# ***Manual On Setting Up, Using, And Understanding Random Forests V3.1***

The V3.1 version of random forests contains some modifications and major additions to Version 3.0. It fixes a bad bug in V3.0. It allows the user to save the trees in the forest and run other data sets through this forest. It also allows the user to save parameters and comments about the run.

I apologize in advance for all bugs and would like to hear about them. To find out how this program works, read my paper "Random Forests" Its available on the same web page as this manual. It was recently published in the Machine Learning. Journal

The program is written in extended Fortran 77 making use of a number of VAX extensions. It runs on SUN workstations f77 and on Absoft Fortran 77 (available for Windows) and on the free g77 compiler. but may have hang ups on other f77 compilers. If you find such problems and fixes for them, please let me know.

**Random forests computes**

classification and class probabilities
intrinsic test set error computation
principal coordinates to use as variables.
variable importance (in a number of ways)
proximity measures between cases
a measure of outlyingness
scaling displays for the data

The last three can be done for the unsupervised case i.e. no class labels. I have used proximities to cluster data and they seem to do a reasonable job. The new addition uses the proximities to do metric scaling of the data. The resulting pictures of the data are interesting and useful.

The first part of this manual contains instructions on how to set up a run of random forests V3.1. The second part contains the notes on the features of random forests V3.1 and how they work.

## I. ***Setting Parameters***

The first seven lines following the parameter statement need to be filled in by the user.

### ***Line 1 Describing The Data***

**mdim**=number of variables
**nsample0**=number of cases (examples or instances) in the data
**nclass**=number of classes
**maxcat**=the largest number of values assumed by a categorical variable in the data
**ntest**=the number of cases in the test set. NOTE: Put ntest=1 if there is no test set. Putting ntest=0 may cause compiler complaints.
**labelts**=0 if the test set has no class labels, 1 if the test set has class labels.
**iaddcl**=0 if the data has class labels. If not, iaddcl=1 or 2 adds a synthetic class as described below

If their are no categorical variables in the data set maxcat=1. If there are categorical variables, the number of categories assumed by each categorical variable has to be specified in an integer vector called cat, i.e. setting cat(5)=7 implies that the 5th variable is a categorical with 7 values. If maxcat=1, the values of cat are automatically set equal to one. If not, the user must fill in the values of cat in the early lines of code.

For a J-class problem, random forests expects the classes to be numbered 1,2, ...,J. For an L valued categorical, it expects the values to be numbered 1,2, ... ,L. At present, L must be less than or equal to 32.

A test set can have two purposes--first: to check the accuracy of RF on a test set. The error rate given by the internal estimate will be very close to the test set error unless the test set is drawn from a different distribution. Second: to get predicted classes for a set of data with unknown class labels. In both cases the test set must have the same format as the training set. If there is no class label for the test set, assign each case in the test set label classs #1, i.e. put cl(n)=1, and set labelts=0. Else set labelts=1.

If the data has no class labels, addition of a synthetic class enables it

it to be treated as a two-class problem with nclass=2. Setting iaddclass=1 forms the synthetic class by independent sampling from each of the univariate distributions of the variables in the original data. Setting iaddclass=2 forms the synthetic class by independent sampling from uniforms such that each uniform has range equal to the range of the corresponding variable.

***Line 2 Setting up the run***

**jbt**=number of trees to grow
**mtry**=number of variables randomly selected at each node
**look**=how often you want to check the prediction error
**ipi**=set priors
**ndsize**=minimum node size

**jbt:**
this is the number of trees to be grown in the run. Don't be stingy--random forests produces trees very rapidly, and it does not hurt to put in a large number of trees. If you want auxiliary information like variable importance or proximities grow a lot of trees--say a 1000 or more. Sometimes, I run out to 5000 trees if there are many variables and I want the variables importances to be stable.

**mtry:**
this is the only parameter that requires some judgment to set, but forests isn't too sensitive to its value as long as it's in the right ball park. I have found that setting mtry equal to the square root of mdim gives generally near optimum results. My advice is to begin with this value and try a value twice as high and half as low monitoring the results by setting look=1 and checking the internal test set error for a small number of trees. With many noise variables present, mtry has to be set higher.

**look:**
random forests carries along an internal estimate of the test set error as the trees are being grown. This estimate is outputted to the screen every look trees. Setting look=10, for example, gives the internal error output every tenth tree added. If there is a labeled test set, it also gives the test set error. Setting look=jbt+1 eliminates the output. Do not be dismayed to see the error rates fluttering around slightly as more trees are added. Their behavior

is analagous to the sequence of averages of the number of heads in tossing a coin.

**ipi:** pi is an real-valued vector of length nclass which sets prior probabilities for classes. ipi=0 sets these priors equal to the class proportions. If the class proportions are very unbalanced, you may want to put larger priors on the smaller classes. If different weightings are desired, set ipi=1 and specify the values of the {pi(j)} early in the code. These values are later normalized, so setting pi(1)=1, pi(2)=2 weights a class 2 instance twice as much as a class 1 instance. The error rates reported are an unweighted count of misclassified instances.

**ndsize:** setting this to the value k means that no node with fewer than k cases will be split. The default that always gives good performances is ndsize=1. In large data sets, memory requirements will be less and speed enchanced if ndsize is set larger. Usually, this results in only a small loss of accuracy for large data sets.

***Line 3 Options on Variable Importance***

i**mp**=1 turns on the variable importances methods described below.

> **impstd**=1 gives the standard imp output
> **impmargin**=1 gives, for each case, a measure of the effect of noising up each variable
> **impgraph**=1 gives for each variable, a plot of the effect of the variable on the class probabilities.

**impstd**=1 computes and prints the following columns to a file

i) variable number
variables importances computed as:
ii) The % rise in error over the baseline error.
iii) 100* the change in the margins averaged over all cases
iv) The proportion of cases for which the margin is decreased minus the proportion of increases.
v) The gini increase by variable for the run

**impgraph**=1 computes and prints out the columns for each variable m--

i) variable number i.e. m
ii) sorted values of x(m) from lowest to highest
iii-iii+nclass) effect of x(m) on the probabilities of class j.

***Line 4 Options based on proximities***

**iprox**=1 turns on the computation of the intrinsic proximity measures between any two cases . This has to be turned on for the following options to work.

**noutlier**=1 computes an outlyingness measure for all cases in the data. If iaddcl=1 then the outlyingness measure is computed only for the original data. The output has the columns :

i) class
ii) case number
iii) measure of outlyingness

**iscale=1** computes scaling coordinates based on the proximity matrix. If iaddcl is turned on, then the scaling is outputted only for the original data. The output has the columns:

i) case number
i) true class
iii) predicted class.
iv) 0 if ii)=iii), 1 otherwise
v-v+msdim ) scaling coordinates

**mdimsc** is the number of scaling coordinates to be extracted. Usually 4-5 is sufficient

***Line 5 Transform to Principal Coordinates***

**ipc=1** takes the x-values and computes principal coordinates from the covariance matrix of the x's. These will be the new variables for RF to operate on. This will not work right if some of the variables are categorical.

**mdimpc:** This is the number of principal components to extract. It has to be <=mdim.

**norm=1** normaizes all of the variables to mean zero and sd one before computing the principal components.

***Line 6 Saving the forest***

**isavef**=1 saves all the trees in the forest to a file named eg. A.

**isavep**=1 creates a file B that contains the parameters used in the run and allows up to 500 characters of text description about the run.

**irunf**=1 reads file A and runs new data down the forest.

**ishowp**=1 reads file B and prints it to the sccreen

The calling code and files names required (except for the name of A) are at the end of the main program. The name for A is entered at the beginning of the program.

***Line 7 Output Controls***

Note: user must supply file names for all output listed below or send it to the screen.

