

ABOUT THE LAB:

We will learn about basic pairwise alignment (Needleman-Wunsch) algorithm and we will introduce some of the Matlab Bioinformatics Toolbox functions for pairwise alignment of sequences and corresponding visualizations.

1. Background. We will talk about the reasons to conduct sequence alignment, global and local alignment.

2. Dot plot. Create the dot plot of two 'GATTCATCCATGGTAC' and 'GTACTTCAATC-CATGC' in Matlab using 'seqdotplot'. What can you conclude about the two sequences based on the dot plot? (Turn in the dot plot for the sequences.)

3. Needleman-Wunsch algorithm. We will go through two simple examples of the Needleman-Wunsch algorithm for pairwise global alignment using the Likic slides (moodle, Needleman-Wunsch algorithm I) and the Dynamics programming tutorial (moodle, Needleman-Wunsch algorithm II).

4. Alignment using the Bioinformatics toolbox. We will use the following two sequence alignment algorithms in Matlab: Needleman-Wunsch (global) algorithm (in Matlab: 'nwalignment') and the Smith-Waterman (local) algorithm (in Matlab: 'swalignment'). We will get the scores and the alignment for both methods and visualize the final alignment with the command 'showalignment'. Use the algorithms on the two sequences given above as well as the following two sequences: 'MYSENENDYIILEDKTATGKKRDWKGKKRRRTNLMAE' and 'MYICVVFSLILIFTSIEILLGGKV'. (Turn in the score, alignment and the 'showalignment' output for the two pairs of sequences; display results of both methods.)