

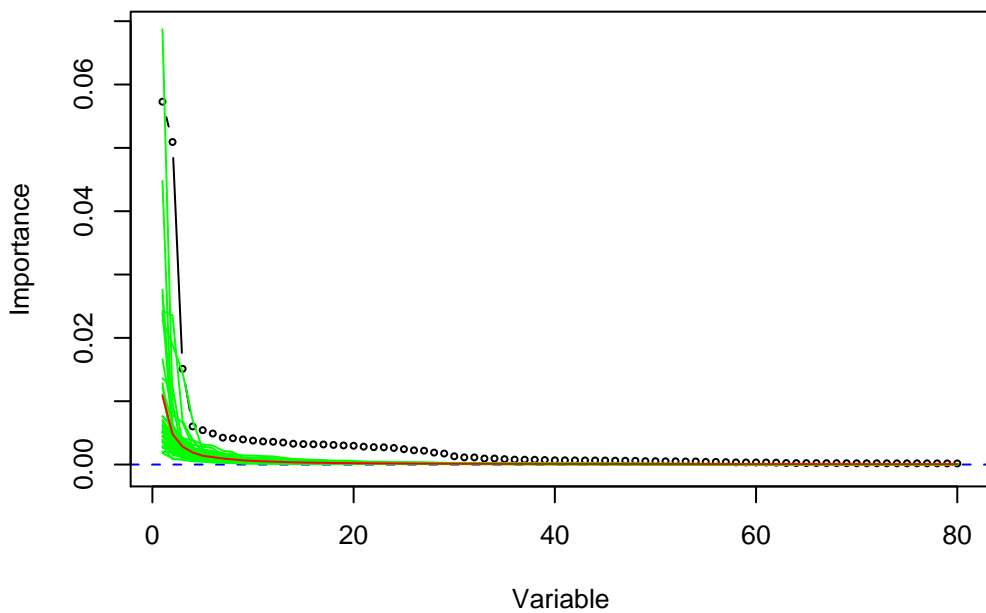
Variable importances: real microarray data sets.

'Scree plots' or 'importance spectrum':

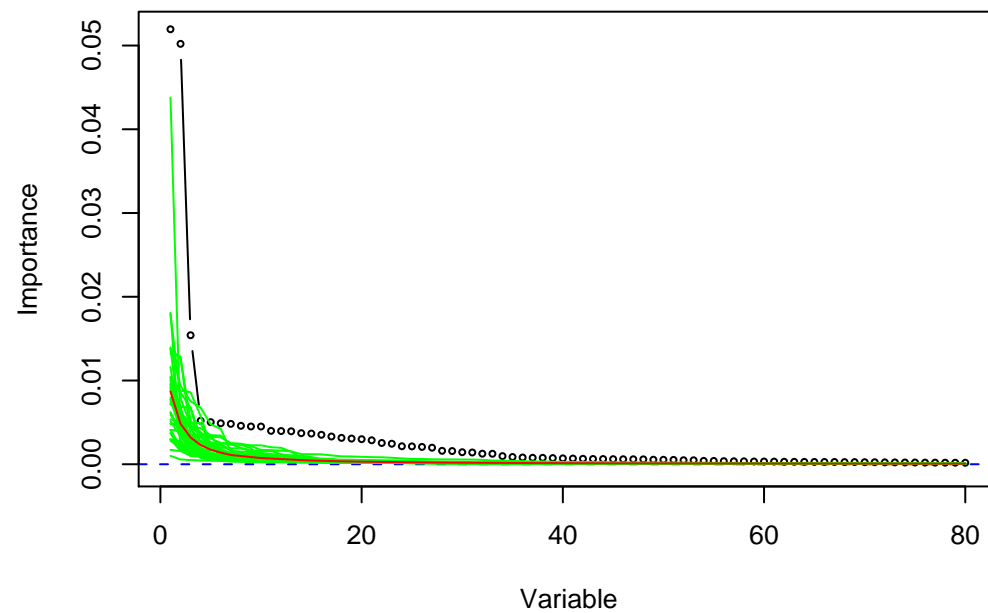
Black: original data sets; green: permuted class labels data sets;

red: average from permuted class labels data sets.