**nsumout**=1 writes out summary data to the screen. This includes errors rates and the confusion matrix

**infout**=1 prints the following columns to a file
i) case number
ii) 1 if predicted class differs from true class, 0 else
iii) true class label
iv) predicted class label
v) margin=true class prob. minus the max of the other class prob.
vi)-vi+nclass) class probabilities

**ntestout**=1 prints the follwing coumns to a file
i) case number in test set
ii) true class (true class=1 if data is unlabeled)
iii) predicted class
iv-iv+nclass) class probabilities

**iproxout**=1 prints to file
i) case #1 number
ii) case #2 number
iii) proximity between case #1 and case #2

**USER WORK:**

The user has to construct the read-in the data code of which I have left an example. This needs to be done after the dimensioning of arrays. If maxcat >1 then the categorical values need to be filled in. If ipi=1, the user needs to specify the relative weights of the classes.

File names need to be specified for all output. This is important since a chilling message after a long run is "file not specified" or something similar.

**REMARKS:**

The proximities can be used in the clustering program of your choice. Their advantage is that they are intrinsic rather than an ad hoc measure. I have used them in some standard and home-brew clustering programs and gotten reasonable results. The proximities between class 1 cases in the unsupervised situation can be used to cluster. Extracting the scaling coordinates from the proximities and plotting scaling coordinate i versus scaling coordinate j gives illuminating pictures of the data. Usually, i=1 and j=2 give the most information (see the notes below).

There are four measures of variable importance: They complement each other. Except for the 4th they are based on the test sets left out on each tree construction. On a microarray data with 5000 variables and less than 100 cases, the different measures single out much the same variables (see notes below). But I have found one synthetic data set where the 3rd measure was more sensitive than the first three.

Sometimes, finding the effective variables requires some hunting. If the effective vzriables are clear-cut, then the first measure will find them. But if the number of variables is large compared to the number of cases, and if the predictive power of the individual variables is small, the other measures can be useful.

Random forests <u>does not overfit.</u> You can run as many trees as you want. Also, it is fast. Running on a 250mhz machine, the current version using a training set with 800 cases, 8 variables, and mtry=1, constructs each tree in .1 seconds. On a training set with 2200 cases, 11 variables, and mtry=3, each tree is constructed in .2 seconds. It takes 4 seconds per tree on a training set with 15000 cases and 16 variables with mtry=4, while also making computations for a 5000 member test set.

The present version of random forests does not handle missing values. A future version will. It is up to the user to decided how to deal with these. My current preferred method is to replace each missing value by the median of its column and each missing categorical by the most frequent value in that categorical. My impression is that because of the randomness and the many trees grown, filling in missing values with a sensible values does not effect accuracy much.

For large data sets, if proximities are not required, the major memory requirement is the storage of the data itself, and the three integer arrays a,at,b. If there are less than 64,000 cases, these latter three may be declared integer*2 (non-negative). Then the total storage requirement is about three times the size of the data set. If proximities are calculated, storage requirements go up by the square of the number of cases times eight bytes (double precision).

## ***Outline Of How Random Forests Works***

### *Usual Tree Construction--Cart*

Node=subset of data. The root node contains all data.

At each node, search through all variables to find best split into two children nodes.

Split all the way down and then prune tree up to get minimal test set error.

### *Random Forests Construction*

Root node contains a bootstrap sample of data of same size as original data. A different bootstrap sample for each tree to be grown.

An integer K is fixed, K<<number of variables. K is the **only** parameter that needs to be specified. Default is the square root of number of variables.

At each node, K of the variables are selected at random. Only these variables are searched through for the best split. The largest tree possible is grown and is not pruned.

The forest consists of N trees. To classify a new object having coordinates **x**, put **x** down each of the N trees. Each tree gives a classification for **x.**

The forest chooses that classification having the most out of N votes.

## Transformation to Principal Coordinates

One of the users lent us a data set in which the use of a few principal components as variables reduced the error rate by 2/3rds. On experimenting, a few other data sets were found where the error rate was significantly reduced by pre-transforming to principal coordinates As a convenience to users, a pre-transformation subroutine was incorporated into this version.

## ***Random Forests Tools***

The design of random forests is to give the user a good deal of information about the data besides an accurate prediction. Much of this information comes from using the "out-of-bag" cases in the training set that have been left out of the bootstrapped training set.

The information includes:

a) Test set error rate.

b) Variable importance measures

c) Intrinsic proximities between cases

d) Scaling coordinates based on the proximities

e) Outlier detection

The following explains how these work and give applications, both for labeled and unlabeled data.

## ***Test Set Error Rate***

In random forests, there is no need for cross-validation or a separate test set to get an unbiased estimate of the test set error. It is gotten internally, during the run, as follows:

Each tree is constructed using a different bootstrap sample from the original data. About one-third of the cases are left out of the bootstrap sample and not used in the construction of the kth tree.

Test Set Error Rate

Put each case left out in the construction of the kth tree down the kth tree to get a classification.

In this way, a test set classification is gotten for each case in about one-third of the trees. Let the final test set classification of the forest be the class having the most votes.

Comparing this classification with the class label present in the data gives an estimate of the test set error.

## **Class probability estimates**

At run's end, for each case, the proportion of votes for each class is recorded. For each member of a test set (with or without class labels), these proportions are also computed. By a stretch of terminology , we call these class probability estimates. These should not be interpreted as the underlying distributional probabilities. But they contain useful information about the case.

The margin of a case is the proportion of votes for the true class minus the maximum proportion of votes for the other classes. The size of the margin gives a measure of how confident the classification is.

## ***Variable Importance.***

Because of the need to know which variables are important in the classification, random forests has four different ways of looking at variable importance. Sometimes influential variables are hard to spot--using these four measures provides more information.

Measure 1

To estimated the importance of the mth variable. In the left out cases for the kth tree, randomly permute all values of the mth variable Put these new covariate values down the tree and get classifications.

Proceed as though computing a new internal error rate. The amount by which this new error exceeds the original test set error is defined as the importance of the mth variable.

Measures 2 and 3

For the nth case in the data, its margin at the end of a run is the proportion of votes for its true class minus the maximum of the proportion of votes for each of the other classes. The 2nd measure of importance of the mth variable is the average lowering of the margin across all cases when the mth variable is randomly permuted as in method 1.

The third measure is the count of how many margins are lowered minus the number of margins raised.

Measure 4

The splitting criterion used in RF is the gini criterion--also used in CART. At every split one of the mtry variables is used to form the split and there is a resulting decrease in the gini. The sum of all decreases in the forest due to a given variable, normalized by the number of trees, froms measure 4.

We illustrate the use of this information by some examples. Some of these were done on version 1 so may differ somewhat from the version 3 output.

## *An Example--Hepatitis Data*

Data: survival or non survival of 155 hepatitis patients with 19 covariates. Analyzed by Diaconis and Efron in 1983 Scientific American. The original Stanford Medical School analysis concluded that the important variables were numbers 6, 12, 14, 19.

Efron and Diaconis drew 500 bootstrap samples from the original data set and used a similar procedure, including logistic regression, to isolate the important variables in each bootstrapped data set.

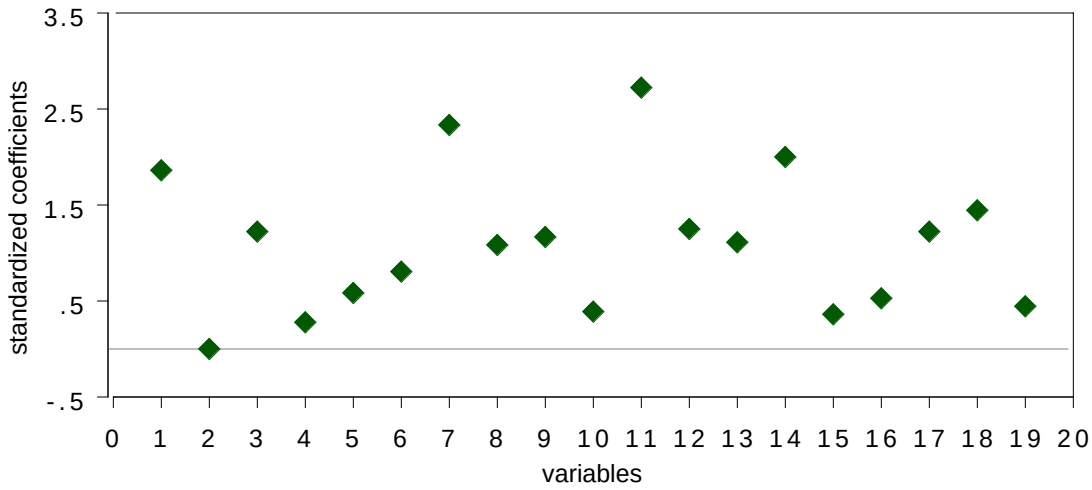
Their conclusion , "Of the four variables originally selected not one was selected in more than 60 percent of the samples. Hence the variables identified in the original analysis cannot be taken too seriously."

