The khmer software package: enabling efficient nucleotide sequence analysis [version 1; peer review: 2 approved, 1 approved with reservations]

Abstract
The khmer package is a freely available software library for working efficiently with fixed length DNA words, or k-mers. khmer provides implementations of a probabilistic k-mer counting data structure, a compressible De Bruijn graph representation, De Bruijn graph partitioning, and digital normalization. khmer is implemented in C++ and Python, and is freely available under the BSD license at https://github.com/dib-lab/khmer/.

Keywords
bioinformatics, dna sequencing analysis, k-mer, kmer, khmer, online, low-memory, streaming
**Introduction**

DNA words of a fixed-length k, or “k-mers”, are a common abstraction in DNA sequence analysis that enable alignment-free sequence analysis and comparison. With the advent of second-generation sequencing and the widespread adoption of De Bruijn graph-based assemblers, k-mers have become even more widely used in recent years. However, the dramatically increased rate of sequence data generation from Illumina sequencers continues to challenge the basic data structures and algorithms for k-mer storage and manipulation. This has led to the development of a wide range of data structures and algorithms that explore possible improvements to k-mer-based approaches.

Here we present version 2.0 of the khmer software package, a high-performance library implementing memory- and time-efficient algorithms for the manipulation and analysis of short-read data sets. khmer contains reference implementations of several approaches, including a probabilistic k-mer counter based on the CountMin Sketch, a compressible De Bruijn graph representation built on top of Bloom filters, a streaming lossy compression approach for short-read data sets termed “digital normalization”, and a generalized semi-streaming approach for k-mer spectral analysis of variable-coverage shotgun sequencing data sets.

khmer is both research software and a software product for users: it has been used in the development of novel data structures and algorithms, and it is also immediately useful for certain kinds of data analysis (discussed below). We continue to develop research extensions while maintaining existing functionality.

The khmer software consists of a core library implemented in C++, a CPython library wrapper implemented in C, and a set of Python “driver” scripts that make use of the library to perform various sequence analysis tasks. The software is currently developed on GitHub under [https://github.com/dib-lab/khmer](https://github.com/dib-lab/khmer), and it is released under the BSD License. There is greater than 87% statement coverage under automated tests, measured on both C++ and Python code but primarily executed at the Python level.

**Methods**

**Implementation**

The core data k-mer counting data structures and graph traversal code are implemented in C++, and then wrapped for Python in hand-written C code, for a total of 10.5k lines of C/C++ code. The command-line API and all of the tests are written in 13.7k lines of Python code. C++ FASTQ and FASTA parsers came from the SeqAn library.

Documentation is written in reStructuredText, compiled with Sphinx, and hosted on ReadTheDocs.org.

We develop khmer on github.com as a community open source project focused on sustainable software development, and encourage contributions of any kind. As an outcome of several community events, we have comprehensive documentation on contributing to khmer at [https://khmer.readthedocs.org/en/latest/dev/](https://khmer.readthedocs.org/en/latest/dev/). Most development decisions are discussed and documented publicly as they happen.

**Operation**

khmer is primarily developed on Linux for Python 2.7 and 64-bit processors, and several core developers use Mac OS X. The project is tested regularly using the Jenkins continuous integration system running on Ubuntu 14.04 LTS and Mac OS X 10.10; the current development branch is also tested under Python 3.3, 3.4, and 3.5. Releases are tested against many Linux distributions, including RedHat Enterprise Linux, Debian, Fedora, and Ubuntu. khmer should work on most UNIX derivatives with little modification. Windows is explicitly not supported.

Memory requirements for using khmer vary with the complexity of data and are user configurable. Several core data structures can trade memory for false positives, and we have explored these details in several papers, most notably Pell et al. 2012 and Zhang et al. 2014. For example, most single organism mRNAseq data sets can be processed in under 16 GB of RAM, while memory requirements for metagenome data sets may vary from dozens of gigabytes to terabytes of RAM.

