

Practice example for global alignment of amino acid sequences
(based on Simplified Needleman-Wunsch algorithm)

Scheme used for scoring in this example:

matches: 1 point
mismatches: -1 point
gaps: -1 point

	gaps	S	A	G	P	T
gaps	0	-2	-4	-6	-8	-10
S	-2	1 -2 -3 -6 -5 -8 -7 -10 -9 -12 -2 1 -1 -1 -3 -3 -5 -5 -7 -7				
V	-4	-3 -1 0 -3 -2 -5 -4 -7 -6 -9 -6 -1 -3 0 -2 -2 -4 -4 -6 -6				
G	-6	-5 -3 -2 -2 1 -2 -3 -6 -5 -8 -8 -3 -5 -2 -2 1 -1 -1 -3 -3				
G	-8	-7 -5 -4 -4 -1 1 0 -3 -2 -5 -10 -5 -7 -4 -4 1 -1 0 -2 -2				
P	-10	-9 -7 -6 -6 -5 -1 2 0 -1 -4 -12 -7 -9 -6 -8 -1 -1 2 0 0				
T	-12	-11 -9 -8 -8 -7 -3 -2 0 3 0 -14 -9 -11 -8 -10 -3 -5 0 0 3				

Here is the traceback process:

	gaps	S	A	G	P	T
gaps	0	-2	-4	-6	-8	-10
S	-2	1-2-21-1-3-3-5-5-7-7				
V	-4	-3-1-6-1-30-2-2-4-4-6-6				
G	-6	-5-3-8-3-5-21-2-3-6-5-8				
G	-8	-7-5-10-5-7-4110-3-2-5				
P	-10	-9-7-12-7-9-61-1200-4				
T	-12	-11-9-14-9-11-8-7-3-2030				

Giving the alignment:

SA_GPT
SVGGPT