### *Logistic Regression Analysis*

Error rate for logistic regression is 17.4%.

Variables importance is based on absolute values of the coefficients of the variables divided by their standard deviations.

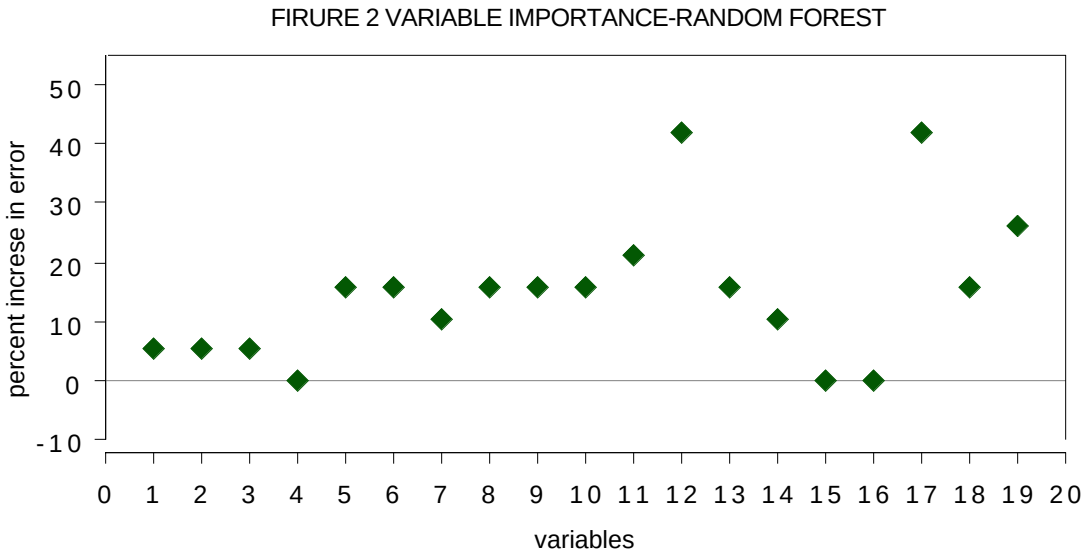
FIGURE 1 STANDARDIZED COEFFICIENTS-LOGISTIC REGRESSION




The conclusion is that variables 7 and 11 are the most important covariates. When logistic regression is run using only these two variables, the cross-validated error rate rises to 22.9% .

*Analysis Using Random Forests*

The error rate is 12.3%--30% reduction from the logistic regression error. Variable importances (measure 1) are graphed below:




Two variables are singled out--the 12th and the 17th The test set error rates running 12 and 17 alone were 14.3% each. Running both together did no better. Virtually all of the predictive capability is provided by a single variable, either 12 or 17. (they are highly correlated)

The standard procedure when fitting data models such as logistic regression is to delete variables; Diaconis and Efron (1983) state , "...statistical experience suggests that it is unwise to fit a model that depends on 19 variables with only 155 data points available."

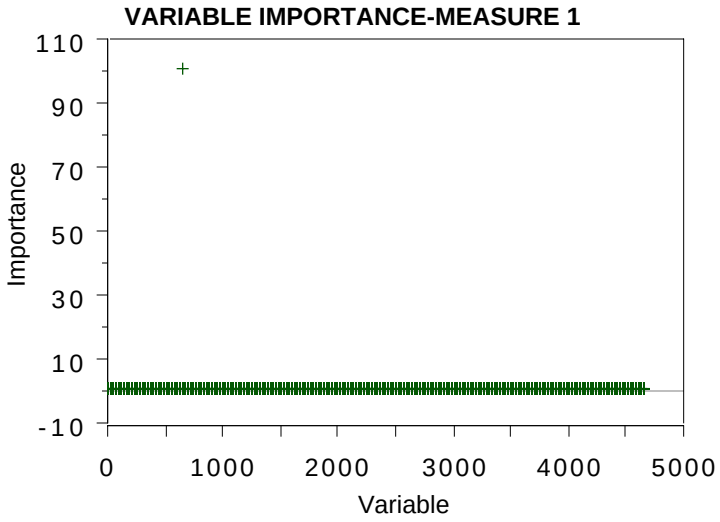
Newer methods in Machine Learning thrive on variables--the more the better. There is no need for variable selection ,On a sonar data set with 208 cases and 60 variables, Random Forests error rate is 14%. Logistic Regression has a 50% error rate.

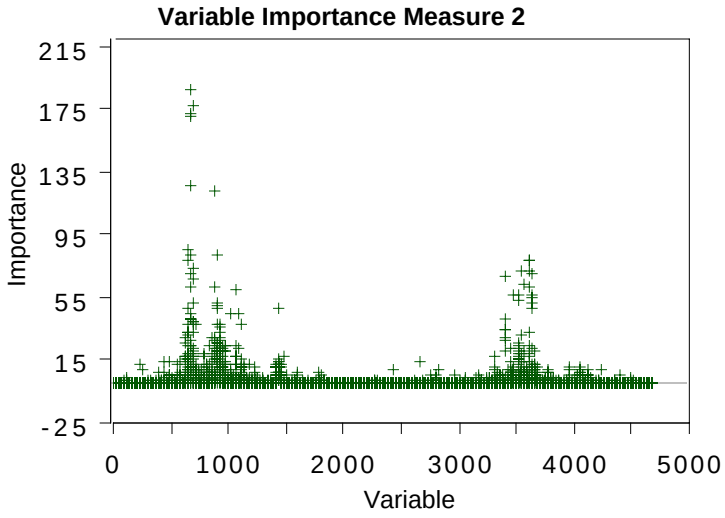
## *Microarray Analysis*

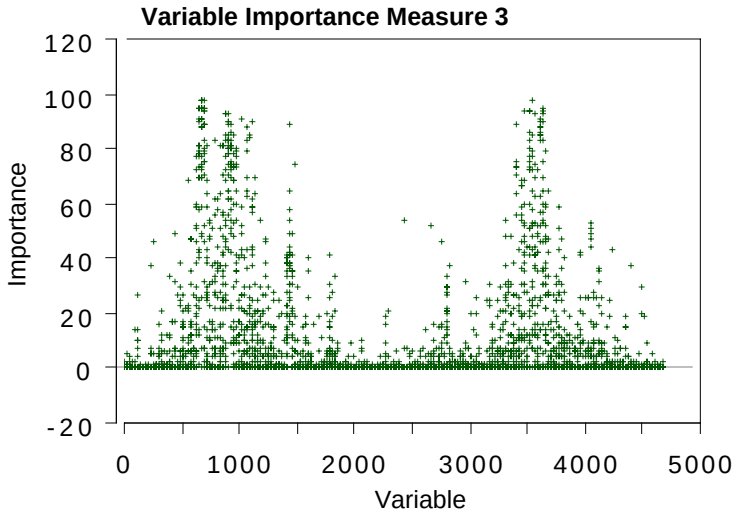
Random forests was run on a microarray lymphoma data set with three classes, sample size of 81 and 4682 variables (genes) without any variable selection. The error rate was low (1.2%) using mtry=150.

What was also interesting from a scientific viewpoint was an estimate of the importance of each of the 4682 genes.