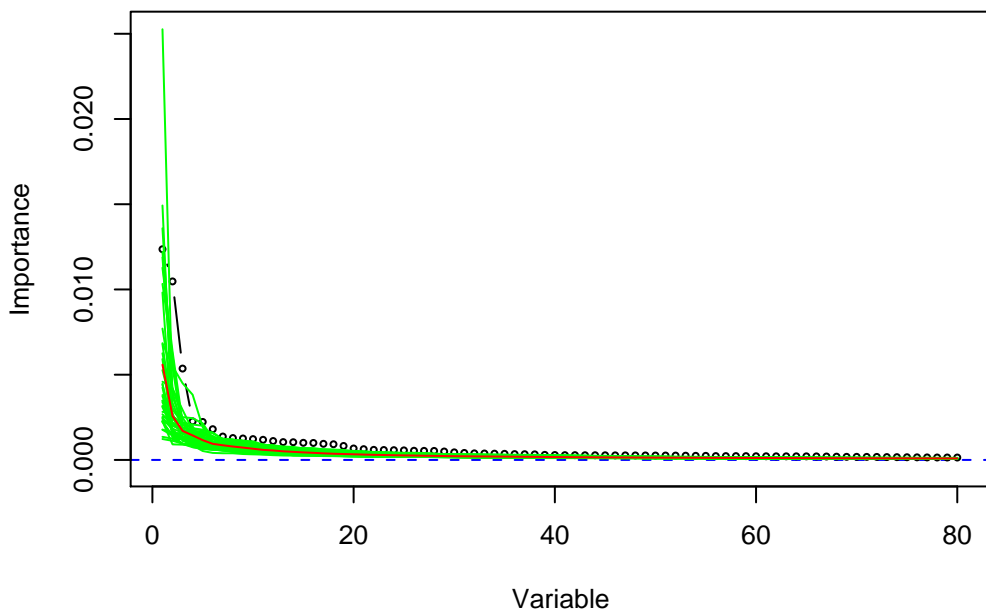
**leukemia; ntree = 5000, mtry = ncol**



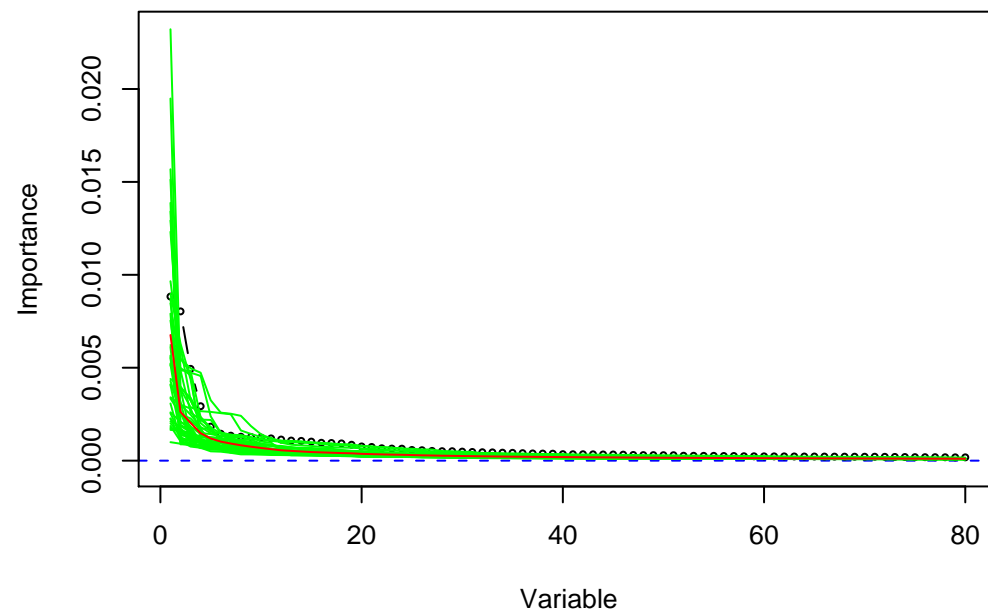
**leukemia; ntree = 5000, mtry = 0.5 \* ncol**



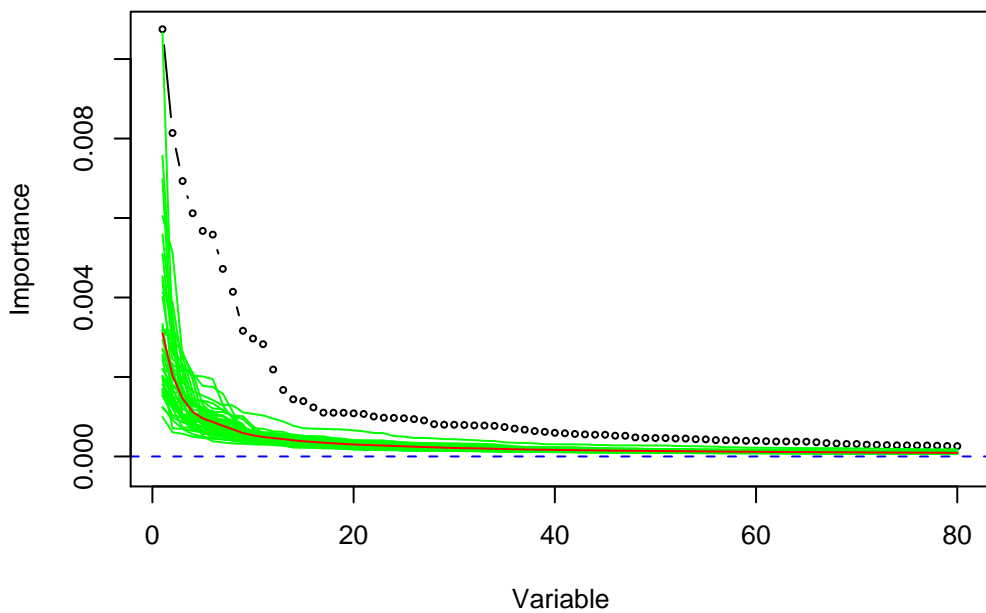
**breast, 2cl; ntree = 5000, mtry = ncol**



