

Resource Summary Report

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Computing Genome Assembly Likelihoods

RRID:SCR_017624

Type: Tool

Proper Citation

Computing Genome Assembly Likelihoods (RRID:SCR_017624)

Resource Information

URL: <https://pachterlab.github.io/cgal/>

Proper Citation: Computing Genome Assembly Likelihoods (RRID:SCR_017624)

Description: Software tool for computing genome assembly likelihoods. Computes likelihood of reads with respect to assembly and statistical model which can be used as metric for evaluating assemblies. Novel likelihood based approach to assembly assessment in absence of ground truth.

Abbreviations: CGAL

Resource Type: data processing software, software resource, image analysis software, alignment software, software application

Defining Citation: [PMID:23360652](#)

Keywords: Computing, genome, assembly, likelihood, read, evaluation

Funding: NHGRI R21 HG006583;
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Resource Name: Computing Genome Assembly Likelihoods

Resource ID: SCR_017624

Alternate URLs: <http://bio.math.berkeley.edu/cgal/>

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260731T043016+0000

Ratings and Alerts

No rating or validation information has been found for Computing Genome Assembly Likelihoods.

No alerts have been found for Computing Genome Assembly Likelihoods.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 106 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Alberoni D, et al. (2023) Alterations in the Microbiota of Caged Honeybees in the Presence of *Nosema ceranae* Infection and Related Changes in Functionality. *Microbial ecology*, 86(1), 601.

Schiavano GF, et al. (2023) *Listeria monocytogenes* Strains Persisting in a Meat Processing Plant in Central Italy: Use of Whole Genome Sequencing and In Vitro Adhesion and Invasion Assays to Decipher Their Virulence Potential. *Microorganisms*, 11(7).

Berner D, et al. (2023) Chromosome-Level Assemblies of the *Pieris mannii* Butterfly Genome Suggest Z-Origin and Rapid Evolution of the W Chromosome. *Genome biology and evolution*, 15(6).

Tolman ER, et al. (2023) A Chromosome-length Assembly of the Black Petaltail (*Tanypteryx hageni*) Dragonfly. *Genome biology and evolution*, 15(3).

Tan C, et al. (2023) First Report on Development of Genome-Wide Microsatellite Markers for Stock (*Matthiola incana* L.). *Plants (Basel, Switzerland)*, 12(4).

Chen W, et al. (2023) Stop or Not: Genome-Wide Profiling of Reassigned Stop Codons in Ciliates. *Molecular biology and evolution*, 40(4).

Farlow AJ, et al. (2023) *Rosenbergiella meliponini* D21B Isolated from Pollen Pots of the Australian Stingless Bee *Tetragonula carbonaria*. *Microorganisms*, 11(4).

Ovchinnikov V, et al. (2023) Caecilian Genomes Reveal the Molecular Basis of Adaptation and Convergent Evolution of Limblessness in Snakes and Caecilians. *Molecular biology and evolution*, 40(5).

Lewis GL, et al. (2023) Association of ISVsa3 with Multidrug Resistance in *Salmonella enterica* Isolates from Cattle (*Bos taurus*). *Microorganisms*, 11(3).

Egorova A, et al. (2023) Plasmid Composition, Antimicrobial Resistance and Virulence Genes Profiles of Ciprofloxacin- and Third-Generation Cephalosporin-Resistant Foodborne *Salmonella enterica* Isolates from Russia. *Microorganisms*, 11(2).

Rudenko N, et al. (2023) Genomic Confirmation of *Borrelia garinii*, United States. *Emerging infectious diseases*, 29(1), 64.

Bologa AM, et al. (2023) The Landscape of the DNA Transposons in the Genome of the Horezu_LaPeri Strain of *Drosophila melanogaster*. *Insects*, 14(6).

Leavitt SD, et al. (2023) Genomic Resources for the First Federally Endangered Lichen: The Florida Perforate *Cladonia* (*Cladonia perforata*). *Journal of fungi* (Basel, Switzerland), 9(7).

Diagne MM, et al. (2023) Novel Amplicon-Based Sequencing Approach to West Nile Virus. *Viruses*, 15(6).

Pan Z, et al. (2022) Chromosomal-Level Genome Assembly of the Springtail *Tomocerus qinae* (Collembola: Tomoceridae). *Genome biology and evolution*, 14(4).

Zhang WP, et al. (2022) Dead-End Hybridization in Walnut Trees Revealed by Large-Scale Genomic Sequence Data. *Molecular biology and evolution*, 39(1).

Hezaveh K, et al. (2022) Tryptophan-derived microbial metabolites activate the aryl hydrocarbon receptor in tumor-associated macrophages to suppress anti-tumor immunity. *Immunity*, 55(2), 324.

Sawadogo Y, et al. (2022) Genomic Epidemiology of SARS-CoV-2 in Western Burkina Faso, West Africa. *Viruses*, 14(12).

Kiel A, et al. (2022) Genome-Based Analysis of Virulence Factors and Biofilm Formation in Novel *P. aeruginosa* Strains Isolated from Household Appliances. *Microorganisms*, 10(12).

Mauldin MR, et al. (2022) Exportation of Monkeypox Virus From the African Continent. *The Journal of infectious diseases*, 225(8), 1367.