An evaluation of the accuracy and speed of metagenome analysis tools

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Abstract

Metagenome studies are becoming increasingly widespread, yielding important insights into microbial communities covering diverse environments from terrestrial and aquatic ecosystems to human skin and gut. With the advent of high-throughput sequencing platforms, the use of large scale shotgun sequencing approaches is now commonplace. However, a thorough independent benchmark comparing state-of-the-art metagenome analysis tools is lacking. Here, we present a benchmark where the most widely used tools are tested on complex, realistic data sets. Our results clearly show that the most widely used tools are not necessarily the most accurate, that the most accurate tool is not necessarily the most time consuming, and that there is a high degree of variability between available tools. These findings are important as the conclusions of any metagenomics study are affected by errors in the predicted community composition. Data sets and results are freely available from http://www.ucbioinformatics.org/metabenchmark.html

With the advent of second-generation sequencing platforms such as 454[1] and Illumina[2], the ease with which any research group can generate gigabases of high-quality sequence data at comparatively low cost has had a major impact on biological research. One field of research that has grown immensely over recent years is metagenomics[3] - the investigation of full communities to address questions about the composition, diversity and functioning of complex systems. The field has moved from amplicon sequencing of specific marker genes to high-throughput shotgun sequencing of total DNA in a sample. The result is large, complex data sets that can be used to investigate both taxonomic composition and, potentially, functional capacity of a sample.

Metagenomic studies have shed light on novel aspects of biology. For instance, studies of the human microbiome has shown possible connections between the bacteria in the gut and diseases as diverse as diabetes[4], depression[5] and rheumatoid arthritis[6]. In ecology, metagenomics make it possible to investigate complex communities in e.g. soil[7], glaciers[8] and air[9]. Some groups are looking at ancient communities and tracing community changes over time by investigating the metagenomes in coprolites[10], teeth[11] and elsewhere[12]. In metatranscriptomics, the expressed RNAs are investigated[13–15], potentially making it possible to infer transcription patterns directly, but as this field is still in its infancy due to technical complexities we focus on metagenomics in this paper.

The results of any metagenomics study relies on computational tools that can analyze large data sets and extract useful and correct information about the community under investigation. Fortunately, a number of tools have been developed to investigate the taxonomic composition of metagenomes and, in some cases, also shed light on the functional composition of the community. These tools can broadly be separated in two groups - those using all available sequences for each data set (e.g. CLARK[16], the EBI metagenomics webserver [17], Genometa [18], GOTTCHA[19], Kraken [20], LMAT [21], MEGAN [22,23], MG-RAST [24], the One Codex webserver, taxator-tk [25]) and those focusing on a set of marker genes (e.g MetaPhlAn [26], MetaPhyler [27], mOTU [28], QIIME [29]).

A previous benchmark used synthetic communities by pooling genomic DNA[30] in order to primarily investigate different sequencing approaches. However, an independent, in-depth benchmark of analysis tools is lacking. Here we present what is to our knowledge the first unbiased, comprehensive benchmark of metagenome analysis tools in which the authors are not involved in any of the tools tested. We use a set of sequences that were sampled from a known taxonomic distribution, these include genomic sequences from characterised taxa, simulated relatives of varying evolutionary distances using phylogenetic modelling and permuted sequences that serve as a negative control. These are realistic synthetic metagenomes that capture many of the complexities encountered in real sequencing experiments. We evaluate 14 tools in order to investigate how well they perform both in terms of taxonomy and, where available, function. This comprehensive benchmark sheds light on the performance of widely used tools and can help researchers decide what tools to use in

their metagenomics studies, which can have a strong impact on the results and conclusions of any study.

Results

Overall performance

The key results are listed in Table 1. The run time varies between tools, ranging from minutes (OneCodex, QIIME) and hours (e.g. mOTU, Kraken) to several days (e.g. MetaPhyler, EBI webserver). However, it should be noted that the input to QIIME is much smaller than the full data sets being analyzed by the other tools as it only contained predicted 16S rRNA sequences. The run time experienced by a user when using a webserver (EBI, MG-RAST, OneCodex) may depend heavily on a number of factors such as current load, software upgrades, priority of the job etc.

The data sets were all designed containing 80% reads that could ideally be mapped to their corresponding genomes of origin (70% bacteria and archaea, 5% *in silico* evolved bacterial genomes, 5% Eukaryote) and 20% sampled from shuffled genomes that should not map. Depending on whether the database used contained Eukaryote genomes or not, each tool should be able to map up to 70%-80% of the reads.

Note, however, that the fraction of reads mapped is not in itself a metric of quality since some tools rely on smaller sets of marker genes. As with the run times, the actual fraction of reads mapped varies greatly between tools. MetaPhlAn, MetaPhyler and mOTU all rely on sets of marker genes, and the EBI webserver uses only predicted rRNA reads, and therefore these four methods map the fewest reads (from 0.08% to appr. 5%). Kraken maps around 72%, whereas Genometa, MEGAN and Taxator-tk all map around 40%, and LMAT, MG-RAST and QIIME map up towards 60% of reads. Interestingly, the number of reads analyzed is not reflected in the run time (e.g. Kraken analyzes many more reads than MetaPhyler but runs much faster).

The 20% reads from shuffled bacterial genomes should not be assigned to any taxa. Overall the tools perform well by assigning very few shuffled reads to phyla. Of the 11 methods tested, four map 0 shuffled reads (EBI, Genometa, MetaPhlAn, QIIME), and three tools map an average of 2-19 shuffled reads (Kraken, MG-RAST, Taxator-tk). MetaPhyler maps more than 600 reads on average, whereas LMAT maps a large number of shuffled reads to the database (on average 1,486,699 reads). For MEGAN and mOTU this information was not readily available. CLARK maps more than the expected maximum 80% (appr. 84%) and since this tool did not include Eukaryotes in its database, the number of shuffled reads that are mapped is large (around 2.5 million reads on average).

