Resolution and accuracy in Congreve & Lamsdell matrices

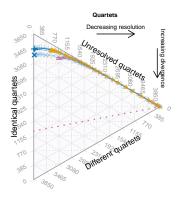
 $Martin\ R.\ Smith\ martin.smith@durham.ac.uk\\ 2019-01-10$

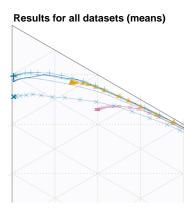
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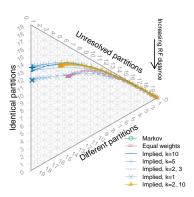
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This page depicts the analytical results of all 100 matrices generated by Congreve & Lamsdell [1] using a ternary plotting approach [2], with quartets and partitions used as distance metrics.

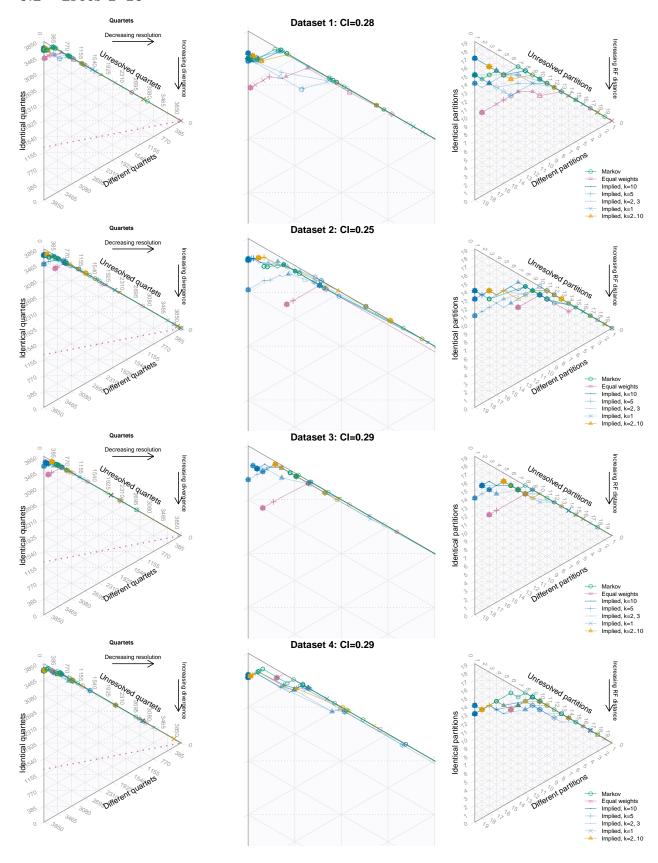
0.1 Summary

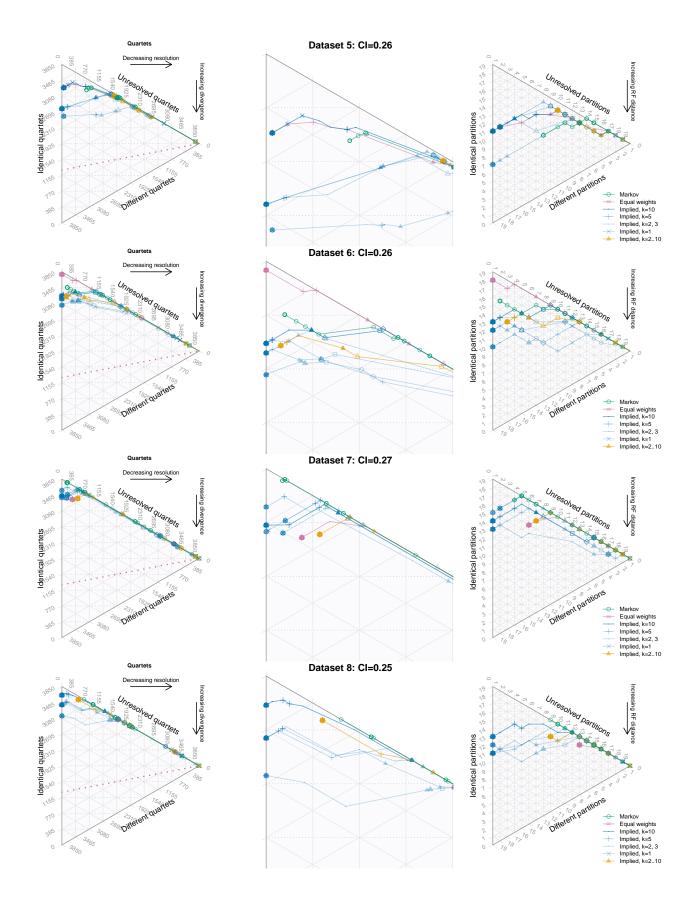


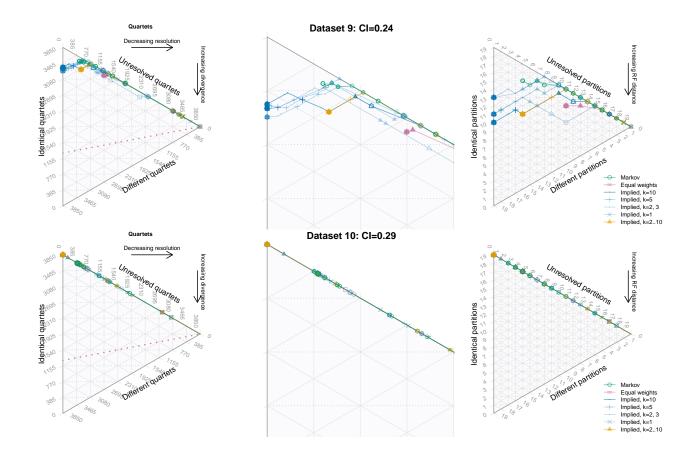




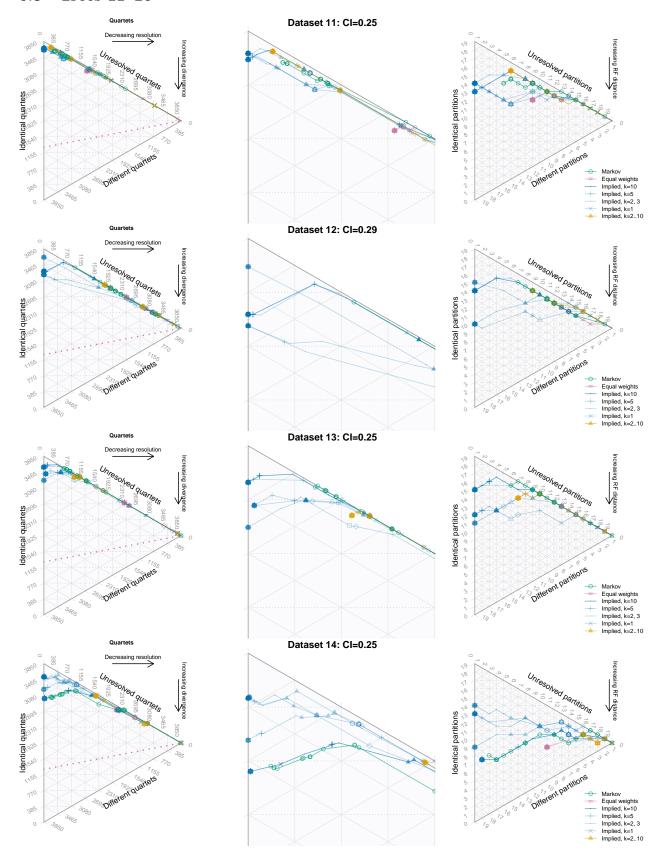
0.2 Trees 1-10