The graphs below were produced by a run of random forests.





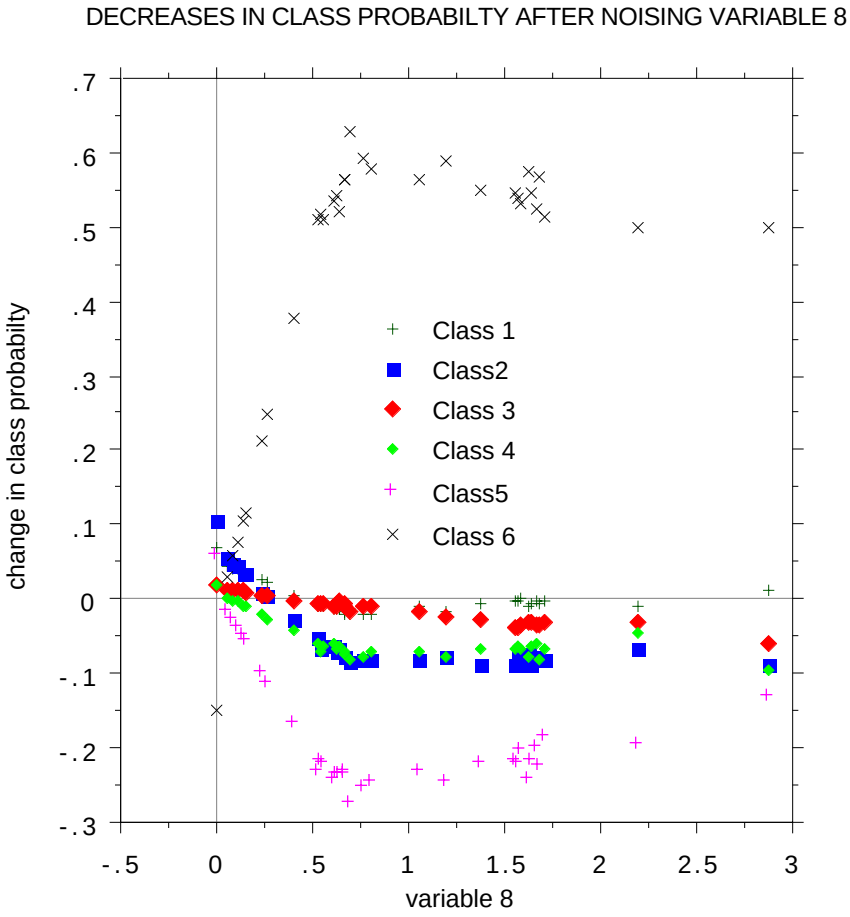

The graphs show that measure 1 has the least sensitivity, showing only one significant variable. Measure 2 has more, showing not only the activity around the gene singled out by measure 1 but also a secondary burst of activity higher up. Measure 3 has too much sensitivity, fingering too many variables.

Measure 4 also has too much sensitivity. On the other hand, on another microarray data set, measure 4 was the only measure that was capable of locating important variables.

## *Effects of variables on predictions*

Besides knowing which variables are important, another piece of information needed is how the values of each variable effects the prediction. To look at this, for each class and each variable m, use as response variable the class probability minus the class probability with the mth variable noised. Plot this against the values of the mth variable and do a smoothing of the curve.

The figure below is a plot of the decreases in class probability due to noising up the 8th variable in the glass data. The sixth class probability is significantly decreased. The other class probabilities increase somewhat. They are happy the variable 8 is out of the picture.




## ***An intrinsic proximity measure***

Since an individual tree is unpruned, the terminal nodes will contain only a small number of instances. Run all cases in the training set down the tree. If case i and case j both land in the same terminal node. increase the proximity between i and j by one. At the end of the run, the proximities are divided by twice the number of trees in the run and proximity between a case and itself set equal to one.

To cluster-use the above proximity measures.

## *Example-Bupa Liver Disorders*

This is a two-class biomedical data set consisting of the covariates

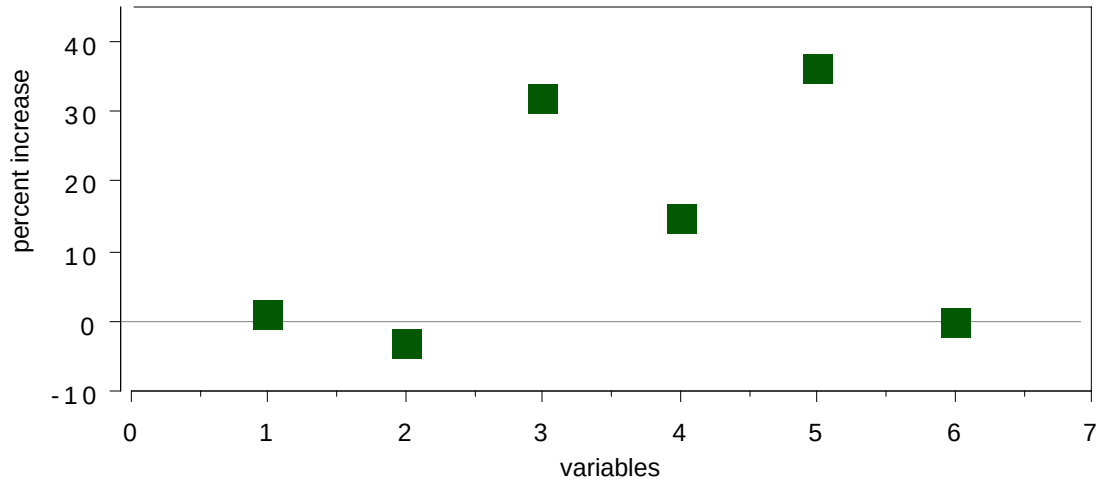
| | |
|---|---|
| 1. mcv | mean corpuscular volume |
| 2. alkphos | alkaline phosphotase |
| 3. sgpt | alamine aminotransferase |
| 4. sgot | aspartate aminotransferase |
| 5. gammagt | gamma-glutamyl transpeptidase |
| 6. drinks | number of half-pint equivalents of alcoholic beverage drunk per day |

The first five attributes are the results of blood tests thought to be related to liver functioning. The 345 patients are classified into two classes by the severity of their liver disorders.

The misclassification error rate is 28% in a Random Forests run. What can we learn about this data?

A) *Variable Importance (method 1)*

FIGURE 2 VARIABLE IMPORTANCE-BUPA LIVER



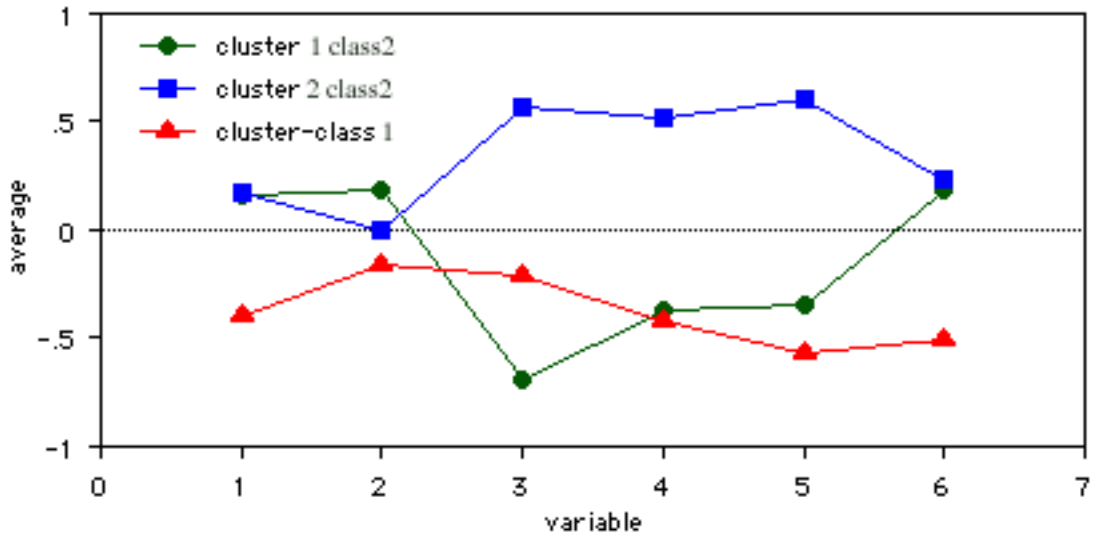

Blood tests 3 and 5 are the most important, followed by test 4.

