



Aeromancer: A Workflow Manager for Large-Scale MapReduce-Based Scientific Workflows

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Outline

- Introduction & Motivation
 - Cloud computing and its benefits
 - SeqInCloud and scalability analysis
- Aeromancer
 - Usage scenario
 - Workflow and architecture
 - Discussion
- Experiments & Initial Results

Introduction & Motivation

I would like
6 virtual machines
for a month

user a

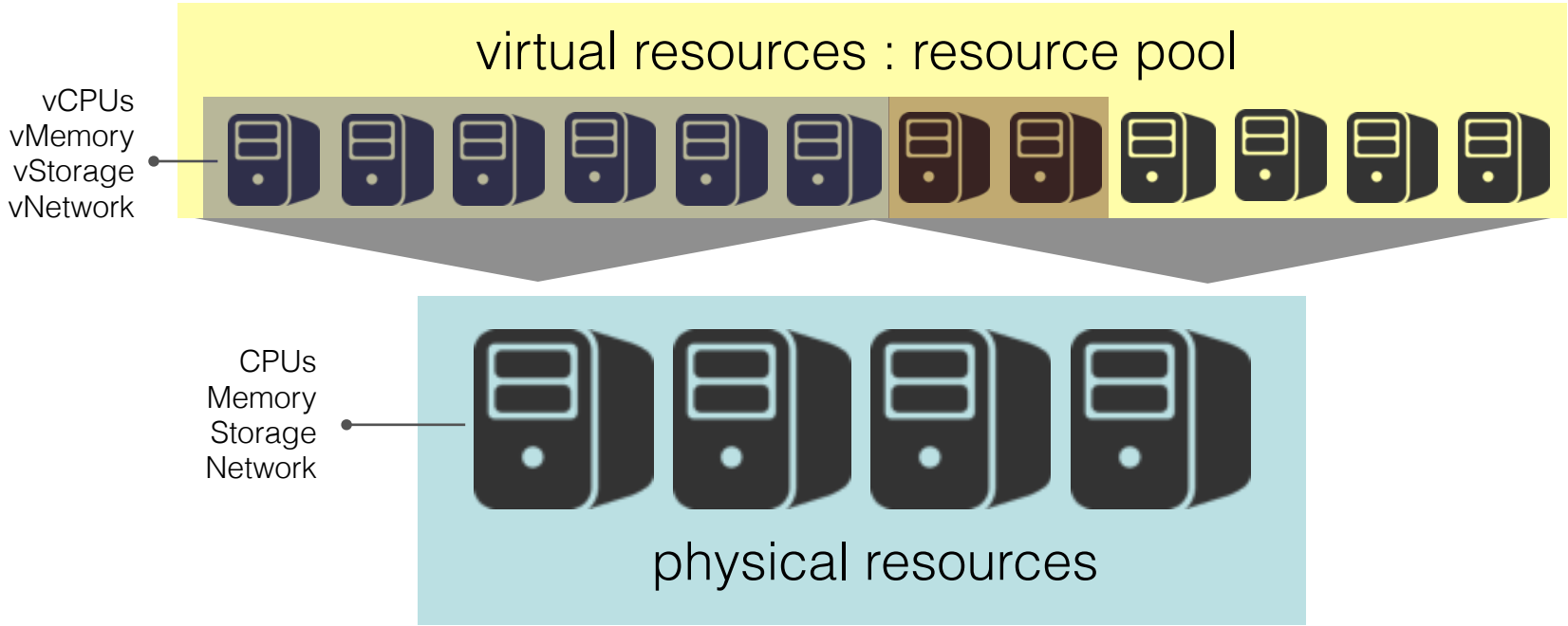


I would like
3 virtual machines
for 2 months

user b



What is Cloud?



How is Cloud beneficial for Us?



Next-generation sequencing (NGS) produces a huge amount of DNA sequence data

{ 2k sequencers produce 15 PB genetic data/year }

Cost of sequencing a human-size genome decreases over time

{ 2011 → \$95M }
{ 2012 → \$6.5k }
{ 2014 → \$1k }

How is Cloud beneficial for Us?



Big Data

How is Cloud beneficial for Us?



