

Aligned seed sequences for a profile-HMM should be trimmed before actual usage. What parts can be removed, and what expected improvements can be achieved through this process?

1. Generally, poorly aligned regions can be removed. These often include non-homogeneous regions at the ends of sequence alignments, which are frequently specific to individual sequences or incomplete. Since these regions can be detrimental to the accuracy of the model, they should be eliminated.
2. HMM models construct statistical models based on information from the given sequences starting from the provided seed. Therefore, removing inaccurately aligned regions can enhance the accuracy of the profile HMM. Additionally, the removal of non-homogeneous regions at the beginning and end of sequences can lead to an emphasis on conserved regions, and the reduction in the length of the seed due to region removal can shorten computing time.