Using BioGrids

for RNA-Seq on AWS and Your Laptop

James Vincent

BioGrids Consortium

Harvard Medical School

TMEC 304

July 25 2019

BioGrids

by Harvard Medical School

Today we will .....

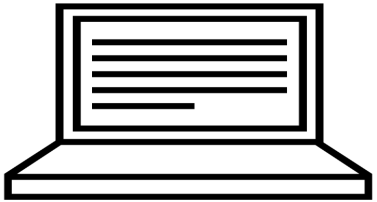
Install software with BioGrids

Run an RNA-Seq workflow

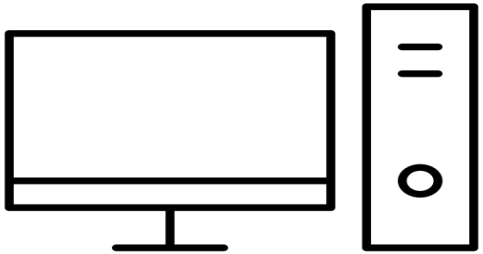
Replicate above on AWS and laptop

BioGrids on AWS

faithful laptop



AWS EC2 Instance



RNA-Seq Workflow

open a terminal

open a browser: biogrids.org/wiki/workshops

Subtle Things

- Capsule Environment
- .bashrc / .profile not changed
- binary installs

Avoid Time Sinks

https://www.biostars.org/p/189261/:

This seems to be a bug when installing fastqc using apt-get install fastqc

STARmanual.pdf

….which creates problems for STAR compilation. One option to avoid this problem is to install gcc …….

http://github.gersteinlab.org/exceRpt/

Manual Installation:

….generally not recommended … <snip> … instructions on how to install exceRpt and its various dependencies will [one day] be listed toward the bottom of this page.

Reproducible Research

Self Documenting

```
$ STAR --sbapp:d

Capsule:STAR using star version 2.5.3a
  Version information for: /programs/i386-mac/star

Default version:                        2.5.3a
In-use version:                         2.5.3a
Other available versions:               none
Overrides use this shell variable:  STAR_M
```

Include in workflow:

```
 STAR     --sbapp:d
 samtools --sbapp:d
```

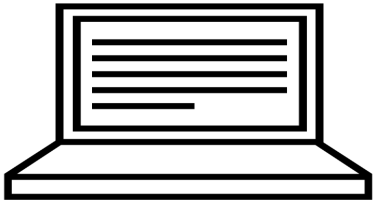
Config File

```
[installer]
site = biogrid-production
key = 70rYFBTDnmCr93VUklfbf1s3M4jdyC9bFVYHew==
user = jvincent1

[packages]
star@2.5.3a = i386-mac
samtools@1.5 = i386-mac
igv@2.4.10 = i386-mac
```

