AWS Cloud Computing of TOPMed Data

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Analysis Pipeline on the Cloud

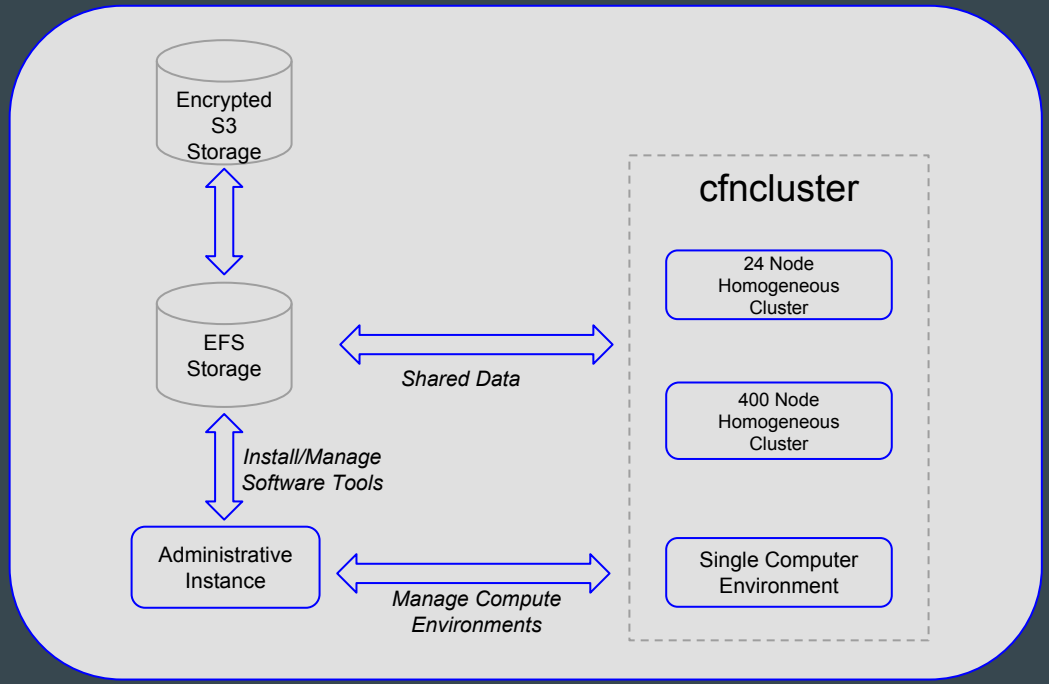
Presentation

- Review High Performance Computing (HPC) Support in Analysis Pipeline
- Overviews
  - AWS *cfncluster*
  - Docker
  - AWS *Batch Service*
- Examples Include:
  - Docker
  - Analysis Pipeline using AWS *Batch Service*
  - Monitoring *Batch Service*