Another important measure is the occurrence of false positives, i.e. how often a tool predicts the presence of phyla that were not included in the data sets. In general, the tools are consistently specific in that they do not mistakenly predict phyla that aren't there. Of the reads being mapped, most tools assign less than 1% to phyla other than those included in the simulation. However, there are two outliers with Taxator-tk assigning around 14% of mapped reads to phyla not represented in the simulated data sets, and the EBI server assigning almost 42% of the mapped reads to "Other" bacteria and archaea although not to any specific phyla.

Taxonomic analysis

For each tool, the predicted relative abundance of each phylum was compared to the known abundance (see Online Methods for details on composition of data sets). The predicted abundance differed significantly from the known abundance ($p<0.05$) in almost every case (see Supplementary Figure 1 and Supplementary Table 1 for details). Only four tools include Eukaryotes (GOTTCHA, MG-RAST, MetaPhlAn, OneCodex) and all significantly underrepresent the Eukaryote component. However, in many cases the Eukaryote databases only include a small subset such as selected fungi. Overall, there was a large variation in the predicted relative abundance of phyla. Interestingly, it is not only the rare phyla that show large variations in the predicted abundances, also two of the most abundant phyla - Acidobacteria and Proteobacteria - showed large variation between tools.

Log odds scores were used to investigate the differences between the known and predicted relative abundance of phyla (Supplementary Figure 2). Scores close to 0 indicate predictions close to the real proportions, a negative score means the program predicted too few, and a positive score means the program predicted too many. On average the dominant phyla (Proteobacteria, Actinobacteria, Acidobacteria) lie closer to 0 as it is less likely to predict a fold change in abundance for these groups. Conversely, the rare phyla show the largest fluctuations. The simulated Spirochaetes are underrepresented by all tools, most likely because the highly divergent genomes are hard to confidently map to genome sequences.

Although all tools generate relative abundances that differ from the actual abundances, the degree to which they diverge is highly variable. In Fig. 1, the sum of absolute log odds scores is shown for each tool, giving an overall indication of how much the results from each tool tend to diverge from the correct proportions (a small sum is preferable). Since Eukaryotes were only predicted by a small subset of tools, and since the databases used by these only included very specific species, the Eukaryote component was ignored (see Supplementary Figure 3 for the plot including Eukaryotes). Also shown is $\log_2$ of the run time in minutes, and there is no correlation between run times and sum of log odds scores (Pearson correlation; $r = 0.24$, $P = 0.41$). However, the sum should not be considered alone as it can be strongly affected by a single prediction being wrong (e.g. Taxator-tk on Gemmatimonadetes). Likewise, the rarer phyla (e.g. Elusimicrobia with only 0.44% of the reads) can have a disproportionate impact on the sum because a small absolute error can have a large relative impact on the log odds. In addition, Pearson correlations between predicted and known

proportions was calculated for each tool (Table 1). For each tool, only phyla predicted by that tool were included in the calculation. Although all the predictions correlate with the real abundances (all $P<0.01$), the coefficients vary from $r = 0.74$ (EBI) to $r = 0.99$ (Kraken). Again, there is no correlation between run times and average Pearson correlations (Pearson correlation; $r = -0.05$, $P = 0.86$) but as expected there is a negative correlation between sum of log odds and average correlations (Pearson correlation; $r = -0.75$, $P = 0.0021$), indicating that a prediction that correlates well with the known composition also has a low sum of log odds scores.

