Managing Galaxy's Built-in Data

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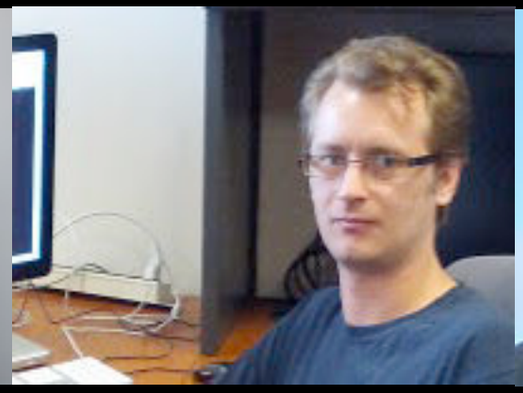

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The Galaxy Team

http://wiki.galaxyproject.org/GalaxyTeam

Overview

Intro to Built-in Datasets

A problem

Data Managers

- What?
- Demo

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Built-in Datasets

BWA example

Map with BWA for Illumina (version 1.2.3)

Will you select a reference genome from your history or use a built-in index?:

Use a built-in index

Select a reference genome:

Arabidopsis lyrata: Araly1

Arabidopsis lyrata: Araly1
Armadillo (Dasypus novemcinctus): dasNov1
Bacillus subtilis subsp. subtilis str. 168: baciSubt
Bordetella bronchiseptica str. RB50: bordBron
Budgerigar (Melopsittacus undulatus): melUnd1
Burkholderia pseudomallei 1106a: burkPseu_1106A
Burkholderia pseudomallei 1710b: 13954
Burkholderia pseudomallei 668: 13953
Burkholderia pseudomallei K96243: 178

umina)

BWA produces SAM with several lines of header information

Execute

Built-in Datasets

BWA example

Reference Genome (*.fasta)

bwa index [-a bwtsw|div|is] [-c] <in.fasta>

BWA Index Files on disk (*.amb, *.bwt, *.rbwt, *.rsa, *.ann, *.pac, *.rpac, *.sa)

File listing paths, genome build, descriptions, etc. of available BWA indexes (bwa_index.loc)

abstraction layer

Tool Data Table (tool_data_table_conf.xml)

Galaxy BWA Tool (bwa_wrapper.xml)

Built-in Datasets

bwa_wrapper.xml

```
<conditional name="genomeSource">
  <param name="refGenomeSource" type="select" label="Will you select a reference gen
    <option value="indexed">Use a built-in index</option>
    <option value="history">Use one from the history</option>
  </param>
  <when value="indexed">
    <param name="indices" type="select" label="Select a reference genome">
      <options from_data_table="bwa_indexes">
        <filter type="sort_by" column="2" />
        <validator type="no_options" message="No indexes are available" />
      </options>
    </param>
  </when>
  <when value="history">
    <param name="ownFile" type="data" format="fasta" metadata_name="dbkey" label="Se
  </when>
</conditional>
```

Built-in Datasets

tool_data_table_conf.xml

```
<tables>
    <!-- Locations of indexes in the BWA mapper format -->
    <table name="bwa_indexes" comment_char="#">
        <columns>value, dbkey, name, path</columns>
        <file path="tool-data/bwa_index.loc" />
    </table>
</tables>
```

```
dan@scofield:~$ cat /galaxy/data/location/bwa_index.loc
#This is a sample file distributed with Galaxy that enables tools
#to use a directory of BWA indexed sequences data files. You will need
#to create these data files and then create a bwa_index.loc file
#similar to this one (store it in this directory) that points to
#the directories in which those files are stored. The bwa_index.loc
#file has this format (longer white space characters are TAB characters):
#
#<unique_build_id>   <dbkey>   <display_name>   <file_path>
#
#So, for example, if you had phiX indexed stored in
#/depot/data2/galaxy/phiX/base/,
#then the bwa_index.loc entry would look like this:
#
#phiX174   phiX   phiX Pretty   /depot/data2/galaxy/phiX/base/phiX.fa
#
#and your /depot/data2/galaxy/phiX/base/ directory
#would contain phiX.fa.* files:
#
#-rw-r--r--  1 james    universe 830134 2005-09-13 10:12 phiX.fa.amb
#-rw-r--r--  1 james    universe 527388 2005-09-13 10:12 phiX.fa.ann
#-rw-r--r--  1 james    universe 269808 2005-09-13 10:12 phiX.fa.bwt
#...etc...
#
#Your bwa_index.loc file should include an entry per line for each
#index set you have stored. The "file" in the path does not actually
#exist, but it is the prefix for the actual index files.  For example:
#
#phiX174             phiX   phiX174          /depot/data2/galaxy/phiX/base/phiX.fa
#hg18canon           hg18   hg18 Canonical   /depot/data2/galaxy/hg18/base/hg18canon.fa
#hg18full            hg18   hg18 Full        /depot/data2/galaxy/hg18/base/hg18full.fa
#/orig/path/hg19.fa  hg19   hg19             /depot/data2/galaxy/hg19/base/hg19.fa
#...etc...
#
#Note that for backwards compatibility with workflows, the unique ID of
#an entry must be the path that was in the original loc file, because that
#is the value stored in the workflow for that parameter. That is why the
#hg19 entry above looks odd. New genomes can be better-looking.
#
Araly1  Araly1  Arabidopsis lyrata: Araly1      /galaxy/data/Araly1/bwa_index/Araly1.fa
dasNov1 dasNov1 Armadillo (Dasypus novemcinctus): dasNov1       /galaxy/data/dasNov1/bwa_index/dasNov1.fa
baciSubt        baciSubt        Bacillus subtilis subsp. subtilis str. 168: baciSubt    /galaxy/data/microbes/baciSubt/bwa_index/baciS
bordBron        bordBron        Bordetella bronchiseptica str. RB50: bordBron   /galaxy/data/microbes/bordBron/bwa_index/bordBron.fa
```

