

An Introduction to *predictiveModeling*

Adam Margolin

July 16, 2012

1 Introduction

TODO

Add some R code here that demos the package, note that this gets executed as part of the package check so it should not take too long to run. For longer running stuff we could also write vignettes but place them in a different directory so that they are not run as part of the package check.

2 Available Functions, Classes, and Objects

```
> library(predictiveModeling)
```

```
randomSurvivalForest 3.6.3
```

Type `rsf.news()` to see new features, changes, and bug fixes.

```
> ls('package:predictiveModeling')
```

```
[1] "CaretModel"
[2] "CoxModel"
[3] "GlmnetModel"
[4] "LinearModel"
[5] "MostCorrelatedFeatures"
[6] "PredictiveModel"
[7] "PredictiveModelFeatureEvaluator"
[8] "PredictiveModelPerformance"
[9] "PredictiveModelResults"
[10] "RSFmodel"
[11] "RSFmodel_500feat_100trees"
[12] "SurvivalModelPerformance"
[13] "SurvivalModelPerformanceCV"
[14] "convertDataFrameToFeatureMatrix"
[15] "createAggregateFeatureDataSet"
[16] "createENetTuneGrid"
[17] "createFeatureAndResponseDataList"
[18] "crossValidatePredictiveModel"
[19] "crossValidatePredictiveSurvivalModel"
[20] "defaultTrainControl"
[21] "exactConcordanceIndex"
[22] "filterNasFromMatrix"
[23] "filterPredictiveModelData"
```

```
[24] "plotPredictiveModelHeatmap"  
[25] "trainPartition"
```

3 Available Demos

```
> demo(package="predictiveModeling")  
[1] "customModelsInCaret "
```

4 Citation

```
> citation("predictiveModeling")
```

To cite package 'predictiveModeling' in publications use:

```
Adam Margolin, Nicole Deflaux, Matt Furia and the Sage Bionetworks  
Software Platform Team (2015). The predictive modeling package allows  
users to write custom predictive models or use off-the-shelf models  
via caret, and compare their performance. R package version 0.12-4.
```

A BibTeX entry for LaTeX users is

```
@Manual{,  
  title = {The predictive modeling package allows users to write custom  
predictive models or use off-the-shelf models via caret, and  
compare their performance.},  
  author = {Adam Margolin and Nicole Deflaux and Matt Furia and {Sage Bionetworks Software Platform Tea  
  year = {2015},  
  note = {R package version 0.12-4},  
}
```

5 Session Information

The output of `sessionInfo` on the build system after running this vignette.

```
> toLatex(sessionInfo())  
  
• R version 2.15.0 (2012-03-30), i386-apple-darwin9.8.0  
• Locale: C  
• Base packages: base, datasets, grDevices, graphics, methods, splines, stats, utils  
• Other packages: Biobase 2.16.0, BiocGenerics 0.2.0, KernSmooth 2.23-7, Matrix 1.0-6, affy 1.34.0,  
  caret 5.15-023, cluster 1.14.2, foreach 1.4.0, glmnet 1.7.3, lattice 0.20-6, plyr 1.7.1,  
  predictiveModeling 0.12-4, proclim 1.3.1, randomSurvivalForest 3.6.3, reshape 0.8.4, survcomp 1.6.0,  
  survival 2.36-12  
• Loaded via a namespace (and not attached): BiocInstaller 1.4.3, SuppDists 1.1-8, affyio 1.24.0,  
  bootstrap 2012.04-0, codetools 0.2-8, grid 2.15.0, iterators 1.0.6, preprocessCore 1.18.0, rmeta 2.16,  
  survivalROC 1.0.0, tools 2.15.0, zlibbioc 1.2.0
```