

Resource Summary Report

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FAST Analysis of Sequences Toolbox

RRID:SCR_024074

Type: Tool

Proper Citation

FAST Analysis of Sequences Toolbox (RRID:SCR_024074)

Resource Information

URL: <https://metacpan.org/dist/FAST>

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Description: Software Fast Analysis of Sequences Toolbox (FAST) is a set of UNIX utilities (for example fasgrep, fascut, fashead and fastr) that extends the UNIX toolbox paradigm to bioinformatic sequence records. FAST workflows are designed for serial processing of flatfile biological sequence record databases per-sequence, rather than per-line, through UNIX pipelines. The default data exchange format is multifasta (specifically, a restriction of BioPerl FastA format). FASTQ format is supported. FAST is designed for learnability, interoperability, interface consistency, rapid prototyping, fine-tuned control, and reproducibility. FAST tools expose the power of Perl and BioPerl to users in an easy-to-learn command-line paradigm.

Abbreviations: FAST

Synonyms: libfast-perl, Fast Analysis of Sequences Toolbox, FAST - FAST Analysis of Sequences Toolbox, fast

Resource Type: software toolkit, software resource

Keywords: Analysis of sequences, UNIX utilities, UNIX toolbox paradigm to bioinformatic sequence records, serial processing, flatfile biological sequence record databases per-sequence, FASTQ format, learnability, interoperability, interface consistency, rapid prototyping, fine-tuned control, reproducibility

Availability: Free, Available for download, Freely available,

Resource Name: FAST Analysis of Sequences Toolbox

Resource ID: SCR_024074

Old URLs: <https://sources.debian.org/src/libfast-perl/>

License: perl_5

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Record Last Update: 20260729T044602+0000

Ratings and Alerts

No rating or validation information has been found for FAST Analysis of Sequences Toolbox.

No alerts have been found for FAST Analysis of Sequences Toolbox.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.