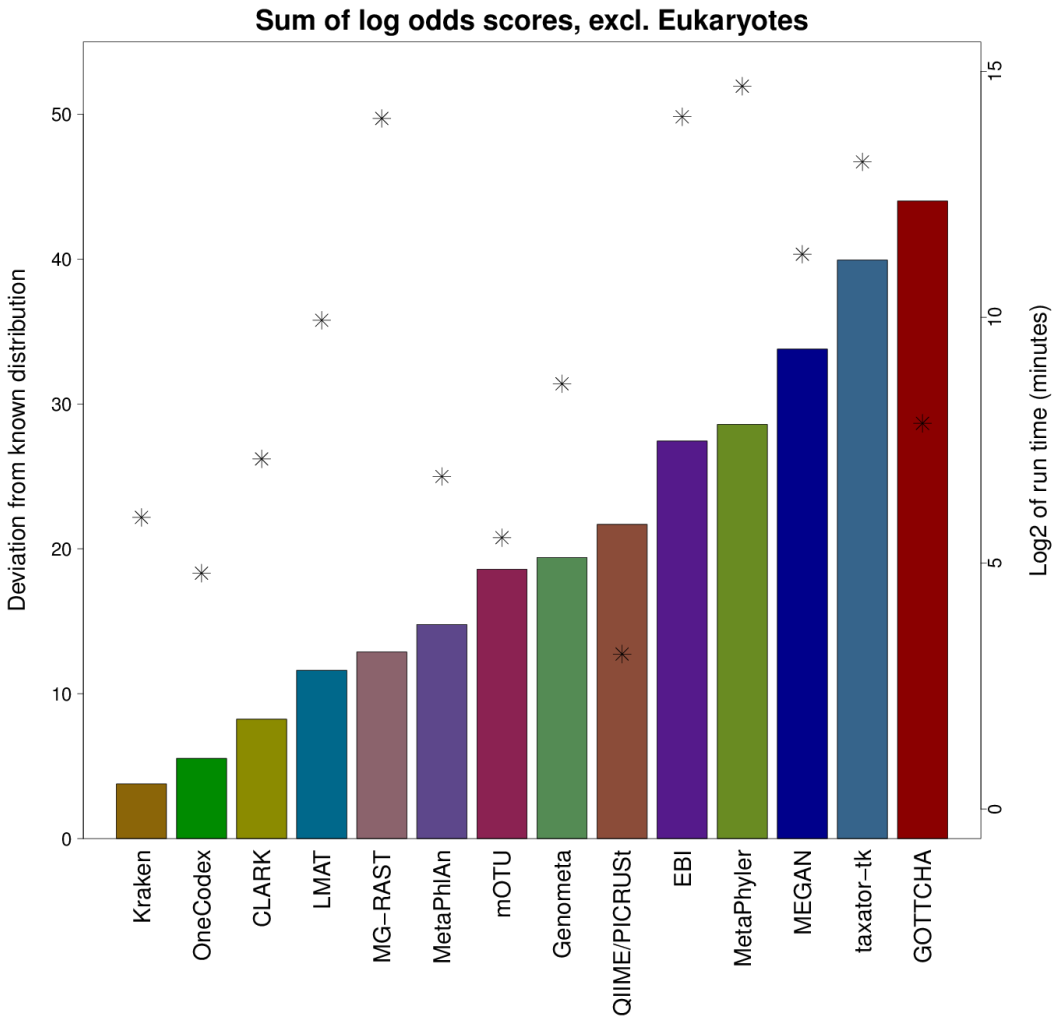

Figure 1: *Sum of absolute log odds scores for each tool (bars) and $\log_2$ of run time in minutes (asterisks, *). Sum of log odds scores indicate the overall performance in terms of deviation from the known proportions. A low sum indicates a high accuracy.*

To visualize the degree of overall similarity between the predicted and the real communities, a non-metric multidimensional scaling (NMDS) ordination of the relative abundances was generated (Fig. 2). There are three replicates of each set with identical proportions. Thus, each tool has three predictions per set, and ideally the corresponding symbols should be on

top of each other. Since most tools do not predict Eukaryote abundances, these were excluded in Fig. 2. However, including them does not change the conclusion (see Supplementary Figure 3).

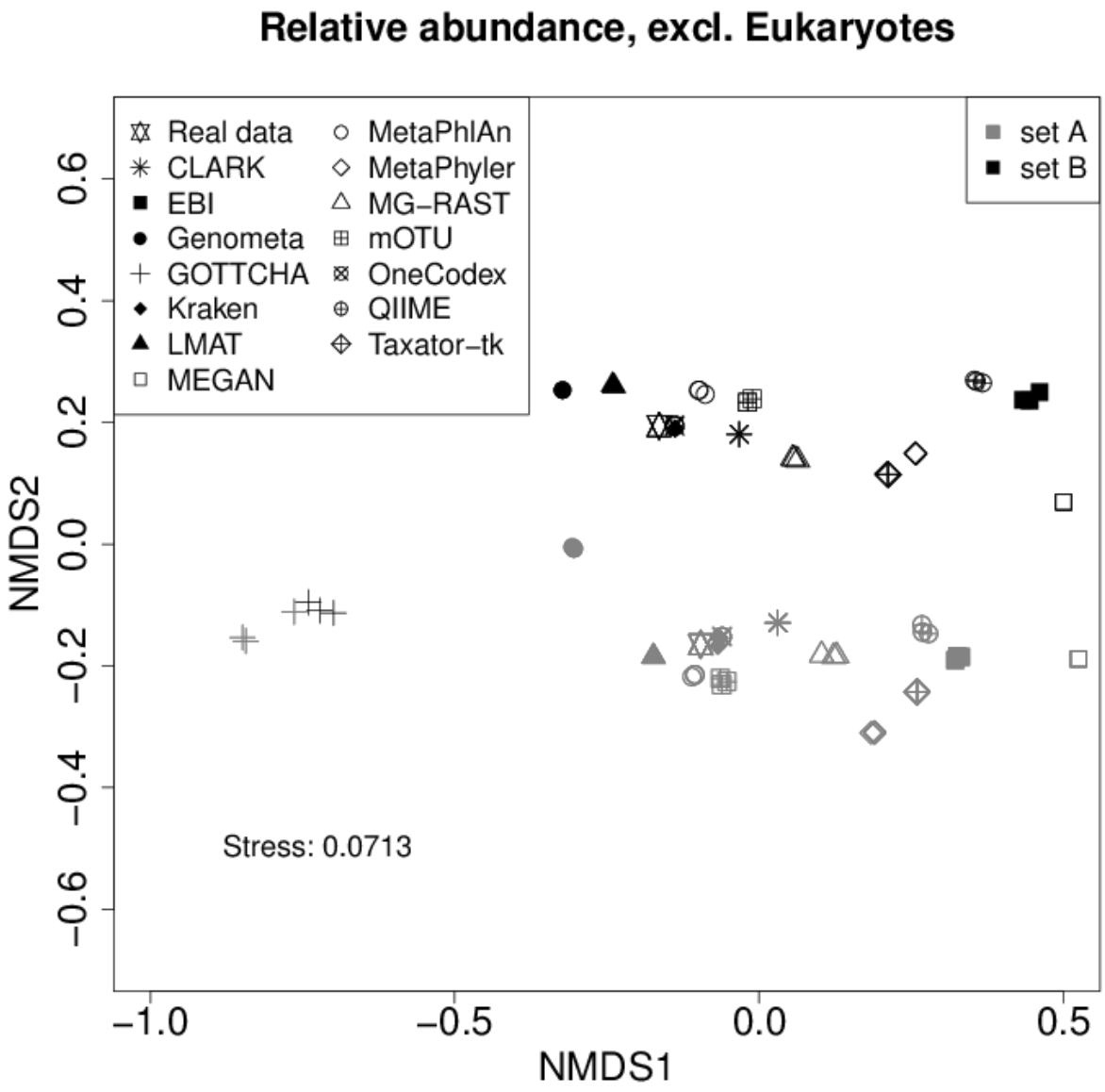

Figure 2: *NMDS plot of relative abundances at the phylum level for the known and predicted communities in replicates. Eukaryotes are not included. Metagenomes in set A are gray, and metagenomes in set B are black. The known communities are shown with a star.*

In Fig. 2, there is a clear separation between sets A and B. Furthermore, most tools predict almost identical relative abundances for the three replicates in each set, placing the three individual points almost on top of each other (the largest variation is seen for CLARK, EBI,

MG-RAST and QIIME). However, the similarity between predicted and known relative abundances (as measured by the distance between a set of predictions and the known proportions) varies between tools. The results from Kraken and OneCodex are the closest to the actual points in both sets of metagenomes followed by CLARK, Genometa, LMAT, MetaPhlAn and mOTU. The results from EBI, GOTTCHA and MEGAN are the most divergent, and the remaining tools produce results in between the two extremes.

