REPORT

Alignment-free tools for metagenomics-data analysis

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Abstract

TODO

Keywords: alignment-free; report; metagenome

Introduction

Metagenomics

A puddle of mud The metagenome is the whole set of genes, of a population, of microorganisms as found in a sample of a microbiome. As such metagenomics is the study and analysis of such metagenomes.[1]

A microbiom is the "home" of countless bacteria, archea and viruses; like all microorganisms >90% of those found in microbioms are uncultured, leaving researchers with the problem of how to study those organisms.

Accumulated data from microbiom samples Choosing a sample is the easiest part of the analysis of a microbiom. the following steps are:

1 DNA isolation from samples
2 construction of DNA libraries (typically in *E. Coli* as host)
3 Mining for clones and DNA sequences of interest
4 Accumulation of desired clones and DNA sequences

as stated in Streit et al [2], to obtain a metagenomic library.

NGS – Next Generation Sequencing The sheer amount of data gathered through such samples – Kakirde et al[3] states 10000 Gb of DNA in a soil sample – leaves researches with the problem of sequencing. While Sanger sequencing is

Goals

The "classical" approach
Alignment-based method

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The good

The bad – Too much data, too little time The analysis of such metagenomes is heavy on computation and time resources, due to the amount of data collected; this results in the pursuit of faster and more effective methods for data analysis

The alternative approach
Alignment-free method

The ugly

Methods

Statistics
The power of statistics

k-tupel approach – Song et al
What is a k-tupel

D_2

Nucleotide bias

Visualization approach
The idea behind

non-linear dimension reduction – Laczny et al
Weiss noch nicht hier

Results

Application of tools on data set
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Content
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Competing interests
Author's contributions
Acknowledgements
References

1. Handelsman, J.: Metagenomics: application of genomics to uncultured microorganisms. Microbiology and molecular biology reviews **68**(4), 669–685 (2004)

2. Streit, W.R., Schmitz, R.A.: Metagenomics – the key to the uncultured microbes. Current Opinion in Microbiology **7**(5), 492–498 (2004). doi:10.1016/j.mib.2004.08.002

3. Kakirde, K.S., Parsley, L.C., Liles, M.R.: Size does matter: Application-driven approaches for soil metagenomics. Soil Biology and Biochemistry **42**(11), 1911–1923 (2010). doi:10.1016/j.soilbio.2010.07.021

Figures

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Figure 2 Sample figure title. Figure legend text.

Tables

Table 1 Sample table title. This is where the description of the table should go.

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