

RpkmVisualizer Plugin Manual

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1 Overview

RpkmVisualizer operates on the output of RNA-Seq to generate a circular bar graph of RPKM values for regions of a genome.

1.1 Intended Use

The plugin is meant to be used as part of gene diversity and abundance analysis of microbial populations. The intended workflow involves assembling and annotating a consensus sequence from DNA reads from a sample of a population, and then using RNA-Seq on this sequence and the original set of DNA reads. Though RNA-Seq is normally purposed for gene expression analysis, it is used here for abundance analysis. Among the resulting table is a column RPKM, which stands for Reads Per Kilobase of exon model per Million mapped reads, and is a measure representing the amount of reads per annotated region (gene). The RPKM values can then be used to infer the relative frequency of the presence of genes in a population. RpkmVisualizer serves to represent these findings graphically by displaying the magnitude of the RPKM values for each region along the genome.

2 Installation

2.1 Downloading

The plugin can be obtained from two locations.

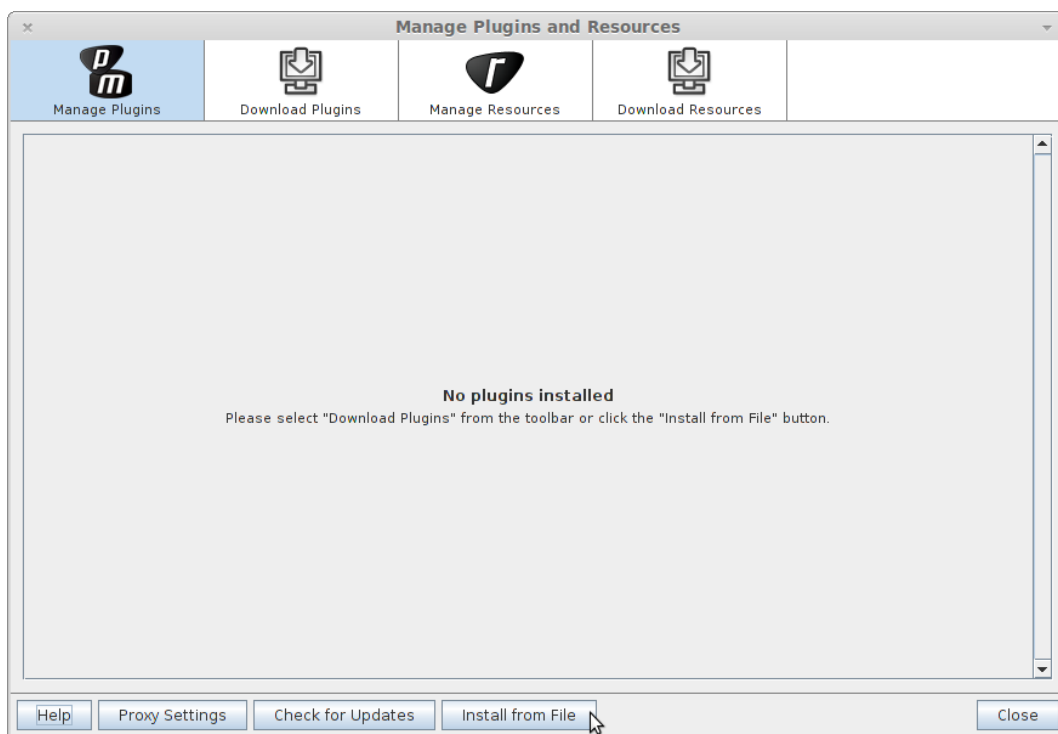
- In source form: <http://github.com/jedbarlow/rpkmvisualizer>
- As a compiled package: <http://www.ualberta.ca/~ejbarlow/biol498/>

2.2 Loading into CLC Genomics Workbench

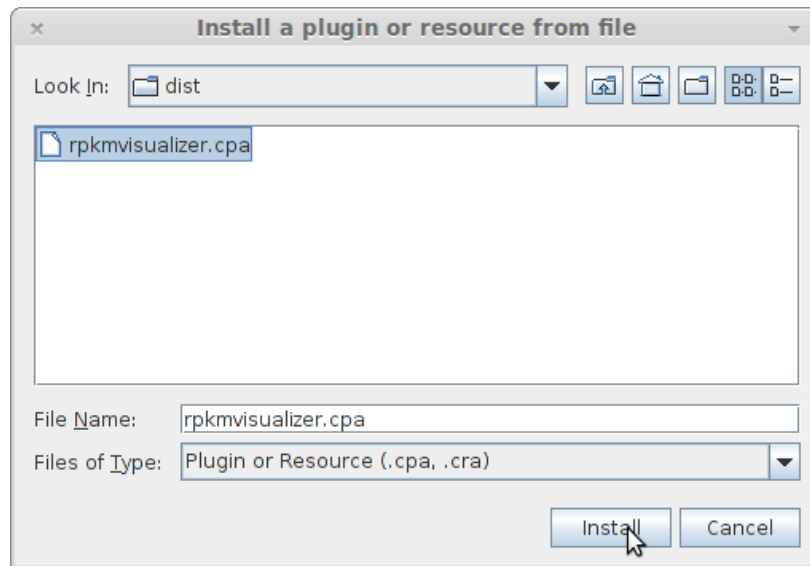
Once obtained, the plugin *rpkmvisualizer.cpa* can be installed as follows. First, click the **Plugins** button in the CLC Genomics Workbench toolbar in the top-right corner of the main window.



