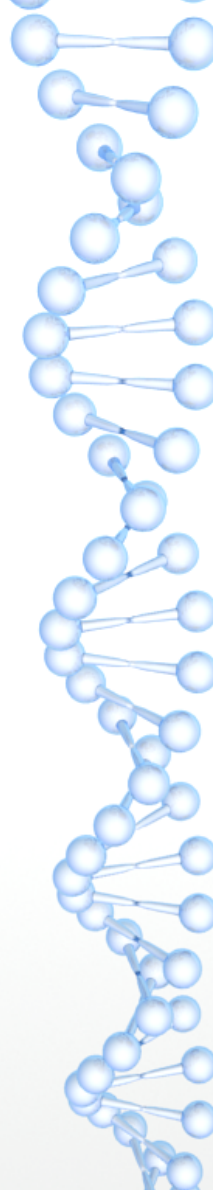




Računanje lokalnog poravnanja koristeći Smith-Watermanov algoritam implementiran na CUDA platformi

Halambek, Tunković, Bartol

Običan Smith-Waterman

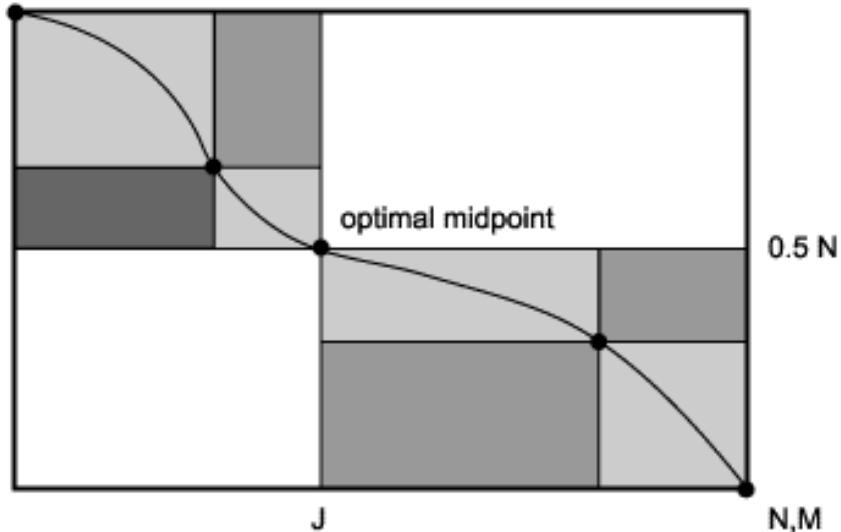


		G	G	C	T	C	A	A	T	C	A
		0	0	0	0	0	0	0	0	0	0
A		0	0	0	0	0	0	2	2	0	0
C		0	0	0	2	0	2	0	1	1	2
C		0	0	0	2	1	2	1	0	0	3
T		0	0	0	0	4	2	1	0	2	1
A		0	0	0	0	2	3	4	3	1	1
A		0	0	0	0	0	1	5	6	4	2
G		0	2	2	0	0	0	3	4	5	3
G		0	2	4	2	0	0	1	2	3	4

Preuzeto sa stranice predmeta *Bioinformatika* - http://www.fer.unizg.hr/_download/repository/bioinformatika_skripta_v1.2.pdf

