Optimization of 16S amplicon analysis using mock communities: implications for estimating community diversity

Andrew Krohn[1,2], Bo Stevens[3], Adam Robbins-Pianka[4], Matthew Belus[5], Gerard J. Allan[1,2], Catherine Gehring[1,6]

[1]Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ
[2]NAU Environmental Genetics and Genomics Laboratory, Flagstaff, AZ
[3]School of Earth Sciences and Environmental Sustainability, Northern Arizona University, Flagstaff, AZ
[4]Department of Computer Science, University of Colorado Boulder, Boulder, CO
[5]Anschutz Medical Campus, University of Colorado Denver, Aurora, CO
[6]Merriam-Powell Center for Environmental Research, Flagstaff, AZ

Corresponding Author:
Andrew Krohn[1,2]

Email address: alk224@nau.edu

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Abstract:

The diversity of complex microbial communities can be rapidly assessed by high-throughput DNA sequencing of marker gene (e.g., 16S) PCR amplicon pools, often yielding many thousands of DNA sequences per sample. However, analysis of such community amplicon sequencing data requires multiple computational steps which affect the outcome of a final data set. Here we use mock communities to describe the effects of parameter adjustments for raw sequence quality filtering, picking operational taxonomic units (OTUs), taxonomic assignment, and OTU table filtering as implemented in the popular microbial ecology analysis package, QIIME 1.9.1. We demonstrate a workflow optimization based upon this exploration, which we also apply to environmental samples. We found that quality filtering of raw data and filtering of OTU tables had large effects on observed OTU diversity. While all taxonomy assignment programs performed with similar accuracy, an appropriate choice of similarity threshold for defining OTUs depended on the method used for OTU picking. Our "default" analysis in QIIME overestimated mock community OTU diversity by at least a factor of ten. Our optimized analysis correctly characterized mock community taxonomic composition and improved the OTU diversity estimate, reducing overestimation to a factor of about two. Though observed relative abundances of mock community member taxa were approximately correct, most were still represented by multiple OTUs. Low-frequency OTUs conspecific to constituent mock community taxa were characterized by multiple substitution and indel errors and the presence of a low-quality base call resulting in sequence truncation during quality filtering. Low-quality base calls were observed at "G" positions most of the time, and were also associated with a preceding "TTT" trinucleotide motif. Environmental diversity estimates were reduced by about 40% from 2508 to 1533 OTUs when comparing output from the default and optimized workflows. We attribute this reduction in observed diversity to the removal of erroneous sequences from the data set. Our results indicate that both strict quality filtering of raw sequencing data and careful filtering of raw OTU tables are important steps for accurately estimating microbial community diversity.

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Introduction:

Over the past decade, amplicon sequencing of marker gene fragments has become the preferred method for profiling the diversity of microbial communities. Briefly, the technique uses the polymerase chain reaction (PCR) to amplify a pool of PCR products from an environmental sample to be resolved by high throughput DNA sequencing. Similar sequences are binned together into operational taxonomic units (OTUs) and compared against a database to obtain taxonomic classifications. Amplicon sequencing is flexible in that a community can be profiled for different genes which may represent markers specifically suited for identification of certain microbial constituents (e.g., 16S for bacteria and archaea, ITS for fungi). Similarly, profiling with functional genes can offer a better understanding of community traits (e.g., Bentzon-Tilia et al., 2015). While communities were originally profiled with high-throughput sequencing on 454 pyrosequencing instruments (Sogin et al., 2006), amplicon sequencing has been adapted to newer instrumentation including sequencers from Illumina (Caporaso et al., 2012) and Pacific Biosciences (Fichot & Norman, 2013). Illumina sequencing is currently the most popular option due to several factors including cost, throughput, instrument availability, and the existence of multiple protocols for amplification and sequencing of marker gene pools on this platform (Caporaso et al., 2012; Bokulich & Mills, 2013; Kozich et al., 2013; Fadrosh et al., 2014).

Accurate determination of community diversity and taxonomic content are often primary aims of community amplicon sequencing projects. Systematic errors experienced during sample preparation, such as PCR and sequencing errors, can contribute to overestimation of diversity (Kunin, 2010). Additionally, signal cross-talk during index sequence cycles on Illumina sequencers can lead to false identification of an organism in a sample (Kircher, Sawyer & Meyer, 2012; Nelson et al., 2014). In the face of such potential complications, careful analysis is necessary to ensure that diversity estimates are not inflated and that data are properly filtered to avoid Type II errors. Several comprehensive tools exist for processing such data including mothur (Schloss et al., 2009), QIIME (Caporaso et al., 2010a), and UPARSE (Edgar, 2013). Many stand-alone tools are also available for performing specific bioinformatic tasks which may or may not be implemented in QIIME, mothur or UPARSE. It may be beneficial in some cases to perform separate bioinformatic steps with different software packages in order to obtain the most

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accurate community representation for a given ecosystem. For instance, the use of various pre-processing tools (e.g., error correction, chimera filtering) may improve the outcome for a given data set. In this instance, the average researcher would require greater familiarity with the production and processing of amplicon sequencing data in order to make the best decisions during data processing.

Automated quality filtering is among the first steps performed in any sequencing project and is a necessity for managing modern DNA sequencing data sets. To achieve the status of "finished," genome sequencing projects require consensus base quality scores where the likelihood of an incorrect base call is less than 1 in 100,000 (q50), whereas assemblies using unfiltered data are considered "standard draft" and are expected to contain errors (Chain & Grafham, 2009). The default parameters in QIIME 1.9.1 require a minimum quality score of q4 as recommended by Bokulich et al. (2013), and should be similarly treated as "draft" data. More reads are retained for downstream analysis, but a low quality score requirement also introduces an unknown degree of sequencing error as base quality scores may vary widely across a single sequencing run. Thus, data generated on runs with higher average error rates are more likely to overestimate alpha diversity if quality scores are not strictly controlled (at the expense of sequencing depth). Inconsistent qualities from sequencing runs can be effectively controlled via quality filtering, and default quality filtering in QIIME retains reads that may be variably trimmed to a range of 75-100% of the original sequence length. Because the quality of different sequences may decrease non-uniformly across a sequencing run, variable read lengths may also contribute to an inflated estimate of OTU richness if reads are not de-replicated or sorted by size prior to clustering. Various error correction algorithms are available for processing Illumina data (e.g., Kelley, Schatz & Salzberg, 2010; Medvedev et al., 2011; Nikolenko, Korobeynikov & Alekseyev, 2013), the use of which may result in an increased number of reads retained following quality filtering. Callahan et al. (2016) recently demonstrated a data processing workflow that utilized error correction with good success, where the number of expected taxa approximately equaled the number of observed OTUs, though we do not explore the use of error correction techniques here. Chimera filtering, commonly performed following quality filtering, is essential to remove PCR artifacts and further improves sequencing data quality.

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Quality-filtered amplicon sequencing data are clustered into OTU definitions, a computational process for which numerous programs are available. CD-HIT (Fu et al., 2012), UCLUST (Edgar, 2010), BLAST (Altschul, 1990), and Swarm (Mahé et al., 2014) are popular options that are all available in QIIME. Reference-based analysis techniques, such as BLAST, are known to incur biases according to the choice of reference database (Nelson et al., 2014), but can easily be parallelized for more efficient computation. UCLUST can utilize a reference database, perform database-independent *de novo* clustering, or, as with the open-reference strategy currently implemented in QIIME, a combination of both methods (Navas-Molina et al., 2013). Pure *de novo* analysis is preferred by many as the approach least likely to impose a bias on the final outcome. One popular option for *de novo* OTU clustering is CD-HIT, but as this program cannot be parallelized it can be time-prohibitive when used with larger data sets. Swarm, another *de novo* OTU clustering program, allows for portions of the *de novo* clustering process to be parallelized, thus eliminating database-specific effects while also optimizing computational requirements. All OTU picking programs require the researcher to choose a similarity or distance threshold beyond which two sequences must be considered as separate OTUs. If present at this stage, PCR or sequencing errors may contribute to OTU inflation to an unknown degree. In addition to ensuring the data are properly filtered, one can also utilize a conservative clustering threshold in order to avoid overestimation of community diversity (i.e., ≤97%; Kunin et al., 2010).

Taxonomic assignment, achieved through comparison of OTU definition sequences to a reference database, can also be performed in a variety of ways. Popular methods include BLAST, UCLUST, and RDP (Wang et al., 2007), and each are available in QIIME. In 2008, Liu et al. reported that RDP provided the most accurate taxonomic assignments. Presently, other techniques continue to be utilized by various amplicon sequencing analysis pipelines (e.g., Giongo et al., 2010; Gweon et al., 2015), revealing a lack of consensus among researchers. Considering that improved taxonomic accuracies may be observed when sequences obtained for study organisms are more similar to those populating the reference database, the relative success of each algorithm may be context-dependent. For environmental data sets, accuracies of taxonomic assignments are estimated by means of a confidence or quality value relevant to the utilized technique (e.g., e-value for BLAST). Careful assessment of taxonomic accuracies can

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only be done when the sequence content of a given sample can be anticipated. This can be achieved with synthetic mock communities created *in silico* by extracting sequences from a database (e.g., Bellemain et al., 2010) or using genomic mock communities that combine DNA extracts from cultured organisms. Neither scenario is likely to provide an outcome that is directly comparable to the natural complexities of environmental communities, yet both can offer a measure of accuracy for taxonomic assignment methods.

