

# An Alternative Way for Genome Analysis on Cloud

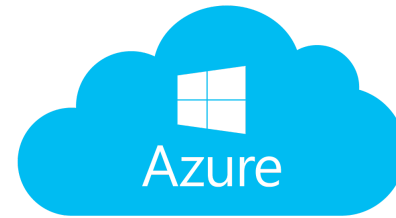
ETL, ExTL, and introduction of its engine: `aws-sub`

Hiromu OCHIAI - National Cancer Center Japan

# Genome analysis on Cloud Resources



Google Cloud Platform



and more

How to use "Cloud"?

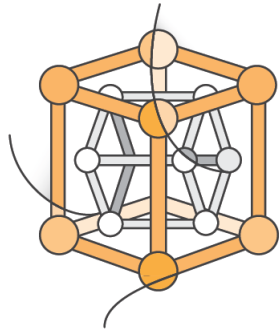


# "Building a Cluster on Cloud"

- Galaxy



- cfn-cluster



- ElastiCluster
- Butler
- etc...

# Pros and Cons of "Cluster on Cloud"

- Pros:

- We are **VERY** used to cluster on HPC
  - *Grid Engine, HTCondor, SLURM, etc...*
  - e.g. `qsub ./my-workflow.sh`

# Pros and Cons of "Cluster on Cloud"

## • Pros:

- We are **VERY** used to cluster on HPC
  - *Grid Engine, HTCondor, SLURM, etc...*
  - e.g. `qsub ./my-workflow.sh`

## • Cons:

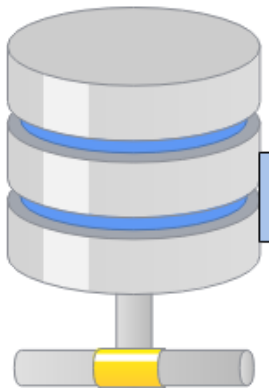
- Persistent static resources
  - Scheduler Node, Queue Database, Filesystem

