Eoulsan
Analyse du séquençage à haut débit dans le cloud et sur la grille

Journées SUCCES

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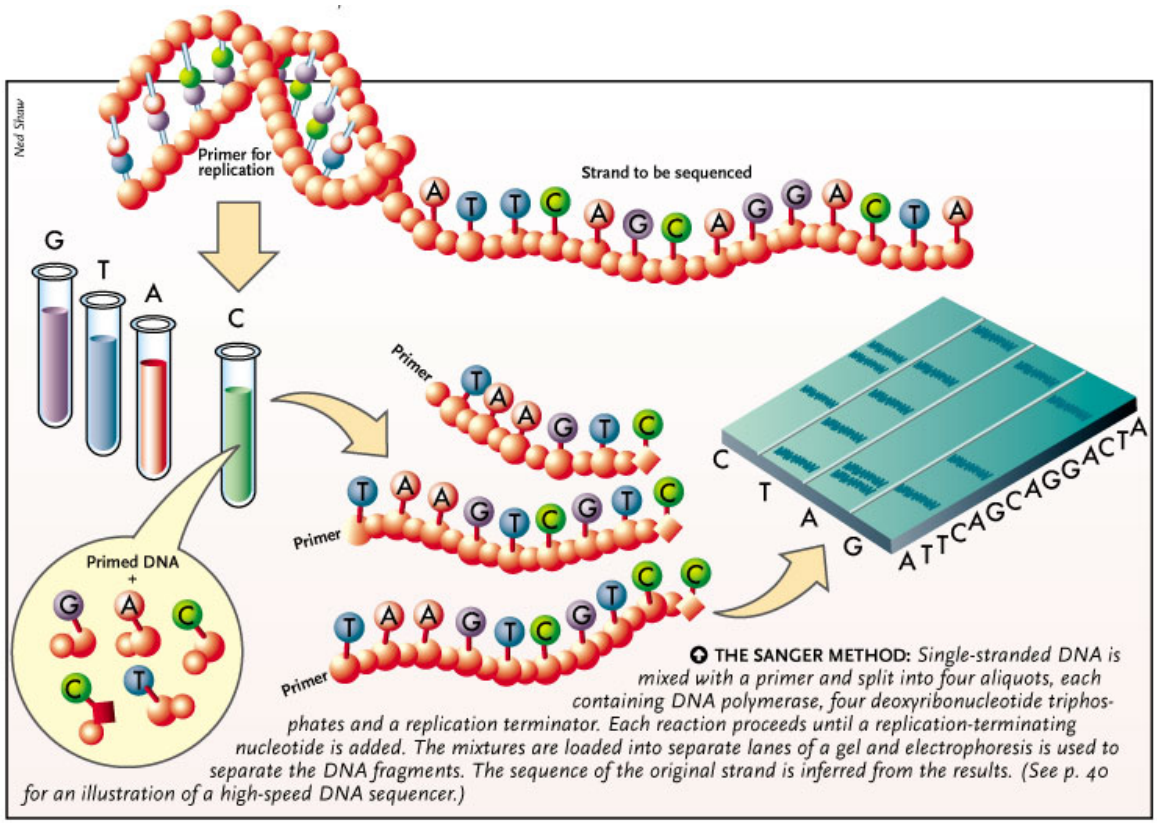
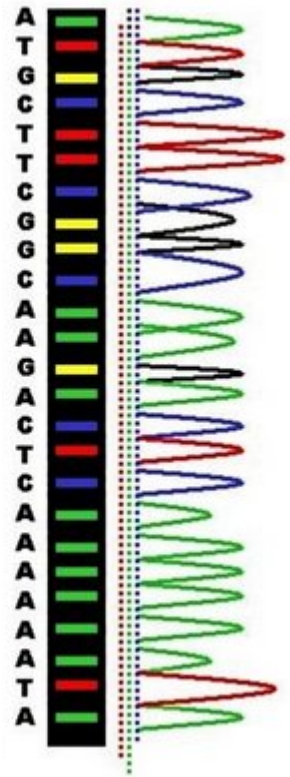
The Sanger DNA sequencing method

- **Sequencing by synthesis** by Frédérick Sanger (**1977**, chemistry nobel price 1980).

