

# HTSeq—a Python framework to work with high-throughput sequencing data

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## ABSTRACT

**Motivation:** A large choice of tools exists for many standard tasks in the analysis of high-throughput sequencing (HTS) data. However, once a project deviates from standard workflows, custom scripts are needed.

**Results:** We present HTSeq, a Python library to facilitate the rapid development of such scripts. HTSeq offers parsers for many common data formats in HTS projects, as well as classes to represent data, such as genomic coordinates, sequences, sequencing reads, alignments, gene model information and variant calls, and provides data structures that allow for querying via genomic coordinates. We also present htseq-count, a tool developed with HTSeq that preprocesses RNA-Seq data for differential expression analysis by counting the overlap of reads with genes.

**Availability and implementation:** HTSeq is released as an open-source software under the GNU General Public Licence and available from <http://www-huber.embl.de/HTSeq> or from the Python Package Index at <https://pypi.python.org/pypi/HTSeq>.

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## 1 INTRODUCTION

The rapid technological advance in high-throughput sequencing (HTS) has led to the development of many new kinds of assays, each of which requires the development of a suitable bioinformatical analysis pipeline. For the recurring ‘big tasks’ in a typical pipeline, such as alignment and assembly, the bioinformatics practitioner can choose from a range of standard tools. For more specialized tasks, and to interface between existing tools, customized scripts often need to be written.

Here we present HTSeq, a Python library to facilitate the rapid development of scripts for processing and analysing HTS data. HTSeq includes parsers for common file formats for a variety of types of input data and is suitable as a general platform for a diverse range of tasks. A core component of HTSeq is a container class that simplifies working with data associated with genomic coordinates, i.e. values attributed to genomic positions (e.g. read coverage) or to genomic intervals (e.g. genomic features such as exons or genes). Two stand-alone applications developed with HTSeq are distributed with the package, namely htseq-qa for read quality assessment and htseq-count for preprocessing RNA-Seq alignments for differential expression calling.

Most of the features described in the following sections have been available since the initial release of the HTSeq package in 2010. Since then, the package and especially the htseq-count script have found considerable use in the research community. The present article provides a description of the package and also reports on recent improvements.

HTSeq comes with extensive documentation, including a tutorial that demonstrates the use of the core classes of HTSeq and discusses several important use cases in detail. The documentation, as well as HTSeq’s design, is geared towards allowing users with only moderate Python knowledge to create their own scripts, while shielding more advanced internals from the user.

## 2 COMPONENTS AND DESIGN OF HTSeq

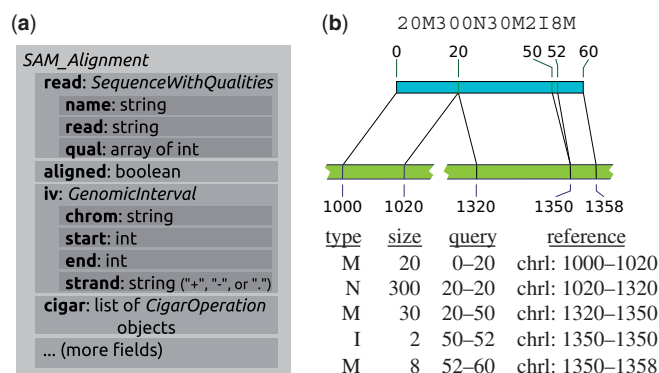
### 2.1 Parser and record objects

HTSeq provides parsers for reference sequences (FASTA), short reads (FASTQ) and short-read alignments (the SAM/BAM format and some legacy formats), and for genomic feature, annotation and score data (GFF/GTF, VCF, BED and Wiggle).