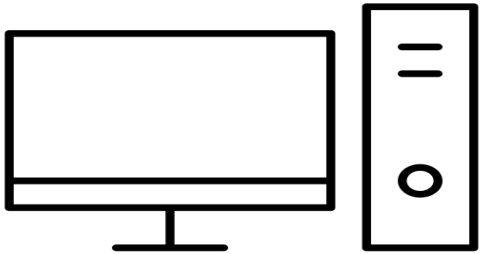
This Is Handy

faithful laptop



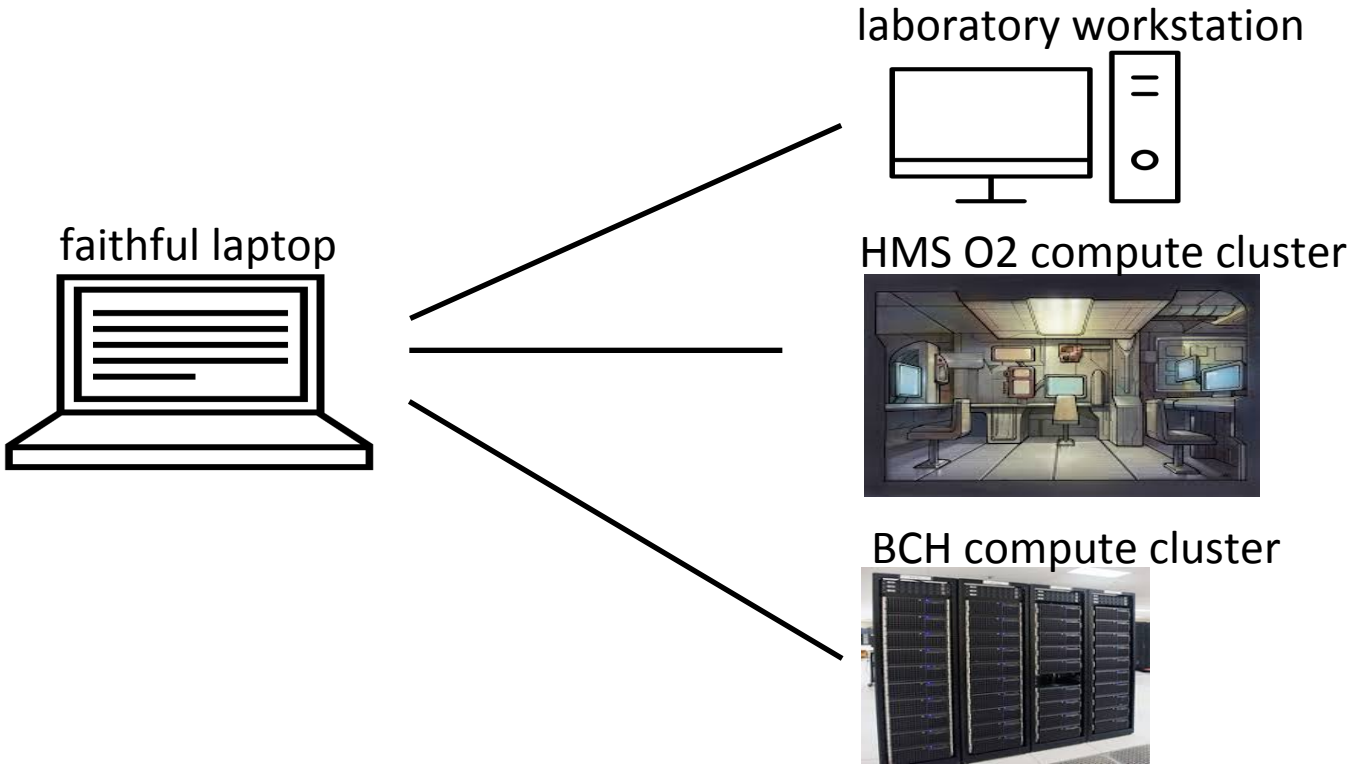
biogrids save mysetup.txt

new workstation



biogrids reactivate mysetup.txt

BioGrids is Portable



BioGrids Benefits

save time - reduce headaches

scale and share workflows

part of reproducible research

BioGrids Consortium

Personnel

SBGrid
BioGrids

Compute Infrastructure

Funding
HMS Tools and Technologies Committee

Why BioGrids?

You  Cover of Nature

compile software
compile libraries
manage dependencies
manage versions
manage paths
change versions
....