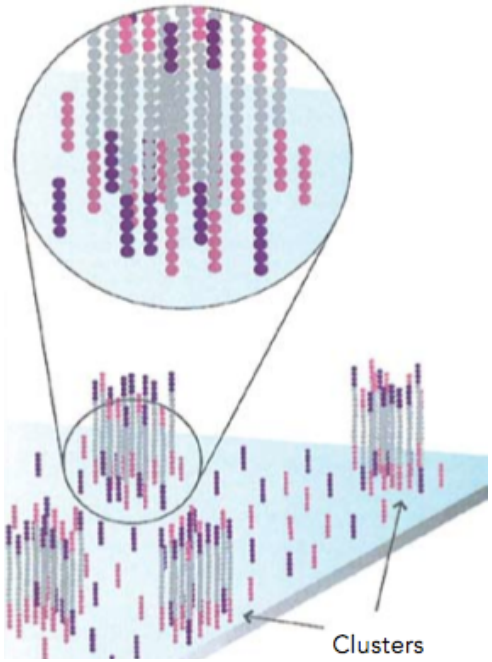


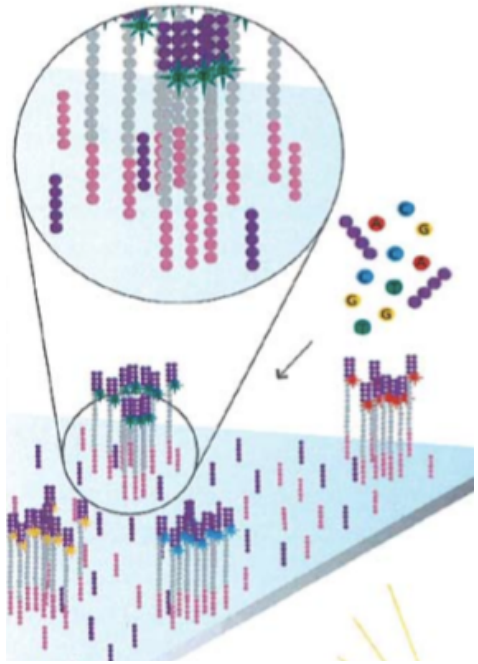


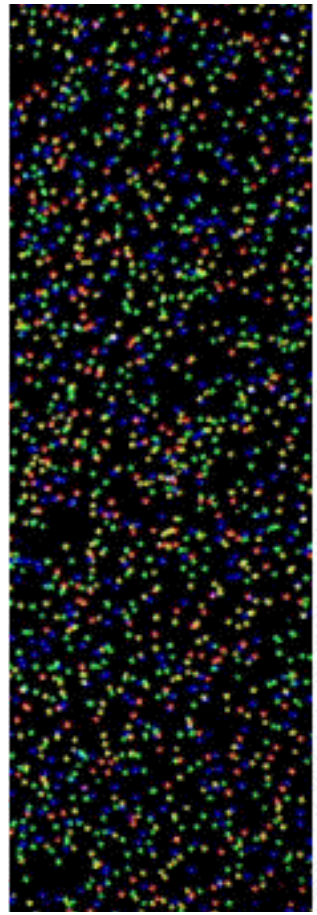
- **126 capillary sequencers** can sequence **one human genome in 12 days**.

From The Scientist

The second generation of sequencing device





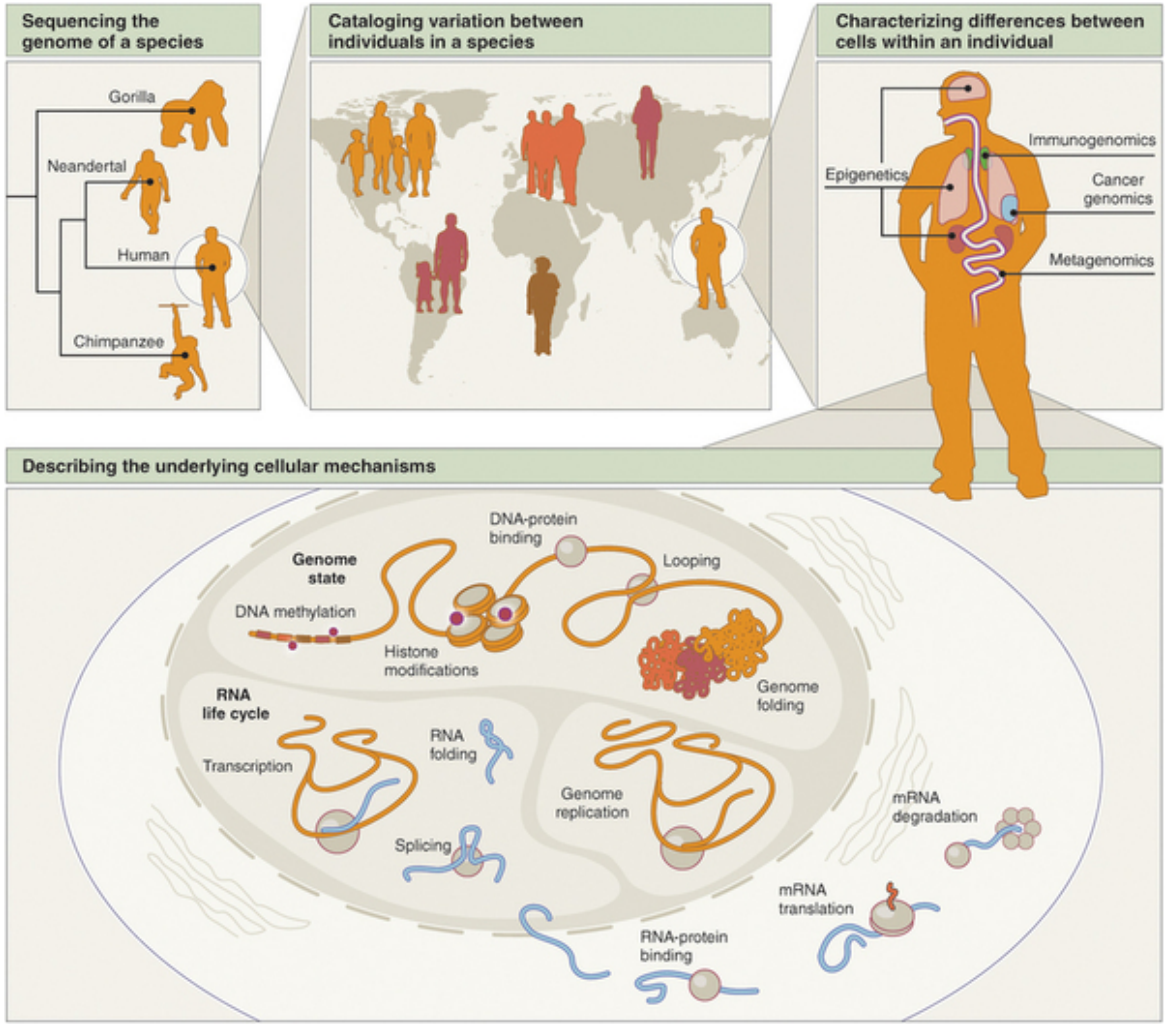


- **One** Illumina **HiSeq** can sequence **two human genomes** in **8 days**.