Once quality filtered sequences have been clustered and taxonomically classified, they are compiled into an OTU table with count data for each observation. As OTUs defined from erroneous sequences may persist to this point in an analysis, the resulting OTU table must be filtered prior to conducting diversity analyses, and the filtering approach can have a profound effect on the final result (Bokulich et al., 2013). Although Bokulich et al. (2013) suggested the inclusion of mock communities on sequencing runs to assess the overall run quality and improve diversity assessments, they also provide a general recommendation to quality filter the final table by removing OTUs that represent less than 0.005% of the total read abundance. This has proven to be a useful guideline for numerous studies in which mock communities were not included. However, this practice ignores the independence of each sample and will treat samples differently according to sequencing depth such that low read count samples will be more severely filtered than samples with higher read counts.

Considering samples independently, Kircher, Sawyer & Meyer (2012) observed an indexing inaccuracy rate of 0.3%, citing cluster mixing during sequencing as a mechanism by which single-indexed Illumina sequences are likely attributed incorrectly to a particular sample. For certain applications, their result argues that such data must be filtered at 0.3% by sample in order to avoid Type II errors. Another common practice is to remove singleton OTUs (by sample or by table) under the assumption that such OTUs represent errors generated during sequencing (see Dickie, 2010). However, errors introduced during early PCR cycles may be faithfully replicated many times so as to appear as valid OTUs, causing overestimation of OTU richness even after singleton filtering (Nguyen et al., 2015). As an alternative, Nguyen et al. (2015) suggest the removal of low-count or low-proportion OTUs by sample at a threshold informed by mock community data. Mock communities used in this way may also identify certain sequence motifs prone to error, which may help to identify whether novel OTUs observed in

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environmental data should be considered suspect. Unfortunately, such controls are not available for many data sets and artificial communities may not perform similarly to environmental communities during sample preparation and analysis. Because samples are amplified independently, PCR errors are likely to be present in the form of private OTUs observed only in a single sample, so removal of unshared OTUs may be another effective precaution against overestimation of diversity due to sequencing error.

As these examples illustrate, accurate filtering of an OTU table is not straightforward. The sequence misattribution rate reported by Kircher, Sawyer & Meyer (2012) is vastly different than the filtering threshold of 0.005% recommended by Bokulich et al. (2013), though their recommendation was to filter across the entire OTU table. Since many amplicon sequencing studies report relatively few taxa present above 0.3% per sample, filtering by sample at this threshold (Kircher threshold) will exclude many valid taxa. The presence of misattributed sequences may also diminish the efficacy of private OTU removal to eliminate PCR errors, though dual-indexing of samples should reduce or eliminate sequence misattribution events (Kircher, Sawyer & Meyer, 2012). Singleton filtering, however applied, is unlikely to be thorough enough to remove errors that are either replicated during the PCR process or systematic errors from the sequencing process. For single- or dual-indexed Illumina data, filtering at 0.005% across the entire table (Bokulich threshold) may represent a viable compromise between confident assignment of sequences to samples and the stringency that one imposes on filtering the final table.

In this study, we used simple genomic mock communities and an environmental data set to describe the effects of parameter adjustments for methods implemented in QIIME 1.9.1 (Caporaso et al., 2010a) on sequence quality filtering, OTU picking, taxonomic assignment, and OTU table filtering. We focused on QIIME because of its popularity and flexibility for processing amplicon sequencing data sets. We hypothesized that observed OTU diversity will be inflated due to the presence of PCR and/or sequencing artifacts, and that such effects will be observable in simple genomic mock communities under the expectation that one OTU should be observed per constituent taxon. Using five mock communities consisting of 4-8 taxa each, we developed a modified protocol for the analysis of 16S community amplicon sequencing data, and demonstrate the method on an environmental data set. By carefully controlling each of the steps

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that we investigated, we were able to describe mock community compositions more correctly than with a default workflow.

Materials and Methods:

Mock communities

DNA was extracted from axenic cultures of *Pseudomonas aeruginosa* (Proteobacteria), *Proteus vulgaris* (Proteobacteria), *Klebsiella pneumoniae* (Proteobacteria), *Escherichia coli* (Proteobacteria), *Bacillus megaterium* (Firmicutes), *Lactococcus lactis* (Firmicutes), *Staphylococcus aureus* (Firmicutes), and *Micrococcus luteus* (Actinobacteria) using a PowerSoil DNA Extraction Kit (MoBio Laboratories, Carlsbad, CA). DNA was quantified by PicoGreen (Life Technologies, Carlsbad, CA) fluorescence, and normalized to approximately 0.75 ng/µL. Five mock communities containing different ratios of bacterial taxa were constructed from the extracted DNA. Community 0 contained equal volumes of DNA from each taxon; Community 1a contained 8% *M. luteus*, 42% *B. megaterium*, 42% *L. lactis*, and 8% *S. aureus*; Community 1b contained 42% *M. luteus*, 8% *B. megaterium*, 8% *L. lactis*, and 42% *S. aureus*; Community 2a contained 8% *E. coli*, 8% *K. pneumoniae*, 42% *P. vulgaris*, and 42% *P. aeruginosa*; Community 2b contained 42% *E. coli*, 42% *K. pneumoniae*, 8% *P. vulgaris*, and 8% *P. aeruginosa*. Final concentrations for each mock community were determined to be ~ 0.75 ng/µL (Table S1). Expected compositions of mock communities were corrected for genome size and copy number against the CBS Genome Atlas Database (Hallin & Ussery, 2004).

Environmental samples

Environmental samples with an expected environmental contrast were collected from the Northern Arizona University Pinyon Pine Common Garden near Sunset Crater National Monument, AZ. During garden installation in October 2009, soil samples were collected from holes dug to plant seedlings ("pre-tree" treatment). Soil core samples were taken from the same seedlings in December 2010 ("post-tree" treatment). The top 2 centimeters (cm) of soil were brushed aside prior to taking cores. A 2.5 cm diameter metal corer was placed 2 cm from the seedling base and driven to a depth of 10 cm. Samples were kept on ice in the field and stored at -20 ^{o}C until DNA extraction. DNA was extracted from homogenized soil cores using a

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PowerSoil DNA Extraction Kit. Only samples which produced a clean ribosomal PCR product were included in this study, resulting in unequal sample sizes between pre-tree (n = 13) and post-tree (n = 28) groups. A random number generator was used to select a subset of post-tree samples (n = 13) for comparisons of data with equal sample sizes. Samples were normalized to c. 1 ng/µL prior to PCR amplification for library construction.

The environmental samples presented here are meant only to allow a demonstration of the effects of a mock community-based workflow optimization on real environmental data. Though we expect the presence of a seedling to create additional niche space which would increase observed diversity, no background soil control samples were collected in order to properly test this hypothesis. Nonetheless, the two sets of soil samples can be expected to vary because of the presence or absence of a seedling and also due to differences in the time of sampling, both year and season.

Library construction and sequencing

Amplicons were produced in a two-step protocol as suggested by Berry et al. (2011). Briefly, samples were amplified in triplicate PCR reactions for the 16S V4 region using the universal bacterial/archaeal primers 515F and 806R (Bates et al., 2011). First round reactions were performed in triplicate in 384 well plates. The 8 µL volumes contained the following: 1 µM each primer (Eurofins MWG Operon, LLC), 200 µM each dNTP (Phenix Research, Candler, NC), 0.01 U/µL Phusion Hot Start II DNA Polymerase (Life Technologies), 1X HF Phusion Buffer (Life Technologies), 3 mM $MgCl_2$, 6% glycerol, and 1 µL normalized template DNA. Cycling conditions were: 2 minutes at 95°C followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 55°C, 4 minutes at 60°C. Triplicate reactions for each sample were pooled by combining 4 µL from each, and 2 µL was used to check for results on a 1% agarose gel. The remainder was diluted 10-fold and used as template in a second PCR reaction in which 12 base Golay indexed sequencing tails (Caporaso et al., 2012) were added. Second round reaction conditions were identical to the first round except only one reaction was conducted per sample and only 15 total cycles were performed. Indexed PCR products were purified using a 1:1 ratio of 18% polyethylene glycol and carboxylated magnetic beads as described in Rohland & Reich (2012), quantified by PicoGreen fluorescence, and an equal mass of each sample was combined into a final sample pool. The pool was purified and concentrated, and subsequently quantified by

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quantitative PCR against Illumina DNA Standards (Kapa Biosystems, Wilmington, MA). Sequencing was carried out on a MiSeq Desktop Sequencer (Illumina Inc, San Diego, CA) running in paired end 2x150 mode.

Sanger sequencing of mock community members

The 16S gene for each mock community member was sequenced by the Sanger method to a minimum depth of 2 in order to provide an accurate sequence for assessing taxonomic assignment methods. Briefly, PCR products were produced using primers 27F (Lane, 1991) and 806R or 515F and 1492R (Turner et al., 1999). Products were bead-purified with 18% PEG and used as template in sequencing reactions containing 0.25 µL BigDye Terminator v3.1 (Life Technologies), 1X BigDye Terminator Sequencing Buffer (Life Technologies), 3 µM primer and 1.5 mM additional $MgCl_2$. Cycling conditions were: 2 minutes at 95°C followed by 60 cycles of 5 seconds at 95°C, 5 seconds at 50°C, 2 minutes at 60°C. Sequencing products were bead-purified with a 3:1 ratio of 25% PEG, resuspended in water, and sequenced on either a 3730xl or a 3130 Genetic Analyzer (Life Technologies). Chromatograms were processed in Staden Package v1.7 (Staden, Beal & Bonfield, 2000) and the resulting sequences used to augment the Greengenes database so that an exact match for each expected OTU would be present during taxonomy assignment. Taxonomic identity for each sequence was confirmed by comparing against the non-redundant database at NCBI using the online BLAST tool (Altschul et al., 1990). Sequences were deposited to GenBank with accession numbers KY007579-KY007586.

