.corRank.20"),
  c("SL.glmnet.0.25", "screen.corRank.50",
    "screen.corRank.20"),
  c("SL.randomForest", "screen.clinical",
    "screen.corP.01", "screen.glmnet"),
  c("SL.bagging", "screen.clinical",
    "screen.corP.01", "screen.glmnet"),
  c("SL.bart", "screen.clinical",
    "screen.corP.01", "screen.glmnet"),
  c("SL.mean", "All"))
SuperLearner

```r
fitSL <- SuperLearner(Y = surv.resp, X = X,
                      SL.library = SL.library,
                      family = binomial(),
                      method = "method.NNLS",
                      control = list(saveFitLibrary = FALSE))

fitSL
```

van’t Veer
Only presenting results for non-zero coefficients. Table does not fit on a slide.
cvSuperLearner

```r
fitSL.CV <- cvSuperLearner(Y=surv.resp, X=X,
V = 20,
SL.library = SL.library,
family = binomial(),
method = "method.NNLS",
cvControl = list(stratifyCV = TRUE))

summary(fitSL.CV)
```
<table>
<thead>
<tr>
<th>Algorithm</th>
<th>subset</th>
<th>Risk</th>
<th>SE</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>SuperLearner</td>
<td>–</td>
<td>0.194</td>
<td>0.017</td>
<td>0.103</td>
<td>0.309</td>
</tr>
<tr>
<td>Discrete SL</td>
<td>–</td>
<td>0.238</td>
<td>0.024</td>
<td>0.127</td>
<td>0.415</td>
</tr>
<tr>
<td>SL.knn(10)</td>
<td>All</td>
<td>0.249</td>
<td>0.020</td>
<td>0.144</td>
<td>0.532</td>
</tr>
<tr>
<td>SL.knn(10)</td>
<td>clinical</td>
<td>0.239</td>
<td>0.019</td>
<td>0.138</td>
<td>0.496</td>
</tr>
<tr>
<td>SL.knn(10)</td>
<td>cor (p &lt; 0.1)</td>
<td>0.262</td>
<td>0.023</td>
<td>0.095</td>
<td>0.443</td>
</tr>
<tr>
<td>SL.knn(10)</td>
<td>cor (p &lt; 0.01)</td>
<td>0.224</td>
<td>0.020</td>
<td>0.088</td>
<td>0.365</td>
</tr>
<tr>
<td>SL.knn(10)</td>
<td>glmnet</td>
<td>0.219</td>
<td>0.028</td>
<td>0.007</td>
<td>0.465</td>
</tr>
<tr>
<td>SL.knn(20)</td>
<td>All</td>
<td>0.242</td>
<td>0.013</td>
<td>0.171</td>
<td>0.397</td>
</tr>
<tr>
<td>SL.knn(20)</td>
<td>clinical</td>
<td>0.236</td>
<td>0.012</td>
<td>0.154</td>
<td>0.382</td>
</tr>
<tr>
<td>SL.knn(20)</td>
<td>cor (p &lt; 0.1)</td>
<td>0.233</td>
<td>0.017</td>
<td>0.108</td>
<td>0.342</td>
</tr>
<tr>
<td>SL.knn(20)</td>
<td>cor (p &lt; 0.01)</td>
<td>0.206</td>
<td>0.018</td>
<td>0.121</td>
<td>0.321</td>
</tr>
<tr>
<td>SL.knn(20)</td>
<td>glmnet</td>
<td>0.217</td>
<td>0.026</td>
<td>0.018</td>
<td>0.405</td>
</tr>
<tr>
<td>SL.knn(30)</td>
<td>All</td>
<td>0.239</td>
<td>0.013</td>
<td>0.171</td>
<td>0.396</td>
</tr>
<tr>
<td>SL.knn(30)</td>
<td>clinical</td>
<td>0.236</td>
<td>0.012</td>
<td>0.169</td>
<td>0.386</td>
</tr>
<tr>
<td>SL.knn(30)</td>
<td>cor (p &lt; 0.1)</td>
<td>0.232</td>
<td>0.014</td>
<td>0.143</td>
<td>0.319</td>
</tr>
<tr>
<td>SL.knn(30)</td>
<td>cor (p &lt; 0.01)</td>
<td>0.215</td>
<td>0.017</td>
<td>0.136</td>
<td>0.346</td>
</tr>
<tr>
<td>SL.knn(30)</td>
<td>glmnet</td>
<td>0.210</td>
<td>0.023</td>
<td>0.039</td>
<td>0.402</td>
</tr>
<tr>
<td>SL.knn(40)</td>
<td>All</td>
<td>0.240</td>
<td>0.011</td>
<td>0.182</td>
<td>0.331</td>
</tr>
<tr>
<td>SL.knn(40)</td>
<td>clinical</td>
<td>0.238</td>
<td>0.010</td>
<td>0.179</td>
<td>0.319</td>
</tr>
<tr>
<td>SL.knn(40)</td>
<td>cor (p &lt; 0.1)</td>
<td>0.236</td>
<td>0.012</td>
<td>0.166</td>
<td>0.316</td>
</tr>
<tr>
<td>SL.knn(40)</td>
<td>cor (p &lt; 0.01)</td>
<td>0.219</td>
<td>0.015</td>
<td>0.154</td>
<td>0.309</td>