From htttp://www.illumina.com

Applications cover a lot of biological fields

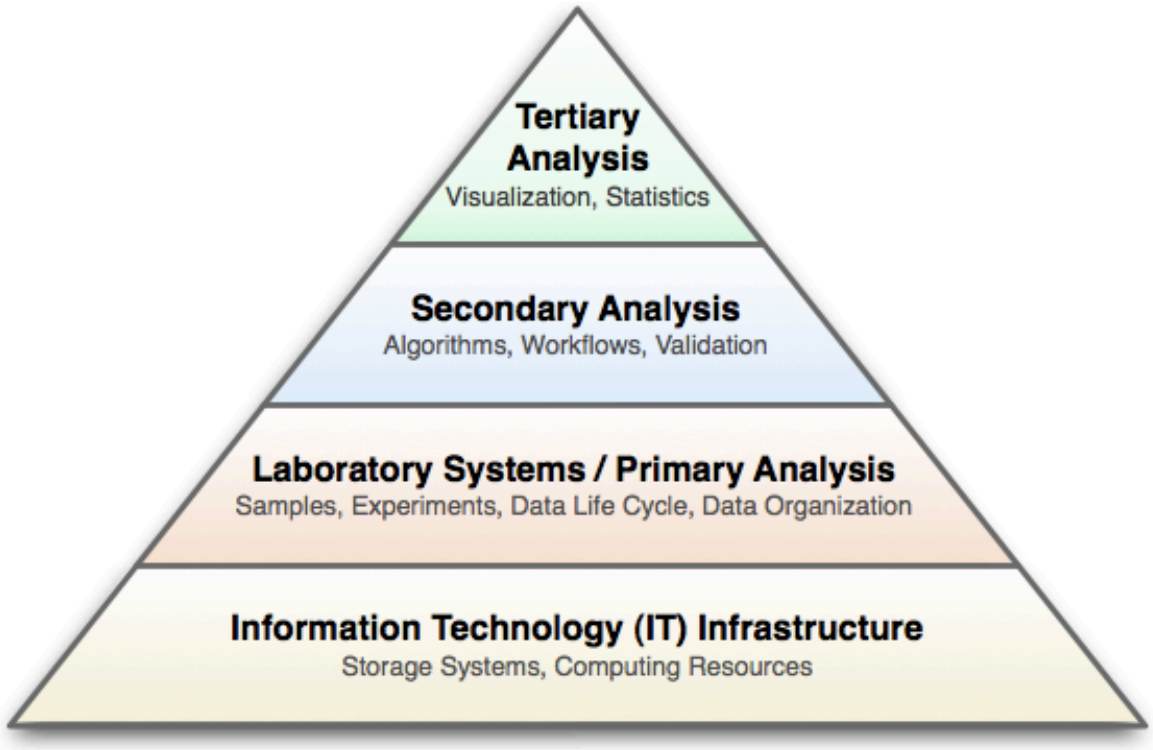
- De novo sequencing;
- Resequencing;
- Functional analysis;
- Metagenomic;
- Diagnostics;
- Personal genomic…



Shendure & Aiden (2012) Nat. Biotech.

Data analysis levels

- Sequencer outputs produce **To of data for each run** and large raw result files.
- Data analysis on big genomes **require calculation power and memory**.

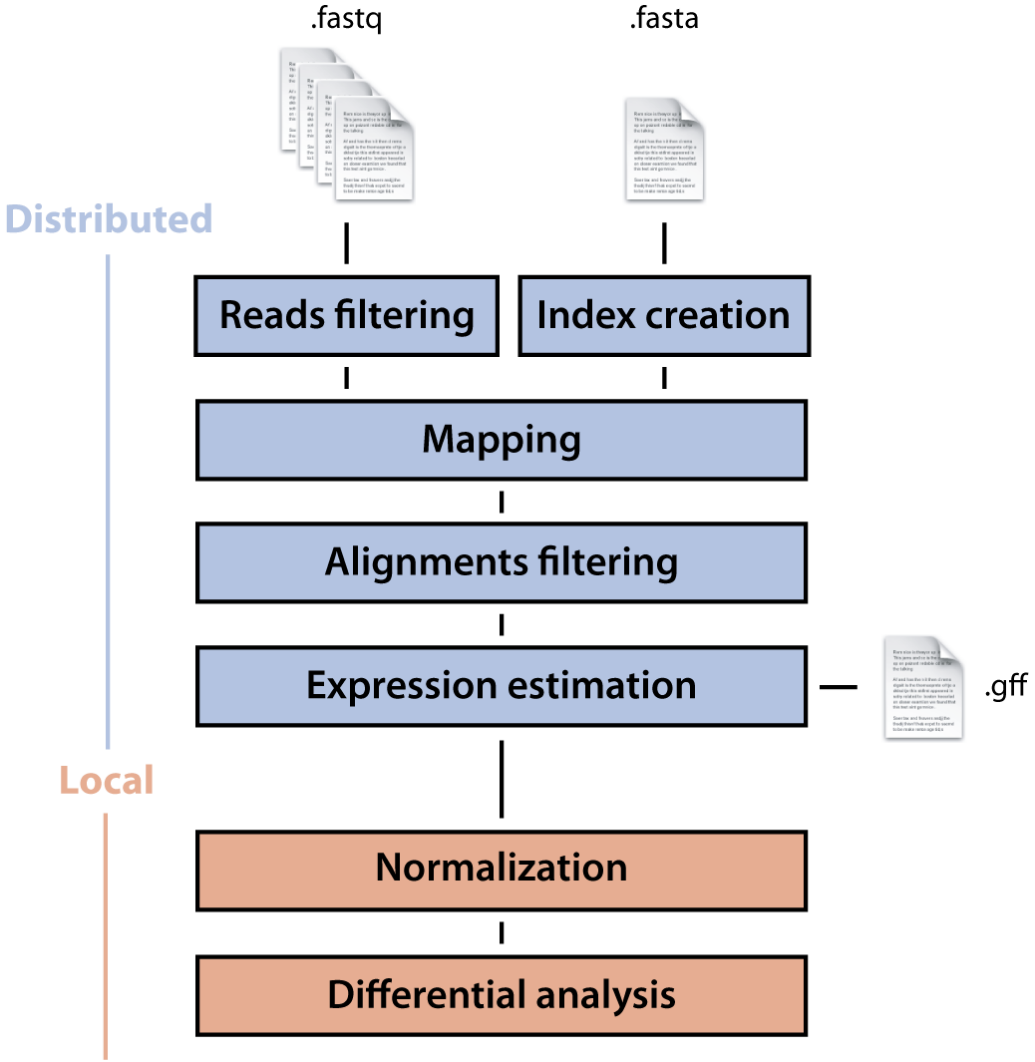


http://www.geospiza.com/finchtalk/labels/Next Generation Sequencing.html

Eoulsan: our RNA-Seq data analysis workflow

- Eoulsan works **from raw sequencer outputs** (Illumina) **to the list of differentially expressed genes**.
- Its **modular** and **flexible** analysis framework runs with various already available analysis solutions (SOAP2, Bowtie, Bowtie2, BWA, GSNAP).
- New **function extension** through external java plug-in.
- **Distributed calculation** to speed up the analysis.

