

# Supplementary Materials: “SCARPA: Scaffolding Reads with Practical Algorithms”

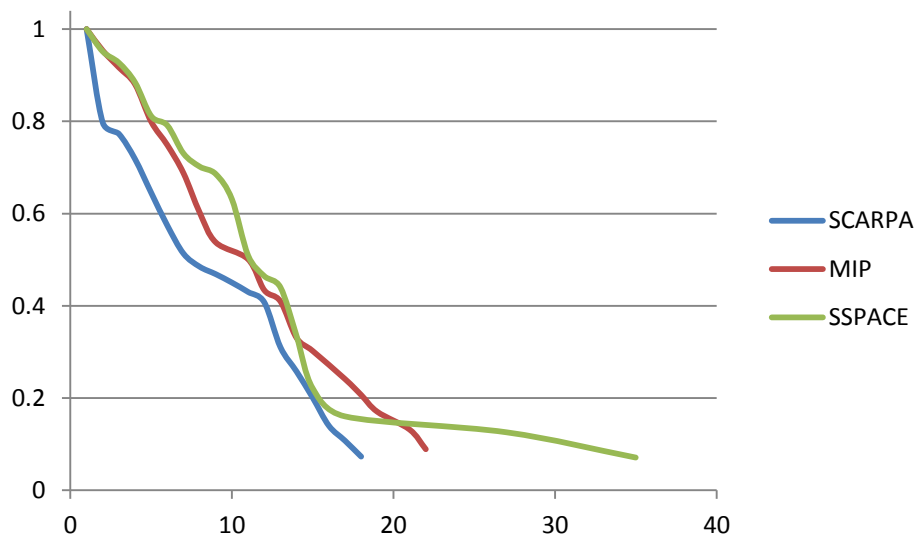
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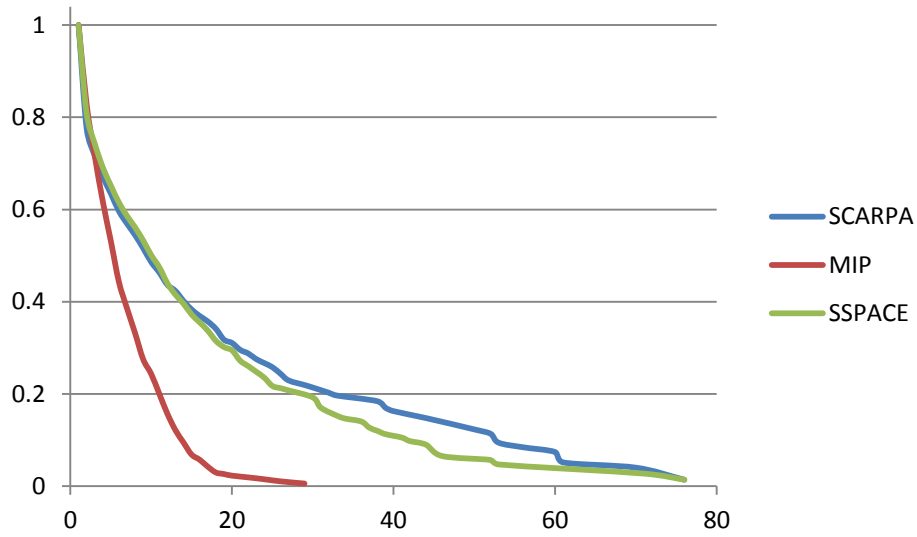
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The figures below compare the number of contigs merged in scaffolds<sup>1</sup> for SCARPA, MIP and SSPACE in the *E. coli*, *G. clavigera* and Assemblathon1 datasets. Below, the X axis denotes the scaffolds containing that many or more contigs, while the Y axis denote the total fraction of contigs covered by these scaffolds.

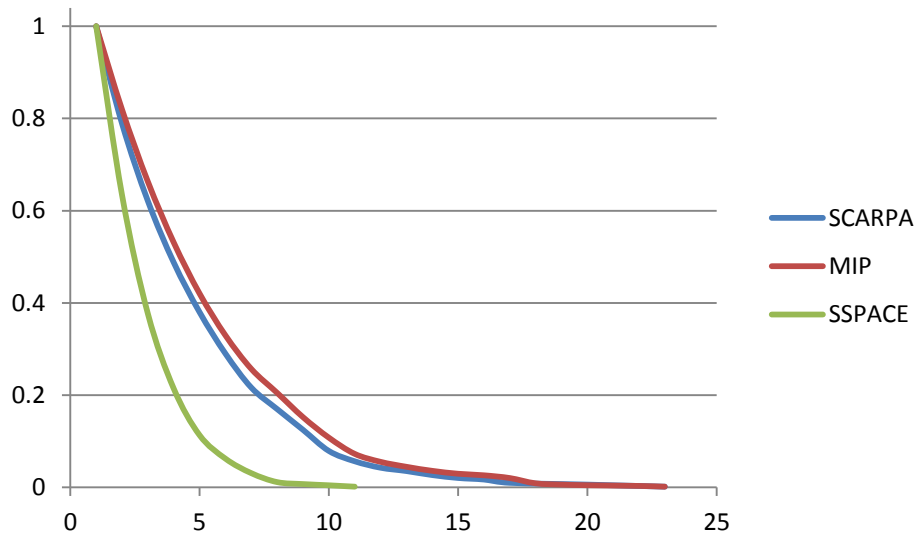


**Supplementary Fig1.** The fraction of *E. coli* contigs (Y axis) covered by scaffolds containing X or more contigs.

<sup>1</sup> We were unable to retrieve the contig content information for SOPRA scaffolds.



**Supplementary Fig2.** The fraction of *G. clavigera* contigs (Y axis) covered by scaffolds containing X or more contigs.



**Supplementary Fig3.** The fraction of Assemblathon1 contigs (Y axis) covered by scaffolds containing X or more contigs.