on the GenomeCloud

Yet another on-demand Galaxy cloud,
but only powered by Apache CloudStack

Youngki Kim

kt, Korea

Outline

- **Introducing GenomeCloud**
  - Who we are, why we start
- Galaxy on the GenomeCloud
- Use cases and lessons learned
- Conclusions

Diversity

GCC 2014 Talks

GCC 2014 Posters

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Introducing GenomeCloud

GenomeCloud

A complete and integrated platform from analyzing genome data to the interpretation of analysis results.

View all services

g-Analysis

Automated genome analysis pipelines at your fingertips.

g-Cluster

Easy-of-use and cost-effective genome research infrastructure

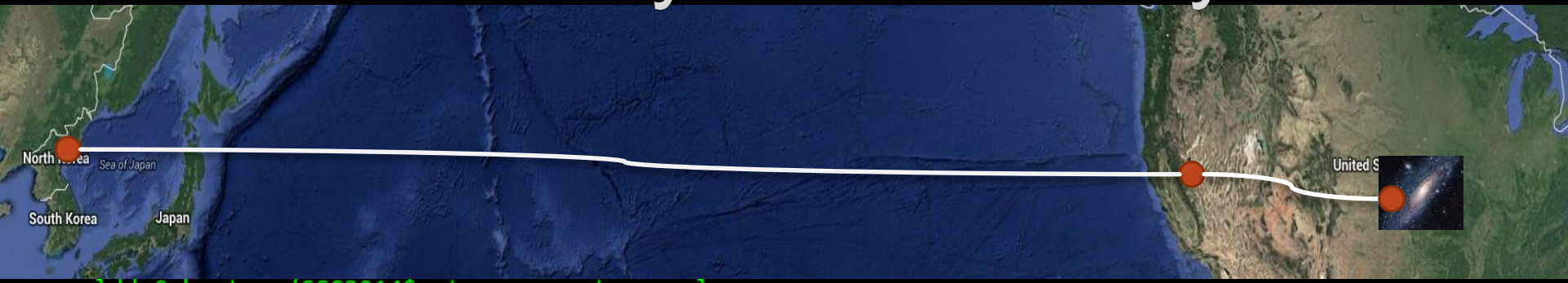
g-Storage

A simple way to store, share and protect data

g-Insight BETA

Accurate analysis and interpretation of biological meaning of genome data

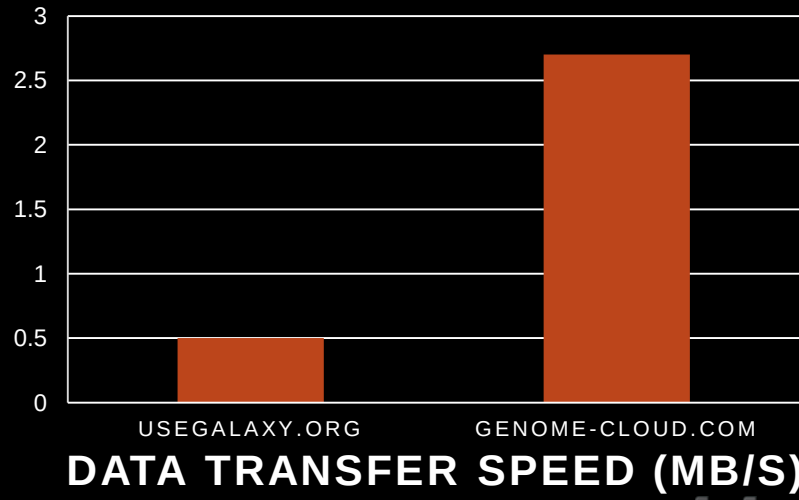
Far away to the Galaxy




```
molddu@ubuntu:~/GCC2014$ mtr --report usegalaxy
HOST: ubuntu                      Loss%   Avg
  1.|-- 192.168.65.2               0.0%   0.5
  2.|-- 192.168.0.1               10.0%   3.8
  3.|-- 14.32.67.254               0.0%  11.4
  4.|-- 121.138.226.65             0.0%  10.3
  5.|-- 61.78.42.162               0.0%   9.5
  6.|-- 121.138.12.137             0.0%  15.6
  7.|-- 112.174.18.21              0.0%  10.8
  8.|-- 112.174.8.122              0.0%  17.5
  9.|-- 112.174.87.113             0.0%   9.9
 10.|-- 112.174.87.234             0.0%  142.3
    `|-- ???
 11.|-- ae7-113.edge6.LosAngeles1  0.0%  143.4
 12.|-- vlan70.csw2.LosAngeles1.L  0.0%  193.8
 13.|-- ae-72-72.ebr2.LosAngeles1  0.0%  197.9
 14.|-- ae-3-3.ebr3.Dallas1.Level  0.0%  208.5
 15.|-- ae-73-73.csw2.Dallas1.Lev  0.0%  209.2
 16.|-- 4.69.146.14               60.0%  1130.
 17.|-- 4.71.198.54                0.0%  292.0
 18.|-- aust-utnoc-core-ge-0-0-0-  0.0%  177.4
 19.|-- 192.124.226.22              0.0%  182.8
 20.|-- vl664-ex9214-roc.net.tacc 10.0%  190.7
 21.|-- fw0.tacc.utexas.edu       10.0%  182.1
 22.|-- galaxy-web-02.tacc.utexas 10.0%  195.2
```