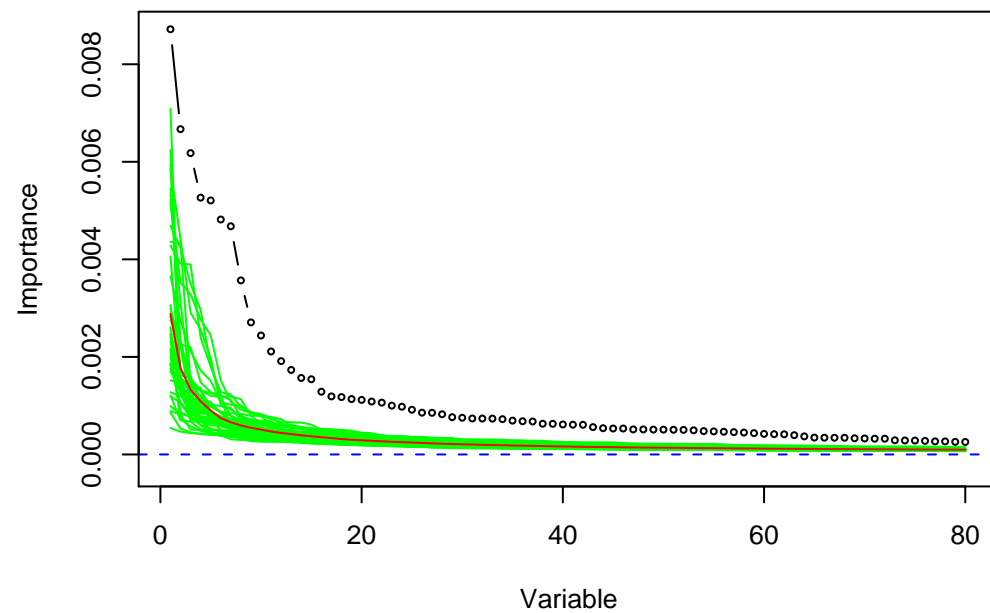
**breast, 2cl.; ntree = 5000, mtry = 0.5 \* ncol**



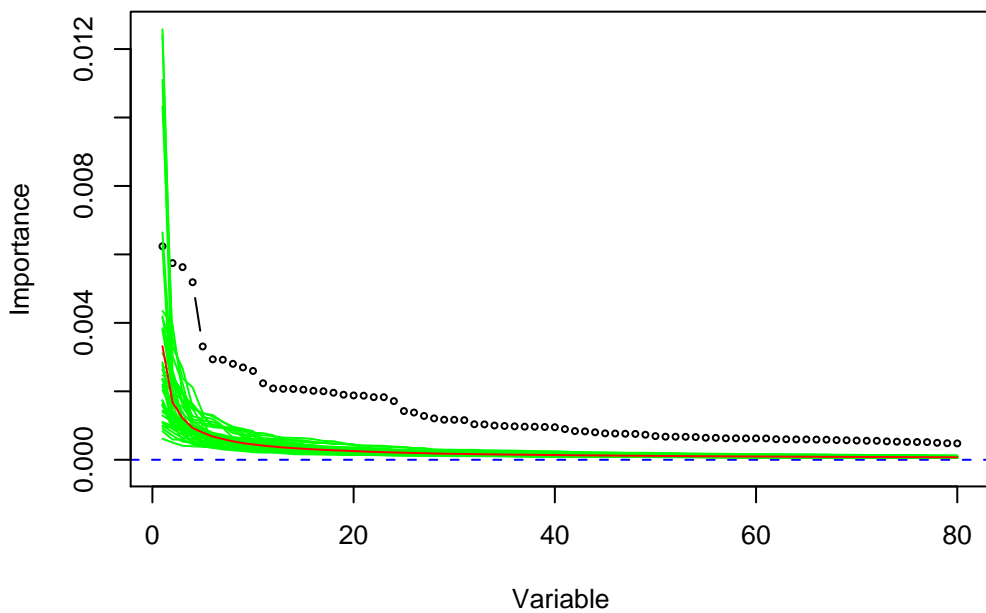
**breast, 3cl; ntree = 5000, mtry = ncol**



