



# FAST: FAST Analysis of Sequences Toolbox

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## ABSTRACT

FAST (FAST Analysis of Sequences Toolbox), built on BioPerl, provides simple, powerful open source command-line tools to filter, transform, annotate and analyze biological sequence data. Modeled after the GNU (GNU's Not Unix) Textutils such as `grep`, `cut`, and `tr`, FAST tools such as `fasgrep`, `fascut`, and `fastr` are designed for rapid prototyping of expressive bioinformatic workflows in a compact and generic command vocabulary. Compact combinatorial encoding of data workflows with FAST commands can facilitate better documentation and reproducibility of bioinformatic protocols, supporting better transparency in big biological data science. Interface self-consistency and conformity with conventions of GNU, Matlab, Perl, BioPerl, R and GenBank, help make FAST easy to learn. FAST automates numerical, text-based, sequence-based and taxonomic searching, sorting, selection and transformation of sequence records and alignment sites based on indices, ranges, tags and feature annotations, and analytics for composition and codon usage. Automated content- and feature-based extraction of sites and support for molecular population genetic statistics makes FAST useful for molecular evolutionary analysis. FAST is portable, easy to install, and secure, with stable releases posted to CPAN and development on Github. The default data exchange format in FAST is Multi-FastA (specifically, a restriction of BioPerl FastA format). Sanger and Illumina 1.8+ FASTQ formatted files are also supported. The command-line basis of FAST makes it easier for non-programmer biologists to interactively investigate and control biological data at the speed of thought.

**Keywords:** Unix philosophy, MultiFASTA, pipeline, bioinformatic workflow, open source, BioPerl, regular expression, NCBI Taxonomy

## 1 INTRODUCTION

Bioinformatic software for non-programmers is traditionally implemented for user convenience in monolithic applications with Graphical User Interfaces (GUIs) (Smith et al., 1994; Rampp et al., 2006; Librado and Rozas, 2009; Waterhouse et al., 2009; Gouy et al., 2010). However, today, the monolithic application paradigm can be easily outscaled by big biological data, particularly Next Generation

Sequencing (NGS) data at gigabyte and terabyte-scale. Better empowerment of non-programmers for genome-scale analytics has been achieved through web-based genome browser interfaces (**Cunningham et al.**, 2015; **Rosenbloom et al.**, 2015; **Markowitz et al.**, 2014). On the other hand, for smaller datasets, sequence and alignment editor applications encourage manual manipulation of data, which is error-prone and essentially irreproducible. To reduce error and increase reproducibility in the publishing of bioinformatic and biostatistical protocols it is important to facilitate the documentation and automation of data science workflows through scripts and literate programming facilities (**Knuth**, 1984) that both completely document and encode scientific workflows for machine processing of biological data.

Reproducibility in bioinformatics and biostatistics protocols is crucial to maintaining public trust in the value of its investments in high-dimensional analysis of complex biological systems (**Baggerly and Coombes**, 2009; **Hutson**, 2010; **Baggerly and Coombes**, 2011; **Huang and Gottardo**, 2013). In one analysis, only two of 18 published microarray gene-expression analyses were completely reproducible, in part because key analysis steps were made with proprietary closed-source software (**Ioannidis et al.**, 2008). Furthermore, even though analytical errors are a major source of retractions in the scientific literature (**Casadevall et al.**, 2014), peer-review and publication of scientific data processing protocols is generally not yet required to publish scientific studies. Adequate documentation of bioinformatic and biostatistical workflows and open source sharing of code upon publication (**Peng**, 2009) facilitates crowd-sourced verification, correction and extension of code-based analyses (**Barnes**, 2010; **Morin et al.**, 2012), and reuse of software and data to enable more scientific discovery returns from public data (**Peng**, 2011). Review and publication of open data science protocols may also help reduce temptations to overinterpret data and encourage more objectivity in data science (**Boulesteix**, 2010), although perhaps it is expanded computational and statistical literacy and training for all scientists that is the ultimate remedy for these problems (**Morin et al.**, 2012; **Joppa et al.**, 2013).

