

Top 20 Useful Bioinformatic Tools

Promoter Scan

功能：启动子预测

网址：<https://www-bimas.cit.nih.gov/molbio/proscan/>



ORF Finder

功能：ORF预测

网址：<https://www.ncbi.nlm.nih.gov/orffinder/>



NCBI-BLAST

功能：序列比对


网址：<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)


QuickBLASTP
 Try QuickBLASTP for a fast protein search of nr.
 Tue, 23 May 2017 13:00:00 EST [More BLAST news...](#)

Web BLAST



Nucleotide BLAST
nucleotide & nucleotide

blastx
translated nucleotide & protein



Protein BLAST
protein & protein

MUSCLE

功能：运行速度比较快的多序列比对

网址：<http://www.ebi.ac.uk/Tools/msa/muscle/#>

MUSCLE

Input form
Web services
Help & Documentation
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Tools > Multiple Sequence Alignment > MUSCLE

Multiple Sequence Alignment

MUSCLE stands for **M**ultiple **S**equence **C**omparison by **L**og-**E**xpectation. MUSCLE is claimed to achieve both better average accuracy and better speed than [ClustalW2](#) or [T-Coffee](#), depending on the chosen options.

Important note: This tool can align up to 500 sequences or a maximum file size of 1 MB.

STEP 1 - Enter your input sequences

Enter or paste a set of sequences in any supported format:

Clustal Omega

功能：DNA、RNA、蛋白的多序列比对

网址：<http://www.ebi.ac.uk/Tools/msa/clustalo/>

Clustal Omega

Input form
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Tools > Multiple Sequence Alignment > Clustal Omega

Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments between **three or more** sequences. For the alignment of two sequences please instead use our [pairwise sequence alignment tools](#).

Important note: This tool can align up to 4000 sequences or a maximum file size of 4 MB.

ClustalW2

功能：应用较广泛的多序列比对

网址：<http://www.ebi.ac.uk/Tools/msa/clustalw2/>

ClustalW2

[Input form](#) | [Web services](#) | [Help & Documentation](#)

[Feedback](#) | [Share](#)

Tools > Multiple Sequence Alignment > ClustalW2

ClustalW2 is a general purpose DNA or protein multiple sequence alignment program for **three or more** sequences. For the alignment of two sequences please instead use our [pairwise sequence alignment tools](#).

Please Note

The ClustalW2 services have been retired. To access similar services, please visit the [Multiple Sequence Alignment tools](#) page. For protein alignments we recommend [Clustal Omega](#). For DNA alignments we recommend trying [MUSCLE](#) or [MAFFT](#). If you have any questions/concerns please contact us via the [feedback link](#) above.

T-Coffee

功能：准确度高,速度慢的多序列比对

网址：<http://www.ebi.ac.uk/Tools/msa/tcoffee/>

T-Coffee

[Input form](#) | [Web services](#) | [Help & Documentation](#)

[Feedback](#) | [Share](#)

Tools > Multiple Sequence Alignment > T-Coffee

Multiple Sequence Alignment

T-Coffee is a multiple sequence alignment program. Its main characteristic is that it will allow you to combine results obtained with several alignment methods.

Important note: This tool can align up to 500 sequences or a maximum file size of 1 MB.

SimiTriX-SimiTetra

功能：多序列比对相似性展示

网址：<http://cotton.hzau.edu.cn/EN/tools/BioERCP/simitrix.php>

G C G I *SimiTriX-SimiTetra*
Group of Cotton Genetic Improvement

[Home](#) | [About](#) | [Blast](#) | [SimiTriX](#) | [SimiTetra](#) | [Help](#)

Control Panel

Input file
Input the value file directly
选择文件 | 未选择任何文件
提交

Dataset Name

Value Cutoff

Canvas Surface

Color Range

Show Information of selected points +

Show Result of Stats +

Venn图

功能：绘制Venn图

网址：<http://www.biovenn.nl/index.php>

Set Image Parameters

title	<input type="text" value="BioVenn"/>	Courier New bold	24	Black
subtitle	<input type="text" value="(C) 2007 - 2017 Tim Hulsen"/>	Courier New bold	18	Black
x title	<input type="text" value="ID Set X"/>	Courier New bold	12	Black
y title	<input type="text" value="ID Set Y"/>	Courier New bold	12	Black
z title	<input type="text" value="ID Set Z"/>	Courier New bold	12	Black

print numbers
 absolute nrs
 percentages

ID Set X	<input type="text"/>	<- Copy and paste your IDs .. Or input a file with IDs: <input type="button" value="选择文件"/> 未选择任何文件	Red
ID Set Y	<input type="text"/>	<- Copy and paste your IDs .. Or input a file with IDs: <input type="button" value="选择文件"/> 未选择任何文件	Lime
ID Set Z	<input type="text"/>	<- Copy and paste your IDs .. Or input a file with IDs: <input type="button" value="选择文件"/> 未选择任何文件	Blue