2X more hosts than GenomeCloud

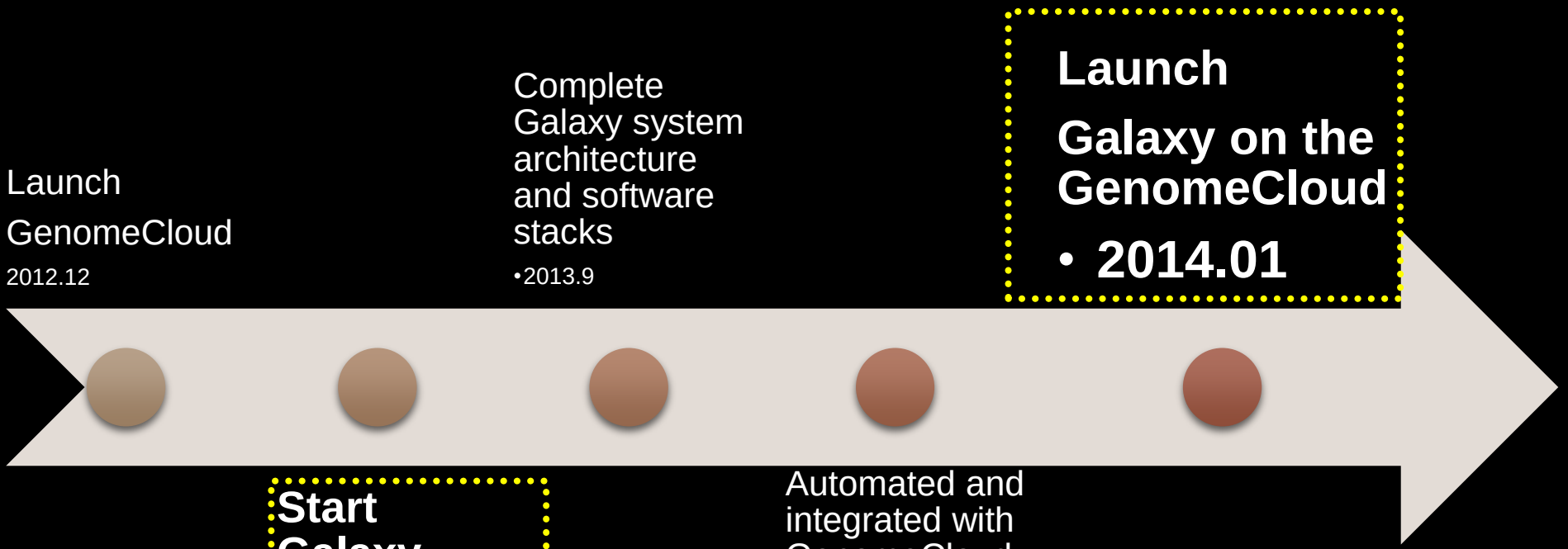
- **5 X more time** than GenomeCloud for data transfer