Data processing and statistical analysis

All bioinformatics were carried out on a Mac Pro (Apple, Inc.) running Ubuntu Linux 14.04 LTS (Canonical Ltd.) or the Monsoon high-performance computing cluster at Northern Arizona University (https://nau.edu/hpc/) running CentOS 6.6 (The CentOS Project). Figures were generated in Veusz v1.24 (http://home.gna.org/veusz/) or Geneious v8.1 (Biomatters Ltd.). As contaminating PhiX Control sequence can complicate sequencing projects (Mukherjee et al., 2015), we calculated the amount of PhiX Control among our demultiplexed data and removed it prior to sample processing. This task was performed with the `akutils phix_filtering` command in akutils v1.2 (Krohn, 2016; https://github.com/alk224/akutils-v1.2) which maps raw

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data against the Enterobacteria phage phiX174 sensu lato complete genome sequence (NC_001422.1) using Smalt 0.7.6 (http://www.sanger.ac.uk/resources/software/smalt/).

Overlapping paired end reads were aligned using the `akutils join_paired_reads` command in akutils which employs the `fastq-join` command from ea-utils (Aronesty, 2011). Demultiplexing and quality filtering of raw, joined data (mean length = 253 bp) was carried out in QIIME with the `split_libraries_fastq.py` script using default parameters, or with more strict requirements of a minimum quality threshold of q20 (q = 19), allowing 0-3 low-quality base calls (r = 1-3), and requiring at least 95% of each read to be high quality (p = 0.95). Chimeras were removed by the UCHIME method (Edgar et al., 2011) as implemented in vsearch 1.1.1 (Rognes et al., 2016) using either the `–uchime_denovo` or `–uchime_ref` option against the Gold reference database (http://drive5.com/uchime/gold.fa). OTU picking and taxonomy assignments were performed using the `akutils pick_otus` command in akutils which calls standard functions in QIIME. After manual inspection of sequence divergence among congeneric mock community members, sequences were dereplicated on the first 100 bases using the prefix_suffix OTU picker in QIIME. OTU picking was performed with multiple similarity or distance thresholds using common OTU picking algorithms (CD-HIT, UCLUST and BLAST at 97%, 95%, 92%, 90%, 85%, and Swarm at $d1$, $d2$, $d3$, $d4$, $d5$). BLAST was used only for closed reference analysis, UCLUST for open reference analysis, and CD-HIT and Swarm for *de novo* analyses. Taxonomy was assigned using BLAST, RDP, and UCLUST options with default settings available in QIIME 1.9.1 (UCLUST option in QIIME actually uses the USEARCH algorithm for database matching steps). Reference-based OTU picking steps and taxonomic assignments were conducted against the Greengenes 97% database (McDonald et al., 2012) which had been formatted to include only the V4 region using the `akutils format_database` command in akutils. Sequence alignments and phylogenetic trees were produced using the `akutils align_and_tree` command in akutils which aligns sequences using PyNAST (Caporaso et al., 2010b) and generates phylogenies with FastTree (Price, Dehal & Arkin, 2009). Diversity analyses were conducted using the `akutils core_diversity` command in akutils.

In order to facilitate assessment of optimal workflow steps, we first sought to establish a method of filtering the final OTU tables by eliminating OTUs resulting from mixed clusters. To

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this end, we processed the mock and environmental data sets through a default QIIME workflow (see below) to assess taxonomic components, and compared methods for filtering OTU tables to remove contaminating taxa from the mock data. An ideal filtering method should remove erroneous OTUs that arise either from sequencing error or cluster mixing. Table filtering was carried out using either the Kircher threshold (0.3% by sample; Kircher, Sawyer & Meyer, 2012), the Bokulich threshold (0.005% by table; Bokulich et al., 2013), singletons removed by table (mc2), or singletons removed by sample (n2). Private OTUs were assumed to be errors and were also removed in the n2 tables. Filtered OTU tables were grouped according to filtering method, and differences in the amount of OTUs classified as contaminating taxa was assessed by one-way ANOVA. Tukey's HSD test was used to determine which groups were statistically distinct.

An optimal workflow was chosen by assessing diversity estimates and taxonomic identities assigned to mock community data. The optimal OTU picking algorithm was determined as the method that yielded the correct diversity result over the broadest range of similarity or distance thresholds. Taxonomic accuracy was determined by seeding the Greengenes database with the expected sequences from the mock community constituent taxa prior to analysis, and inspecting the results. OTU tables from the optimal workflow across the accurate range of similarity thresholds were filtered at each of the four thresholds described above. Our "default QIIME workflow" was identical to the optimal workflow with the following changes: the `split_libraries_fastq.py` command was performed with default settings; OTU picking was performed with the `pick_open_reference_otus.py` command; taxonomic assignment was performed with UCLUST; OTU tables were filtered with the Bokulich threshold. Results from the optimal workflow were compared to the result obtained from our default workflow. Environmental data was then processed using the best workflow determined from this process and compared to the default result.

Diversity analyses for mock community data were calculated on OTU tables that had been rarefied to 10,000 reads, or 5,000 reads for environmental data. Comparison of observed mock community composition to the *a priori* expectation (Table S1) was conducted with Spearman's rank correlation using species-level assignments. Comparison of observed OTU diversity between environmental sample groupings was performed with nonparametric t-tests. A

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random subset of post-tree samples from the environmental data (n = 13) was selected to determine if unequal sample sizes were contributing to observed OTU diversity. Distance matrices were calculated from environmental data for weighted UniFrac distance (Lozupone & Knight, 2005). Tests of differences of total beta diversity were carried out on distance matrices using PERMANOVA (Anderson, 2001), and differences in multivariate dispersion were detected with PERMDISP (Anderson, Ellingsen & McArdle, 2006).

Representative sequences for the optimized mock community result were extracted from the output data. When multiple OTU definition sequences represented the same taxonomic identity, they were aligned with Mafft v7.123b (Katoh & Standley, 2013) using the L-INS-i setting. The lower abundance OTU for each multi-OTU taxon was assumed to be erroneous and base differences compared to the major OTU were characterized. Trinucleotide motifs preceding each base difference and terminal truncation position were tabulated. Because 2x150 sequencing data does not fully overlap for 515F-806R amplicons (mean length = 253 bp), terminal base and preceding trimers were considered in the context of the second read. Environmental data processed through the optimal workflow was also investigated for terminal truncation positions and preceding trinucleotide motifs. Because we have no reliable reference sequence for many environmental OTUs, we investigated only OTUs that shared a taxonomic designation with at least one other OTU, and had been truncated by more than 3 bases during quality filtering. For mock and environmental data, motif and terminal base representations were tested against the assumption of random occurrence with Chi-square tests.

We attempted to determine actual sequencing error rates for data used in either the default QIIME workflow or our optimized workflow. Mock community reads were demultiplexed in QIIME with `split_libraries_fastq.py` under default or strict quality filtering, utilizing the `--store_demultiplexed_fastq` option. Demultiplexed fastq files were imported into Geneious and aligned against the Sanger sequencing data for each mock community member, requiring a 95% similarity in order to exclude contaminant sequences from the alignments. The resulting alignments were exported in SAM format and SAM "NM" flags were calculated in SAMtools v1.19 (Li et al., 2009). The `sam-stats` command in ea-utils was used to calculate mismatch rates ("snp rate" field).

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Results:

The sequencing run clustered at 1119 k/mm^2 (+/- 70) and resulted in 17.96 million total reads passing filter, an overall error rate of 0.36%, and 91% of reads exceeded q30. PhiX Sequencing Control v3 sequences (Illumina, Inc.) constituted 8.31% of the total run (percent aligned). Once demultiplexed, mock community data contained 4.35% PhiX (103,070/2,371,510 reads) while the environmental data contained 4.10% PhiX (259,366/6,332,586 reads). Mock community data demultiplexed under default parameters were determined to have an average error rate of 0.3661% while stringent quality filtering yielded an improved error rate of 0.0990%. Actual error rates varied for each taxon (Table S2). Denovo chimera detection found zero chimeric reads, while reference-based detection consistently identified chimeras at a rate of about 1% for each data set. As the more conservative option, we chose to utilize reference-based chimera detection for the remainder of this study. Sample metadata is available in Table S11. Raw sequencing data for samples used in this study are publicly available in the NCBI Sequence Read Archive (study accession SRP091609; BioProject PRJNA348617).