Cloud can accelerate our ability
to identify the cure for cancer

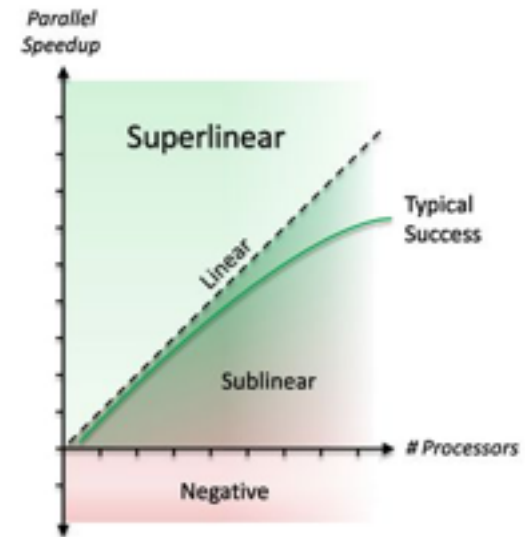
Big Data Challenge



Provisioning compute and storage resources to analyze the exponentially increasing genomic data

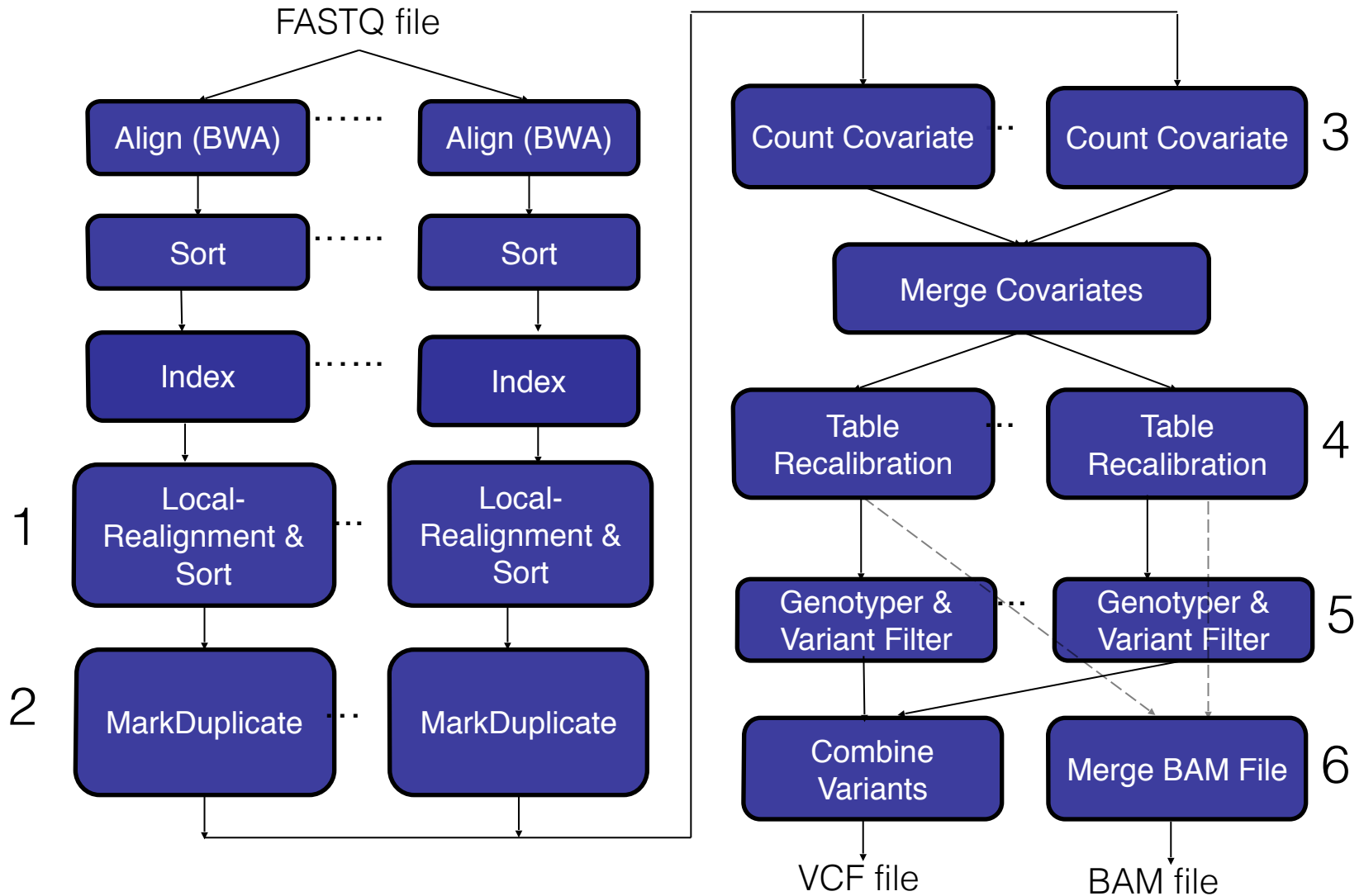
SeqInCloud

- It is implemented based on GATK (Genome Analysis Toolkit)
- All six stages have to be executed in order
- Each stage is implemented as a small separated Hadoop program
 - It can be broken down into small jobs and run on multiple computers/processors
 - We expect a **linear speed-up** on every stage

