



Healthcare research: HPC and cloud.

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WORKSHOP GARR 2019, 8-10 ottobre 2019, Rome

IEO Hospital



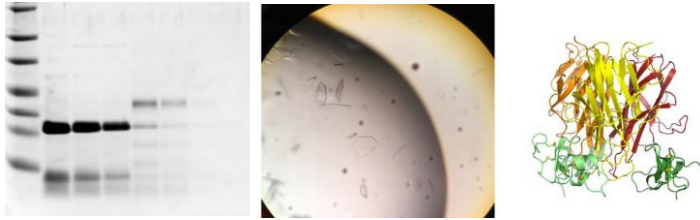
Department of Experimental Oncology



Clinical and basic research, Integration within IEO Clinical Programs, PhD program
> 20 bioinformaticians

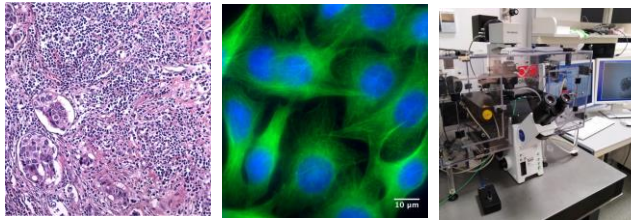
Technological units: raw & processed data

Crystallography



- Few users
- 1 TB/year
- Analyses: Memory and GPUs

imaging



- ~50 TB/year
- ~10 users
- Big images visualization

genomics

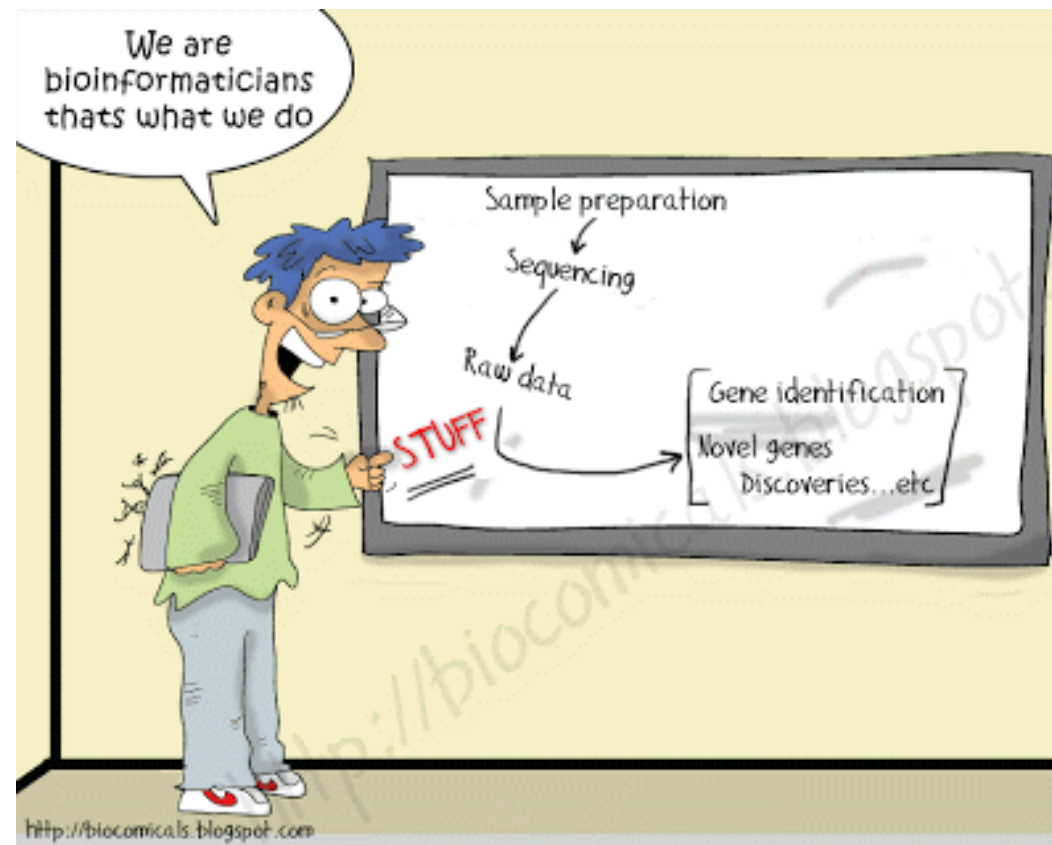


- > 20 TB/year
- cpus and memory for data preparation and analyses

Proteomics, Radiomics, ...