**Suggestion: "On-Demand ETL"**

# ETL is

- Extract, Transform, Load
- Data processing model for general purpose

## Data Source



**Extract**

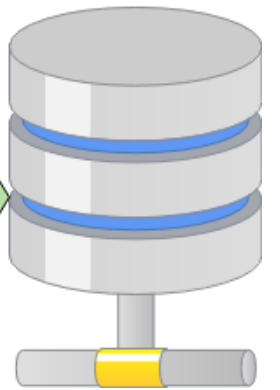
## Computing Resources



**Transfrom**



## Data Destination

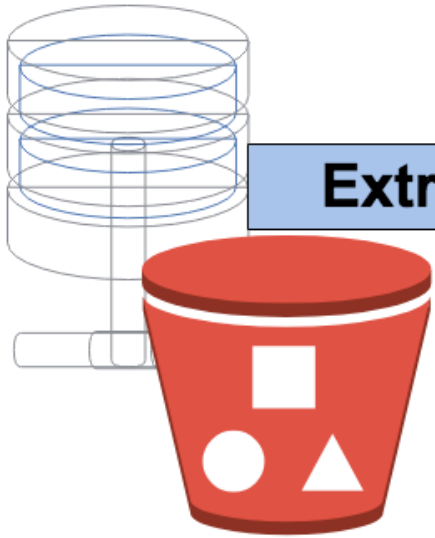


**Load**



# Do it on Cloud

**Data Source**

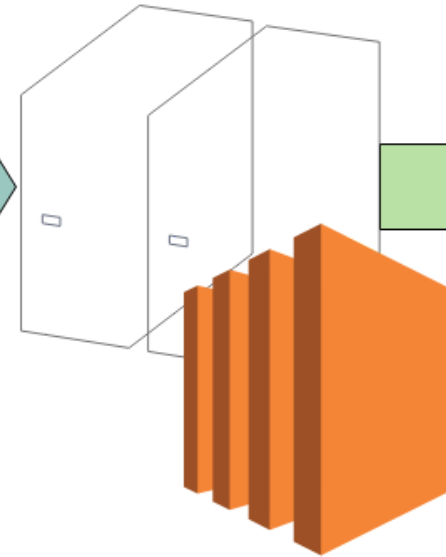


**Extract**

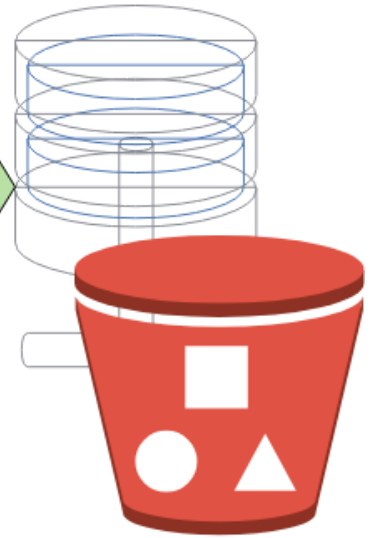
**Computing Resources**



**Transfrom**

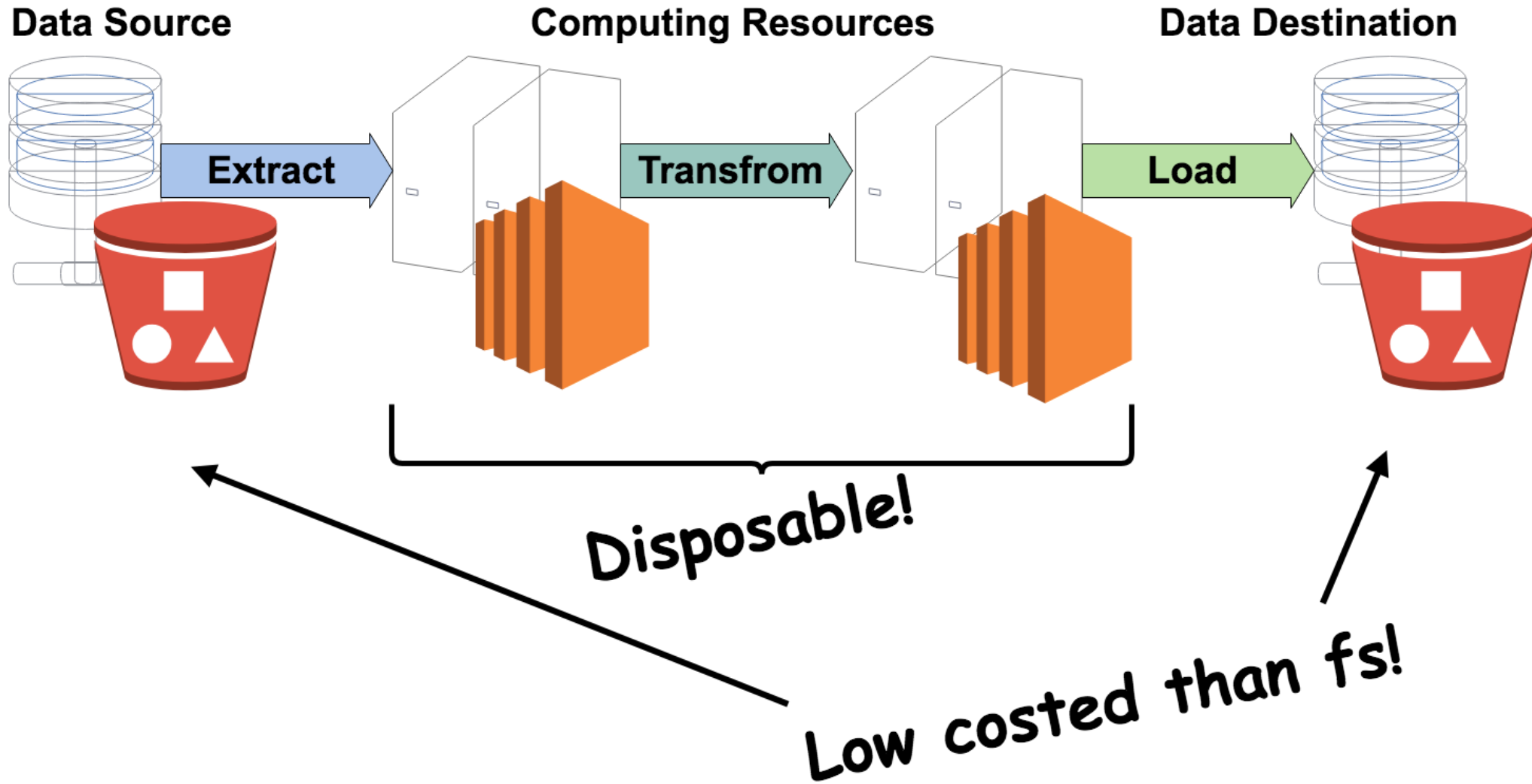


**Data Destination**



**Load**

# Do it on Cloud



Do it with `awscli` !

# If you have 4 Fastq samples

**Your actual  
sample data**



**Common Data  
e.g. Reference**



**List of  
data locations  
on the storage**

# Specify workflow script and samples

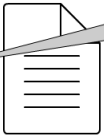
Your actual  
sample data



Common Data  
e.g. Reference



```
$ aws \
  --tasks ./my-samples.csv \
  --script ./my-workflow.sh
```