Under default QIIME assessment, the mock community data showed substantial OTU inflation; where there should have been just 8 OTUs, there were 127 (Table S3). When the environmental data set was processed through the same workflow, 73 OTUs were classified at the family level as Sphingomonadaceae. Together, these OTUs made up 5.3% of environmental sequences, and Sphingomonadaceae was the most abundant classification observed at the family level (Table S4). Three OTUs representing about 0.13% of the mock community data set were also classified as Sphingomonadaceae, a designation which should be absent from the mock data. This result led us to surmise that sequences from the environmental data set were contaminating the mock communities during sequencing. Such sample cross-talk presumably arises from the cluster mixing effect described by Kircher, Sawyer & Meyer (2012) where the index read from a flowcell cluster is spuriously attributed to a neighboring cluster. The mock data also contained 3 OTUs classified as Planococcaceae (<0.03%) and 1 OTU classified as Methylobacteriaceae (<0.01%), again corresponding with OTUs observed within the environmental data. Sphingomonadaceae sequences were observed across all five mock communities, whereas Planococcaceae was only associated with communities 0, 1a, and 1b, suggesting that cluster-mixing events may occur non-randomly. Methylobacteriaceae was present as just a single read

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among community 1b. Three mock community OTUs were observed at low levels in communities from which they should be absent, indicating additional cluster-mixing within the mock community data.

As the most prevalent non-target taxon observed among the mock community data, we sought to establish a method for filtering OTU tables that would eliminate the presence of Sphingomonadaceae reads. OTU tables generated for the mock communities by each of the OTU picking, taxonomy assignment and table filtering methods were compared for the presence of Sphingomonadaceae contaminants. Considering filtering method (mc2, n2, Kircher threshold, or Bokulich threshold) as the predictive variable, we found strong differences among them in removing non-target OTUs ($F_{3,239} = 89.301$, $p < 0.0001$). The least severe filtering method (mc2) retained the most Sphingomonadaceae OTUs (2.50 +/- 1.21) followed by n2 (2.45 +/- 1.21), and Bokulich threshold (1.85 +/- 0.86). Only the Kircher threshold completely removed Sphingomonadaceae contamination from the mock community OTU tables effectively (Tukey's HSD, $p < 0.05$).

Default quality filtering and OTU picking in QIIME resulted in overestimation of mock community diversity regardless of how the final OTU table was filtered (Figure 1a-d; Figure S1: Default mock community rarefactions). Diversity estimates were inflated up to 35 times when singletons were removed by table, compared to nearly 3.5 times when filtering with the Kircher threshold. Despite the reduction of OTU inflation by an order of magnitude, these results indicate that revisions to initial processing steps may yield improved results. We therefore sought to establish an optimized workflow that would produce the correct number of OTUs for an input of known constituents. Using data that had been filtered according to strict standards during the `split_libraries_fastq.py` step in QIIME ($q = 19$, $r = 0$, $p = 0.95$), a correct result was achieved for each of the OTU picking algorithms tested. However, each algorithm differed in which similarity threshold was required for the optimal result (Table 1). Closed reference OTU picking with BLAST overestimated diversity above a similarity threshold of 92%. Open reference OTU picking with UCLUST overestimated diversity at every threshold except 95% similarity. *De novo* OTU picking using CD-HIT at thresholds below 92% and Swarm resolutions below *d*4 underestimated diversity. Swarm yielded the correct result over the broadest range of tested distance thresholds (*d*1-*d*4), and offers other attractive features that made it stand out

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among the tested OTU pickers (e.g., *de novo* picking, multi-threaded analysis). Thus, Swarm was chosen as the optimal OTU picking method for the remainder of the study. We chose *d*4 distance as the optimal threshold as it was the most conservative setting to yield a correct result.

Taxonomic accuracy for Swarm-picked OTUs (*d*4) was assessed for the different taxonomy assigners using default parameters in QIIME 1.9.1. To control for reference database bias, we added representative sequences from each of the correct OTUs to our Greengenes reference with a unique identifier. We observed that BLAST returned the representative sequence 100% of the time, while RDP and UCLUST never found the exact match (Table 2). Even though RDP and UCLUST did not find optimal sequences, assignments were correct, though less specific in taxonomic depth. BLAST yielded similar results when the representative sequences were not present in the database (Table 2). While BLAST offers the advantage of obtaining the best sequence match when available in the database, RDP and UCLUST both offer an advantage in substantially reducing computational time while providing reasonable accuracy for most applications. For the analysis presented here, we chose BLAST as the optimal taxonomy assigner for its superior accuracy.

A perfect result for analysis of our mock communities requires stringent quality filtering of the raw data. Default quality filtering in QIIME 1.9.1 was established according to Bokulich et al. (2013). This imposes a minimum Phred quality score of 4 ($q = 3$), truncates sequences after three bases are observed below this threshold ($r = 3$), and retains truncated reads that represent a minimum of 75% of the original sequence length ($p = 0.75$). In contrast, we performed strict quality filtering using $q = 19$, $r = 0$, and $p = 0.95$. This more stringent filtering protocol ensures that data used for analysis are of much higher quality with approximately uniform read lengths. An important consequence of such stringency is that much of the raw data is discarded. Of the 2,373,247 raw mock community sequences, default quality filtering retained 2,020,542 reads (85.1%), whereas stringent parameters retained just 657,544 reads (27.7%). Holding constant $q = 19$ and $p = 0.95$, we found that increasing r during quality filtering had a profound effect on the amount of data retained (Figure 2a). Allowing $r = 1$ resulted in an increase of data retention from approximately 27% (r = 0) to over 56%. When $r = 2$ and $r = 3$, increases in data retention showed diminishing returns, with 70% and 75% of the data retained, respectively. However, we also found that allowing $r > 0$ will generally cause an inaccurate estimate of the number of

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OTUs, depending on the criteria used for OTU picking (Figure 2b). With the *d*1 resolution, increasing *r* will create a proportional inflation in the number of OTUs determined by Swarm. At *d*2 resolution, allowing *r* = 1 still correctly described our simple mock community whereas allowing *r* = 2 or *r* = 3 caused diversity to be overestimated. At resolutions *d*3 and *d*4, allowing *r* > 0 caused underestimates of diversity. This suggests that the best result is obtained with the most stringent quality filter, which we selected for our optimal workflow (*q* = 19). Similar results using more data may be possible by allowing a small amount of errors (e.g., *r* = 1) and picking OTUs with a more conservative similarity or distance threshold (e.g., Swarm at *d*2 resolution).

The Kircher threshold was effective at removing contaminating OTUs in our mock community data thus yielding a near-perfect result (Figure 3). However, we anticipated that such filtering could be too stringent for environmental analysis given the low per-sample OTU frequencies commonly reported (e.g., Sogin et al., 2006). We compared the expected mock community results to those observed with either default settings, or optimized settings for quality filtering, OTU picking and taxonomy assignment, using each of the final OTU table filtering methods we tested. For all comparisons, Spearman's rank correlation yielded significant p-values (<0.001), so we present only correlation values and 95% confidence intervals (CI) here. When comparing the default analysis to the expected outcome, Spearman's *r* showed a negative correlation ($r = -0.3494$; CI = [−0.4280, −0.2655]). Optimized results exhibited strong positive correlations regardless of filtering threshold used. Lower values for Spearman's *r* occured when diversity was overestimated and when contaminants were present. Correlation with the expected outcome improved as filtering stringency increased with every filtering method producing a dramatic improvement over the default workflow (mc2: $r = 0.8075$, CI = [0.7663, 0.8420]; n2: $r = 0.8702$, CI = [0.8344, 0.8987]; Bokulich threshold: $r = 0.9135$, CI = [0.8841, 0.9357]; Kircher threshold: $r = 0.9646$, CI = [0.9495, 0.9752]). The Bokulich threshold was chosen as our optimal OTU table filtering method because it yielded the best correlation without being overly strict.

Output for the environmental data using either the default or optimized workflow was examined for basic diversity statistics. Default analysis identified 2508 OTUs classified into 388 taxonomic assignments (OTUs per taxon: mean = 6.46, median = 2; Figure S3: Default environmental rarefactions). The optimized analysis identified 1533 OTUs classified into 328 taxonomic assignments (OTUs per taxon: mean = 4.67, median = 2; Figure S4: Optimized

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environmental rarefactions). By treatment, OTU diversity was reduced about twofold when assessed via the optimized workflow and compared to the default results (Figure 4a-4b). In the default analysis, pre-tree soils hosted 978.30 +/- 128.42 OTUs while post-tree soils had 1138.35 +/- 86.34 OTUs (nonparametric T-test = 4.578, $p < 0.001$). In the optimized analysis, pre-tree soils contained 543.28 +/- 79.32 compared to 674.95 +/- 50.21 OTUs in post-tree soils (nonparametric T-test = 6.277, $p < 0.001$). Differences in beta diversity were observed between treatments for each workflow using weighted UniFrac distance matrices (Figure 4c-4d; default PERMANOVA = 8.181, $p < 0.001$; optimized PERMANOVA = 9.355, $p < 0.001$). We also noticed an increase in multivariate dispersion in the optimized workflow, though the differences were not found to be significant in either case (default PERMDISP = 1.086, $p = 0.294$; optimized PERMDISP = 2.160, $p = 0.158$). When data was processed with equivalent sample sizes, the same patterns were observed for both alpha diversity (pre-tree = 545.76 +/- 78.84, post-tree = 679.00 +/- 47.86; nonparametric T-test = 5.004, $p < 0.001$) and beta diversity (PERMANOVA = 6.585, $p < 0.001$), though statistical power was slightly reduced, and multivariate dispersion increased (PERMDISP = 3.248, $p = 0.071$), consistent with a reduction in sample size.

