Cloud Computing For Biology

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The Sanger Institute

Funded by Wellcome Trust.

- 2nd largest research charity in the world.
- ~700 employees.
- Based in Hinxton Genome Campus, Cambridge, UK.

Large scale genomic research.

- Sequenced 1/3 of the human genome. (largest single contributor).
- We have active cancer, malaria, pathogen and genomic variation / human health studies.

All data is made publicly available.

- Websites, ftp, direct database. access, programmatic APIs.

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Use Cases

Virtual Co-location

Scientific SaaS

Smart Archives

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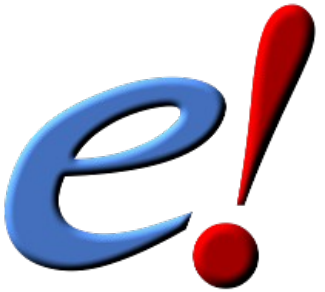
Ensembl



Ensembl is a system for genome Annotation.

Data visualisation / Mining web services.

- www.ensembl.org
- Provides web / programmatic interfaces to genomic data.
- 10k visitors / 126k page views per day.

Compute Pipeline (HPTC Workload)

- Take a raw genome and run it through a compute pipeline to find genes and other features of interest.
- Ensembl at Sanger/EBI provides automated analysis for 51 vertebrate genomes.

- Software is Open Source (apache license).
- Data is free for download.

We have web services and HPTC workloads running on Iaas.

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Virtual Co-location

Virtual Co-location for Web services

- Was hosted in a single datacentre at the Genome Campus, UK.
- 1 datacentre = Single point of failure.
- Access slow if you were not in western Europe.

Cloud Application

- Build worldwide network of mirrors on Amazon AWS (IaaS).
- Mirrors currently in US and Asia.

Deployment times:

- Very time consuming to put machines into a co-lo facility.
- Especially abroad. (death by FCC paperwork.)

Flexibility:

- Simple to add new machines into the virtual Colo, terminate contracts.

Costs:

- Pay as you go model more cost effective that tiered model provided by co-lo (not the primary motive)...