## B) *Clustering*

Using the proximity measure outputted by Random Forests to cluster, there are two class #2 clusters.

In each of these clusters, the average of each variable is computed and plotted:

FIGURE 3 CLUSTER VARIABLE AVERAGES




Something interesting emerges. The class two subjects consist of two distinct groups: Those that have high scores on blood tests 3, 4, and 5 Those that have low scores on those tests. We will revisit this example below.

## ***Scaling Coordinates***

The proximities between cases n and k form a matrix {prox(n,k)}. From their definition, it is easy to show that this matrix is symmetric, positive definite and bounded above by 1, with the diagonal elements equal to 1. It follows that the values 1-prox(n,k) are squared distances in a Euclidean space of dimension not greater than the number of cases. For more background on scaling see "Multidimensional Scaling" by T.F. Cox and M.A. Cox

Let prox(n,-) be the average of prox(n,k) over the 2nd coordinate. and prox(-,-) the average over both coordinates. Then the matrix:

$$\text{cv((n,k)=.5*(prox(n,k)-prox(n,-)-prox(k,-)+prox(-,-))}$$

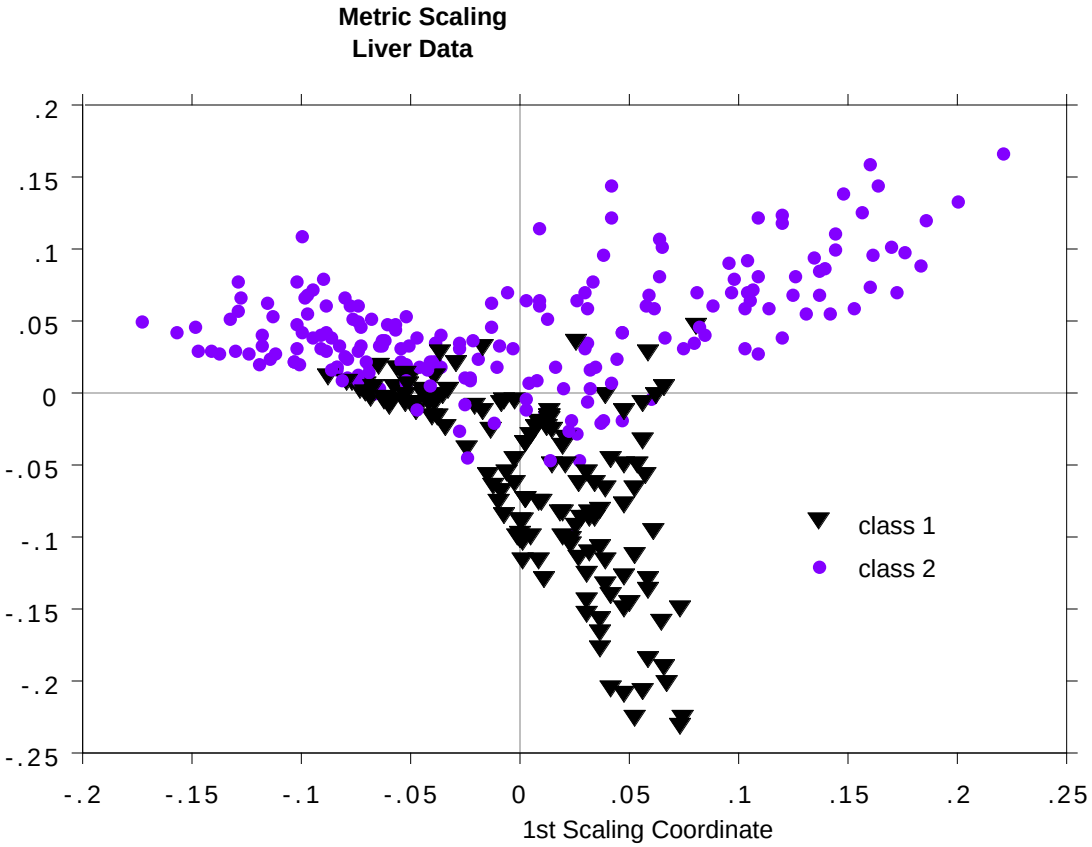
is the matrix of inner products of the distances and is also positive definte symmetric. Let the eigenvalues of cv be $\lambda(l)$_and the eigenvectors $v_l(n)$_Then the vectors

$$x(n) = (\sqrt{\lambda(1)}v_1(n), \sqrt{\lambda(2)}v_{2,}(n), \ldots)$$

have squared distances between them equal to 1-prox(n,k). We refer to the values of $\sqrt{\lambda(j)}v_j(n)$_ as the jth scaling coordinate.

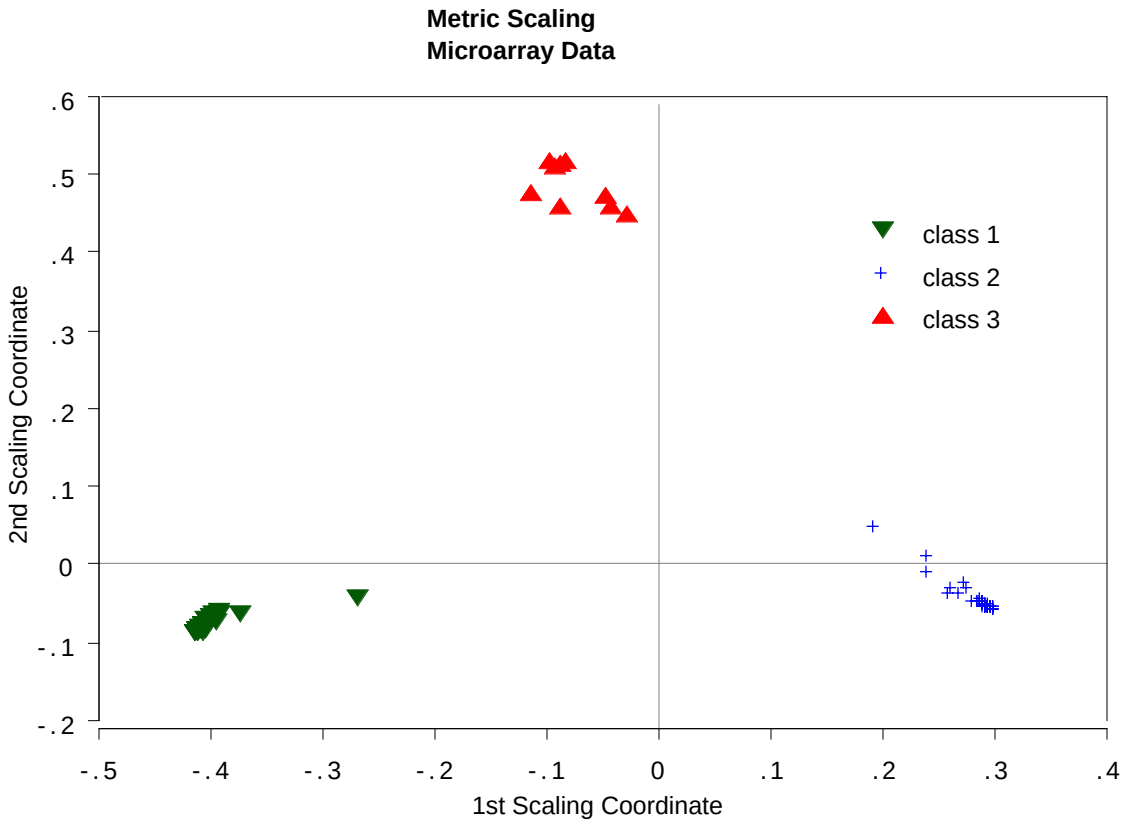
In metric scaling, the idea is to approximate the vectors **x**(n) by the first few scaling coordinates. This is done in random forests by extracting the number msdim of the largest eigenvalues and corresponding eigenvectors of the cv matrix. The two dimensional plots of the ith scaling coordinate vs. the jth often gives useful information about the data. The most useful is usually the graph of the 2nd vs. the 1st.