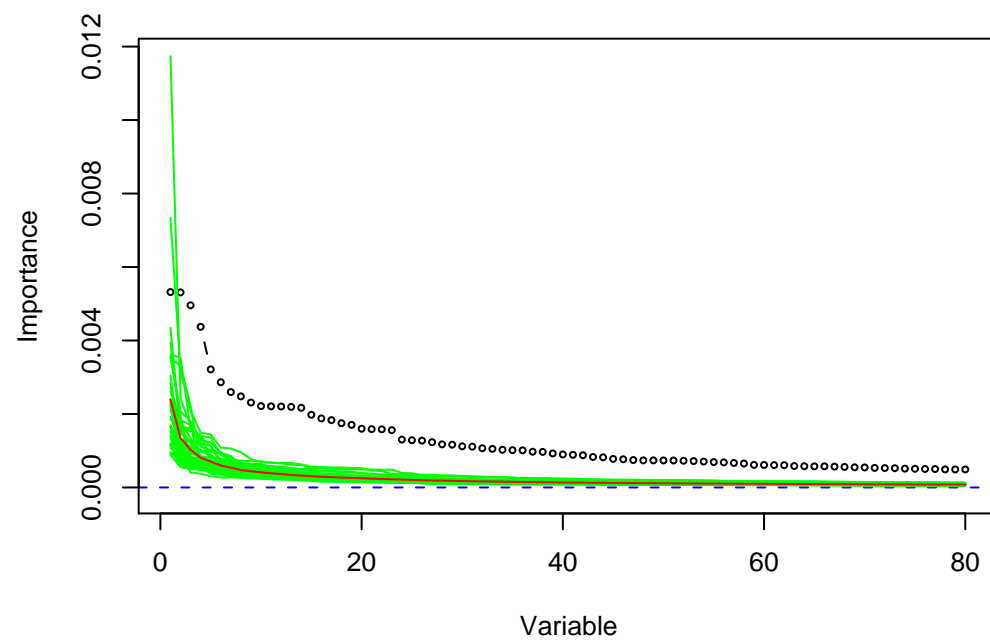
**breast, 3cl.; ntree = 5000, mtry = 0.5 \* ncol**



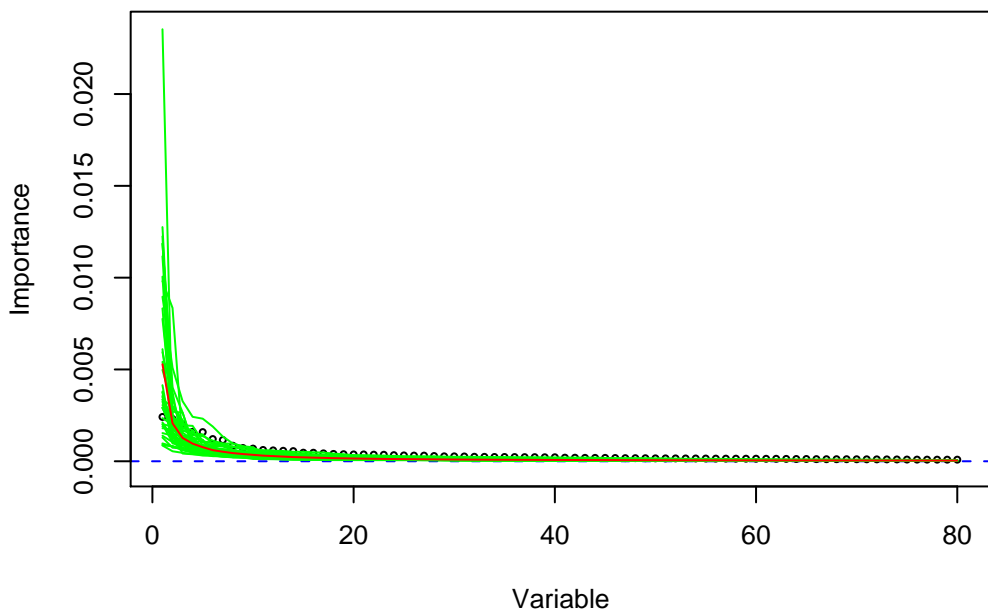
**NCI; ntree = 5000, mtry = ncol**



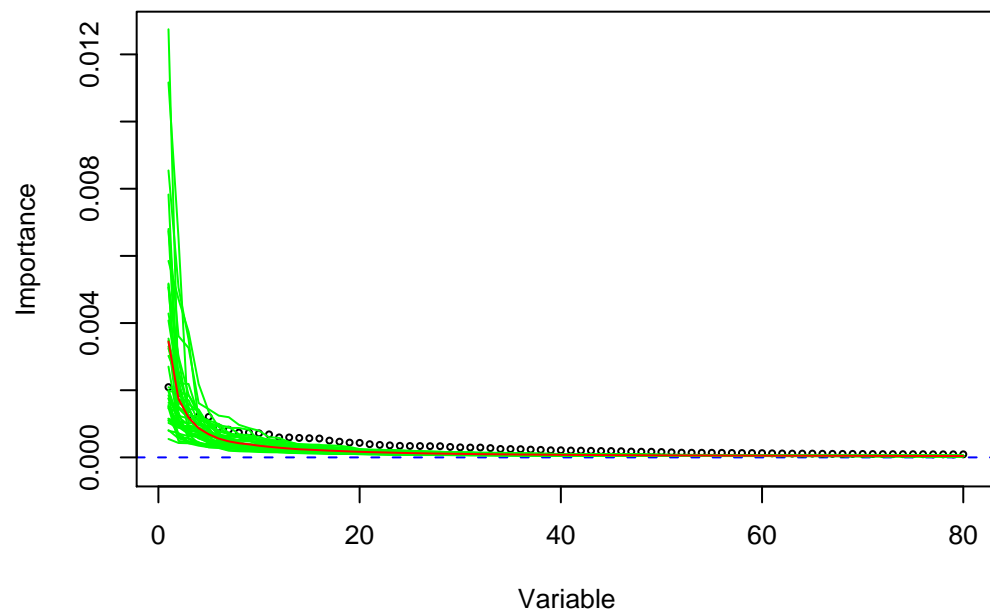
**NCI.; ntree = 5000, mtry = 0.5 \* ncol**