Of the 17 OTUs observed in the optimized mock result, the nine extra OTUs therein were composed of three contaminants and six spurious OTUs representing sequence variants of the target taxa. All extra OTUs were present at low levels ranging from 0.003% to 0.17% per sample (Table S5). That sequence counts of contaminant OTUs were observed in all samples, but only for select taxa, strongly suggests that cluster mixing events occur non-randomly during Illumina sequencing. Species-level mock community observations from the optimized workflow describe the eight constituent taxa at approximately the correct proportions. However, six of the eight taxa were represented by two OTUs each. The main OTU for each taxon was present as 6.30% to 19.09% of the total community while the rates of lower frequency OTUs ranged from 0.01% to 0.05%. Manual inspection of conspecific OTU sequence alignments revealed multiple substitution and indel positions within the first 100 bases which prevented these sequences from dereplicating into the correct sequence during our workflow (Table S6). Additionally, these sequence variants were shorter than the main constituent sequence by at least seven bases, indicating that they derive from inherently lower quality reads. Inspection of trinucleotide motifs preceding each substitution or indel position did not reveal any pattern relating to the observed

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errors (Table S7). Consistent with the results of Schirmer et al. (2015), we observed a higher rate of errors among A or C bases than G or T (error ratio = 1.67). Since A and C or G and T bases share fluorescence excitation wavelengths during Illumina 4-channel sequencing-by-synthesis (SBS), this result suggests that some of the errors we observed were indeed the result of systematic errors during sequencing, although this study was not designed to distinguish between such errors and those generated during PCR. Examining the terminal trinucleotide motif immediately preceding truncation positions (Table S8) we observed "TTT" 83% of the time (X^2_{63} = 271.333, $p < 0.0001$). Additionally, the correct base at the truncation position was "G" 83% of the time (X^2_3 = 11.33, $p = 0.0101$). An example alignment for the two OTUs representing *B. megaterium* is presented in Figure 5a, illustrating the "TTT" motif preceding a "G" truncation position (reverse complimented).

Truncation positions and preceding trimers were also characterized for environmental data, resulting in 34 "suspect" OTUs (Table S9). Of these, 27 OTUs had been truncated at a "G" position (79.41%; X^2_3 = 54.235, $p < 0.0001$), and just 10 possible trimers were represented preceding the truncation position. The motifs "TTT" and "TTC" were substantially overrepresented, being observed 14 (41.18%) and 7 (20.59%) times, respectively (X^2_{63} = 474.235, $p < 0.0001$). An example alignment for 5 OTUs classified to the family level as Sphingomonadaceae is presented in Figure 5b, and includes one such suspect OTU with a "TTT" motif preceding a "G" truncation position (reverse complemented).

Discussion:

Our results show that amplicon sequencing data from Illumina MiSeq instruments requires stringent quality filtering in order to provide the most accurate estimates of diversity. Kunin et al. (2010) found that diversity was grossly overestimated for their mock community data until a quality threshold of q27 was implemented. Similarly, Nelson et al. (2014) observed high overestimation of mock community diversity (25-125 times expected) unless the data was carefully controlled. Our optimal workflow still overestimated the OTU diversity of our simple mock communities by a factor of about two. While this is still an overestimation, it is an improvement over results obtained by default processing. Our optimized protocol yielded a reasonable characterization of taxonomic content for mock communities (Table S5) and

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environmental data (Table S10) alike, though it is important to recognize that mock community results may not always generalize well to environmental samples.

Some authors have suggested that excessive OTU diversity may be at least partially explained by the presence of unfiltered chimeric reads (Edgar, 2013), ribosomal paralogs (Pei et al., 2010), or laboratory contaminants (Nelson et al., 2014). It seems worth noting that the level of chimeric reads in our data was very low compared to rates observed by others (e.g., Schloss, Gevers & Westcott, 2011; Edgar, 2013). We speculate this is due the use of a high-fidelity polymerase and low cycling conditions during library construction, consistent with the results of Gohl et al. (2016). As chimeras are thought to form primarily when incomplete products from the previous cycle act as primers during the extension step (Haas et al., 2011), we made use of an extra-long, low temperature extension of 4 minutes at 60 ^{o}C in an attempt to minimize this effect. We tested the cycling conditions by amplifying serial dilutions of 16S products by qPCR (data not shown) and found it yielded an efficiency of about 1, lending further support to the possibility that our data is virtually chimera-free. Intragenomic ribosomal diversity is also an unlikely explanation for OTU inflation in our mock community results. While structural changes are often associated with diversity of the ribosomal operon (Lim, Furuta & Kobayashi, 2012), these should have little impact on the sequence diversity of the 16S V4 region. In fact, Sun et al. (2013) found that the V4-V5 region suffers from lower rates of intragenomic diversity compared to other variable regions of the 16S rRNA gene. Using a quality cut-off of q20 across a 253 nt sequence, paralogous sequences may remain, though we did not observe any such sequences at a rate high enough to be considered as potential paralogs. Further, the observed proportion of each constituent was quite close to expected proportions after accounting for genome size and 16S rRNA gene copy numbers (Figure 3). All contaminants that we observed in the mock community data could be directly attributed to taxa present in the environmental data set.

Schirmer et al. (2015) observed that error rates reported by Illumina MiSeq sequencers, according to the PhiX Control v3, do not accurately reflect those of amplicon sequences. Their conclusion that actual error rates were higher than those indicated by q-scores reported by the MiSeq has important implications for the use of Illumina sequencing in estimating microbial diversity. It is possible that newer imaging strategies (e.g., 2-channel SBS chemistry used by Illumina NextSeq and MiniSeq instruments) will provide improved parity between the estimated

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and actual error rates, but this will require careful testing. Interestingly, when we attempted to determine actual error rates through alignment of mock community sequences (demultiplexed under default settings) to their expected result, we observed a very close correlation compared to the error reported by PhiX Control (0.36% vs. 0.37%). This result was not consistent across different mock community constituent taxa, suggesting that error rates can be taxon-specific (Table S2). We further note that data filtered under our strict filtering conditions, which stipulated a minimum per-base quality of q20, yielded an average mismatch rate of just 0.099% (q30), indicating that most of our data is of exceptional quality following quality filtering.

Of the non-target OTUs present in our optimized mock community result, one third were contaminants arising from cluster mixing events during sequencing and two thirds were sequence variants of the constituent OTUs which may have arisen during PCR, sequencing, or a combination of the two. Cluster mixing can be controlled by dual-indexing of samples (Kircher, Sawyer & Meyer, 2012), but errors arising during PCR or sequencing represent systematic errors inherent to the procedure of amplicon sequencing which are difficult, if not impossible, to completely eliminate irrespective of indexing strategy. Even though dual-indexing offers a clear advantage over single indexing with regard to sample attribution, single-indexed protocols (e.g., Caporaso et al., 2012) remain popular and widely used. Single-indexed data still yields valuable information and should not be discounted, as long as researchers are aware of the limitations. Dual-indexed designs should be encouraged for new research projects (e.g., Kozich et al., 2013; Fadrosh et al., 2014).

We echo the recommendation by others (e.g., Bokulich et al., 2013; Schirmer et al., 2015) to include control mock community samples to guide data analysis. PhiX Control v3 is still needed to improve sequence diversity for the purpose of cluster map generation (https://goo.gl/NpauDN), but an alternative reference sequence could be used with onboard mock communities to more directly estimate error profiles for community amplicon sequencing data. PhiX sequence itself likely contributes little, if at all, to inflation of diversity estimates, and is easily quantified and removed. Though such an effect is direct evidence of cluster mixing, the rate of PhiX infiltration is likely much higher than the rate of sample mixing because PhiX Control is unindexed, producing no fluorescent signal during indexing cycles. Spurious OTUs

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defined from contaminating PhiX sequence may be more prevalent amid sequence data which was accompanied by higher concentrations of PhiX Control v3 during sequencing.

Although this study was not designed for careful investigation of errors generated during amplicon sequencing projects, we were able to observe that certain bases and motifs were more frequently associated with low-quality base calls than should be expected by chance. The presence of a "TTT" or "TTC" motif immediately preceding a "G" position near the end of a sequence (near the start of the second read) was most frequently associated with an erroneous or suspect OTU (Table S8). Indeed, mock community diversity was inflated on account of this effect, but determining the source of such error requires more careful investigation than is possible here, given that this study derives from a single MiSeq run with limited taxonomic diversity. In addition to the terminal truncation observations, we note that all other observed errors in the mock community sequences occurred within the first 100 bp of sequence, specific to the non-overlapping region of the first sequencing read (Figure 5a). It is likely that the errors we observed here would have occurred less frequently had we used fully-overlapping reads for this study. Importantly, the motif-specific patterns we observed were consistent between the mock and environmental data sets (Figure 5; Table S8; Table S9).

Estimates of alpha diversity are more sensitive than beta diversity calculations to the effects of cluster mixing and systematic errors. Increasing the number of allowed low-quality reads (*r* parameter in `split_libraries_fastq.py`) increases the amount of data available for processing, but also changes observed diversity. For this reason, we suggest that alpha diversity estimates should be performed only with data that has been stringently filtered for quality. Because errors in amplicon sequencing data may follow sequence-specific patterns (Schirmer et al., 2015; this study), spurious OTUs may provide artificial support to the statistical separation of experimental treatments. Alternatively, spurious OTUs arising from taxa which are not differentially represented among treatments could provide artificial noise, making it more difficult to detect real differences. In either scenario, careful quality filtering can diminish such effects.

