Enabling Economical Genome Analyses through Optimization and Scalable Workflows

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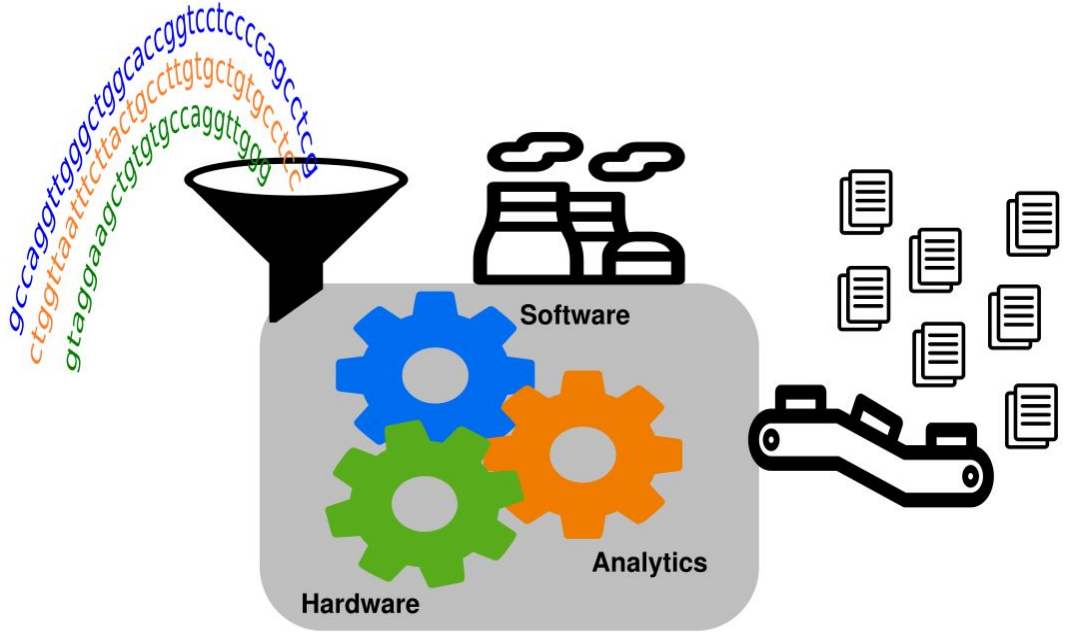
The genomic data science machine