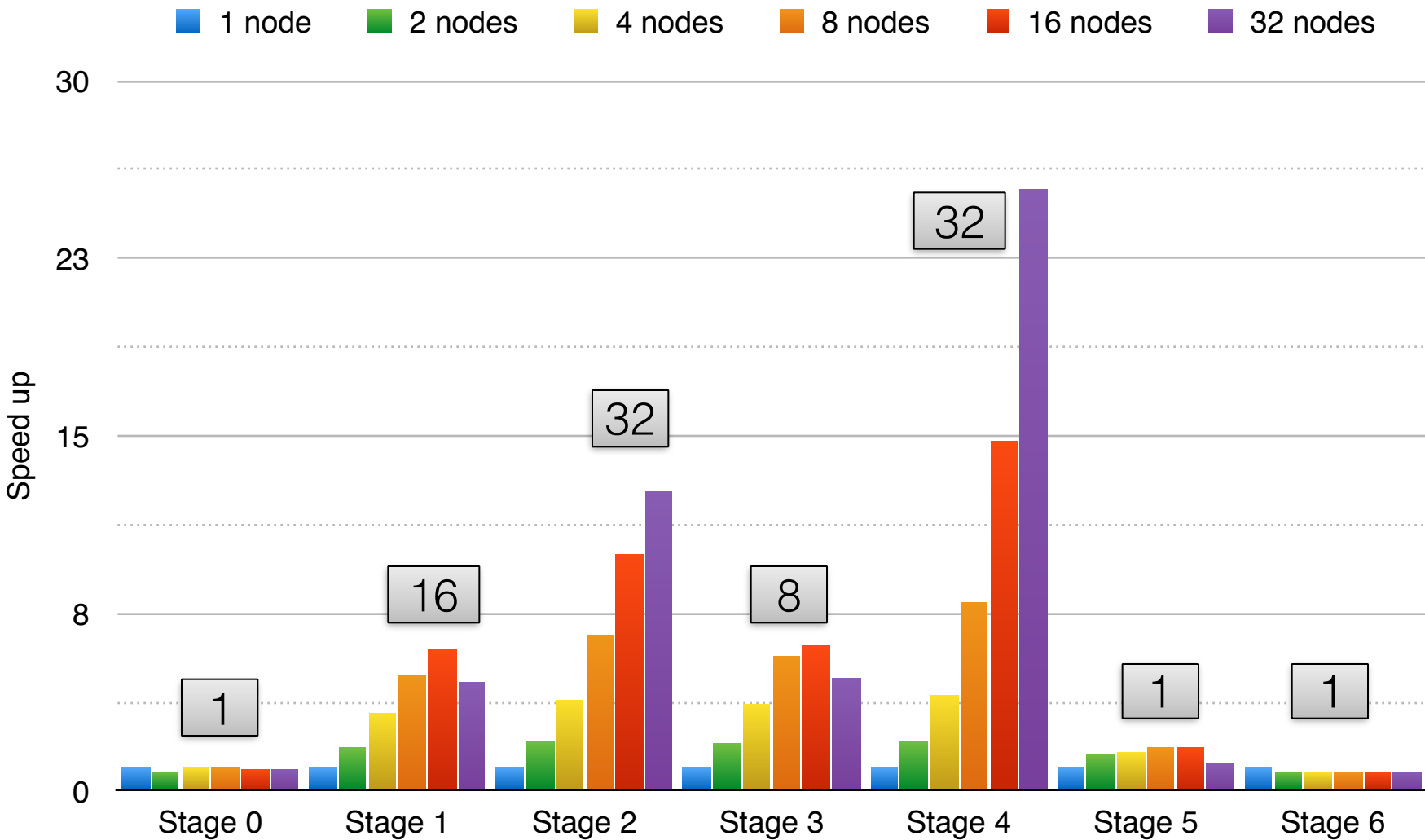


SeqInCloud

Genome variant analysis pipeline



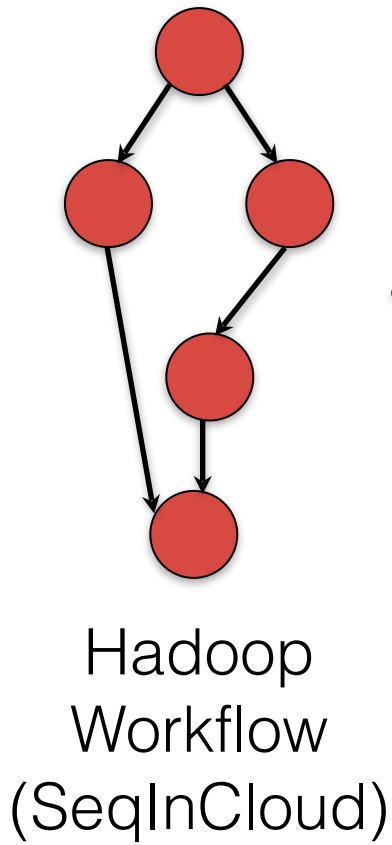
SeqInCloud Scalability Analysis



SeqInCloud Scalability Analysis

- To run SeqInCloud efficiently on Hadoop
 - Number of compute nodes must be varied based on the scalability of each stage
- Challenges
 1. How many nodes do we need for each stage?
 2. How to rapidly adjust a number of nodes with negligible overhead?

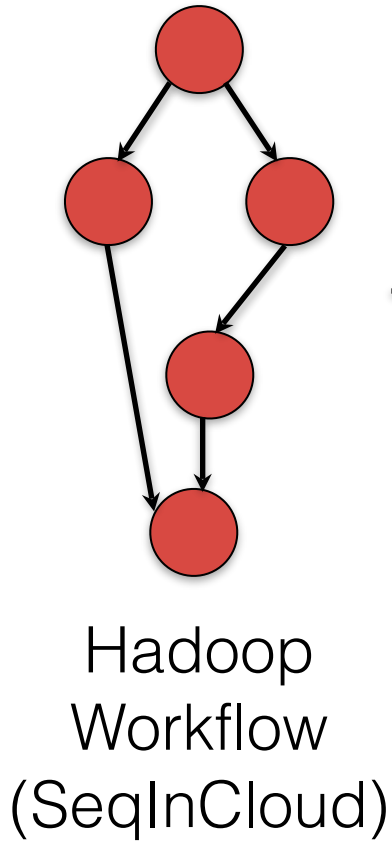
An automatic Hadoop workflow execution is needed!



Hadoop
Workflow
Manager



Cloud



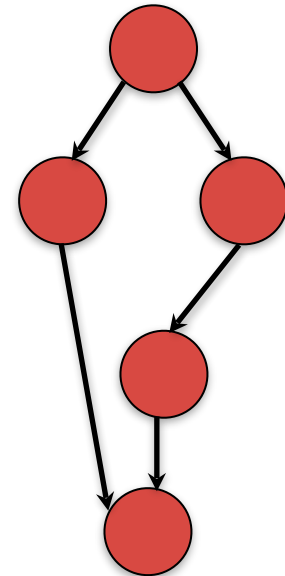
Aeromancer



Cloud

Aeromancer

- Platform for executing the scientific Hadoop workflows
 - Based on Hadoop
 - MapReduce
 - HDFS
 - Build on top of CloudGene
 - Workflow (DAG)
 - Node/Stage
 - Edge (represent dependency between two stages)



Aeromancer Usage Scenario



1

Add a new application to
Aeromancer

Aeromancer Usage Scenario

```
cloudgene.yaml
name: CloudBurst
description: Highly Sen
version: 1.1.0
