



# Canadian Bioinformatics Workshops

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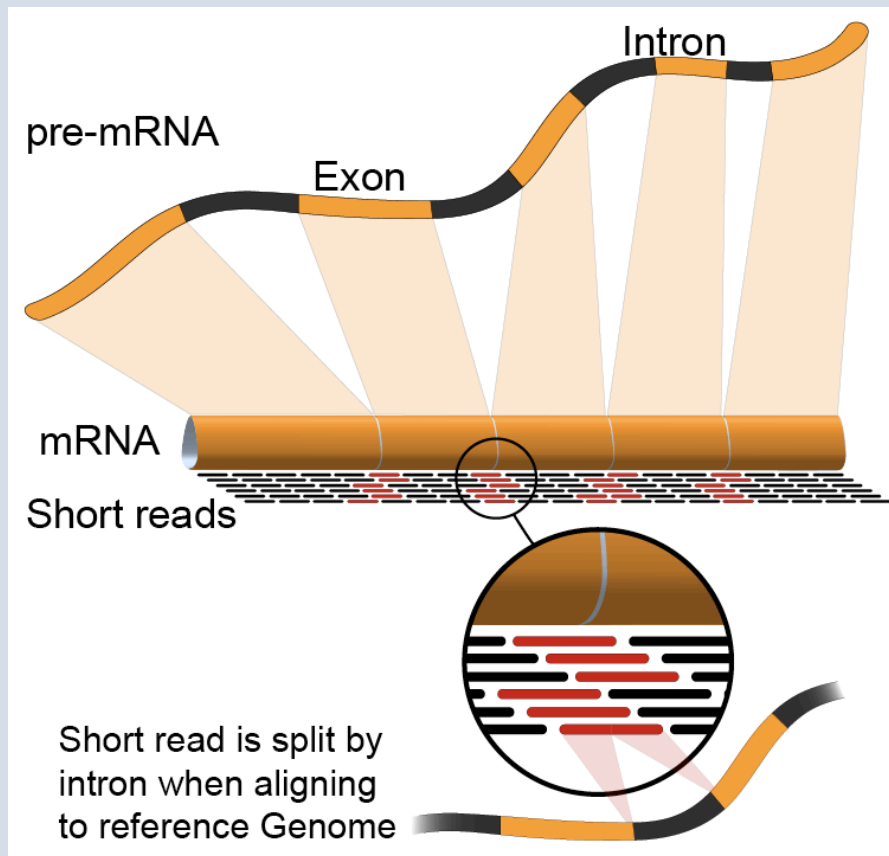
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# Introduction to Genome Analysis Platforms

Malachi Griffith, Obi Griffith, Jason Walker

Informatics for RNA-seq analysis

June 16 - 17, 2016



# What is a genome analysis 'platform'?

- Means different things to different people...
  - Lost of jargon and buzzwords
- Hardware
  - e.g. 'Dell Genomic Data Analysis Platform'
- Pipelines
- Cloud computing
  - 'Private clouds'
  - 'Public clouds' - Amazon AWS, Google Cloud, digital ocean, etc.
- Virtualization and virtual machines
  - VirtualBox (vagrant), OpenStack, VMWare
- Workflow management systems
- Software development kits (SDKs)
- Application programming interfaces (APIs)
- Distributed storage and processing (e.g. 'Hadoop')
- Job schedulers. e.g. pbs, lsf, sge, openlava,

# List of existing genome analysis platforms

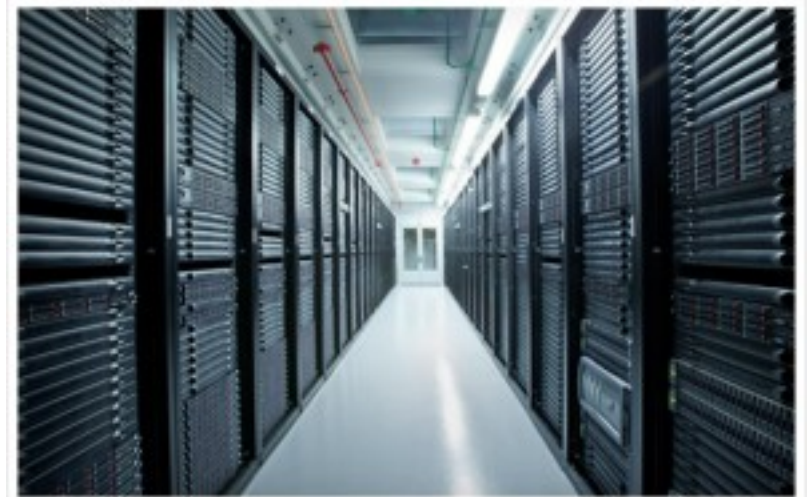
- <https://docs.google.com/spreadsheets/d/1o8iYwYUy0V7IECmu21Und3XALwQihioj23WGv-w0itk/pubhtml>
- Genome Modeling System (GMS), Galaxy, bcbio-nextgen, Omics Pipe, Illumina BaseSpace, BINA Genomic Analysis System, SeqWare, DNA Nexus Platform, gkno, NGSANE, Appistry's Ayrris, GATK's Queue, Curoverse's Arvados, CGA's Firehose, Seven Bridges Genomics, MIT STAR, GenomOncology, ga4gh, IBM's PowerGene Orchestrator, etc.