Scaling cancer research



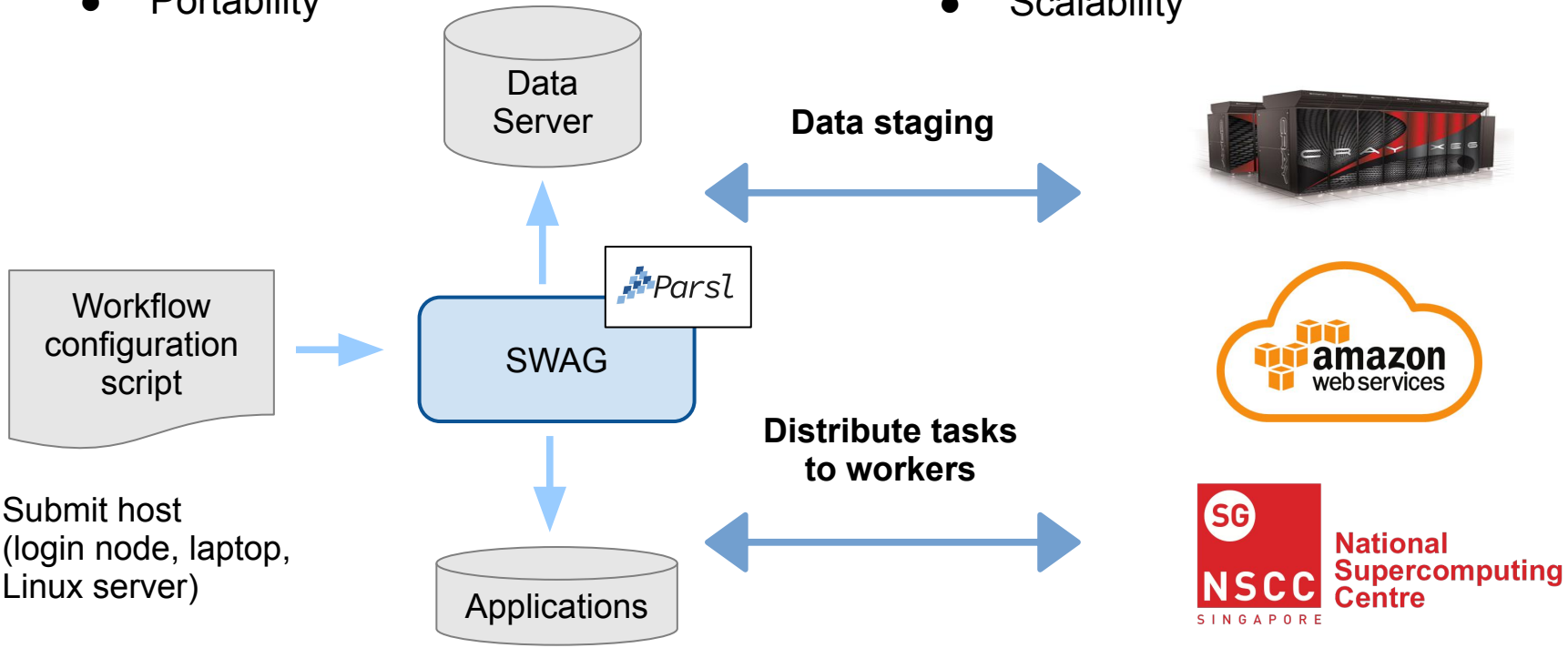
Cloud Platforms

Supercomputing Clusters

Compute Cost

SWAG: Scalable Workflows for Analyzing Genomes

- Transparent parallelism
- Portability
- Robust to failures
- Scalability



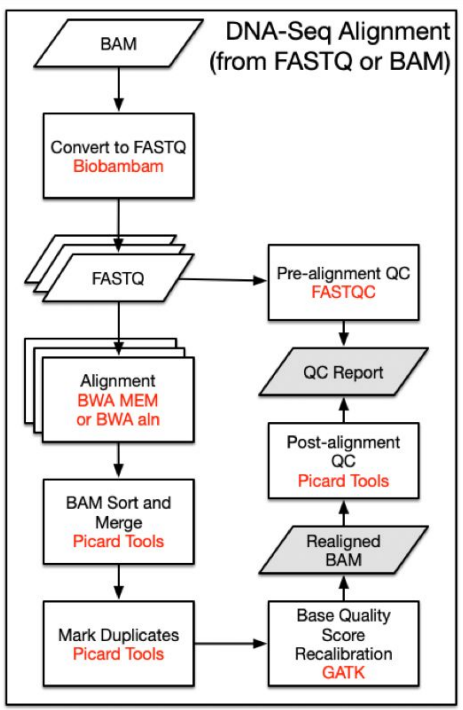
Integrating local and public DNAseq samples

Problem: we want to compare our collection of locally generated DNAseq samples to those in public repositories

Possible solutions:

1. Download all raw data and process locally
    a. Computationally and monetarily expensive
2. Take data as is (e.g. different pipelines on the respective datasets)
    a. Highly prone to technical artifacts; datasets are not comparable
3. Emulate a trusted pipeline locally