</tr>
<tr>
<td>SL.knn(40)</td>
<td>glmnet</td>
<td>0.211</td>
<td>0.021</td>
<td>0.060</td>
<td>0.346</td>
</tr>
<tr>
<td>SL.glmnet(α = 1.0)</td>
<td>corRank.50</td>
<td>0.229</td>
<td>0.029</td>
<td>0.078</td>
<td>0.445</td>
</tr>
<tr>
<td>SL.glmnet(α = 1.0)</td>
<td>corRank.20</td>
<td>0.208</td>
<td>0.026</td>
<td>0.048</td>
<td>0.424</td>
</tr>
<tr>
<td>SL.glmnet(α = 0.75)</td>
<td>corRank.50</td>
<td>0.221</td>
<td>0.027</td>
<td>0.077</td>
<td>0.420</td>
</tr>
<tr>
<td>SL.glmnet(α = 0.75)</td>
<td>corRank.20</td>
<td>0.209</td>
<td>0.026</td>
<td>0.046</td>
<td>0.421</td>
</tr>
<tr>
<td>SL.glmnet(α = 0.50)</td>
<td>corRank.50</td>
<td>0.226</td>
<td>0.027</td>
<td>0.077</td>
<td>0.426</td>
</tr>
<tr>
<td>SL.glmnet(α = 0.50)</td>
<td>corRank.20</td>
<td>0.211</td>
<td>0.026</td>
<td>0.059</td>
<td>0.419</td>
</tr>
<tr>
<td>SL.glmnet(α = 0.25)</td>
<td>corRank.50</td>
<td>0.229</td>
<td>0.027</td>
<td>0.084</td>
<td>0.424</td>
</tr>
<tr>
<td>SL.glmnet(α = 0.25)</td>
<td>corRank.20</td>
<td>0.216</td>
<td>0.025</td>
<td>0.072</td>
<td>0.406</td>
</tr>
<tr>
<td>SL.randomForest</td>
<td>clinical</td>
<td>0.198</td>
<td>0.019</td>
<td>0.098</td>
<td>0.391</td>
</tr>
<tr>
<td>SL.randomForest</td>
<td>cor (p &lt; 0.01)</td>
<td>0.204</td>
<td>0.018</td>
<td>0.101</td>
<td>0.341</td>
</tr>
<tr>
<td>SL.randomForest</td>
<td>glmnet</td>
<td>0.220</td>
<td>0.025</td>
<td>0.072</td>
<td>0.378</td>
</tr>
<tr>
<td>SL.bagging</td>
<td>clinical</td>
<td>0.207</td>
<td>0.016</td>
<td>0.108</td>
<td>0.408</td>
</tr>
<tr>
<td>SL.bagging</td>
<td>cor (p &lt; 0.01)</td>
<td>0.205</td>
<td>0.018</td>
<td>0.107</td>
<td>0.353</td>
</tr>
<tr>
<td>SL.bagging</td>
<td>glmnet</td>
<td>0.206</td>
<td>0.022</td>
<td>0.077</td>
<td>0.388</td>
</tr>
<tr>
<td>SL.bart</td>
<td>clinical</td>
<td>0.202</td>
<td>0.018</td>
<td>0.109</td>
<td>0.365</td>
</tr>
<tr>
<td>SL.bart</td>
<td>cor (p &lt; 0.01)</td>
<td>0.210</td>
<td>0.021</td>
<td>0.092</td>
<td>0.376</td>
</tr>
<tr>
<td>SL.bart</td>
<td>glmnet</td>
<td>0.220</td>
<td>0.028</td>
<td>0.043</td>
<td>0.423</td>
</tr>
<tr>
<td>SL.mean</td>
<td>All</td>
<td>0.250</td>
<td>0.003</td>
<td>0.246</td>
<td>0.251</td>
</tr>
</tbody>
</table>
Installing suggested packages

```r
install.packages(c("glmnet","randomForest","class","gam","gbm","nnet","polspline","MASS","e1071","stepPlr","arm","party","spls","LogicReg","nnls","multicore","SIS","BayesTree","quadprog","ipred","mlbench","rpart","caret","mda","earth"),
type="source",
repos="http://cran.cnr.Berkeley.edu",
dependencies=c("Depends","Imports"))
# missing DSA, not available on CRAN
```

Can remove type = ‘source’ if system not setup to install packages from source.
Colophon

- Slides created with \LaTeX\ package \textbf{Beamer}
- Code blocks adapted from the \textbf{tikzDevice} \texttt{R} package
- \LaTeX\ package \texttt{tikz} and \texttt{sweave} for code styles
- \texttt{R} version 2.13.0 and \texttt{SuperLearner} version 2.0-1
- Other packages: arm 1.4-10, BayesTree 0.3-1, caret 4.88, class 7.3-3, DSA 3.1.4, e1071 1.5-25, earth 2.6-2, gam 1.04, gbm 1.6-3, glmnet 1.6, Hmisc 3.8-3, ipred 0.8-11, leaps 2.9, lme4 0.999375-39, LogicReg 1.4.10, MASS 7.3-13, mda 0.4-2, mlbench 2.1-0, modelUtils 3.1.4, nnet 7.3-1, nnls 1.3, party 0.9-9994, polspline 1.1.5, quadprog 1.5-4, randomForest 4.6-2, rpart 3.1-50, SIS 0.6,