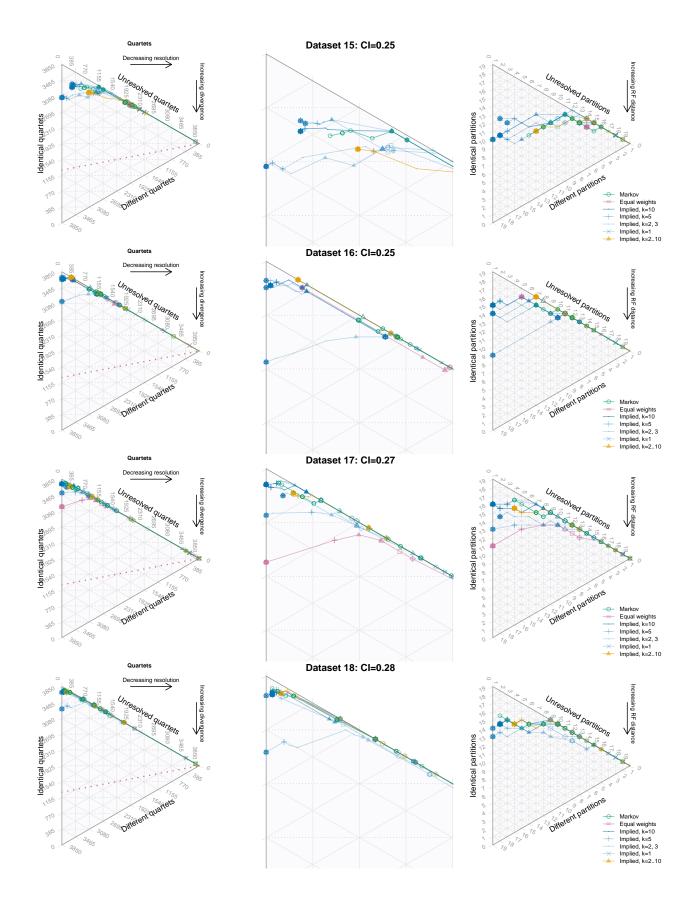


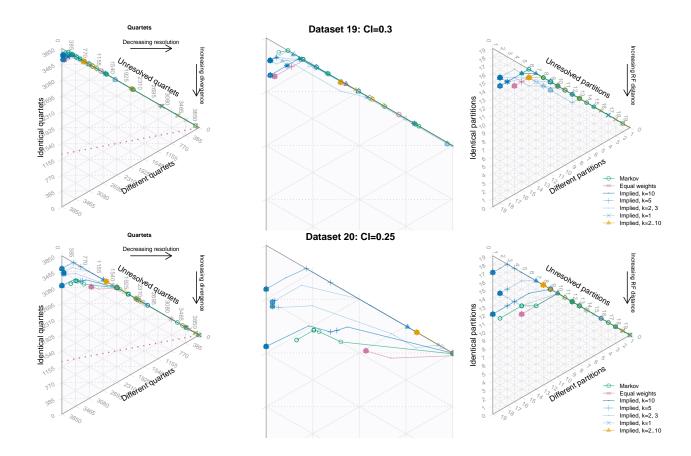




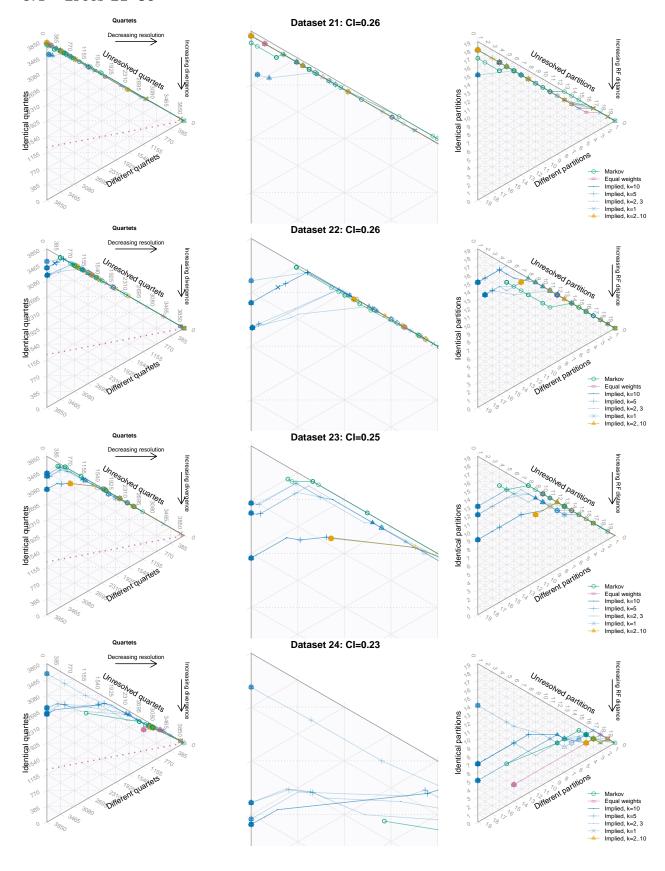
0.3 Trees 11-20

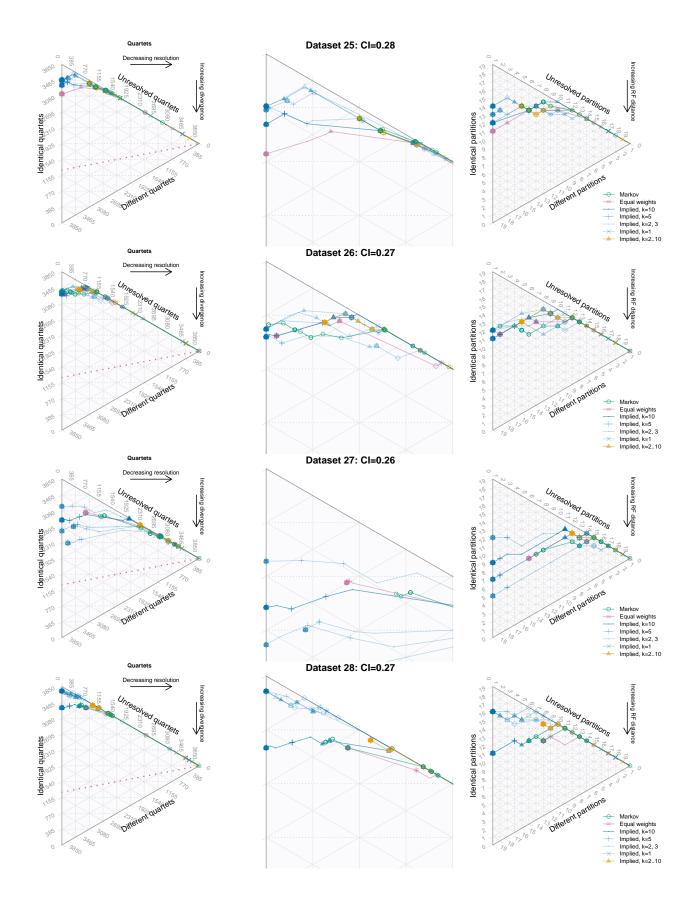


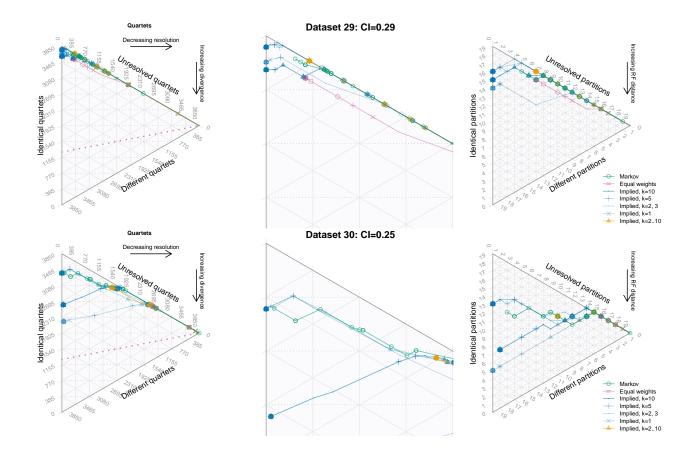




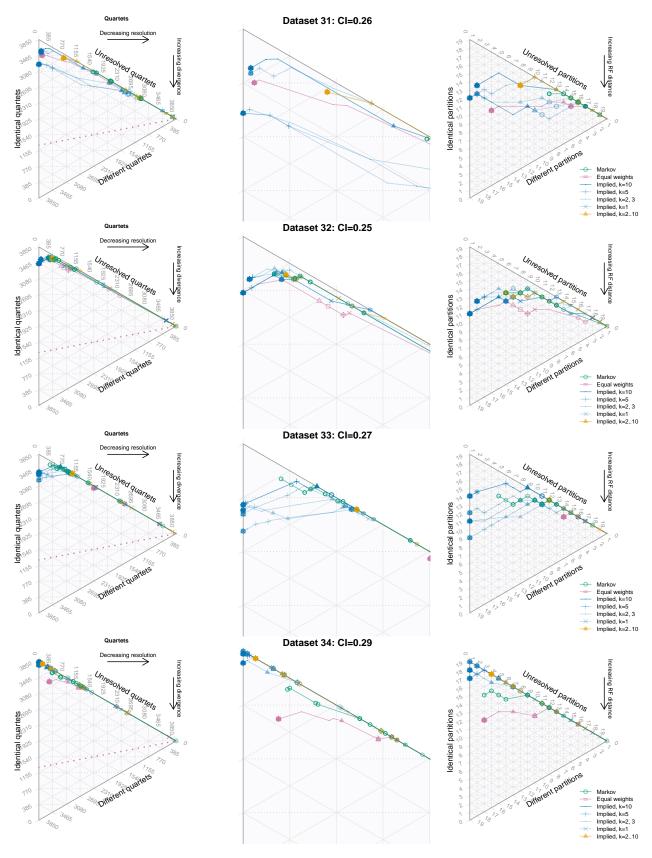
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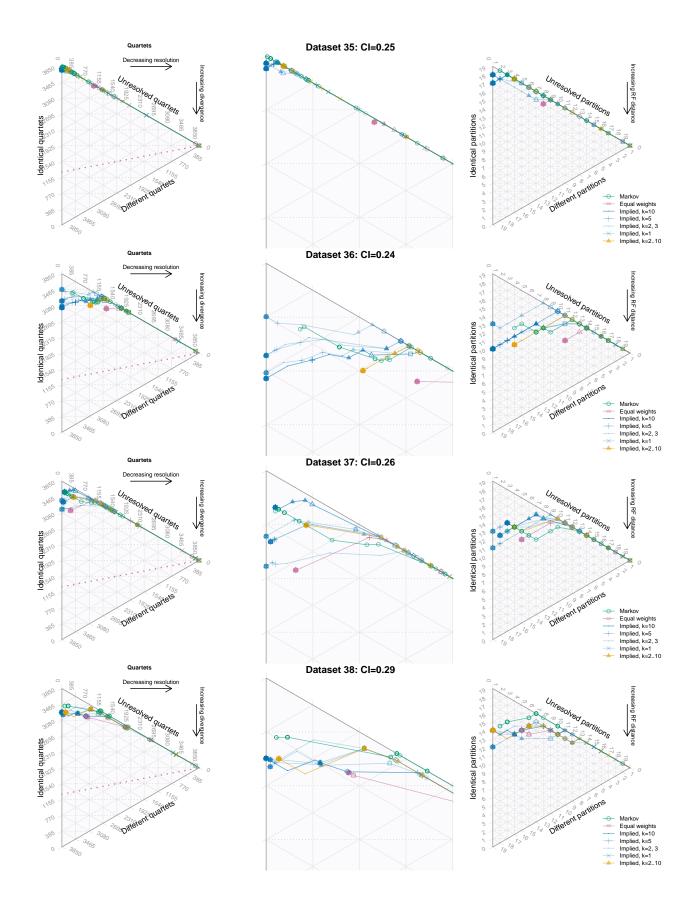


