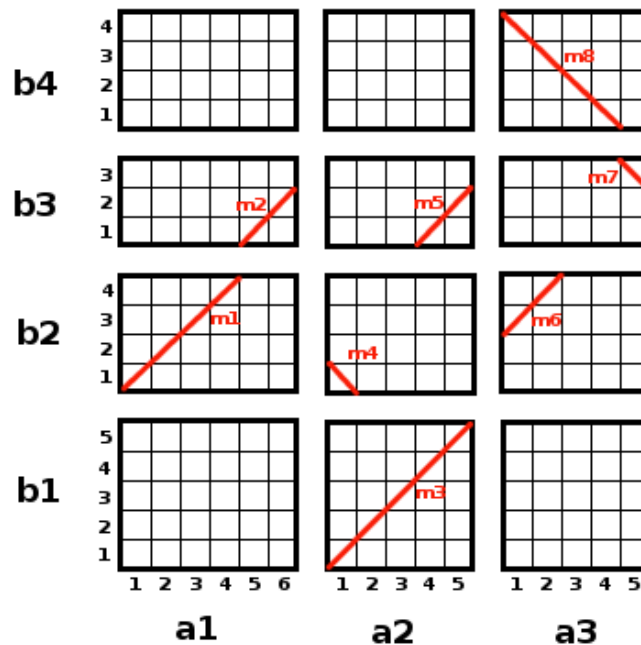


Whole Genome Comparison Assembly Comparison

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1 OSL - a small example



Given Assemblies $A = (a_1, a_2, a_3)$ and $B = (b_1, b_2, b_3, b_4)$ and the following matches:

- $m_1 = (a_1, 1, 4, b_2, 1, 4, 1)$
- $m_2 = (a_1, 5, 6, b_3, 1, 2, 1)$
- $m_3 = (a_2, 1, 5, b_1, 1, 5, 1)$
- $m_4 = (a_2, 1, 1, b_2, 1, 1, -1)$
- $m_5 = (a_2, 4, 5, b_3, 1, 2, 1)$
- $m_6 = (a_3, 1, 2, b_2, 3, 4, 1)$
- $m_7 = (a_3, 5, 5, b_3, 3, 3, -1)$
- $m_8 = (a_3, 1, 4, b_4, 1, 4, -1)$

Apply the OSL algorithm to layout the contigs of assembly A .

Hints:

1. The weight of a match is represented by its length. So the match m_1 gets for example the weight 4.
2. You can draw a diagonal extension between two connectors c and c' if the heights of the connectors differ at most in one position.