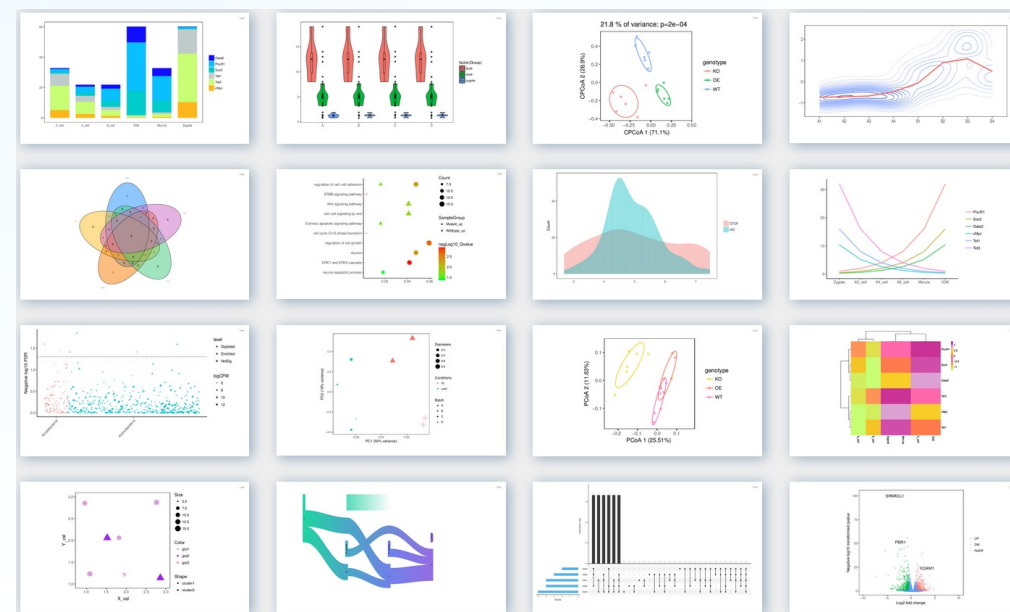
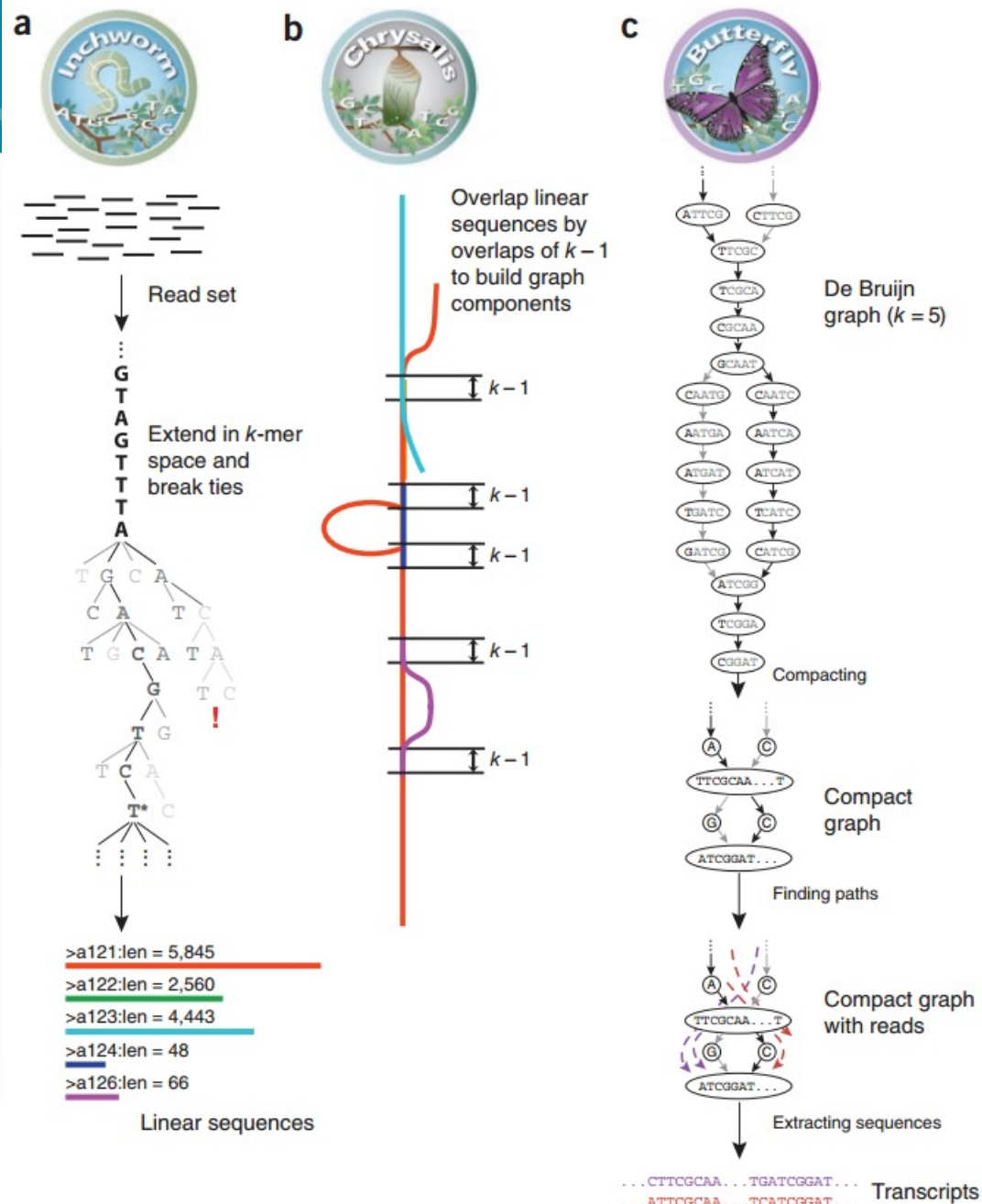