Then click the Install From File button.



Then navigate to the folder containing the `rpkvisualizer.cpa` file, select the file, and click the Install From File button.



Then follow the on-screen steps of the wizard. Once installed, RPKM Heat Map should appear inside the **Show** viewing option in the right-click menu as indicated by the figure in the next section below.

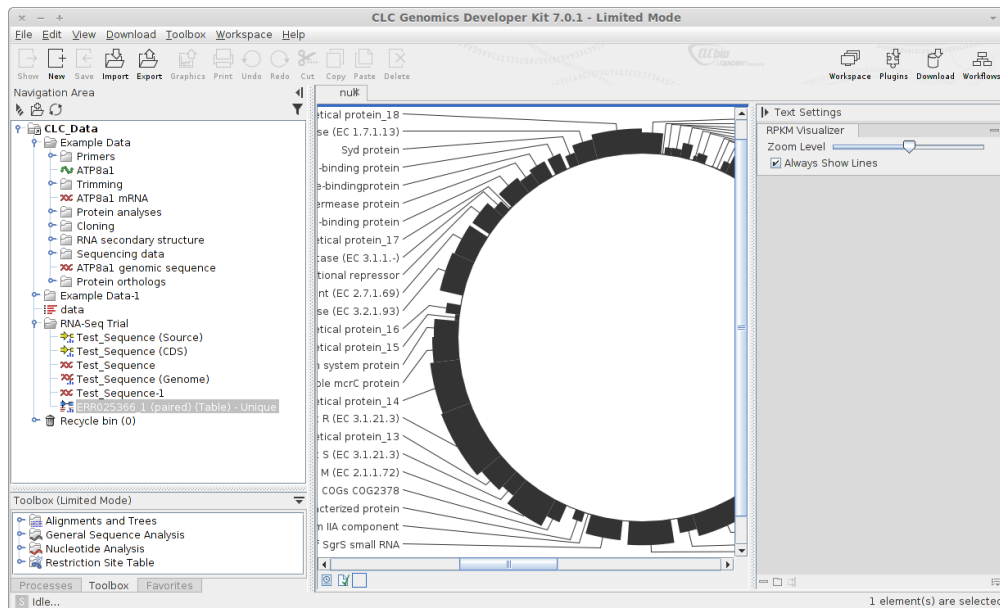
3 Operation

3.1 Accessing the Plugin

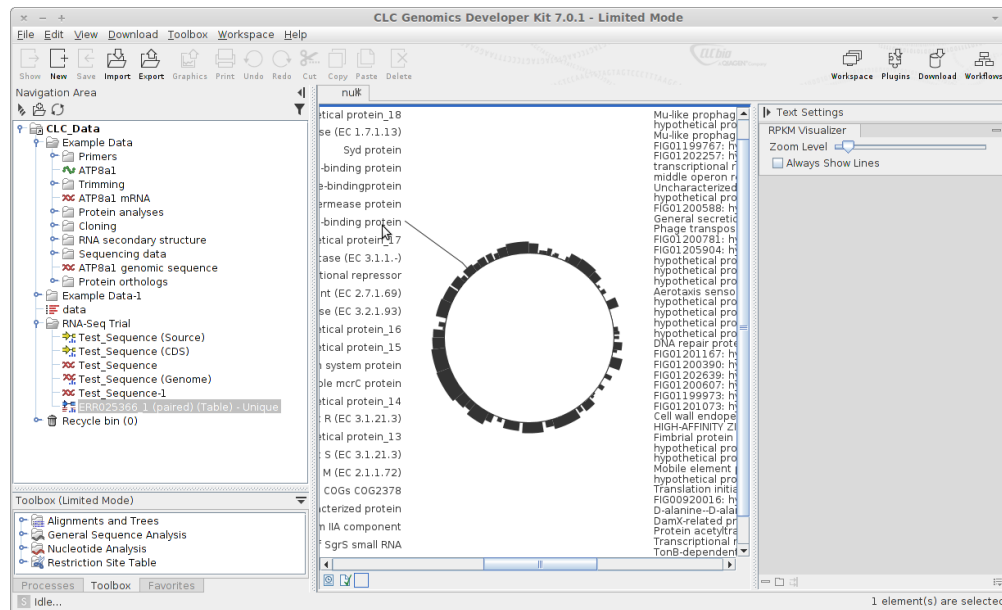
In the CLC Genomics Workbench explorer pane, right-click on the result table of the RNA-Seq tool, and navigate to the RPKM Heat Map option as shown in the following screenshot.

3.2 Plugin Configuration

A sidebar with options can be accessed by clicking the arrow near the top-right corner of the figure, next to the vertical scrollbar.



These options can be used to adjust basic parameters of the figure, such as zoom level and other layout options. For example, the following image demonstrates a change in zoom level and line visibility options.



4 Additional Information and URLs

RpkmVisualizer is being actively developed by Jed Barlow at the Boucher Lab (Department of Biological Sciences, University of Alberta) under the direction of Yan Boucher.

- Boucher Lab: http://www.biology.ualberta.ca/boucher_lab/Boucher_Lab/Welcome.html