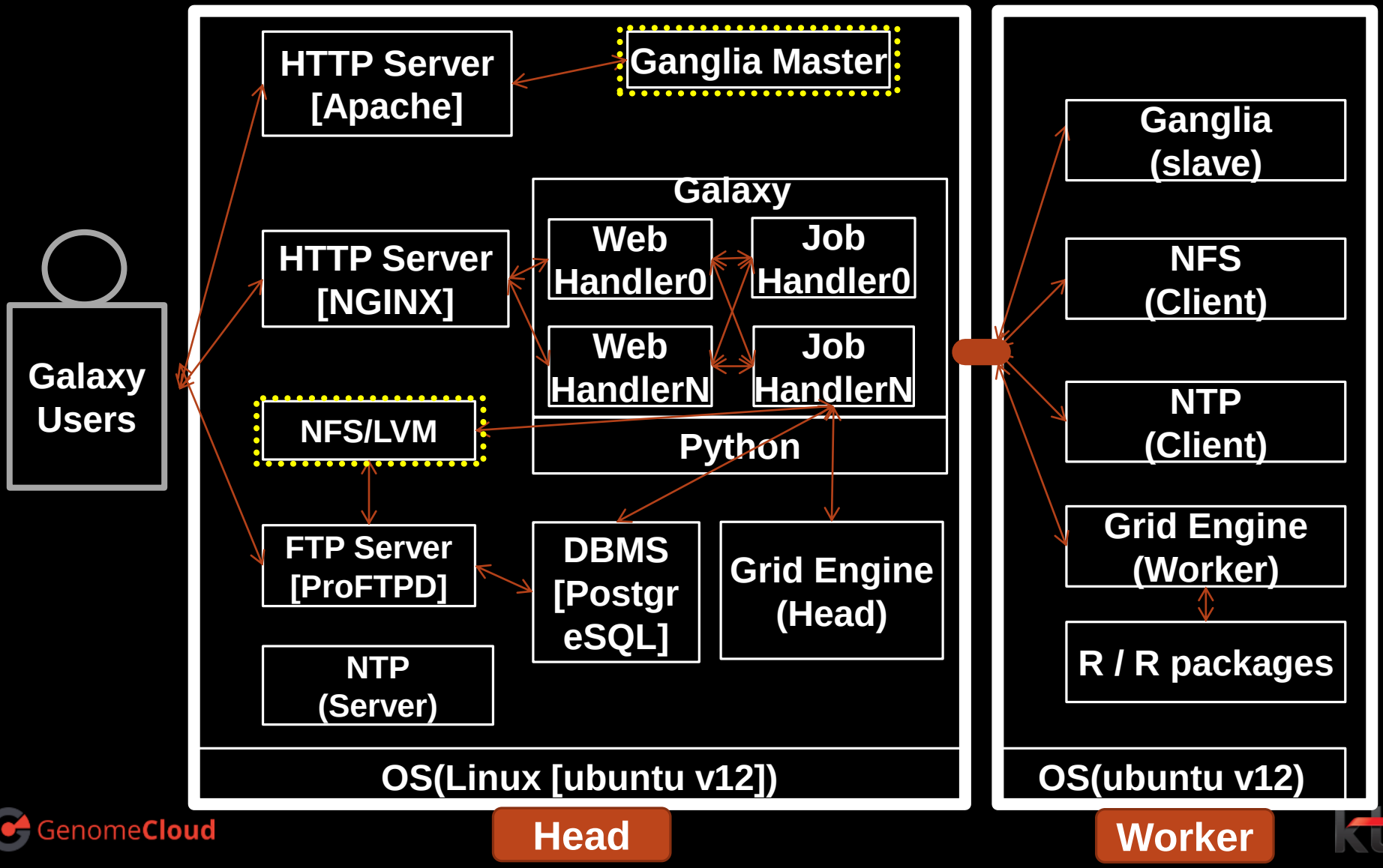
Outline

- Introducing GenomeCloud
- **Galaxy on the GenomeCloud**
  - Software stack, system architecture, automation and add-ons
- Use cases and lessons learned
- Conclusions

Timeline

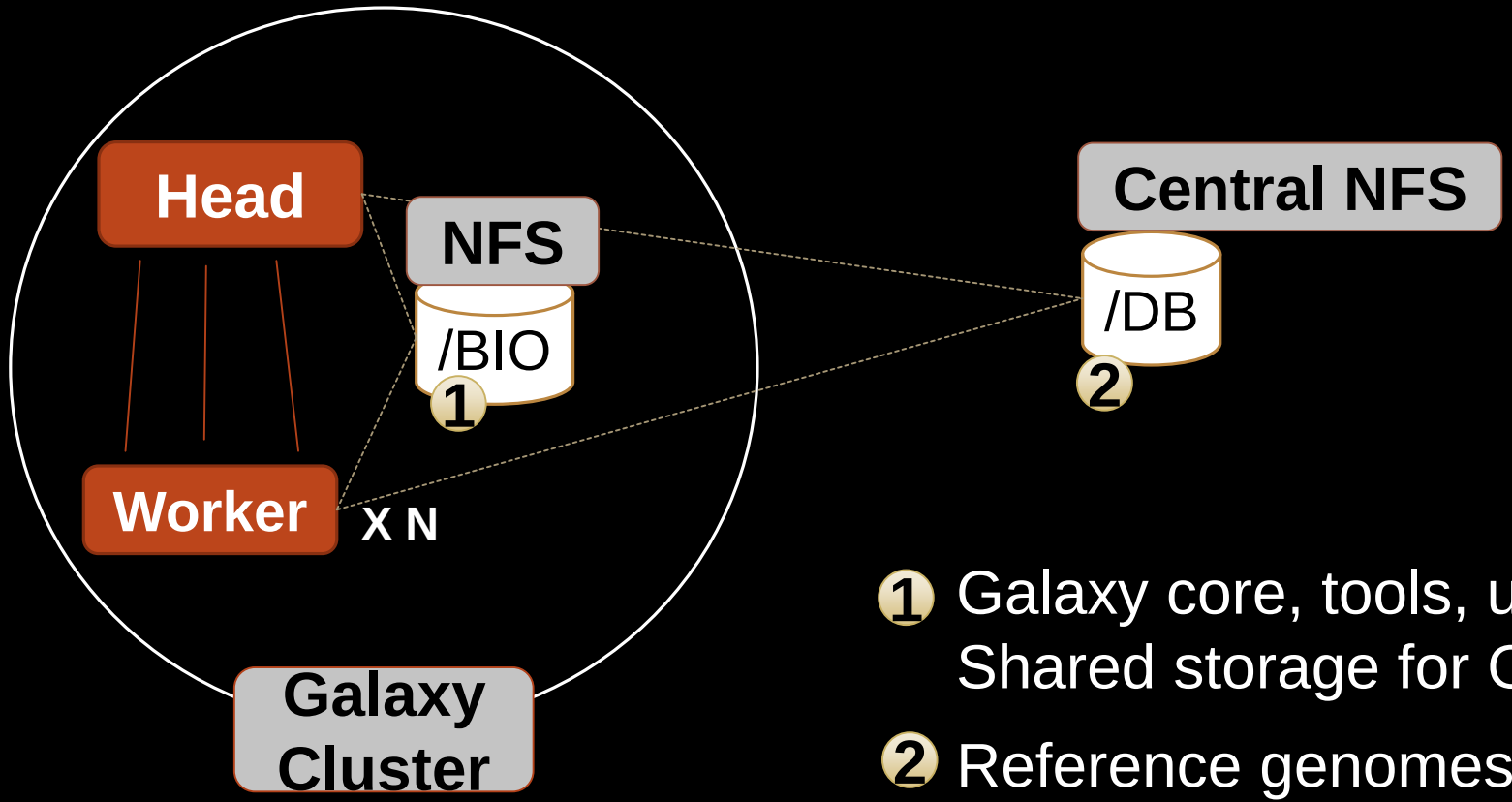

Launch
GenomeCloud
2012.12
Start
Galaxy
setup in
servers
• 2013.7
Complete
Galaxy system
architecture
and software
stacks
•2013.9
Automated and
integrated with
GenomeCloud
•2013.12
Launch
Galaxy on the
GenomeCloud
• 2014.01