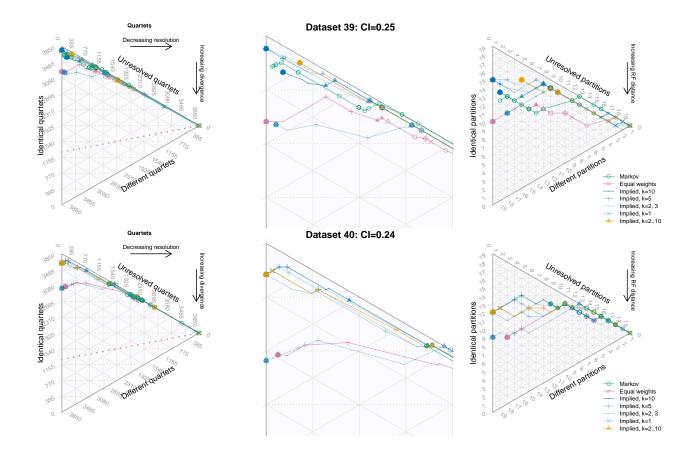




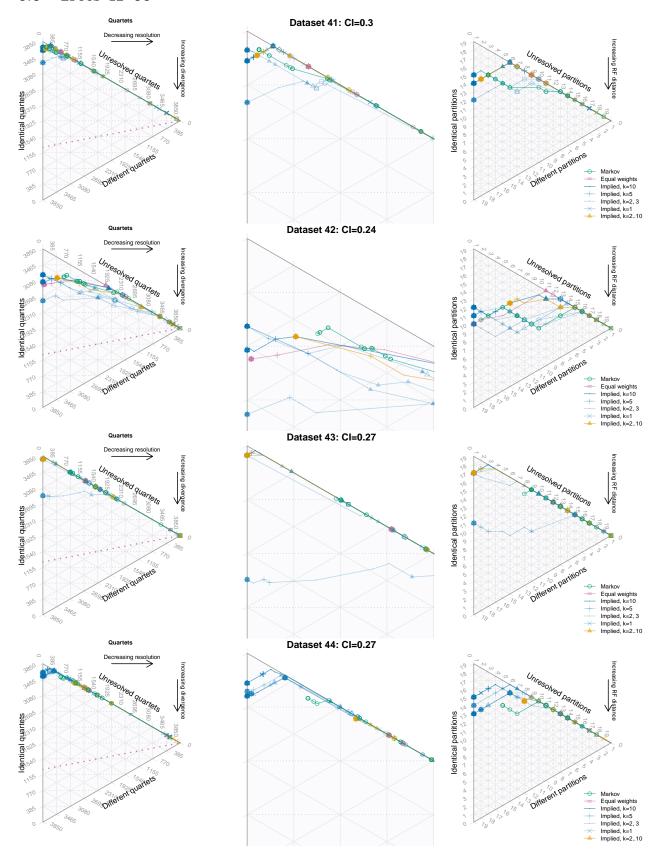
0.5 Trees 31-40

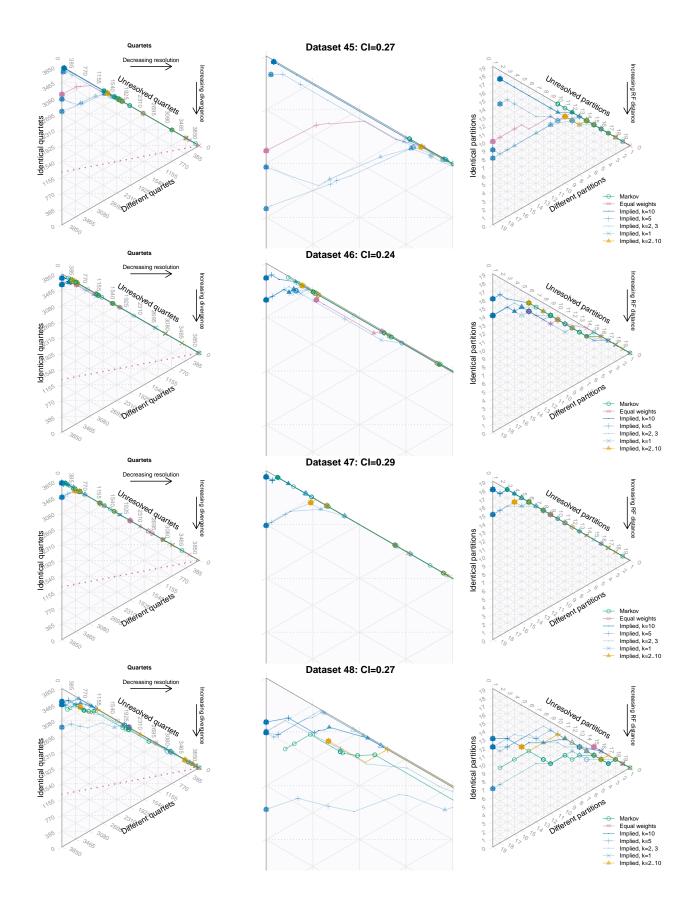


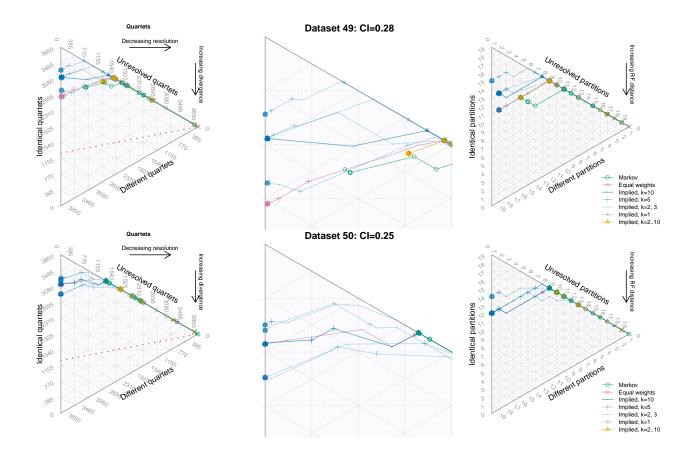