We illustrate with three examples. The first is the graph of 2nd vs. 1st scaling coordinates for the liver data



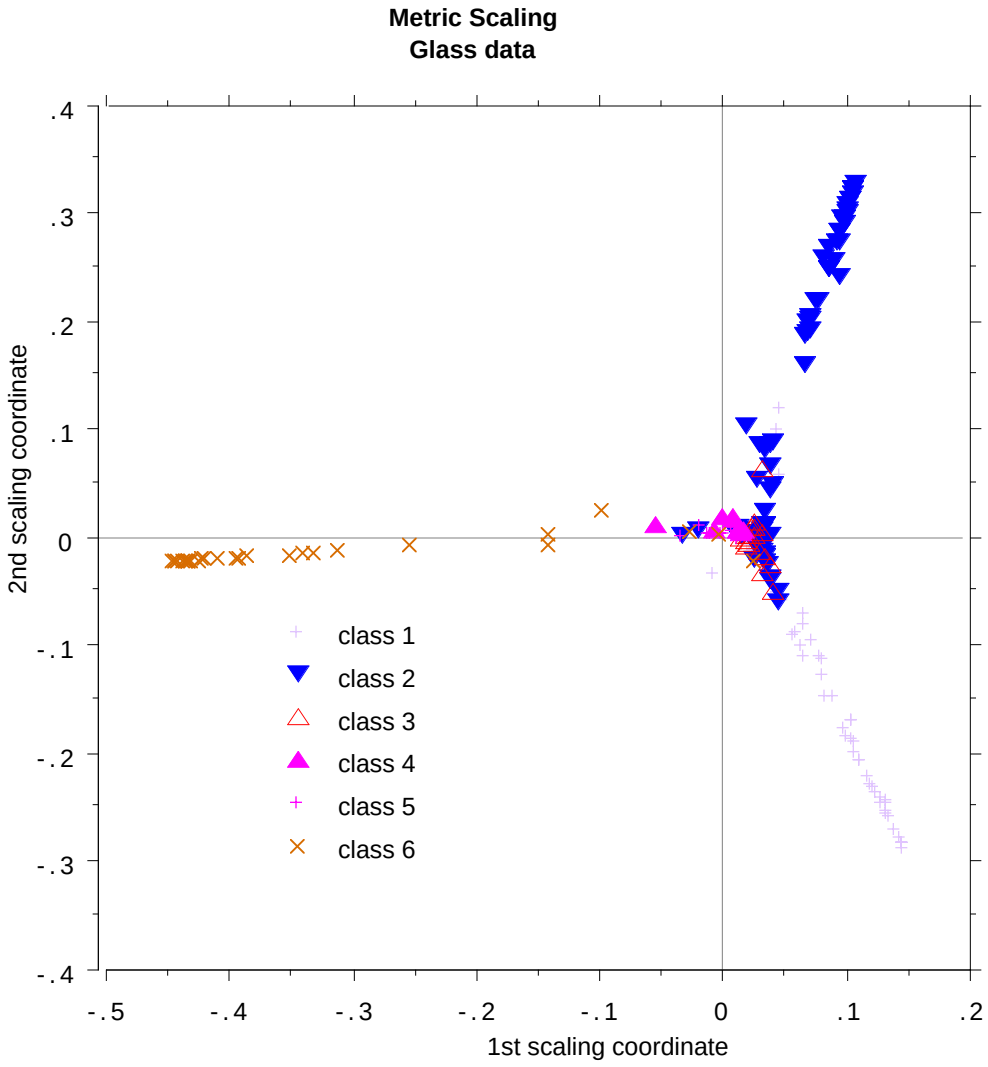

The two arms of the class #2 data in this picture correspond to the two clusters found and discussed above.

The next example uses the microarray data. With 4682 variables, it is difficult to see how to cluster this data. Using proximities and the first two scaling coordinates gives this picture:




Random forests misclassifies one case. This case is represented by the isolated point in the lower left hand corner of the plot.

The third example is glass data with 214 cases, 9 variables and 6 classes. This data set has been extensively analyzed (see Pattern recognition and Neural Networkks-by B.D Ripley). Here is a plot of the 2nd vs. the 1st scaling coordinates.:

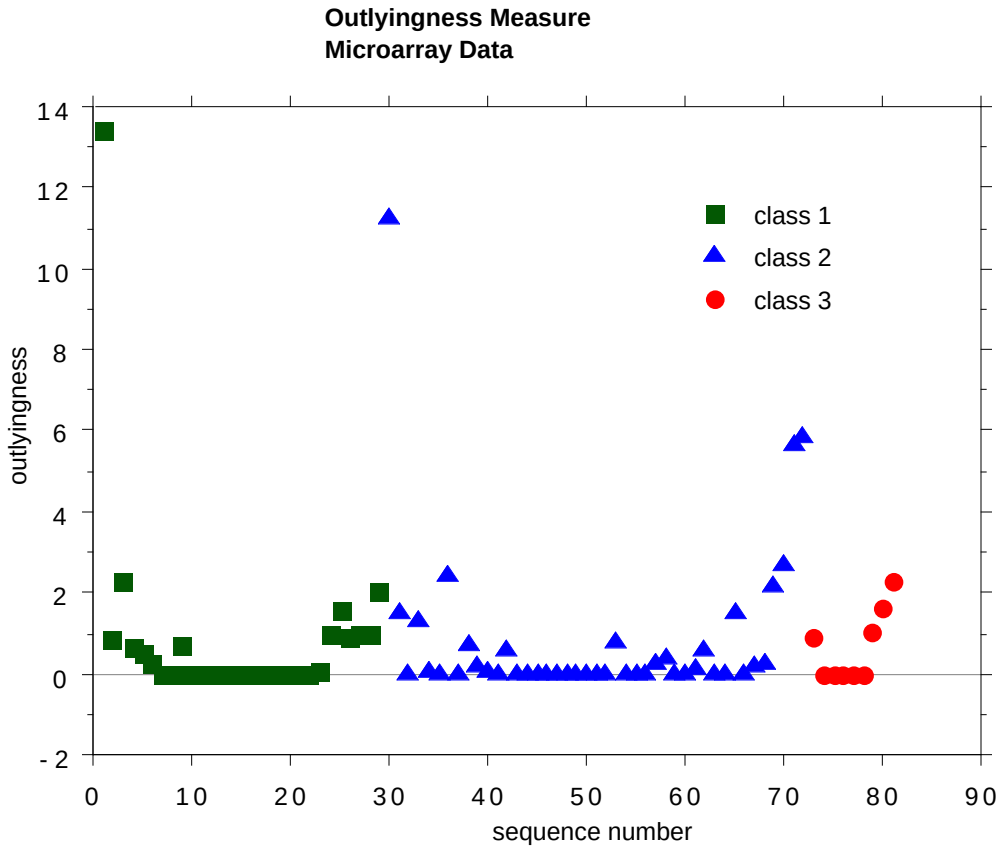



None of the analyses to data have picked up this interesting and revealing structure of the data--compare the plots in Ripley's book.