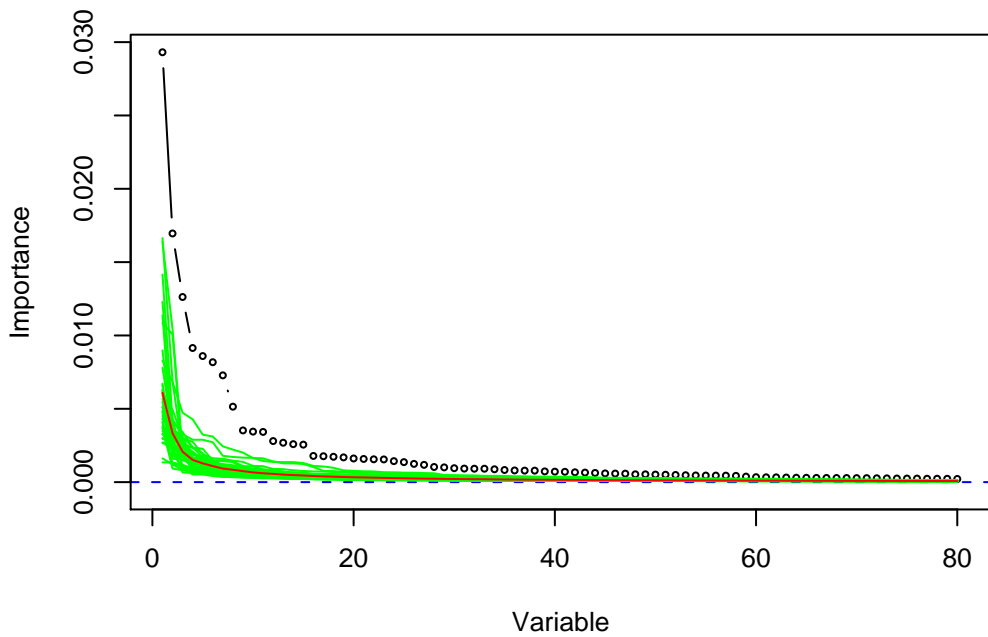
**adenoc; ntree = 5000, mtry = ncol**



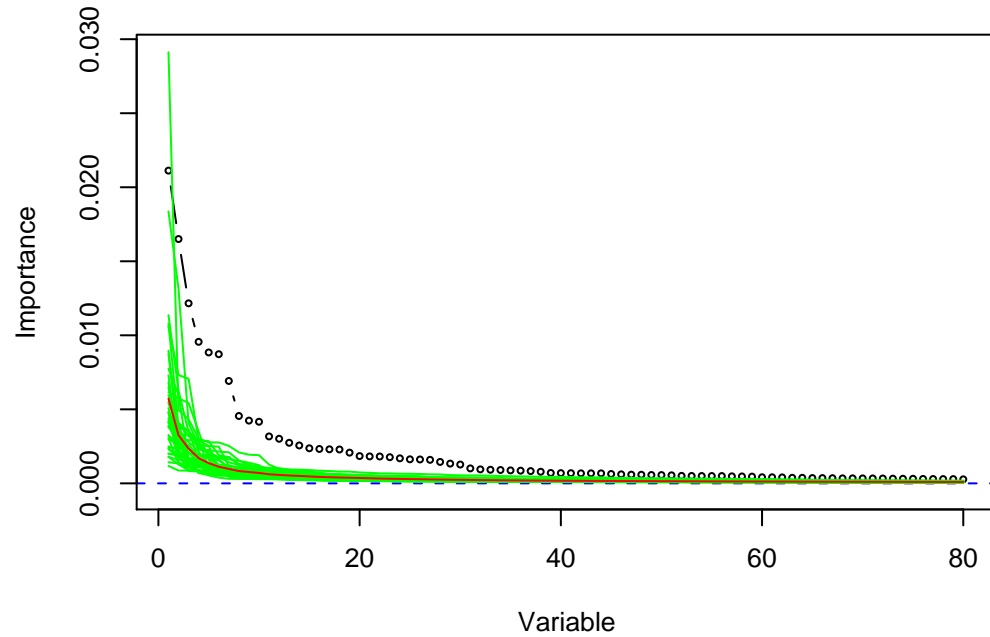
**Adenoc.; ntree = 5000, mtry = 0.5 \* ncol**