Our results suggest that alpha diversity can be overestimated if sequencing error rates are not carefully controlled. Here we observed this effect with a QIIME-based workflow, although QIIME is just one of a variety of tools used in data analysis for such work. Because errors may

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arise systematically during PCR or sequencing implies that a similar effect is likely to be observed regardless of which analysis pipeline is used to assess the data. We made use of a high-fidelity polymerase (Phusion Hot Start II) in contrast to many studies which continue to utilize Taq polymerase, with which PCR-derived errors will be more prevalent. Lower fidelity will promote more PCR-derived errors, and those generated during early cycles will be highly perpetuated, an effect which would be more problematic under high-cycling conditions. This effect was recently demonstrated by Gohl et al. (2016), who also showed that PCR-chimeras are virtually absent from protocols utilizing low-cycling conditions. Because errors may follow sequence-specific patterns, some diversity estimates may be particularly inflated for certain taxa, which can further affect studies using taxonomic content to predict community function (e.g. Langille et al., 2013). The use of phylogenetic metrics (e.g., phylogenetic diversity for alpha diversity, UniFrac for beta diversity) during data analysis will likely diminish the effects of complications associated with systematically-inflated OTU diversity. Though the quality-filtering recommendations outlined by Bokulich et al., (2013) have subsequently provided valuable guidance to numerous researchers, newer quality-filtering methods promise improvements in accuracy and read retention (e.g., Puente-Sánchez, Aguirre & Parro, 2016). Careful consideration of the results presented here and elsewhere (Kunin et al., 2010; Schirmer et al., 2015) will improve upon our collective interpretation of microbial diversity across environments.

Conclusions:

In this study, we observed that each of the various workflow components tested (quality filtering, OTU picking, taxonomic assignment, and OTU table filtering) affect the outcome of an amplicon sequencing project. Though high quality output can be achieved through a variety of means, in this study the optimal result was achieved with a specific set of steps. We outline them here as a general recommendation for processing community amplicon data generated on MiSeq instruments through QIIME 1.9.1 (Caporaso et al., 2010a). Analysis parameters can and should be adjusted as necessary for individual data sets. The optimal workflow as performed in this study was as follows (optimized steps in bold):

1. Remove PhiX Control v3 contamination with Smalt

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2. Align read pairs with fastq-join
3. **Strict quality filter in QIIME (*q* = 19, *r* = 0, *p* = 0.95)**
4. Chimera filtering with vsearch
5. Sequence dereplication with prefix/suffix OTU picker
6. **Pick OTUs with Swarm (*d*4 resolution, adjust as necessary)**
7. **Assign taxonomy with BLAST (default settings)**
8. **Filter output table at the Bokulich threshold**

Our results were consistent with the hypothesis that mock community diversity would be inflated due to the presence of PCR or sequencing errors in the data. By imposing more rigorous quality filtering of raw sequencing data, much of this error is removed. The effects of remaining errors can be minimized by utilizing a conservative similarity or distance threshold during OTU picking. By characterizing mock communities at multiple thresholds, one can identify a sufficiently conservative similarity or distance value (*d*4 in our case) which should offer improved confidence when measuring environmental diversity. If mock communities are unavailable, we advocate the use of a workflow based upon the above optimization. For studies utilizing an alternative locus, we suggest adjusting the clustering threshold based on the length of the amplicon (e.g., more conservative clustering for longer amplicons) until mock communities can be employed to determine a more informed threshold.

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Table 1: Mock community OTU picking results. Comparison of OTU picking methods using mock communities with eight total taxa. Cell values represent the number of OTUs returned for a given algorithm and similarity or distance threshold. Correct results are emphasized with bold text.

	97%/*d*1	**95%/*d*2**	**92%/*d*3**	**90%/*d*4**	**85%/*d*5**
BLAST	9	9	**8**	**8**	**8**
CD-HIT	**8**	**8**	**8**	5	5
UCLUST	11	**8**	9	9	11
Swarm	**8**	**8**	**8**	**8**	5

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992 Table 2: Mock community taxonomic assignment results. Comparison of taxonomic assignment methods using mock communities
993 with eight total taxa. Representative sequences were added to Greengenes to test each of the assigners for the ability to return the
994 optimal sequence from a database search. Resulting taxonomic assignments for each method are listed with method-specific
995 confidence values indicated in parentheses (BLAST: e-value, RDP: bootstrap confidence, and UCLUST: p-value). An asterisk (*)
996 indicates an exact match against the correct representative sequence. The final column shows results with BLAST when the
997 representative sequences are excluded from the database.

OTU ID	Expected result	BLAST	RDP	UCLUST	BLAST (Greengenes only)
denovo 0	*Escherichia coli*	**Escherichia coli* (1e-139)	*Escherichia coli* (0.860)	Enterobacteriaceae (1.00)	Enterobacteriaceae (1e-139)
denovo 1	*Staphylococcus aureus*	**Staphylococcus aureus* (6e-135)	*Staphylococcus* (0.980)	*Staphylococcus epidermidis* (0.67)	*Staphylococcus* (6e-135)
denovo 2	*Bacillus megaterium*	**Bacillus megaterium* (2e-137)	*Bacillus cereus* (0.720)	*Bacillus* (0.67)	*Bacillus cereus* (2e-137)
denovo 3	*Klebsiella pneumoniae*	**Klebsiella pneumoniae* (1e-139)	Enterobacteriaceae (1.000)	Enterobacteriaceae (0.67)	Enterobacteriaceae (1e-139)
denovo 4	*Proteus vulgaris*	**Proteus vulgaris* (1e-139)	*Proteus* (0.960)	*Proteus* (0.67)	*Proteus* (2e-137)
denovo 5	*Lactococcus lactis*	**Lactococcus lactis* (1e-136)	*Lactococcus* (0.640)	*Lactococcus* (1.00)	*Lactococcus* (1e-136)
denovo 6	*Micrococcus*	**Micrococcus luteus*	*Micrococcus* (0.900)	*Micrococcus* (0.67)	*Micrococcus* (2e-

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	luteus	(2e-137)			137)
denovo 7	*Pseudomonas aeruginosa*	**Pseudomonas aeruginosa* (1e-139)	*Pseudomonas* (0.520)	Pseudomonadaceae (0.67)	*Pseudomonas* (1e-139)
Matches		8/8 (100%)	0/8 (0%)	0/8 (0%)	0/8 (0%)

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Figure 1: Alpha diversities of mock communities by default analysis. Alpha diversity comparisons for mock communities using default analysis settings and rarefied to 10,000 sequences per sample. Mean values are represented by an "x" while median values are represented by a straight line. Each plot depicts a different OTU table filtering method: (a) singletons removed across the entire table (mc2), (b) private alleles and singletons removed per sample (n2), (c) OTUs removed that do not exceed 0.005% of the total data (Bokulich), and (d) OTUs removed that do not exceed 0.3% per sample (Kircher). In every case, diversity estimates are inflated (expected values are Community 0: 8 OTUs; Communities 1a, 1b, 2a, 2b: 4 OTUs each).