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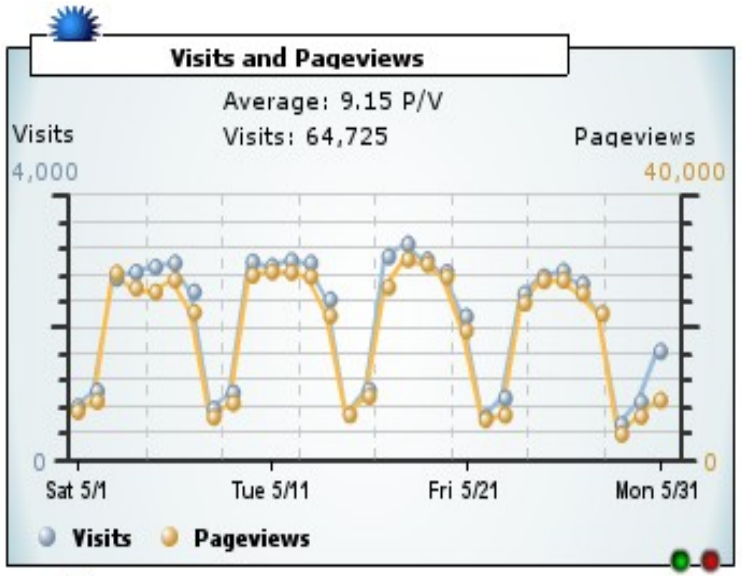
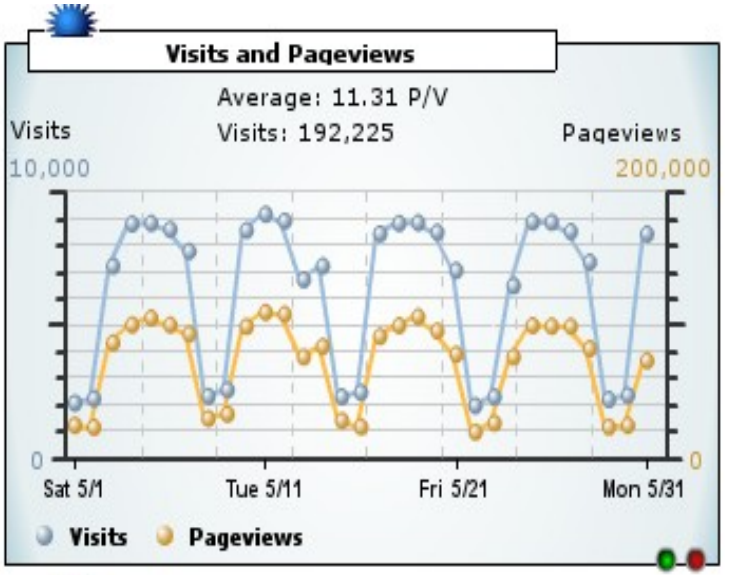
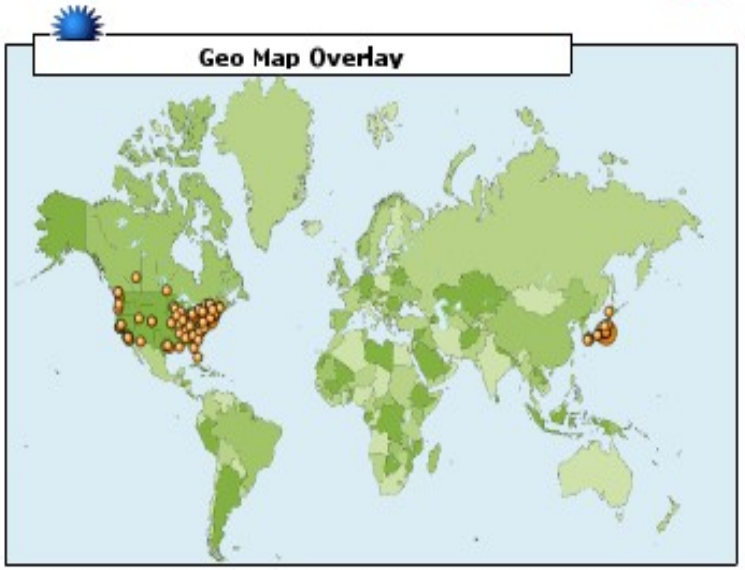
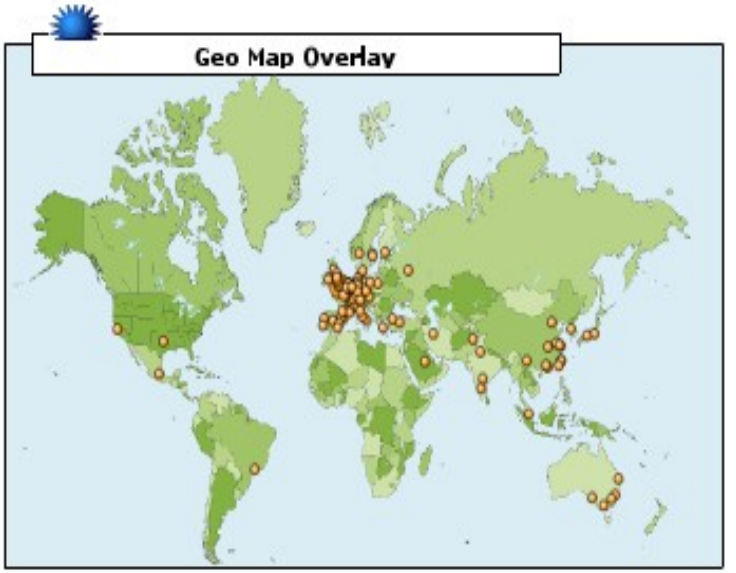
Usage









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Sequencing Informatics

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Economic Trends:

As cost of sequencing halves every 12 months.

- *cf* Moore's Law

The Human genome project:

- 13 years.
- 23 labs.
- $500 Million.

A Human genome today:

- 3 days.
- 1 machine.
- $10,000.
- Large centres are now doing studies with 10,000s of genomes.

Trend will continue:

- Generation 3 sequencers are on their way.
- $500 genome is probable within 5 years.

