Resource Summary Report

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NanoFilt

RRID:SCR_016966
Type: Tool

Proper Citation

NanoFilt (RRID:SCR_016966)

Resource Information

URL: https://github.com/wdecoster/nanofilt

Proper Citation: NanoFilt (RRID:SCR_016966)

Description: Software tool written in Python to perform its filtering based on mean read quality and GC content and read length. Used for filtering and trimming of long read sequencing data.

Resource Type: software application, software resource, data processing software

Keywords: filtering, trimming, long, sequencing, data, read

Funding:

Availability: Free, Available for download, Freely available

Resource Name: NanoFilt

Resource ID: SCR_016966

Alternate URLs: https://sources.debian.org/src/nanofilt/

License: GNU General Public License v3.0

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250412T060043+0000

Ratings and Alerts

No rating or validation information has been found for NanoFilt.

No alerts have been found for NanoFilt.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 196 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Morita D, et al. (2025) Genomic epidemiology and genetic characteristics of clinical Campylobacter species cocirculating in West Bengal, India, 2019, using whole genome analysis. Antimicrobial agents and chemotherapy, 69(1), e0110824.

Chudhary A, et al. (2025) Characterization of chemosensory genes in the subterranean pest Gryllotalpa Orientalis based on genome assembly and transcriptome comparison. BMC genomics, 26(1), 33.

Ye F, et al. (2025) Comprehensive genome annotation of the model ciliate Tetrahymena thermophila by in-depth epigenetic and transcriptomic profiling. Nucleic acids research, 53(2).

Bejaoui S, et al. (2025) Comparison of Illumina and Oxford Nanopore sequencing data quality for Clostridioides difficile genome analysis and their application for epidemiological surveillance. BMC genomics, 26(1), 92.

Gatins R, et al. (2024) Whole genome assembly and annotation of the King Angelfish (Holacanthus passer) gives insight into the evolution of marine fishes of the Tropical Eastern Pacific. GigaByte (Hong Kong, China), 2024, gigabyte115.

Zhong L, et al. (2024) Nanopore-based metagenomics analysis reveals microbial presence in amniotic fluid: A prospective study. Heliyon, 10(6), e28163.

LeBlanc NR, et al. (2024) Green Waste Compost Impacts Microbial Functions Related to Carbohydrate Use and Active Dispersal in Plant Pathogen-Infested Soil. Microbial ecology, 87(1), 44.

Pan J, et al. (2024) Molecular basis of phenotypic plasticity in a marine ciliate. The ISME journal, 18(1).

Meyer C, et al. (2024) Temperature modulates dominance of a superinfecting Arctic virus in its unicellular algal host. The ISME journal, 18(1).

Herman EK, et al. (2024) Bacterial enrichment prior to third-generation metagenomic sequencing improves detection of BRD pathogens and genetic determinants of antimicrobial resistance in feedlot cattle. Frontiers in microbiology, 15, 1386319.

Dhanji-Rapkova M, et al. (2024) Investigating Non-Native Ribbon Worm Cephalothrix simula as a Potential Source of Tetrodotoxin in British Bivalve Shellfish. Marine drugs, 22(10).

Tsuchiya J, et al. (2024) Time course transcriptomic profiling suggests Crp/Fnr transcriptional regulation of nosZ gene in a N2O-reducing thermophile. iScience, 27(11), 111074.

Lü Z, et al. (2024) Chromosome-level genome assembly and annotation of eel goby (Odontamblyopus rebecca). Scientific data, 11(1), 160.

Rheman S, et al. (2024) Nanopore sequencing for identification and characterization of antimicrobial-resistant Escherichia coli and Salmonella spp. from tilapia and shrimp sold at wet markets in Dhaka, Bangladesh. Frontiers in microbiology, 15, 1329620.

Gand M, et al. (2024) Towards facilitated interpretation of shotgun metagenomics long-read sequencing data analyzed with KMA for the detection of bacterial pathogens and their antimicrobial resistance genes. Frontiers in microbiology, 15, 1336532.

Erlandson SR, et al. (2024) Sterile sentinels and MinION sequencing capture active soil microbial communities that differentiate crop rotations. Environmental microbiome, 19(1), 30.

Pilgrim J, et al. (2024) Comparative genomics of a novel Erwinia species associated with the Highland midge (Culicoides impunctatus). Microbial genomics, 10(4).

Quinn MW, et al. (2024) Apirhabdus apintestini gen. nov., sp. nov., a member of a novel genus of the family Enterobacteriaceae, isolated from the gut of the western honey bee Apis mellifera. International journal of systematic and evolutionary microbiology, 74(4).

Raymond BB, et al. (2024) Snow alga Sanguina aurantia as revealed through de novo genome assembly and annotation. G3 (Bethesda, Md.), 14(10).

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. Nature communications, 15(1), 6297.