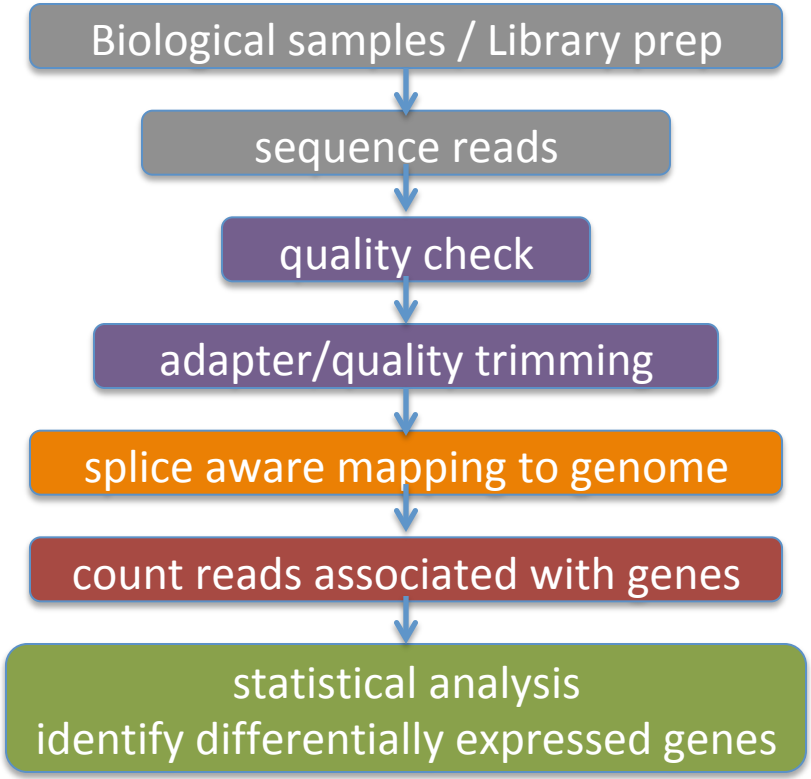
learn to use software
optimize workflow
get science done

RNA-Seq Overview

Harvard Chan Bioinformatics Core (HBC)

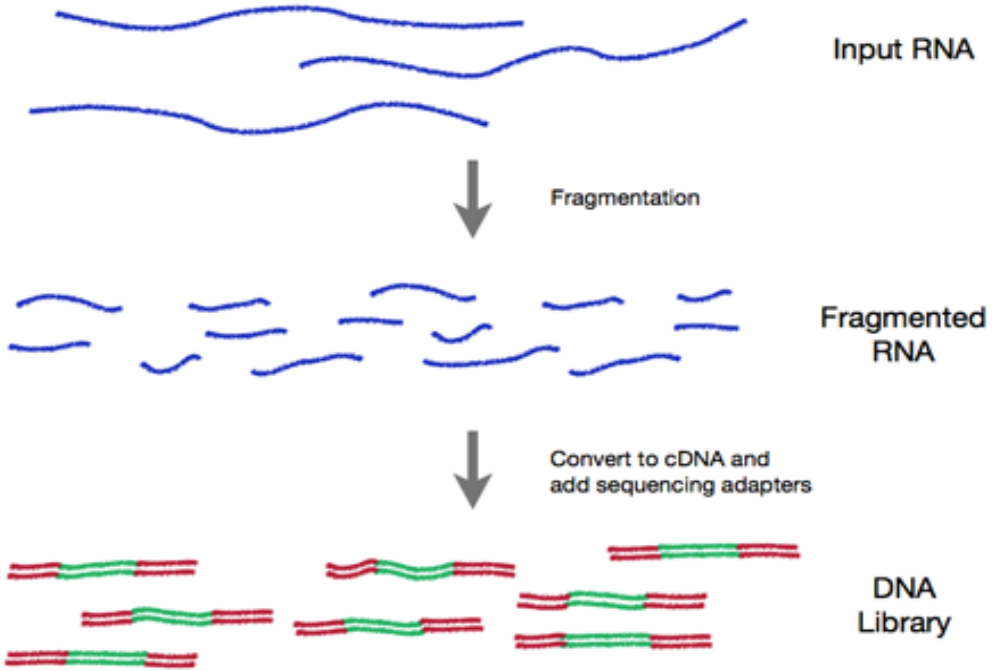
http://bioinformatics.sph.harvard.edu/training

