Resource Summary Report

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Stampy

RRID:SCR_005504
Type: Tool

Proper Citation

Stampy (RRID:SCR_005504)

Resource Information

URL: http://www.well.ox.ac.uk/project-stampy

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Description: A software package for the mapping of short reads from illumina sequencing machines onto a reference genome. It''s recommended for most workflows, including those for genomic resequencing, RNA-Seq and Chip-seq. Stampy excels in the mapping of reads containing that contain sequence variation relative to the reference, in particular for those containing insertions or deletions. It can map reads from a highly divergent species to a reference genome for instance. Stampy achieves high sensitivity and speed by using a fast hashing algorithm and a detailed statistical model. Stampy has the following features: * Maps single, paired-end and mate pair Illumina reads to a reference genome * Fast: about 20 Gbase per hour in hybrid mode (using BWA) * Low memory footprint: 2.7 Gb shared memory for a 3Gbase genome * High sensitivity for indels and divergent reads, up to 10-15% * Low mapping bias for reads with SNPs * Well calibrated mapping quality scores * Input: Fastq and Fasta; gzipped or plain * Output: SAM, Maq''s map file * Optionally calculates per-base alignment posteriors * Optionally processes part of the input * Handles reads of up to 4500 bases

Abbreviations: Stampy

Resource Type: software resource

Defining Citation: PMID:20980556

Keywords: bio.tools

Funding:

Resource Name: Stampy

Resource ID: SCR_005504

Alternate IDs: OMICS_00691, biotools:stampy

Alternate URLs: https://bio.tools/stampy

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250420T014253+0000

Ratings and Alerts

No rating or validation information has been found for Stampy.

No alerts have been found for Stampy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 176 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Cornetti L, et al. (2024) Long-term balancing selection for pathogen resistance maintains trans-species polymorphisms in a planktonic crustacean. Nature communications, 15(1), 5333.

Officer K, et al. (2024) Genomic insights into anthropozoonotic tuberculosis in captive sun bears (Helarctos malayanus) and an Asiatic black bear (Ursus thibetanus) in Cambodia. Scientific reports, 14(1), 7343.

Liu X, et al. (2024) A genome-wide association study reveals the relationship between human genetic variation and the nasal microbiome. Communications biology, 7(1), 139.

Kingsley EP, et al. (2024) Adaptive tail-length evolution in deer mice is associated with differential Hoxd13 expression in early development. Nature ecology & evolution, 8(4), 791.

Tapanes E, et al. (2024) The genetic basis of divergent melanic pigmentation in benthic and limnetic threespine stickleback. Heredity, 133(4), 207.

Miyazaki S, et al. (2023) Zfp296 knockout enhances chromatin accessibility and induces a

unique state of pluripotency in embryonic stem cells. Communications biology, 6(1), 771.

Durak MR, et al. (2023) Genome-Wide Discovery of Structural Variants Reveals Distinct Variant Dynamics for Two Closely Related Monilinia Species. Genome biology and evolution, 15(6).

Li X, et al. (2023) Comparing genomic variant identification protocols for Candida auris. Microbial genomics, 9(4).

Lee CK, et al. (2023) Successful Confirmation of Dual Genital Herpes Co-Infection with Herpes Simplex Virus 1 and Herpes Simplex Virus 2 Using Unbiased Metagenomic Next-Generation Sequencing. Viruses, 15(9).

Pan B, et al. (2022) Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome biology, 23(1), 2.

Lange JD, et al. (2022) A Population Genomic Assessment of Three Decades of Evolution in a Natural Drosophila Population. Molecular biology and evolution, 39(2).

Freitas S, et al. (2022) Parthenogenesis in Darevskia lizards: A rare outcome of common hybridization, not a common outcome of rare hybridization. Evolution; international journal of organic evolution, 76(5), 899.

Mongue AJ, et al. (2022) Population differentiation and structural variation in the Manduca sexta genome across the United States. G3 (Bethesda, Md.), 12(5).

Koska M, et al. (2022) Distinct Long- and Short-Term Adaptive Mechanisms in Pseudomonas aeruginosa. Microbiology spectrum, 10(6), e0304322.

Carlier J, et al. (2021) Convergent Adaptation to Quantitative Host Resistance in a Major Plant Pathogen. mBio, 12(1).

Tortelli BA, et al. (2021) The structure and diversity of strain-level variation in vaginal bacteria. Microbial genomics, 7(3).

Baxley RM, et al. (2021) Bi-allelic MCM10 variants associated with immune dysfunction and cardiomyopathy cause telomere shortening. Nature communications, 12(1), 1626.

Barthlott T, et al. (2021) Indispensable epigenetic control of thymic epithelial cell development and function by polycomb repressive complex 2. Nature communications, 12(1), 3933.

Chatzinakos C, et al. (2021) Increasing the resolution and precision of psychiatric genome-wide association studies by re-imputing summary statistics using a large, diverse reference panel. American journal of medical genetics. Part B, Neuropsychiatric genetics : the official publication of the International Society of Psychiatric Genetics, 186(1), 16.

Rodríguez Cruz PM, et al. (2021) Presynaptic congenital myasthenic syndrome due to three novel mutations in SLC5A7 encoding the sodium-dependant high-affinity choline transporter. Neuromuscular disorders : NMD, 31(1), 21.