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1. [arXiv:2211.08157](#) [pdf] [cs.DS](#) [q-bio.GN](#) [q-bio.QM](#)**Genome-on-Diet: Taming Large-Scale Genomic Analyses via Sparsified Genomics****Authors:** [Mohammed Alser](#), [Julien Eudine](#), [Onur Mutlu](#)

Abstract: ...applicability. We show that sparsifying genomic sequences greatly accelerates the state-of-the-art read mapper (minimap2) by 2.57-5.38x, 1.13-2.78x, and 3.52-6.28x using real **illumina**, HiFi, and ONT reads, respectively, while providing up to 2.1x smaller memory footprint, 2x smaller index size, and more truly detected small and structural variations compared... [▽ More](#)

Submitted 9 July, 2024; **v1** submitted 15 November, 2022; **originally announced** November 2022.

2. [arXiv:1007.5075](#) [pdf, ps, other] [q-bio.GN](#) [q-bio.QM](#) [doi](#) [10.1371/journal.pone.0015406](#)**Microbiome profiling by illumina sequencing of combinatorial sequence-tagged PCR products****Authors:** [Gregory B. Gloor](#), [Ruben Hummelen](#), [Jean M. Macklaim](#), [Russell J. Dickson](#), [Andrew D. Fernandes](#), [Roderick MacPhee](#), [Gregor Reid](#)

Abstract: We developed a low-cost, high-throughput **microbiome** profiling method that uses combinatorial sequence tags attached to PCR primers that amplify the rRNA V6 region. Amplified PCR products are sequenced using an... [▽ More](#)

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