website: http://sourcef
author: Nabanita
category: Genetics

cloud:
  provider: Azure
  host: seqincloud.azurehdinsight.net
  user: admin
  pass: Abcde-1234
  storageprefix: asy
  storageacct: seqincloud
  storagekey: yTtIG1PrvgUv8l25yp2Q5e/c9r9xvMKiY0sRCFDi+ihqx CZ4LWN800awSdRCpiR6/vDatXv0LBBvh@oXtZgVeg==
  storagecontainer: seqincloud
  localuser: Nabanita

mapred:
  steps:
    - name: CloudBurst1
      jar: $ipjar
      mainclass: $referen
      params: $reads1 $ou
      64 2
      alias: s1
      dependency: none
      runstep: 1
      runlocation: $loc1
      compress: 0
      isDelete: $isDelete
      datanodes: $nodes1
      stepinput: $referen
      stepoutput: $output
      - Execution command
      - Stage dependencies
      - Data dependencies
      alignment 2 2 2 2

    - name: CloudBurst2
      jar: $ipjar
      mainclass: $reference
      params: $reads2 $output2 $min_read_len $max_read_len $k $allowdifferences $filteralignment 2 2 2 2
      64 2
      alias: s2
      dependency: none
      runstep: 2
      runlocation: $loc2
```

