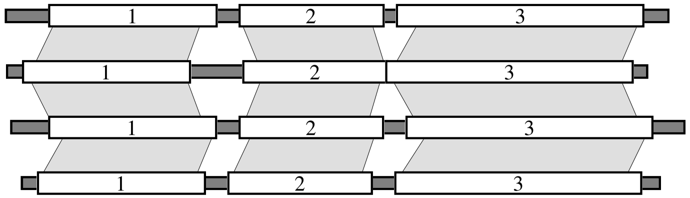
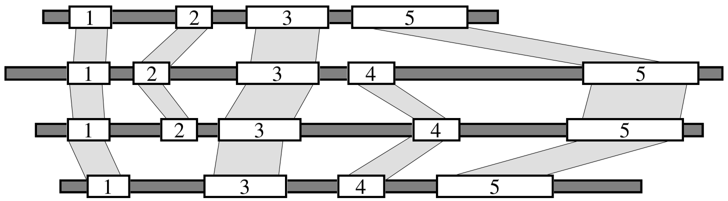
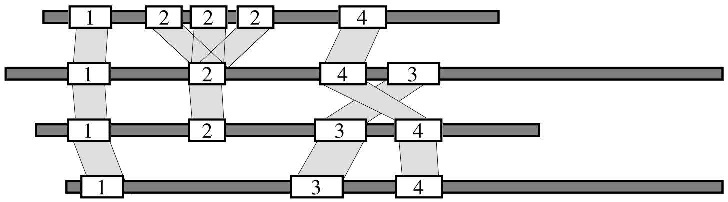
		Comment	Appropriate approach
a)		Sequences are related over their entire length.	Progressive global alignment method (e.g. CLUSTAL W).
b)		Sequences share conserved blocks, separated by non-conserved regions containing large indels. Blocks are consistent (i.e. in the same order) but not necessarily uniform (i.e. some blocks may be missing in some sequences).	Block-based global alignment method (e.g. DIALIGN, ITERALIGN). Compare alignments produced by different programs (including progressive methods).
c)		Sequences contain a non-consistent set of conserved blocks (i.e. some blocks are duplicated or occur in a different order along sequences).	Motif-based local alignment method (e.g. MEME). Compare alignments produced by different programs.

1 Conserved block
Non-conserved region

Fig. 4
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Bioinformatics - a practical approach