Hadoopizer : a cloud environment for bioinformatics data analysis

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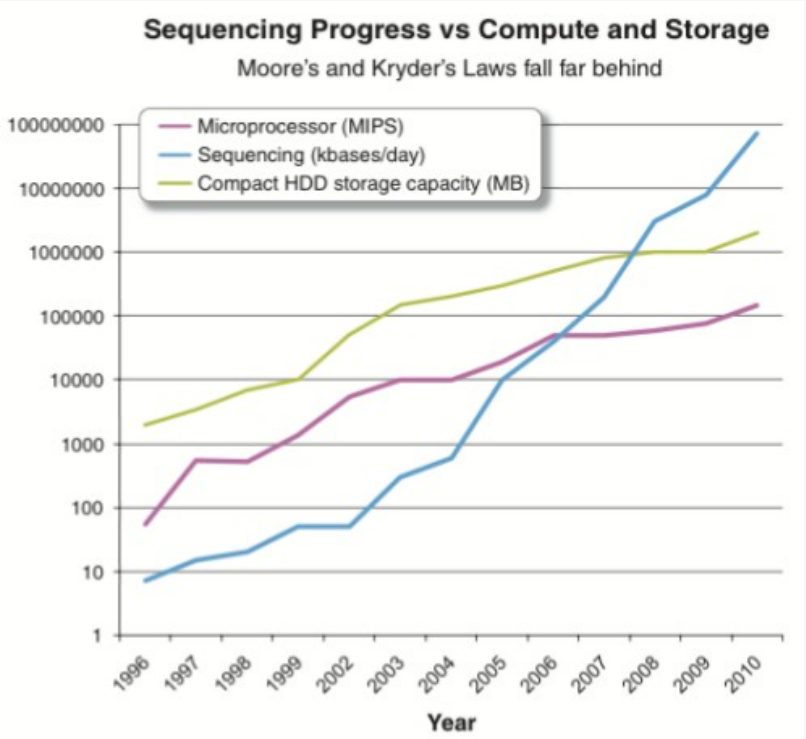
Data deluge in biology

Next generation sequencing (NGS)

- Very cheap DNA sequencing
- Compute and storage grow slower than sequence production
- “Data deluge”
  - This is the first wave
    - Proteomic
    - Imaging
    - ...



Kahn. On the future of genomic data. Science (2011) vol. 331 (6018) pp. 728-9

Next Generation Sequencing technologies

DNA

- Alphabet = A, T, G, C (1 letter = 1 “base”)
- Human genome = 3 Gb

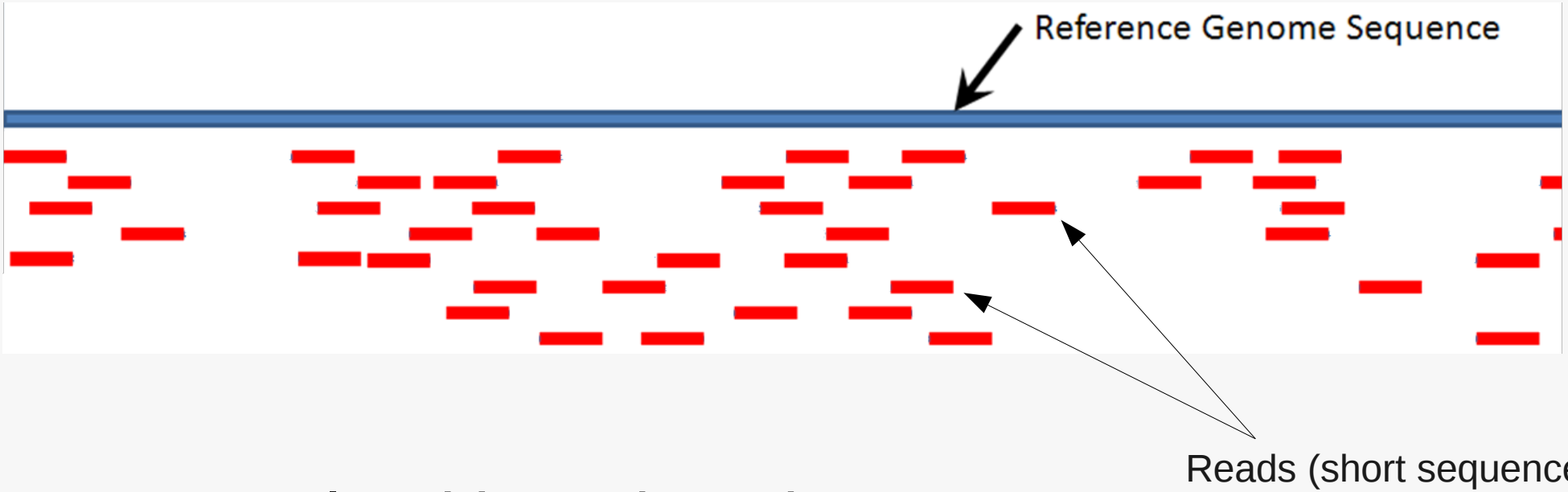
Next generation sequencing (NGS)

- 1 run (11 days) = 6 Billion reads of 100 b

Many methods

- De novo assembly of a genome
- Mapping on a genome
- ...