Application details

Public cloud details

Execution details

- Execution command
- Stage dependencies
- Data dependencies

YAML file

Aeromancer Usage Scenario



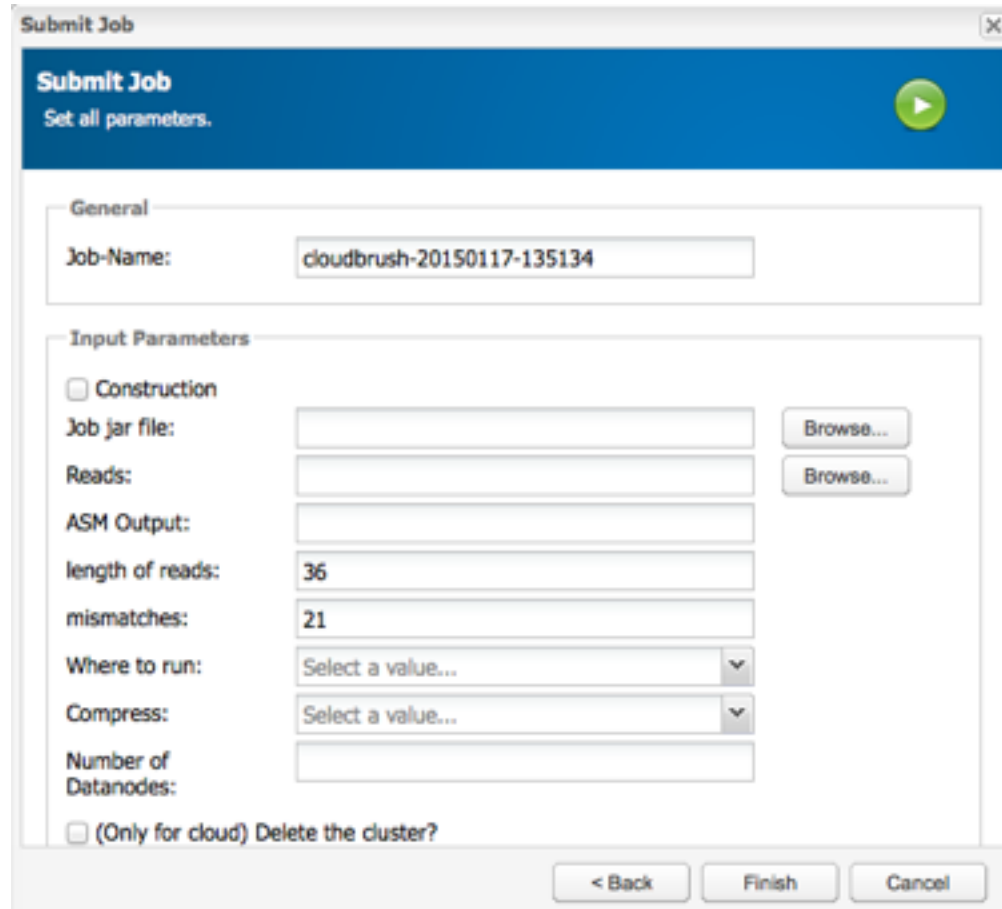
1

Add a new application to
Aeromancer

2

Submit a new job

Aeromancer Usage Scenario



The screenshot shows a web-based form titled "Submit Job" with a blue header bar containing the text "Submit Job" and "Set all parameters." and a green play button icon. The form is divided into two main sections: "General" and "Input Parameters".

General

Job-Name:

Input Parameters

Construction

Job jar file:

Reads:

ASM Output:

length of reads:

mismatches:

Where to run:

Compress:

Number of Datanodes:

(Only for cloud) Delete the cluster?

At the bottom of the form are three buttons: "< Back", "Finish", and "Cancel".