Functional analysis

Inferring function from metagenomes is much more challenging than inferring taxonomy. However, the extra information not only makes better use of the shotgun data but also adds a new and more ecologically relevant layer of information to the study. The tools LMAT, MG-RAST, MEGAN, QIIME/PICRUSt and the EBI metagenomics server all analyze the functional capacity of the metagenomes by looking at the protein coding genes (with the exception of PICRUSt that infers protein-coding gene content from taxonomic profiles generated by QIIME).

The test datasets have been created with changes to the relative abundance of cyanobacteria (photosynthesis; more abundant in set A), *Bradyrhizobium* and *Rhizobium* (nitrogen fixation; more abundant in set A), and known pathogens (more abundant in set B). Using the known shifts in taxa as a proxy for the expected functional shifts makes it possible to compare the predicted differences to what the expected change should be. Although the magnitude might differ due to e.g. the number of genes involved in the trait, the genome size and the number of species sampled, the direction should be the same.

MEGAN, MG-RAST and LMAT all use the SEED hierarchy for functional annotation, and we used the same subset of SEED subsystems for these analyses although some subsystems were not predicted by all tools. PICRUSt uses KEGG, and the EBI webserver uses Gene Ontology (see Supplementary Material for the exact categories used, and Supplementary Table 3 for the predicted proportions). If more than one category was used for a function the average log fold change is reported. The shifts in functional categories are shown in Figure 3.

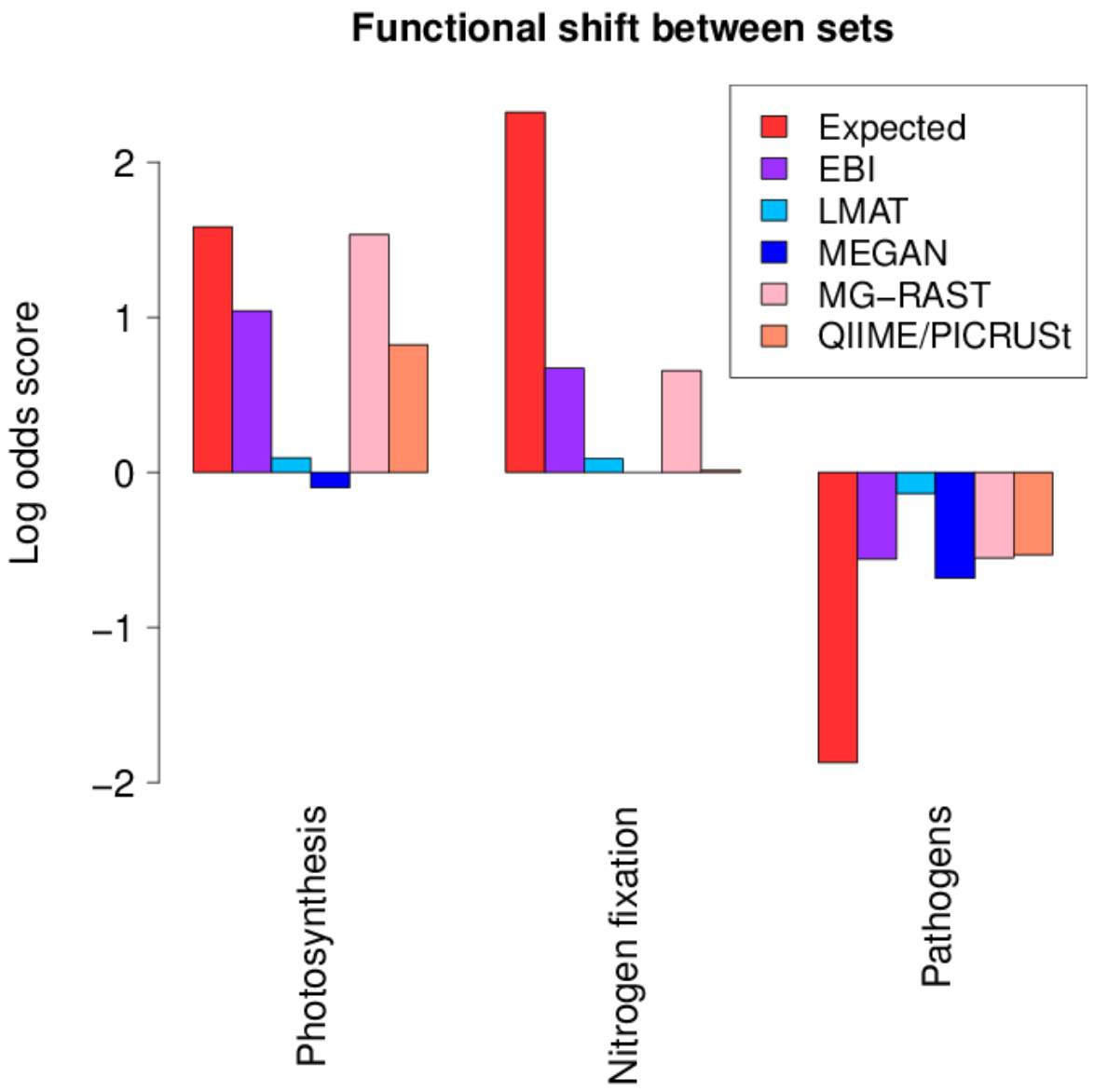

Figure 3: *Shifts in relative abundance for the three functional categories that vary between set A and set B for the tools that analyze the functional capacity of metagenomes. A positive log odds score means an increase in set A relative to set B, and a negative log odds score means a decrease in set A relative to set B.*

Only MG-RAST and the EBI webserver capture the overall pattern of functional changes in all three categories. The direction is correct in all cases but the magnitude of the shifts differ. The closest match is in the photosynthesis category with MG-RAST almost mirroring the expected shift. For both nitrogen fixation and pathogens the shift is much less than what would be expected based on read counts alone. For the pathogens, one explanation is that a number of

categories are used, some of which are not exclusive to pathogens. Thus, we would not expect a clean “pathogens” signal.