The user interface for khmer is via the command line. The command line interface consists of approximately 25 Python scripts; they are documented at [http://khmer.readthedocs.org/](http://khmer.readthedocs.org/) under User Documentation. Changes to the interface are managed with semantic versioning which guarantees command line compatibility between releases with the same major version.

khmer also has an unstable developer interface via its Python and C++ libraries, on which the command line scripts are built.

**Use cases**

khmer has several complementary feature sets, all centered on short-read manipulation and filtering. The most common use of khmer is for preprocessing short read Illumina data sets prior to de novo sequence assembly, with the goals of decreasing compute requirements for the assembler as well as potentially improving the assembly results.

**Prefiltering sequence data for de novo assembly with digital normalization**

We provide an implementation of a novel streaming “lossy compression” algorithm in khmer that performs abundance normalization of shotgun sequence data. This “digital normalization” algorithm eliminates redundant short reads while retaining sufficient information to generate a contig assembly. The algorithm takes advantage of the online k-mer counting functionality in khmer to estimate per-read coverage as reads are examined; reads can then be accepted as novel or rejected as redundant. This is a form of error reduction, because the net effect is to decrease not only the total number of reads considered for assembly, but also the total number of errors considered by the assembler. Digital normalization results in a decrease of the amount of memory needed for de novo assembly of high-coverage data sets with little to no change in the assembled contigs.

Digital normalization is implemented in the script `normalize-by-median.py`. This script takes as input a list of FASTA or FASTQ files, which it then filters by abundance as described above;
see 3 for details. The output of the digital normalization script is a
downsamled set of reads, with no modifications to the individual
reads. The three key parameters for the script are the k-mer size, the
desired coverage level, and the amount of memory to be used for
k-mer counting. The interaction between these three parameters and
the filtering process is complex and depends on the data set being
processed, but higher coverage levels and longer k-mer sizes result
in less data being removed. Lower memory allocation increases the
rate at which reads are removed due to erroneous estimates of their
abundance, but this process is very robust in practice3.

The output of normalize-by-median.py can be assembled using a de novo assembler such as Velvet6, IDBA8, Trinity12 or
SPAdes13.

K-mer counting and read trimming
Using a memory-efficient CountMin Sketch data structure, khmer
provides an interface for online counting of k-mers in streams
of reads. The basic functionality includes calculating the k-mer
frequency spectrum in sequence data sets and trimming reads at
low-abundance k-mers. This functionality is explored and benchmarked in 1.

Basic read trimming is performed by the script filter-abund.py, which takes as arguments a k-mer countgraph (created by
khmer’s load-into-counting.py script) and one or more sequence data files. The script examines each sequence to find
k-mers below the given abundance cutoff, and truncates the sequence at the first such k-mer. This truncates reads at the location
of substitution errors produced by the sequencing process. When processing sequences from variable coverage data sets, filter-
abund.py can also be configured to ignore reads that have low estimated abundance.

K-mer abundance distributions can be calculated using the script
abundance-dist.py, which takes as arguments a k-mer count
graph, a sequence data file, and an output filename. This script
determines the abundance of each distinct k-mer in the data file
according to the k-mer countgraph, and summarizes the abundances
in a histogram output.

We recently extended digital normalization to provide a general-
ized semi-streaming approach for k-mer spectral analysis4. Here,
we examine read coverage on a per-locus basis in the De Bruijn
graph and, once a particular locus has sufficient coverage, call
errors or trim bases for all following reads belonging to that graph
locus. The approach is “semi-streaming”4 because some reads must
be examined twice. This semi-streaming approach enables few-pass
analysis of high coverage data sets. More, the approach also makes
it possible to apply k-mer spectral analysis to data sets with uneven
coverage such as metagenomes, transcriptomes, and whole-genome
amplified samples.

Because our core data structure sizes are preallocated based on
estimates of the unique k-mer content of the data, we also provide
fast and low-memory k-mer cardinality estimation via the script
unique-kmers.py. This script uses the HyperLogLog algorithm
to provide a probabilistic estimate of the number of unique k-mers
in a data set with a guaranteed upper bound4. A manuscript on this
implementation is in progress (Irber and Brown, unpublished).

