Sequence analysis

Higher classification sensitivity of short metagenomic reads with CLARK-S

Rachid Ounit and Stefano Lonardi*

Department of Computer Science and Engineering, University of California, Riverside, CA 92521, USA

*To whom correspondence should be addressed.

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Abstract

Summary: The growing number of metagenomic studies in medicine and environmental sciences is creating increasing demands on the computational infrastructure designed to analyze these very large datasets. Often, the construction of ultra-fast and precise taxonomic classifiers can compromise on their sensitivity (i.e. the number of reads correctly classified). Here we introduce CLARK-S, a new software tool that can classify short reads with high precision, high sensitivity and high speed.

Availability and Implementation: CLARK-S is freely available at http://clark.cs.ucr.edu/

Contact: stelo@cs.ucr.edu

Supplementary information: Supplementary data are available at Bioinformatics online.

1 Introduction

One of the primary goals of metagenomic studies is to determine the taxonomical identity of bacteria and viruses in a heterogeneous microbial sample (e.g. soil, water, urban environment, human microbiome). This analysis can reveal the presence of unexpected bacteria and viruses in a newly explored microbial habitat, or in the case of the human body, elucidate relationships between diseases and imbalances in the microbiome.

Arguably, the most effective and unbiased methods to study these microbial samples is via high-throughput sequencing. The associated computational problem is to assign sequenced (short) reads to a taxonomic unit. Several methods and software tools are available, but faster and more accurate algorithms are needed to keep pace with the increasing throughput of modern sequencing instruments. In Ounit et al. (2015) we introduced CLARK, a taxonomy-dependent binning method whose classification speed is currently unmatched. A recent independent evaluation of fourteen taxonomic binning/profiling methods (Kraken by Wood and Salzberg, 2014, MEGAN by Huson et al., 2007 and many others) showed that the classification precision of CLARK is comparable (sometimes better) than the state-of-the-art classifiers (Lindgreen et al., 2016). Although CLARK’s speed and precision are very high, its classification sensitivity (i.e. the fraction of reads that it correctly classifies) can be significantly improved with the methods described next.

We recall that CLARK is a k-mer based method. Briefly, it assigns a read $r$ to a reference genome $G$ if $r$ and $G$ share more discriminative $k$-mers (i.e. $k$-mers that appear exclusively in one reference genome) than other genomes in the database. Here we show that the classification sensitivity can be increased by allowing mismatches between shared $k$-mers in a limited number of (carefully predetermined) positions, while maintaining the requirement for $k$-mers to be discriminative. The idea of allowing mismatches to improve the sensitivity of seed-and-extend alignment methods was pioneered in Ma et al. (2002) with the notion of spaced seed. While spaced seeds have been used in some metagenomic binning/profiling methods (e.g. MEGAN), the use of discriminative spaced $k$-mers is novel. Here we describe an extension of the algorithmic infrastructure of CLARK based on spaced seed, called CLARK-S.

2 Methods

Given an integer $k$ and $m$ reference genomes $\{g_1, g_2, \ldots, g_m\}$, the discriminative $k$-mers $D_i$ for genome $g_i$ is the set of all $k$-mers in $g_i$ that do not occur (exactly) in any other genome (Ounit et al., 2015). A spaced seed $s$ of length $k$ and weight $w<k$ is a string over the alphabet $\{1, \ast\}$ that contains $w$ ‘1’ and $(k-w)$ ‘∗’ Matches are required at a ‘1’ positions, while mismatches are allowed at the ‘∗’ locations. The set of discriminative spaced $k$-mers $E_{i,s}$ is the set of all
k-mers of $D_j$ that do not occur in any other set $D_i$ ($j \neq i$) when mismatches are allowed at “*” positions in $s$.

The common model to align a short (Illumina) read $r$ of fixed length to a reference genome $G$ is a short alignment (Brown et al., 2004; Ma et al., 2002). Finding an optimal set of spaced seeds through a dynamic programming method implemented by Ilie et al. (2011) on a region of 100bp, we selected the three spaced seeds with the highest ‘hit probability’ ($Ma et al., 2002$), namely $1111*1111*1111*1111*1111*11111$ (hit probability $0.998111$), $11111*1111*1111*1111*11111*11111$ ($0.999099$) and $11111*1111*1111*1111*11111*11111$ ($0.998093$).

In the pre-processing stage, CLARK-S stores on disk, for each genome $i$ and each spaced seed $s$, the set of discriminative spaced k-mers $E_s$. When compared with CLARK’s classification phase, CLARK-S requires three look-ups for each k-mer in a read (one look-up per spaced seed).