List of  
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# Security Group

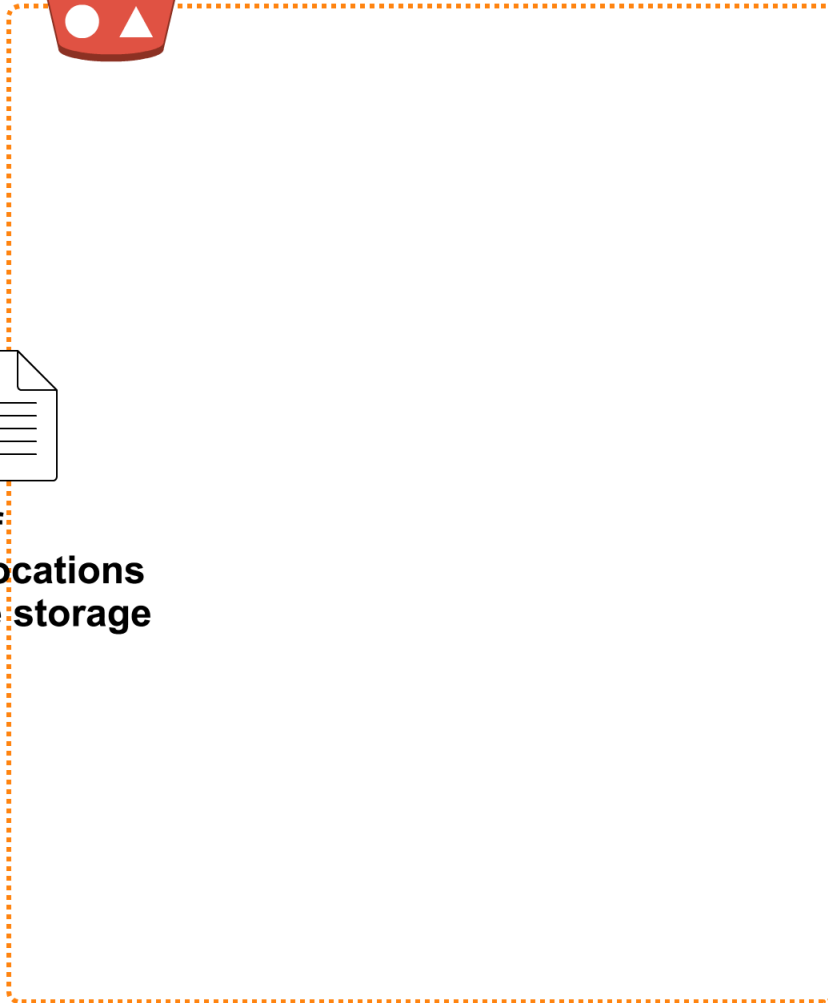
**Your actual  
sample data**



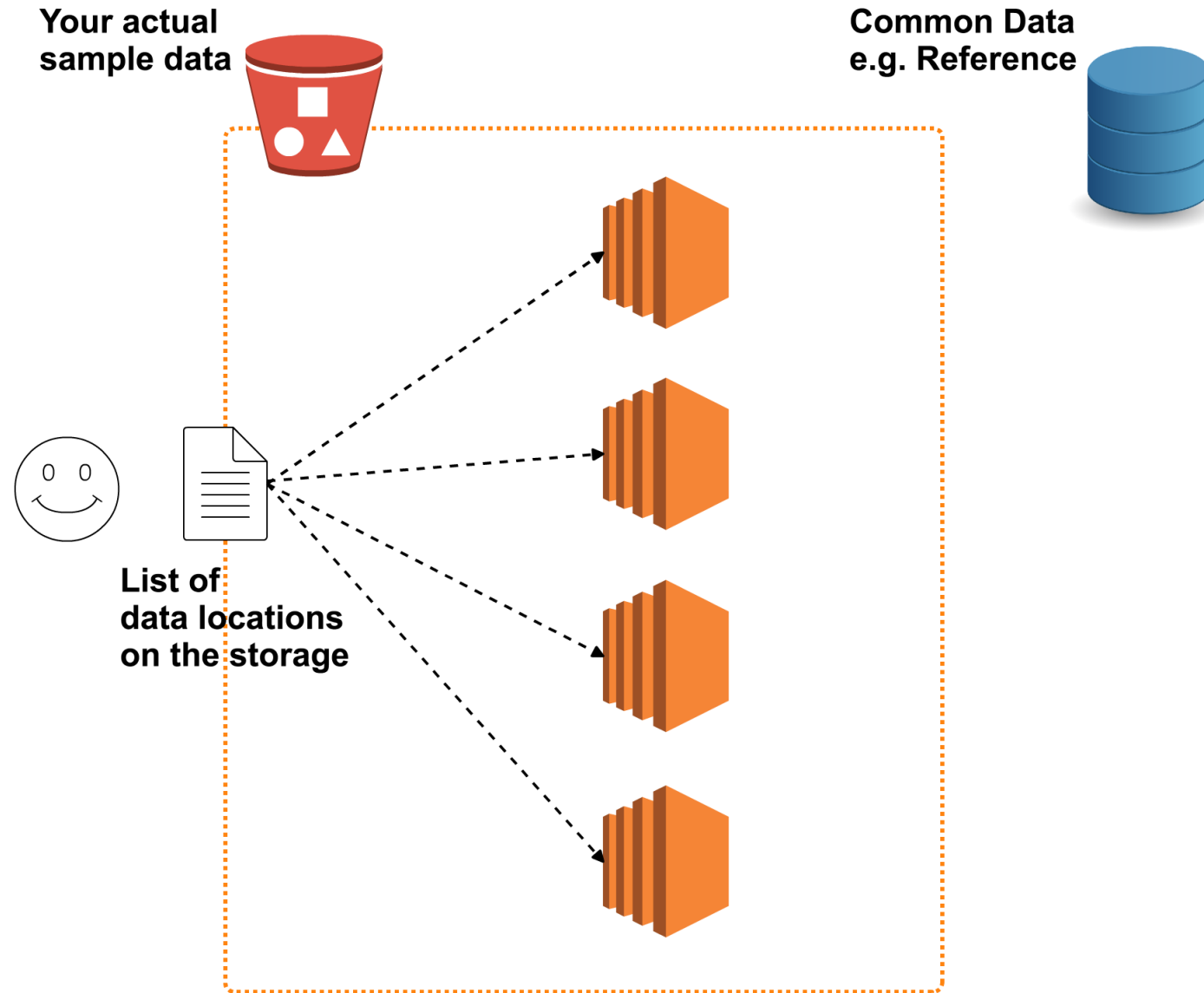
**Common Data  
e.g. Reference**



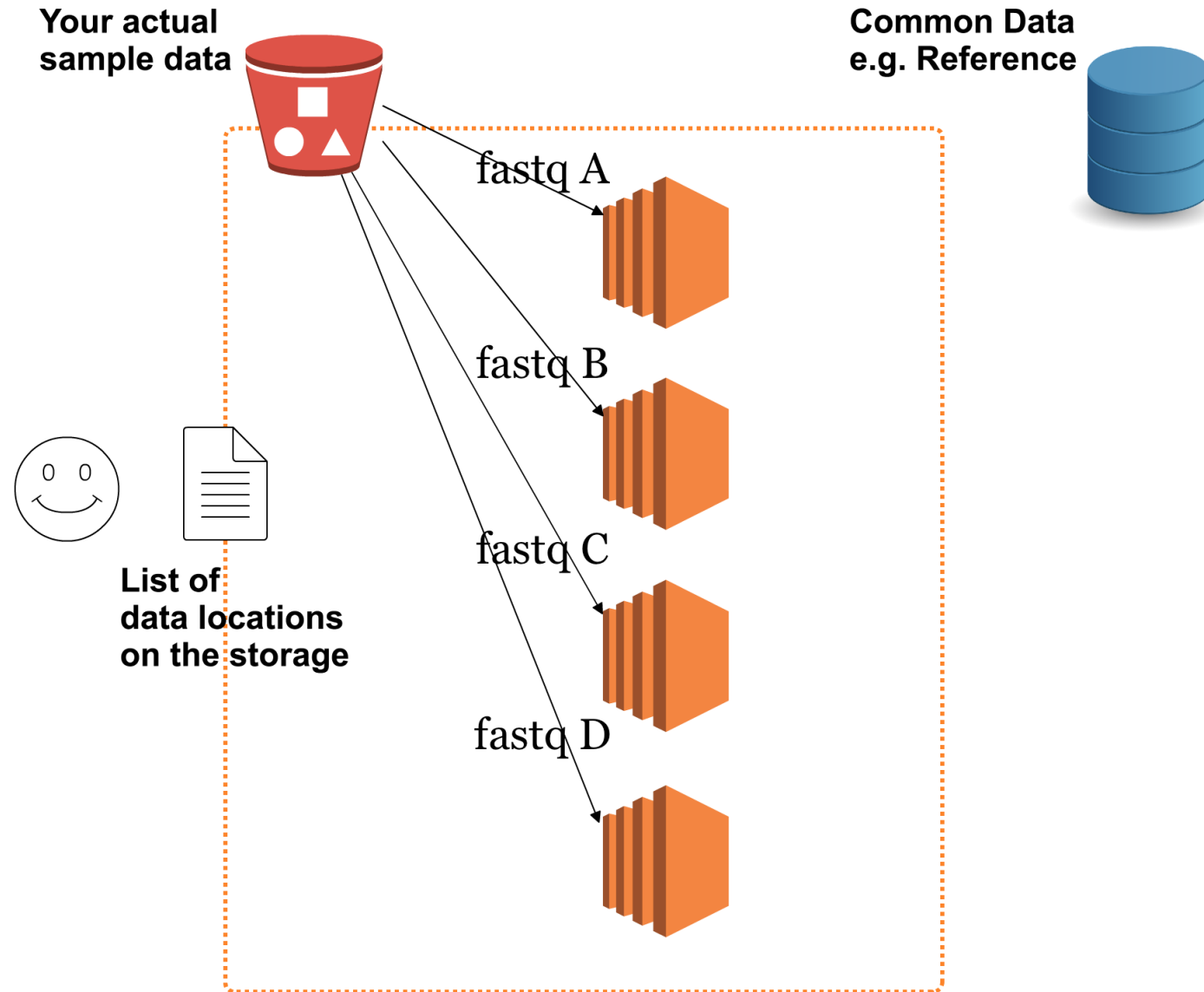
**List of  
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# Instances for each sample