Galaxy software stack



Galaxy system architecture

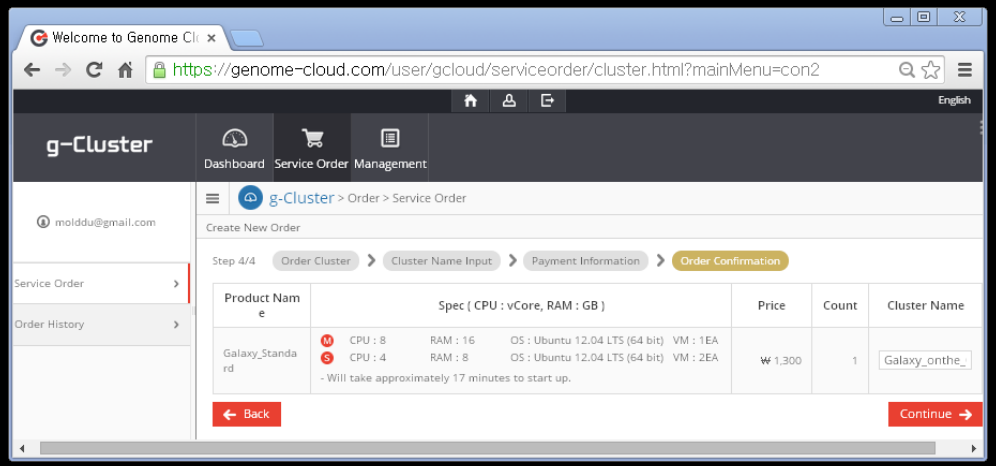
- Decoupled shared storages

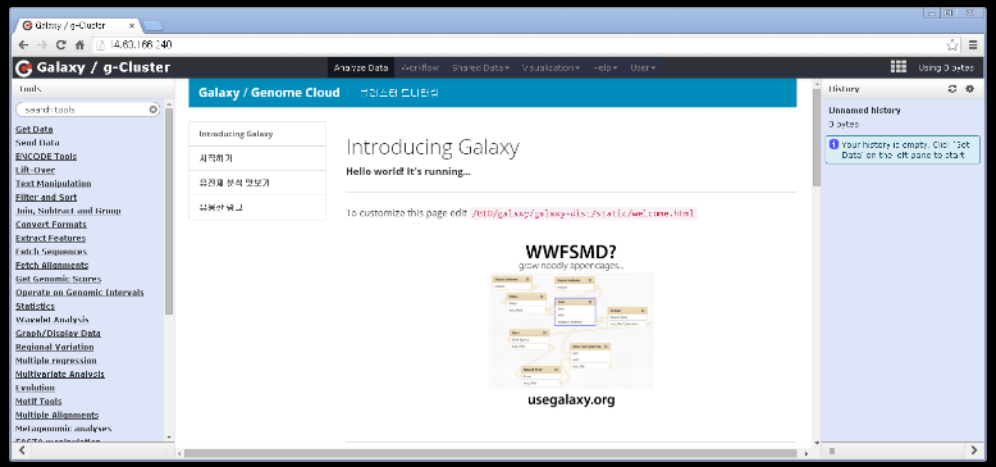


1. Galaxy core, tools, user data
   Shared storage for Grid Engine
2. Reference genomes data,
   Genome data locations

Fully automated cluster creation

- Select cluster type ➔ name it ➔ use it





1. Deploy head node
2. Associate public IP
3. Create port forwarding rule
4. Create and attach disk volumes
5. Deploy worker nodes