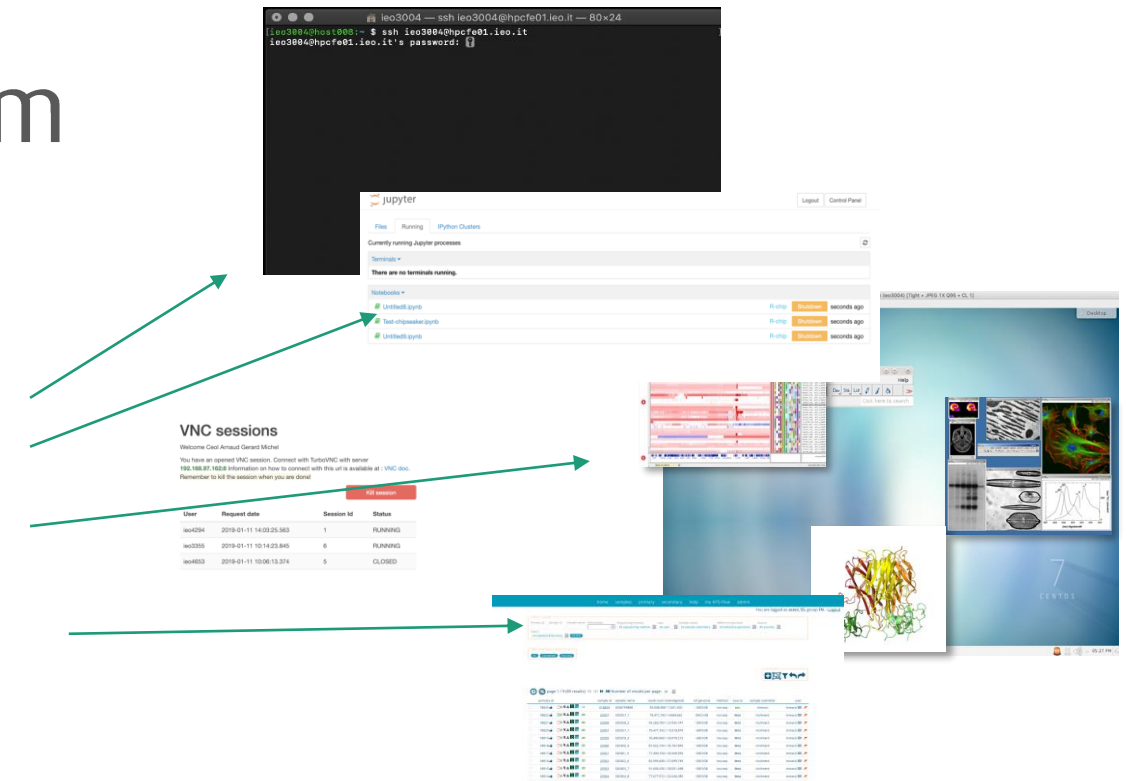
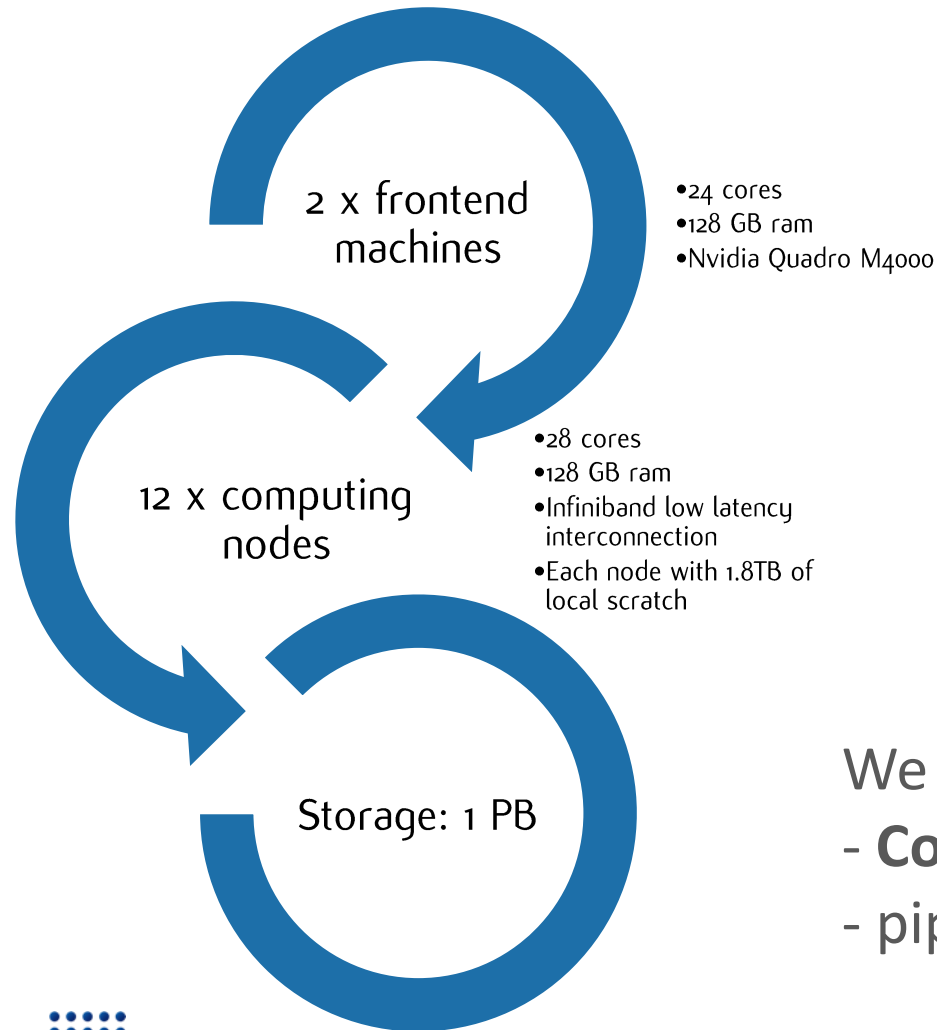


