The number of middling alignment scores of unrelated sequences does not inspire confidence in the accuracy of local alignment due to the possibilities of false positives. Determining a poorly aligned but related sequence could be indeterminable from a completely unrelated sequence. This corresponds with lecture and text through the accuracy of basic smith-waterman and how poorly it does at determining actually related alignments on poorly related sequences. This paired with the fact that sometimes multiple highest local alignment scores will show up, showing a likely false positive. We can help correct this by determining the probability of getting sequence alignments of length L in nonhomologous sequences and then focus on the alignments of greater length than L, still taking into account the determined probability.