

HTProcess_Jellyfish-2.0.0

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Community rating: ?????

Part of the HTProcess group of applications. Runs Jellyfish on all the reads in a library and analyzes the kmer population.

Quick Start

- To use **HTProcess_Jellyfish-2.0.0**, import your data in the form of the HTProcess_Reads directory output from the HTProcess_prepare-directories-and-run-fastqc app.
- **Resources:** <http://www.cbcb.umd.edu/software/jellyfish/>

Test Data



Test data for this app appears directly in the Discovery Environment in the Data window under *Community Data* -> *iplantcollaborative* -> *example_data* -> *htprocess1* -> *HTProcess_Jellyfish*

Input File(s)

Use the directory **HTProcess_Reads** in the directory above as test input.

Parameters Used in App

When the app is run in the Discovery Environment, use the following parameters with the above input file(s) to get the output provided in the next section below.

Set the kmer values to 21, 27, and 35.

Output File(s)

Expect the files found in *Community Data* -> *iplantcollaborative* -> *example_data* -> *htprocess1* -> HTProcess_Jellyfish. Click on *jellyfish_report.html* to open the report from Jellyfish in the DE. For each kmer setting entered 3 graphs will be produced in the same row – each being the same graph with a different Y axis limit to provide different views of the data.

Tool Source for App

- https://pods.iplantcollaborative.org/wiki/display/DEapps/HTProcess_Jellyfish-2.0.0