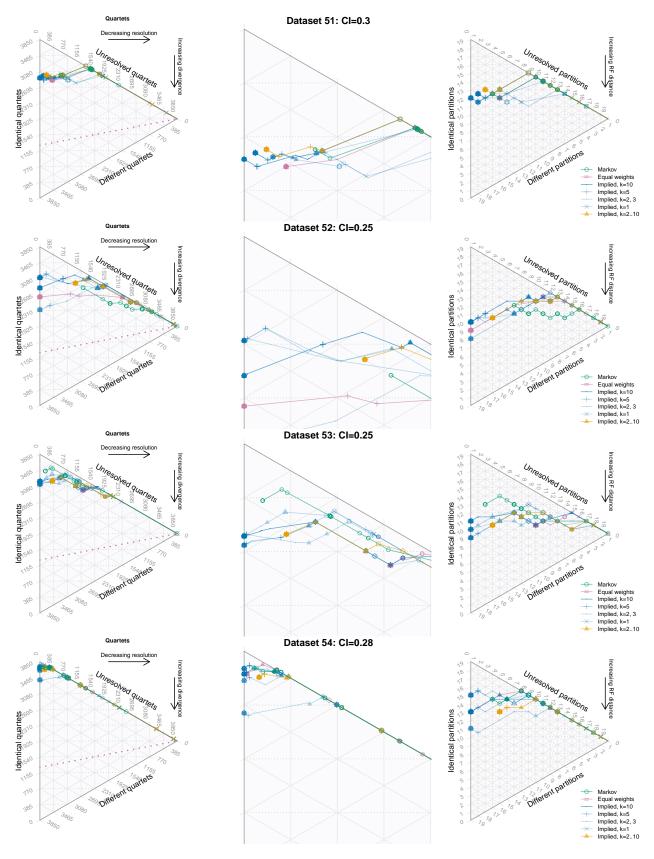
0.6 Trees 41-50

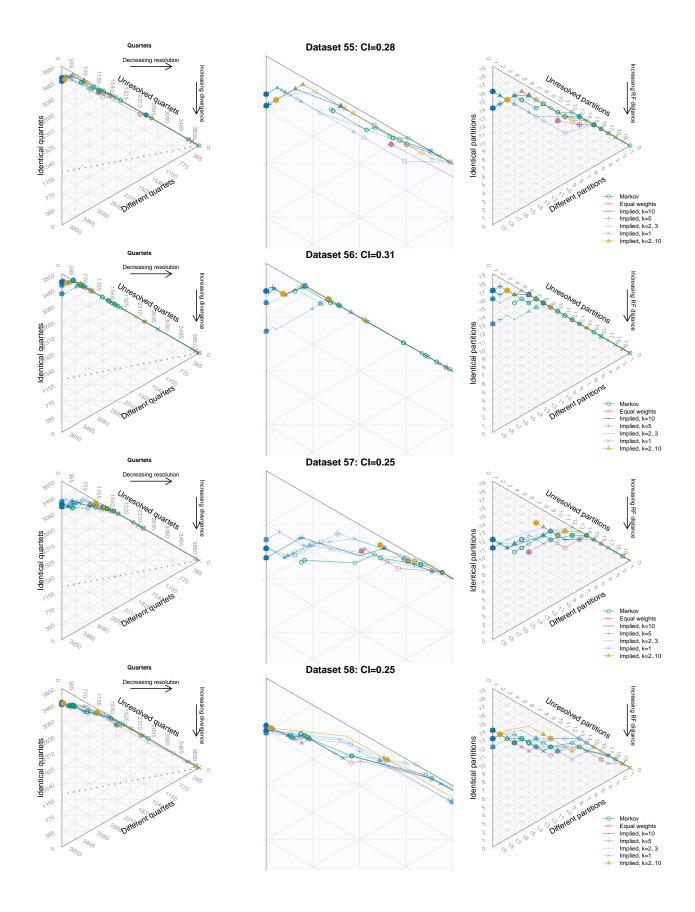


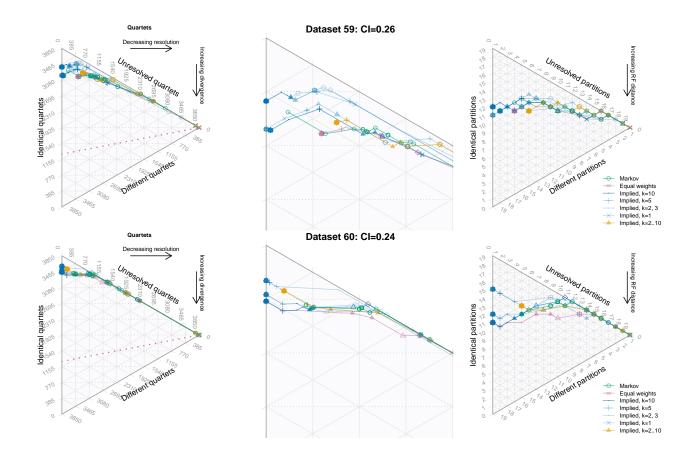




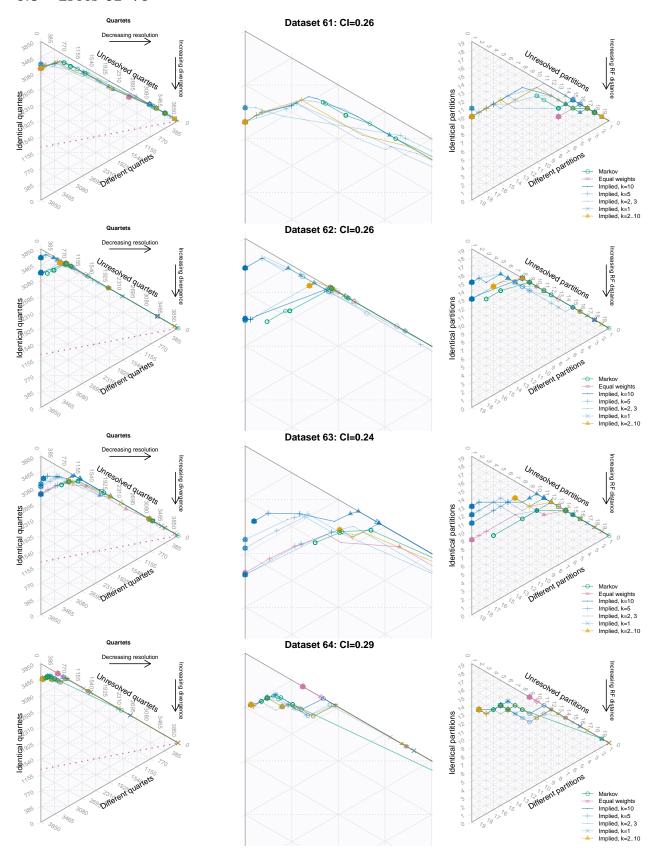
0.7 Trees 51-60

