Initialize the similarity matrix to be equal to a given similarity matrix.

Initialize the high and low values the number of changes and unchanged to be zero.

While the number of changes is less than a given iteration amount or the unchanged is less than the convergence rate:

For a given amount of perturbations:

Randomly choose different values in the similarity matrix and randomly increase or decrease those values by a given percentage

End for

For each peptide in the list of high binding peptides:

Set the high value to be equal to the sum of the found similarity scores of high binding peptides to each of the other high binding peptides.

Set the low value to be equal to the sum of the found similarity scores of high binding peptides to each of the other low binding peptides.

End for

If the found high value is greater than the previous high value, and the found low value is lower than the previous low values:

Save the current changed matrix as the new-found matrix

Increase the changed value by 1

Set the unchanged value to 0

Else:

Increase the unchanged value by 1

Revert the changes to the similarity matrix to the previous step.

End else

End while

Save the final matrix as the converged matrix.