Computational Biosciences Institute Workshop 5

Informatics for RNA-sequence analysis

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How to run the pipeline under linux?

- Totorial_Workshop5_Linux
  - Create QC reports using FASTQC.
  - Trim the reads.
  - Use Bowite2/Tophat2 to align reads to the genome.
  - Do post-alignment QC.
  - Use Cufflinks to quantify gene expression.
  - Use Cuffdiff to do differential expression analysis.
  - Use Cummerbund to examine the data.

Totorial_Workshop5_Linux

http://tinyurl.com/n4ujbf6

Totorial_Workshop5_Linux

Updated Feb 24, 2014

#Tutorial_Workshop5_Linux.txt

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#The rest of the tutorial should be conducted in a linux Terminal session @ hoffman cluster.

#All lines starting with a '#' are comments and will not be executed.

log into hoffman server
ssh YOURID@hoffman2.idre.ucla.edu

request a working node
qrsh -l h_data=4G,time=4:00:00

HOW TO GET THE DATA
cd $HOME
cp -r /u/scratch/k/kzhang/cbi_workshop5 .

How to submit your jobs to hoffman?

qsub Statement From the Command Prompt

SGE commands

> qsub -l h_data=4G,time=2:00:00 -N brain_s1 -cwd -b y "YOUR COMMAND"

indicates command is a script or an executable binary

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Workshops

Submitted by collaboratory on Wed, 01/09/2013 - 20:47

Workshop 1: Introduction to UNIX command-line

Workshop 2: Introduction to Galaxy Server and Genome Browsers

Workshop 3: Introduction to R and Bioconductor

Workshop 4: Short read mapping - QC, alignment to reference and quantification

Workshop 5: Informatics for RNA-sequence Analysis

Workshop 6: DNA methylation using BS-sequencing data

Workshop 7 : Analysis of ChIP-seq data

Tags:
Workshops

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Questions/Discussion.