RNA-Seq Overview

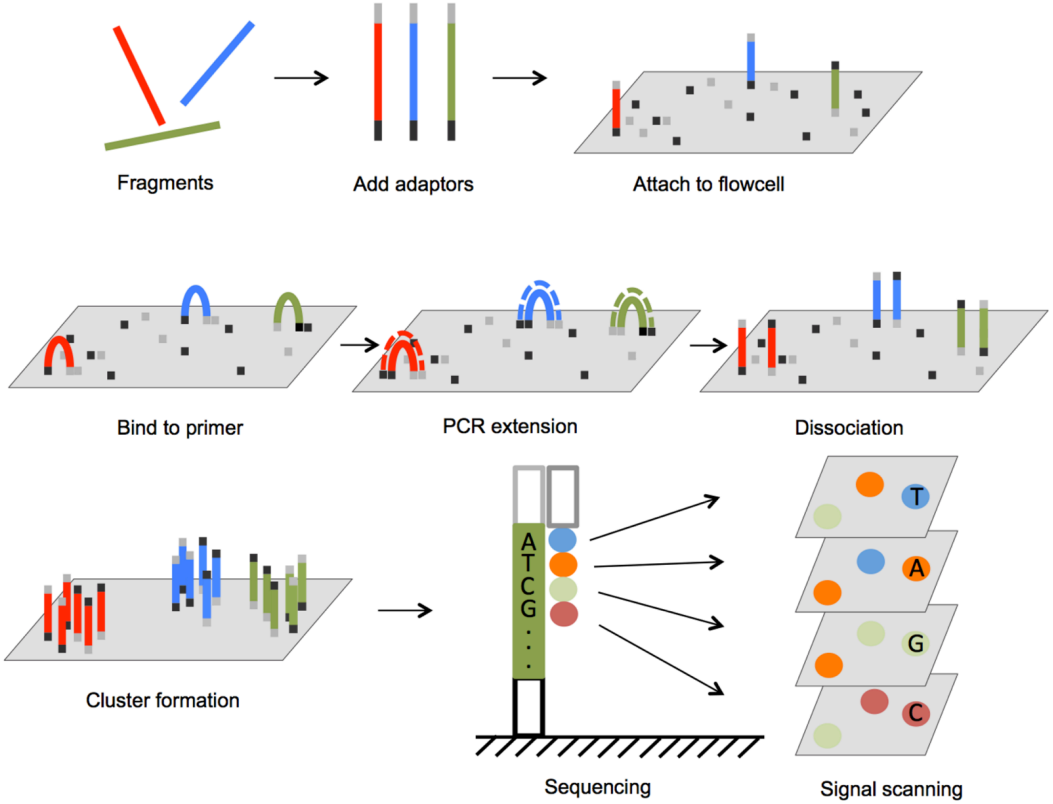


hbctraining.github.io/Intro-to-rnaseq-hpc-O2

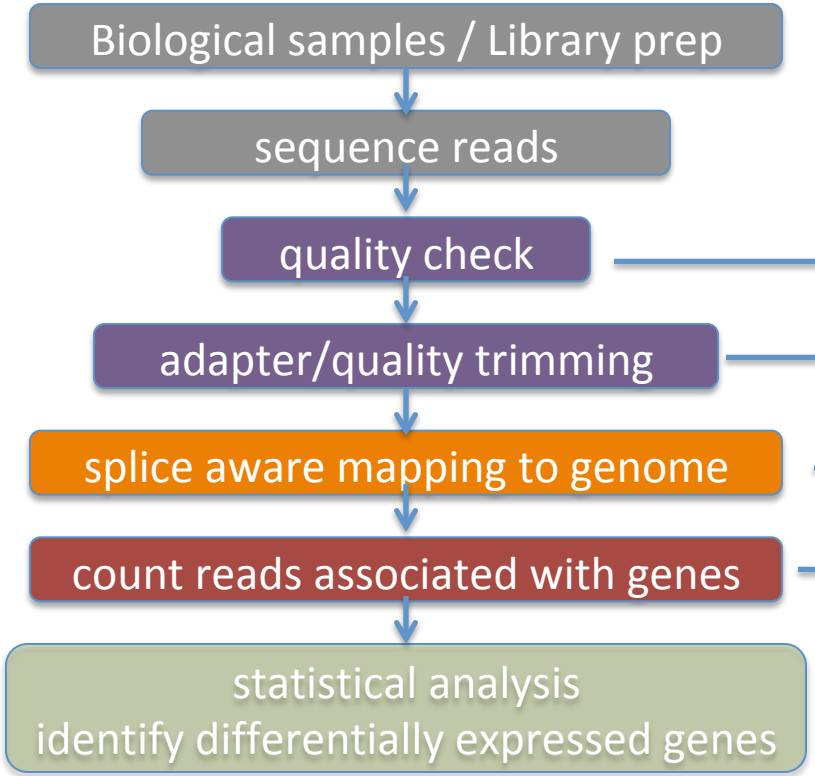
RNA Prep


Input RNA
Fragmentation
Fragmented RNA
Convert to cDNA and add sequencing adapters
DNA Library