Eoulsan

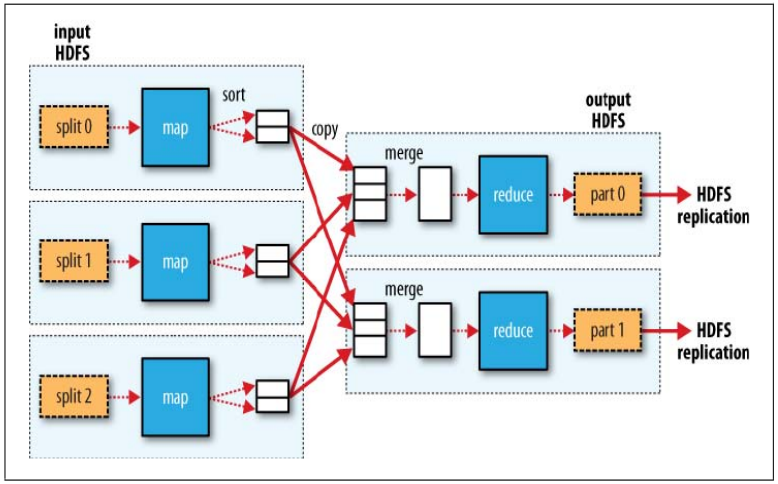


Jourdren (2012) *Bioinformatics*

http:/transcriptome.ens.fr/eoulsan/

We use MapReduce to increase analysis speed

- **MapReduce** is used for parallel computation and **automatically handles duties**, such as job scheduling, fault tolerance and distributed aggregation.



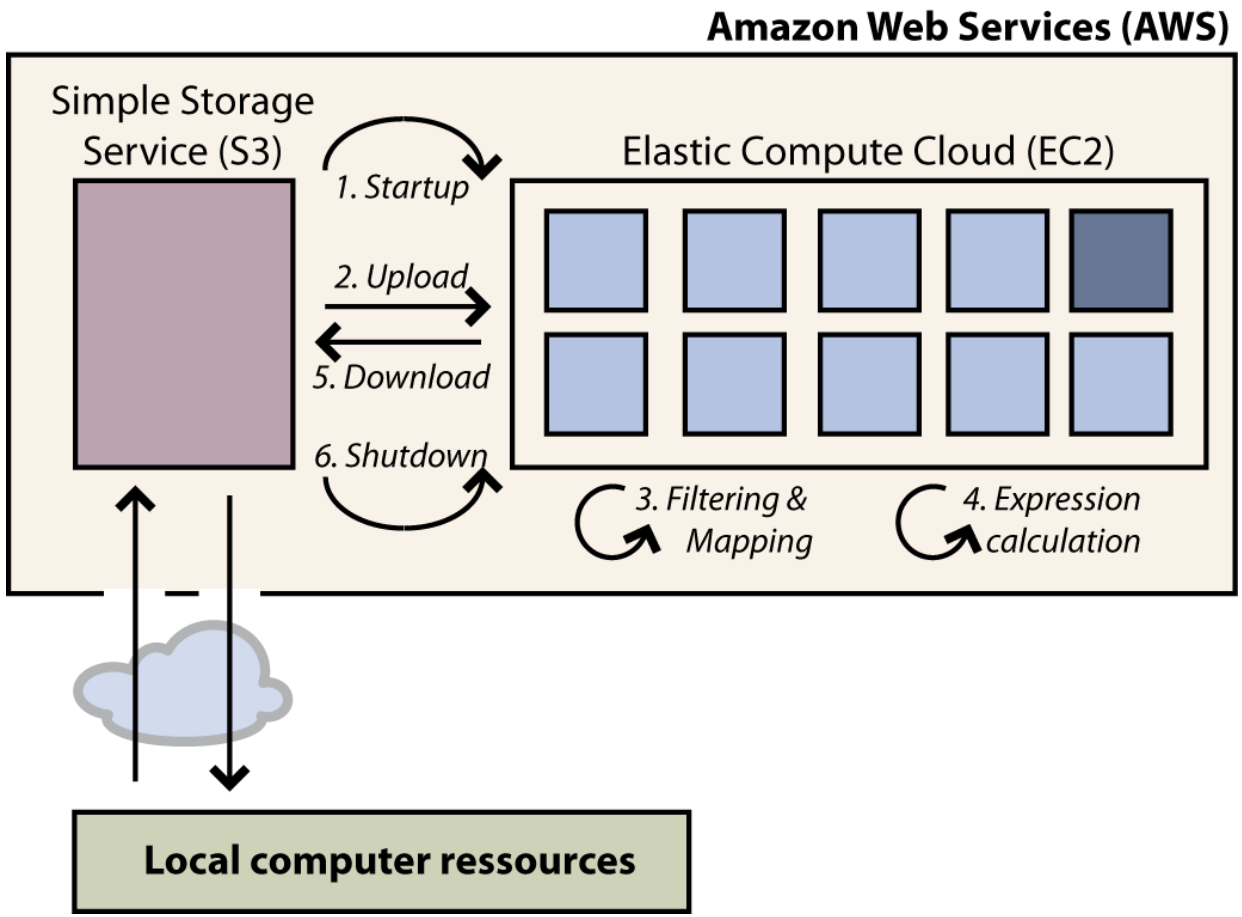
White (2009) *O'Reilly Media*

```
Map(id_alignment, alignment)
    → list(id_exon, 1)

Sort(id_exon,1)

Reduce(id_exon, list(1,1...1))
    → list(id_exon, count)
```

- **Hadoop** is a popular (Twiter, facebook, eBay …) **open-source implementation** of the MapReduce framework as the original Google implementation is not public.

