

Lab 11

Note: the following free software can be used to visualize chromatogram files generated by a sequencer. You can download to install on your own computer. Do not download it in the lab. As I do not have such a sample file, you do not need to test it. Chromas lite:

http://www.technelysium.com.au/chromas_lite.html

More information related to sequencing service can be found, for example, at <http://seqcore.brcf.med.umich.edu/>

Multiple Genome Alignment

In this lab you will learn how to use Mauve – a tool for multiple genome alignment to investigate gene gain, loss and rearrangement.

The tool can be downloaded from:

<http://darlinglab.org/mauve/user-guide/introduction.html>

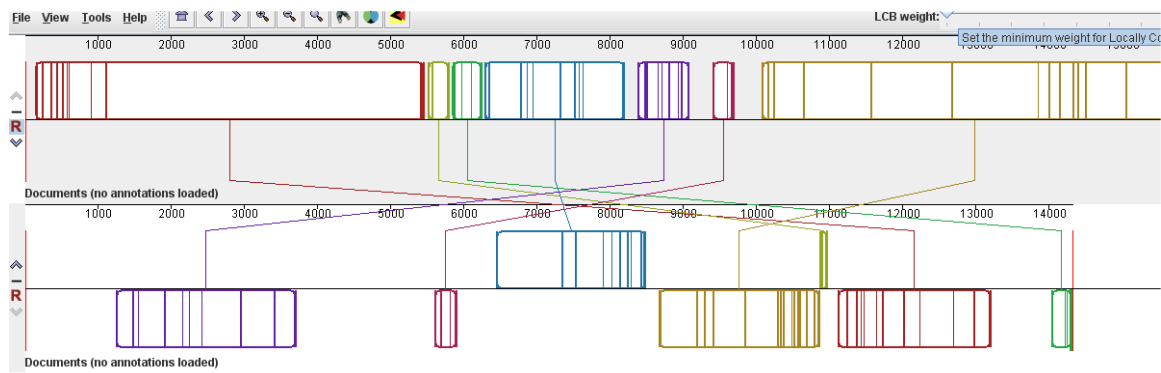
You can also find two publications that provide details of the tool algorithm and development.

Lab procedure:

1) Go to “NCBI organelle genome resources” (using google to search), then you can choose either mitochondrial genomes or plastid genomes. Download 3 – 5 mt genomes or plastid genomes from different species (distantly related species will give you more interesting pictures). Save each genome in individual fasta file.

Then you can start aligning them using Mauve.

Here is an example of output for two mt genomes: human vs worm.



- 2) Using the papaya X.fas and HSY.fas to do the alignment – you should expect to produce a picture as below