NGS application: example of mapping



Many algorithms (101*)

- Sequencing errors, mutations, repetitions, gaps

Parallelization

- Indexed genome
- Each read can be mapped individually

* source: seqanswers.com wiki

Data management

- Production facilities
  - Sequencing centers
    - Genoscope, BGI, companies, ...
  - Sequencers in labs => disseminated
- Computing resources
  - Disseminated too => transfers
    - in labs, on platforms (or none)
  - Peaks of activity

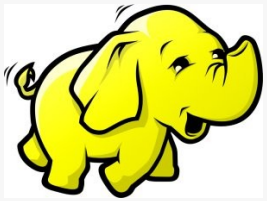
=> Engineering challenges

Why the cloud

- Extensible computing resources
  - Amazon, Azure, private clouds
- Parallelization
  - SGE or Hadoop clusters
- Reproducible results
  - Shareable virtual machines

Hadoop

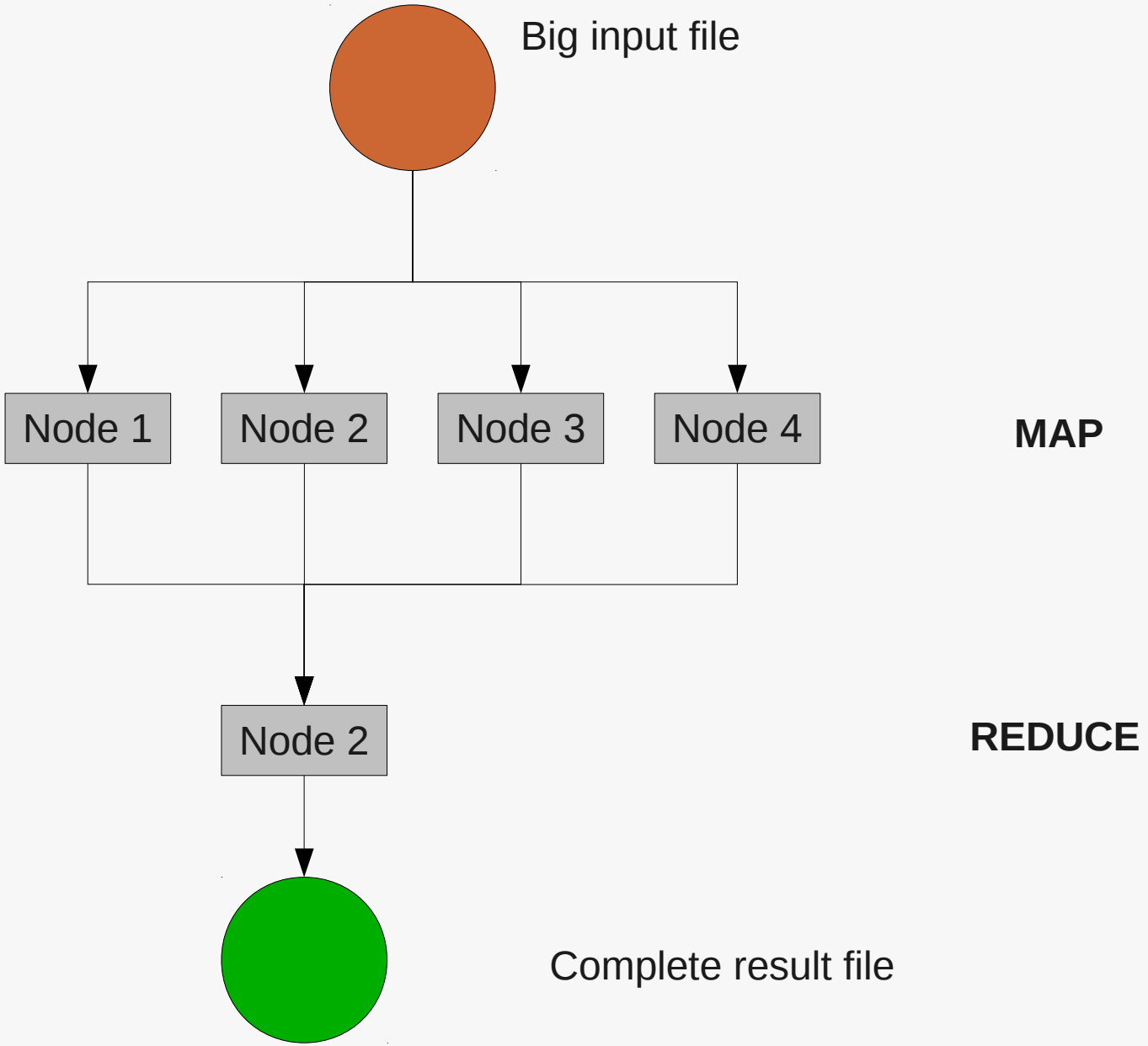
- MapReduce framework
- Distributed processing of large datasets
- Scalability
  - 1 to thousands of nodes
- Fault tolerance
  - Detect node failure and retry
- Hadoop-related projects
  - Hbase, Hive, Cassandra, Pig, ...



