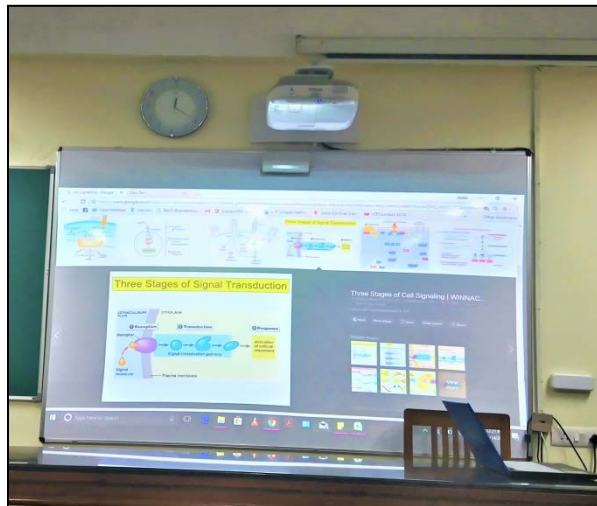
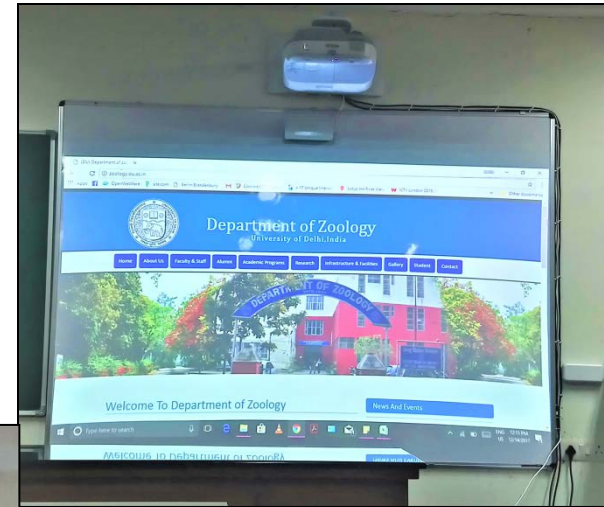


Smart Boards in
Classrooms
Department of Zoology







ABySS: A parallel assembler for short read sequence data

BC Cancer Agency
CARE + RESEARCH
An agency of the Provincial Health Services Authority

Research Centre
Canada's Michael Smith Genome Sciences Centre

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- Adapter Trimming for Small RNA Sequencing
- Sealer
- LINKS
- Konnector
- Spark
- TASR
- XpressAlign: FPGA Short Read Aligner

ABySS

Assembly By Short Sequences - a de novo, parallel, paired-end sequence assembler

Project Description

ABySS v2

ABySS is a *de novo*, parallel, paired-end sequence assembler that is designed for short reads. The single-processor version is useful for assembling genomes up to 100 Mbases in size. The parallel version is implemented using MPI and is capable of assembling larger genomes.

To assemble transcriptome data, see [Trans-ABySS](#).

Awards

June 2015, 12th [BC]² Conference in Basel, Switzerland: ABySS was the winner of the

Project Resources

- Releases
- Documentation
- Issue tracker
- Support
- Contact address

Project owner: Anthony Raymond

Assembly Algorithm

- Partitioning Read Space
- Aggregation Generation
- Trimming
- Builds Puppets

UGENE is a free bioinformatics software for multiple sequence alignment, genome sequencing data analysis, amino acid sequence visualization.

Unipro UGENE

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Unipro UGENE 1.28

October, 2017

UGENE is free open-source cross-platform bioinformatics software

It works perfectly on Windows, Mac OS and Linux and requires only a few clicks to install

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Cite Us

Okonechnikov K, Golosova O, Fursov M, the UGENE team. **Unipro UGENE: a unified bioinformatics toolkit.** *Bioinformatics* 2012 28: 1166-1167. doi:10.1093/bioinformatics/bts091

Support and Services

Feel free to contact us if you need [technical support](#).

Free Resources

- Browse the documentation

News

November 20th, 2017
UGENE 1.28.1 has been released

November 5th, 2014
Article about NGS pipelines in UGENE

Podcast

Ep51: What's new in UGENE 1.27?
Ep50: What's new in UGENE 1.20 & 1.21?

Board

>Feature Requests: Donate a little bit
>Feature Requests: Re: DNA-Star file conversion

Issues

PhyloPhlAn is a computational pipeline for reconstructing highly accurate and resolved phylogenetic trees based on whole-genome sequence information.