Harmonizing to the Genomic Data Commons

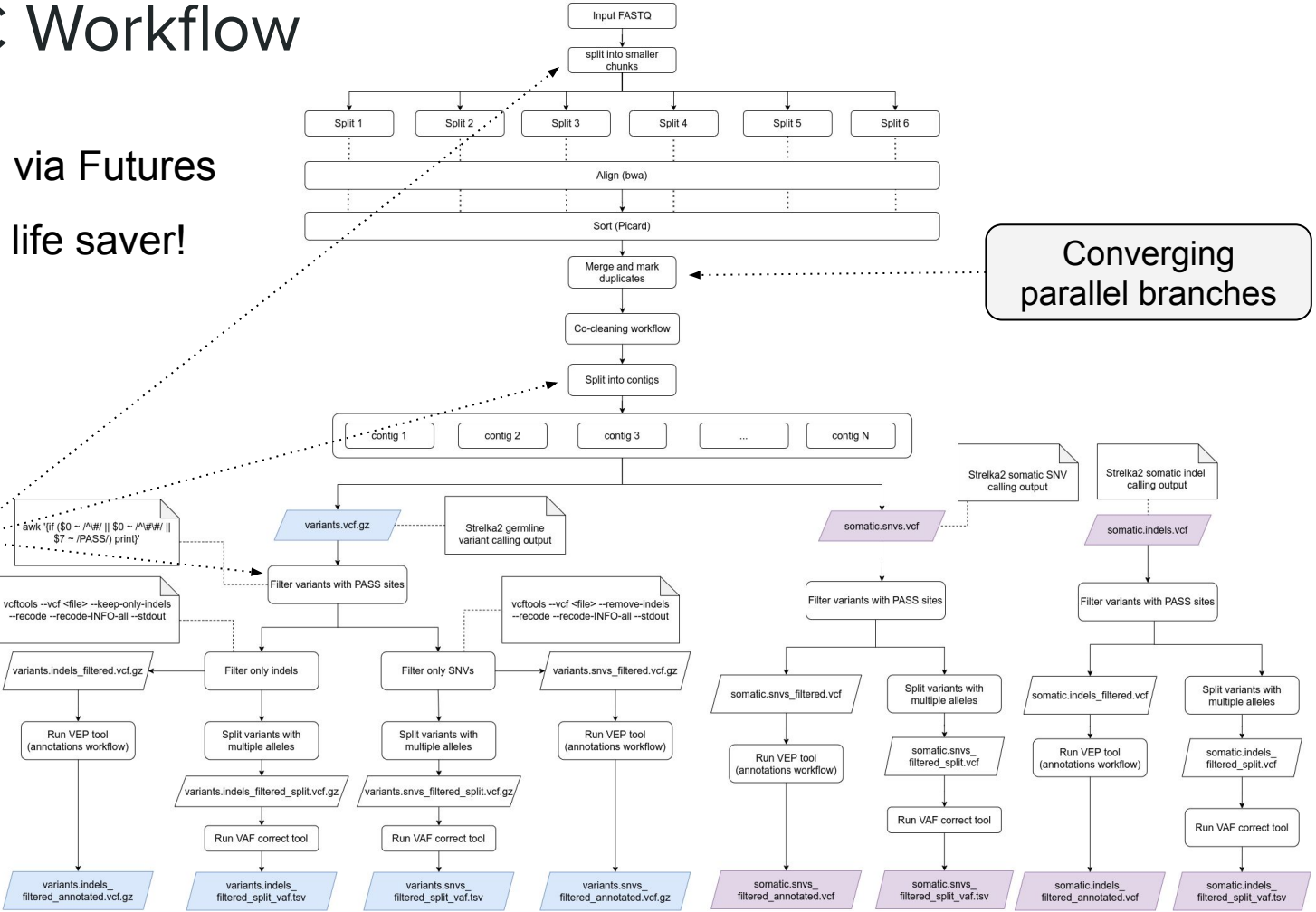


*** hg38 used as ref genome**

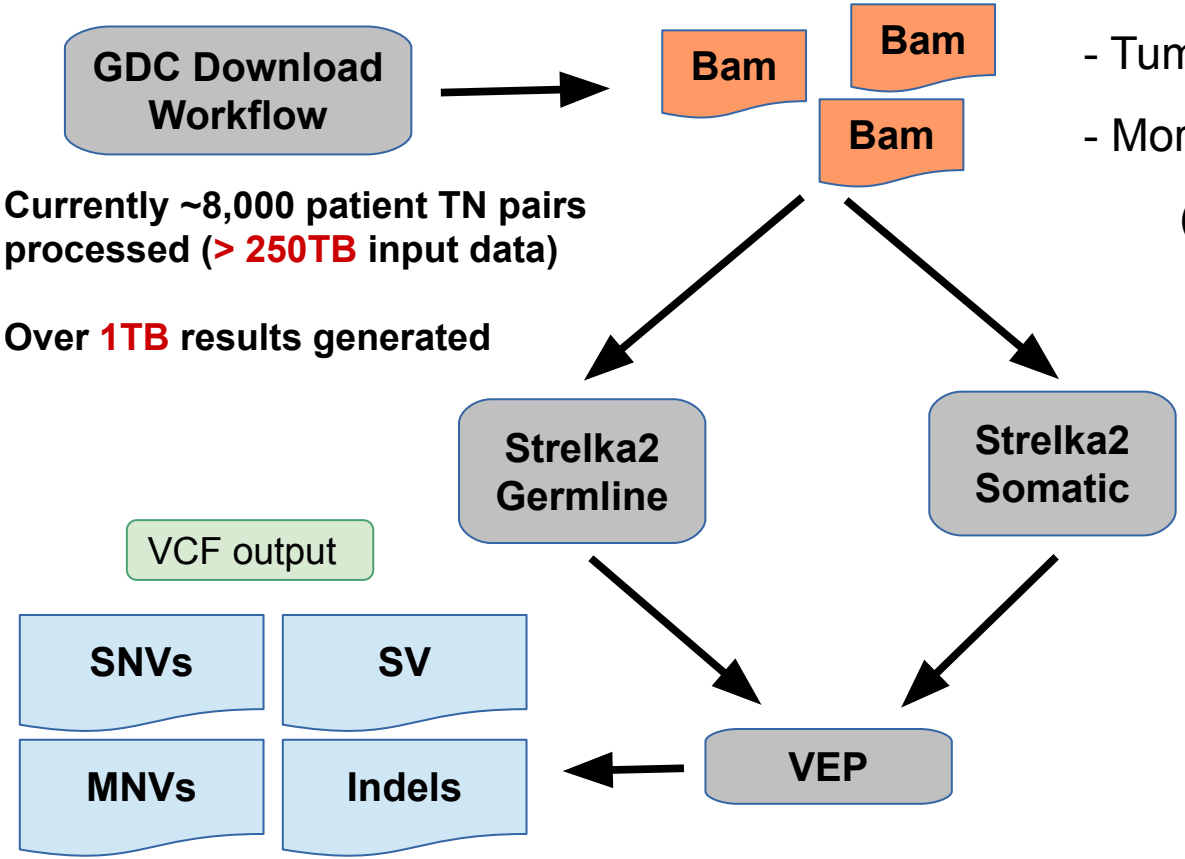
- Tens of thousands of sequenced (panel, exome, & genome) cancer samples
- All samples processed through the same pipeline
- A scalable GDC analytical workflow not yet provided

SWAG - GDC Workflow

- Parsl app chaining via Futures
- Checkpointing is a life saver!



