Resource Summary Report

Generated by dkNET on Apr 29, 2025

AGORA

RRID:SCR_005070

Type: Tool

Proper Citation

AGORA (RRID:SCR_005070)

Resource Information

URL: http://www.biomedcentral.com/1471-2105/13/189

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Description: An algorithm to use optical map information directly within the de Bruijn graph framework to help produce an accurate assembly of a genome that is consistent with the optical map information provided. AGORA takes as input two data structures: OpMap? an ordered list of fragment sizes representing the optical map; and Edges? a list of de Bruijn graph edges with their corresponding sequences.

Abbreviations: AGORA

Synonyms: Assembly Guided by Optical Restriction Alignment

Resource Type: software resource

Defining Citation: PMID:22856673

Keywords: genome assembly, genome, reconstruction

Funding:

Resource Name: AGORA

Resource ID: SCR_005070

Alternate IDs: OMICS 00039

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250420T014243+0000

Ratings and Alerts

No rating or validation information has been found for AGORA.

No alerts have been found for AGORA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 79 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Nychas E, et al. (2025) Discovery of robust and highly specific microbiome signatures of non-alcoholic fatty liver disease. Microbiome, 13(1), 10.

Qian Y, et al. (2025) A data-driven modeling framework for mapping genotypes to synthetic microbial community functions. bioRxiv: the preprint server for biology.

Carr A, et al. (2024) Personalized Clostridioides difficile engraftment risk prediction and probiotic therapy assessment in the human gut. bioRxiv: the preprint server for biology.

Al-Nijir M, et al. (2024) Metabolic modelling uncovers the complex interplay between fungal probiotics, poultry microbiomes, and diet. Microbiome, 12(1), 267.

Vavougios GD, et al. (2024) SARS-CoV-2-Induced Type I Interferon Signaling Dysregulation in Olfactory Networks Implications for Alzheimer's Disease. Current issues in molecular biology, 46(5), 4565.

Gelbach PE, et al. (2024) Flux sampling in genome-scale metabolic modeling of microbial communities. BMC bioinformatics, 25(1), 45.

Xu Q, et al. (2024) Simulate Scientific Reasoning with Multiple Large Language Models: An Application to Alzheimer's Disease Combinatorial Therapy. medRxiv: the preprint server for health sciences.

Zhu J, et al. (2024) Integrative analysis with microbial modelling and machine learning uncovers potential alleviators for ulcerative colitis. Gut microbes, 16(1), 2336877.

Najer T, et al. (2024) Mitochondrial genome fragmentation is correlated with increased rates of molecular evolution. PLoS genetics, 20(5), e1011266.

Yu W, et al. (2024) Disease-Associated Neurotoxic Astrocyte Markers in Alzheimer Disease Based on Integrative Single-Nucleus RNA Sequencing. Cellular and molecular neurobiology, 44(1), 20.

Wright CJ, et al. (2024) Comparative genomics reveals the dynamics of chromosome evolution in Lepidoptera. Nature ecology & evolution, 8(4), 777.

Groen In 't Woud S, et al. (2024) Genetic and environmental factors driving congenital solitary functioning kidney. Nephrology, dialysis, transplantation: official publication of the European Dialysis and Transplant Association - European Renal Association, 39(3), 463.

Tassoulas LJ, et al. (2024) Insights into the action of the pharmaceutical metformin: Targeted inhibition of the gut microbial enzyme agmatinase. iScience, 27(2), 108900.

Balzerani F, et al. (2024) q2-metnet: QIIME2 package to analyse 16S rRNA data via high-quality metabolic reconstructions of the human gut microbiota. Bioinformatics (Oxford, England), 40(11).

Park T, et al. (2024) Genome-wide transcriptome analysis of A? deposition on PET in a Korean cohort. Alzheimer's & dementia: the journal of the Alzheimer's Association, 20(12), 8787.

Hedin KA, et al. (2024) Saccharomyces boulardii enhances anti-inflammatory effectors and AhR activation via metabolic interactions in probiotic communities. The ISME journal, 18(1).

Srinak N, et al. (2024) Metabolic cross-feeding interactions modulate the dynamic community structure in microbial fuel cell under variable organic loading wastewaters. PLoS computational biology, 20(10), e1012533.

Román L, et al. (2024) Genome-scale metabolic modeling of the human milk oligosaccharide utilization by Bifidobacterium longum subsp. infantis. mSystems, 9(3), e0071523.

Versluis DM, et al. (2024) 2'-Fucosyllactose helps butyrate producers outgrow competitors in infant gut microbiota simulations. iScience, 27(3), 109085.

Palanikumar I, et al. (2024) Panera: An innovative framework for surmounting uncertainty in microbial community modeling using pan-genera metabolic models. iScience, 27(7), 110358.