Euler V2.0

Tech ID: 19272 / UC Case 2004-827-0

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://nbcr.sdsc.edu/euler/.

Site License.

CONTACT

University of California, San Diego
Office of Innovation and Commercialization
innovation@ucsd.edu
tel: 858.534.5815.



OTHER INFORMATION

KEYWORDS

genome assembly, PCR, sequence finishing, EST assembly

CATEGORIZED AS

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

RELATED CASES

2004-827-0

© 2009 - 2012, The Regents of the University of California
Terms of use
Privacy Notice