- Hadoop is a **Java framework** that can be executed on any cluster.

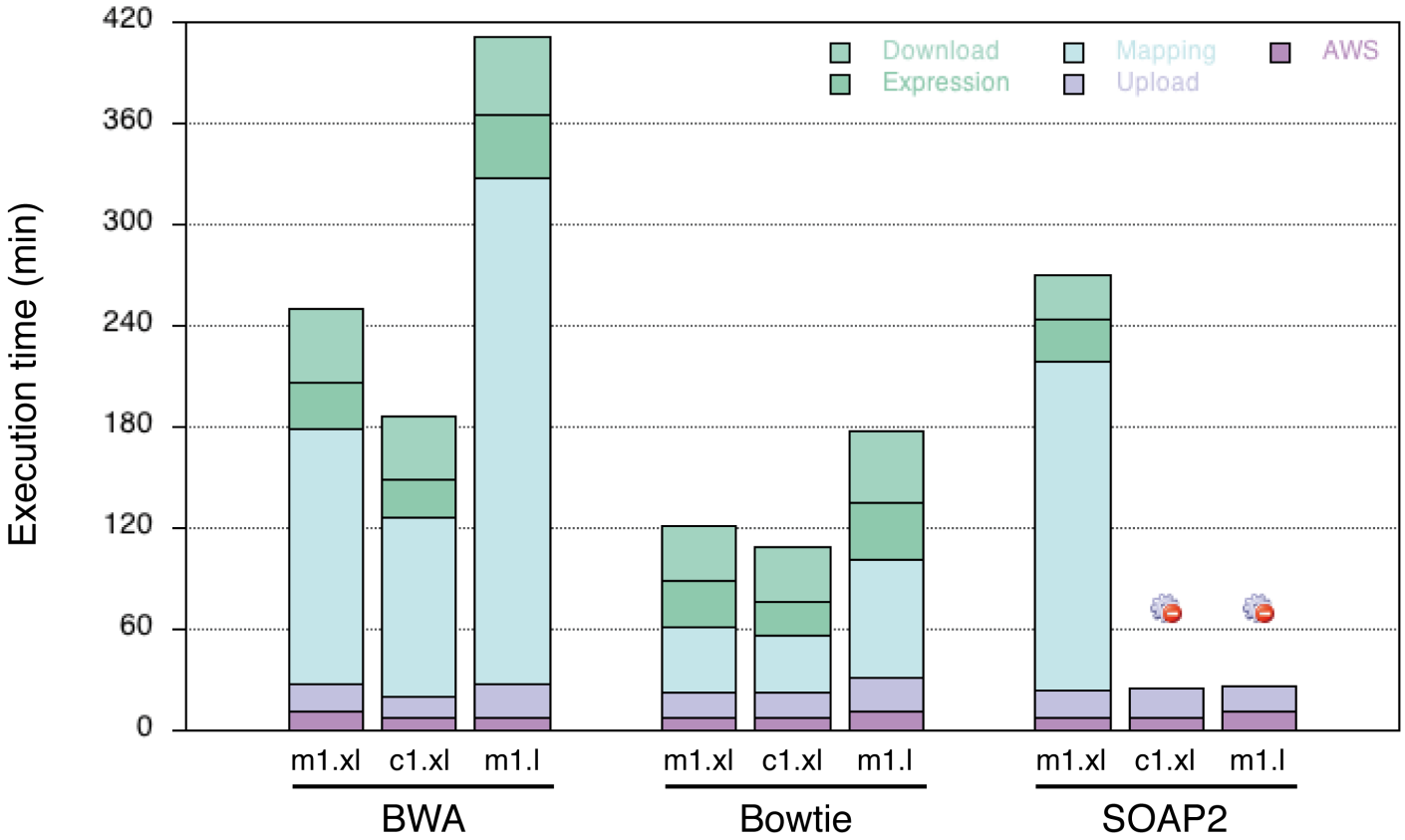
Eoulsan workflow on Amazon Web Services




```
$ eoulsan.sh -conf conf-aws.txt awsexec -d "Job name" param-aws.xml design.txt
s3://sgdb-test/demo
```

