BiobankCloud – A PaaS for Storage, Analysis and Inter-connection of Biobank Data

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www.biobankcloud.eu is financed by the European Commission 7th Framework Programme.
HiSeq X Ten^ => ~18,000 genomes/year
Volume  => ~5.2 PB/year*
Velocity => ~45 MB/sec*

^Cost ~$10 million
*5.2 PB assumes a replication factor of 3

See: http://goo.gl/OCgJ36
Schizophrenia is not based on genomic variation

There are 60 mutations associated with schizophrenia

[Images source: Patterson, Fighting the Big C with the Big D, 2014]
Network effects: Biggest Dataset wins!

Centralized dataset: technically feasible, politically hard.
Federated dataset: technically hard, politically feasible.
The BiobankCloud Project

www.biobankcloud.eu
The biobank “concept” is defined (by Swedish law) as:

“biological material from one or several human beings collected and stored indefinitely or for a specified time and whose origin can be traced to the human or humans from whom it originates”

In Sweden, they have the goal of digitizing biological material in biobanks (e-biobanking).

≈ 500,000 people
BiobankCloud PaaS

- Biobankers
  - NGS data producers
    - Collections, samples
  - Non-programmers

- Bioinformaticians
  - NGS data analysts
  - Programmers
    - Python, R, Matlab, scripts

BiobankCloud LIMS

- Cuneiform/HiWAY
- Hops-YARN
- Hops-HDFS

Kerberos
CharonFS

IT Admins
LIMS: Lab Information Management System

- LIMS for NGS Data
  - Multi-tenancy
  - Study-level
  - Role-Based Access Control
  - Two-factor authentication
  - Audit trails
  - Plugin model for apps
  - REST APIs
Manage Sample Collections and Studies

Collections

- LifeGene
- Stockholm-2

Select a collection in the panel on the left.

Add collection

Dataset(s) uploader

Drag & Drop Genomic data here to upload or Select data from your computer

Check Uploaded Samples
Data Storage: HopsFS

- A modified version of HDFS
- Customizable and Scalable Metadata
- High throughput for read and write operations
- NameNode failover time ≈ 5 seconds (vs ~1 minute for HDFS)
HopsFS Erasure Coding

HDFS 2.x
Triple Replication (+200%)

2x Replication + XOR (+120%)

Reed-Solomon (+40%)
Run Cuneiform Workflows on YARN

Cuneiform jobs

History

Untitled job
- Run on: Mon Jan 26 11:11:34 CET 2015
- Run by: Test
- State: FINISHED
- Execution time: 2192526 ms
- Logs: stdout.log, stderr.log
- Results: 4379648099 1 result

Run configuration

- Job name
- Upload workflow file: + Upload
- Uploaded file: wordcount.cf

Input parameters

- Execute

Typical Workflow

- FastQ
- Align
- BAM
- Variant Calling
- VCF
- Annotate
- Annotated Results
Cuneiform