# What is a job scheduler?

- A **job scheduler** is a computer application for controlling unattended background program execution (commonly called batch processing).
- For example, in genomics data processing, a researcher might use a job scheduler to submit 100 tophat alignment jobs to a cluster of computers at their institute's data center

# What is cloud computing?

- The practice of using a network of remote servers hosted on the Internet to store, manage, and process data, rather than a local server or a personal computer.
- For example, instead of using a local server or buying 25 computers with 8 CPU's each, 70Gg of RAM, etc. for the RNA-seq course we rented these computers on the Amazon 'Cloud'. All analysis for the course actually happened at a massive data center in Northern Virginia



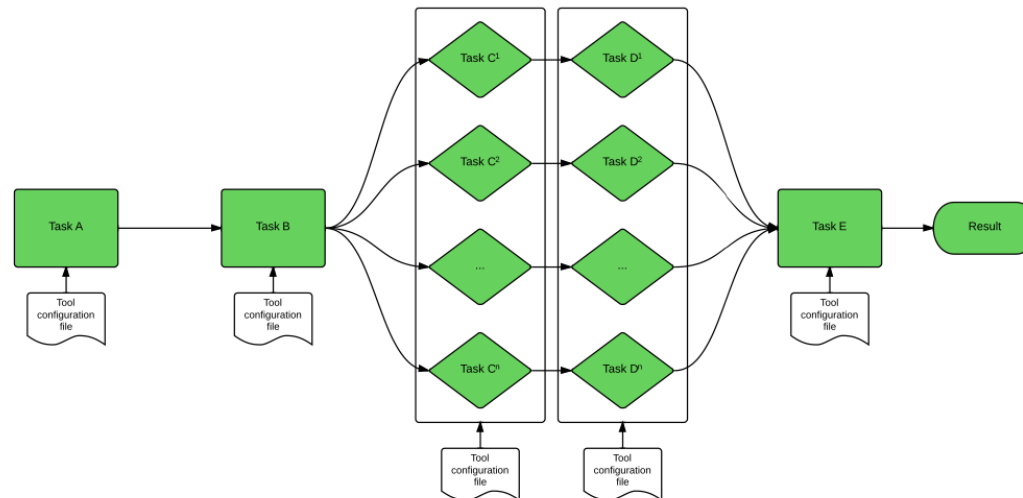
# What is a virtual machine?

- A *virtual machine* (VM) is an operating system OS or application environment that is installed on software which imitates dedicated hardware. The end user has the same experience on a *virtual machine* as they would have on dedicated hardware.
- In the context of genome analysis pipelines a virtual machine may sometimes be used to allow researchers to share and distribute very complex computing environments (may dependencies) that are difficult to set up.



# What is a workflow management system?

- A **workflow management system** (WfMS) is a software **system** for the execution of a defined sequence of tasks, arranged as a **workflow**.
- For example, the RNA-seq analysis has many steps with interconnected dependencies
  - TopHat alignment of several lanes of data needs to happen before they can all be merged into a final BAM file, and merging needs to happen before indexing of the BAM, and so on.
  - Some steps can happen in parallel, other in series. Workflow systems help handle these dependencies



# What is a software development kit (SDK)?

- A software development kit (SDK) is a set of software development tools that facilitates the creation of applications for a certain software framework
- E.g. DNA Nexus Platforms provides software development kit with support for several programming languages to help you build pipelines efficiently in their system

# What is an application programming interface (API)

- An API is a set of routines, protocols, and tools for building software applications. An API expresses a software component in terms of its operations, inputs, outputs, and underlying types. An API defines functionalities that are independent of their respective implementations, which allows definitions and implementations to vary without compromising each other.

# What is distributed storage and processing (e.g. 'Hadoop')?

- Hadoop is an open-source software framework for distributed storage and distributed processing of Big Data on clusters of commodity hardware. Its Hadoop Distributed File System (HDFS) splits files into large blocks and distributes the blocks amongst the nodes in the cluster. For processing the data, the Hadoop Map/Reduce moves code (software) to the nodes that have the required data, and the nodes then process the data in parallel. This approach takes advantage of data locality, in contrast to conventional HPC architecture which usually relies on a parallel file system (compute and data separated, but connected with high-speed networking).