Although the input to QIIME/PICRUSt is not ideal for these programs, they predict a shift in the expected direction in both the photosynthesis and pathogens categories. There was no nitrogen fixation category predicted so the ‘Nitrogen Metabolism’ was used showing no difference between the two sets. The strategy employed by PICRUSt differs fundamentally from the other tools used so the performance is worth noting.

MEGAN shows a shift close to 0 in photosynthesis and assigns no reads to the nitrogen fixation subsystem. Only in the pathogens category does the prediction match the expected change, showing the largest fold change of the tested tools. LMAT predicts minor shifts in all three categories, all in the right direction but too close to 0 to be useful for most downstream analyses.

Given that the “pathogens” category contains a number of functional categories for which we would expect a mix of pathogens and non-pathogens, it is interesting to see that most tools predict the expected shift between the sets. Moreover, the tools seem to agree on the magnitude of the shift as well. This is relevant for analysis of complex traits by using a combination of categories incorporating different functional aspects that have been linked to a given trait but are not exclusive to this trait. The photosynthesis category shows the best match between both direction and magnitude of the shift for three of the tools. For nitrogen fixation, only two tools (the EBI webserver and MG-RAST) predicted the expected shift.

Discussion

This paper presents the first large independent benchmark of metagenome analysis tools using complex, realistic simulated data sets with replicates. The results show that the run time of individual tools vary by many orders of magnitude, and that the fraction of reads analyzed varies dramatically (from <1% to >70%). Although no tool predicts the actual relative abundances of bacterial phyla correctly (all tools differed significantly from the actual distributions), some predictions are much more similar to the correct answer than others. Interestingly, there is no correlation between the number of reads used, quality of the result and run time. Indeed, the best tool in terms of both similarity to the correct answer and the fraction of reads used is also one of the fastest tools tested, namely Kraken, followed by One Codex and CLARK.

However, Kraken only analyzes the taxonomic distribution and does not look at the potential functional differences in terms of gene content. For the tools that were able to perform this type of analysis (LMAT, MEGAN, MG-RAST, QIIME/PICRUSt, EBI), the predictions differed starkly between the tools. The EBI and MG-RAST webservers both predicted the expected direction of change in all three functional categories. Interestingly, using QIIME and PICRUSt predicted two of the functional changes, although the data used is not what these methods were developed for. The remaining methods predicted one (MEGAN) or none (LMAT) of the functional shifts.

The field of metagenomics is changing rapidly, and there is still room for improvement in the development of analysis tools. For taxonomic assignment, there are now tools that we show to perform well on controlled but complex and realistic data sets. One area of further research could be to focus on broadening the taxonomic range to include at least some Eukaryotes and Viruses of interest. When it comes to functional analysis, there seems to still be room for improvement on existing tools. Most of the tools available that are able to look at the functional capacity of metagenomes are among the slowest tools tested, so it might be fruitful to look at other approaches - potentially inspired by the fastest tools for taxonomic assignment. More importantly, only two of the five tested methods predicted all the functional changes, whereas the others did not. It might be worth looking into the underlying assumptions behind the functional assignments of reads. Here, it seems that the approaches taken by the EBI webserver and MG-RAST perform the best, but it is also worth noting the performance of PICRUSt although it only considers the taxonomic predictions from QIIME. This approach seems to be a relevant area for further research.

Methods

To make the benchmark unbiased and realistic, the data sets used for testing had to mimic the complexities - both in terms of number of taxa present, observed shifts in the abundance of taxa, sequencing errors, unknown reads etc. - that real shotgun metagenomes produce. A suite of analysis tools were then used to analyze the same data sets using the recommended settings for each tool, and the output from each tool was parsed in order to assess performance. In the following, details on the design of data sets, selection of tools, and analyses are presented.

Creating test data sets

Designing the data sets was the most crucial part of the analysis. To ensure that the assessment was realistic and fair, we created data sets that closely mimic the complexities, size and characteristics of real data. Furthermore, to test whether the tools could distinguish between metagenomes from different communities we generated two sets - set A and set B - with different composition. For both set A and set B, we generated three replicates. All replicates from a set have the same relative abundance of each phyla, but the actual genomes sampled as well as the positions within the genomes were randomized. Therefore, the benchmark was performed on 2 sets of data (set A and set B) with different characteristics (see below), each set contains 3 groups of simulated reads for a total of 6 simulated metagenomes.

For a number of reasons, the focus of the benchmark is on the phylum level predictions. From a practical perspective, comparing the phylum level predictions between tools is much easier and less prone to differences in e.g. naming conventions. It is also worth noting that a tool that performs poorly at the phylum level will also perform poorly at the lower taxonomic levels. The relative ranking of tools at the phylum level will therefore mirror the relative ranking at lower levels. In a real life metagenome study, many sequences will not match specific species due to biases in the databases and undersampling of large regions of the phylogeny. Thus, by necessity the focus will often be at the phylum level. Even more important, it has been shown that higher taxonomic levels of bacteria show ecological coherence making phyla a very relevant unit for understanding ecological patterns[31,32]. Thus, in many real life scenarios the analysis would focus on the phylum level composition making this benchmark the most appropriate.

To capture the intricacies of next-generation sequencing, the data sets were based on real sequencing results obtained from pooling 6 soil DNA samples on a single HiSeq 2000 lane and generating 2x100 PE shotgun reads (unpublished, manuscript in preparation). The real sequence reads were discarded for this benchmark, but an error profile was calculated for each of the 6 libraries using ART[33] based on the reported quality scores. Using ART and the error profiles, read pairs were simulated (read length 100, mean insert size 500, standard

deviation 25) from both real, simulated and shuffled genomes (see below). The resulting 6 metagenomes contain between 27 and 37 million read pairs.