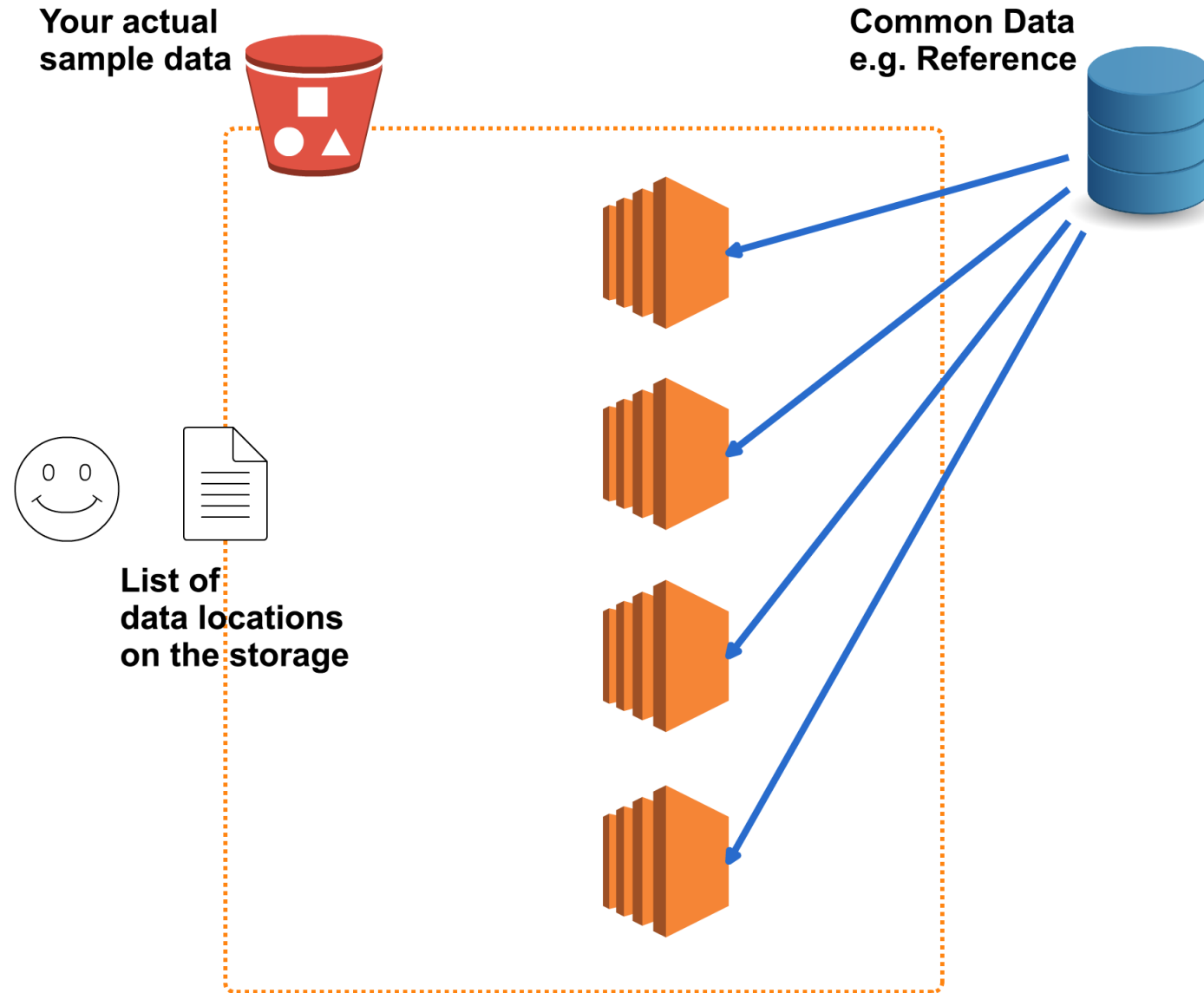


# Fetch specific sample data according to the location

