## Computational Molecular Biology 2019 -Homework One

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February 2019

## **Question One**

Given sequence S of length N and sequence T of length M, how many possible alignments are there? Give an expression in N and M.

Given a sequences of length N and M, we construct a Needleman-Wunsch grid with sides n+1 and m+1 when we include the gap, as show in the completed example in Figure 1. Each path from the top left of the grid to the bottom right taking right, down or down-right diagonal steps provides a valid solution to the problem.

Needleman-Wunsch								
match = 1			mismatch = -1			gap = -1		
		G	С	Α	т	G	С	U
	0	-1	-2	-3	-4	-5	-6	-7
G	-1	1	- 0	-1	2	-3	-4	-5
A	-2	0	0		0 <	1 →	2	3
т	-3	-1	-1	Ô	2	1 :	- 0	1
т	-4	-2	-2	-1		1	0	-1
A	-5	-3	-3	-1	0	0	0	-1
С	-6	-4	-2	-2	-1	-1	4	0
Α	-7	-5	-3	-1	2	-2	0	0

Figure 1: Needleman-Wunsch

This problem can be described using **Delannoy numbers**. Therefore, we can describe the expression for the number of possible alignments in terms of n and m as:

$$\sum_{k=0}^{\min(m,n)+1} \binom{n+1}{k} \binom{m+1}{k} 2^k$$