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A Problem

Hi,

We have a local install of galaxy and I'm trying to add the reference index files for bwa using the information provided in the following link

http://wiki.g2.bx.psu.edu/Admin/NGS%20Local%20Setup

I have modified the bwa_index.loc file present in the ../tool-data directory by adding the path to where the index is on our server (Also attached). However, even after restarting the server, the reference genome does not show when choosing the "use a built-in index option". I'm not sure whether the loc file is correctly created and whether any other configuration file needs to be changed/updated. Help in the matter greatly appreciated.

Thanks,

Aarti

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Hi Aarti,

Check the name of your ref file. If it is hg19.fa, then modify loc file as
"hg19 hg19 HG19_BWA /root/Ref_INDEX/HG19BWAIndex/base/hg19.fa"

Avik Datta

Aarti

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Help?

Avi

Thank

Aarti

Check the name of your ref file. If it is hg19.fa, then modify loc file as "hg

Also make sure you are using TABs to separate the fields in the .loc file, this has bitten me several time in the past. My vim config places 4 spaces instead of TAB, to deactivate this option you can do ":set noexpandtab".

Hope it helps,
Carlos

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Check the name of your ref file. If it is hg19.fa, then modify loc file as

"hg19 hg19 HG19 BWA /root/Ref_INDEX/HG19BWAIndex/base/hg19.fa"

Also make sure you are using TABs to separate the fields in the .loc

Hello Carlos,
Thanks a lot for the tip. The tab trick has fixed the problem.

Regards,
Aarti

Other concerns

Accessible?

- Manually download genome FASTA files
- Download, compile, run bwa index; which options?

Reproducible?

- Only if the person performing manual steps keeps good notes

Transparent?

- Send email to sysadmin asking for notes

Need to restart Galaxy server when new entries are added

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Data Managers

- Allows for the creation of built-in (reference) data
  - underlying data
  - data tables
    - *.loc files
- Specialized Galaxy tools that can only be accessed by an admin
- Defined locally or installed from Tool Shed

Data Managers

- Flexible Framework
  - not just Genomic data
  - Interactively Run Data Managers through UI
  - Workflow compatible
  - API
- Examples:
  - Fetching Genome (FASTA) sequences
  - Building short read mapper indexes for genomes

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Data Manager Demo

- Fetch the Genome Sequence for sacCer2
  - UCSC as the source
  - Install fetching tool from Tool Shed
  - all_fasta table is populated automatically
- Build BWA indexes for sacCer2
  - Install indexing tool from Tool Shed
  - Build indexes
  - bwa_index table is populated automatically
- Align some reads to the newly added reference genome

Data Manager Demo: Full Disclosure

- The default CloudMan instance comes with sacCer2 pre-installed, but I deleted it.
- The sequencing reads to be aligned with BWA were created locally from the reference genome before uploading
- Setup Galaxy admin account already

http://gcc2013-demo.dblankenberg.org/

Make Your Own

http://wiki.galaxyproject.org/Admin/Tools/DataManagers/HowTo/Define

Several examples available in the test Tool Shed (search for "data_manager")

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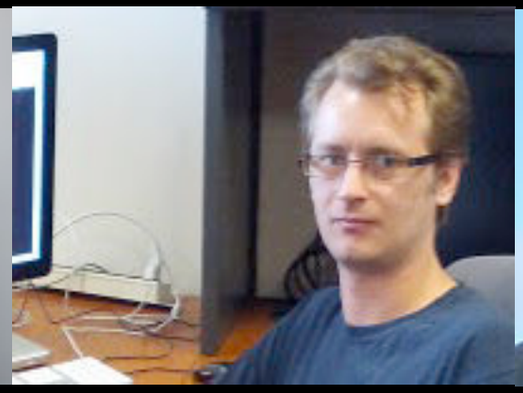

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