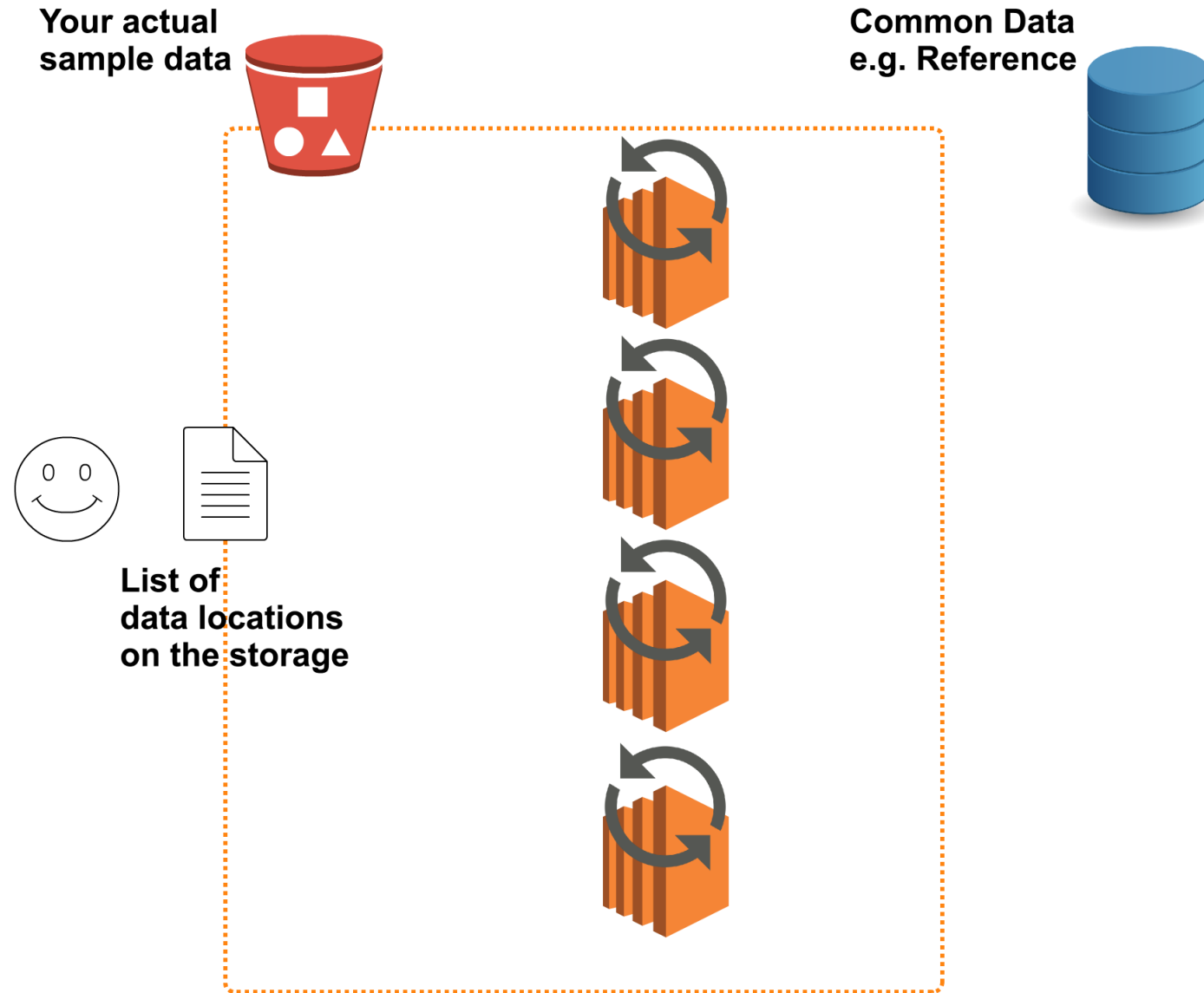




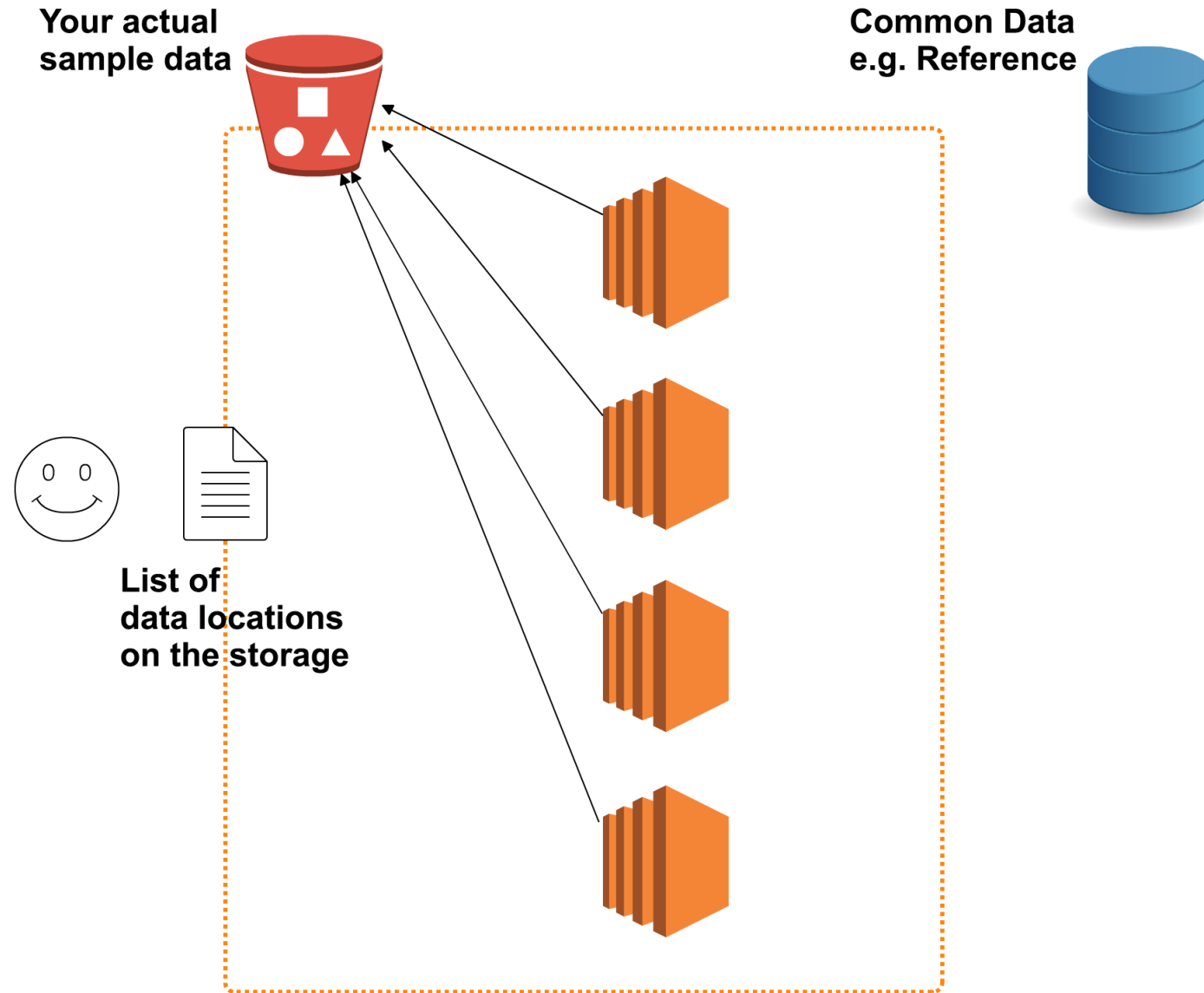
# Fetch reference data from common data source