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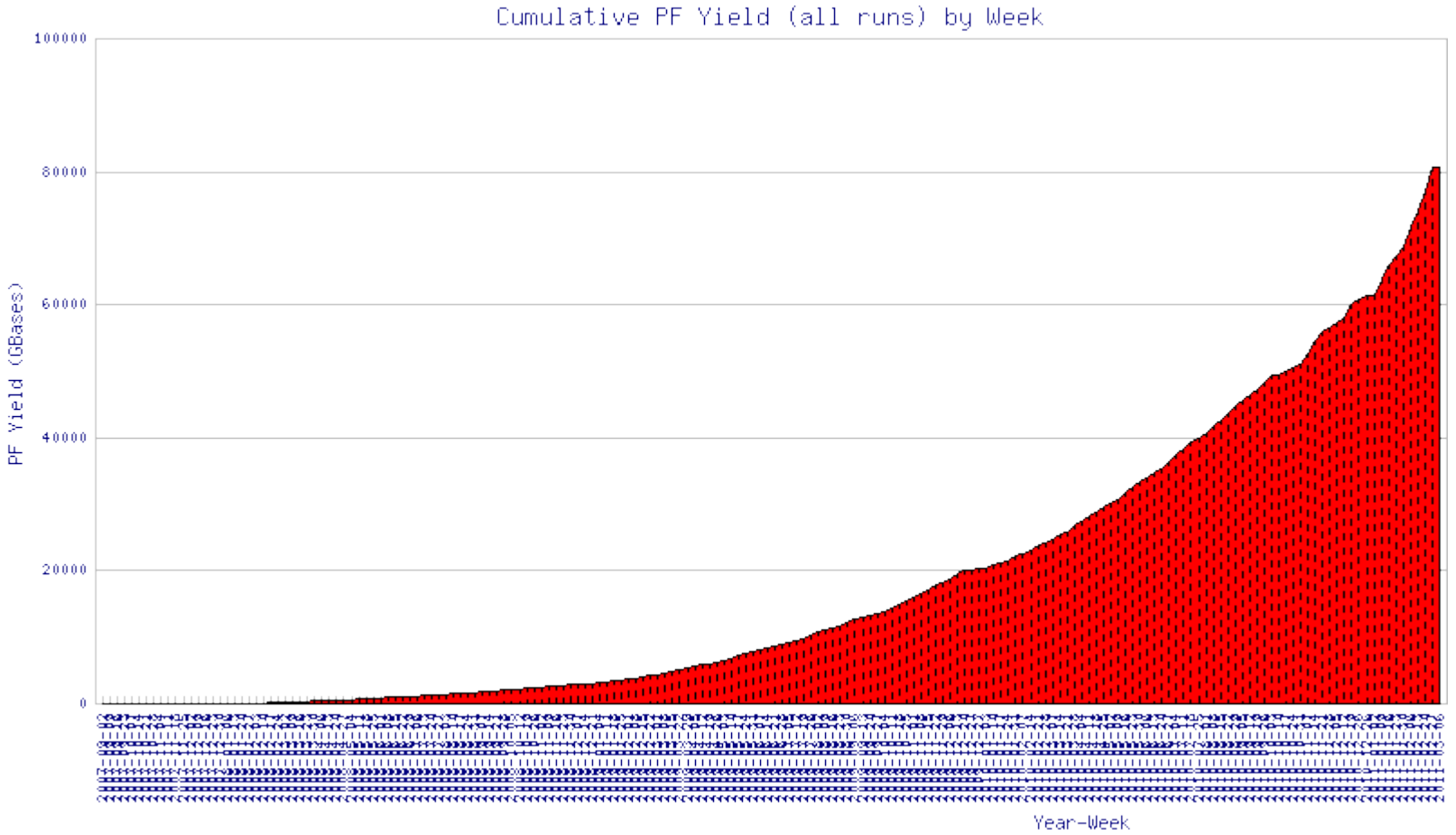
The Scary Graph



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Managing Growth & Change

We have exponential growth in storage and compute.

- Storage /compute doubles every 12 months.
  - 2010 ~12 PB raw.

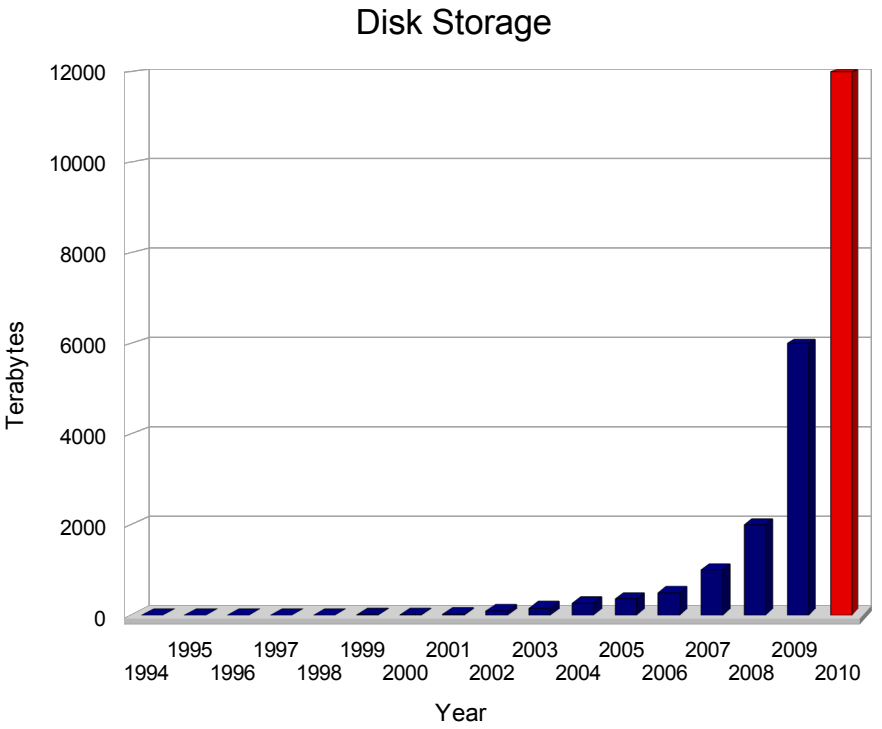
Processes change constantly.

