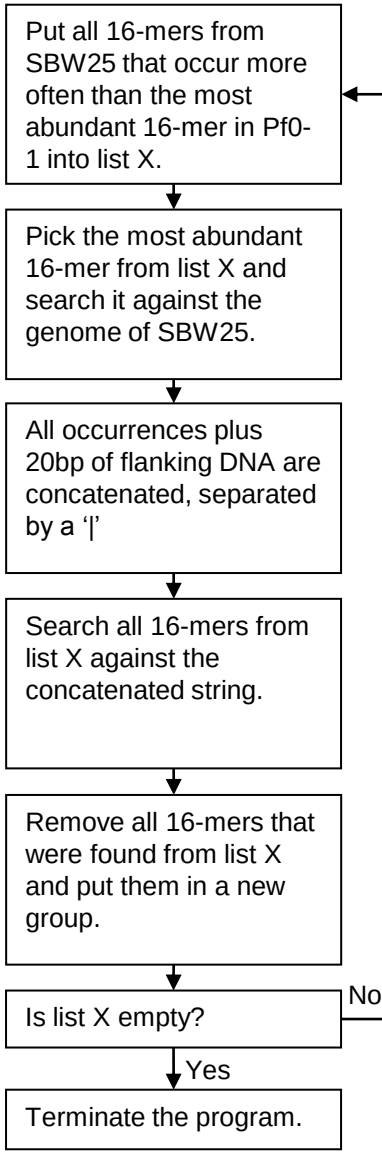
Put all 16-mers from SBW25 that occur more often than the most abundant 16-mer in Pf0-1 into list X.
Pick the most abundant 16-mer from list X and search it against the genome of SBW25.
All occurrences plus 20bp of flanking DNA are concatenated, separated by a '|'
Search all 16-mers from list X against the concatenated string.
Remove all 16-mers that were found from list X and put them in a new group.
Is list X empty?
No
Yes
Terminate the program.