Smanjenje memorijske složenosti #1

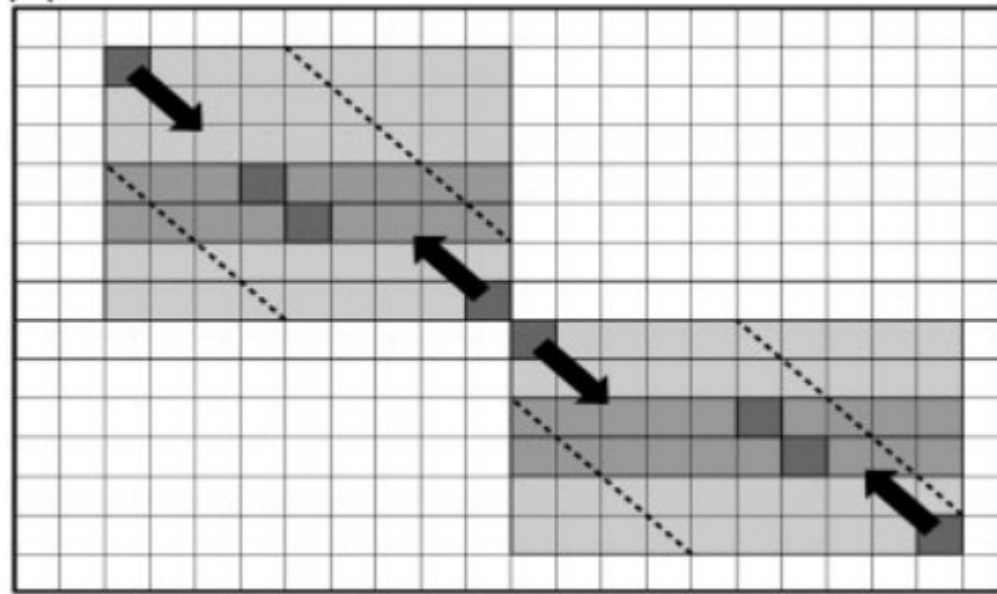
Mayers-Millerov algoritam



Preuzeto s <http://www.bioinformaticsonline.org/ch/ch03/supp-3.html>

Smanjenje memorijske složenosti #2

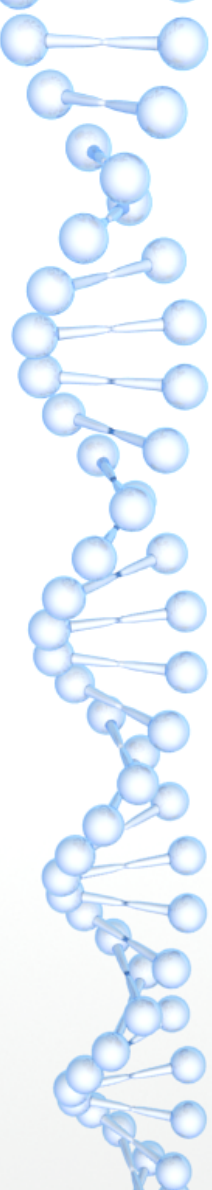
Nalaženje početnog elementa rekonstrukcije



Preuzeto iz originalnog rada - Korpar, Šikić (2013), <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3777108/pdf/btt410.pdf>

Smanjenje vremenske složenosti – CUDA

Wavefront metoda



d ₁	d ₂	d ₃	d ₄	d ₅	d ₆	↘	d ₈	d ₉
d ₂	d ₃	d ₄	d ₅	d ₆	↘	d ₈	d ₉	d ₁₀
d ₃	d ₄	d ₅	d ₆	↘	d ₈	d ₉	d ₁₀	d ₁₁
d ₄	d ₅	d ₆	↘	d ₈	d ₉	d ₁₀	d ₁₁	d ₁₂
d ₅	d ₆	↘	d ₈	d ₉	d ₁₀	d ₁₁	d ₁₂	d ₁₃

Preuzeto iz Sandes, Melo (2013), <http://ieeexplore.ieee.org/document/6226380/>



Rezultati

Tablica 4.1. Trajanje izvođenja algoritma u sekundama

Duljina sekvence	SW#	SW
100	1.06	1.22
1000	1.35	1.22
10000	1.70	1.46
100000	1.59	2.77
1000000	12.87	137.31

Tablica 4.2. Iznosi poravnanja (alignment score)

Duljina sekvence	SW#	SW
100	7	7
1000	10	10
10000	13	13
100000	17	17
1000000	19	19