## ***Outlier Location***

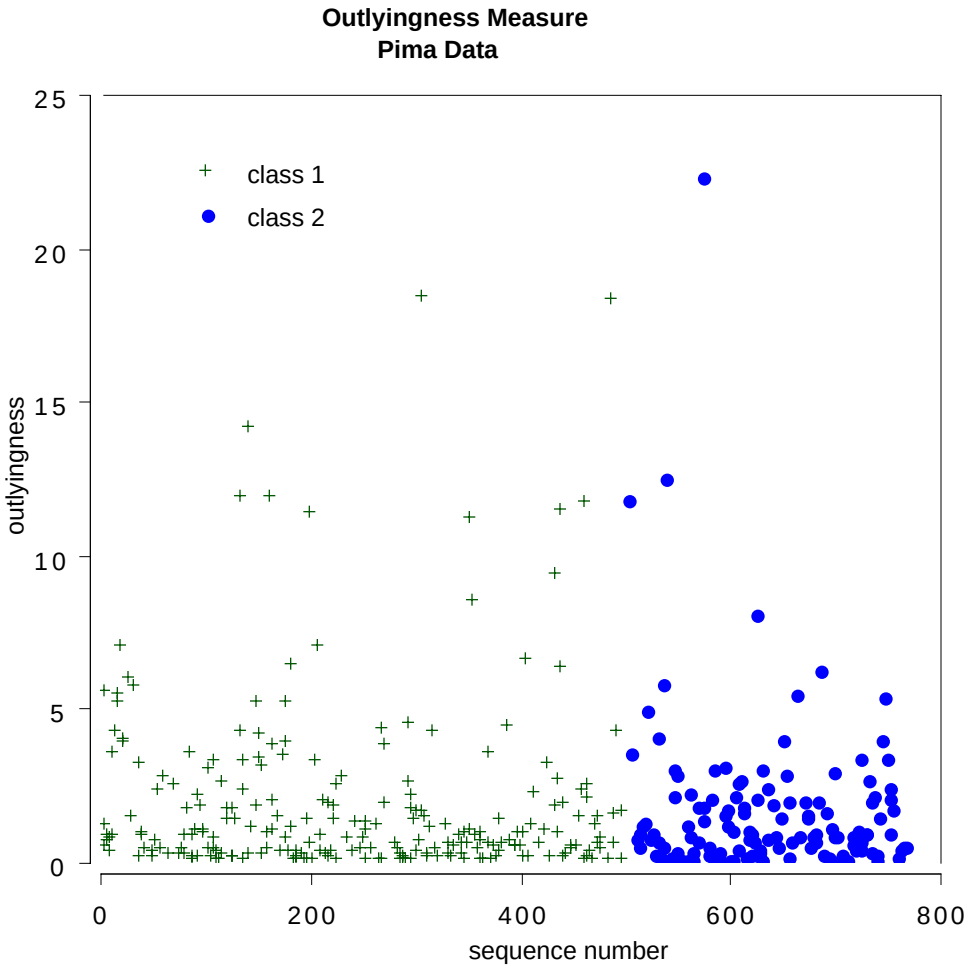
Outliers are defined as cases having small proximities to all other cases. Since the data in some classes is more spread out than others, outlyingness is defined only with respect to other data in the same class as the given case. To define a measure of outlyingness, we first compute, for a case n, the sum of the squares of prox(n,k) for all k in the same class as case n. Take the inverse of this sum--it will be large if the proximities prox(n,k) from n to the other cases k in the same class are generally small. Denote this quantity by out(n).

For all n in the same class, compute the median of the out(n), and then the mean absolute deviation from the median. Subtract the median from each out(n) and divide by the deviation to give a normalized measure of outlyingness. Yhe values less than zero are set to zero. Generally, a value above 10 is reason to suspect the case of being outlying. Here is a graph of outlyingness for the microarray data




There are two possible outliers--one is the first case in class 1, the second is the first case in class 2.

As a second example, we plot the outlyingness for the Pima Indians hepatitis data. This data set has 768 cases, 8 variables and 2 classes. It has been used often as an example in Machine Learning research but has been suspected of containing a number of outliers.




If 10 is used as a cutoff point, there are 12 cases suspected of being outliers.

## ***Analyzing Unlabeled Data***

Unlabeled date consists of N vectors {**x**(n)} in M dimensions. Using the iaddcl option in random forests, these vectors are assigned class label 1. Another set of N vectors is created and assigned class label 2. The second synthetic set is created by independent sampling from the one-dimensional marginal distributions of the original data.

For example, if the value of the mth coordinate of the original data for the nth case is x(m,n), then a case in the synthetic data is constructed as follows: its first coordinate is sampled at random

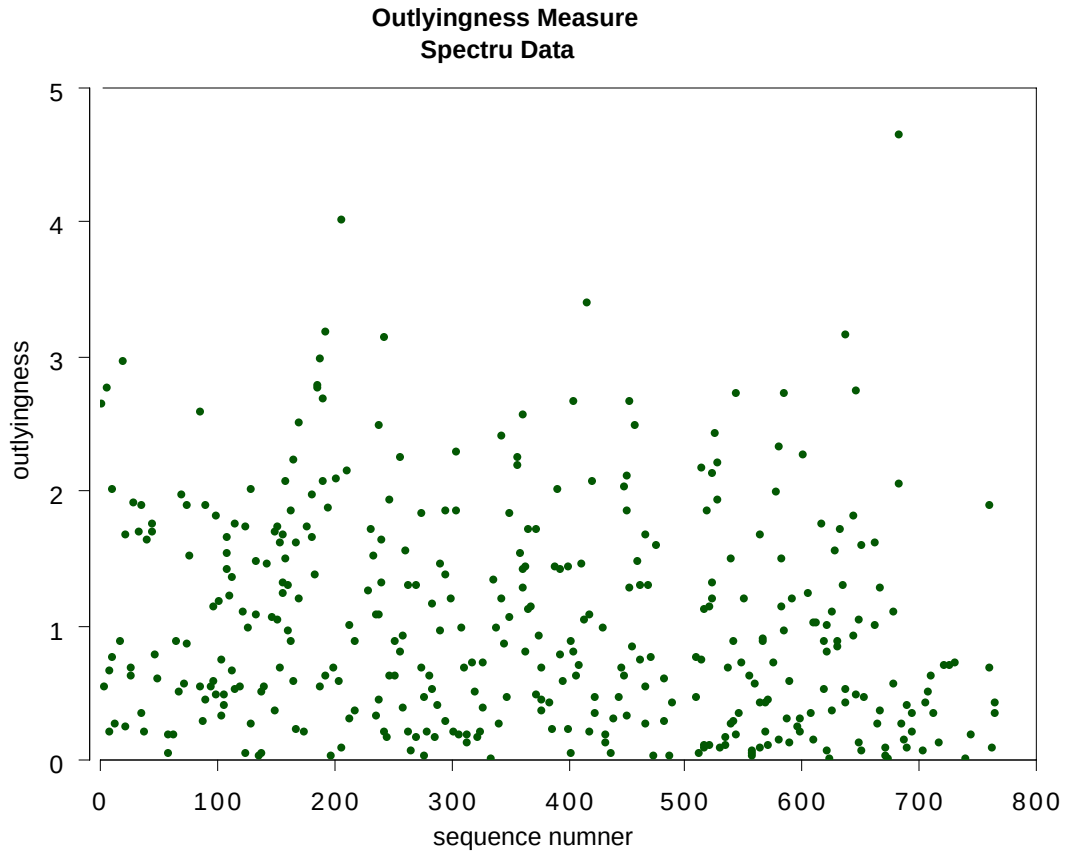
from the N values x(1,n), its second coordinate is sampled at random from the N values x(2,n), and so on. Thus the synthetic data set can be considered to have the distribution of M independent variables where the distribution of the mth variable is the same as the univariate distribution of the mth variable in the original data.

When this two class data is run through random forests a high misclassification rate--say over 40%, implies that there is not much dependence structure in the original data. That is, that its structure is largely that of M independent variables--not a very interesting distribution. But if there is a strong dependence structure between the variables in the original data, the error rate will be low. In this situation, the output of random forests can be used to learn something about the structure of the data. The following is an example.