无参转录组组装和注释



无参组装步骤





- Trinity --seqType fq --left reads_1.fq --right reads_2.fq --CPU 6 --max_memory 20G

<https://github.com/trinityrnaseq/trinityrnaseq/wiki>





- 拼装完成之后得到Transcripts.fasta，用Salmon定量，DESeq2差异分析。



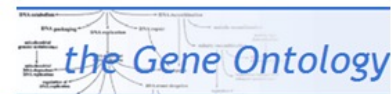
Trinotate



Pfam



eggNOG
version 3.0



RNA-Seq → Trinity → Transcripts/Proteins → Functional Data → Discovery

Automated Higher Order Biological Analysis

Eggnog在线注释



 **EggNOG 5.0.0**

Search protein or OG

Navigation

Home

Sequence search

eggNOG-mapper v2
(Batch Functional Annotation)

Downloads

API

Methods

EggNOG v5.0

A database of orthology relationships, functional annotation,
and gene evolutionary histories.

Organisms	Viruses	Orthologous Groups	Tree & Algs
5,090	2,502	4.4M	4.4M

Search

Citation

eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses.
Jaime Huerta-Cepas, Damian Szklarczyk, Davide Heller, Ana Hernández-Plaza, Sofia K Forslund, Helen Cook, Daniel R Mende, Ivica Letunic, Thomas Rattei, Lars J Jensen, Christian von Mering, Peer Bork
Nucleic Acids Res. 2019 Jan 8; 47(Database issue): D309–D314. doi: 10.1093/nar/gky1085

Previous versions

News

Contact

Tweets by @eggnogdb

EggNOG database

Retweeted

Ben Orsburn

@ProteomicsNews

Replying to @ProteomicsNews

Round 1 with @EggNogDB -- cuts the number of "unknown function" proteins from 61.3% of the total to <30% of the FASTA. For perspective, this is THE most well-characterized strain of Plasmodium falciparum (the most fatal human malaria parasite.) Coming back to this later.

♡

↗

Sep 23, 2020

EggNOG database

Retweeted

Jaime Huerta-Cepas

@jhcepas

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6



GenomicsTools

TOOLS

eggNOG-mapper

SUPPORT

Frequent Questions

Documentation

Standalone version

About



Annotate FASTA file

Upload Sequences (Up to 100,000 CDS/protein sequences in **FASTA** format)

浏览... 未选择文件。

Email address: (Required for job scheduling and notifications)

Enter email

Taxonomic Scope

(annotations will only be transferred from orthologs in the selected taxa group)

Auto adjust per query (RECOMMENDED)

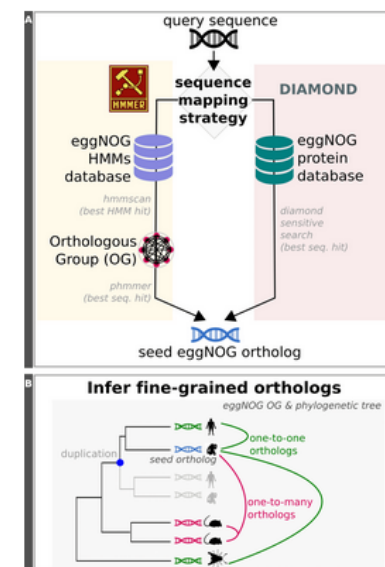
Orthology restrictions

Transfer annotations from any ortholog

Advanced Options

Method Overview

eggNOG-mapper v2 is a tool for functional annotation of large sets of sequences based on fast orthology assignments using precomputed **eggNOG v5.0** clusters and phylogenies. The method is illustrated in the following figure:



无参转录组分析Wiki



- Trinity Wiki Home
- Installing Trinity
 - Trinity Computing Requirements
 - Accessing Trinity on Publicly Available Compute Resources
 - Run Trinity using Docker
- Running Trinity
 - Genome Guided Trinity Transcriptome Assembly
 - Gene Structure Annotation of Genomes
- Trinity process and resource monitoring
 - Monitoring Progress During a Trinity Run
 - Examining Resource Usage at the End of a Trinity Run
- Output of Trinity Assembly
- Assembly Quality Assessment
 - Counting Full-length Transcripts
 - RNA-Seq Read Representation
 - Contig Nx and ExN50 stats
 - Examine strand-specificity of reads
- Downstream Analyses
 - Transcript Quantification
 - QC Samples and Bio Replicates
 - Differential Transcript or Gene Expression
 - Sample Specificity Analysis in Many Sample Comparisons
 - SuperTranscripts
 - Differential Transcript Usage
 - Identifying Sequence Polymorphisms or Variants
 - Coding Region Identification
 - Functional Annotation of Transcripts
 - Gene Ontology term functional category enrichments
- Miscellaneous additional functionality that may be of interest
 - In silico normalization of fastq files
- Community contributions
 - Defining a reduced 'best' transcript set
- Trinity Tidbits
- Frequently Asked Questions (FAQ)





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