3 Experimental setup

As said, a recent independent evaluation of several published taxonomic binning methods showed that CLARK and Kraken are the two most accurate tools at the genus and phylum level (Lindgreen et al., 2016). Instead of comparing CLARK-S to all published binning methods, it is therefore sufficient to compare it against CLARK and Kraken. To guarantee a consistent and fair evaluation, we ran CLARK-S, CLARK and Kraken on the same set of reference genomes, namely all microbial genomes in the NCBI RefSeq database (total of 5747 species: 1335 bacteria, 123 archaea and 4289 viruses). Evaluations were carried out on simulated datasets and real metagenomic data, as explained next.

We created six synthetic datasets, each representing a distinct microbial habitat and containing reads from the related dominant organisms (see Supplementary Materials S1 for full details). We included samples from the human mouth (characterized by 12 dominant species), city parks (48 species), human gut (20 species), household (two datasets, 31 and 21 species) and soil (50 species). A seventh dataset included reads from 525 randomly chosen bacterial/archaeal species (see Supplementary Materials S1). All these datasets are composed of 100 bp reads generated by ART (Huang et al., 2012) using the Illumina error model with default settings. Since two distinct species $i$ and $j$ can have sequence similarity as high as 98.8% (Stackebrandt and Goebel, 1994), a short read $r$ generated from genome $g_i$ may appear in another genome $g_j$ for a given error rate or number of mismatches. Ignoring the possibility of ambiguity in reads classification is likely to lead to incorrect conclusions on precision and sensitivity. In order to carry out an unbiased evaluation, we created additional datasets (called ‘unambiguous’, see Supplementary Materials S2 for details) in which no read can be mapped to more than one species with the same error rate or number of mismatches. We tested the three tools on fourteen datasets containing a total of 23.5 M reads from 647 species (see Supplementary Table S1). We also added three negative control samples containing short reads that do not exist in any genome in the NCBI/RefSeq database (see Supplementary Materials S1). We used the precision and sensitivity metrics defined in Ounit et al. (2015) to evaluate the classification performance.

For experiments on real metagenomes, we chose a large dataset from a recent study on the microbial profile of the New York City subway system, the Gowanus canal and public parks (Afshinnekoo et al., 2015). We selected twelve datasets containing a total of 105M reads from various microbial habitat (e.g. bench, garbage can, kiosk, stairway rail, water, etc.), subway stations and riders usage (see Supplementary Table S3). Although the ground truth for these data is unknown, the abundance of bacteria, eukaryotes and viruses present in these samples were provided in Afshinnekoo et al. (2015). We trimmed raw reads as it was done in Afshinnekoo et al. (2015) (see Supplementary Table S3), then compared the results of CLARK-S with the findings in Afshinnekoo et al. (2015) (see Supplementary Tables S4 and S5).

4 Results and discussion

Observe in Supplementary Table S2 that the sensitivity achieved by CLARK-S on the 14 simulated datasets is consistently higher than other tools, while maintaining high precision (the increase in sensitivity is even higher on unambiguous datasets). Also, note that CLARK-S did not classify any reads from the negative control samples. Supplementary Table S7 shows that CLARK-S classifies about 200 000 short reads per minute (using one CPU), while CLARK classifies about 3.5 M short reads per minute. If one can take advantage of eight cores, CLARK-S classifies about 1 M short read per minute, which is sufficiently fast to process large metagenomic datasets in few minutes (see Supplementary Materials S3). CLARK-S requires more time to build the database than CLARK or Kraken, but its RAM usage is comparable to the other tools (see Supplementary Table S8).

Observe in Supplementary Table S6 (real datasets) that CLARK-S classifies more reads than CLARK or Kraken. On average, CLARK-S classifies 10% more reads than Kraken, and 27% more reads than CLARK. Supplementary Table S5 indicates the reads count assigned by each tool to each species listed in Afshinnekoo et al. (2015) and present in the database. CLARK-S achieves consistently the highest agreement with Afshinnekoo et al. (2015) on all samples. For instance, in P00589 and P00720, CLARK-S detected both Brucella ovis and phage HK97 but CLARK/Kraken did not; in sample P01136, CLARK-S detected Brucella ovis but CLARK/Kraken failed to do so. In general, CLARK-S identified more relevant organisms than the other tested tools, as observed by a recent study focusing on water samples (Thompson et al., 2016).

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References


