
labibi Documentation

Release 0.8.3

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This is a set of protocols for doing genomic data analysis – specifically, de novo mRNAseq assembly and de novo metagenome assembly – in the cloud.

The latest released version of these protocols is v0.8.3; please follow the instructions at the following URL, and use this URL in citations and discussions:

<https://khmer-protocols.readthedocs.org/en/v0.8.3/>

(The URL <https://khmer-protocols.readthedocs.org/> will always go to the latest released version.)

Protocols:

1.1 mRNAseq assembly: the Eel Pond Protocol

`mrnaseq/index`

This is a lightweight protocol for assembling up to a few hundred million mRNAseq reads, annotating the resulting assembly, and doing differential expression with RSEM.

1.2 Metagenome assembly: the Kalamazoo Protocol

`metagenomics/index`

This is a protocol for assembling low- and medium-diversity metagenomes. Marine sediment and soil data sets may not be assemblable in the cloud just yet.

Additional information

Need help? Either post comments on the bottom of each page, OR [sign up for the mailing list](#).

Have you used these protocols in a scientific publication? We'll have citation instructions up soon.

Funding

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TODO:

- remove/transition stuff from the angus site.
- add sfg/stanford: <http://sfg.stanford.edu/>
- send to biostar-ninjas