CloudStack APIs

6. Clustering, Software setup, Galaxy setup

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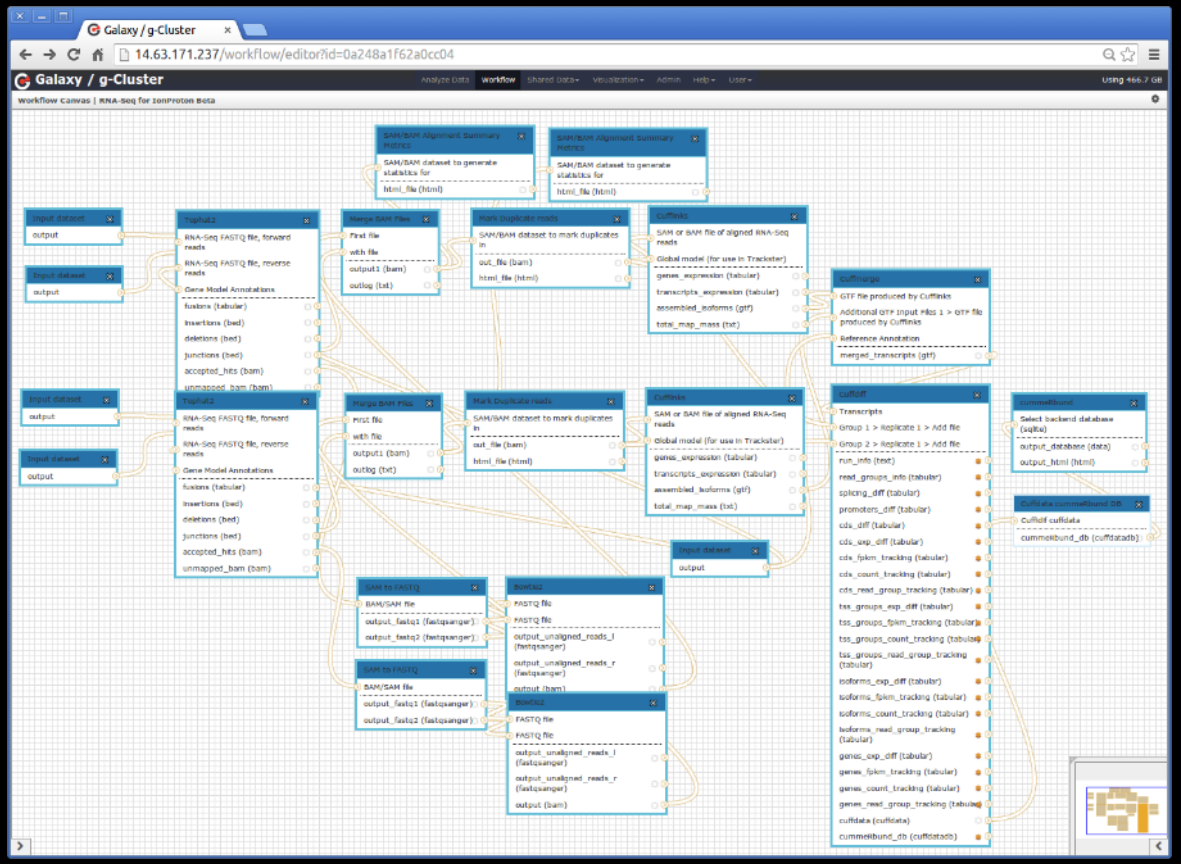
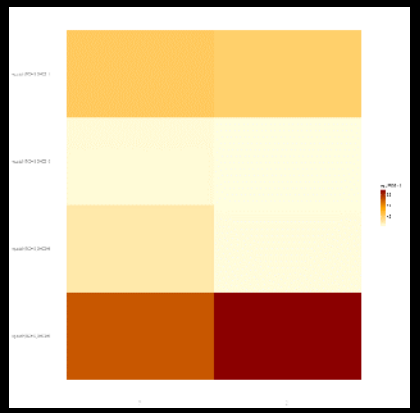
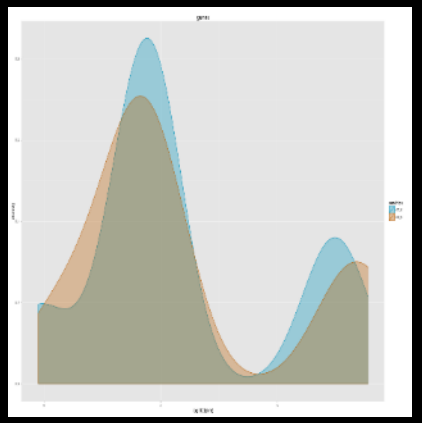
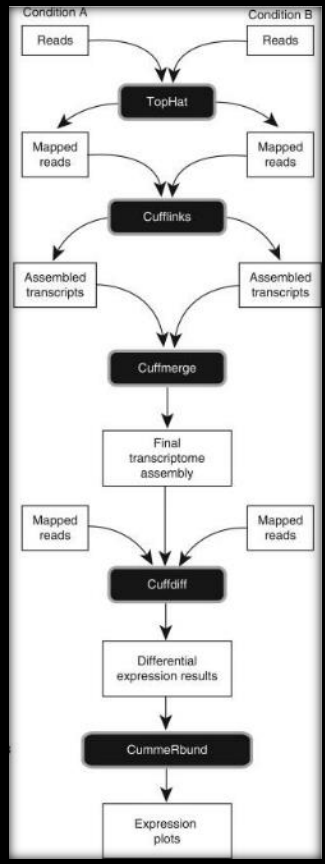
Pre-installed pipelines