ID Type:
 map Affymetrix/EntrezGene IDs to Ensembl Gene IDs

background transparency background color

image width image height

(Click [here](#) to see an example)

Venn图

功能：绘制Venn图

网址：http://bioinformatics.psb.ugent.be/cgi-bin/liste/Venn/calculate_venn.html

BIOINFORMATICS & EVOLUTIONARY GENOMICS

PEOPLE - RESEARCH - GENOMES - PUBLICATIONS - SOFTWARE - JOBS - LIBRES - INTRANET - PRESS



Calculate and draw custom Venn diagrams



Venn图

功能：绘制Venn图

网址：<http://bioinfogp.cnb.csic.es/tools/venny/index.html>

1. Paste up to four lists. One element per row ([example](#)),
2. Click the numbers to see the results,
3. Right-click the figure to view and save it
(actual size in pixels: 1280x1280)

UPPERCASE lowercase ←cannot be undone!

List 1 0

[clear](#)

List 2 0

[clear](#)

List 3 0

[clear](#)

List 4 0

[clear](#)

WEGO

功能：绘制GO注释结果图

网址：<http://wego.genomics.org.cn/cgi-bin/wego/index.pl>

BGI WEGO Web Gene Ontology Annotation Plotting

Introduction:

The GO (Gene Ontology) project began as the collaboration of Flybase, Saccharomyces Genome Database (SGD) and Mouse Genome Base. And now it has gone beyond what it used to be. There are so many GO resources and tools that help biologists explore the depth of gene analysis, from several genes to large-scale.

WEGO (Web Gene Ontology Annotation Plot) is a useful tool for plotting GO annotation results. It has been widely used in many important biological research projects, such as the rice genome project [Yu, J. et al. Science 296, 79-92 (2002); Yu, J. et al. PLoS Biol 3, e38 (2005)] and the silkworm genome project [Xu, Q. et al. Science 306, 1937-40 (2004)]. It has become one of the daily tools for downstream gene annotation analysis, especially when performing comparative genomics tasks. WEGO along with two other tools, namely External to GO Query and GO Archive Query, are freely available for all users. Any suggestions are welcome at wego@genomics.org.cn. Here is a sample output generated by WEGO (Fig. 1).

There are three steps to work with WEGO. The first is to upload annotation results. The input file(s) can be in WEGO native format, or if you are using InterProScan as the annotation tool, the result(s) could be used directly. We support InterProScan text, raw and XML output formats as the input format of WEGO. Then, you will be redirected to a webpage with hierarchical GO tree in which all the GO terms contained in the files uploaded are included. You could choose any GO terms interested at this page to display in the output histogram. The last step is figure setting, such as the figure caption, histogram color(s) and legend description. Currently, WEGO support SVG, PNG, PostScript, EPS and GIF as output graph format. You can also get the results by our feedback Email.

Fig 1. The sample figure of WEGO output, from the rice genome paper published on science.

CIRCOS

功能：绘制圈图

网址：<http://mkweb.bcgsc.ca/tableviewer/visualize/>



20 imperatives of information design — BioVis 2012

visualize settings samples archive about

→ 0 . READ SLOGAN BADGES

→ 1 . CHECK DATA FORMAT

Before uploading a data file, check the [samples gallery](#) to make sure that your data format is compatible.

→ 6 . WHAT IS THIS?

The Circos table viewer uses the [Circos](#) application to turn data tables into chord diagrams.

	A	B	C	D	E	F	G
A	105	450	92	94	5	301	195
B	20	46	78	33	53	28	83
C	118	553	94	317	25	89	287
D	100	18	108	104	105	25	173
H	23	83	123	342	98	40	205
I	173	428	103	325	82	215	23
J	305	173	138	49	81	258	207

into circularly composited visualizations like this

CIRCexplorer

功能：进行circRNA分析

网址：<http://circexplorer2.readthedocs.io/en/latest/>

iPath

功能：进行可视化通路图在线分析

网址：<http://pathways.embl.de/>

Select the desired version by clicking the map icons below:

iPath v2: the main interface

The default version of iPath comes with 3 overview pathways maps based on KEGG data:

- Metabolic pathways
- Regulatory pathways
- Biosynthesis of secondary metabolites

iPath v1: original version

This is the initial interactive Pathways Explorer version, which contains only the original version of the metabolic pathways overview map.

iMyc: Mycoplasma pneumoniae map

Hand curated map showing an overview of *M. pneumoniae* metabolism. Currently still using the iPath version 1 interactive interface.