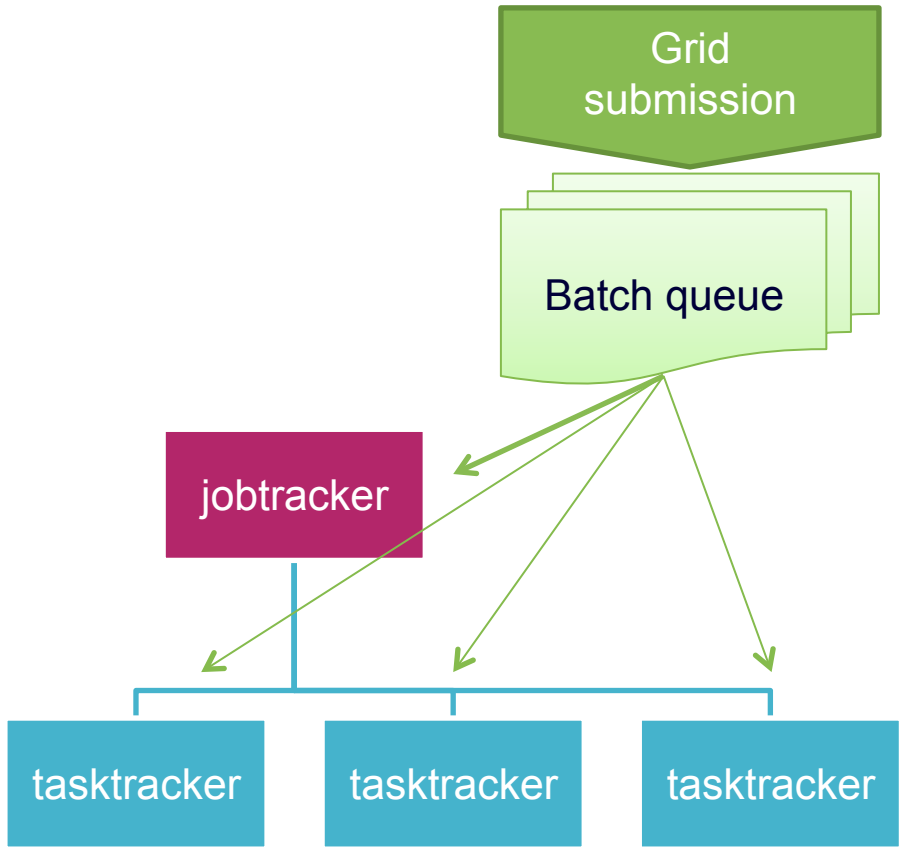
Tests for instance and mapper types

Instance	Memory (Go)	CPU (EC2 unit)	I/O performance	Price USD/hour
m1.large	7.5	4	high	$0.44
m1.xlarge	16.0	8	high	$0.88
c1.xlarge	7.0	20	high	$0.88



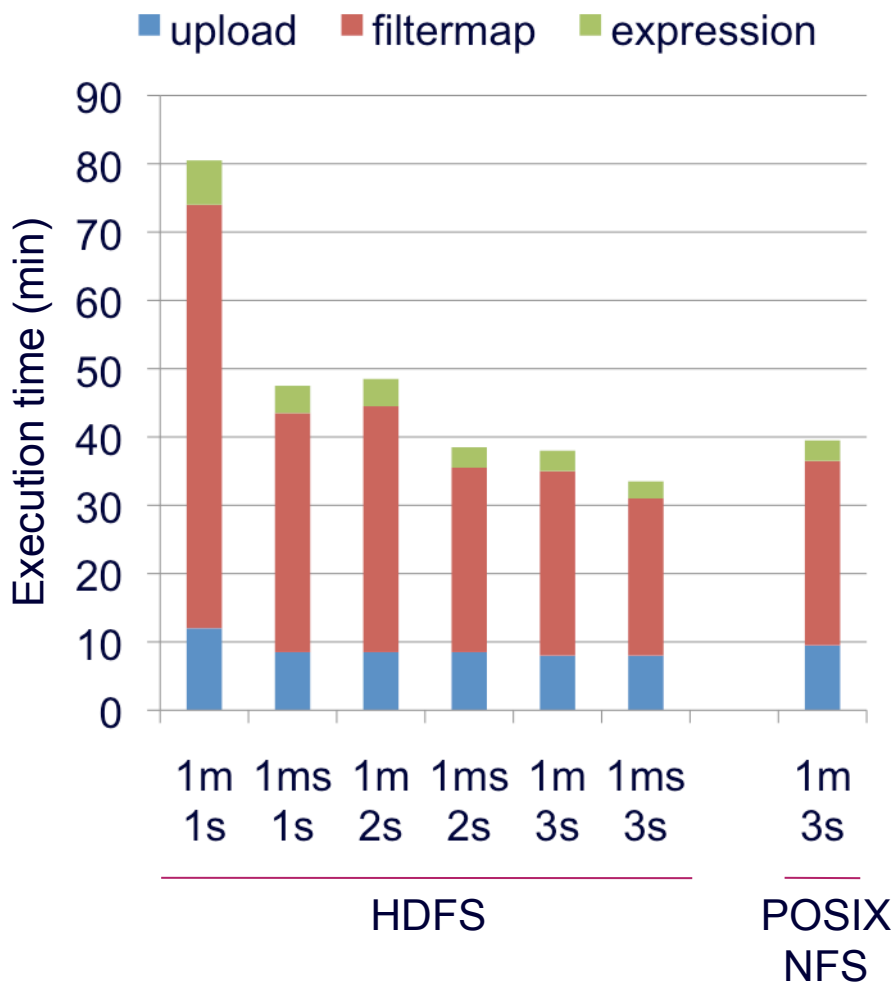
Can we run Eoulsan on a grid infrastructure?

- **Is Hadoop compatible with grid cluster?**
- Several technical solutions need to be addressed.
- **Task management**
  - Master and slaves on the grid cluster;
  - Or, only slaves on the grid cluster.
- **Data storage**
  - HDFS storage available on site;
  - POSIX/NFS storage to build HDFS;
  - HDFS cluster run locally on nodes.



First results

- Tests using a **R&D grid cluster at LLR**.
- **4 identical nodes**
  - E5520 2.27GHz 16 virtual cores;
  - 48GB RAM;
  - 250GB hard drive;
  - 1Gb/s Ethernet connection;
  - OS Scientific Linux 6.3 64bit;
- hadoop-1.0.4-1.x86_64
- **Storage**
  - Dedicated HDFS cluster;
  - Or POSIX/NFS storage.
- **Same** Mouse RNA-Seq **data** than the one we use on **AWS**.