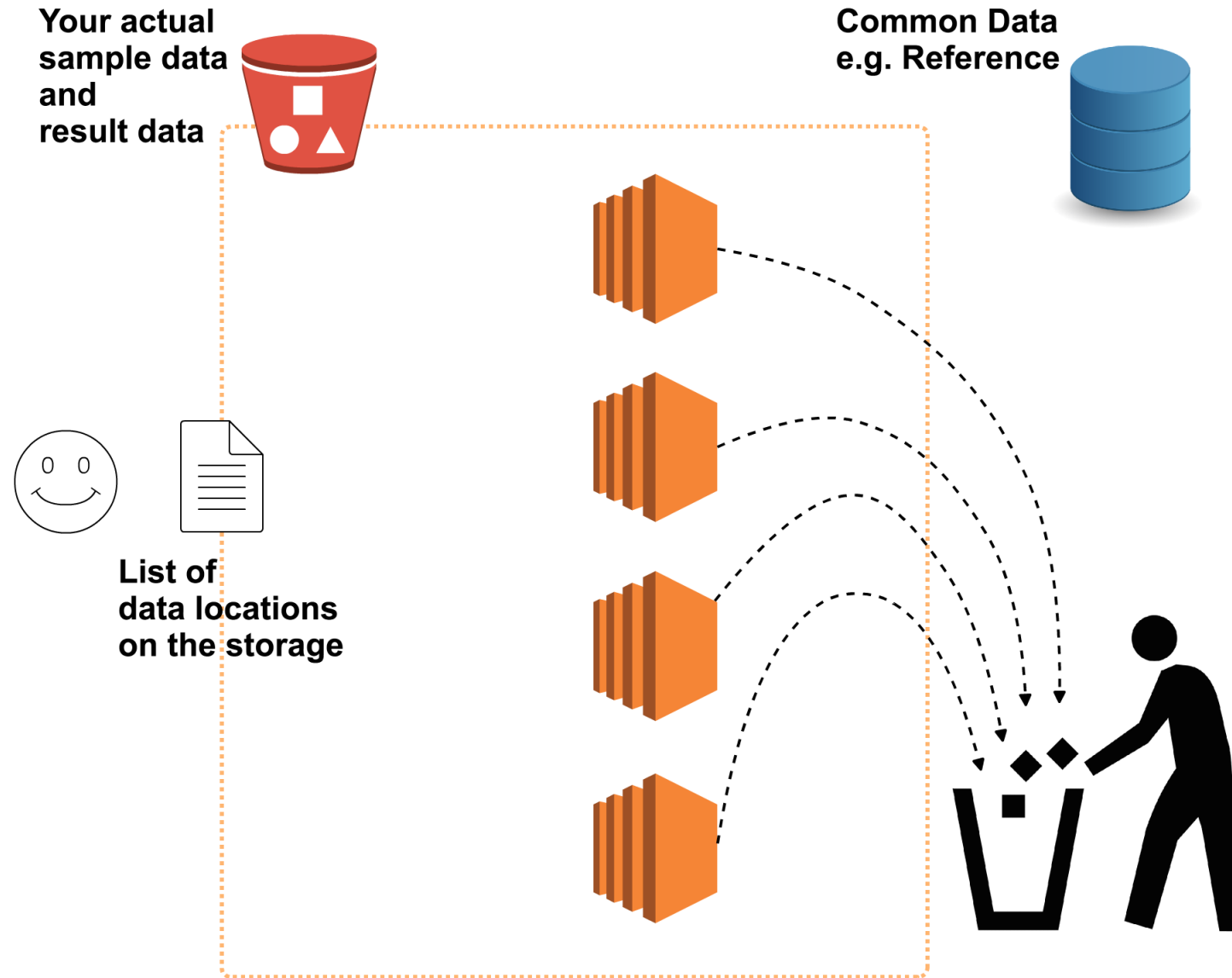
# Execute your workflow for each



# Push the result data back to the storage



# Dispose all the computing resources no longer used



# All you got is the result data!

Your actual  
sample data  
and  
result data

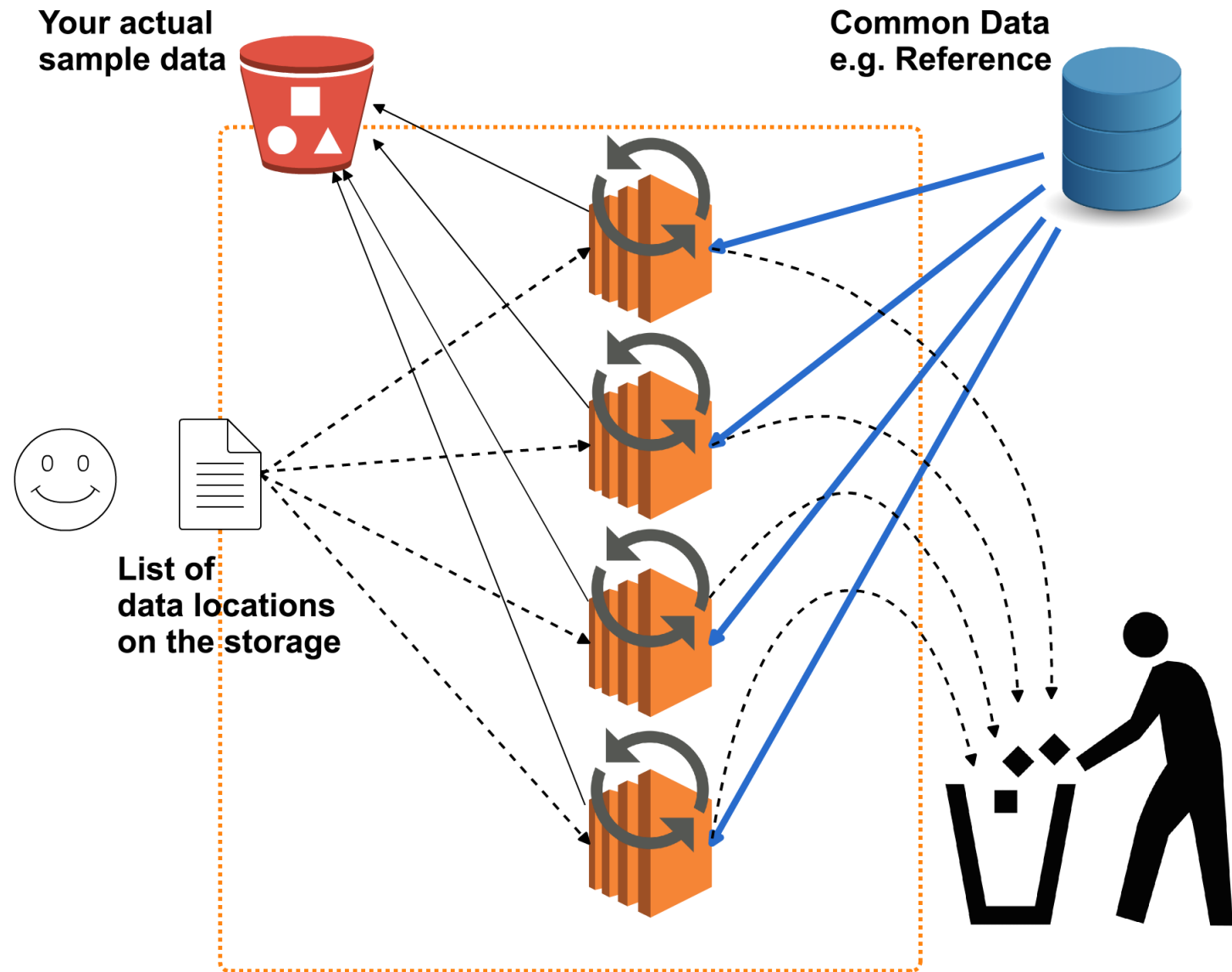


Common Data  
e.g. Reference



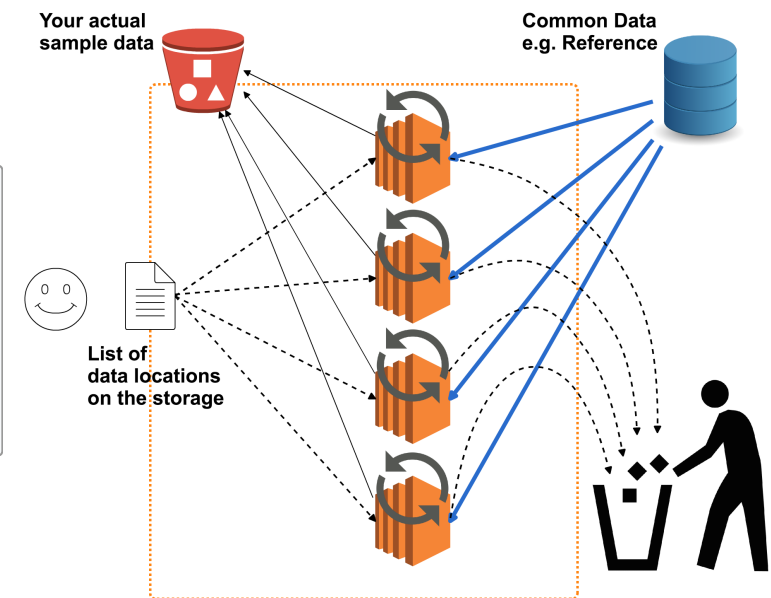
List of  
data locations  
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# Overall