- Driven by changes in machine chemistry.
- LIMs, compute pipelines and algorithms in constant flux.

Moore's law will not save us.

- Transistor/disk density: T_d=18 months
- Sequencing cost: T_d=12 months
- Sequencing output: Td=3-6 months

This is hard!



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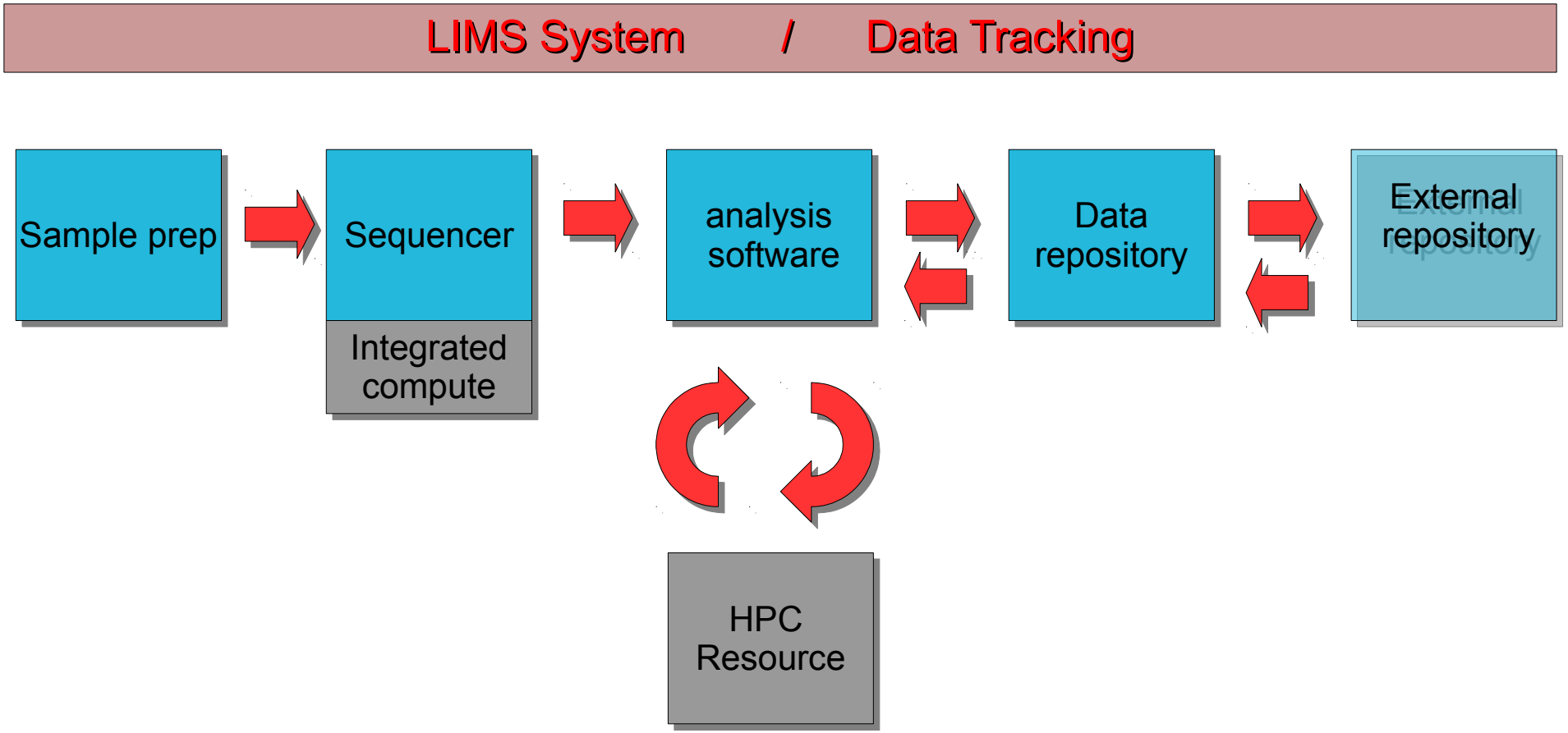
What do you need to do sequencing?