To make comparison between tools possible, the relative abundance of individual phyla was controlled by sampling read pairs from sequenced genomes in well defined proportions (see Supplementary Table 1 for the exact proportions and number of reads, and Supplementary Table 2 for the list of genomes used in the different categories). Some phyla were included in equal proportions in all data sets, while others varied either subtly or more substantially between sets A and B. Note that Eukaryotes are treated as a single “phylum” although the chromosomes used come from various phyla (including e.g. Arabidopsis, chicken and human).

In many published metagenome studies, a large number of the reads can not be given a taxonomic assignment, the most likely reason being that a lot of sequences are from unknown organisms that are not present in the reference databases being used. To mimic this pool of unknown reads, all the simulated metagenomes contain 20% shuffled reads obtained by shuffling a set of 110 genomes using the shuffle program from the HMMER package[34] (using parameters “-d -w 500” to use a local window and preserve dinucleotide distribution) and sampling reads from these shuffled “genomes”. These reads served as a negative control as the genomes of origin were not included in the simulated communities.

Since taxonomic assignment is based on sequenced genomes, there will be an inherent bias towards classification of reads from groups that have been sampled frequently (e.g. human pathogens) whereas genomes from more understudied branches of the tree of life (e.g. Archaea) will often not be assigned. Furthermore, reads from an unsequenced relative of a known species might be easy or hard to assign depending on the evolutionary distance between the two. To test how the different tools perform on sequences that diverge from the available genomes but are not shuffled as in the above test, we used Rose version 1.3 [35] to simulate evolution and generate simulated relatives of the Spirochaete, *Leptospira interrogans* (EMBL ID AE016823). In total, a set of 32 genomes was generated containing 8 genomes with either little, medium, mixed or high divergence. No other Spirochaete genomes were included in the data sets. Since these genomes are not random but simulated using an evolutionary model, the reads should be assigned to the correct clade.

Some tools are able to not only determine community composition from a metagenome but can also infer “functional capacity” by analyzing the predicted protein coding sequences. To test the latter, the two sets were designed with functional differences as well: 1) The Proteobacteria contain different proportions of known pathogens, 2) the genera Rhizobium and Bradyrhizobium, which are capable of nitrogen fixation, vary, and 3) the relative abundance of Cyanobacteria (photosynthesizers) differ between the two sets. The different contributions of these groups to set A and set B should be reflected in both the relative abundance of phyla and functional categories.

To evaluate the performance of each tool, no single metric was used as this is a complex problem where multiple factors should be considered. Instead, we investigated a number of performance metrics comparing the predicted to the known community structure, or looking at the specific performance of a tool:

- **Run time:** For the end user, the time spent analyzing data can be a significant bottleneck. We used the '`GNU time`' (version 1.7) function to determine the cpu time spent on each data set, taking into account the use of multiple cores etc. A user can then assess if the time needed for a given tool to finish is realistic, and if the extra time required for some tools compared to others yields a proportional increase in the quality of the prediction.
- **Ease of use:** For the end user, how easy it is to use a tool can be a decisive factor. We did not specifically evaluate how user friendly a tool is, but we list some key things to consider: Can you use the zipped, paired-end Fastq files directly? Do you have to unzip the files? Do you have to convert the Fastq files to Fasta files? Does the tool utilize paired-end information? The number of steps involved varies between tools. In Section 2 of the supplementary material, we list the commands used in the analyses so the reader can judge how easy it is to run a tool.
- **Information provided:** Most tools only provide information on the community composition, while some provide functional information as well.
- **Reads mapped:** Since some tools use a limited set of marker genes for the analyses, whereas others use much broader databases, the fraction of reads mapped in itself might not be useful. However, in case two tools both use the same or similar databases, it can be of interest to know how large a fraction of the reads each tool was able to analyze.
- **Shuffled reads mapped:** As a measure of specificity, it is of interest to know how many of the shuffled reads (generated from shuffled genomes) each tool maps to a phylum since this can reflect how often real reads might be wrongly assigned as well.
- **Non-existing phyla:** As we know exactly which phyla have been included in the data sets, we can also test how often a tool predicts the presence of a phylum that is not included in the data.
- **Divergence from real distribution:** Each predicted relative abundance of a phylum was compared to the actual abundance, and the overall divergence for each tool was evaluated.
- **Correlation with known community composition:** By comparing the relative abundance of phyla generated by each tool to the known composition, Pearson correlation coefficients were calculated giving the overall concordance between prediction and the real abundances.
- **Multivariate analysis:** The overall agreement between tools, and between tools and the real distributions, were visualized with non-metric multidimensional scaling (NMDS) plots which group similar predictions together and give a broad overview of agreements and disagreements.

In combination, these different metrics will help the end user decide which tool is best suited for their particular needs.

Selection of tools

There are many tools available for analyzing metagenomes. For the present analysis, the following criteria were used to include tools:

- **Availability:** The tool should be freely available either as download or webserver.
- **Usability:** The tool should have a proper manual, readme file or help function describing how to use it. In case of problems, the respective authors were contacted.
- **Adoption:** The tool should be widely used, or show potential of being widely adopted in the future.

Any selection will by necessity leave out tools that some researchers would find useful. However, it is infeasible to test all available tools, and using the above criteria gives a clear way of narrowing down the options. Some tools were considered but excluded due to lack of support, lack of details on how to use the tool, or nonfunctioning webservers.