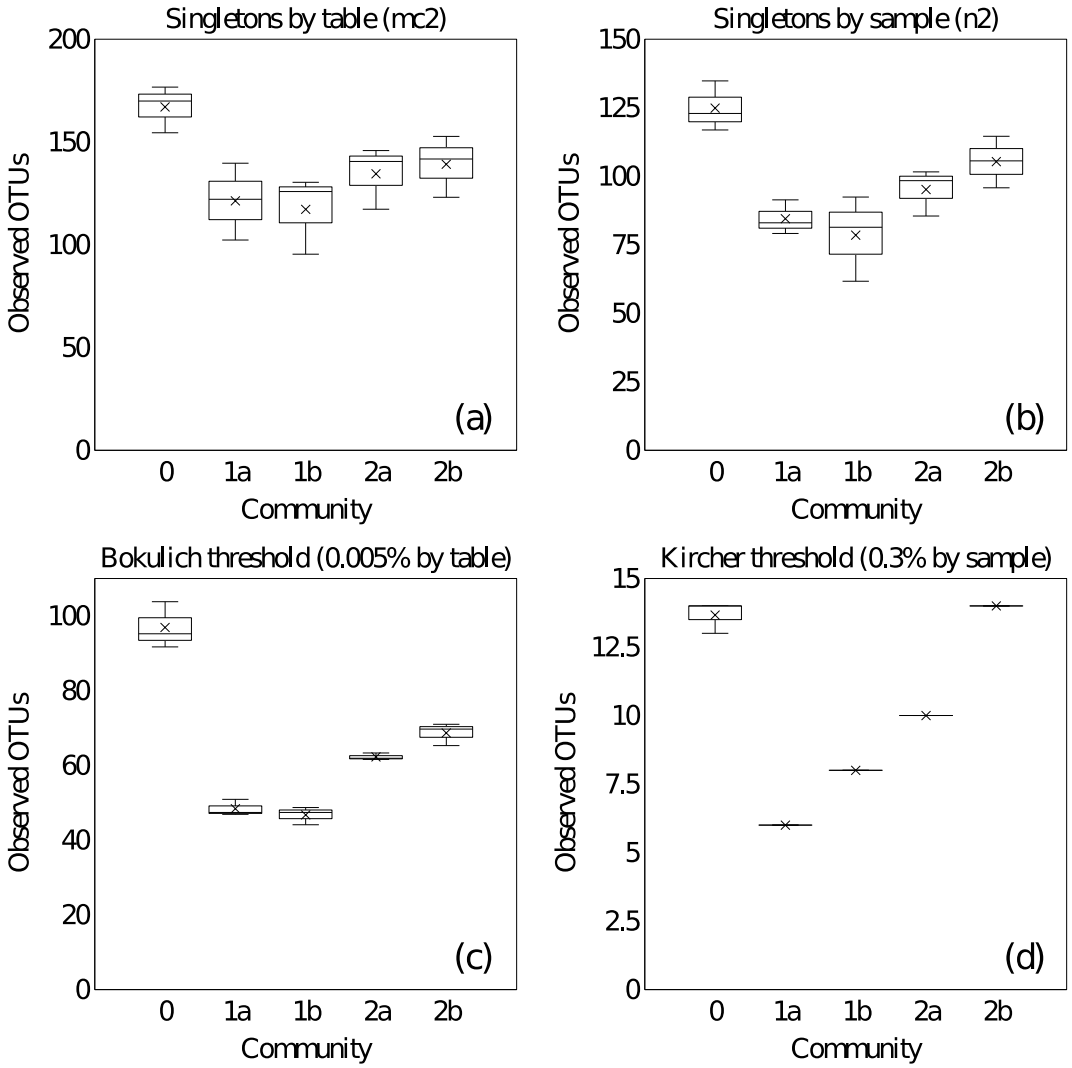

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Figure 2: Effect of allowed low-quality reads on data retention and observed OTU diversity. The effect of adjusting (a) the r parameter (allowed low quality reads), in the split_libraries_fastq.py command in QIIME, on the percent of raw reads retained after data processing (Swarm d4 only), and (b) the observed number of OTUs in the mock community data compared to expected values (expressed as percent of total) across Swarm resolutions d1-d4.

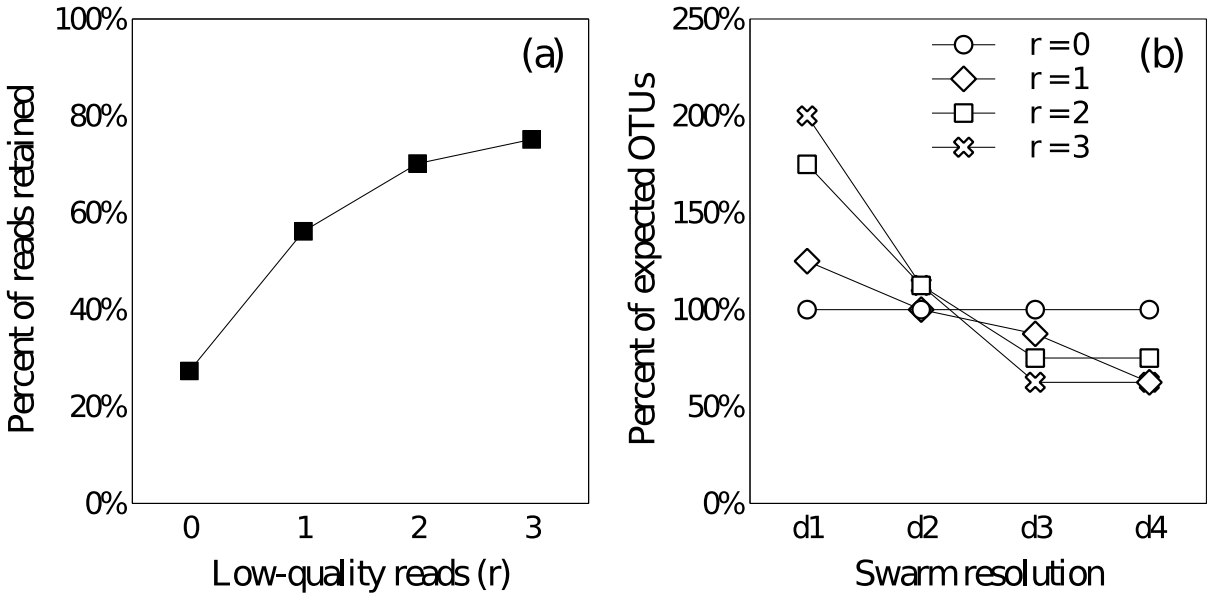

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Figure 3: Observed versus expected mock community compositions. Observed mock community compositions (Obs) plotted against expected values (Exp) for each separate community. Data presented here are for the optimized analysis using the Kircher threshold for OTU table filtering, and yielded a strong positive correlation to the expected result (Spearman's r = 0.9646, CI = [0.9495, 0.9752]).

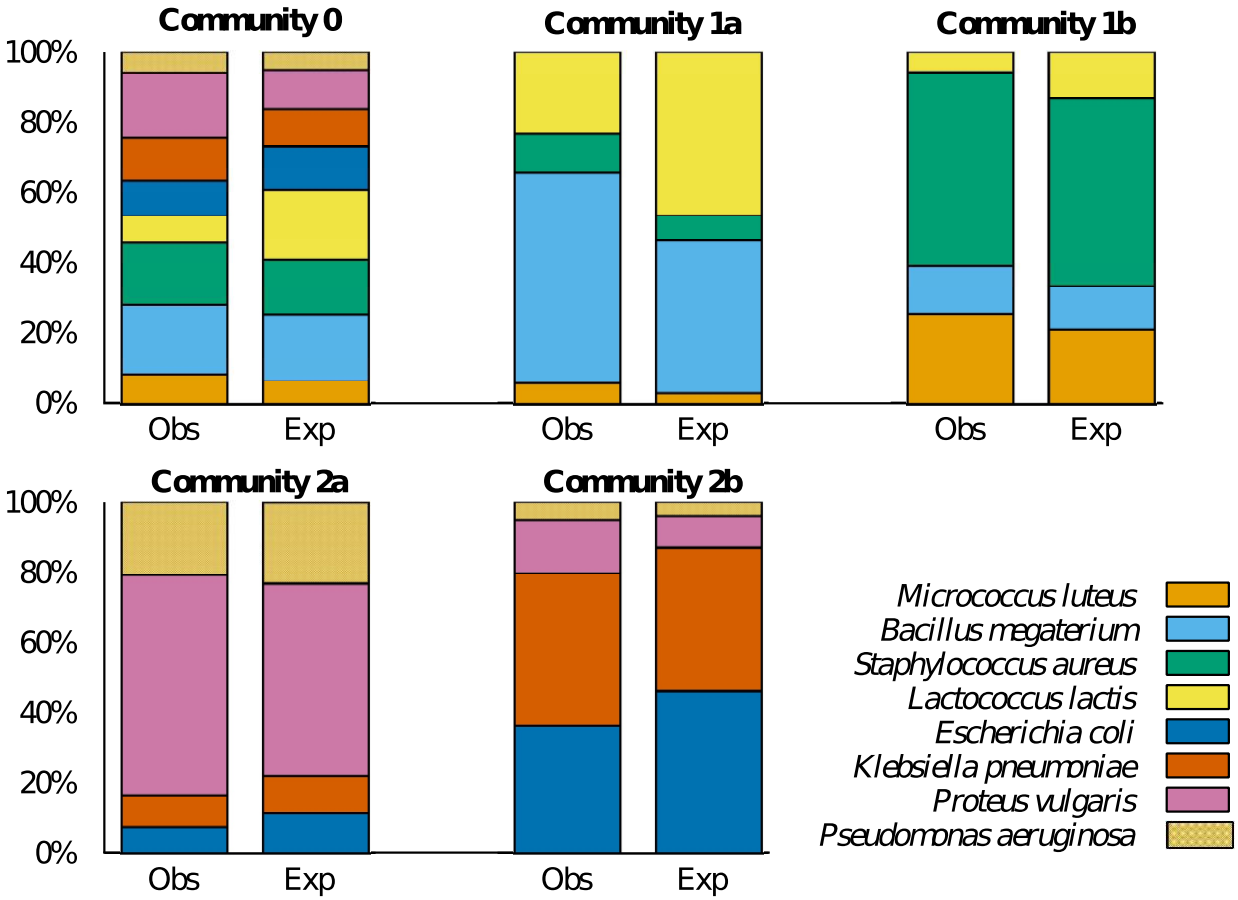

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Figure 4: Diversity analyses for environmental data rarefied to 5000 reads per sample. Alpha diversity as assessed by default (a) or optimized (b) workflow. Beta diversity assessed by default (c) or optimized (d) workflow (white squares: pre-tree; black circles: post-tree). All data show the same trends with strong statistical support (see text). Optimization has a strong effect on the interpretation of alpha diversity results while results are similar between workflows for beta diversity analyses