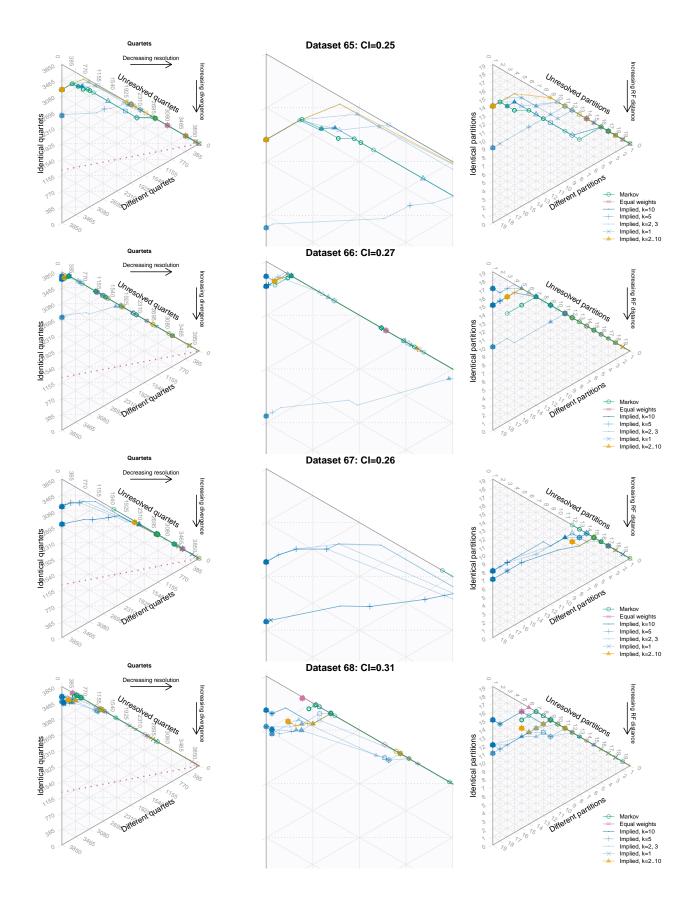


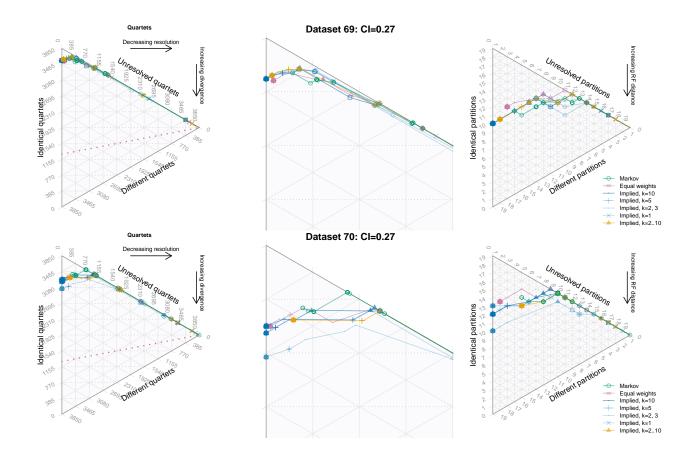




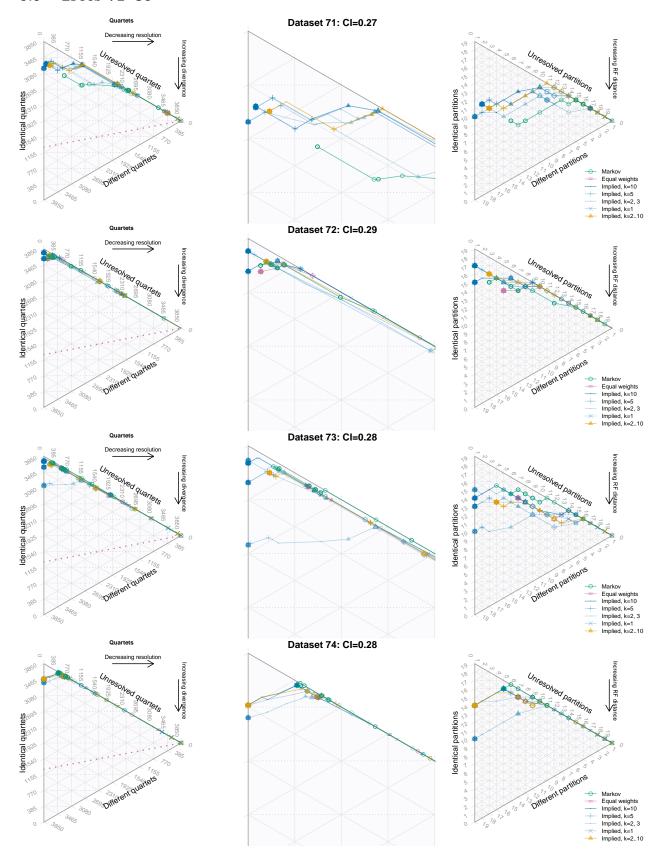
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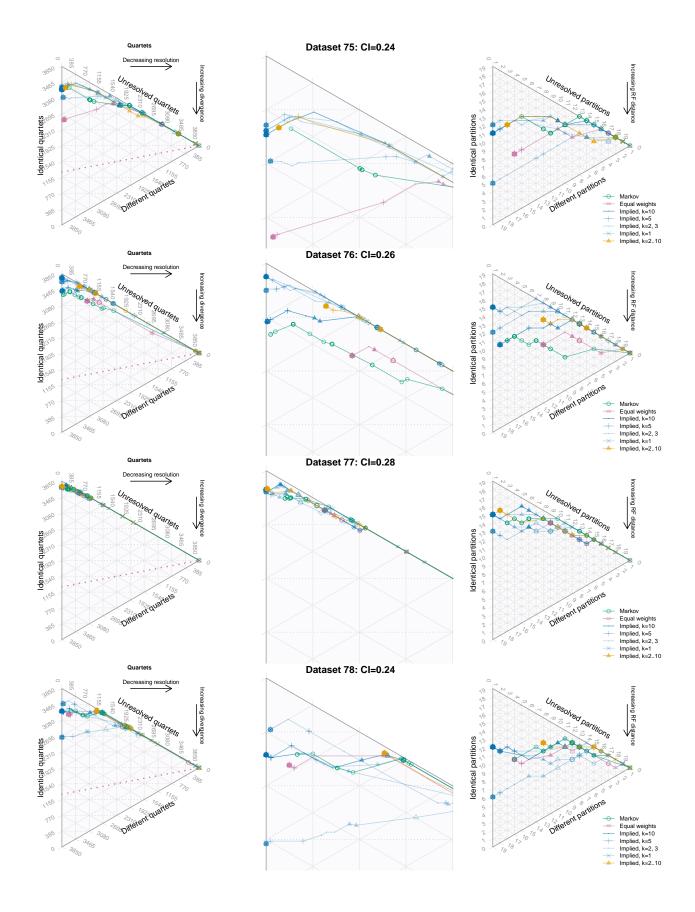