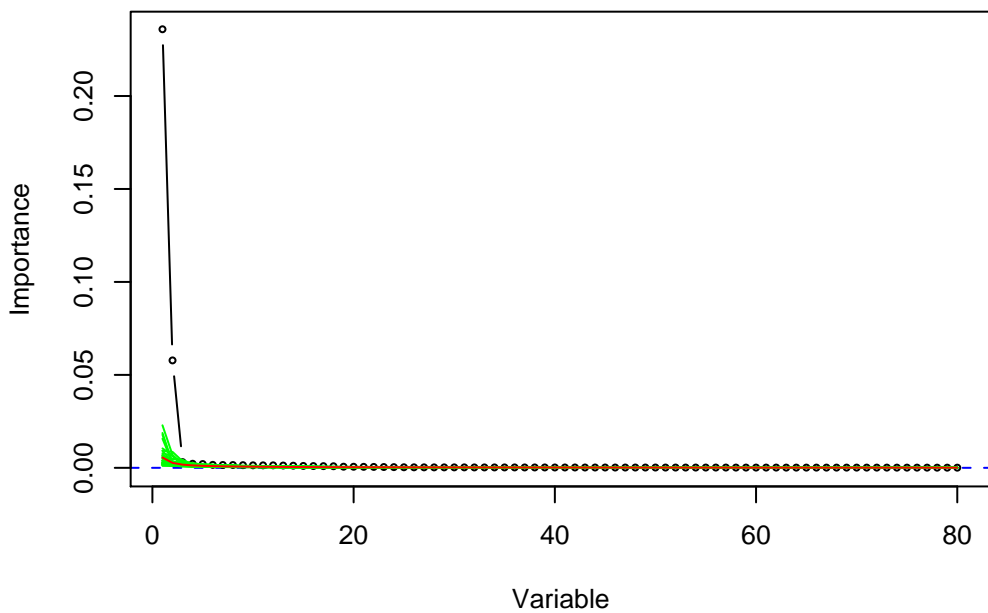
**colon; ntree = 5000, mtry = ncol**



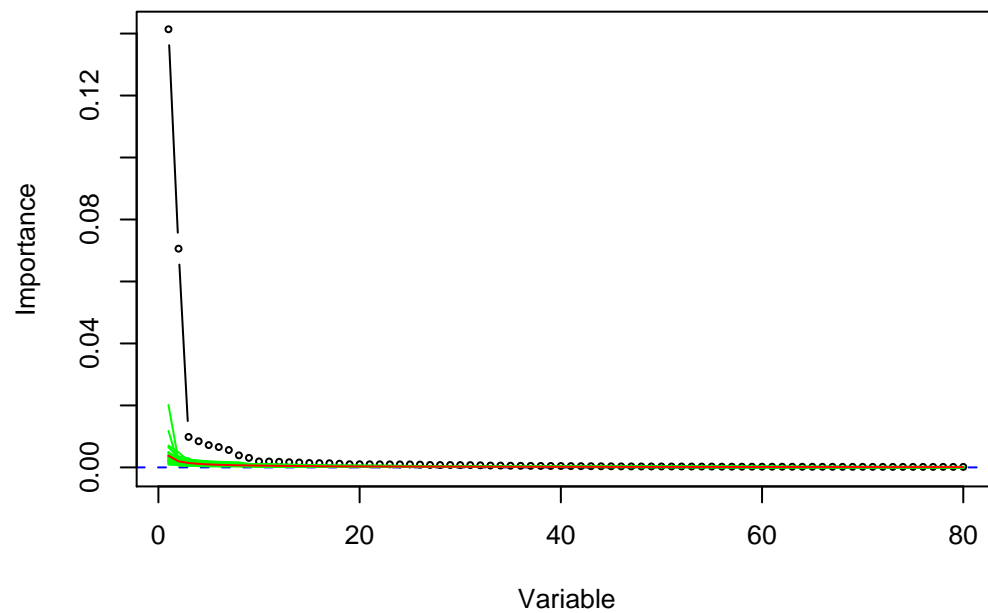
**colon.; ntree = 5000, mtry = 0.5 \* ncol**