Web-based open-source workflow suites such as Galaxy (**Blankenberg and Hillman-Jackson**, 2014), Taverna (**Oinn et al.**, 2006) and BioExtract (**Lushbough et al.**, 2011) are a recent innovation in the direction of greater reproducibility in bioinformatics protocols for genome-scale analytics. However, the most powerful, transparent and customizable medium for reproducible bioinformatics work is only available to specialists through programming Application Programming Interfaces (APIs) such as BioPerl and Ensembl (**Yates et al.**, 2015). Both workflow design suites and programming APIs require dedication and time to learn.

There is a need for more software falling between GUIs and APIs, that provides non-programmers greater bioinformatic power and more direct, real-time access to their biological data for interactive and reproducible exploration, control, and analysis. Closer inspection of data and interactive construction and control of data flows makes it so much easier to rapidly prototype error-free workflows. Nipping errors in the bug that can completely confound downstream analyses. The time-tested paradigm in scientific computing for rapid prototyping of reproducible data workflows is the Unix command-line.

In this tradition we present FAST: FAST Analysis Sequences Toolbox, modeled after the standard Unix toolkit (**Peek**, 2001), now called Coreutils. FAST is written in Perl and BioPerl, but its users don't need to know Perl, only Unix. The FAST tools follow the Unix philosophy to "do one thing and do it well" and "write programs to work together." (**Stutz**, 2000). Command-line utilities for bioinformatics such as the EMBOSS package (**Rice et al.**, 2000), the FASTX tools (**Gordon**, 2009) or the scripts that come with BioPerl (**Stajich et al.**, 2002) typically offer suites of tools with simple, well-defined functions that lend themselves to scripting, but are not necessarily designed according to the Unix toolbox philosophy specifically to interoperate through serial composition. Similarly, FaBox is a free and open online server with functions that overlap with FAST tools, but is not designed for serial composition. On the other hand, the Unix toolbox model has been used before in more or less more specialized bioinformatics applications such as the popular SAMTools suite (**Li et al.**, 2009) and in the processing of NMR data (**Delaglio et al.**, 1995).

The FAST tools are written in Perl using BioPerl packages (**Stajich et al.**, 2002). This makes FAST utilities easy to adopt if you are familiar with the Unix toolbox and allows fast sequence analysis even on

Table 1. FAST 1.0 utilities

Tool	Function	Textutil analog	Default element processed
fasgrep	regex selection of records	grep	identifiers
fasfilter	numerical selection of records		identifiers
fastax	taxonomic selection of records		descriptions
fashead	order-based selection of records	head	
fastail	order-based selection of records	tail	
fascut	index-based selection and reordering of data	cut	sequences
fasuniq	record reduction by content and order	uniq	sequences
alncut	selection of sites by content		sequences
gbfalncut	selection of sites by features		sequences
fassort	numerical or text sorting of records	sort	identifiers
fastaxsort	taxonomic sorting of records		identifiers
fastpaste	merging of records	paste	sequences
fastr	character transformations on records	tr	identifiers
fassub	regex substitutions on records		identifiers
faslen	annotate sequence lengths		descriptions
fascomp	annotate monomeric compositions		descriptions
fascodon	annotate codon usage		descriptions
fasxl	annotate biological translations		descriptions
fasrc	annotate reverse complements		descriptions
fasconvert	convert format of records		
gbfcut	emit sequences by regex matching on features	grep	features
alnpi	molecular population genetic statistics		
faswc	tally sequences and characters	wc	sequences

76 large datasets. Extensive documentation has been developed for each FAST utility along with useful error  
77 messages following recommended practice (Seemann, 2013). FAST is free and open source, available to  
78 anyone for re-use, verification and extension. This is in line with the call to make science generally more  
79 accessible, open, and reproducible by other scientists and the public (Groves and Godlee, 2012).

2 DESIGN

80 The Unix textutils paradigm allows users to treat plain-text files as databases in which *records* correspond  
81 to single lines containing *fields* separated by *delimiters* such as commas, tabs, or strings of white-space  
82 characters. FAST extends this paradigm to biological sequence data, allowing users to treat collections of  
83 files of sequence data as databases for complex queries, transformations and analytics. The textutils model  
84 is generalized exactly by FAST because it models sequence record *descriptions* as an ordered collection  
85 of fields (see below).

