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RNA-Seq Pipeline in Galaxy

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RNA-Seq Pipeline in Galaxy

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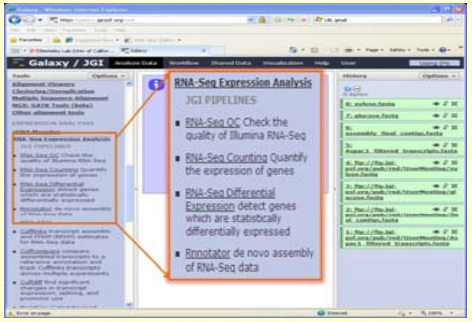
Galaxy at the JGI

Galaxy is an open, innovative web-based computing platform for accelerating life science data analysis. This platform integrates many common life science tools and data sources needed for performing the wide array of analyses used in genome studies. Galaxy's user friendly interface allows biologists, without the need to learn how to run specific tools from the command line prompt, to start data analysis right away. Moreover, all installed tools seamlessly connect to the powerful computing cluster, which brings the high performance computing to biology by simply clicking a button.

At JGI, the Galaxy enables a wide range of genomic tasks, from basic sequence data manipulation, sequence alignment, expression analysis, annotation, customized tools to de novo assembly. The web site is open to all JGI users and collaborators at https://galaxy.jgi-psf.org/

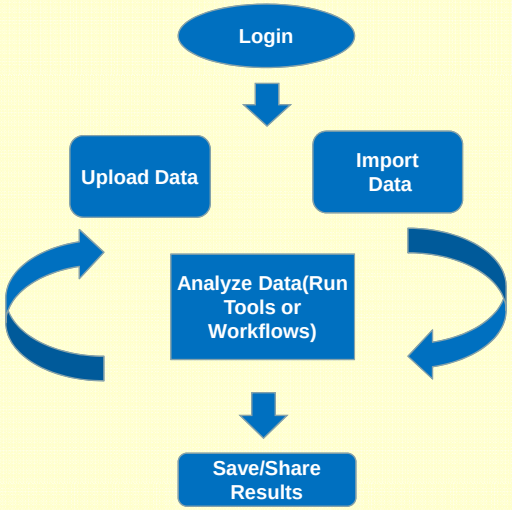
RNA-Seq Tools in Galaxy



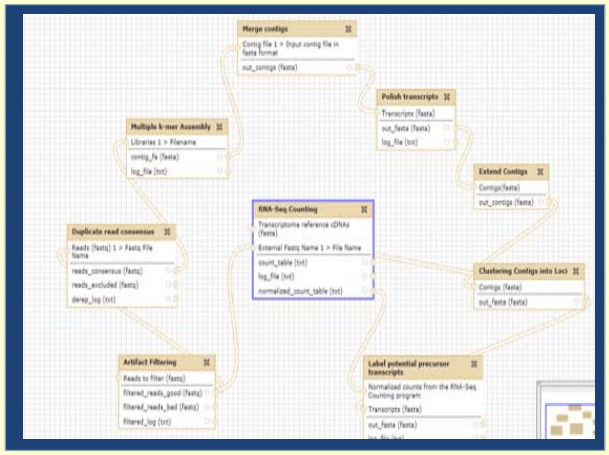
RNA-Seq Pipeline

- **QC** :
  To find out if RNA-Seq experiments worked
- **Counting & Statistics**:
  To detect genes which are up/down regulated
- **Assembly:**
  To assemble reads without reference transcriptome

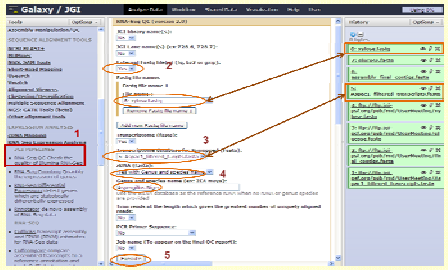
Data Workflow in Galaxy



RNA-Seq *de novo* Assembly Workflow in Galaxy

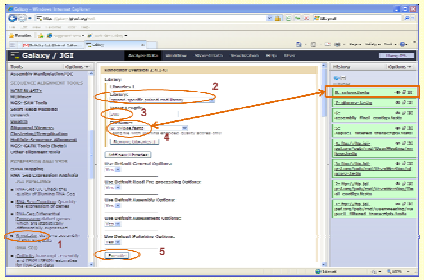


5 Steps to run QC Pipeline



QC Report

5 Steps to Run an Assembly in Galaxy



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