# Examples

- **Assuming you have some NGS data, how should you analyze it?**
- Depends where you are on the informatics spectrum. Do you want to:
  - Build a completely novel process, a custom pipeline, develop algorithms, write software, etc.
    - Maximum flexibility. Performance and scalability are determined by how well you engineer it.
  - Build on top of someone else genome analysis platform
    - Don't have to start from scratch but still have a lot of flexibility.
    - e.g. GMS, Arvados, DNA Nexus, bcbio-nextgen, Gkno, etc.
  - Upload data in web browser, use graphical user interface
    - Sacrifices flexibility for ease of use
    - Galaxy, Illumina BaseSpace
  - Have someone do the analysis for you and give you the results

# Companies whose platforms amount to bioinformatics for hire...

- Appistry's Ayrris
- Seven Bridges Genomics
- GenomOncology
- IBM's PowerGene Orchestrator
- BINA Genomic Analysis System
  - Sort of. They provide a pre-configured hardware + software solution, help you install it and connect it to your in house data production
- Etc.

# Galaxy

- <http://galaxyproject.org/>
- Open Source academic project.
- Example RNA-seq workflow
  - <https://usegalaxy.org/u/mwolfien/w/rnaseq-wolfien-pipeline>
- A web based interface that allows you to run existing workflows or create custom analyses by combining tools in the Galaxy ‘toolshed’

# Illumina BaseSpace

The screenshot shows the Illumina BaseSpace dashboard. At the top is a navigation bar with the BaseSpace logo, a 'Dashboard' button, and icons for 'Prep', 'Runs', 'Projects', 'Apps', 'Public Data', and 'Help'. On the right of the navigation bar is a search icon, a user profile for 'Malachi Griffith', and the 'illumina' logo. The main content area is divided into several sections. On the left, a 'NOTIFICATIONS' section lists four items: 'Shotgun metagenomics can now be analyzed in the BaseSpace platform.' (Nov 17, 2014), 'Upcoming BaseSpace Developer Conference in San Francisco!' (Nov 06, 2014), 'Proteomics? There are Apps for that!' (Oct 03, 2014), and 'Taking Out the Trash' (Sep 15, 2014). Below this is a 'RUNS' section showing two completed runs: '2x151PhiX' and 'BacillusCereus'. To the right of the notifications is a 'TIP OF THE DAY' section with a message about transferring ownership. Below the tip is a 'PROJECTS' section listing 'WASHU', 'Illumina FastTrack Services Cancer Analysis D...', 'BaseSpaceDemo', and 'TumorNormal\_WGS\_HiSeq2000\_CSW\_0.23'. On the far right is an 'ANALYSES' section showing four analysis entries, each with a 'WASHU' icon and a link to a specific analysis (e.g., 'iPathwayGuide', 'Cufflinks Assembly & DE 08/26...', 'RNA Express 08/26/2014 4:16:19', 'RNA Express 08/26/2014 3:09:40'). A vertical 'contact us' button is on the right edge of the dashboard.

- Use integrated 'apps' and automated pipelines.
- Graphical interface
- <https://basespace.illumina.com>



# DNA Nexus Platform

DNA Nexus

PLATFORM SCIENCE SUPPORT COMPANY

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YOUR VISION.

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De novo computational biology and cloud

Control Your Data  
Certified ISO 27001 framework to

Remove All Limits on Scale

- Build your own pipeline or use an existing one
- DNA Nexus handles cloud deployment, etc. for you
- <https://www.dnanexus.com/>

# Other pipeline development platforms to build on top of

- Gkno
  - <http://gkno.me/>
- Genome Modeling System (GMS)
  - <https://github.com/genome/gms>
- Arvados
  - <https://arvados.org/>
- Bcbio-nextgen
  - <https://bcbio-nextgen.readthedocs.org/en/latest/>
- OmicsPipe
  - <http://sulab.org/tools/omics-pipe/>
- NGSANE
  - <https://github.com/BauerLab/ngsane>

# The Global Alliance for Genomics Health (ga4gh)

- An international coalition, formed to enable the sharing of genomic and clinical data.
- Work on data models and APIs for Genomic data.
- Not yet entirely clear what is available to be used by end users beyond the 'beacon' project:
- <http://genomicsandhealth.org/>
- <http://ga4gh.org/#/>
- <https://github.com/ga4gh>
- <http://ga4gh.org/#/beacon>

# We are on a Coffee Break & Networking Session