Hadoop in a few words

1. Load input data as key/values
2. Distribute them to computing node
3. Map(): transform to new key/values pairs
4. Reduce(): combine values having the same key
5. Write to output file

Hadoop


Big input file
Node 1
Node 2
Node 3
Node 4
MAP
Node 2
REDUCE
Complete result file

The project

- Cloud computing and bioinformatics data:
  - Does it work?
  - Do we miss some tools?
  - Will it be efficient?
- Private cloud setup: GenoCloud
- Inventory of existing solutions
- Development of Hadoopizer

Private cloud

- Private cloud for test purpose
- Based on OpenNebula
  - 240 cores, 940 Gb memory, 8 Tb storage
  - EC2 compatibility
- Ready to use images
  - Sge cluster
  - Hadoop cluster

http://genocloud.genouest.org

Inventory

Already existing tools:

- CloudAligner
  - Mapping (specific algorithm)
- CloudBurst
  - Mapping (RMAP algorithm)
- Contrail
  - De novo assembler (specific algorithm)
- Crossbow
  - SNPs detection (uses Bowtie and SOAPsnp)
- Myrna
  - RNAseq, differential expression (bowtie, R/Bioconductor)

Inventory

- Less specific tools:
  - Eoulsan
    - Filtering, mapping, differential expression
    - Pipelines
    - Extendable (but not simple)
  - CloudMan
    - SGE cluster (with console) + Galaxy frontend

Bioinfo applications in the cloud

Main limitations

- Fast evolution of both data & algorithms
  - Obsolescence of algorithms (myrna, cloudburst, contrail)
- Evolution cost
  - Test new algorithms
  - Custom code/scripts (very common)
- Incompatible dependencies