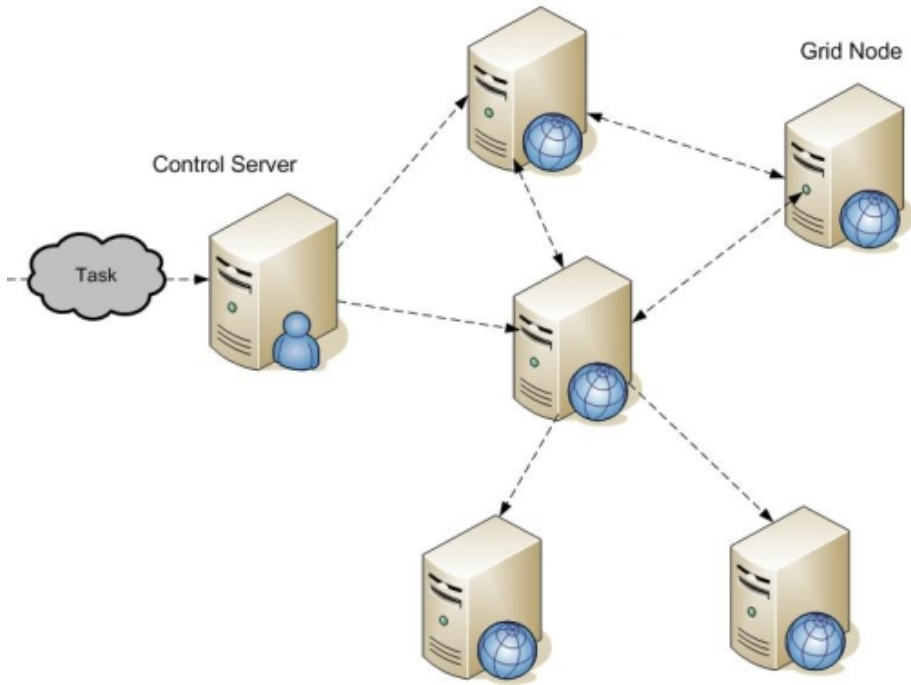


Conclusion

- The **first tests are very promising**: Hadoop can work on grid cluster.
- Eoulsan delivers **quicker results** than using Amazon Web Services.
- **Storage choice as no influence** on analysis performance.
- There is a **maximum number of slaves** after which the gain is minimal (5 for the task we used for the tests).
- **Interface for downloading/uploading** data from/to HDFS/NFS/HTML/Grid storage is available.
- The workflow heavily uses **whole node scheduling**. This is now a standard tool on the GRID but it may be nontrivial to effectively implement it.

Future work

- **Benchmark larger datasets** to compare performances between grid and AWS.
- Allow Eoulsan to remotely run on the grid.
- **Final goal**: make the **choice** of the computing infrastructure **transparent for final users**
- By **creating generic VM** to run Hadoop everywhere:
  - CNRS Research Cloud;
  - GenoCloud (BioGenOuest);
  - Stratuslab cloud…



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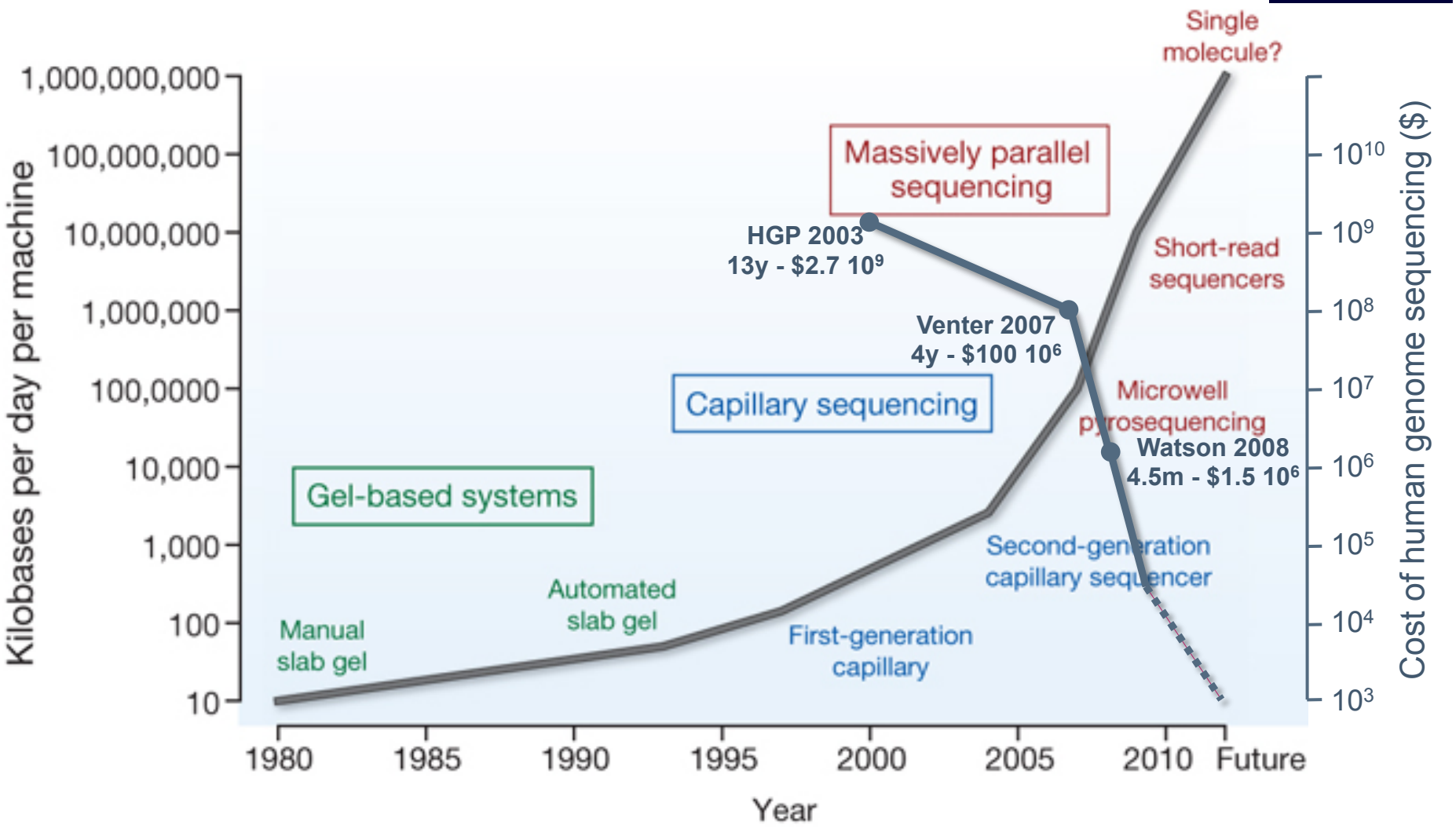
Evolution of sequencing technologies