Each parser is provided as a class whose objects are tied to a file name or open file or stream and work as iterator generators, i.e. they may be used in the head of a *for* loop and will yield a sequence of record objects that are taken up by the loop variable. These record objects are instances of suitable classes to represent the data records. Wherever appropriate, different parsers will yield the same type of record objects. For example, the record class *SequenceWithQualities* is used whenever sequencing read with base-call qualities needs to be presented, and hence yielded by the *FastqParser* class and also present as a field in the *SAM\_Alignment* objects yielded by *SAM\_Reader* or *BAM\_Reader* parser objects (Fig. 1). Specific classes (*GenomicPosition* and *GenomicInterval*) are used to represent genomic coordinates or intervals, and these are guaranteed to always follow a fixed convention (namely, following Python conventions, zero-based, with intervals being half-open), and parser classes take care to apply appropriate conversion when the input format uses different convention. The same is true for functions to write files.

To offer good performance, large parts of *HTSeq* are written in *Cython* (Behnel *et al.*, 2011), a tool to translate Python code augmented with type information to *C*. While the code for reading and writing all text-based formats, including text SAM files, is written in Python/Cython and hence has no external dependencies, the classes *BAM\_Reader* and *BAM\_Writer* wrap around

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**Fig. 1.** (a) The *SAM\_Alignment* class as an example of an *HTSeq* data record: subsets of the content are bundled in object-valued fields, using classes (here *SequenceWithQualities* and *GenomicInterval*) that are also used in other data records to provide a common view on diverse data types. (b) The *cigar* field in a *SAM\_alignment* object presents the detailed structure of a read alignment as a list of *CigarOperation*. This allows for convenient downstream processing of complicated alignment structures, such as the one given by the cigar string on top and illustrated in the middle. Five *CigarOperation* objects, with slots for the columns of the table (bottom) provide the data from the cigar string, along with the inferred coordinates of the affected regions in read ('query') and reference

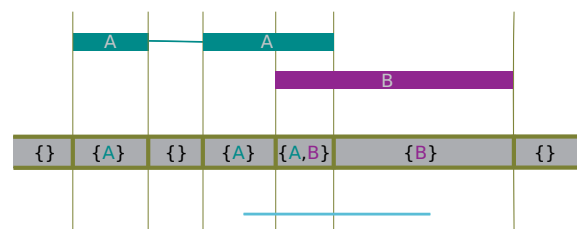
functionality from *PySam* (<http://code.google.com/p/pysam/>) and are available only if that package has been installed.

The *SAM\_Alignment* class offers functionality to facilitate dealing with complex, e.g. gapped, alignments (Fig. 1b), with multiple alignments and with paired-end data. The latter is challenging because, in the SAM format, an alignment of a read pair is described by a pair of alignment records, which cannot be expected to be adjacent to each other. *HTSeq* provides a function, *pair\_SAM\_alignments\_with\_buffer*, to pair up these records by keeping a buffer of reads whose mate has not yet been found, and so facilitates processing data on the level of sequenced fragments rather than reads.

## 2.2 The GenomicArray class

Data in genomics analyses are often associated with positions on a genome, i.e. coordinates in a reference assembly. One example for such data is read coverage: for each base pair or nucleotide of the reference genome, the number of read alignments overlapping that position is stored. Similarly, gene models and other genomic annotation data can be represented as objects describing features such as exons that are associated with genomic intervals, i.e. coordinate ranges in the reference.

A core component of *HTSeq* is the class *GenomicArray*, which is a container to store any kind of genomic-position-dependent data. Conceptually, each base pair position on the genome can be associated with a value that can be efficiently stored and retrieved given the position, where the value can be both a scalar type, such as a number, or a more complex Python object. In practice, however, such data are often piecewise constant, and hence, the class internally uses a tree structure to store 'steps', i.e. genomic intervals with a given value. This has been implemented in C++, building on the *map* template of the C++ standard library, which is typically realized as a red-black tree



**Fig. 2.** Using the class *GenomicArrayOfSets* to represent overlapping annotation metadata. The indicated features are assigned to the array, which then represents them internally as steps, each step having as value a set whose elements are references to the features overlapping the step

(Josuttis, 1999). To link C++ and Python code, we used SWIG (Beazley *et al.*, 1996). Alternatively, the class also offers a storage mode based on NumPy arrays (van der Walt *et al.*, 2011) to accommodate dense data without steps. If such data become too large to fit into memory, NumPy's *memmap* feature may be used, which swaps currently unused parts of the data out to disk. The choice of storage back-end is transparent, i.e. if the user changes it, no changes need to be made in the code that uses the *GenomicArray* objects.

