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

Distribute tasks to workers

Data staging

Data Server

Workflow configuration script

Submit host (login node, laptop, Linux server)

Parsl

Applications

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
• 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
Converging parallel branches

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

Fork into multiple branches
SWAG - Supplementing Data from GDC

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

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

Over 1TB results generated
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 ≠ N2)

- Improved support for remote task execution
  - Non-shared file system between Parsl and workers
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