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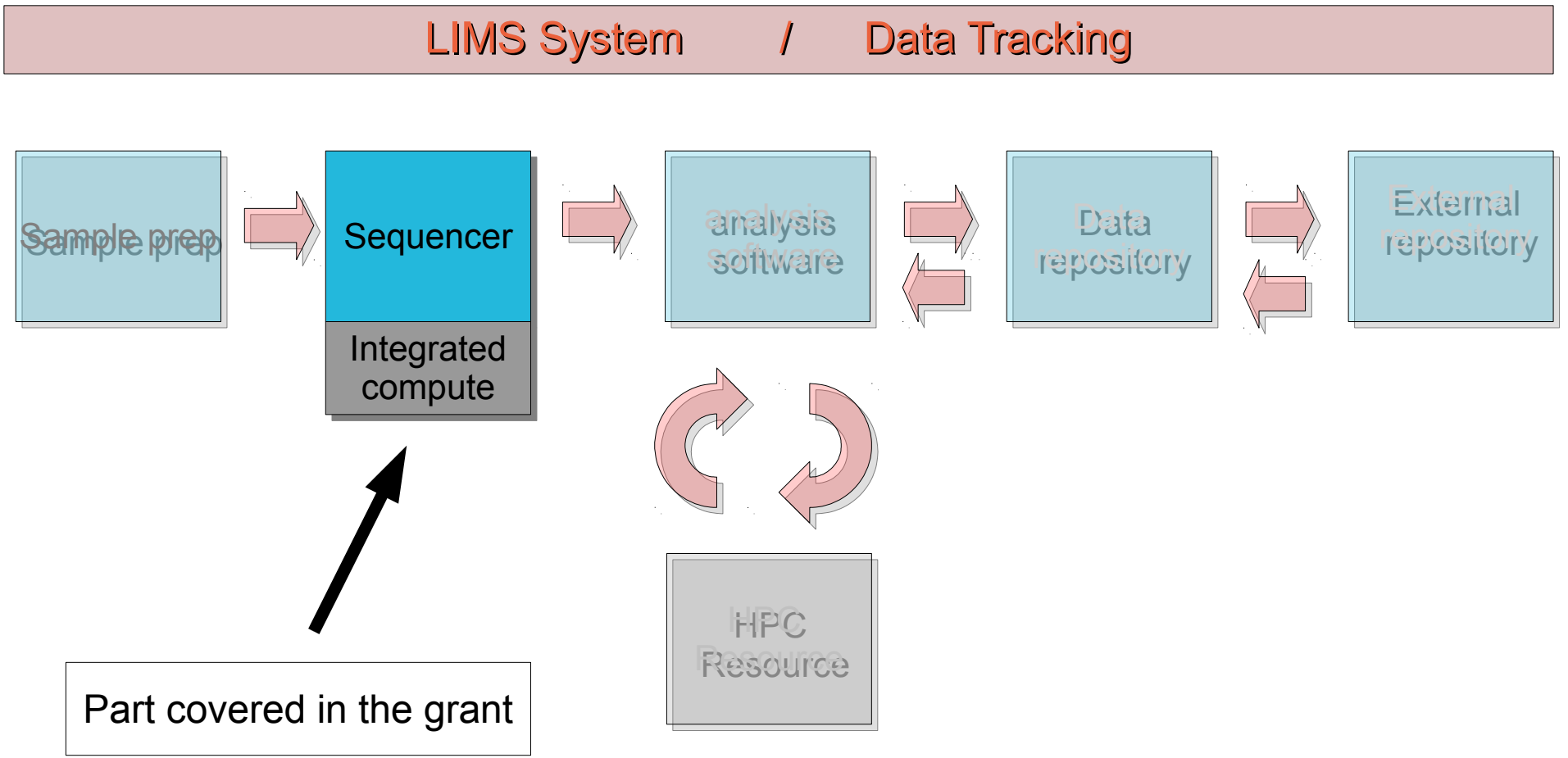

How can cloud help?

