

# Euler V2.0

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## TECHNOLOGY DESCRIPTION

This approach abandons the classical "overlap - layout - consensus" approach in favor of a new graph approach that, for the first time, resolves the problem of repeats in fragment assembly. The graph approach, in contrast to the Celera assembler, does not mask repeats but uses them instead as a powerful fragment assembly tool. The software also works with 454 contigs.

For general information about the EULER project see Pevzner, et al, PNAS, 98, 2001 and <http://nbcv.sdsc.edu/euler/>.

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## OTHER INFORMATION

### KEYWORDS

genome assembly, PCR, sequence  
finishing, EST assembly

### CATEGORIZED AS

- ▶ **Biotechnology**
- ▶ Bioinformatics
- ▶ **Medical**
- ▶ Research Tools

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