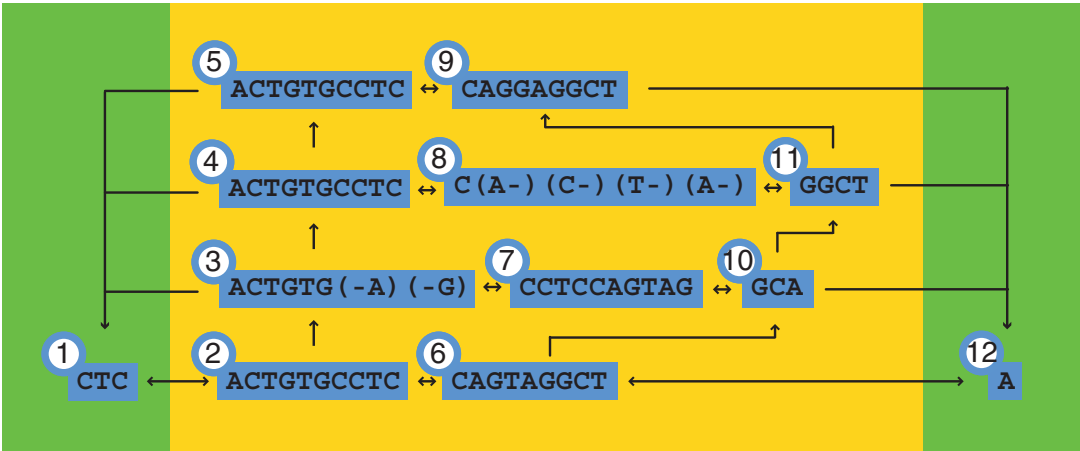


(a)

Genome 4:	CTCACTGTG--CCTCCAGGAGGCTA	Conserved
Genome 3:	CTCACTGTG--CCTCC---GGCTA	
Genome 2:	CTCACTGTGAGCCTCCAGTAGGCAA	Diverged
Ref. seq. :	CTCACTGTG--CCTCCAGTAGGCTA	

(b)

Block length: 10
k: 7



(c)

Read: CTCACTGTGAGCCTCCGGCTA

Best alignment against Genome 3:

Read: CTCACTGTGAGCCTCCGGCTA
Genome 3: CTCACTGTG--CCTCCGGCTA

GM Alignment Format: CTCACTGTG [-A] [-G] CCTCCGGCTA

Transformed alignment against Ref. Seq.:

Read: CTCACTGTGAGCCTCC---GGCTA
Ref. seq.: CTCACTGTG--CCTCCAGTAGGCTA

GM Alignment Format: CTCACTGTG [-A] [-G] CCTCC (A-) (G-) (T-) (A-) GGCTA