- Workflows for RNA-Seq(Tuxedo, Ion Proton) analysis



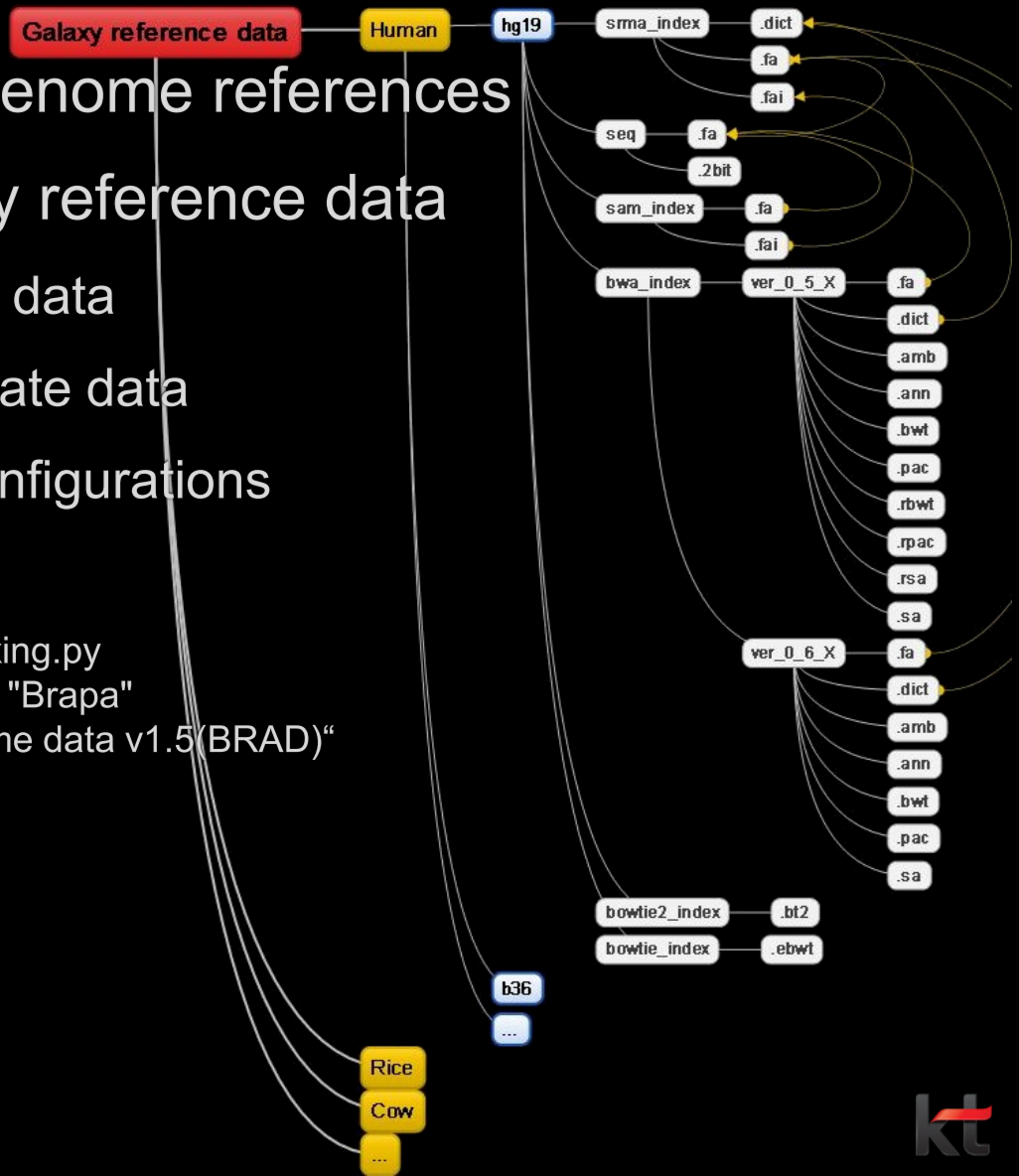






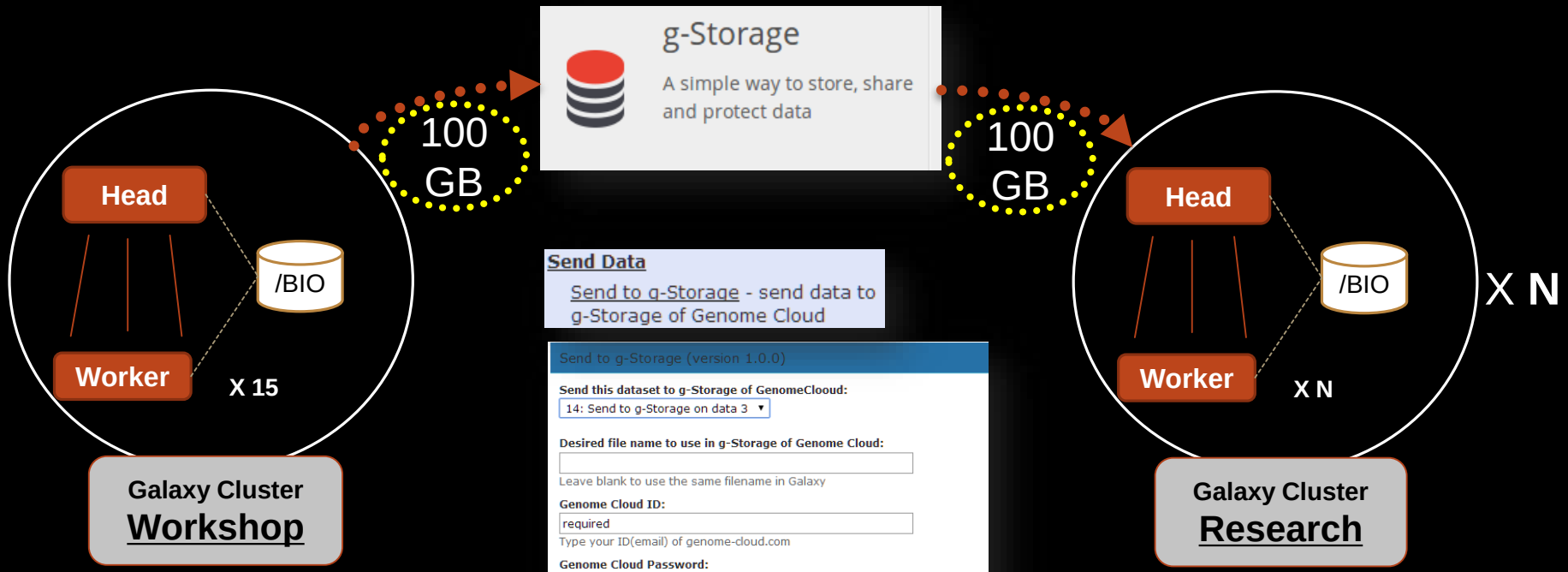
Supporting diverse genome references

- Rapid support of new genome references
- A python tool for Galaxy reference data
  - Index reference genome data
  - Make directories and locate data
  - Change 10 + location configurations
  - Example:
    - python galaxy_reference_indexing.py
      -i "Brapa_sequence_v1.5.fa" -s "Brapa"
      -d "brapa_1.5" -e "Brapa genome data v1.5(BRAD)“



Integration with g-Storage

- Inter Galaxy cluster data transfer