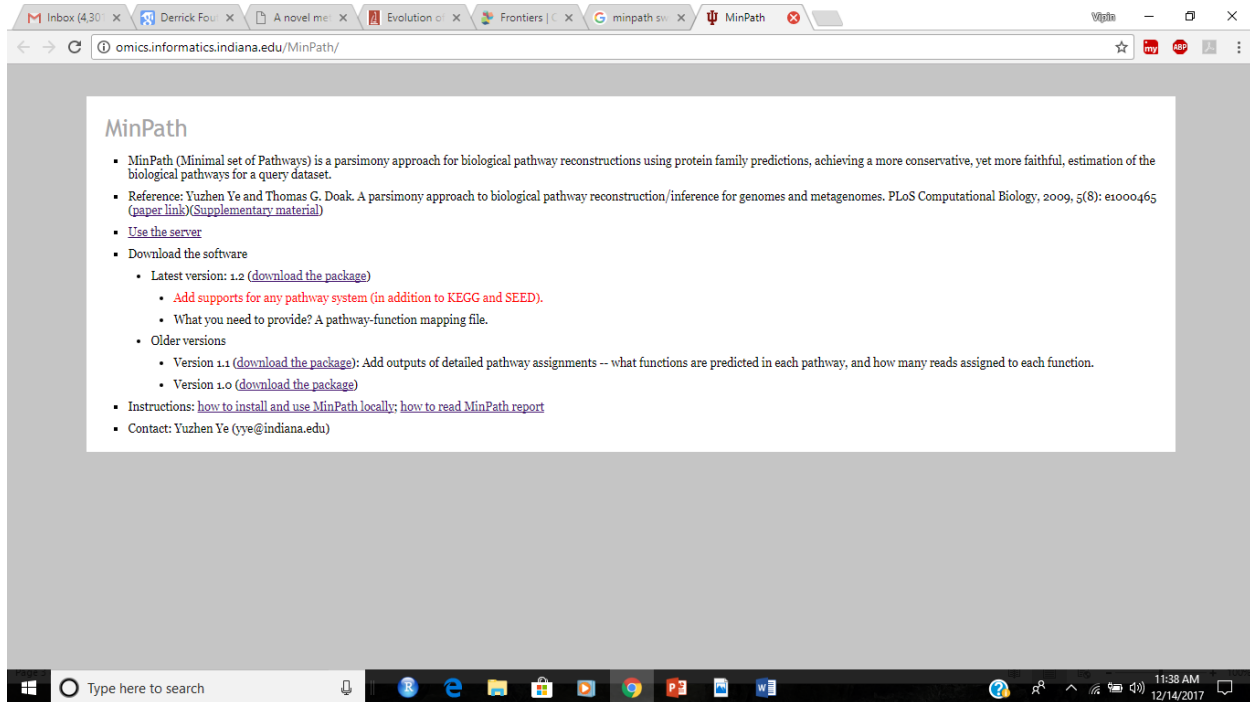
The screenshot shows the homepage of the PhyloPhlAn website. The browser address bar displays the URL <https://huttenhower.sph.harvard.edu/phylophlan>. The website header features the logo of The Huttenhower Lab, which includes a stylized 'H' and 'L' with a DNA double helix. Below the logo, the text reads "The Huttenhower Lab" and "Department of Biostatistics, Harvard T.H. Chan School of Public Health". A navigation menu contains links for HOME, RESEARCH, TEACHING, DOCUMENTATION, PEOPLE, CONTACT, and PUBLICATIONS. The main content area has a breadcrumb trail "Home / PhyloPhlAn" followed by the title "PhyloPhlAn" in a large blue font. Below the title is a subtitle: "PhyloPhlAn: microbial Tree of Life using 400 universal proteins". A paragraph of text describes the pipeline: "PhyloPhlAn is a computational pipeline for reconstructing highly accurate and resolved phylogenetic trees based on whole-genome sequence information. The pipeline is scalable to thousands of genomes and uses the most conserved 400 proteins for extracting the phylogenetic signal. PhyloPhlAn also implements taxonomic curation, estimation, and insertion operations." Below this is a section titled "The main features of PhyloPhlAn are:" followed by a bulleted list:

- completely automatic, as the user needs only to provide the (unannotated) protein sequences of the input genomes (as multifasta files of peptides – not nucleotides)
- very high topological accuracy and resolution because of the use of up to 400 previously identified most conserved proteins
- the possibility of integrating new genomes in the already reconstructed most comprehensive tree of life (3,171 microbial genomes)
- taxonomy estimation for the newly inserted genomes
- taxonomic curation for the produced phylogenetic trees

KAAS. KAAS (KEGG Automatic Annotation Server) provides functional annotation of genes by BLAST or GHOST comparisons against the manually curated **KEGG GENES** database.