RAP

功能：在线分析RNA-seq

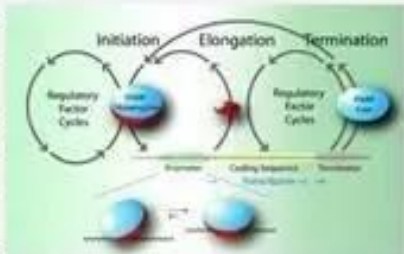
网址：<https://bioinformatics.cineca.it/rap/>

RAP

RAP: RNA-Seq Analysis Pipeline

RNA-Seq technology is becoming widely used in various transcriptomics studies; however, analyzing and interpreting the RNA-Seq data face serious challenges due to transcriptome complexity. A complete RNA-seq analysis involves several steps and the data can be investigated under many points of view (gene and transcript expression, differential expression, alternative splicing, polyA signals, fusion transcripts, etc.)

RAP is a web tool that performs a quite complete and customizable RNA-Seq pipeline and provides an easy and intuitive access through a web interface to intermediate and final results. The main aim of RAP is to provide to users a RNA-Seq pipeline without any installation and IT requirements. The web interface provides an easy and intuitive access for data submission and a user-friendly browsing facility of results. Users can access through RAP to several RNA-Seq algorithms, each integrated with other to maximize the overall quality and quantity of results.



The diagram illustrates the RNA-Seq process. It shows a linear sequence of events: Initiation, Elongation, and Termination. In the Initiation phase, a Regulatory Factor Cycle (represented by a blue and red sphere) binds to a promoter region, leading to the recruitment of RNA polymerase II. In the Elongation phase, RNA polymerase II moves along the DNA template, synthesizing an RNA transcript. In the Termination phase, the RNA transcript is released, and the Regulatory Factor Cycle is recycled. The diagram also shows a 'Coding sequence' and 'Termination' signal on the DNA template.

AUGUSTUS

功能：基因外显子内含子，UTR,注释

网址：<http://bioinf.uni-greifswald.de/webaugustus/prediction/create>



Gene Prediction with AUGUSTUS

Navigation for: [Submit Prediction](#)

- AUGUSTUS Web Server Navigation**
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- [About AUGUSTUS](#)
- [Accuracy](#)
- [Training Tutorial](#)
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- Other AUGUSTUS Resources**
- [AUGUSTUS Wiki](#)
- [AUGUSTUS Forum](#)

Data Input for Running AUGUSTUS

Use this form to submit your data for running AUGUSTUS on new genomic data with already available pre-trained parameters.

Please read the [prediction tutorial](#) before submitting a job for the first time. Example data for this form is available [here](#). You may also use the button below to insert sample data. Please note that you will always need to enter the verification string at the bottom of the page, yourself, in order to submit a job!

Current problem: Regrettably, our server is currently connected to the internet via a rather unreliable connection. This may cause connection timeouts (caused by server side) when uploading big files. Please use the web link upload option, instead, if you experience such problems. We apologize for the inconvenience!

[Fill in Sample Data](#)

We recommend that you specify an **E-mail address**.

E-mail [Help](#)

You must **either** upload a *.tar.gz archive with AUGUSTUS species parameters from your computer **or** specify a project identifier: [Help](#)

AUGUSTUS species parameters *

Upload an archive file (max. 100 MB):

[选择文件](#) 未选择任何文件

[Help](#)

GSDS

功能：基因外显子内含子，UTR,domain等区域特征展示

网址：<http://gsds.cbi.pku.edu.cn/>

The screenshot shows the GSDS 2.0 Gene Structure Display Server interface. At the top, there is a header with the logo and navigation links: Home | Help | About || Links: PlantRegMap. Below the header, there is a section for "Gene Features" with a dropdown menu set to "BED". A text area is provided for "Input features in BED format" with an "Example" button. Below this, there is a section for "Other Features to Display" with a dropdown menu set to "SVG". At the bottom, there are "Reset" and "Submit" buttons.