  - Develop a galaxy tool for sending large data



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Use case

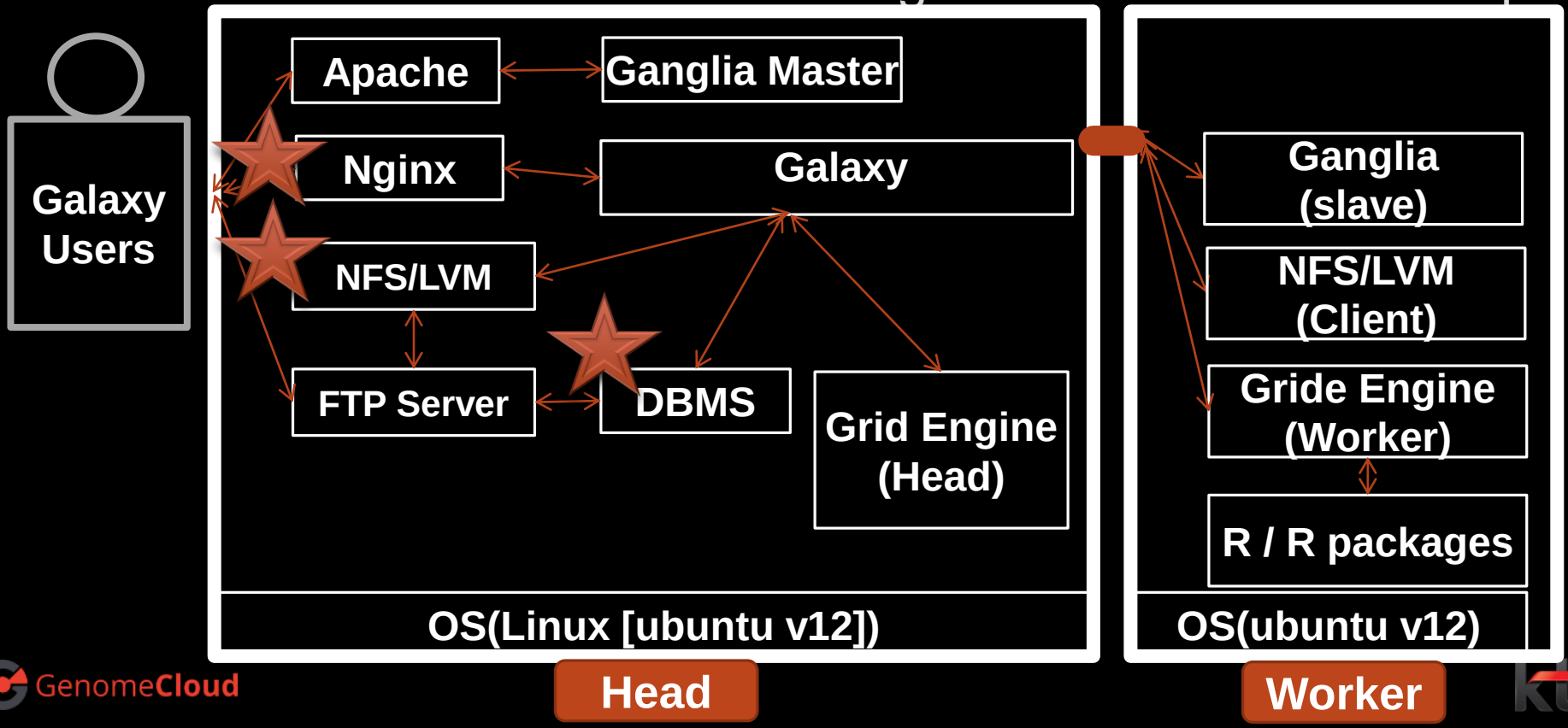
- Bioinformatics education support

Use case

- 4 half-day bioinformatics workshops
  - Date: 13th, 20th May, 3rd,10th Jun
  - **Attendees : 50 +**
  - Galaxy : 8 core 16GB X 16 servers
  - **Contents : from fastQC to RNA-Seq Analysis**
  - Off site workshop and home works
    - # of executed jobs: 5,000 +
  - Feedback: good enough for further research
  - Lessons learned:
    - Be aware of bottlenecks
    - Fix it or adapt to it