- > 100 TB/year ?
- CPUs, GPUs



Dry-lab Researchers (bioinformaticians): analyze the data

The bioinfo (HPC) platform



We encourage the usage of:

- **Containers:** 100% reproducible results
- pipeline managers (Nextflow, Snakemake)

```
1  #!/usr/bin/env nextflow
2
3  /* ...
12 params.bam
13 params.parameters
14 params.regionBed
15 params.refGenome
16 params.outputDir
17
18
19 process tvc {
20
21     cpus 4
22     time '4h'
23
24     script:
25     """
26     mkdir -p ${params.outputDir}
27     variant_caller_pipeline.py --num-threads 4 \
28         --input-bam ${params.bam} \
29         --parameters-file ${params.parameters} \
30         --reference-fasta ${params.refGenome} \
31         --region-bed ${params.regionBed} \
32         --output-dir ${params.outputDir}
33     """
34
35 }
36
```

```
1  singularity.enabled = true
2  process.container = '/hpcnfs/techunits/bioinformatics/singularity/smith.simg'
3  singularity.runOptions = ' --bind /hpcnfs/ '
4  process.executor = 'pbs'
```

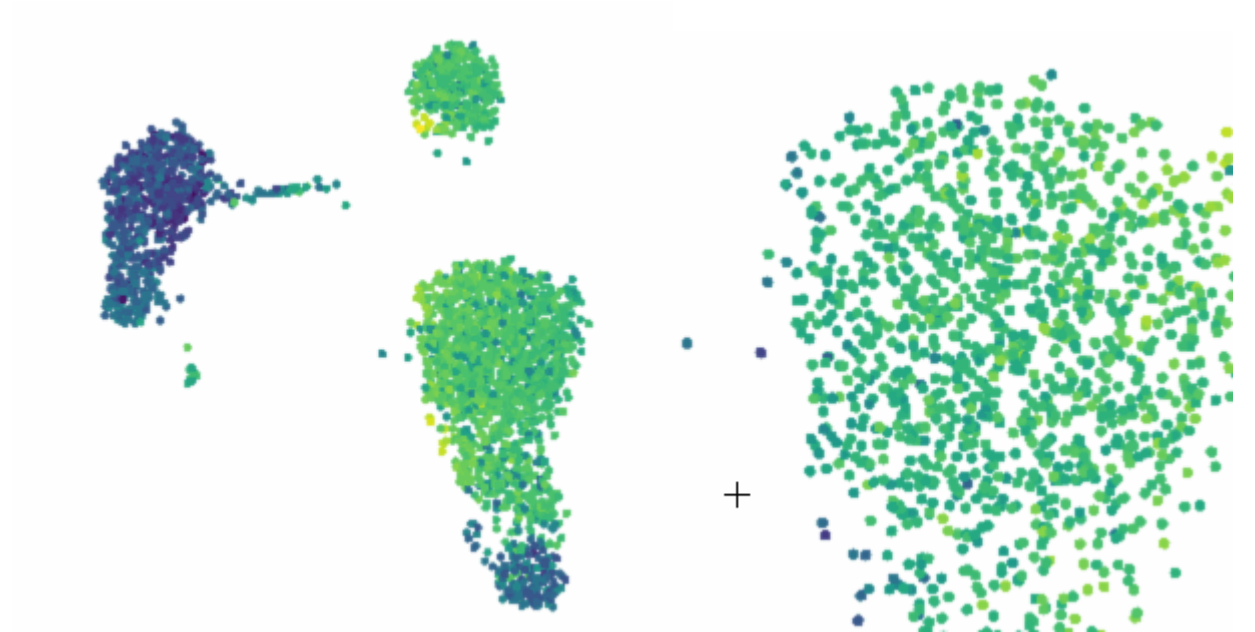
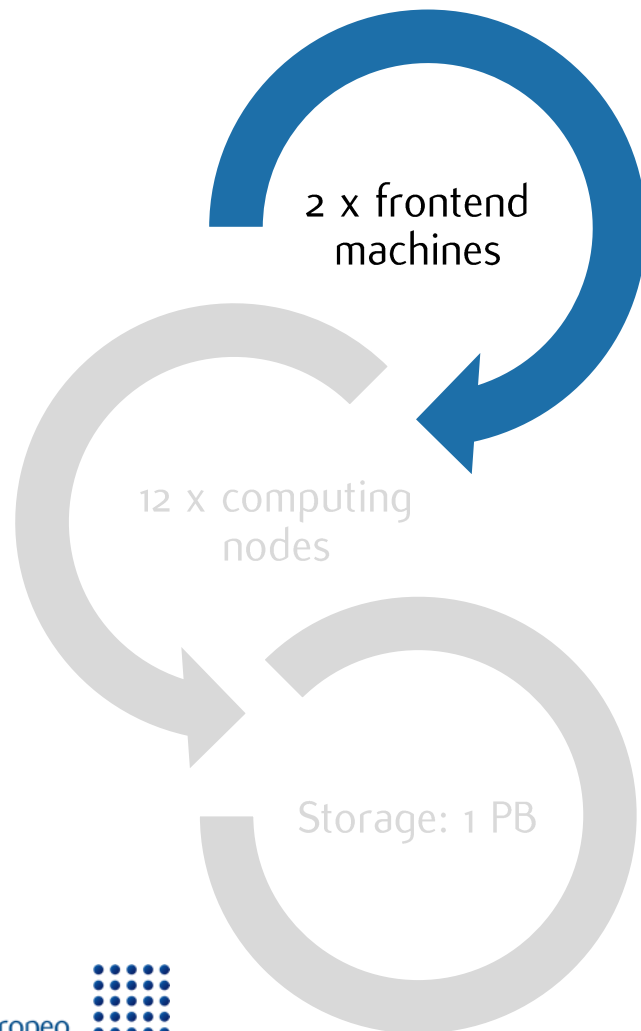
Executors

- Local
- SGE
- LSF
- SLURM
- PBS/Torque
- PBS Pro
- Moab
- NQSII
- HTCondor
- Ignite
- Kubernetes
- AWS Batch
- Google Pipelines
- GA4GH TES



