As noted, in a recent article by Semple (2003): ‘Of particular interest are the relative rates of misassembly (sequence assembled in the wrong order and/or orientation) and the relative coverage achieved by the three protocols. Unfortunately, the UCSC groups were alone in having published assessments of the rate of misassembly in the contigs they produced [ADD: see references (*) on subsequent assembly analysis and comparison].

*Whole-genome shotgun assembly and comparison of human genome assemblies.*
doi:10.1073/pnas.0307971100

- Page 155, right column, paragraph 4:
Note that, traditionally, assemblers have optimized/approximated one of the properties [ADD: only], listed above...

- Page 156, left column, paragraph 2:
Since Unitig construction can be computationally expensive, large-scale assemblers like CELERA/CABOG have adopted [ADD: (**)] a strategy, where Unitigs are computed as chains of mutually unique adjacent reads with best overlap between each other. [ADD: This technique takes time and space linear in the number of reads.]

*Aggressive assembly of pyrosequencing reads with mates.*

doi:10.1093/bioinformatics/btn548

- Page 158, right column, paragraph 4:
The experimental results show that SUTTA has competitive performance to the best state-of-the-art assemblers [ADD: based on contig size comparison].

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