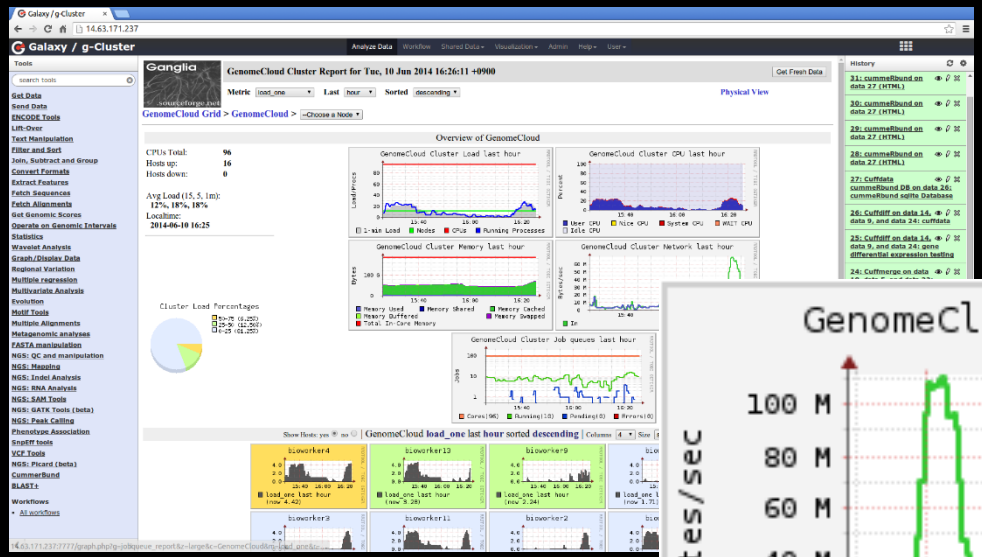
Bottlenecks

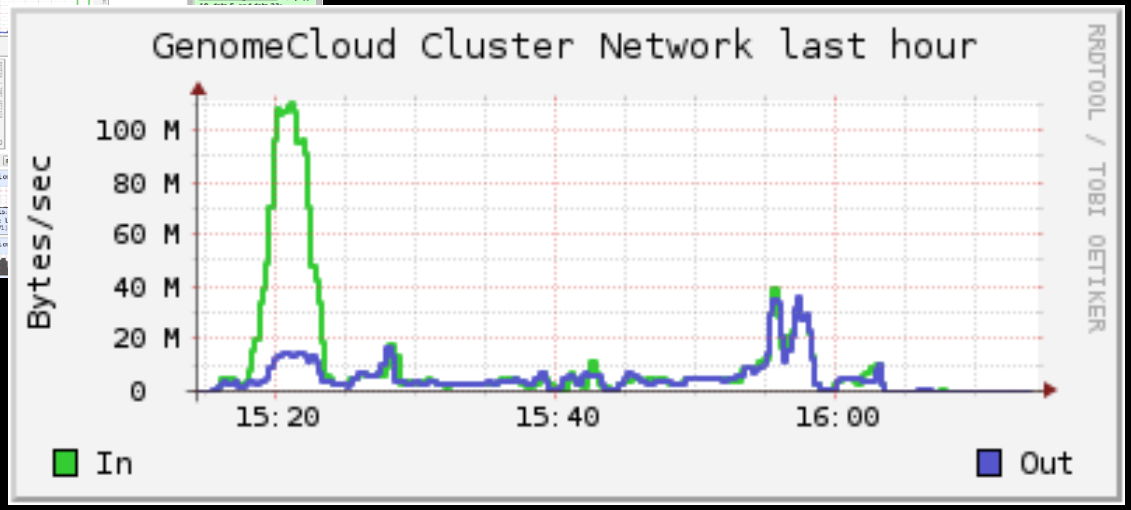
- DBMS: ➔ fix by tuning configuration
- Get data: ➔distribute
- Data transfer from shared storage: ➔ be aware and adapt



Network bottleneck

- Some NGS tools(BWA, bowtie …) saturate the network bandwidth
  - → expect 5 to 10 minutes lead time





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Lessons we learned

- Don’t re-invent the wheel
  - Similar demands and questions were asked and answered
  - 2 anecdotes (run_reports.sh, data manager)
- The more you know, the more you will find the value of Galaxy

Conclusions

Galaxy on the GenomeCloud provides more use cases to the Galaxy Community

- Geography
- Infrastructure
- Users

Galaxy is becoming a door to the diverse bioinformatics research in Korea.

And,

GenomeCloud helps them unlock the door.

Acknowledgment

- **Galaxy team**
  - → We could never **start** this without you
- **GenomeCloud team**
  - → We could never **finish** this without you
  - Daechul choi, Changbum hong, Kwangjoong kim, Wanpyo hong, Hankyu choi, Hosang jeon, Sehyuk yoon, Eunjean jo