REPORT

Alignment-free tools for metagenomics-data analysis

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Abstract

TODO

Keywords: alignment-free; report; metagenome

Introduction

The Metagenome

A puddle of mud The metagenome is a set of genes, of a population, of microorganisms as found in a sample (e.g. from the gut of organisms, soil, water). As such metagenomics is the study and analysis of such metagenomes.[1] Typically the microorganisms found in these samples are uncultured; researchers are interested in cooperation of microorganisms, and microorganisms and microbiome.

NGS – Next Generation Sequencing

Goals

The "classical" approach
Alignment-based method

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

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
title

Content

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Section title

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Sub-sub-sub heading for section Text for this sub-sub-sub-heading . . . In this section we examine the growth rate of the mean of Z_0, Z_1 and Z_2. In addition, we examine a common modeling assumption and note the importance of considering the tails of the extinction time T_x in studies of escape dynamics. We will

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first consider the expected resistant population at vT_x for some $v > 0$, (and temporarily assume $\alpha = 0$)

$$E\big[Z_1(vT_x)\big] = E\left[\mu T_x \int_0^{v \wedge 1} Z_0(uT_x) \exp\big(\lambda_1 T_x(v-u)\big)\, du\right].$$

If we assume that sensitive cells follow a deterministic decay $Z_0(t) = xe^{\lambda_0 t}$ and approximate their extinction time as $T_x \approx -\frac{1}{\lambda_0} \log x$, then we can heuristically estimate the expected value as

$$
\begin{aligned}
E\big[Z_1(vT_x)\big] &= \frac{\mu}{r} \log x \int_0^{v \wedge 1} x^{1-u} x^{(\lambda_1/r)(v-u)}\, du \\
&= \frac{\mu}{r} x^{1-\lambda_1/\lambda_0 v} \log x \int_0^{v \wedge 1} x^{-u(1+\lambda_1/r)}\, du \\
&= \frac{\mu}{\lambda_1 - \lambda_0} x^{1+\lambda_1/rv} \left(1 - \exp\left[-(v \wedge 1)\left(1 + \frac{\lambda_1}{r}\right) \log x\right]\right) \quad (1)
\end{aligned}
$$

Thus we observe that this expected value is finite for all $v > 0$ (also see).

Competing interests
The authors declare that they have no competing interests.

Author's contributions
Text for this section . . .

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

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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Additional file 2 — Sample additional file title
Additional file descriptions text.