86 Another design feature of Unix tools that also characterizes the FAST tools is their ability to accept  
87 input not only from one or more files but also from what is called *standard input*, a data-stream supported  
88 by the Unix shell, and to output analogously to *standard output*. It is this facility that allows FAST tools  
89 to be serially composed in Unix *pipelines* that compactly represent an infinite variety of expressive bioin-  
90 formatic workflows. The serial composability of FAST tools is represented in the overview of the project  
91 shown in Figure 1. FAST utilities may be categorized as for selection, transformation, and annotation and  
92 analysis. Utilities in the selection category select sequences or alignment sites based on various criteria.  
93 For example, `fasgrep` selects sequence records by matching regular expressions against identifiers, de-  
94 scriptions, sequences or specified components of descriptions. A full description of all utilities included  
95 in FAST 1.0 is shown in Table 1.

96 The default data exchange format for FAST tools is the universally recognized FastA format (**Lipman**  
 97 **and Pearson**, 1985). While no universal standard exists for this format, for FAST, "FastA format"  
 98 means what is conventionally called "multi-fasta" format of sequence or alignment data, largely as  
 99 implemented in BioPerl in the module `Bio::SeqIO::fasta` (**Stajich et al.**, 2002).

100 In the FAST implementation of FastA format, multiple sequence records may appear in a single file or  
 101 input stream. Sequence data may contain gap characters. The logical elements of a sequence record are  
 102 its *identifier*, its *description* and its *sequence*. The identifier (indicated with `id` in the example below)  
 103 and description (`desc`) together make the *identifier line* of a sequence record, which must begin with the  
 104 sequence record start symbol `>` on a single line. The description begins after the first block of white-space  
 105 on this line (indicated with `<space>`). The *sequence* of a record appears immediately after its identifier  
 106 line and may continue over multiple lines until the next record starts.

107 In FAST, users may specify fields in sequence records using delimiters (indicated by `<delim>`) quite  
 108 generally using perl-style *regular expressions*. FAST uses one-based indexing of fields as indicated in this  
 109 example:

```
110 >seq1-id<space>seq1-desc-field1<delim>seq1-desc-field2<delim>...
111 seq1-sequence
112 seq1-sequence
113 ...
114 seq1-sequence
115 >seq2-id<space>seq2-desc-field1<delim>seq2-desc-field2<delim>...
116 seq2-sequence
117 seq2-sequence
118 ...
119 seq2-sequence
```

120 In FAST, the sequence identifier is thought as the zero<sup>th</sup> field of the identifier line. One-based indexing of  
 121 description fields in FAST is therefore consistent with zero-based indexing in Perl and one-based indexing  
 122 of sequence coordinates, making all indexing consistent and uniform in FAST.

123 Most FAST tools extend the field-based paradigm further by supporting *tagged values* in sequence  
 124 record descriptions. Tagged values are name-value pairs with a format "name=value" as common in Gen-  
 125 eral Feature Format (GFF) used in sequence annotation. Support for tagged values makes it possible to  
 126 operate on sequence records using unordered or heterogeneous annotations in descriptions. Also, many  
 127 FAST tools have an "annotation" option directing them to augment sequence records with their own output  
 128 calculations, vastly expanding the types of operations and queries that FAST can represent.

### 3 IMPLEMENTATION DETAILS AND BENCHMARKING

129 Nearly all FAST utilities process sequence records inline and therefore have linear runtime complexity  
 130 in the number of sequences. Exceptions are `fassort` and `fastail` which both require some paging  
 131 of data into temporary files. We performed benchmarking of FAST tools using randomly generated se-  
 132 quences and the Benchmark v1.15 perl module on a MacBook Pro 2.5 Ghz Intel i7, with 8 Gb of RAM.  
 133 We examined average CPU runtime over 100 replicates, comparing input sizes of 25K, 250K, or 1M se-  
 134 quence records of length 100, 10K, 100K, or 1M bp. Our benchmarking results show that despite data  
 135 paging, `fassort` runtimes scale linearly with input size (fig 2).

136 The BioPerl backend of FAST 1.0 is version 1.6.901 downloaded in January, 2012. `Bio::SeqIO`  
 137 components were updated to version 1.6.923 on June 4, 2014 and some `Bio::Root` components were  
 138 updated on July 10, 2014 (github commit 50f87e9a4d). We introduced a small number of customizations

139 to the BioPerl code-base, primarily to enable the translation of sequences containing gaps. All of the  
140 BioPerl dependencies of FAST are isolated under its own FAST name-space.