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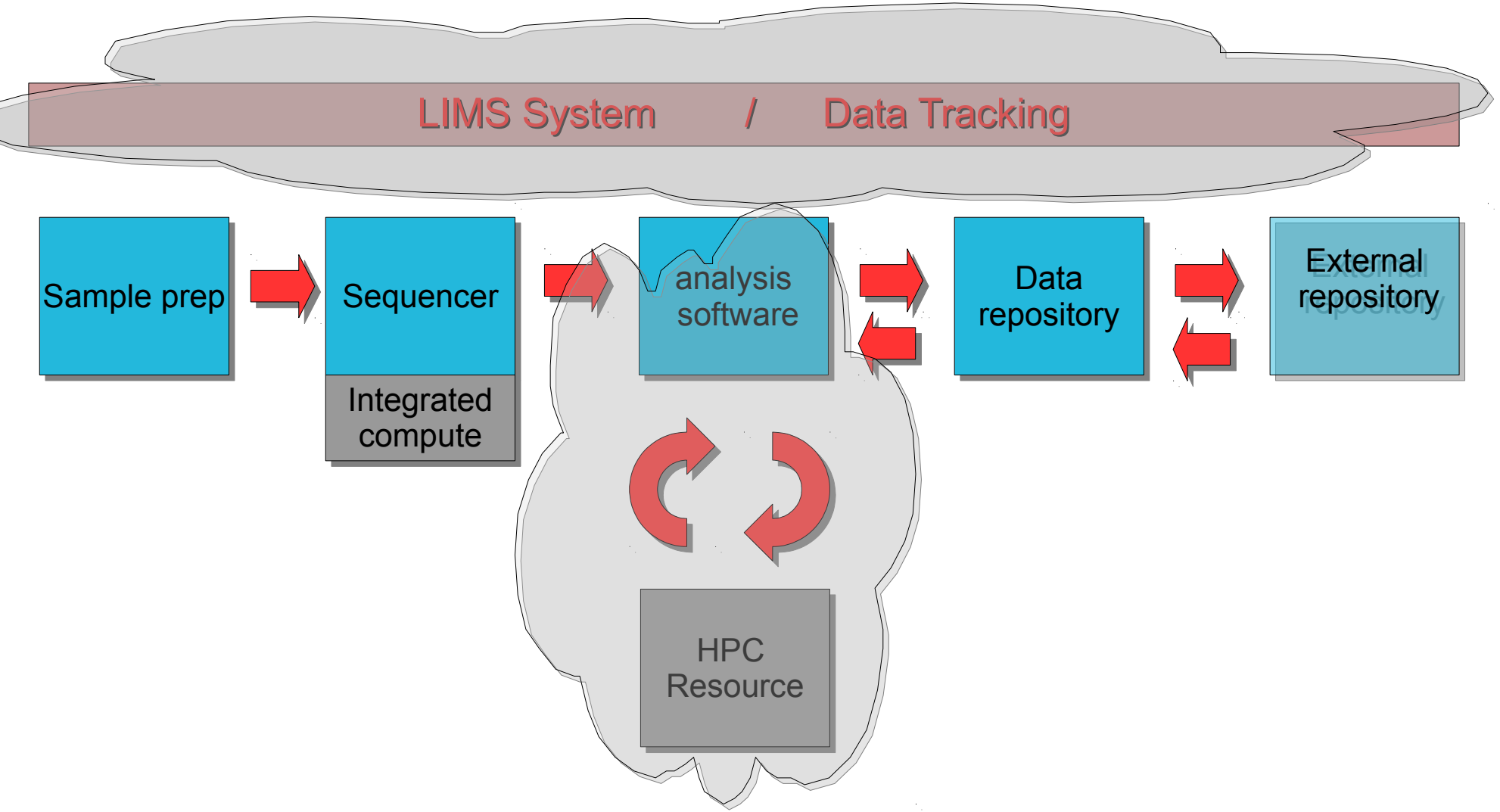
Cloud SaaS



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Commercial or Academic?

Commercial sequencing SaaS exists today.

- Upload data straight from sequencer into cloud.
- Lims, data analysis, archiving.

Problems:

- Data transfers across the public internet make it difficult to get data off the sequencers fast enough.
- Potential data protection issues.

There is a role for academic providers.

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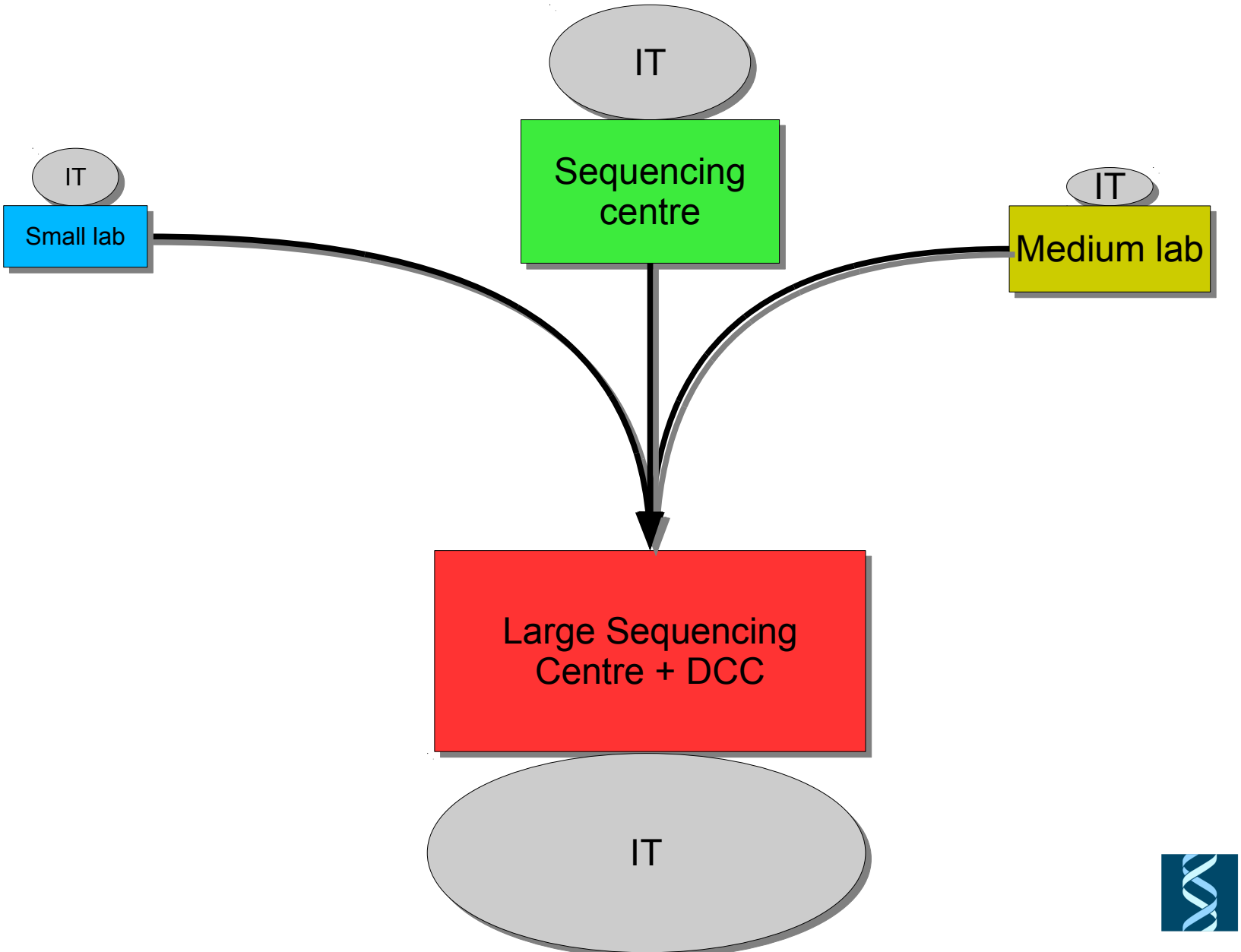
Traditional Collaboration