The following 14 tools were included in the analysis (also see Table 2):

- **CLARK**[16]: CLARK uses a *k*-mer approach where all the common *k*-mers between the targets in the database (e.g. a collection of all bacterial genomes) are removed. This gives a set of genomic regions that uniquely describes each target. A read is assigned to the target with which it shares the highest number of *k*-mers. In the most accurate mode, CLARK uses the full database of targets and assigns a confidence score to the assignment.
- **EBI metagenomics webserver** [17]: Hosted by the European Molecular Biology Laboratory-European Bioinformatics Institute (EMBL-EBI), the webserver ties in with the European Nucleotide Archive (ENA) for data storage and demands a minimum of metadata. The raw reads are cleaned, trimmed using sff-trim from BioPython [36] and trimmomatic [37], clustered to remove duplicates using UCLUST [38], and repeats are masked using RepeatMasker [39]. Paired end reads are joined using SeqPrep [40]. Potential rRNA genes are found using rRNAselector [41], and the taxonomy is predicted from these using QIIME [29] against RDP [42] and GreenGenes [43]. Protein coding genes are predicted using FragGeneScan [44], and the functional annotations are added using InterProScan [45] against a set of databases (including Gene3D [46], Pfam [47] and PROSITE [48]), and each predicted gene is associated with a set of Gene Ontology terms [49].
- **Genometa** [18]: Genometa is a GUI program building on the Integrated Genome Browser (IGB) [50] and using the Bowtie mapper [51]. Reads are mapped to a custom genome database and results can be exported from the GUI program for downstream analysis. The most recent database was used (April 2012) together with Bowtie v1.1.0 which is the only option in the program.
- **GOTTCHA**[19]: GOTTCHA aims at limiting the number of false positives in their predictions by only focusing on genomic regions that are unique to each reference.

These regions are found using a combination of empirical data on coverage and machine learning approaches. GOTTCHA first trims the reads based on qualities followed by fragmentation to obtain a uniform read length. A read is split on every low quality base (Q<20) and then divided into all non-overlapping 30-mers. Matching is done at the species level using exact matches with BWA[52].

- **Kraken** [20]: Kraken classifies reads by breaking each into overlapping k-mers. Each k-mer is mapped to the lowest common ancestor of the genomes containing that k-mer in a precomputed database. For each read, a classification tree is found by pruning the taxonomy and only retaining taxa (including ancestors) associated with k-mers in that read. Each node is weighted by the number of k-mers mapped to the node, and the path from root to leaf with the highest sum of weights is used to classify the read.
- **LMAT** [21]: LMAT works by first generating a searchable database of k-mers from a large collection of genomes. For each k-mer, the lowest common ancestor in the taxonomy tree is calculated. A smaller "marker library" (kML) of the most informative k-mers is generated by separating k-mers into disjoint sets and discarding all sets with fewer than 1000 k-mers, and all k-mers where the lowest common ancestor is above the family level. When assigning taxonomy to a read, the information for each k-mer in the read is extracted from the library, and the path from the highest scoring node to its lowest common ancestor is created. This path is pruned by each conflicting assignment until the score drops below the threshold. Function is assigned in a similar fashion using a customized library.
- **MEGAN** [23]: MEGAN is a GUI (Graphical User Interface) program aimed at analyzing a set of reads that have been mapped to a sequence database. The mapped reads are assigned a taxonomic label by finding the "lowest common ancestor" in the NCBI taxonomy based on sequence similarity. Functional analysis can be performed using different databases. Here, we use the SEED hierarchy [53]. MEGAN assigns function to a read by mapping it to the best matching gene with a known function in the hierarchy. The initial mapping is performed using the RefSeq database ver. 66 [54] using the Diamond aligner [55] from the same group as MEGAN.
- **MetaPhlAn** [26]: MetaPhlAn uses a set of around 1 million markers for taxonomic assignment and, thus is not expected to map all reads. The marker set is based on clade-specific sequences, where a clade can be as specific as a species or as broad as a phylum, and marker sequences have to be strongly conserved within a clade without being locally similar to sequences outside the clade. Taxonomic assignment is accomplished by mapping all reads against the marker set using Bowtie2 [56].
- **MetaPhyler** [27]: MetaPhyler relies on a custom database of 31 marker genes for taxonomic assignment and is therefore not expected to map all reads in a data set. The marker set are mostly universal single-copy genes and Metaphyler has a specific classifier for each [57]. MetaPhyler uses BLASTX [58] to assign reads to marker genes and uses the bit score (adjusted for alignment (HSP) length and marker gene) to assign taxonomy from genus to phylum level.
- **MG-RAST** [24]: The MG-RAST webserver allows the user to upload metagenome data sets for analysis. The server offers an easy to use pipeline that performs both

taxonomic and functional analyses using custom databases M5nr [59] for proteins and M5rna (combining SILVA [60], GreenGenes [43] and RDP [42]) for rRNA analysis. Gene calling is performed on the reads using FragGenescan [44] and predicted proteins are clustered using UCLUST [38]. BLAT [61] is used for calculating similarities for representatives from each cluster. Potential rRNA reads are found using BLAT against a reduced version of the SILVA database, reads are clustered using UCLUST, and BLAT is used against the M5rna database.

- **mOTU** [28]: mOTU uses a set of 10 universal single-copy marker genes to assign taxonomic information to reads. These marker genes were chosen from a larger set of 40 genes as the ones that performed best in an internal benchmark by the authors. A large number of genomes and metagenomes were scanned for these marker genes, and the results clustered into “metagenomic operational taxonomic units” (mOTUS). Taxonomic assignment of reads is performed by mapping them against this mOTU database.
- **One Codex**[62]: One Codex is a web platform (free for academic use) that uses a *k*-mer approach to compare uploaded FASTQ or FASTA files to their in-house index of microbial genomes. Exact *k*-mer matches are used to find the most specific taxonomic assignment for each read, using a lowest common ancestor approach. The output presents the results with a graphical overview of the sample composition, a break-down into high, medium and low abundance species, and direct access to read level classifications.
- **QIIME** [29]: It is important to note that QIIME is a software package aimed at analyzing amplicon data (e.g. SSU rRNA sequences) and is thus not designed for the analysis of shotgun data sets such as the ones used in this paper. However, since QIIME is widely adopted and highly flexible, we found it interesting to test how it might be used on this type of data. Using HMMER (ver 3.1b1) [34] and rRNA alignments from Rfam (ver 12.0) [63] potential reads from 16S rRNA genes were found. This type of data differs from what QIIME is designed for, because it consists of short, random segments that cover different parts of the rRNA gene and that therefore differ in their taxonomic informativeness. It is therefore not the optimal input. QIIME was used to pick open-reference OTUs from Greengenes 13_8 [43] using UCLUST [38] and representative sequences were picked. Taxonomy was assigned using UCLUST. A functional analysis of the metagenomes is performed using PICRUSt [64], a tool that predicts the functional profile of microbial community. The gene content of each organism in a phylogeny (here GreenGenes) is precomputed. Next, the relative abundance of 16S rRNA genes is used to infer the gene content of the metagenome samples, taking into account the copy number of 16S genes. The final functional prediction is based on the KEGG Orthology [65].
- **Taxator-tk** [25]: taxator-tk can use BLASTN [58] or LAST [66] to search with the reads against a local reference database. Overlapping local alignments between the read and a number of reference sequences are joined to form longer segments. Each segment is assigned a taxon ID, and a consensus taxonomic assignment is derived by assigning a weight to each segment based on similarities to the reference sequence.