141 To help reduce the overall installation footprint of FAST, BioPerl dependencies of FAST scripts were  
142 analyzed with the Cava packager (<http://www.cavapackager.com>).

143 Further implementation details of individual FAST tools follows.

### 3.1 FASGREP

144 Mainly for fine-grained regular expression-based searching and selection of sequence records, `fasgrep`  
145 also supports motif-based sequence selections and general analysis of sequence patterns as represented by  
146 Perl regular expressions. The BioPerl `Bio::Tools::SeqPattern` library supports optional ambiguity  
147 expansion of IUPAC codes for nucleotides and proteins in regular expression arguments. All of the  
148 search and selection utilities in FAST support optional complementation and case-insensitive searching.

### 3.2 FASFILTER

149 `fasfilter` supports precise numerical-based selections of sequence records from numerical data in  
150 identifiers, descriptions, fields or tagged-values in descriptions. Both open, closed and compound ranges  
151 are supported in different syntax.

### 3.3 FASCUT

152 `fascut` supports index-based selections of characters and fields in sequence records allowing repetition,  
153 reordering, variable steps, and reversals. A sequence of selection indices and index-ranges are specified  
154 conventionally by comma-separated lists of integers and integer ranges in Perl-style or Genbank coord-  
155 inate style (“from..to”) in R/Octave-style (“from:to”) or Unix `cut`-style (“from-to”). Negative indices  
156 count backwards from last characters and fields. `fascut` outputs the concatenation of data selections for  
157 each sequence record. Variable step-sizes in index ranges conveniently specify first, second or third codon  
158 positions in codon sequence records, for example.

### 3.4 ALNCUT

159 Content-based selection of sites in alignments including gap-free sites, non-allgap sites, variable or  
160 invariant sites and parsimoniously informative sites, or their set-complements, all with the option of  
161 state-frequency-thresholds applied per site.

### 3.5 GBFCUT

162 Allows annotation-based sequence-extraction from GenBank format sequence files, useful for extracting  
163 all sequences that correspond to sets of genes or other annotated features in genome data.

### 3.6 FASSORT

164 Our implementation of `fassort` handles numerical and textual sorting of records by their components,  
165 including reversals. Pages of data are sorted with optimized routines in Perl `Sort::Key` that if necessary  
166 are written to temporary files and merged with `Sort::MergeSort`.

### 3.7 FASUNIQ

167 With `fasuniq` the user may remove records that are duplicates with respect to a specified component  
168 or field. Like their Unix Coreutil analogs, `fasuniq` only compares subsequent records on input, usually  
169 requiring that its input is sorted first by `fassort`.

### 3.8 FASTAX AND FASTAXSORT

170 Taxonomic searching and sorting of sequence records, when those records are already annotated with  
171 NCBI taxonomic identifiers, is enabled by the FAST tools `fastax` and `fastaxsort` using taxonomic  
172 data from NCBI taxonomy (Benson et al., 2009; Sayers et al., 2009). Taxonomic selections may be  
173 logically negated and/or restricted to valid NCBI taxonomic identifiers. A sample of data from tRNAdb-  
174 CE (Abe et al., 2014), which includes taxonomic names from NCBI Taxonomy, is included with the  
175 package and referred to in the documentation, showing how these utilities may be used.

### 3.9 FASTER AND FASSUB

176 `fastr` handles all character-based transformations of sequence records including transliterations, dele-  
177 tions and “squashing” (deletion of consecutive repeats). Includes support to restrict or remap sequence  
178 data to strict or IUPAC ambiguity alphabets and removal of gap characters from sequencing. `fassub`  
179 allows more arbitrary substitutions on sets of strings matched to Perl regexes, analogous to the Perl `s///`  
180 substitution operator.

### 3.10 FASCOMP, FASXL AND FASCODON

181 Annotation and analytics of compositions, translations, and codon usage frequencies of sequence records  
182 (with start and stop codons counted distinctly, in the last case). All genetic codes included in BioPerl,  
183 ultimately from NCBI Entrez, are supported.