HPC: limitations, and how the cloud can help

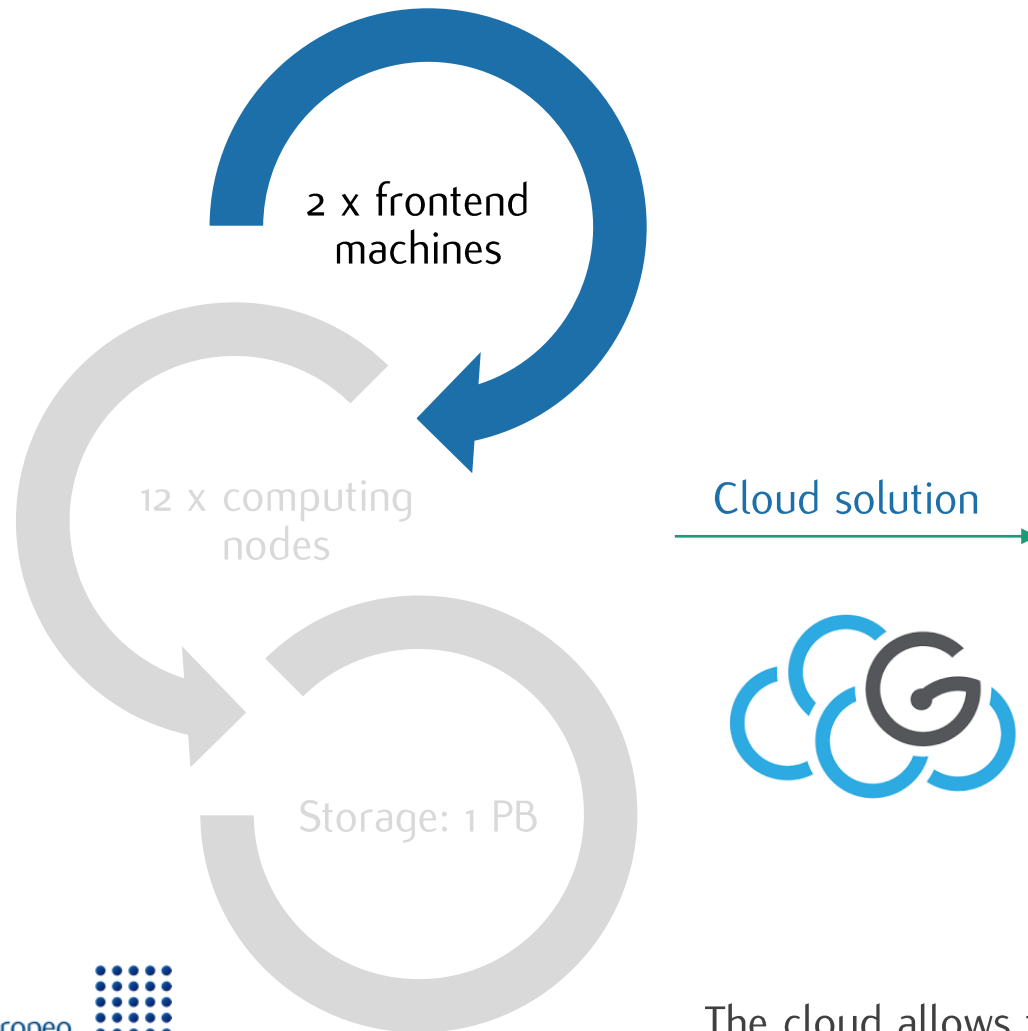
Limitation(s) 1: no admin, no Docker, no web-serving, no outside access



Example: testing **docker-based web application** for the visualization and analyses of single cell sequencing