User Portal

Aeromancer Usage Scenario

1

Add a new application to
Aeromancer

2

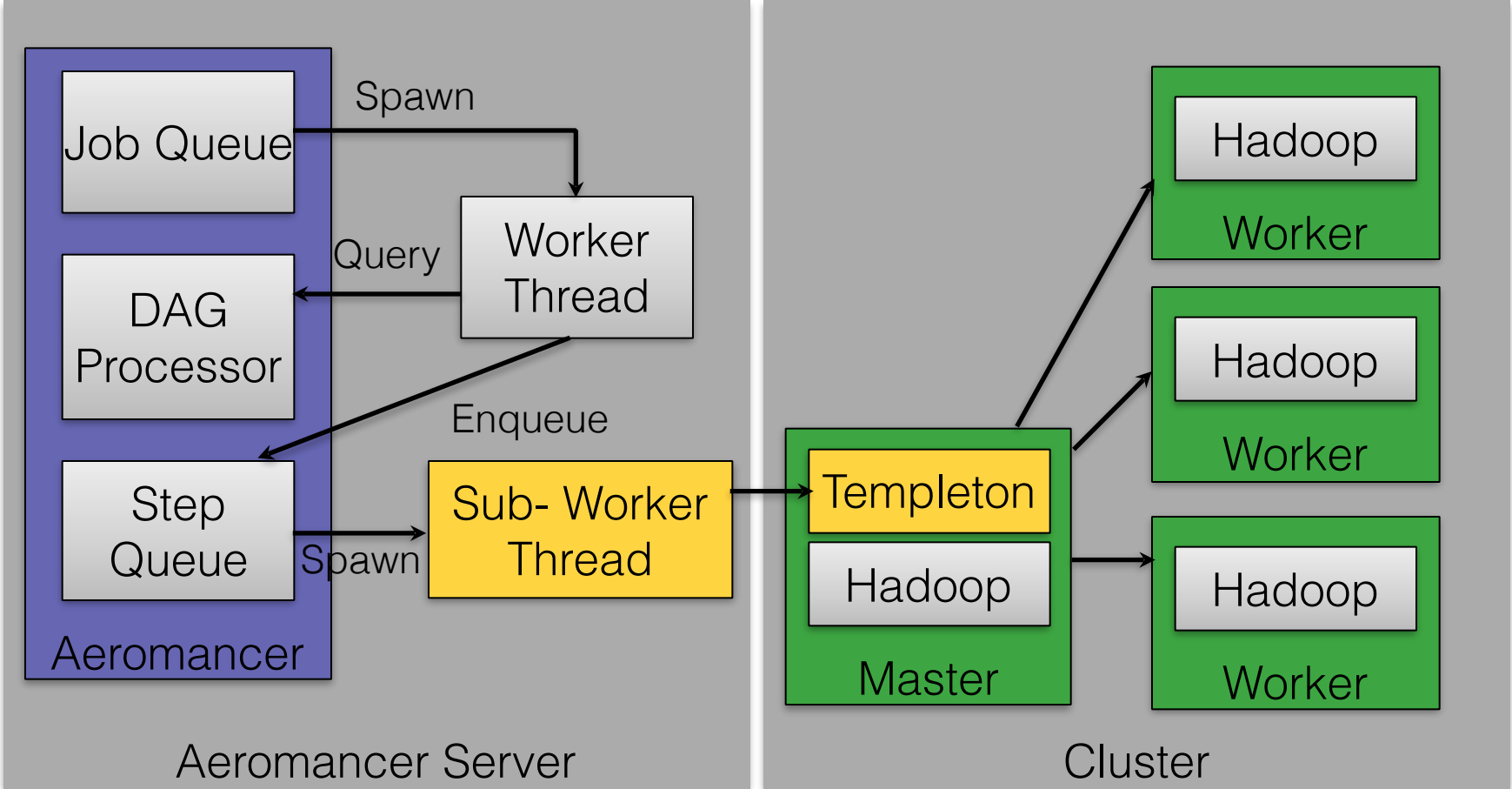
Submit a new job

3

Wait for the execution to
complete



Aeromancer Workflow & Architecture

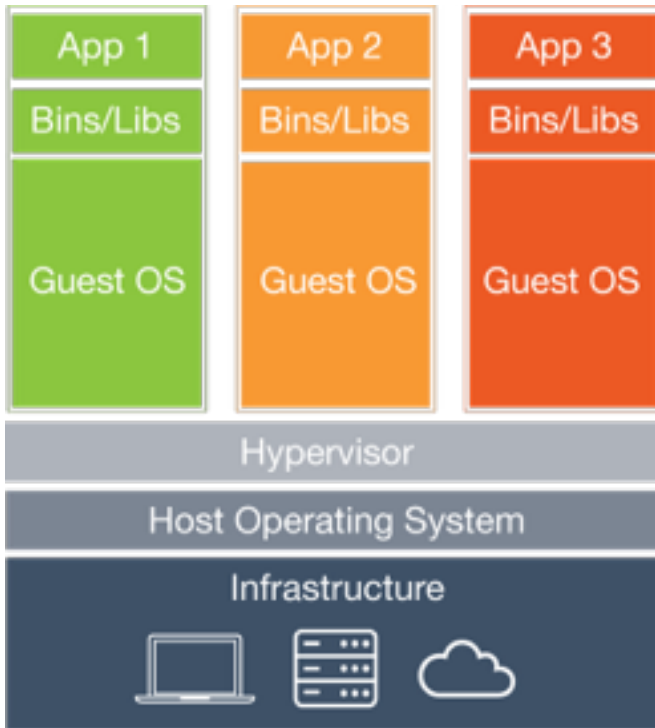


Aeromancer Discussion

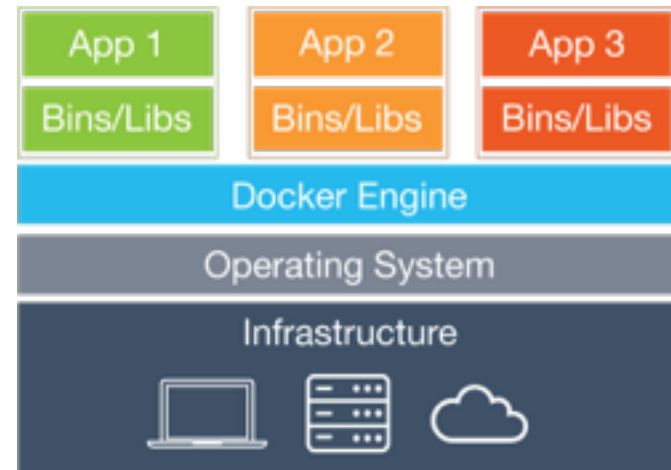
- Currently, Aeromancer worker nodes are **virtual machines** in the cloud
- Pro
 - Number of worker nodes are flexibly adjustable upon demand
- Con
 - The overhead of creating/deleting worker nodes is high
 - Execution speed drops significantly