Partitioning reads into disconnected assembly graphs
We have also built a De Bruijn graph representation on top of a
Bloom filter, and implemented this in khmer. The primary use for
this so far has been to enable memory efficient graph partitioning, in
which reads contributing to disconnected subgraphs are placed into
different files. This can lead to an approximately 20-fold decrease
in the amount of memory needed for metagenome assembly3, and
may also separate reads into species-specific bins15.

Reformatting collections of short reads
In support of the streaming nature of this project, our preferred
paired-read format is with pairs interleaved in a single file. As an
extension of this, we automatically support a “broken-paired” read
format where orphaned reads and pairs coexist in a single file. This
enables single input/output streaming connections between tools,
while leaving our tools compatible with fully paired read files as
well as files containing only orphaned reads.

For converting to and from this format, we supply the scripts
extract-paired-reads.py, interleave-reads.py, and split-paired-reads.py to respectively extract fully
paired reads from sequence files, interleave two files containing
read pairs, and split an interleaved file into two files containing read
pairs.

In addition, we supply several utility scripts that we use in our
own work. These include sample-reads-randomly.py for
performing reservoir sampling of reads and readstats.py for
summarizing sequence files.

Summary
The khmer project is an increasingly mature open source scientific
software project that provides several efficient data structures and
algorithms for analyzing short-read nucleotide sequencing data.
khmer emphasizes online analysis, low memory data structures
and streaming algorithms. khmer continues to be useful for both
advancing bioinformatics research and analyzing biological data.

Software availability
Software available from
https://khmer.readthedocs.org/en/v2.0/

Link to source code
https://github.com/dib-lab/khmer/releases/tag/v2.0

Link to archived source code as at time of publication
http://dx.doi.org/10.5281/zenodo.31258

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Author contributions
CTB is the primary investigator for the khmer software package. MRC is the lead software developer from July 2013 onwards. Many significant components of khmer have their own paper describing them (see “Use Cases”, above). The remaining authors each have one or more Git commits in their name.

Competing interests
No competing interests were disclosed.

Grant information
khmer development has largely been supported by AFRI Competitive Grant no. 2010-65205-20361 from the USDA NIFA, and is now funded by the National Human Genome Research Institute of the National Institutes of Health under Award Number R01HG007513, as well as by the the Gordon and Betty Moore Foundation under Award number GBMF4551, all to CTB.

I confirm that the funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

References

This paper describes version 2 of the khmer software suite. The software is developed to provide both a set of directly usable tools (e.g. normalize-by-median for digital normalization) as well as an experimental framework for developers looking to design new algorithms and methods. It has proven very useful on both of these fronts. The repository is highly watched and starred on GitHub, the developers are very responsive (see more below), and both the senior author’s group and other researches seem to be leveraging this framework to build new tools and algorithms.

The paper itself does a good job of describing the software at a high level, including the overall design and goals. I would have appreciated slightly more detail about the motivation behind the design decisions, and the tradeoffs they entail (e.g. Why have a Python front-end? Why use hand-written binding code rather than a binding generator, like SWIG, that would allow interfaces to other languages as well?). I understand that a comprehensive description is not feasible in a manuscript of this length. It would be very interesting to know, however, the cost paid for using the high-level interface rather than the C++ library directly. When the underlying computation is trivial, simply having to iterate over an enormous number of things in Python could add non-trivial overhead. Despite these desiderata, I find that the paper is generally well written and does a good job of describing what a new user might want to know about khmer, and so I approve of this manuscript.

Like Daniel, I also downloaded and built the software using the instructions provided in the ReadTheDocs documentation. The process was simple, and worked well, with the exception of a minor glitch running the tests. After debugging the cause of the problem, I posted an issue to the GitHub repository, and received a response in less than a day. I bring this up because, while not an aspect of the paper itself, good developer support is crucial to the long-term survival and utility of a software package — khmer seems to have this.