by using **aws**ub

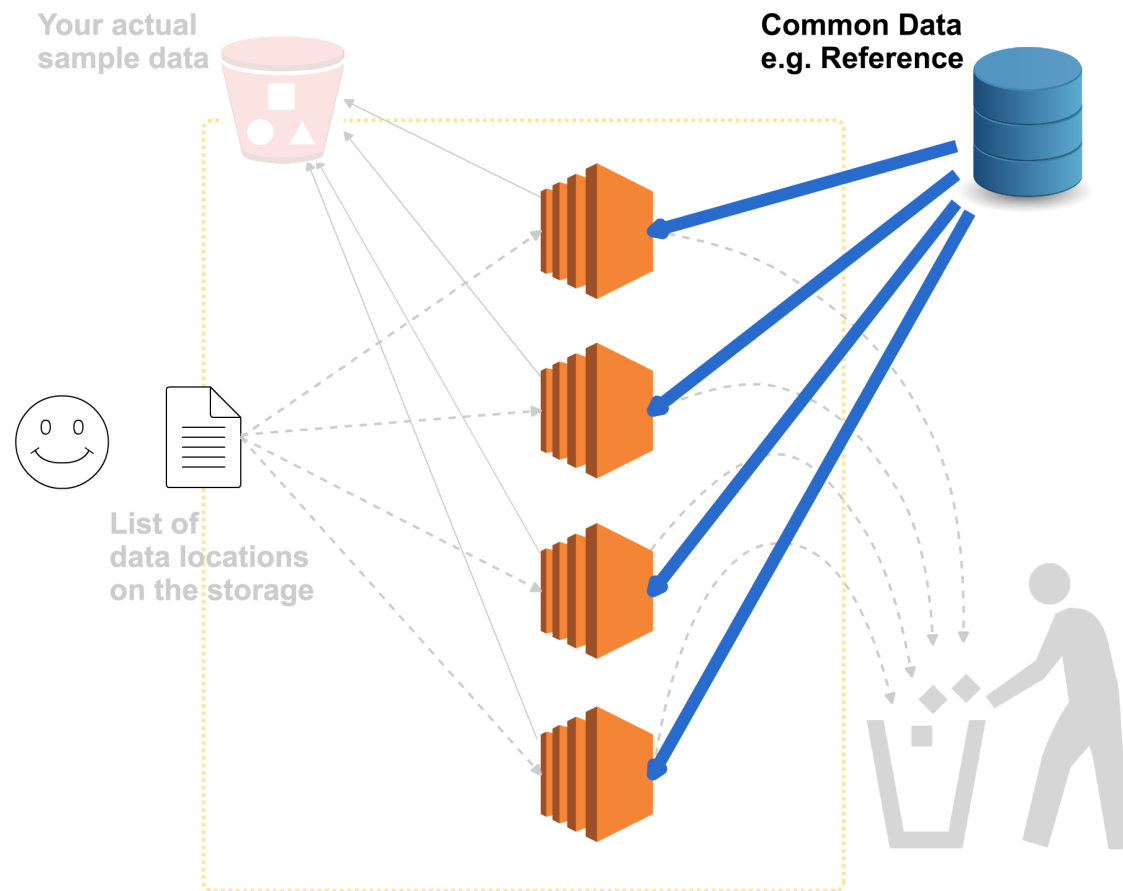
```
$ aws sub \
  --tasks ./my-samples.csv \
  --script ./my-workflow.sh \
  --image otiai10/STAR-alignment # any Docker image
```



# Problems of ETL on Bioinformatics



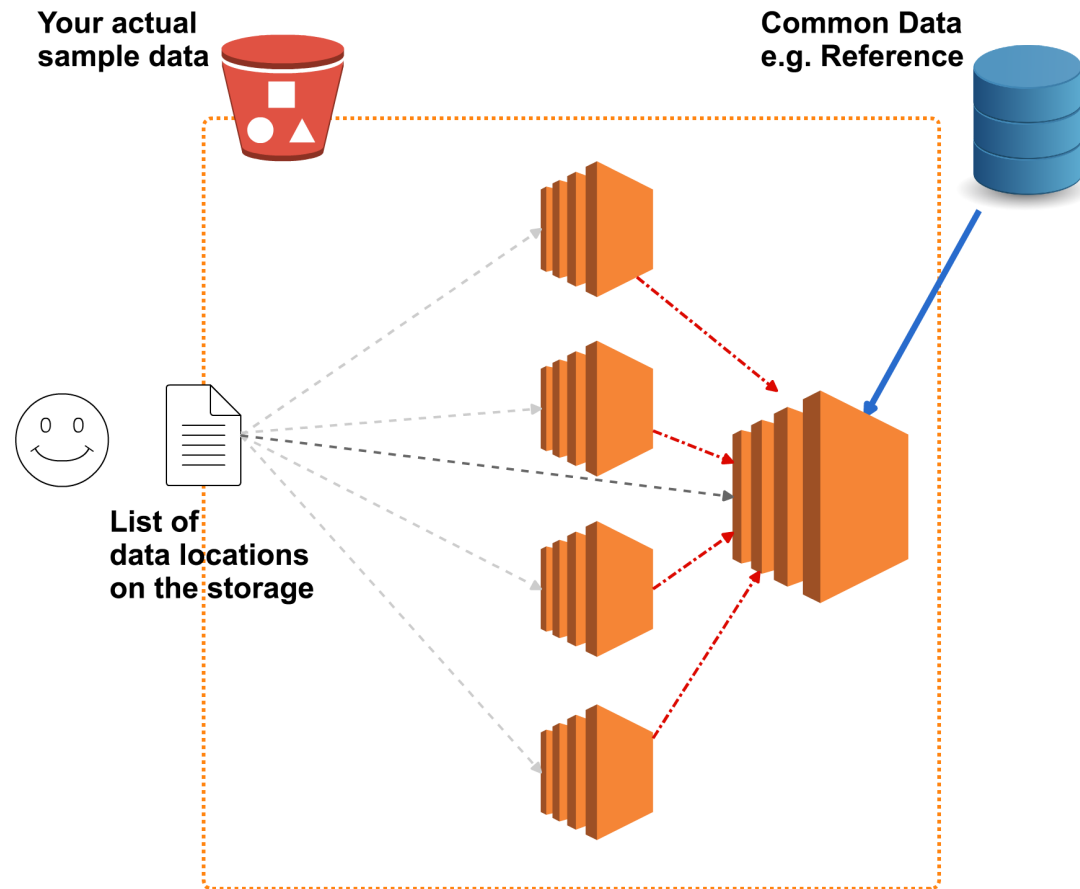
# Problems of ETL on Bioinformatics



- Common Reference Data is so huge
  - Copying huge reference data uses
    - inefficient **traffic**
    - inefficient **instance time**
    - inefficient **storage area**
  - e.g. Human Reference for STAR alignment: **30GB**

