

Overview

Download

Browse source

Issue tracker

Documentation

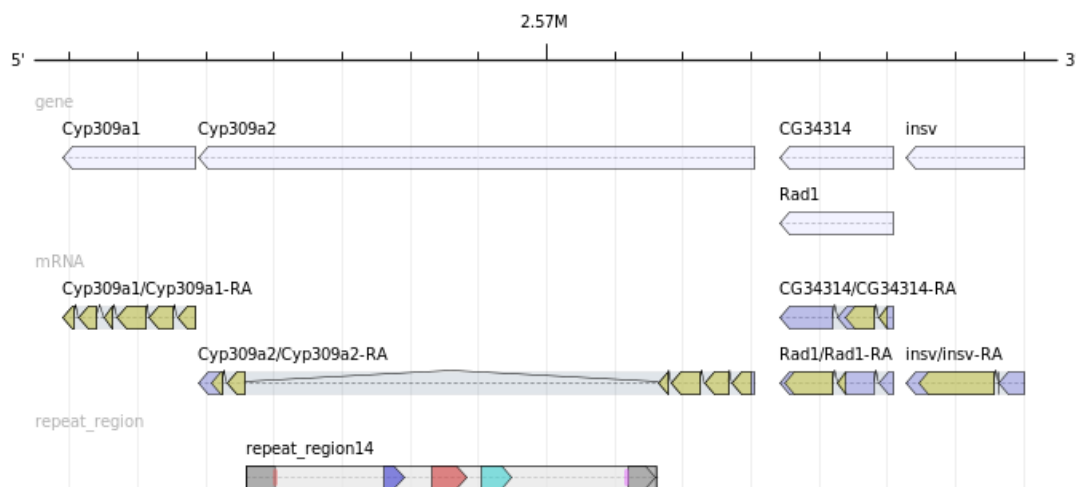
AnnotationSketch

GFF3 validator

License

GenomeTools

The versatile open source genome analysis software



The *GenomeTools* genome analysis system is a [free](#) collection of bioinformatics [tools](#) (in the realm of genome informatics) combined into a single binary named *gt*. It is based on a C library named "libgenometools" which consists of several modules.

If you are interested in gene prediction, have a look at [GenomeThreader](#).

Platforms

GenomeTools has been designed to run on every [POSIX](#) compliant [UNIX](#) system. For example, Linux, Mac OS X, and OpenBSD. A [Windows version](#) which requires a [Cygwin](#) installation is available. Please report problems with it to our [mailing list](#).

GenomeTools publication

G. Gremme, S. Steinbiss and S. Kurtz.

GenomeTools: a comprehensive software library for efficient processing of structured genome annotations.

[IEEE/ACM Transactions on Computational Biology and Bioinformatics 2013, 10\(3\):645–656](#)

Published software in *GenomeTools*

The *GenomeTools* distribution includes several published software tools:

- [LTRharvest](#), an efficient and flexible software tool for *de novo* detection of LTR retrotransposons.
D. Ellinghaus, S. Kurtz, and U. Willhoeft.
LTRharvest, a efficient and flexible software for *de novo* detection of LTR retrotransposons.
[BMC Bioinformatics 2008, 9:18](#)
- [Tallymer](#), a collection of flexible and memory-efficient programs for *k*-mer counting and indexing of large sequence sets.
S. Kurtz, A. Narechania, J.C. Stein, and D. Ware.
A new method to compute K-mer frequencies and its application to annotate large repetitive plant genomes.
[BMC Genomics 2008, 9:517](#)

- **uniquesub**, a program for computing minimum unique substrings.
S. Gräf, F.G.G. Nielsen, S. Kurtz, M.A. Huynen, E. Birney, H. Stunnenberg, and P. Flícek.
Optimized design and assessment of whole genome tiling arrays.
[Bioinformatics 2007, 23\(13\):i195-i204](#)
- **AnnotationSketch**, a library for drawing genome annotations.
S. Steinbiss, G. Gremme, C. Schärfer, M. Mader and S. Kurtz.
AnnotationSketch: a genome annotation drawing library.
[Bioinformatics 2009, 25\(4\):533-534](#)
- **LTRdigest**, a software tool for automated annotation of internal features of LTR retrotransposons.
S. Steinbiss, U. Willhoeft, G. Gremme and S. Kurtz.
Fine-grained annotation and classification of *de novo* predicted LTR retrotransposons.
[Nucleic Acids Research 2009, 37\(21\):7002-7013](#)
- **MetaGenomeThreader**, a software to predict genes, such as PCS's (predicted coding sequences) in sequences of metagenome projects.
D.J. Schmitz-Hübsch and S. Kurtz.
MetaGenomeThreader: A software tool for predicting genes in DNA-sequences of metagenome projects.
In R. Daniel and W. Streit (Eds.), *Metagenomics. Methods in Molecular Biology*, 325-338, Humana Press, Totowa, NJ, ISBN 978-1-60761-822-5
- **GtEncseq**, a compressed biosequence representation with many features.
S. Steinbiss and S. Kurtz.
A New Efficient Data Structure for Storage and Retrieval of Multiple Biosequences.
[IEEE/ACM Transactions on Computational Biology and Bioinformatics 2012, 9\(2\):345-357](#)
- **Readjoinder**, a sequence assembler based on the assembly string graph framework.
G. Gonnella and S. Kurtz.
Readjoinder: a fast and memory efficient string graph-based sequence assembler.
[BMC Bioinformatics 2012, 13:82](#)

The following software tools are based on the *GenomeTools* library:

- **GenomeThreader**, a software tool to compute eukaryote gene structure predictions.
G. Gremme, V. Brendel, M.E. Sparks, and S. Kurtz.
Engineering a software tool for gene structure prediction in higher organisms.
[Information and Software Technology 2005, 47\(15\):965-978](#)
- **FISH Oracle**, a web server for visualizing cancer genomics data.
M. Mader, R. Simon, S. Steinbiss and S. Kurtz.
FISH Oracle: a web server for flexible visualization of DNA copy number data in a genomic context.
[Journal of Clinical Bioinformatics 2011, 1:20](#)
- **ParsEval**, a tool for comparing genome annotations.
D.S. Standage and V.P. Brendel.
ParsEval: parallel comparison and analysis of gene structure annotations.
[BMC Bioinformatics 2012, 13:187](#)
- **LTRsift**, a graphical interface for working with LTR retrotransposon predictions.
S. Steinbiss, S. Kastens and S. Kurtz.
LTRsift: a graphical user interface for semi-automatic classification and postprocessing of *de novo* detected LTR retrotransposons.
[Mobile DNA 2012, 3:18](#)
- **FISH Oracle 2**, a web-based software tool for the integrative analysis of cancer genomics data.
M. Mader, R. Simon, and S. Kurtz.
FISH Oracle 2: a web server for integrative visualization of genomic data in cancer research.
[Journal of Clinical Bioinformatics 2014, 4:5](#)

Contact

The *GenomeTools* are being developed by:

Gordon Gremme, Sascha Steinbiss, Stefan Kurtz and [others](#)

[Genome Informatics Research Group](#)

[Center for Bioinformatics, University of Hamburg](#)