### 3.11 ALNPI

184 `alnpi` outputs molecular population genetic statistics cited in Table 2 for each alignment on input. It can  
185 output a set of statistics for each alignment on input in plain text or L<sup>A</sup>T<sub>E</sub>X format. `alnpi` also supports  
186 sliding window and pairwise analysis of input data. This code computed the sliding window analyses  
187 published in (Ardell et al., 2003). All of the code for these calculations has been reviewed and compared  
188 against calculations produced from DNASP (Librado and Rozas, 2009) as described previously (Ardell,  
189 2004).

## 4 INSTALLATION AND USAGE EXAMPLES

### 4.1 INSTALLATION AND DEPENDENCIES

190 FAST requires a working Perl installation and is distributed through the Comprehensive Perl Archive  
191 Network (CPAN). In a manual install, after download, installation follows standard Perl install proce-  
192 dure: `perl Makefile.PL; make; make test; (sudo) make install`. A small footprint  
193 of BioPerl dependencies has been packaged together in the FAST namespace. Other CPAN dependencies  
194 can be detected and installed by the `cpan` package manager. A fully automated install may on many  
195 systems be initiated by executing `perl -MCPAN -e 'install FAST'`.



**Table 2.** Molecular Population Genetic Statistics in FAST

Statistic	Symbol	Citation
Number of sequences	$n$	
Number of alleles/distinct sequences	$k$	
Number of segregating sites	$S$	
Fraction of segregating sites	$s$	
Average number of pairwise differences	$\Pi$	(Nei and Li, 1979)
Nucleotide Diversity	$\pi$	(Nei and Li, 1979)
Watterson estimator	$\theta_W$	(Watterson, 1975)
Expected number of alleles	$E(K)$	(Ewens, 1972)
Tajima's D	$D$	(Tajima, 1989)
Fu and Li's F	$D^*$	(Fu and Li, 1993)
Fu and Li's F*	$F^*$	(Fu and Li, 1993; Simonsen et al., 1995)
Fu and Li's Eta S	$\eta_S$	(Fu and Li, 1993)
Fu and Li's Eta	$\eta$	(Fu and Li, 1993)

## 4.2 TEST SUITE AND DOCUMENTATION

196 FAST includes rudimentary test suites for each utility, and a FAST Cookbook has been contributed to the  
197 installation package.

## 4.3 SELECTING SEQUENCES BY ENCODED MOTIFS

198 An advantage of the annotation approach in FAST is the ability to select and sort sequences by at-  
199 tributes computed and annotated into data by utilities upstream in the pipeline. For example, to select  
200 protein-coding genes from a file `cds.fas` whose translations contain the *N*-glycosylation amino acid  
201 motif (Kornfeld and Kornfeld, 1985), one could execute:

```
202 fasx1 -a cds.fas | fasgrep -t x10 "N[^P][ST][^P]" | fascut -f 1..-2
```

203 The first command in the pipeline translates each sequence and appends the translation to the description  
204 with the tag “x10” (indicating translation in the zeroth reading frame). The second command in the pipeline  
205 does a regex match using the specified motif pattern on the value of a “name:value” pair in the description  
206 with tag “x10”, hence processing the annotations produced by `fasx1`. The regex argument to `fasgrep` is  
207 quoted to protect the argument from interpretation by the shell. The last command in the pipeline removes  
208 the last field in the description, restoring records as they were before they were annotated by `fasx1`.

## 4.4 SORTING RECORDS BY THIRD CODON POSITION COMPOSITION

209 Another example illustrates the powerful expression of ranges in `fascut`. An optional “by” parameter  
210 in ranges allows increments or decrements in steps larger than one. To extract third-position bases from  
211 codon sequence records, compute and annotate their compositions into record descriptions, ultimately  
212 sorting records by their third-position adenosine contents, do:

```
213 fascut 1:-1:3 cds.fas | fascomp | fassort -nt comp_A
```

## 5 CONCLUDING REMARKS AND FUTURE DIRECTIONS

214 Planned additions in future versions of FAST include `fasrand` and `alnrand` for automated sampling,  
215 permutations and bootstrapping of sequences and sites, respectively, and `fasgo` and `fasgosort` for  
216 selection and sorting of records by Gene Ontology categories (The Gene Ontology Consortium, 2015).