Sequencing


Fragments
Add adaptors
Attach to flowcell
Bind to primer
PCR extension
Dissociation
Cluster formation
ATCG...
Sequencing
T
A
G
C
Signal scanning

RNA-Seq Overview



BioGrids Apps

FastQC

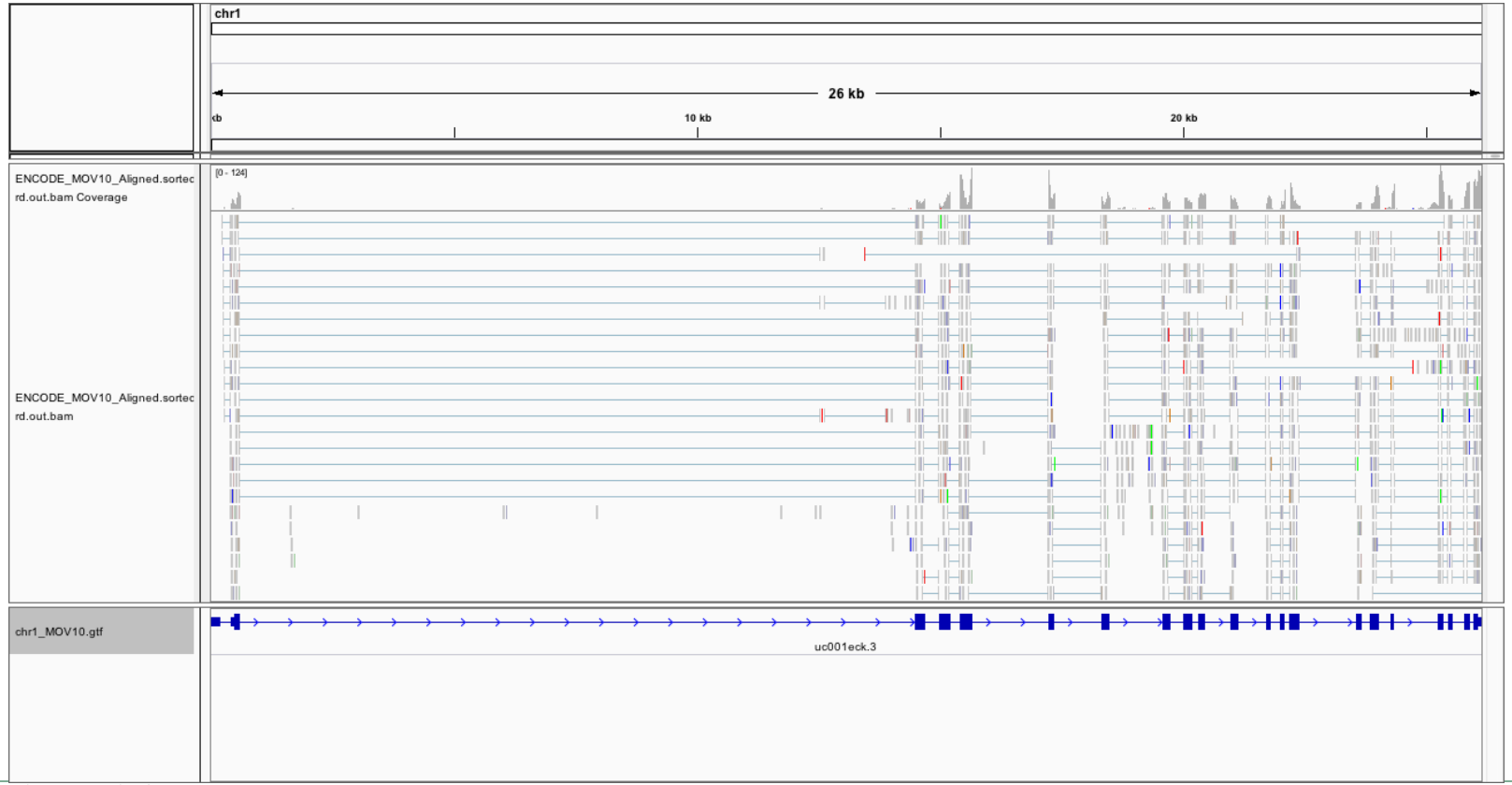
(trimmomatic)

