What is SAM/PAM?

Significance Analysis of Microarrays (SAM)

Significance Analysis of Microarrays (SAM) is statistical technique for finding significant genes in a set of microarray experiments. The software was developed at Stanford University and is free to academic users. SAM is a convenient MS Excel add-in. The input to SAM is gene expression measurements (the normalized gene expression ratio for each gene) from a set of microarray hybridizations and a response variable from each experiment. SAM works with data from both cDNA and oligo arrays and can also be applied to protein expression and SNP array data. In the one-class response variable, SAM tests whether the mean gene expression differs from zero.

Site: http://www-stat.stanford.edu/~tibs/SAM/

Prediction Analysis of Microarrays (PAM)

Prediction Analysis of Microarrays (PAM) performs sample classification from gene expression data using the nearest shrunken centroid method. PAM provides a list of significant genes whose expression characterizes each diagnostic class. The software was developed at Stanford University and is free to academic users. PAM is a convenient MS Excel add-in. It works with both cDNA and oligo arrays and can be applied to protein expression data and SNP array data.

Site: http://www-stat.stanford.edu/~tibs/PAM/

What is the Nearest Shrunken Centroid Method?

The method computes a standardized centroid for each class. This is the average gene expression for each gene in each class divided by the within-class standard deviation for that gene. Nearest centroid classification takes the gene expression profile of a new sample, and compares it to each of these class centroids. The class whose centroid that it is closest to, in squared distance, is the predicted class for that new sample.

Nearest shrunken centroid classification makes one important modification to standard nearest centroid classification. It "shrinks" each of the class centroids toward the overall centroid for all classes by an amount we call the threshold . This shrinkage consists of moving the centroid towards zero by threshold, setting it equal to zero if it hits zero. For example ifthreshold was 2.0, a centroid of 3.2 would be shrunk to 1.2, a centroid of -3.4 would be shrunk to -1.4, and a centroid of 1.2 would be shrunk to zero. After shrinking the centroids, the new sample is classified by the usual nearest centroid rule, but using the shrunken class centroids. This shrinkage has two advantages: 1) it can make the classifier more accurate by reducing the effect of noisy genes, and 2) it does automatic gene selection. The user decides on the value to use for threshold. Typically one examines a number of different choices.

(Taken from the PAM website)