A subclass of *GenomicArray*, the *GenomicArrayOfSets* is suitable to store objects associated with intervals that may overlap, such as genes or exons from a gene model reference. This is implemented using Python sets (Fig. 2): Each step's value is a set of references to the actual objects. When data are inserted into the array, steps get split and sets get duplicated as needed. When querying an interval, the sets overlapped by the query interval are returned, and their union will contain all objects overlapped by the query interval.

## 3 DOCUMENTATION AND CODING STRATEGIES

*HTSeq* comes with extensive documentation to guide developers. Care has been taken to expect only moderate experience with Python from the reader. A 'Tour' offers an overview over the classes and principles of *HTSeq* by demonstrating their use in simple examples. Then, two common use cases are discussed in detail to show how *HTSeq* can be applied to complex tasks.

The first use case is that of aggregate coverage profiles: given ChIP-Seq data, e.g. from histone marks, we want to calculate the profile of these marks with respect to specific positions in the genome, such as transcription start sites (TSSs), by aligning coverage data in windows centred on the TSSs and averaging over the TSSs of all genes or a subset thereof. In this use case, one needs to integrate information from two position-specific data sources, namely a list of TSSs obtained from annotation data and the aligned reads. Hence, one may either iterate through the reads first, store this information in a *GenomicArray* and then use position-specific access to it when iterating through the list of TSSs, or, first store the TSSs in a *GenomicArray* and use this afterwards when iterating through the reads. In either case, one dataset is kept in memory in a form allowing for fast random access, whereas the other is iterated through with only summary information being kept.

These approaches are prototypical for scripts built on HTSeq and hence explained and demonstrated in detail in the documentation (Section ‘A detailed use case: TSS plots’).

The second use case discussed in detail is that of counting for each gene in a genome how many RNA-Seq reads map to it. In this context, the HTSeq class *CigarOperation* is demonstrated, which represents complex alignments in a convenient form (Fig. 1b). This section of the documentation also explains HTSeq’s facilities to handle multiple alignments and paired-end data.

The remainder of the documentation provides references for all classes and functions provided by HTSeq, including those classes not used in the highlighted use cases of the tutorial part, such as the facilities to deal with variant call format (VCF) files.

#### 4 HTSEQ-COUNT

We distribute two stand-alone scripts with HTSeq, which can be used from the shell command line, without any Python knowledge, and also illustrate potential applications of the HTSeq framework. The script *htseq-qc* is a simple tool for initial quality assessment of sequencing runs. It produces plots that summarize the nucleotide compositions of the positions in the read and the base-call qualities.

The script *htseq-count* is a tool for RNA-Seq data analysis: Given a SAM/BAM file and a GTF or GFF file with gene models, it counts for each gene how many aligned reads overlap its exons. These counts can then be used for gene-level differential expression analyses using methods such as *DESeq2* (Love et al., 2014) or *edgeR* (Robinson et al., 2010). As the script is designed specifically for differential expression analysis, only reads mapping unambiguously to a single gene are counted, whereas reads aligned to multiple positions or overlapping with more than one gene are discarded. To see why this is desirable, consider two genes with some sequence similarity, one of which is differentially expressed while the other one is not. A read that maps to both genes equally well should be discarded, because if it were counted for both genes, the extra reads from the differentially expressed gene may cause the other gene to be wrongly called differentially expressed, too. Another design choice made with the downstream application of differential expression testing in mind is to count fragments, not reads, in case of paired-end data. This is because the two mates originating from the same fragment provide only evidence for one cDNA fragment and should hence be counted only once.