This brings me to my final point, about the (currently) controversial authorship policy on this paper, which is ancillary to the quality of the paper (and software) itself. At this point, I must reserve judgement on whether I think the authorship policy adopted by this paper is "good" or "bad" (for science, the community, etc.). Incidentally, this is a dichotomy that does not capture the subtlety or importance of this issue well.
In the manuscript, the authors state "We develop khmer on github.com as a community open source project focused on sustainable software development, and encourage contributions of any kind." Thus, contributions to khmer are of a potentially wide variety in character (and also, I believe, not simply related to improving or maintaining the code). Those who contribute to the design, improve the usability, work on documentation, support new and existing users, and develop and propagate best practices are all contributing something valuable to the khmer software "ecosystem". It is unreasonable to expect a piece of software that is ~25k lines of code (and growing) to be actively developed, maintained, and supported by only a small contingent of people, many of whom may be graduate students soon to graduate and move on. Thus, if we are interested in the long-term viability and quality of such software, we must adopt a system of credit that values and recognizes a variety of different types of contribution. On the other hand, I do share the concern that, in the midst of the current authorship system, bestowing that recognition in the form of authorship may have the adverse effect of diminishing the public perception of the very credit one is trying to grant. Perhaps there is a solution along the lines adopted by this paper, or perhaps something drastically different needs to be considered.

**Competing Interests:** No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.
**Competing Interests:** No competing interests were disclosed.

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**Reviewer Response 06 Oct 2015**

**Daniel S. Katz,** University of Chicago, Chicago, USA

In addition to my report, regarding software papers in general under F1000, I believe that much more should be required from their reviewers, and what **is required** should be made clear. Software journals (e.g., Ubiquity Press’s Journal of Open Research Software, Elsevier’s Software X) have specific statements of what a reviewer should do, which say a lot about the quality of the review. For JORS, this is defined on a web page (http://openresearchsoftware.metajnl.com/about/editorialPolicies/). For Software X, the criteria are not on the web (as far as I know) but are embedded in the review form/process, and are roughly equivalent.

**Competing Interests:** none

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**Reader Comment 08 Oct 2015**

**F1000 Research, UK**

Thanks for this helpful feedback on our guidelines.

Our current guidelines for reviewing software tools are focused around the content of the article itself, and what information should be included. However, reporting issues with the software itself is clearly also important, so we would always encourage referees to download and test the software and include any feedback within the referee reports, so the authors may rectify them. We’ll revise our instructions to software tool referees in light of your comments to make this clearer.

**Competing Interests:** No competing interests were disclosed.

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**Reviewer Report 05 October 2015**

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**Ewan Birney**

European Molecular Biology Laboratory, European Bioinformatics Institute, Hinxton, UK

This is an update of a widely used tool, khmer, which is in broad use in the technical community around de Bruijn graphs and short reads, based on Bloom filters. It is a good update, provides link to the code, and is sensibly written with tests. I have no concern about the scientific aspect of this paper.
I do find the author inclusion list taking a concept and going to the extreme, and I don't think it is sensible to have an anonymised author (en zyme) on the list, with in effect no way to attribute to a person this. Science's openness in publication is also about attribution. Although I understand Titus' consistency of having all git commiters as authors, I think it is sensible to make a distinction of substantial/scientific changes, of which the vast majority of the authors are. Acknowledgements are precisely there to handle these other cases.

I believe it is uncontroroversial to appropriately trim the author list, to use the acknowledgements for anonymous improvement (happens regularly in science) and small details (again, a commonplace practice).

**Competing Interests:** No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

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**Comments on this article**

**Version 1**

Reader Comment 29 Sep 2015

**Russell Neches**, UC Davis, USA

I would like to make a comment regarding Lior Pachter's comment.

The use of pseudonyms has a long and important history in scientific discourse.