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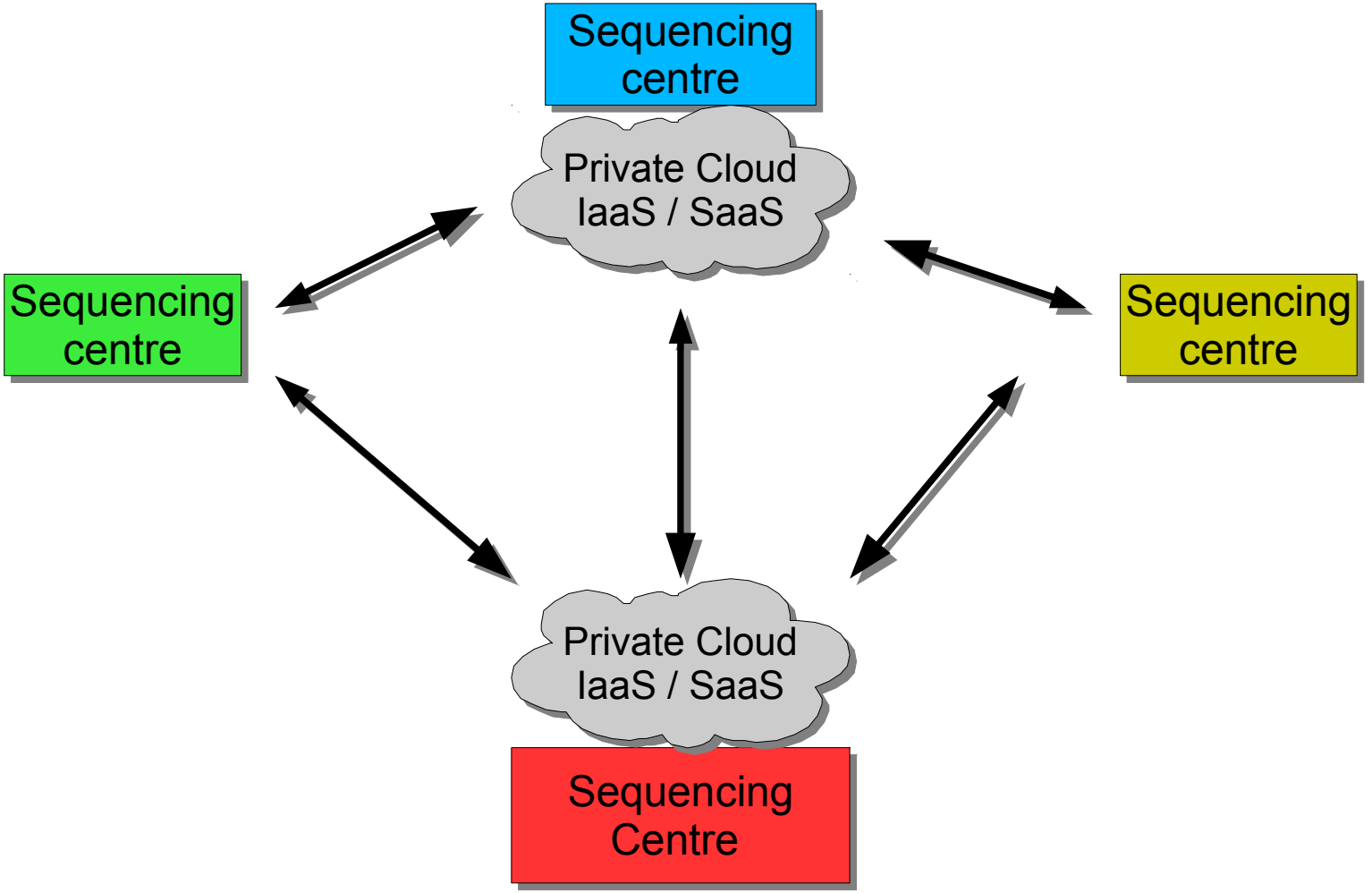
Cloud Collaborations