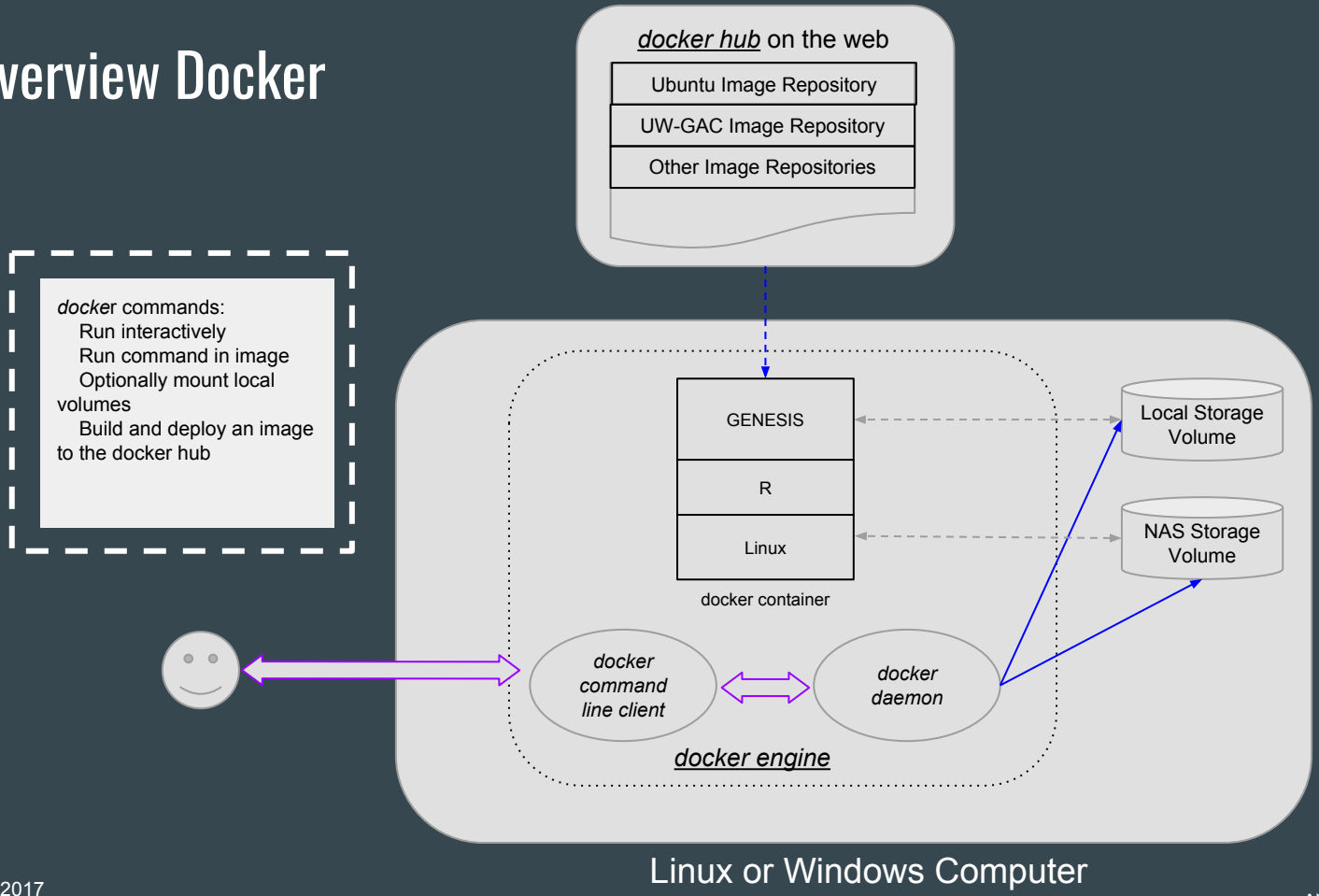
High Performance Computing (HPC) Support in Analysis Pipeline

- Currently Supported
  - Local linux cluster with *SGE* job scheduler
  - AWS *cfncluster* with *SGE* job scheduler (traditional)
  - AWS *batch* with *docker* images (new)
- To Be Investigated
  - Microsoft *Azure* using *Batch/Docker*
  - Google Cloud using *Batch/Docker*