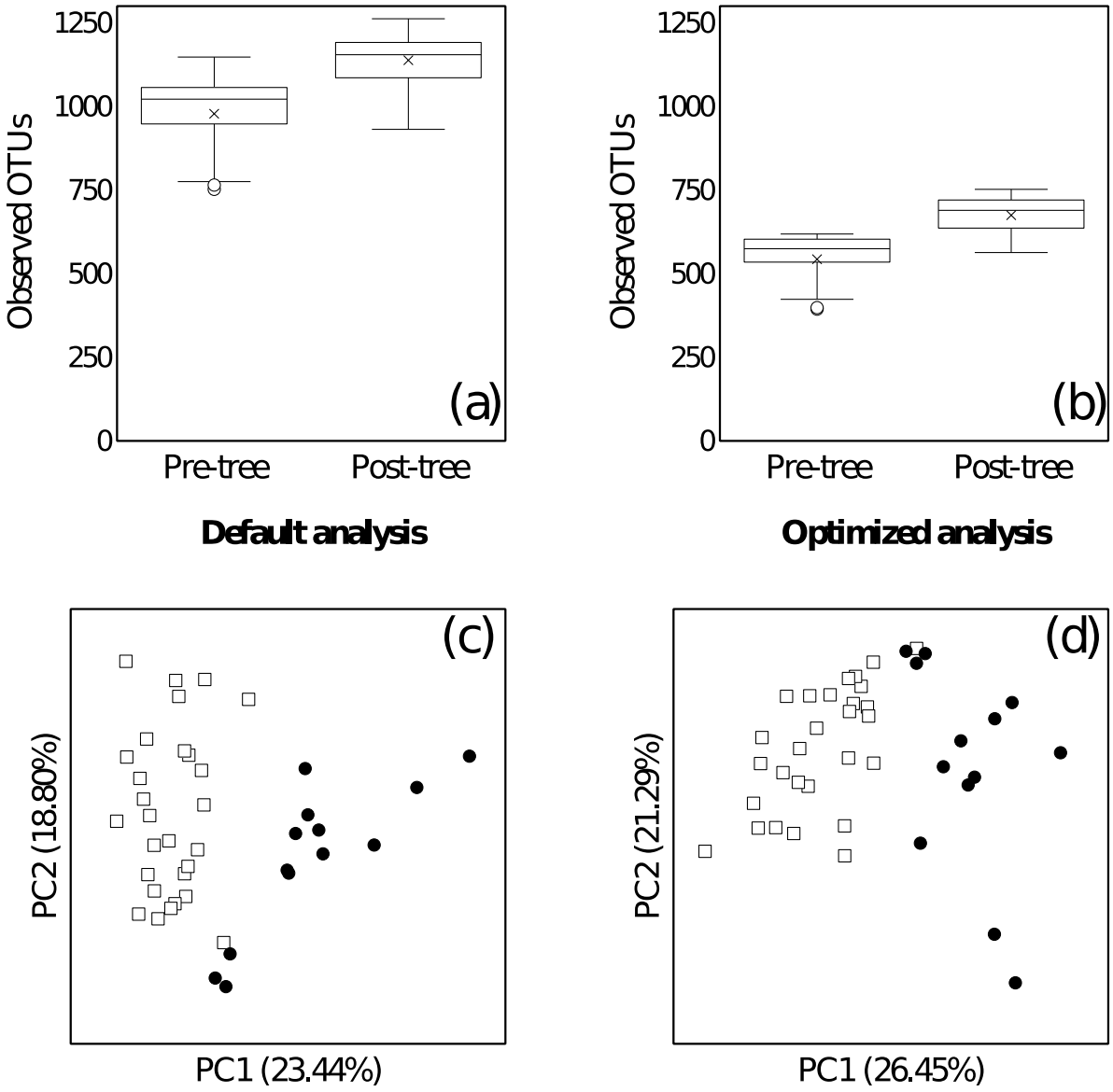

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Figure 5: Mafft alignments illustrating typical truncation of low-frequency OTUs for mock and environmental sequences. Mafft alignments for (a) two OTUs constituting mock community member Bacillus megaterium, and (b) five environmental OTUs classified to the family level as Sphingomonadaceae. Sequences are labelled with de novo OTU designations from the optimized workflow, and base positions are indicated above the sequence alignments. Highlighted bases indicate differences from the alignment consensus (not shown) and are colored according to identity. Overlapping and non-overlapping regions of the first and second reads are indicated above the alignments. Pink and blue positions indicate a “TTT” trimer preceding a “G” truncation position respectively. In each case, the bottom sequence represents a low-frequency OTU which was truncated during quality filtering.

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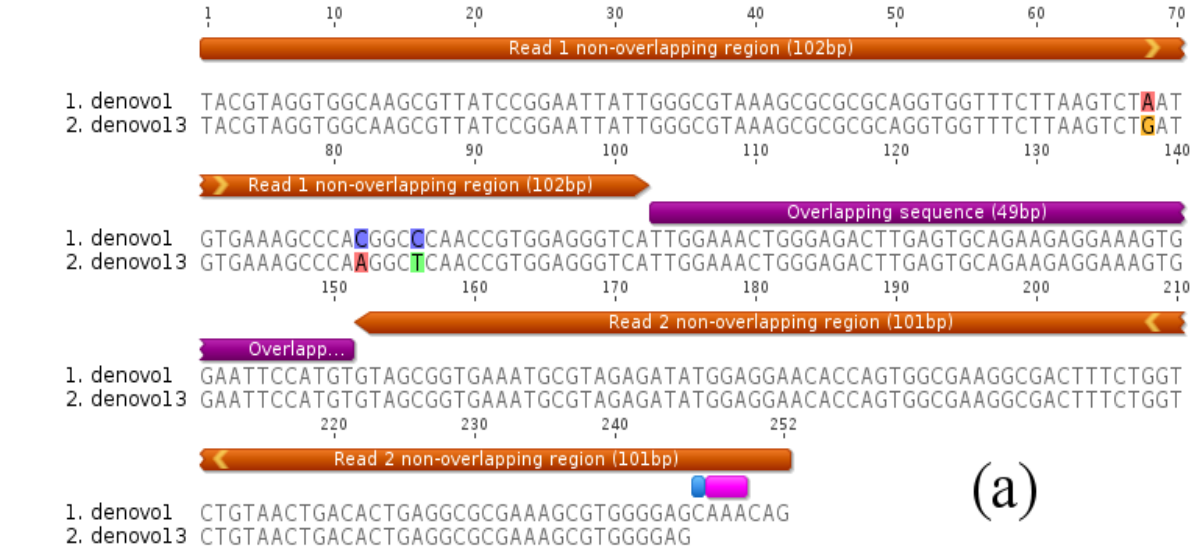

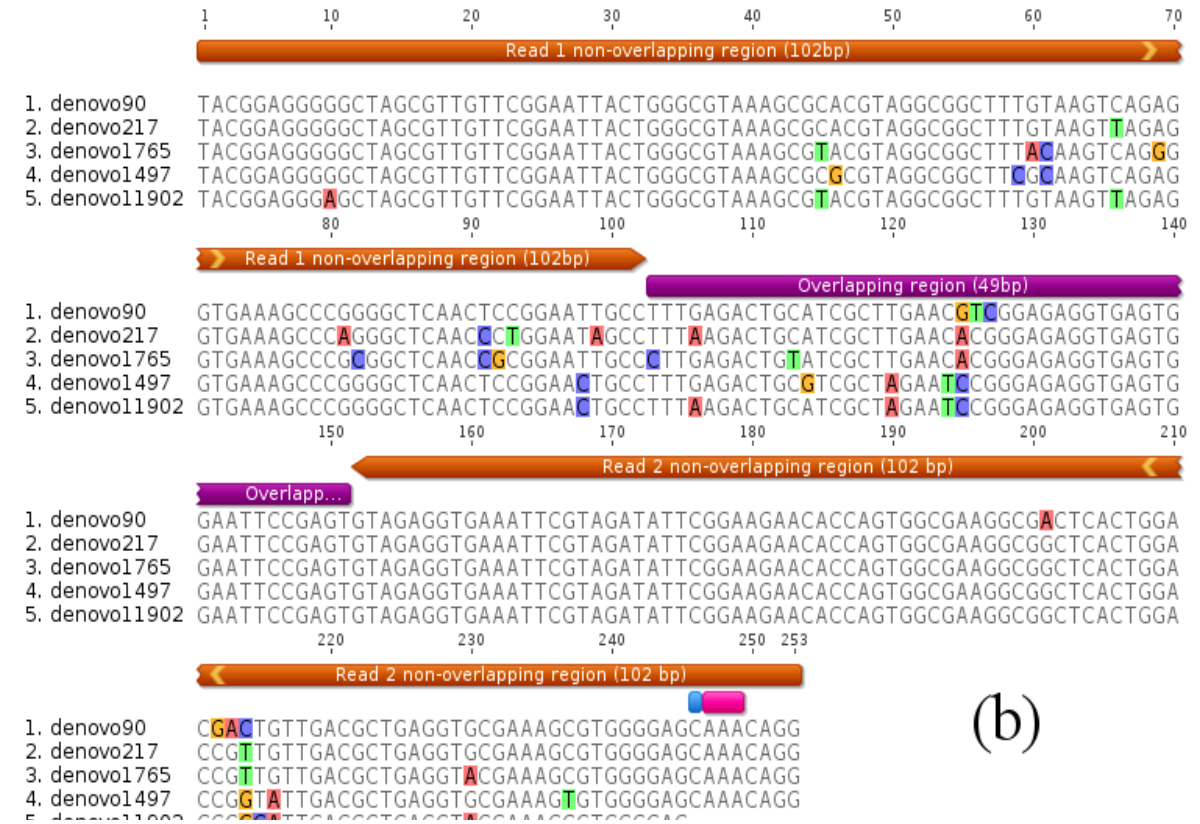

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