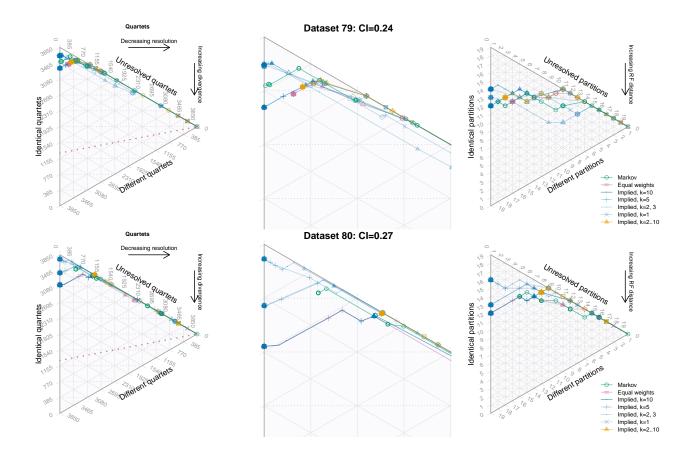




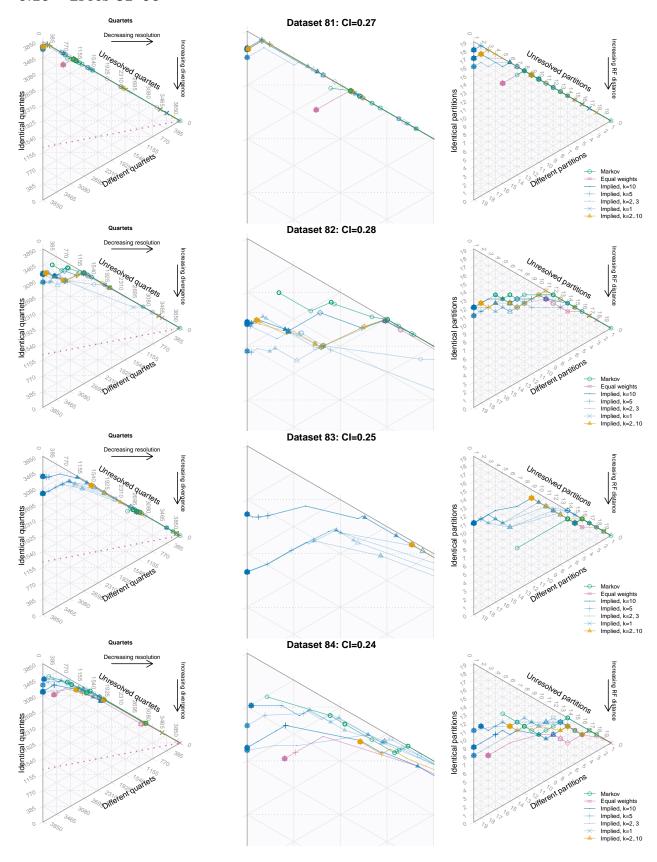
0.9 Trees 71–80

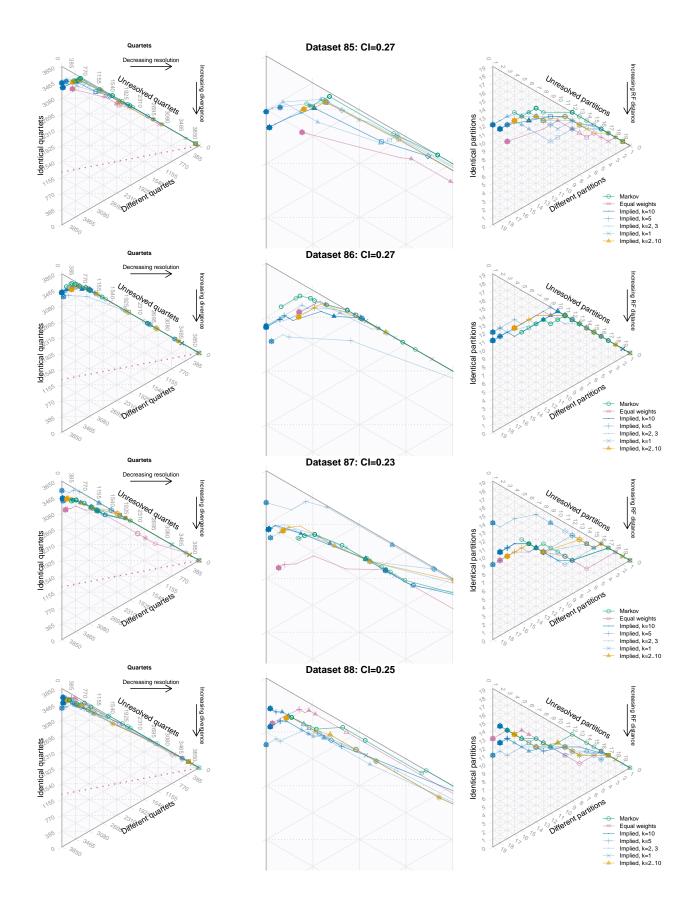


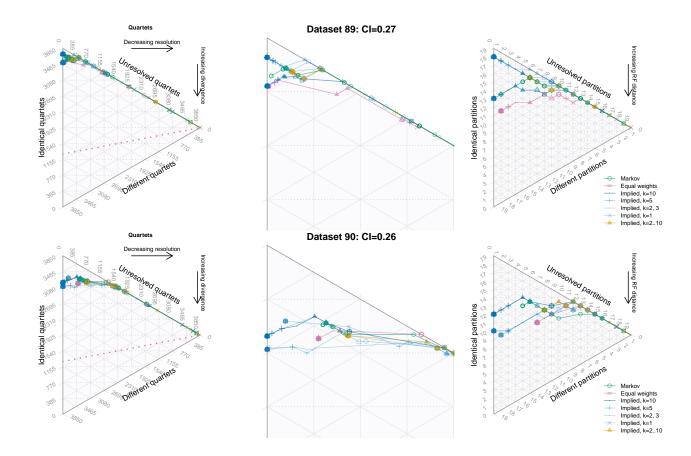




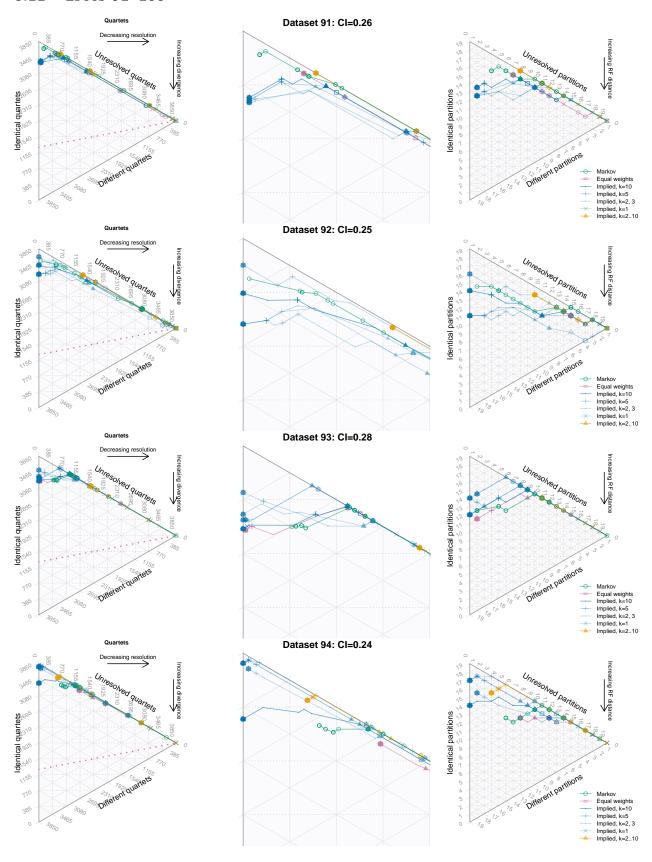
0.10 Trees 81-90

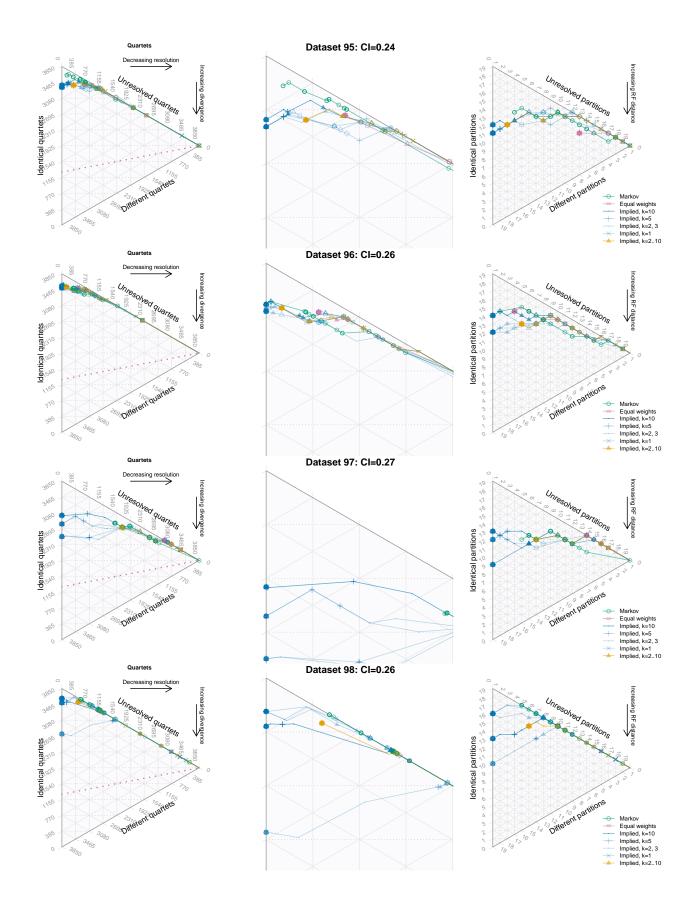


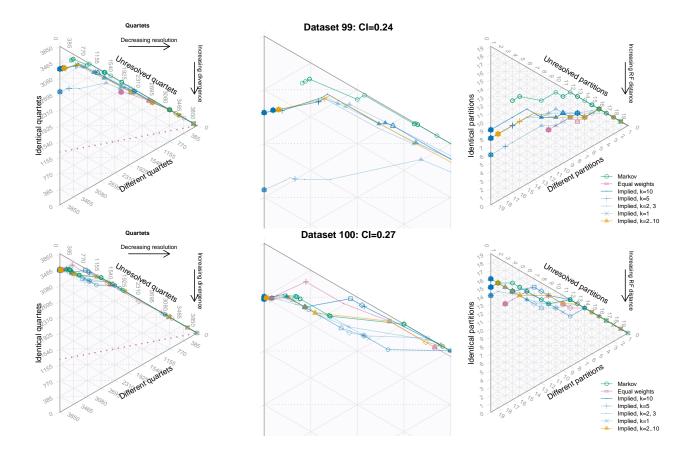




0.11 Trees 91–100







References

- 1. Congreve CR, Lamsdell JC. 2016 Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices. Palaeontology **59**, 447–465. (doi:10.1111/pala.12236)
- 2. Smith MR. In press. Bayesian and parsimony approaches reconstruct informative trees from simulated morphological datasets. $Biology\ Letters;\ preprint\ at\ BioRxiv\ (doi:10.1101/227942)$