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Consortium Cloud

SaaS Advantages:

- Small organisations leverage expertise of big organisations.
  - Frees up staff to concentrate on science, not IT.
- Software and IT infrastructure easily shared with consortium.
  - Ensures consistency across a large project.
- Academia tends to be linked by fast research networks.
  - Moving data is easier.
- Consortium will be signed up to data-access agreements.
  - Simplifies data governance.
- Opens up new opportunities:

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Data Archives

Sequencing data is held in public archives.

- Strong community drive for open science.
- Raw data available for researchers and industry.

Managing archives is difficult.

- All the data is in one place.
- Large burden on the people looking after it.

Data in current archives is "dark".

- You cannot compute across it.

Getting data out is hard:

- Moving TBs across the internet is difficult.

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Example problem:

“We want to run out pipeline across 100TB of data currently in European Genotyping Archive.”

We will need to de-stage the data to Sanger, and then run the compute.

- Extra 0.5 PB of storage, 1000 cores of compute.
- 3 month lead time.
- ~$1.5M capex.

(and the data is actually hosted on our datacentre!)

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Cloud archives

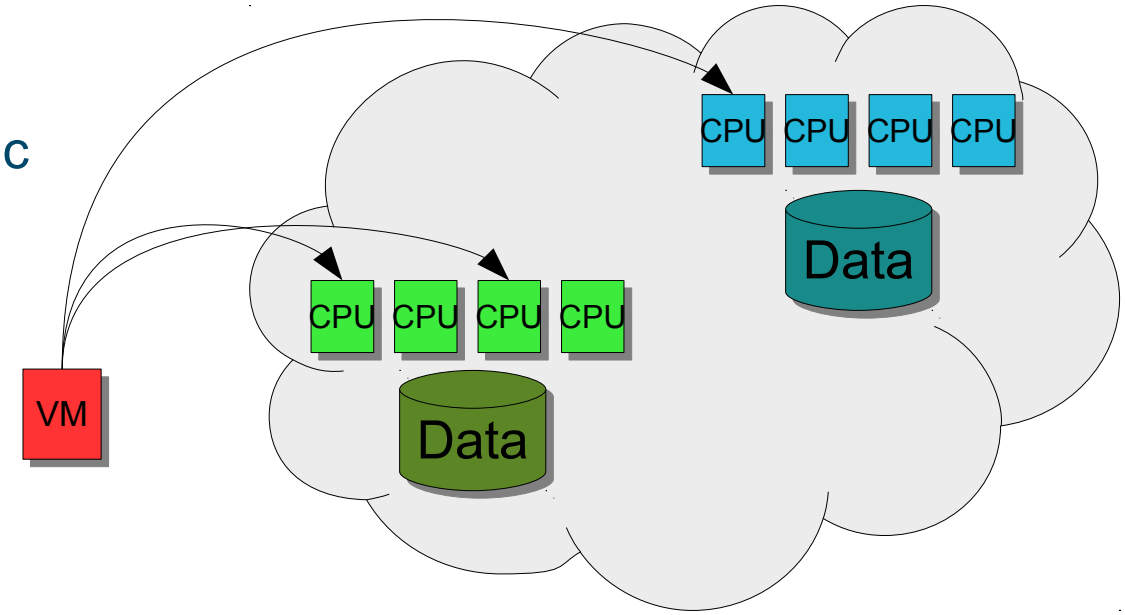
Host data on consortium cloud infrastructures.

Move the compute to the data.

- Upload workload onto VMs.
- Upload VMs into the academic cloud infrastructure.

Federated between centres

- Grid software build on top of cloud components.
- Avoids scaling problems inherent in putting large datasets all in on one place.



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Challenges

None of this infrastructure exists yet!

- Academic service providers have to invest in infrastructure & people.

Funding models:

- How are cost recouped from end users?
- Selling services / charge-back can be tricky in some environments.
  - eg research charities.

Can we do it as well as the big internet companies?

- We have to provide better value than commercial operators.
- Do we build scientific services on top of public IaaS?

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Acknowledgements

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