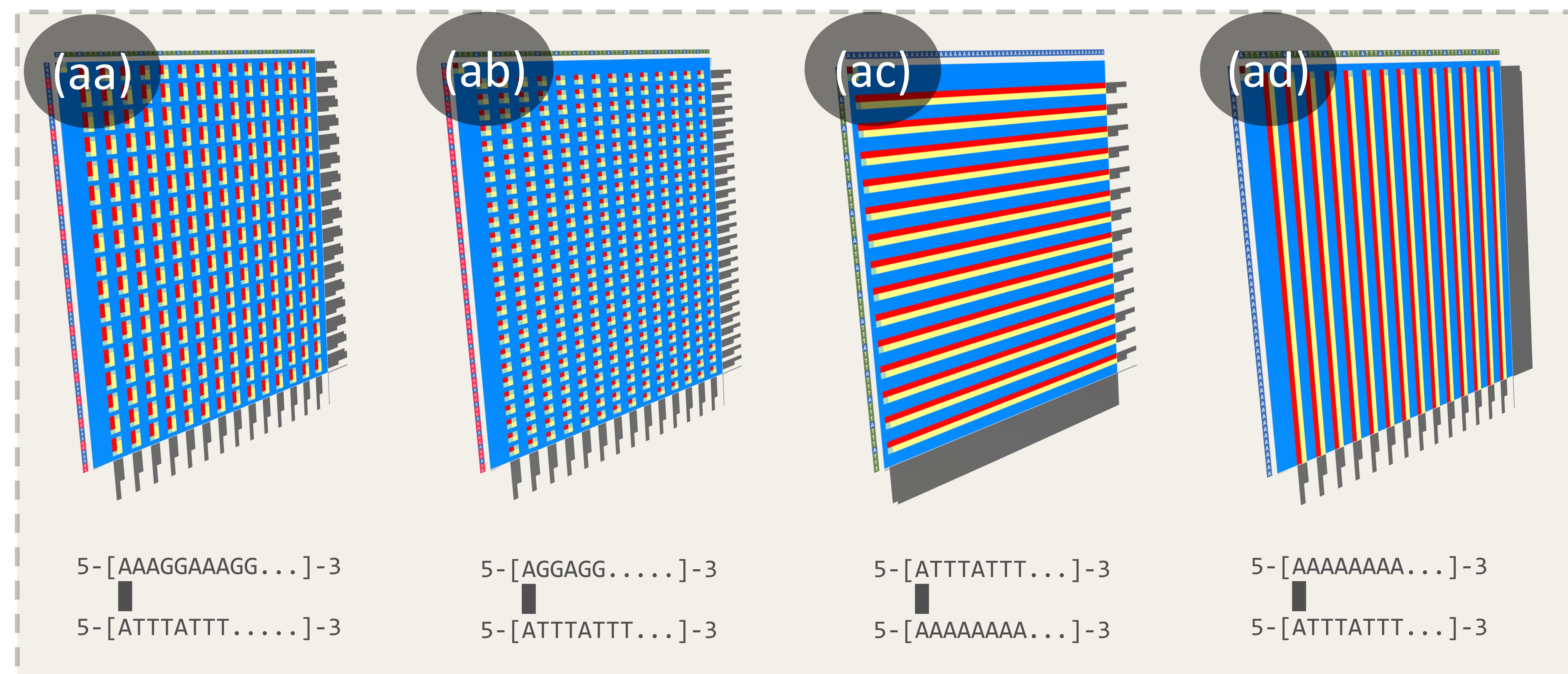


5-[AGAG.....]-3
 5-[ATTTATTT...]-3
 5-[AGGAGG.....]-3
 5-[ATTTATTT...]-3
 5-[AGGAGG.....]-3
 5-[ATTTATTT...]-3
 5-[TTTTA-AAAA...]-3
 5-[ATTTATTT...]-3
 5-[GTAGTAGTA...]-3



A score matrix dissection through specially constructed sequences

A score matrix dissection through specially constructed sequences. Each heatmap represents a score matrix. These heatmaps represent different sequence alignment configurations based on specially constructed sequences. The alignment shows that the optimal alignment area does not follow the main diagonal. **(a-k)** Show different patterns that can appear on the score matrix if special sequences are used. **(k)** Shows the symmetry present on the heatmap in the case of a perfect alignment between two sequences of the same size. **(l-s)** Show islands of high value numbers on the score matrix and presents the meaning of different areas on the score matrix. **(t-v)** shows a patterned grid. **(w-ad)** It shows a variety of possibilities for clean granular patterns.



Cite this work as:

Paul A. Gagniuc. *Algorithms in Bioinformatics: Theory and Implementation*. John Wiley & Sons, Hoboken, NJ, USA, 2021, ISBN: 9781119697961.