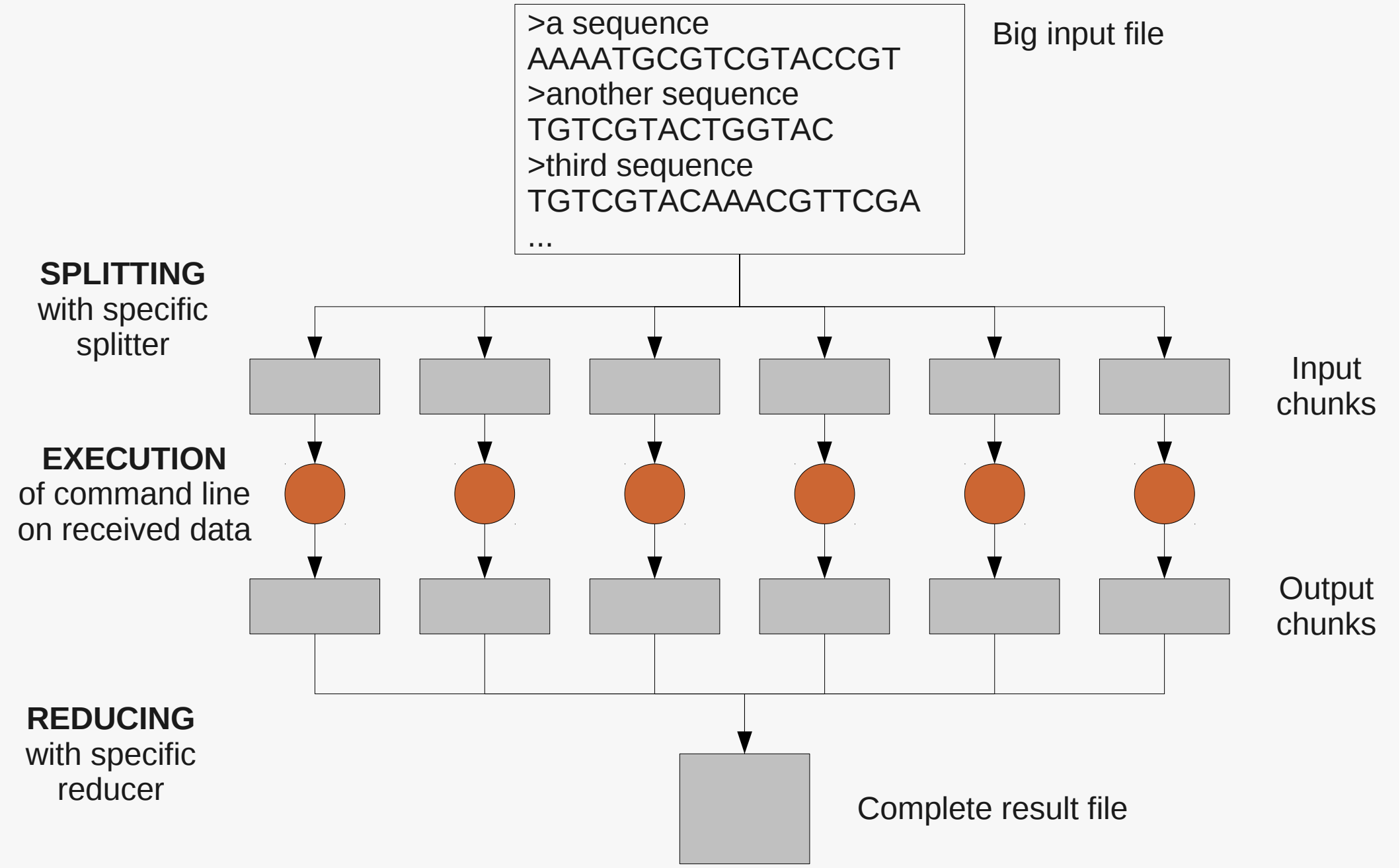
Missing

- Launching custom command line
- Splitters adapted to bioinformatics data formats
- Some glue to make life easier

=> Hadoopizer

Non parallelized treatment

Hadoopizer: how it works



Hadoopizer: using it

Xml example

```
<?xml version="1.0" encoding="utf-8"?>
<job>
    <command>
        bowtie -m 1 --best --strata -S ${genome} ${reads} > ${mapped}
    </command>

    <input id="genome">
        <url autocomplete="true">/home/example/indexed_genome</url>
    </input>

    <input id="reads" split="true">
        <url splitter="fastq">/home/example/reads.fastq</url>
    </input>

    <outputs>
        <url>/home/example/output_mapping/</url>
        <output id="mapped" reducer="sam" />
    </outputs>
</job>
```

Command line example

hadoop jar hadoopizer.jar -c job_config.xml -w hdfs://master_node_ip/bowtie_tmp/

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Hadoopizer: other features

Software deployment

- hadoop jar hadoopizer.jar -b binaries.tar.gz [...]
- Extracted in work dir on each node

Supported formats

- Fasta, Fastq, Sam, (Bam)

Compression

- Input and output

Multiple input+output

- Support of paired sequences

Mapping example: first results

- First results on mapping:
  - Reference genome: 400 Mb
  - Reads: 11 Gb
- With hadoopizer
  - 343 splits on 10 nodes
  - 55 min for map step, 3h for reduce step
    - This is a test cloud, not optimized for performances
    - Configuration tuning, code improvements, ...
- Same command on 1 machine (same config)
  - 4h30

Hadoopizer: performances

- Benchmarks
  - The next step of the project
  - Comparison with:
    - non parallelized
    - SGE parallelized
    - other implementations using Hadoop
  - Take into account the transfer time
- Expected results:
  - Overhead due to I/O on computing nodes

Hadoopizer conclusion

- Coarse grain parallelism
- For embarrassingly parallel problems
- Works with any command line
- Perspectives
  - Support more data formats (bed, wiggle, gff, ...)
  - Performance issues

Perspectives

- 6 months work
- 1.0 released on github
  - https://github.com/genouest/hadoopizer
- Open position to continue the project
  - Benchmarks
  - Public clouds
  - Support other formats, new features
  - Real life applications

Thank you!

www.genouest.org
genocloud.genouest.org
github.com/genouest/hadoopizer

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