## AVAILABILITY

217 Stable versions of FAST are released through the Comprehensive Perl Archive Network (CPAN) at  
218 <http://search.cpan.org/~dhard/>. Development of FAST is through its GitHub at <https://github.com/tlawrence3/FAST>. For latest news on the FAST project please check the Ardell  
219 Lab homepage at <http://compbio.ucmerced.edu/ardell/software/FAST/>.  
220

## DISCLOSURE/CONFLICT-OF-INTEREST STATEMENT

221 The authors declare that the research was conducted in the absence of any commercial or financial  
222 relationships that could be construed as a potential conflict of interest.

## AUTHOR CONTRIBUTIONS

223 D.H.A. conceived, designed, and wrote much of FAST. T.J.L. contributed major code factorizations and  
224 reorganization and `fastail`. K.T.K. contributed code including `faspaste`, and `fashead`. R.S.L.  
225 contributed an analysis of code dependencies for the FAST installer. P.J.B. tested installation and running  
226 on Windows using Strawberry Perl. All authors, especially D.L.C. and C.J.C., contributed documenta-  
227 tion, testing, and code fixes. K.C.H.A. and D.H.A. wrote the FAST Cookbook. D.H.A. wrote the paper  
228 with major contributions from D.L.C. and T.J.L. All authors made minor contributions to the manuscript,  
229 reviewed the final version of the manuscript and agree to be accountable for its contents.

