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CoverM: A Configurable, Easy-to-Use DNA Read Coverage and Relative Abundance Calculator for Metagenomics Applications ## Introduction [Image description: Diagram showing the relationship between metagenomics, CoverM, and DNA read coverage] CoverM aims to be a configurable, easy-to-use, and fast DNA read coverage and relative abundance calculator focused on metagenomics applications. With its user-friendly interface and robust features, CoverM helps researchers calculate the coverage of genomes, MAGs, or individual contigs in their metagenomic samples. ## Installation [Image description: Screenshot showing the installation process of CoverM] CoverM can be installed through the bioconda conda channel. After initial setup, you can install it using statically compiled binaries available on the releases page. For developers, CoverM can also be installed from source, using the cargo build system after installing Rust. ### Installation Methods * **Conda Channel**: Install CoverM and its dependencies through the bioconda conda channel. * **Static Compilation**: Download statically compiled binaries from the releases page. * **Source Code**: Install CoverM from source, using the cargo build system after installing Rust. ## Modes of Operation CoverM operates in several modes: ### Genome Mode * Calculate coverage of genomes * [Example](### Contig Mode * Calculate coverage of contigs * [Example](### Utility Modes * **make**: Generate BAM files through alignment filter * **cluster**: Dereplicate and cluster genomes * **shell-completion**: Generate shell completion scripts ## Usage Example [Image description: Screenshot showing the usage example of CoverM] To calculate the coverage or relative abundance of a set of genomes in a metagenomic sample, you can use CoverM. Here's an example: ```bash coverm genome --coupled sample_1.1.fq.gz sample_1.2.fq.gz --genome-fasta-files genome_1.fna genome_2.fna genome_3.fna genome_4.fna genome_5.fna genome_6.fna genome_7.fna genome_8.fna -t 8 -m mean relative_abundance covered_fraction -o output_coverm.tsv ``` This will calculate the mean coverage, relative abundance, and covered fraction for each genome in the sample. ## Links * [CoverM Documentation](* [GitHub Repository](Looking at half of our sample diversity, we see that the file output_coverm.tsv shows genome samples with varying metrics. The columns include Genome, Mean, Relative Abundance (%), and Covered Fraction for each sample. For instance, genome_1 has a mean coverage of 0.941, while genome_5 shows no coverage at all. Looking at the covered fraction, we see that most genomes have low values due to sub-sampling to 100,000 reads from the full sample. ###ARTICLECoverM is a tool for analyzing read alignment statistics in metagenomics, as published in the journal Bioinformatics by Tyson and Woodcroft in 2025. CoverM is available under the GPL3+ license and provides detailed information on read alignment data, which can be useful for researchers and scientists studying microbial communities.