The screenshot shows the KAAS (KEGG Automatic Annotation Server) website. The browser address bar displays the URL www.genome.jp/tools/kaas/. The website header features the KAAS logo, which is a stylized 'K' and 'A' with a DNA double helix. Below the logo, the text reads "KAAS - KEGG Automatic Annotation Server" and "for ortholog assignment and pathway mapping". The main content area is divided into two columns. The left column is titled "Request" and contains sections for "About KAAS", "Complete or Draft Genome", "Partial Genome", and "Metagenomes". The right column is titled "Example of Results" and contains sections for "KO assignment" and "KEGG pathway mapping". The "KO assignment" section shows a list of query genes and their corresponding KEGG Orthology (KO) assignments. The "KEGG pathway mapping" section shows a diagram of a metabolic pathway with various enzymes and metabolites.

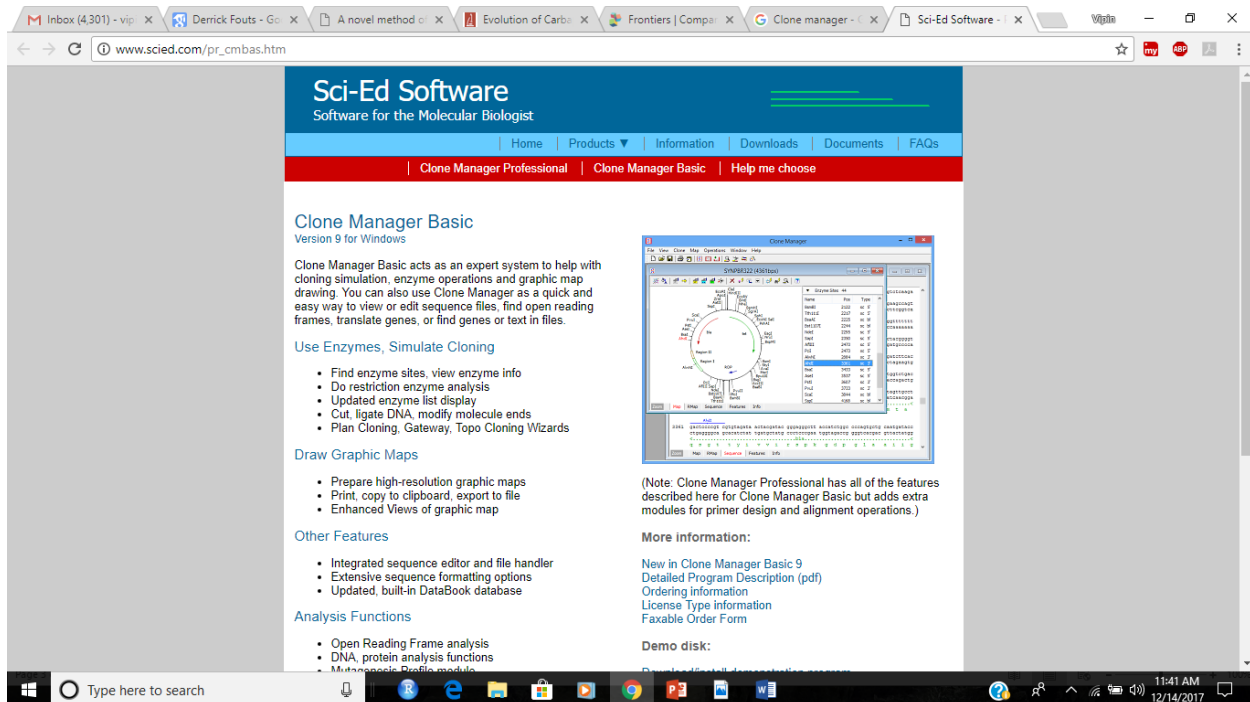
MinPath (Minimal set of Pathways) is a parsimony approach for biological pathway reconstructions using protein family



MinPath

- MinPath (Minimal set of Pathways) is a parsimony approach for biological pathway reconstructions using protein family predictions, achieving a more conservative, yet more faithful, estimation of the biological pathways for a query dataset.
- Reference: Yuzhen Ye and Thomas G. Doak. A parsimony approach to biological pathway reconstruction/inference for genomes and metagenomes. PLoS Computational Biology, 2009, 5(8): e1000465 ([paper link](#))([Supplementary material](#))
- [Use the server](#)
- Download the software
 - Latest version: 1.2 ([download the package](#))
 - Add supports for any pathway system (in addition to KEGG and SEED).
 - What you need to provide? A pathway-function mapping file.
 - Older versions
 - Version 1.1 ([download the package](#)): Add outputs of detailed pathway assignments -- what functions are predicted in each pathway, and how many reads assigned to each function.
 - Version 1.0 ([download the package](#))
- Instructions: [how to install and use MinPath locally](#); [how to read MinPath report](#)
- Contact: Yuzhen Ye (yze@indiana.edu)

Clone manager



Sci-Ed Software
Software for the Molecular Biologist

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Clone Manager Basic

Version 9 for Windows

Clone Manager Basic acts as an expert system to help with cloning simulation, enzyme operations and graphic map drawing. You can also use Clone Manager as a quick and easy way to view or edit sequence files, find open reading frames, translate genes, or find genes or text in files.