Stratton (2009) *Nature*

A ready-to-use software solution

- **Aim:** to automate the analysis of a large number of samples at once.
- With **minimal file requirements**.
  - Data: several Fastq files (.bz2)
    1 reference genome (.fasta)
    1 annotation file (.gff3)
  - Set up: 1 XML parameter file
    1 design file

```
<!-- Filter reads -->
<step skip="false">
        <name>filterreads</name>
        <parameters>
                <parameter>
                        <name>lengthThreshold</name>
                        <value>11</value>
                </parameter>
                <parameter>
                        <name>qualityThreshold</name>
                        <value>12</value>
                </parameter>
        </parameters>
</step>
```

- A design file inspired from the limma R package.

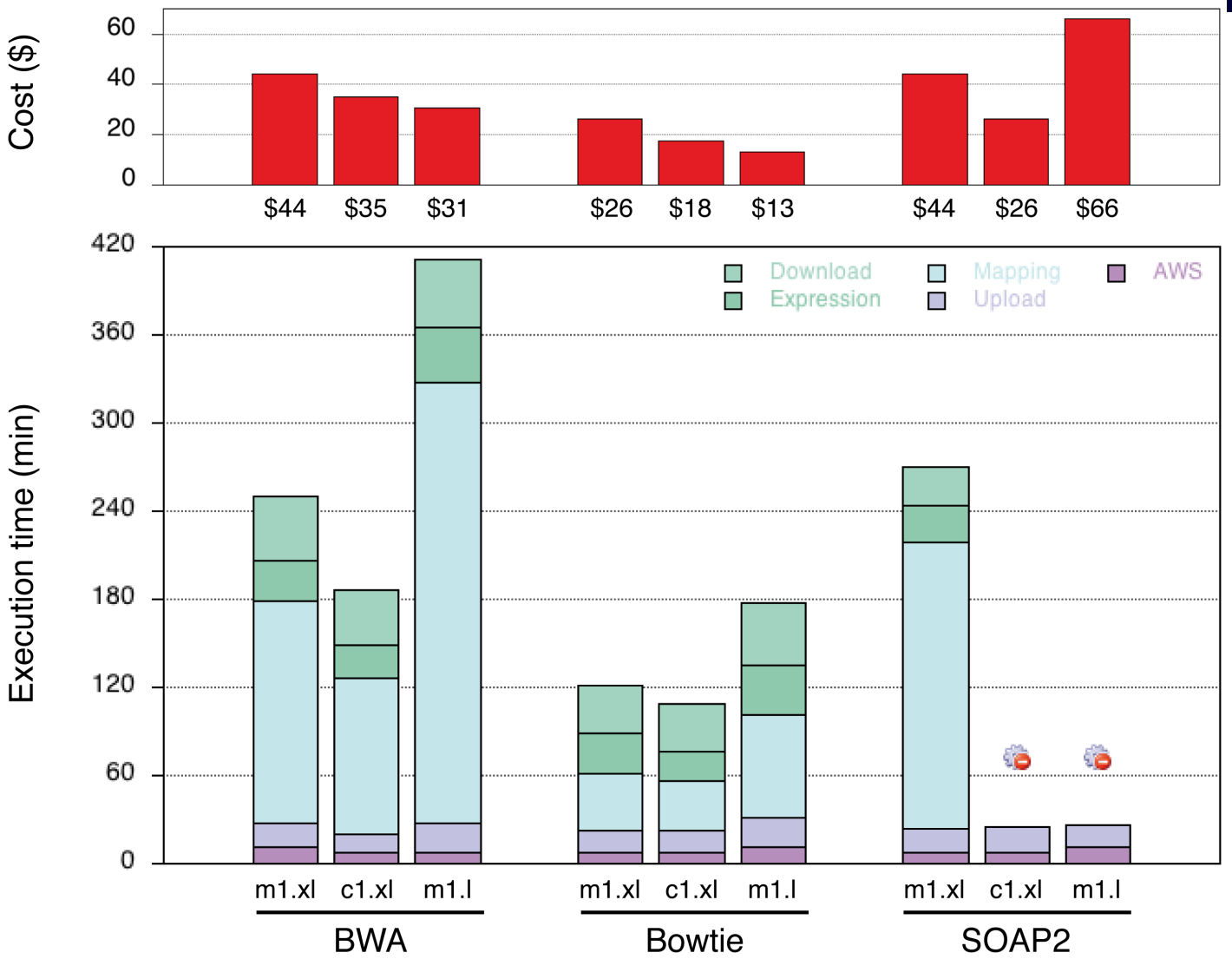
SampleNumber	Name	FileName	Genome	Annotation	Condition	ReplicateType
1	s1	s1.fq	mouse_build37.fasta	mouse_build37.gff	c1	B
2	s2	s2.fq	mouse_build37.fasta	mouse_build37.gff	c2	B
3	s3	s3.fq	mouse_build37.fasta	mouse_build37.gff	c1	B
4	s4	s4.fq	mouse_build37.fasta	mouse_build37.gff	c2	B

- And **one command line** to launch the whole process.

```
$ eoulsan.sh exec parameter_file.xml design_file.txt
```

http:/transcriptome.ens.fr/eoulsan/

Tests for instance and mapper types



Conclusion

- Eoulsan **automates** the analysis of **a large number of samples at once**;
- Its **modular** and **flexible** analysis **framework** runs with various already **available analysis solutions**;
- On **several computer infrastructure** types.

- **Final goal**: make the **choice** of the computing infrastructure **transparent** for final users.
- By **creating generic VM** to run Hadoop everywhere (Private Cloud, Stratuslab)

http:/transcriptome.ens.fr/eoulsan/

Standalone version

Distributed version

Local clusters

Cloud Computing

Grids