SWAG - Supplementing Data from GDC



Currently ~8,000 patient TN pairs processed (> 250TB input data)

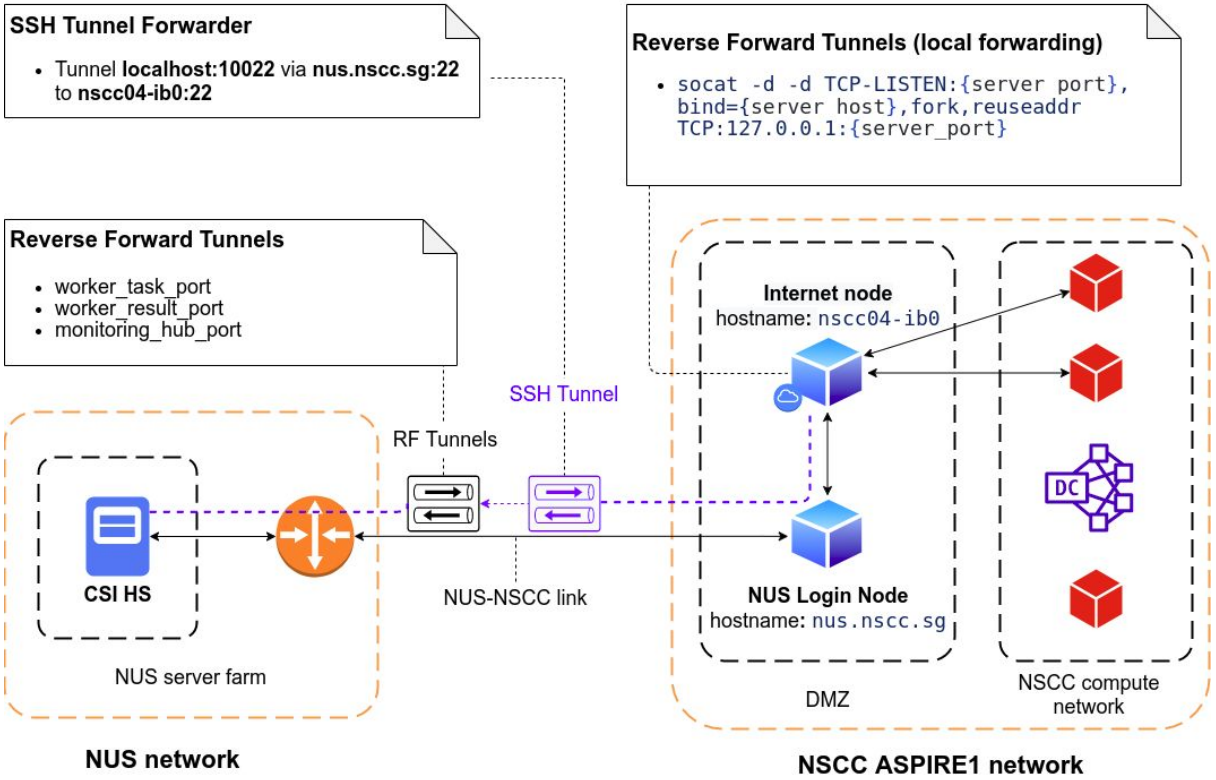
Over 1TB results generated

- Tumor-normal (TN) pairs from TCGA
- More than **10k** cancer patients

  (**33** cancer types)

ASIPRE1
(~700 nodes & ~30,000 cores)

GDC Download Workflow - Infrastructure



- Use LocalProvider with SSHChannel to execute apps on remote nodes
- Create SSH reverse forward tunnels to connect workers to interchange
- Useful when Parsl cannot be executed on a remote instance directly
- Workers should be able to resume work without significant wastage

Wishlist

- More flexibility in packing tasks across multiple executors
  - Deal with task scheduling queue limitations
  - ASPIRE1 medium queue - 24hrs timeout, N1 cpus max
  - ASPIRE1 long queue - 120hrs timeout, N2 cpus max , ($N1 \neq N2$)
- Improved support for remote task execution
  - Non-shared file system between Parsl and workers

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