STAR

subRead

hbctraining.github.io/Intro-to-rnaseq-hpc-O2

Mapped Reads



Check Results

IGV

1: Genomes / Load Genome from File... (chr1_MOV10.fa)

2: File / Load from file... (.gtf file)

3: File / Load from file... (.bam file)

DevOps with BioGrids

workflow	software stack	compute resources
bioinformatics	*BioGrids*	*laptop* *HMS O2* *AWS*

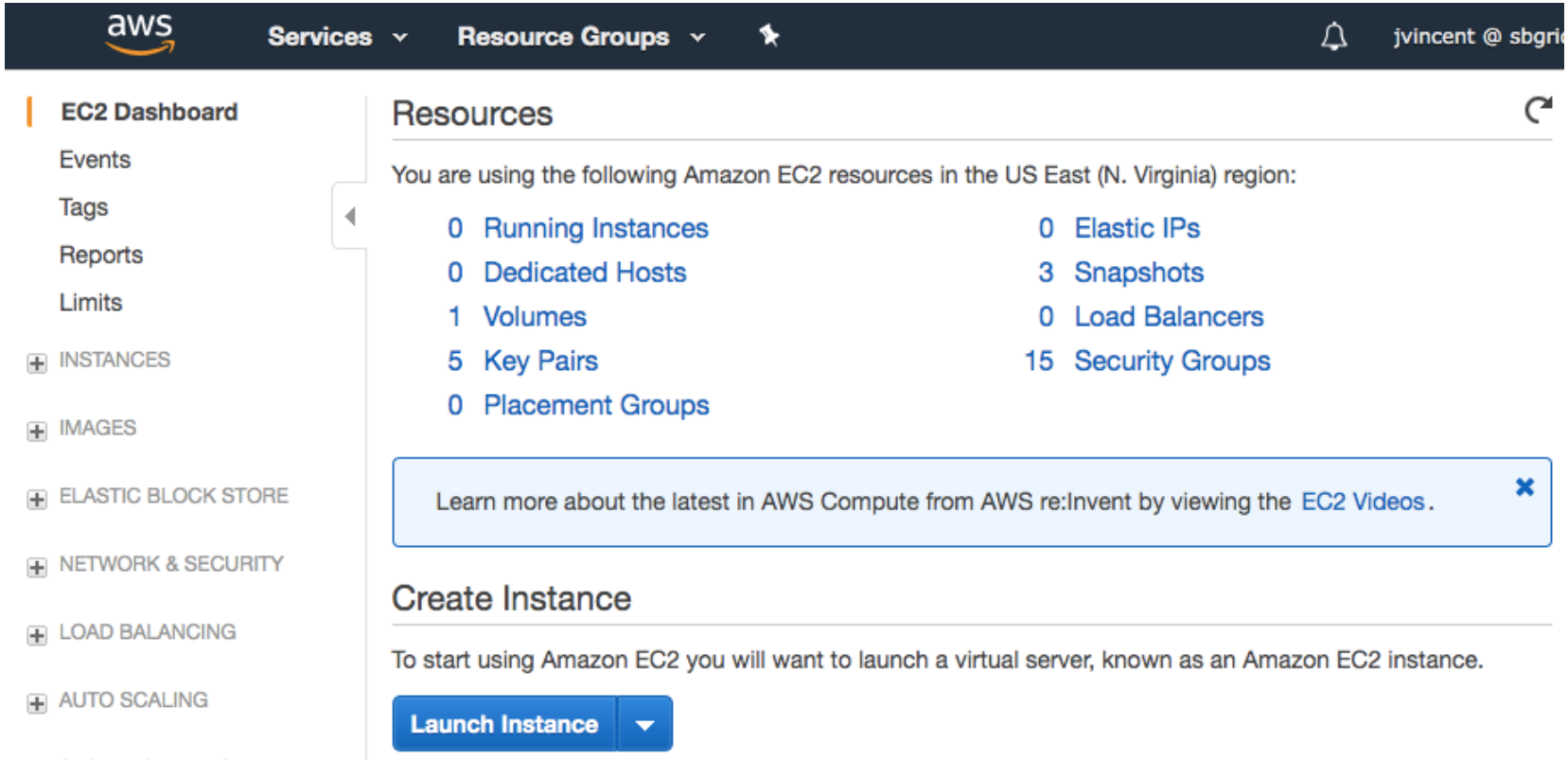
AWS Hands On

https://sbgrid.signin.aws.amazon.com/console

username: **workshop21**

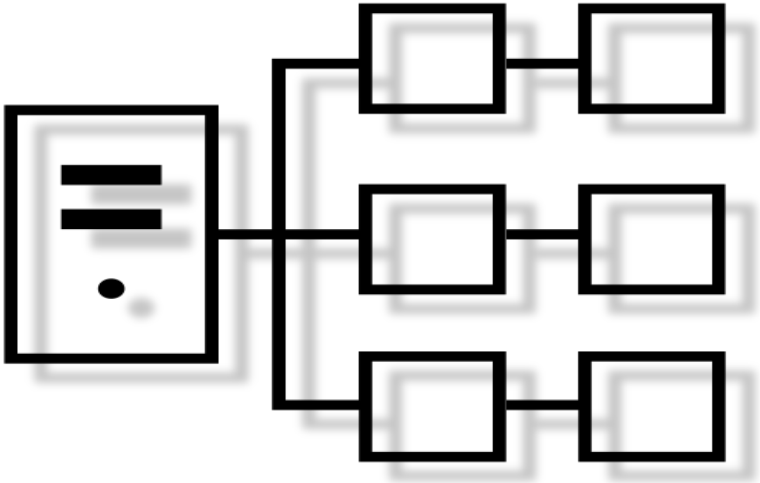
password: **Biogrids_Workshop1**

AWS - Amazon Web Services



AWS Parallel Cluster

aws-parallelcluster.readthedocs.io



scalable HPC cluster

help@biogrids.org

BioGrids is funded by the
Harvard Medical School
Tools and Technologies Committee

Additional Resources

ENCODE data files can be found here for CalTech RNA-Seq :
http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeCaltechRnaSeq/

Use this bam file: wgEncodeCaltechRnaSeqK562R1x75dAlignsRep1V2

Region of MOV10 gene: chr1:113,214,934-113,243,900

How to download whole genome:
- UCSC ftp site: hgdownload.cse.ucsc.edu
- UCSC web site: http://hgdownload.cse.ucsc.edu/goldenPath/hg19/chromosomes/
- UCSC recommends using an ftp client for large file downloads
- chr1 is only 70M

References

TRAINING

hbctraining.github.io/Intro-to-rnaseq-hpc-O2

AWS

https://aws.amazon.com/ec2/getting-started

ENCODE

https://www.encodeproject.org

IMAGES

https://www.diagenode.com/en/categories/Library-preparation-for-RNA-seq

https://rnaseq.uoregon.edu