Limitation 1: no admin and web serving



Virtual Machine 1:
Managed by the user:
Docker + floating IP

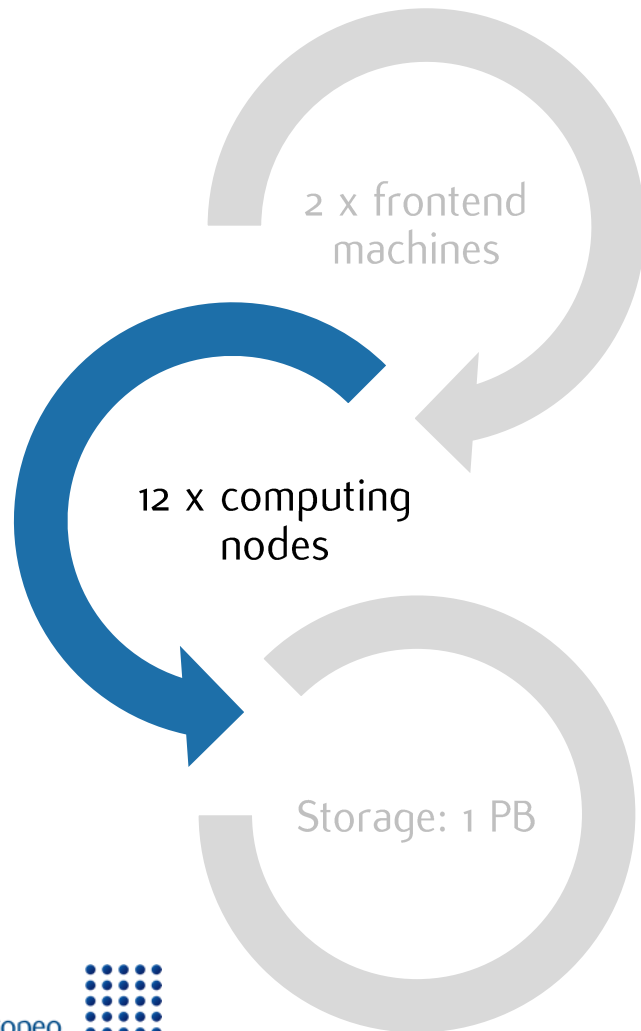


Virtual Machine 2:
Provide to all users of
the institute a “HPC-
like” image.



The cloud allows to create testing environment & publish web servers/services

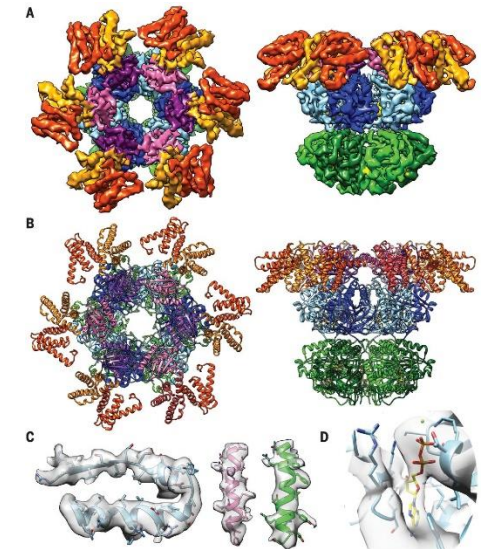
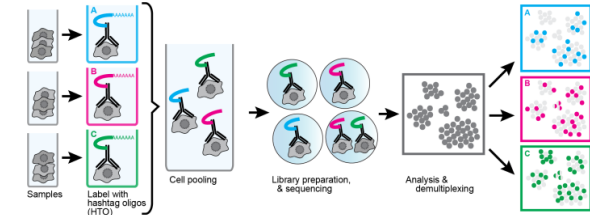
Limitation 2: cores, GPU, RAM



Example 1: CRISPR screening orthogonal interference of 1M cells with multiplexing-enabling. 5TB raw data to be analyzed **100000 cpu/hour** and for the integration and analysis we need a **512GB ram** machine

Example 2: DeepVariant is an analysis pipeline that uses a deep neural network to call genetic variants from next-generation DNA sequencing data: needs VM with **64 CPUs 240 GB RAM**