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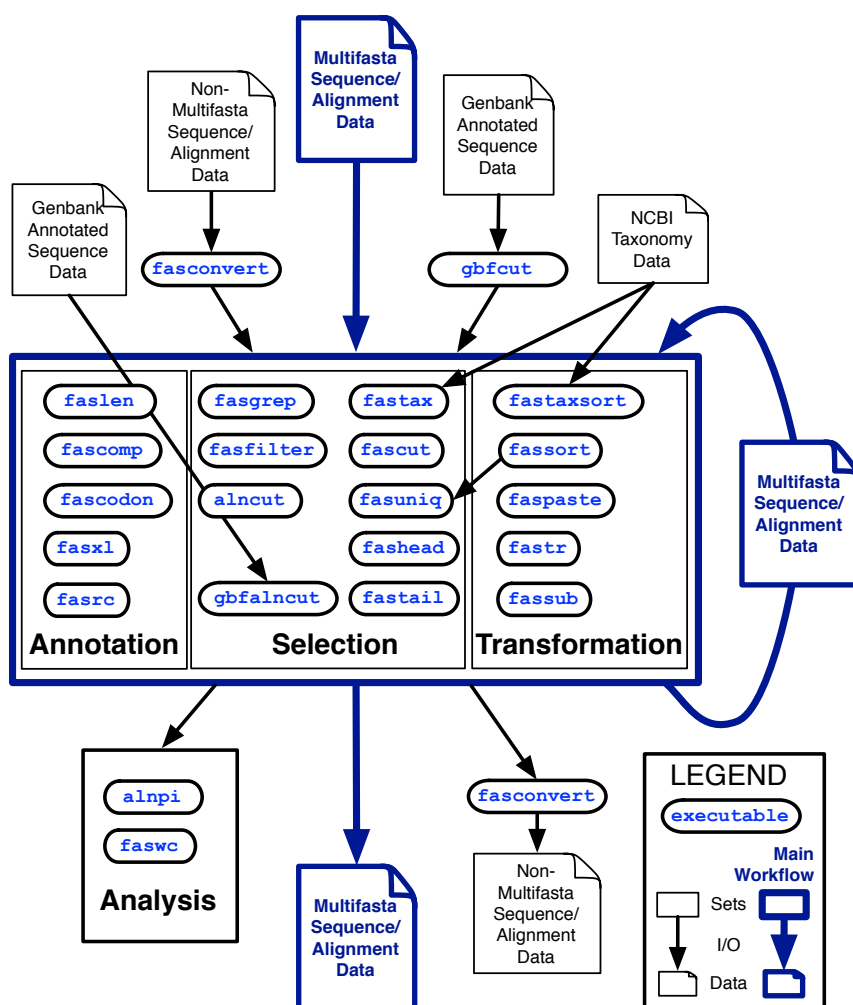
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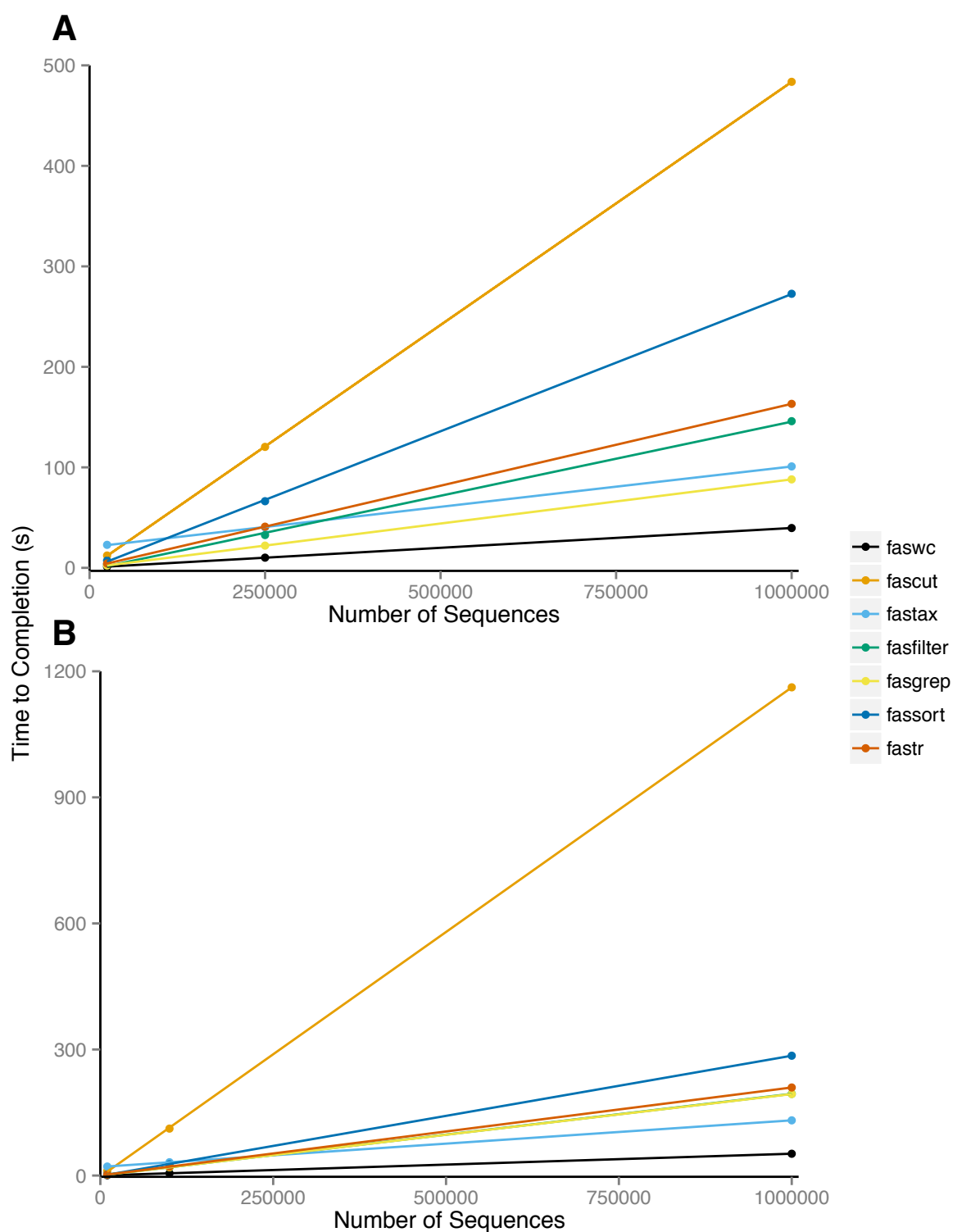
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**Figure 1.** FAST version 1.0 with data and workflow dependencies indicated.

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## FIGURES



**Figure 2.** Average processor time of 100 repetitions required to complete analysis using indicated utility. Utilities were run on six datasets consisting of (a) 25000, 250000, and 1000000 100bp sequences and (b) 10000, 100000, and 1000000 1000bp sequences.