Each tool was run using default settings and with the database recommended by the authors (i.e. a custom database in most cases). If needed, the authors of the individual tools were contacted to verify or troubleshoot the commands used. All authors of the tools used in this study have received a draft of the paper prior to publication in order to give their feedback. Command lines and settings for each tool can be found in the supplementary material.

Predicted abundances were extracted at the phylum level and analyzed as follows: All hits to Eukaryotes were grouped together as a single Eukaryote “phylum”. Due to inconsistencies in naming, hits to Tenericutes and Firmicutes were summed and treated as Firmicutes. All hits to phyla not included in the simulated data sets were grouped and treated as “other”. R [67] was used to do all statistical analyses and to generate all the plots. The result from each tool was compared to the simulated abundances (excluding Eukaryotes for tools that only mapped to bacteria and archaea) calculating Pearson correlations coefficients in R using cor.test. The divergence from simulated abundances was calculated doing simple log odds (i.e. $\log_2$(predicted/simulated)). When summing these, the absolute values were used to measure total divergence irrespective of whether a tool over- or underrepresented specific phyla. NMDS plots were generated using method metaMDS from the vegan [68] package with Bray-Curtis distances. For functional predictions, categories related to photosynthesis and nitrogen-fixation were assessed directly. For pathogens, a number of functional categories that have been shown to potentially be associated with pathogenicity were used (apart from virulence these include motility [69], sporulation [70] and quorum sensing [71]).

Author contributions

SL, KLA and PPG designed the experiment. SL created the data sets, ran the tools and analyzed the results. SL wrote the paper with input from KLA and PPG. All authors read and approved the final manuscript.

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Analysis tool	Fraction	Shuffled	False positives	Run time	Correlation
CLARK	83.60%	2,549,754	0.43%	139.02	0.9749
EBI	0.08%	**0**	41.74%	~ 12 days	0.7427
Genometa	39.91%	**0**	0.83%	401	0.9136
GOTTCHA	43.10%	?	**0.00%**	229.49	0.1777
Kraken	71.98%	19	**0.00%**	60.95	**0.9915**
LMAT	56.61%	1,486,699	0.63%	981.21	0.9395
MEGAN	42.21%	NA	0.49%	2489.65	0.7728
MetaPhlAn	5.09%	**0**	0.75%	108.51	0.9552
MetaPhyler	0.45%	649	0.05%	26586.15	0.7989
MG-RAST	56.17%	3	0.27%	16881.8	0.9209
mOTU	0.16%	NA	0.10%	45.8	0.9334
One Codex	71.65%	23	**0.00%**	27.77	0.9647
QIIME	58.23%	**0**	0.28%	**8.88**	0.7772
Taxator-tk	45.67%	2	14.07%	9147.92	0.8561

Table 1: *Performance of the selected tools. Where applicable, the best performance in each category is highlighted in bold. Fraction: Average fraction of all reads that the tool mapped. Shuffled: Average number of shuffled reads mapped. False positives: Fraction of mapped*

reads assigned to non-existing phyla. Run time: CPU time in minutes per metagenome (where applicable). Correlation: The average Pearson correlation coefficient between predicted and known relative abundances of phyla in the data sets. GOTTCHA failed on setB3 so the average of sets B1 and B2 is used instead.

Tool	Version	Taxonomy	Function	Fastq	Zipped	Paired
CLARK	1.1.2	Yes	No	Yes	Yes	Yes
EBI	NA	Yes	Yes	Yes	Yes	Yes
Genometa	0.51	Yes	No	Yes	No	Yes
GOTTCHA	1.0a	Yes	No	Yes	No	Yes
Kraken	0.10.4 beta	Yes	No	Yes	Yes	Yes
LMAT	1.2.4	Yes	Yes	No	No	Yes[1]
MEGAN[2]	5.7.0	Yes	Yes	Yes	No	(No)[3]
MetaPhlAn	2	Yes	No	Yes	Yes	Yes
MetaPhyler	1.25	Yes	No	No	No	Yes[4]
MG-RAST	3.3.6	Yes	Yes	Yes	Yes	(Yes)[5]
mOTU	NA	Yes	No	Yes	Yes	Yes
One Codex	NA	Yes	No	Yes	Yes	Yes
QIIME[6]	1.8.0	Yes	No	Yes	Yes	Yes
Taxator-tk	1.2.1	Yes	No	No	No	Yes[7]

Table 2: *The metagenome analysis tools included in this benchmark. For each tool, it is shown if it does taxonomic analysis and/or functional analysis, and whether it can analyze Fastq files directly, if you can use zipped input files, and if it utilizes paired end information.*
[1] You need to concatenate the input files with an N between paired reads.
[2] Input to MEGAN was generated using the aligner Diamond (v0.6.3) from the same group.
[3] MEGAN supports paired end data. However, Diamond does not explicitly support this.
[4] Each file is treated separately, but the final results can be combined by the tool.
[5] The server recognizes paired end data but seems to treat reads separately.
[6] QIIME is highly flexible and can handle both zipped and unzipped fastq files, and both single- and paired-end reads. However, in this analysis we adapted QIIME to work with fasta output from HMMER and could not use these features.
[7] Although no direct support, the authors provided a way to use the paired information (see Supplementary Material section 2.10 for details).