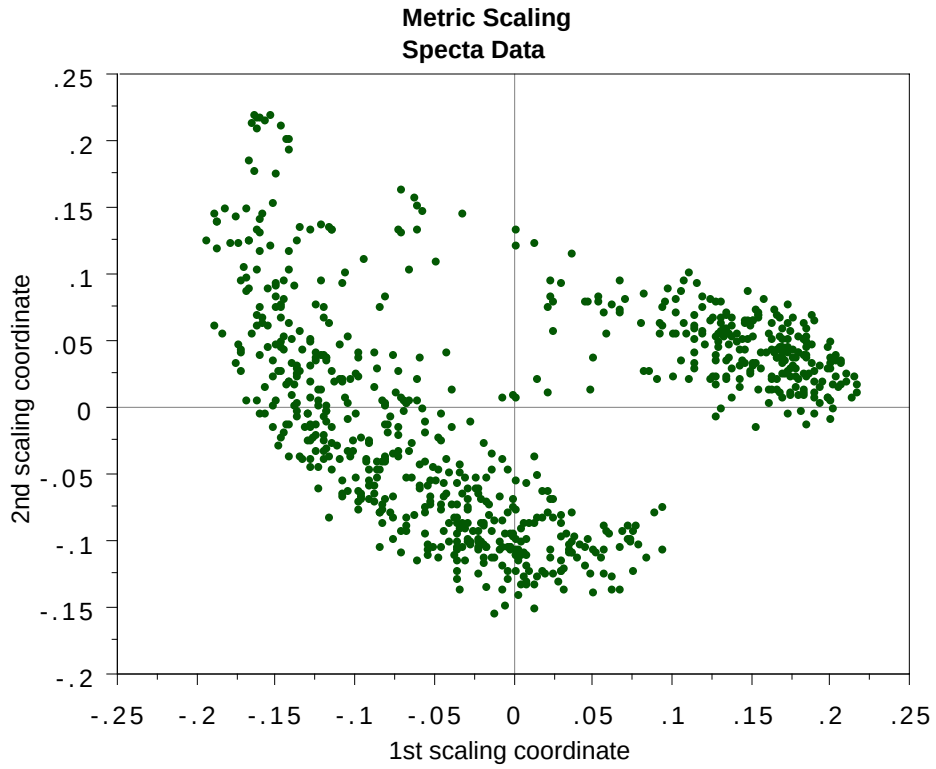
## *An Application to Chemical Spectra*

Data graciously supplied by Merck consists of the first 468 spectral intensities in the spectrums of 764 compounds. The challenge presented by Merck was to find small cohesive groups of outlying cases in this data. Using the iaddcl option, there was excellent separation between the two classes, with an error rate of 0.5%, indicating strong dependencies in the original data.

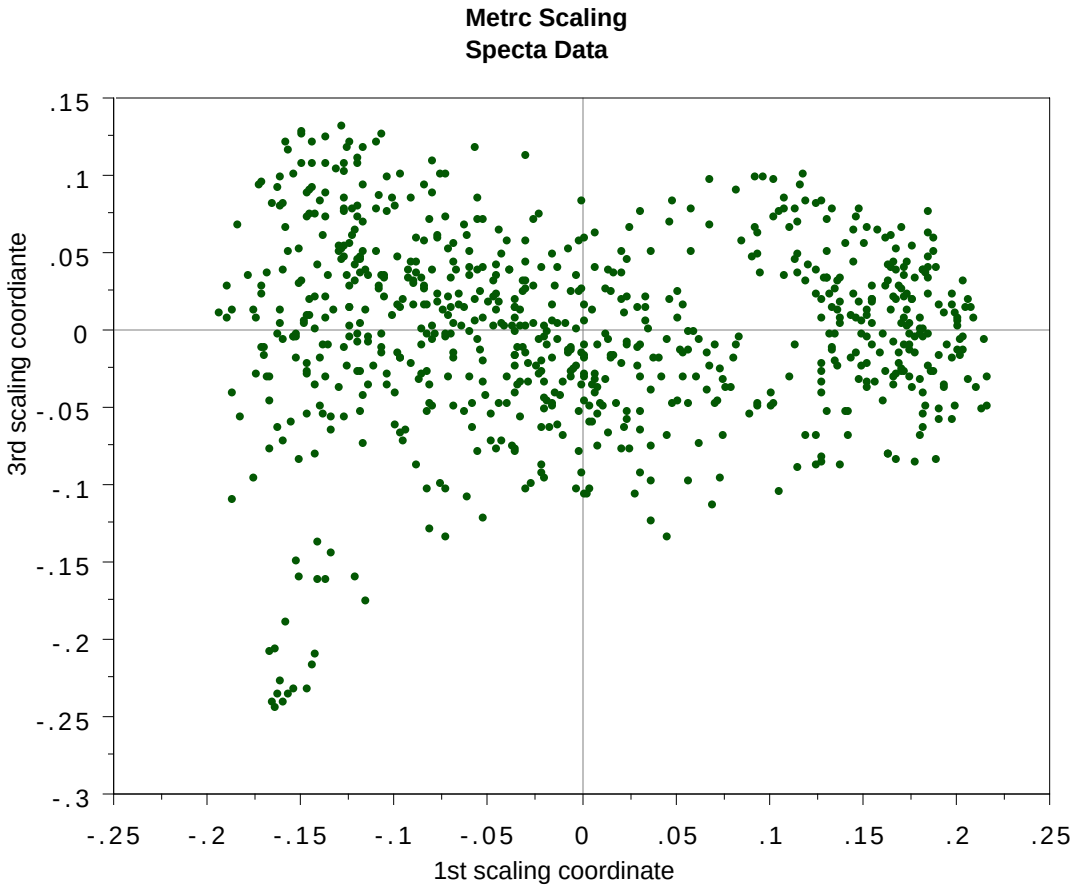
We looked at outliers and generated this plot.




This plot gives no indication of outliers. But outliers must be fairly isolated to show up in the outlier display. To search for outlying groups scaling coordinates were computed. The plot of the 2nd vs. the 1st is below:




This shows, first, that the spectra fall into two main clusters. There is a possiblity of a small outlying group in the upper left hand corner. To get another picture, the 3rd scaling coordinate is plotted vs. the 1st.




The group in question is now in the lower left hand corner and its separation from the body of the spectra has become more apparent.

## ***Saving Forests and Parameters***

If the data set is large with many variables, a run growing 100 trees may take awhile. If there is another set of data with the same parameters except for sample size, the user may want to run this 2nd set down the forest either to get classifications or to use the data as a test set. In this case put isavef=1 and isavep=1.

When isavef is on, the variable values saved to file (which the user must name-say 'forest55') are enough to reconstruct the forest. If irunf =1, then first, the new data are read in. Then the statement open(1, file='forest55',status='old') runs the new data down the forest.

If labelts is set =1, that implies that the new data has labels, and the program will output the error after each tree. If labelts=0, then the new data has no class labels. But data must still be read in as

though there were values of the labels. Simply assign each label the value 1. As soon as these parameter values are filled in and the new data read in, iut goes down the forest. If inewcl=1, then at the end of the run, all predicted class labels will be saved to a file.

The user knows ntest--the sample size of the data to run down the reconstituted forest. But may not remember the other values that need to be put in the parameter statement. However, if when doing the initial run, isavep was put equal to 1 and a filename given in the lines just before the end of the main program, then all the needed parameters will be saved to the file as well as a textual description of up to 500 characters. The only thing that the user provides is the file name and the textual description.

For these new runs modify the parameter statment as follows.
1. all options should be turned off,
2 set nsample0=1, ntest=sample size of the new data, and replace the value of nrnodes by the value given in the parameter file.
3. all other values stay the same as in the original run.

Parameters of the original run given by the file are nsample0,mdim, maxcat, nclass, jbt, nrnodes,the out-of-bag error rate, as well as the original nsample0. The other parameters in the parameter statement such as mtry have no effect in the rerun.

If I have left anything out of this manual, let me know. (leo@stat.berkeley.edu). Please report bugs either to me or Adele Cutler (adele@sunfs.math.usu.edu)