Paper Impact: Assembly of long, error-prone reads using repeat graphs

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Key References

- Assembly of long error-prone reads using de Bruijn graphs.
- Authors: Yu Lin (First), Pavel A. Pevzner (Last and corresponding)
- Journal: PNAS (113 (52), 8396-8405)
- Year: 2016
- Citations: 126 (Google scholar)
- Reason: The presented algorithm Flye is an improvement of the tool presented in this article.
- De novo repeat classification and fragment assembly.
- Authors: Paul A. Pevzner (First), Glenn Tesler (Last and corresponding)
- Journal: CSH Press, Genome Research (volume 14, 1786-1796)
- Year: 2004
- Citations: 294 (Google scholar)
- Reason: Basics on the repeat graph and the repeat classification problem.
- Ancestral reconstruction of segmental duplications reveals punctuated cores of human genome evolution.
- Authors: Zhaoshi Jiang (First), Evan E Eichler (Last and corresponding)
- Journal: Nature Genetics (volume 39, 1361-1368)
- Year: 2007
- Citations: 192 (Google scholar)
- Reason: The information, that repeat graphs can be used to represent mosaic structures.
- What is the difference between the breakpoint graph and the de Bruijn graph?
- Authors: Yu Lin (First), Pavel A Pevzner (Last and corresponding)
- Journal: BMC Genomics volume 15, Suppl 6 (S6)
- Year: 2014
- Citations: 23 (Google scholar)
- Reason: Groundwork publication from Pevzner. Information on the graph structure used to implement Flye. Assembly graphs created from the repeat graph are special cases of breakpoint graphs.
- Haplotype and Repeat Separation in Long Reads.
- Authors: Tischler-Höhle G.

- Journal: Computational Intelligence Methods for Bioinformatics and Biostatistics, CIBB 2017, 103-114
- Year: 2017
- Citations: 3 (Google scholar)
- Reason: The publication describes methods for repeat & haplotype seperation with long reads. Resolving unbriged and highly similar repeats is realted to the challenge of overlap-filtering repeat resolution described in this publication.

Citations of our article

- Citations: 564 (Google scholar); 264 (PubMed); 273 (Web of Science); 356 (Cross Ref)
- Yearly
- o PubMed: 2019: 24; 2020: 141; 2021: 108
- Altmetric: 2017: 1; 2018: 3; 2019: 58; 2020: 280; 2021: 199
- Citations per year (Altmetric)
 Citations per year (Altmetric)
- Articles which cite the given paper:
- Fast and accurate long-read assembly with wtdbg2 (Nature Methods) (cited by: 313, Google scholar), (impact score: 10.93, 2020)
- De novo assembly of haplotype-resolved genomes with trio binning (Nature Biotechnology) (cited by: 151, Google scholar), (impact score: 10.71, 2018)
- Telomere-to-telomere assembly of a complete human X chromosome (Nature) (cited by: 180, Google scholar) (impact score: 42.778, 2019)
- Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome (Science) (cited by: 160, Google scholar), (impact score: 12.84, 2019)
- Opportunities and challenges in long-read sequencing data analysis (Genome Biology) (cited by: 180, Google scholar) (impact score: 11.71, 2020)

Corresponding author Pevzner

• SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing

- Reason: last author, 12583 citations, widely used assembly tool, (impact score 2.09; 2013)
- Initial sequencing and comparative analysis of the mouse genome
- Reason: first sequencing and assembly of the mouse genome, 7438 citations, (impact score 36; 2010)
- De novo identification of repeat families in large genomes
 - Reason: corresponding author, groundwork for the given paper (Assembly of long-error prone reads) /groundwork for assembly of repeat rich genomes, 1211 citations, (impact score 5.15; 2013)
- An Eulerian path approach to DNA fragment assembly
 - Reason: first author, groundwork for further short read assembly tools, 1571 citations, (impact score 9.81; 2013)
- De Novo Peptide Sequencing via Tandem Mass Spectrometry
 - Reason: last author, development of de novo peptide sequencing which is still used today, 747 citations, (impact score 2.09; 2013)