**KitA/KitO Classifier Algorithm**

Here are the details of the KitO/KitA Classifier. It should be a particularly simply algorithm to implement. I’ve also included a text file that has the PC1 coefficients for each Classifier probeset. The first column are the AxiomCEU probeset IDs (which are also the probeset IDs for ASI and Han Chinese), the second column are the Genome Scan Probeset IDs (which you probably won’t need), the third column are the UCSF probeset IDs, the fourth column has the PC1 coefficient values, and the last column are the means for each probesets from the training data.

1. Compute signal\_size for each classifier probeset for each sample [signal\_size = log2(A + B)/2]. A and B are the normalized probe intensities.
2. Subtract off training means from each sample following signal\_size computation being sure to keep the order of probeset IDs the same. For each sample, compute the dot product of the classifier probeset post means subtraction with the PC1 coefficient values again being sure to keep the order the same, i.e.
3. If the dot product value is greater than 4.5, the sample is classified as KitO.
4. If the dot product value is less than -4.5, the sample is classified as KitA.
5. If the value is in between, the sample is classified as “Unknown”.

That’s it!