As the *htseq-count* script has found widespread use over the past 3 years, we note that we recently replaced it with an overhauled version, which now allows processing paired-end data without the need to sort the SAM/BAM file by read name first. See the documentation for a list of all changes to the original version.

#### 5 DISCUSSION

HTSeq aims to fill the gap between performant but monolithic tools optimized for specialized tasks and the need to write data processing code for HTS application entirely from scratch. For a number of the smaller tasks covered by HTSeq, good

stand-alone solutions exist, e.g. *FastQC* (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) for quality assessment or *Trimmomatic* (Bolger et al., 2014) for trimming of reads. If the specific approaches chosen by the developers of these tools are suitable for a user’s application, they are easier to use. However, the need to write customized code will inevitably arise in many projects, and then, HTSeq aims to offer advantages over more narrow programming libraries that focus on specific file formats, e.g. *PySam* and *Picard* (<http://picard.sourceforge.net/>) for SAM/BAM files, by integrating parsers for many common file formats and fixing conventions for data interchange between them. For R developers, similar functionality is now available within the *Bioconductor* project (Gentleman et al., 2004) with packages like *Rsamtools* and *GenomicRanges* (Lawrence et al., 2013). Within Python, HTSeq complements Biopython (Cock et al., 2009), which provides similar functionality for more ‘classic’ bioinformatics tasks such as sequence analysis and phylogenetic analyses but offers little support for HTS tasks.

Although most uses of HTSeq will be the development of custom scripts for one specific analysis task in one experiment, it can also be useful for writing more general tools. The *htseq-count* script, for example, prepares a count table for differential expression analysis, a seemingly easy task, which, however, becomes complicated when ambiguous cases have to be treated correctly. Despite being written in Python, *htseq-count* offers decent performance: Tested on a standard laptop computer, *htseq-count* (version 0.6.1) processed about 1.2 million reads (0.6M read pairs) per minute, using about 250 MB of RAM to hold the human gene annotation in memory. When the file was sorted by position rather than read name, so that mate pairs were not in adjacent records, processing time increased to a bit less than twice as much, and, for a SAM file of 26 GB, less than 450 MB of additional space in RAM were needed for the buffer holding reads with outstanding mates.

When HTSeq was first released in 2010, *htseq-count* was the first comprehensive solution for this task, and has since then been widely used. Recently, further tools for this task have become available, including the *summarizeOverlap* function in the *GenomicRanges* Bioconductor package (Lawrence et al., 2013) and the stand-alone tool *featureCount* (Liao et al., 2014), which achieves fast runtimes because of being implemented in C. In a recent benchmark, Fonseca et al. (2014) compared *htseq-count* with these other counting tools and judged the accuracy of *htseq-count* favourably. Nevertheless, neither *htseq-count* nor the other tools offer much flexibility to deal with special cases, which is why the HTSeq documentation (section ‘Counting reads’) discusses in detail how users can write their own scripts for this important use case.

Interval queries are a recurring task in HTS analysis problems, and several libraries now offer solutions for different programming languages, including BEDtools (Quinlan and Hall, 2010; Dale et al., 2011) and IRanges/GenomicRanges (Lawrence et al., 2013). Typically, these methods take two lists of intervals and report overlaps between them. HTSeq uses a different paradigm, namely that one list of intervals is read in and stored in a *GenomicArrayOfSets* object, and then the other intervals are queried one by one, in a loop. This explicit looping can be more intuitive; one example is the read counting problem

discussed above, where split reads, gapped alignments, ambiguous mappings, etc. cause much need for treatment of special cases that is addressed by branching statements within the inner loop.

In conclusion, HTSeq offers a comprehensive solution to facilitate a wide range of programming tasks in the context of HTS data analysis.

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