Overview AWS *cfncluster*



Overview Docker



Docker Examples

1. Log into AWS docker instance

```
$ ssh -i ~/.ssh/xxx.pem ubuntu@xx.xx.xx
```

2. List docker images and containers

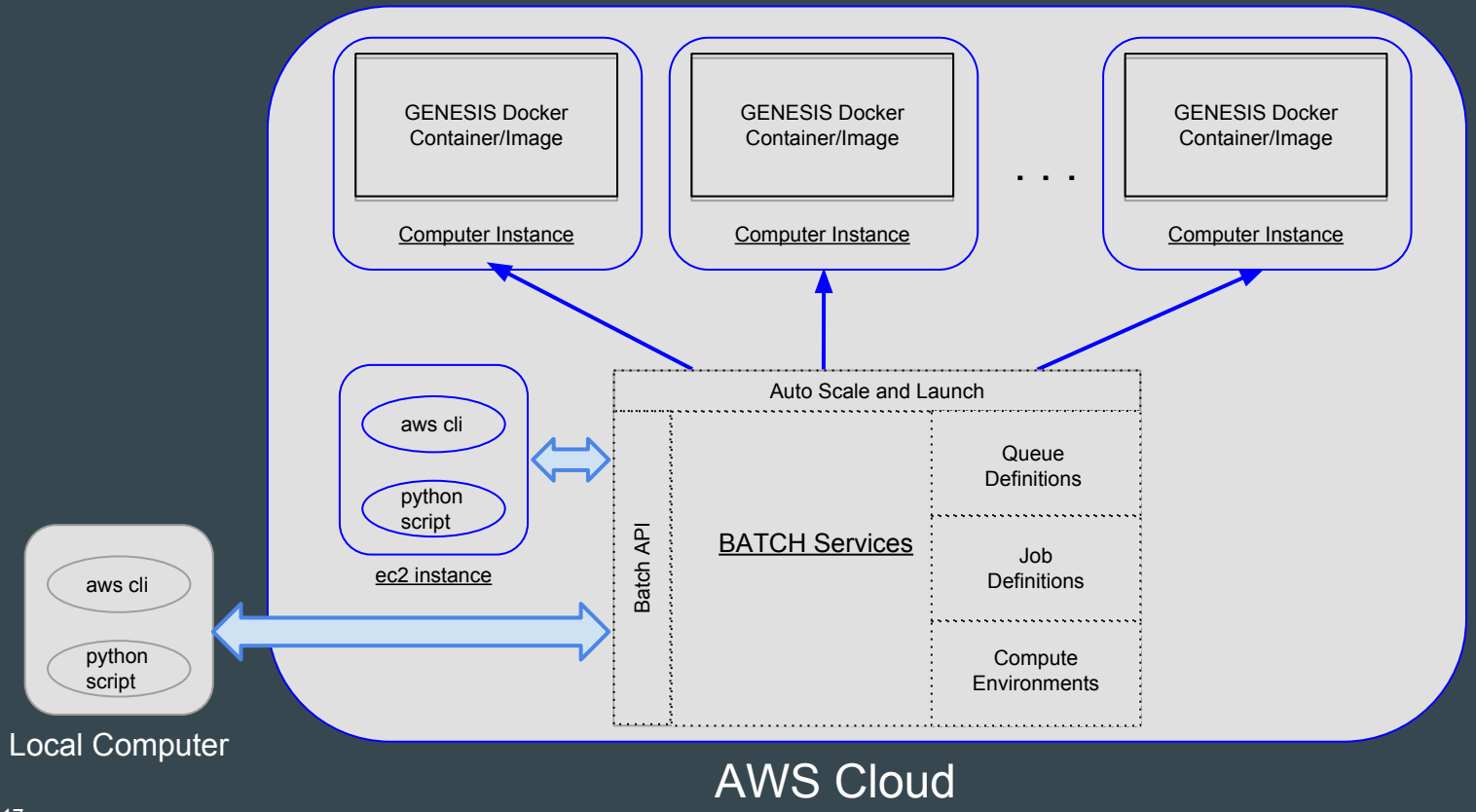
```
$ docker images    # list images
. . .
$ docker ps        # list containers
. . .
```

Docker Examples

3. Run the R TOPMed docker image

```
$ docker run -it uwgac/r-topmed:dev /bin/bash
# R
library(SeqArray)
data.path <-
"https://github.com/smgogarten/analysis_pipeline/raw/devel/testdata"
vcffile <- "1KG_phase3_subset_chr1.vcf.gz"
if (!file.exists(vcffile)) download.file(file.path(data.path, vcffile),
vcffile)
gdsfile <- "1KG_phase3_subset_chr1.gds"
seqVCF2GDS(vcffile, gdsfile, fmt.import="GT", storage.option="LZMA_RA",
verbose=FALSE)
gds <- seqOpen(gdsfile)
gds
```

Overview AWS *Batch Service*



Analysis Pipeline and AWS *Batch* Examples

4. Preliminaries

```
$ # cd to working directory
$ cd /projects/topmed/analysts/kuraisa/tm-workshop
$ # vi the config file
$ vi assoc_window_burden.config
. . .
```

5. Print out commands

```
$ # use print option and cluster_type AWS_Batch
$ python /projects/topmed/dev_code . . .
```

Analysis Pipeline and AWS *Batch* Examples

6. Execute pipeline

```
$ # specify cluster_type AWS_Batch and cluster cfg
$ # file for using test data/environment
$ python /projects/topmed/dev_code/analysis_pipeline . . .
. . .
```

7. Monitor jobs
    a. Batch Console
        i. Dashboard (overview)
        ii. Job queue (Optimal_topmed_testdata)
        iii. Logs
    b. ec2 instances

Questions

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