Use Enzymes, Simulate Cloning

- Find enzyme sites, view enzyme info
- Do restriction enzyme analysis
- Updated enzyme list display
- Cut, ligate DNA, modify molecule ends
- Plan Cloning, Gateway, Topo Cloning Wizards

Draw Graphic Maps

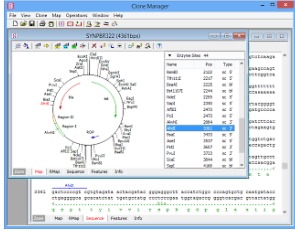
- Prepare high-resolution graphic maps
- Print, copy to clipboard, export to file
- Enhanced Views of graphic map

Other Features

- Integrated sequence editor and file handler
- Extensive sequence formatting options
- Updated, built-in DataBook database

Analysis Functions

- Open Reading Frame analysis
- DNA, protein analysis functions
- [Metagenomic Profile module](#)



Name	Site	Type	Restriction
BamHI	GGATCC	HF	GGATCC
BclI	TGATCA	HF	TGATCA
BglII	AATCTG	HF	AATCTG
BglIII	AGATCT	HF	AGATCT
BlnI	ATATAT	HF	ATATAT
BlnII	ATATAT	HF	ATATAT
BlnIII	ATATAT	HF	ATATAT
BlnIV	ATATAT	HF	ATATAT
BlnV	ATATAT	HF	ATATAT
BlnVI	ATATAT	HF	ATATAT
BlnVII	ATATAT	HF	ATATAT
BlnVIII	ATATAT	HF	ATATAT
BlnIX	ATATAT	HF	ATATAT
BlnX	ATATAT	HF	ATATAT
BlnXI	ATATAT	HF	ATATAT
BlnXII	ATATAT	HF	ATATAT
BlnXIII	ATATAT	HF	ATATAT
BlnXIV	ATATAT	HF	ATATAT
BlnXV	ATATAT	HF	ATATAT
BlnXVI	ATATAT	HF	ATATAT
BlnXVII	ATATAT	HF	ATATAT
BlnXVIII	ATATAT	HF	ATATAT
BlnXIX	ATATAT	HF	ATATAT
BlnXX	ATATAT	HF	ATATAT

(Note: Clone Manager Professional has all of the features described here for Clone Manager Basic but adds extra modules for primer design and alignment operations.)

More information:

- New in Clone Manager Basic 9
- Detailed Program Description (pdf)
- Ordering information
- License Type Information
- Faxable Order Form

Demo disk:

Multiple Sequence Alignment by CLUSTALW

The screenshot shows the web interface for Multiple Sequence Alignment by CLUSTALW. The browser address bar shows the URL www.genome.jp/tools-bin/cluster. The page has a navigation bar with tabs for ETE3, MAFFT, CLUSTALW (selected), and PRRN. The main content area is titled "Multiple Sequence Alignment by CLUSTALW" and includes a "General Setting Parameters" section with options for Output Format (CLUSTAL), Pairwise Alignment (FAST/APPROXIMATE or SLOW/ACCURATE), and Enter your sequences (with labels) below (copy & paste) for PROTEIN or DNA. There is a text input field for sequences and a "Choose File" button for uploading a file. Below this is a "More Detail Parameters..." section with Pairwise Alignment Parameters for FAST/APPROXIMATE (K-tuple(word) size: 1, Window size: 5, Gap Penalty: 3, Number of Top Diagonals: 5, Scoring Method: PERCENT) and SLOW/ACCURATE. The Windows taskbar at the bottom shows the time as 11:43 AM on 12/14/2017.

Primer-BLAST: Finding primers specific to your PCR template

The screenshot shows the web interface for Primer-BLAST. The browser address bar shows the URL <https://www.ncbi.nlm.nih.gov/tools/primer-blast/>. The page title is "Primer-BLAST: Finding primers specific to your PCR template (using Primer3 and BLAST)". The interface is divided into several sections: "PCR Template" with a text input field for the sequence and a "Range" section for Forward and Reverse primers; "Primer Parameters" with fields for PCR product size (70-1000), # of primers to return (10), and Primer melting temperatures (Tm) (57.0-63.0); and "Exon/intron selection" with options for Exon junction span, Exon junction match, and Intron inclusion. The Windows taskbar at the bottom shows the time as 11:44 AM on 12/14/2017.