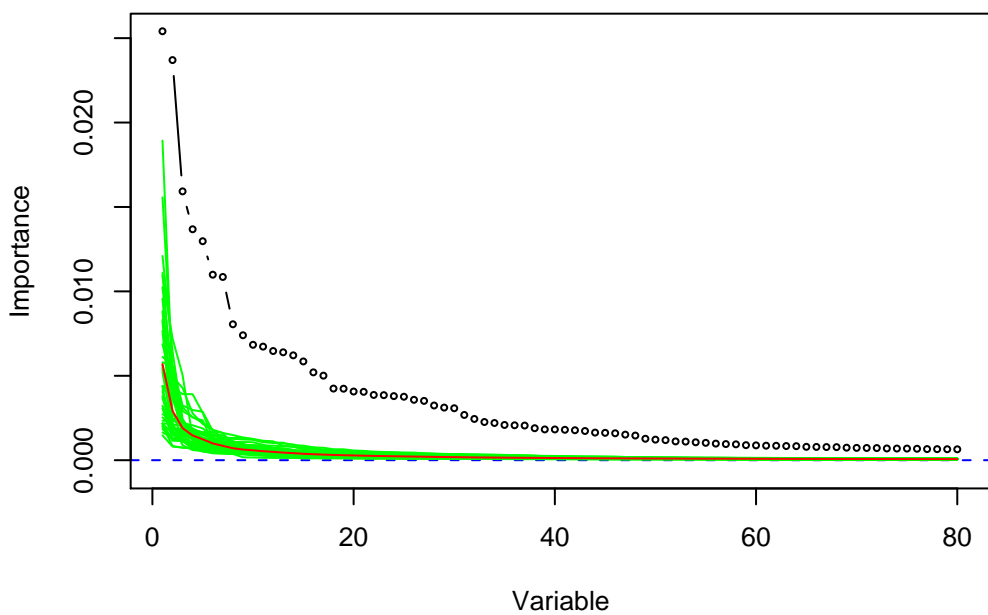
prostate; ntree = 5000, mtry = ncol



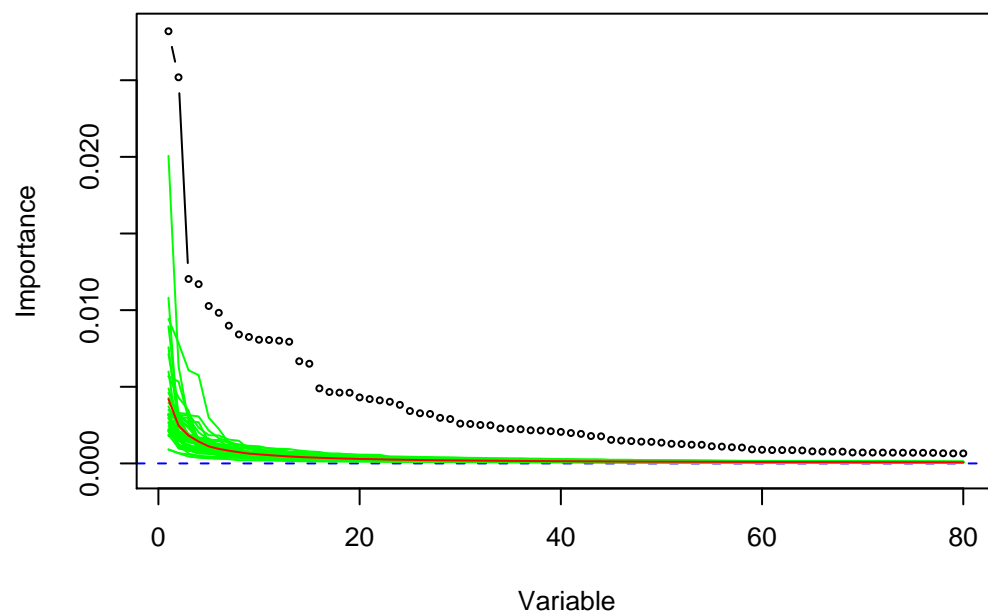
prostate; ntree = 5000, mtry = 0.5 \* ncol