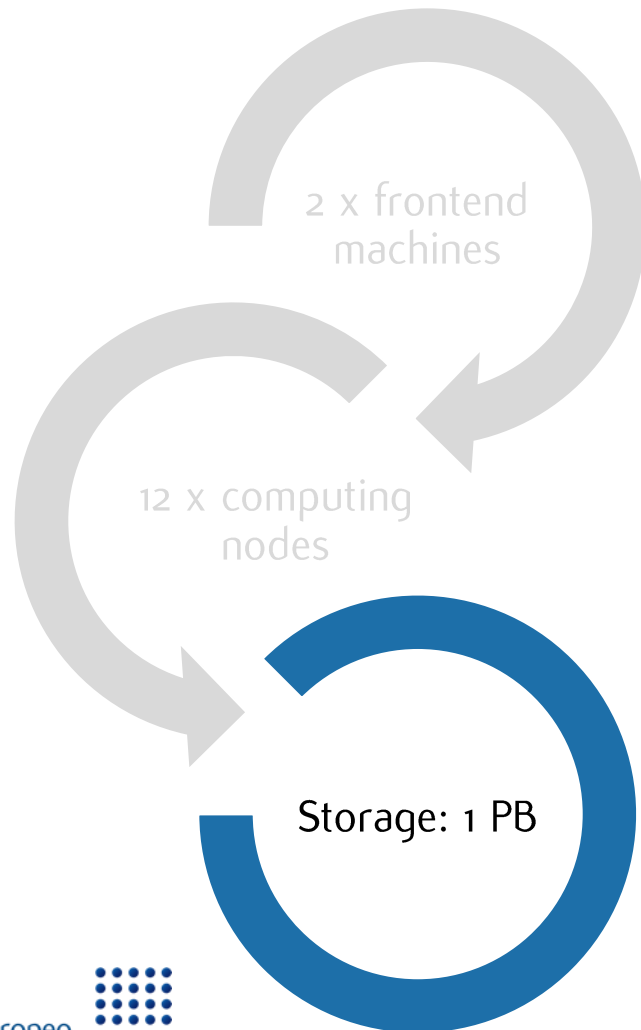
Example 3: Cryo-EM analyze large, complex and flexible structures. 1 project = **3 weeks to 6 months** with **2 GPUs**



Cloud solution



Limitation 3: storage of archives



Storage: Isilon (1PB)

Growth rate: ~ 100 TB/year (only raw data), but will increase.

Cold data: > 300 TB

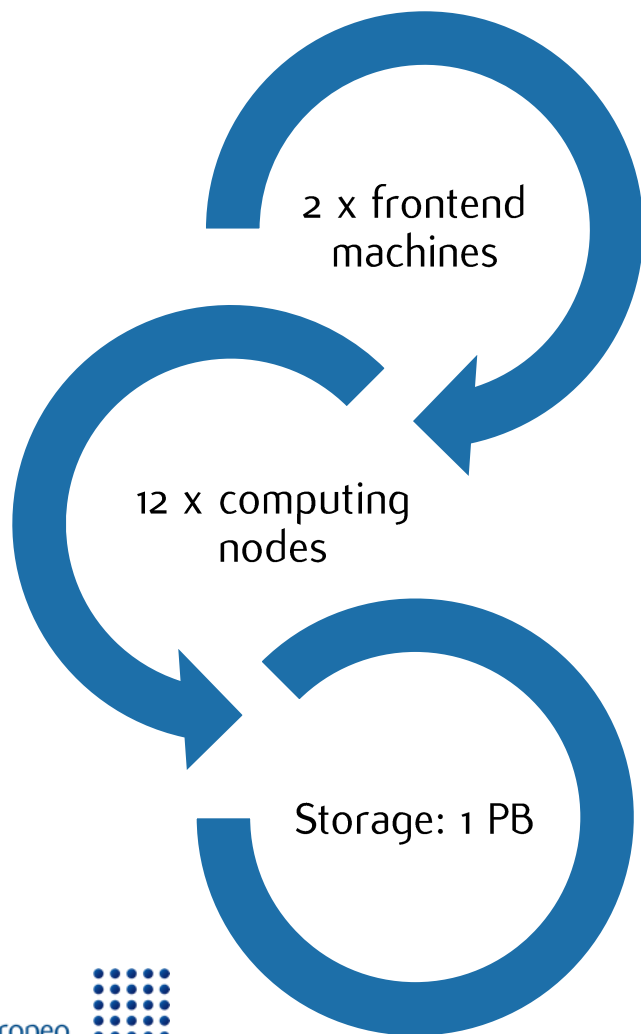
- 90 % will not be used anymore
- cannot be deleted (publication, patents, etc.)

Cloud storage:

- > admin-based management
- > user-based management

Limitation 1: exchange and collaboration

HPC and storage accessible only from the IEO network (intranet).



Cloud solution →



Summary and further considerations

Cloud for: **freedom**, **BIG stuff**, **long term**



Virtual data centers
for collaborative projects

Clinical/biomedical data



Solutions & guidance are
welcome





1994-2019

25 anni di ricerca e innovazione
per la lotta al cancro,
25 anni di Istituto Europeo di Oncologia



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