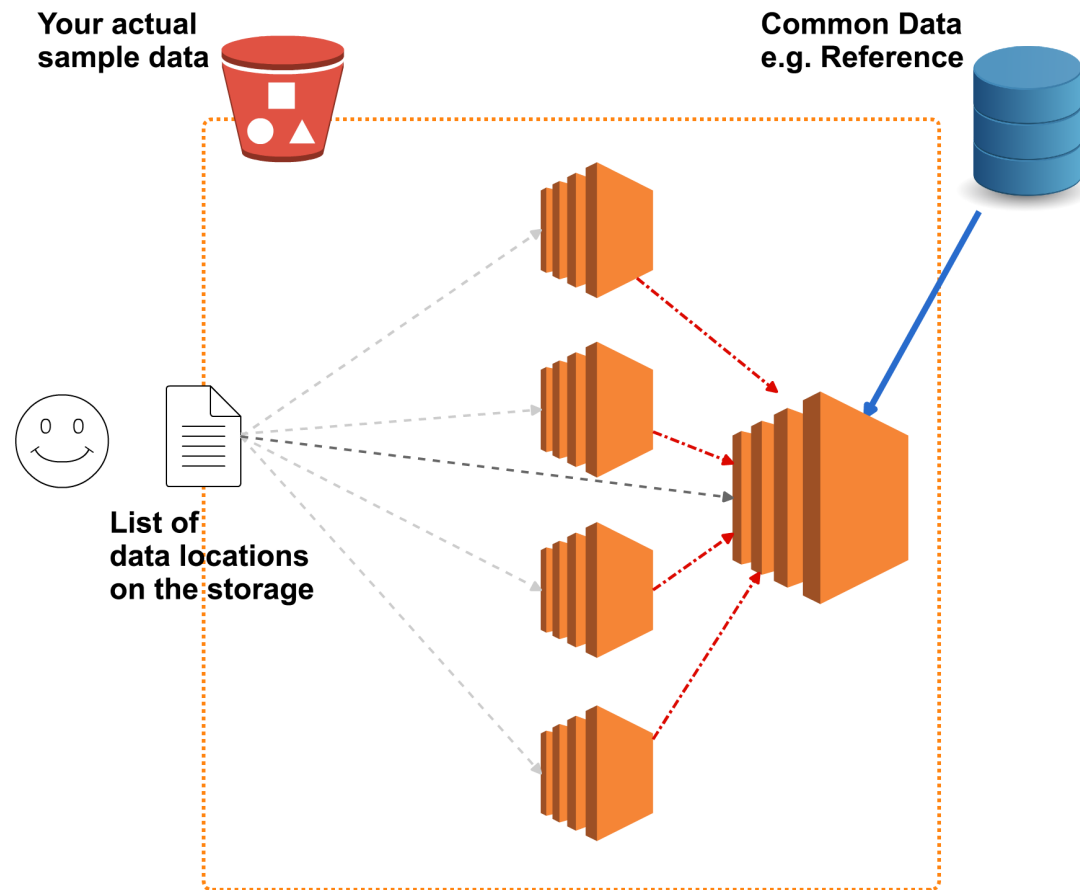
**Suggestion: *Extended* ETL (ExTL)**

# Suggestion: *Extended* ETL (ExTL)



- Create a **Shared Data Instance**
- Fetch external common data **once**
- Let computing instances **mount**

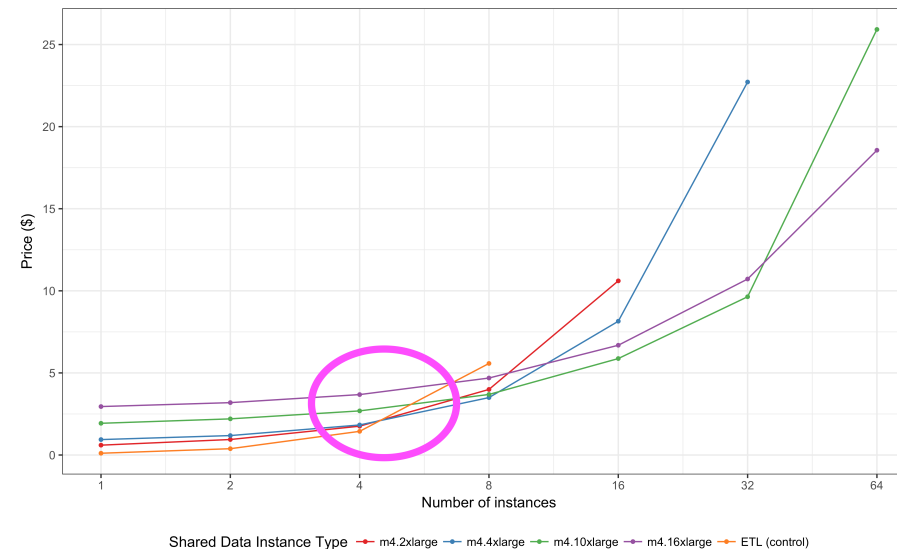
# Suggestion: *Extended* ETL (ExTL)



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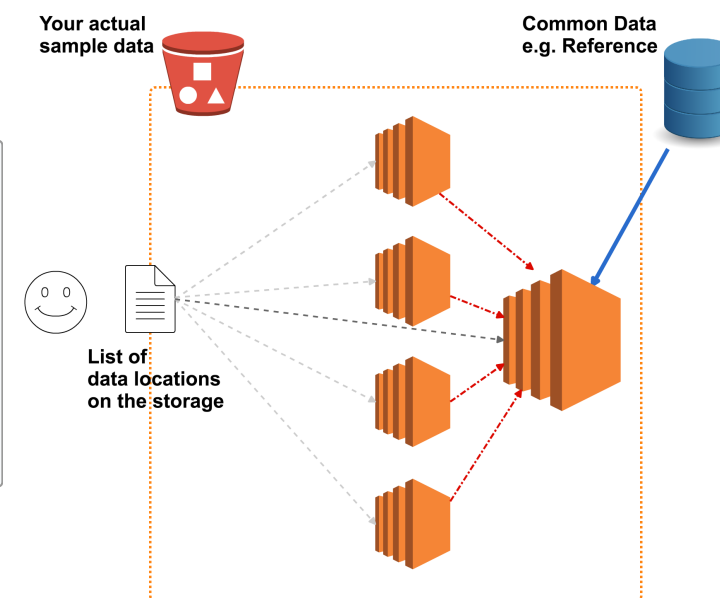
## Cost Saving!

- Network traffic, instance time, ...



# ExTL by using `awsub`

```
$ awsub \  
  --tasks ./my-samples.csv \  
  --script ./my-workflow.sh \  
  --image otiai10/STAR-alignment \  
+ --shared REFERENCE=s3://bucket/huge/reference
```



# Summary

- Another approach than "Cluster on Cloud"
  - **"On-demand ETL on Cloud"**
- Huge common data can be a problem of "ETL on Cloud"
- **"Extended ETL" (ExTL)**
- Working Example Implementation of ExTL: **aws****sub**

# More on the poster

about

- How to **Get started**
- **Google Cloud**, Microsoft Azure, OpenStack and more
- Common Workflow Language (**CWL**)
- Execution **Protocol** and Security Groups / IAM Instance Profile
- **Go** implementation
- etc...

Come to poster **B29**, and any feedback is welcome!

<https://github.com/otiai10/awsub>