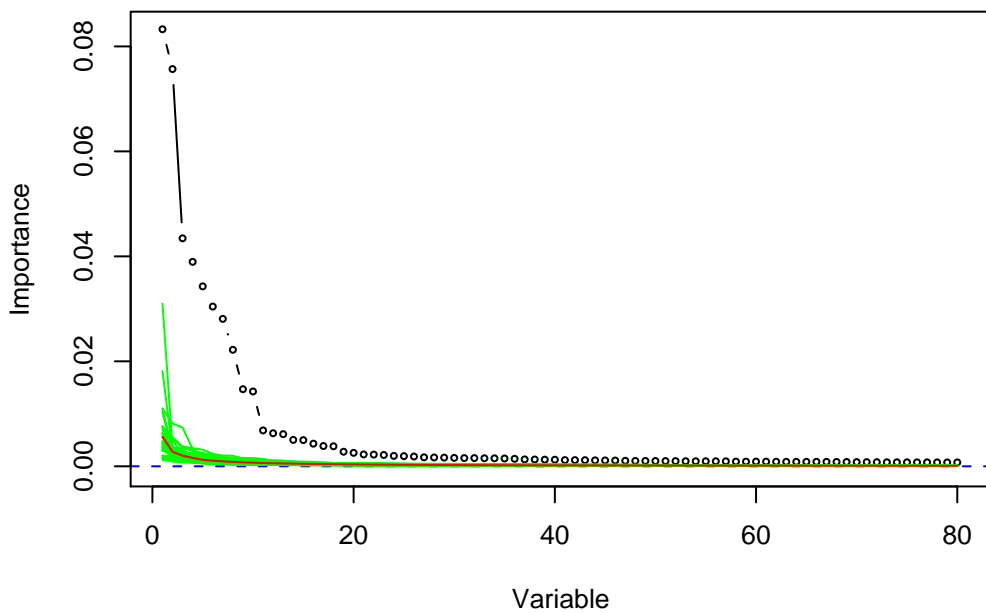
lymphoma; ntree = 5000, mtry = ncol



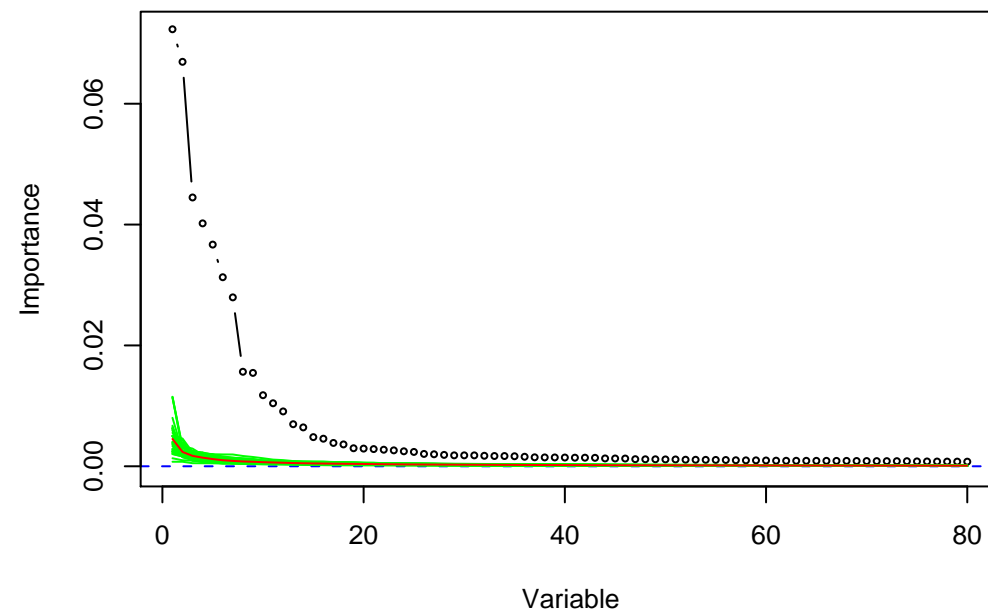
lymphoma; ntree = 5000, mtry = 0.5 \* ncol



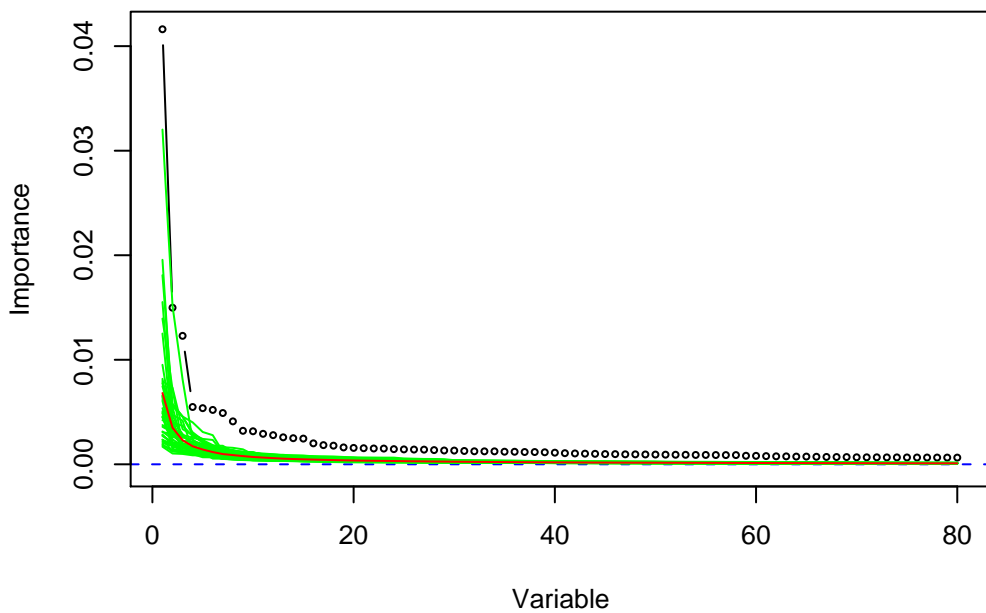
**srbct; ntree = 5000, mtry = ncol**



**srbct; ntree = 5000, mtry = 0.5 \* ncol**



**brain; ntree = 5000, mtry = ncol**



**brain; ntree = 5000, mtry = 0.5 \* ncol**