Despite the fact that we now know its author's identity, the t-statistic is known as "Student's t-test" because that was the name under which he published it. Pseudonyms can be ad hoc tools used to allow researchers to participate in science despite prejudice among their peers. For example, mathematician Sophie Germain studied, corresponded and published under the name Monsieur Antoine Auguste Le Blanc owing to the near-total exclusion of women from all domains of science in the eighteenth century. Pseudonyms have also been deployed to shield researchers from prejudice beyond the scientific community; mathematician Jacques Feldbau published under the less-Jewish-sounding name Jacques Laboureur shortly before he was deported to Auschwitz. Sometimes the motives behind the choice to publish pseudonymously are obscure or personal, such as Carl Ludwig Siegel's choice in 1926 to publish his reduction of a hyperelliptic equation to a unit equation under the name "X." Even Isaac Newton published his alchemical dabblings as "Jehovah Sanctus Unus."

There is a long-standing tradition of etiquette regarding pseudonyms in science. Simply put, one endeavors to respect the author's choice. Of course, there are limits to how far to carry this respect. Most people agree that the courtesy ought not be extended to protect people who use pseudonyms to obtain impunity when attacking others.
Lior writes that, "Authors who did contribute should be listed with full name with affiliation so that they can be contacted if the need arises." The author that Lior has singled out here has made him/herself available for anyone to contact under their pseudonym via email, Twitter, LinkedIn and in person at a variety of professional conferences. Even if one accepts the premise under which it was raised, the objection is unfounded. I respectfully suggest the editors expunge the identifying information Lior placed in his comment. I also feel that Lior's actions in this matter should remain part of the record.

**Competing Interests:** Russell Neches is a graduate student at the same university as some of the authors, though shares no departmental affiliations, program affiliations, publications or funding sources with them. They do, however, occasionally enjoy beer together.

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Reader Comment 28 Sep 2015

**F1000 Research, UK**

Thank you for bringing this to our attention.

Because F1000Research does not have editors and the authors are in charge of their publication, one of the key requirements for publication is that the ‘lead’ authors, who have to engage in the public discussion with referees and readers, are active researchers and meet our authorship criteria. For an author-driven model to work, this is a key check done on submission.

The ICMJE “Uniform requirements”, which specify what type of contribution justify full authorship, constitute best practice in STM publishing and are listed in our policy; the Author Contribution section is meant to ensure transparency for readers, outlining why authors were indeed included in the author list.

We appreciate that readers may not always agree that an individual author's contribution in a paper is ‘substantial’ enough to justify full authorship. However, consistent with the F1000Research publishing ethos generally applied to the content of a paper (where no editors judge whether the finding in a paper is ‘significant’ or substantial enough to justify publication), the in-house editorial team does not usually judge whether an individuals' contribution is sufficient to justify authorship – a call that can be subjective. As with many traditional journals, on submission, we ask the submitting authors confirm that all the co-authors have agreed to the submission of the article.

**Competing Interests:** No competing interests were disclosed.

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Reader Comment 26 Sep 2015

**Lior Pachter, Department of Mathematics, University of California, Berkeley, USA**

This article appears to violate the F1000 criteria for authorship mentioned [here](#) and defined in the "uniform requirements". Specifically, the contribution of "one or more Git commits" in the code which is the sole contribution listed for the majority of authors fails to satisfy the first requirement, namely

- Substantial contributions to the conception or design of the work; or the acquisition, analysis, or interpretation of data for the work.
Most of the authors' Git commits consist of fixing very minor typos (e.g. see here and here). Such "contributions" clearly do not rise to the level of authorship qualification as specified in the "uniform requirements" and the individuals who made such contributions should instead be mentioned in the acknowledgements section.

Authors who did contribute should be listed with full name with affiliation so that they can be contacted if the need arises. This may be necessary to confirm another "uniform requirement" for authorship:

- Agreement to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

I noticed that "en zyme" is listed as an author with the affiliation of "independent Researcher in Boston, MA". This individual appears to be Nathan Kohn, a part time lecturer at Boston University Metropolitan College and should be listed as such (assuming his contribution merits authorship).

**Competing Interests:** I have no competing interests to disclose.

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