- Light-weight statically typed functional dataflow language
- Compiles into dynamic pipelines of black-box tools
- Aims
  - Make foreign code integration as easy as possible
  - Allow complex, iterative workflows
  - Deduce options for parallelism automatically

```cunef
deftask per-chromosome(
    vcf( File )
    : fa( File )
    [fastq1( File ) fastq2( File )] ) {
    bt2idx = bowtie2-build( fa: fa );
    fai = samtools-faidx( fa: fa );
    sam = bowtie2-align(
        idx: bt2idx
        fastq1: fastq1
        fastq2: fastq2 );
    bam = samtools-view( sam: sam );
    sortedbam = samtools-sort( bam: bam );
    mpileup = samtools-mpileup(
        sortedbam: sortedbam
        fa: fa
        fai: fai );
    vcf = varscan( mpileup: mpileup );
}
Hi-Way

- **Hi-Way Workflow Application Master for YARN**
- Executes workflows on Hadoop YARN
  - Scalability, maintenance, fault tolerance, ...
- Full provenance tracing, *executable provenance*
- Runs **Cuneiform**, Galaxy, Pegasus (DAX)
- Various *(adaptive)* schedulers
- Dynamic workflow interface
Integration with Public Clouds
Two Problems...

- How to use public clouds to increase the storage capacity of BiobankCloud platform deployments?

- How to interconnect different BiobankCloud platform deployments in a federation?

  (Important: how to do that without endangering **security** and with minimal **management effort**?)
Charon FS

- Windows Azure
- Google
- Rackspace
- Amazon S3

Charon
BiobankCloud PaaS

Charon
BiobankCloud PaaS

Charon
BiobankCloud PaaS

Hadoop
DepSky: Dependable Cloud-of-Clouds Object Storage


Why multiple clouds?

Survive cloud-wide outages
Avoid vendor lock-in
Better read performance
Tolerance to data corruption
- Bugs
- Malicious insiders
- Attacks and intrusions
DepSky Storage Efficiency and Confidentiality

Data

encrypt

randomly generated key

secret sharing

K

F_1
F_2
F_3
F_4

S_1
S_2
S_3
S_4

Cloud A
Cloud B
Cloud C
Cloud D

F_1
F_2
F_3
F_4

S_1
S_2
S_3
S_4

erasure code

Inverse process for reading from f+1 shares/fragments.

F_1
S_1

F_2
S_2

F_3
S_3

F_4
S_4
1. Most bioinformatics tools also work directly over files, avoiding thus import/export operations.

2. The popularity of Dropbox-like services evidences that working with files is simple and intuitive.

3. A file system allows one to transparently store files in several locations (e.g., local storage, remote sites, clouds, cloud-of-clouds).
Charon Design Principles

- **Separation of file data and metadata**
  - Metadata: file name, size, permissions, stored in *name service* objects
  - Data: file contents in blocks of up to 16MB

- **Files can be stored in different locations**
  - Using semantic cues as in WheelFS (MIT). Examples:
    - `/shared/studies/.Site=CoC/rawreads`
    - `/shared/studies/.Site=local/vcfs`

- **No write/write file conflicts**
  - Files and directories are locked for write

- **Serverless design**
  - There are no explicit servers in a Charon infrastructure, only cloud (storage) services
  - All storage and coordination protocols are *data-centric*, based on the services cloud providers have to offer
Charon Architecture

Public Cloud A

Public Cloud B

metadata

d1

d2

A

B

C

D

A

B

C

Site 1

Site 2

Charon

Charon

Cache

Cache

TLS Channel
Finally, the results showed that prefetching file blocks significantly reduces end-to-end latency, which will be dictated by the third fastest cloud. The rapidity of the cloud-of-clouds (three out of four) to finish the write, thus the latency of clouds for different file sizes is presented in the cloud-of-clouds (C-CoC). The cloud-of-clouds (C-CoC) takes advantage of the fact that we need to update the data in a Byzantine environment.

The best performance for sequential workloads is provided by HARON. This happens because S3QL does not perform well with small files (256kB and 1MB). However, when working with big files (up to 1GB), HARON presents at least 25% better sequential write throughputs compared to the other cloud-backed file systems. In particular, S3QL and NFS provide a lower, but similar, read throughput (sequential and random) when compared with ext4. SCFS and HARON use compression and erasure codes, reducing significantly the amount of transmitted data, and consequently the experienced latency.

When considering write throughput, ext4 and NFS present a similar efficiency in reading and writing from a private repository in different locations: private repository in a local machine (C-Local), hard disk in a server (C-LAN), single cloud in Amazon S3 (C-S3), and cloud-of-clouds (C-CoC). In the last scenario, we use a repository in different locations: HARON, S3, and cloud-of-clouds (C-CoC). The cloud-of-clouds (C-CoC) does not support the big files (up to 1GB) used in this scenario and reports average values. C-CoC has a latency between the three evaluated systems, providing a lower, but similar, read throughput.
Summary

- **BiobankCloud PaaS**
  - One-click Cluster deployment
    - Chef/Karamel

- **Big Data Storage**
  - HopsFS – modified HDFS with scalable metadata and erasure code

- **Workflow Execution Engine**
  - Cuneiform – workflow language
  - Hi-way – execution engine on top of YARN

- **Multi-cloud Storage and Big Data Sharing**
  - Charon – Serverless Cloud-of-Clouds File System
  - Secure integration of public cloud storage to the system
  - Minimal infrastructure requirements

- The software will be made available in the next months
The Team

www.biobankcloud.eu

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