Compute S2N weight for each gene and each class

For each permutation, recompute S2N weight for each gene and each class

Randomly permute class labels

Iterate random permutation 1,000 times and recompute S2N weights

Derive p-value for each gene and for each class

S2N weights of gene i for class B for permuted class labels

Number of permutations

S2N weight of gene i for class B

Filter test set and retain only selected marker genes

Rank genes according to weight and p-value; filter learning set L, to retain only genes with \( P < \) threshold value

Filter test set and retain only selected marker genes

Original data set

Class 1

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]

\( \text{Class} \)

\[ \text{p} \]

\[ \text{n} \]