Containerization may be able to improve Aeromancer's performance

Virtualization



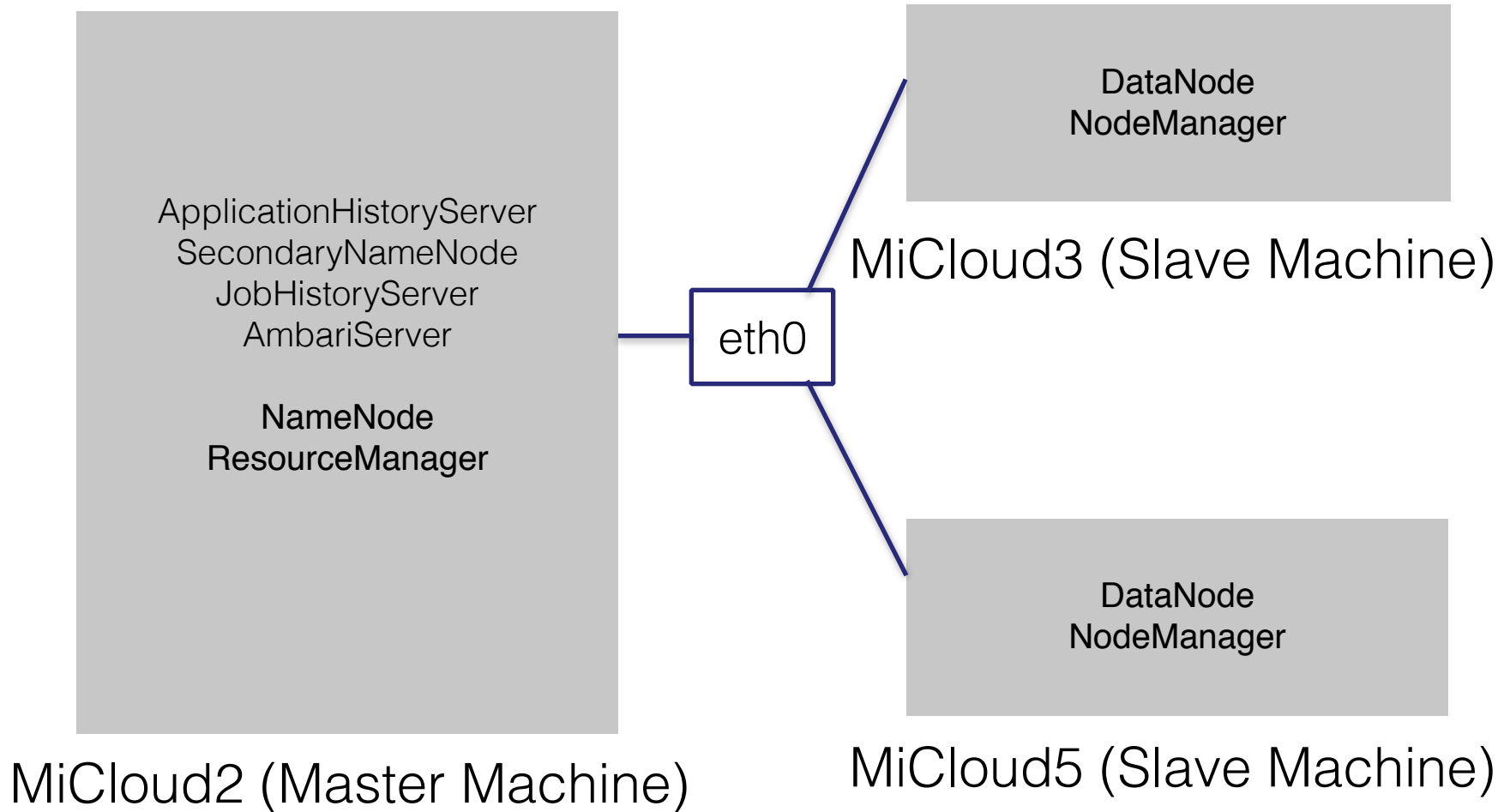
Containerization



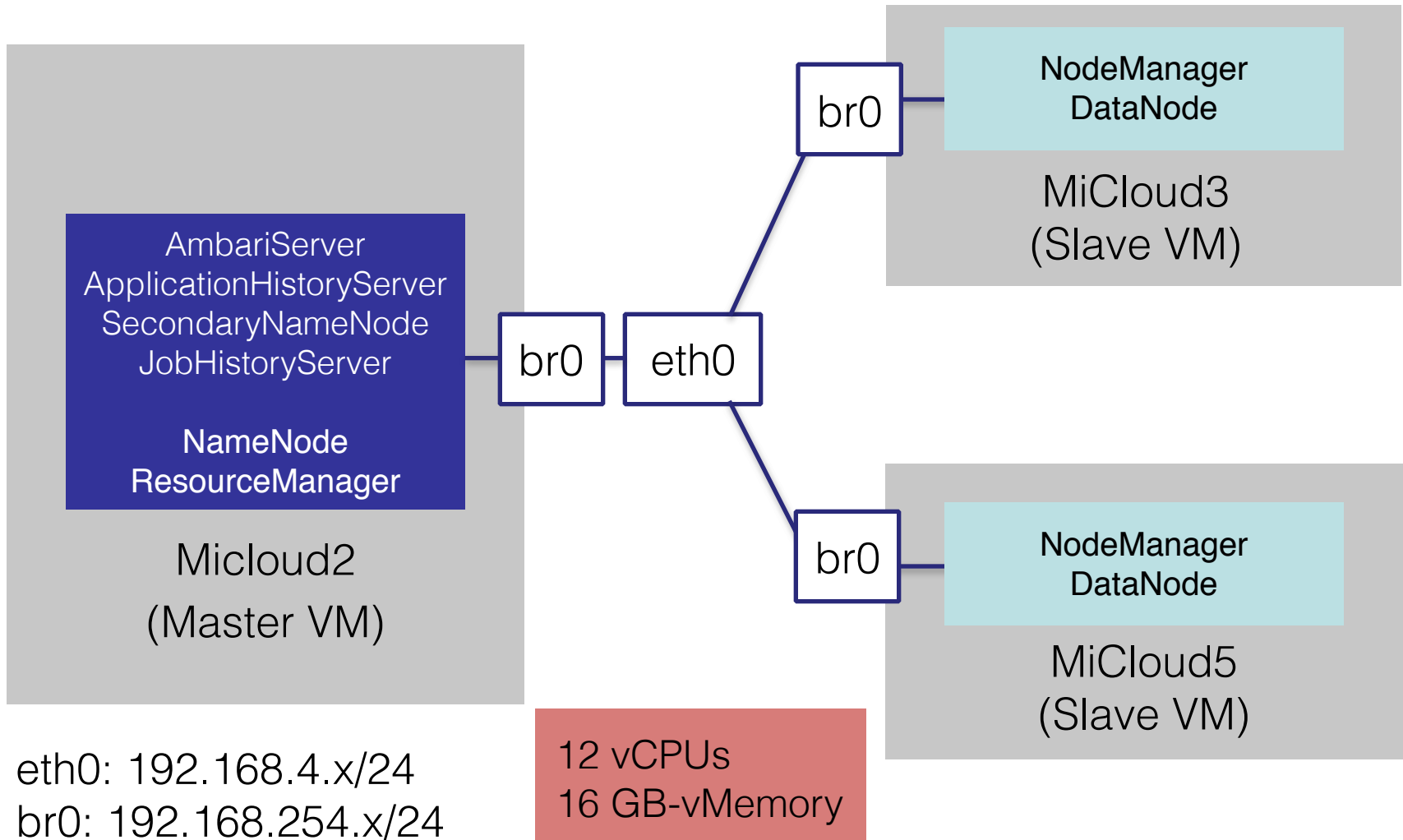
Experiment

- Platforms
 - Bare metal machines
 - KVM
 - Docker
- Benchmarks (HiBench)
 - Sort
 - WordCount
 - TeraSort
 - Nutch Indexing
 - PageRank
 - EnhancedDFSIO
- Performance
 - Speed (execution time)
 - HDFS throughput

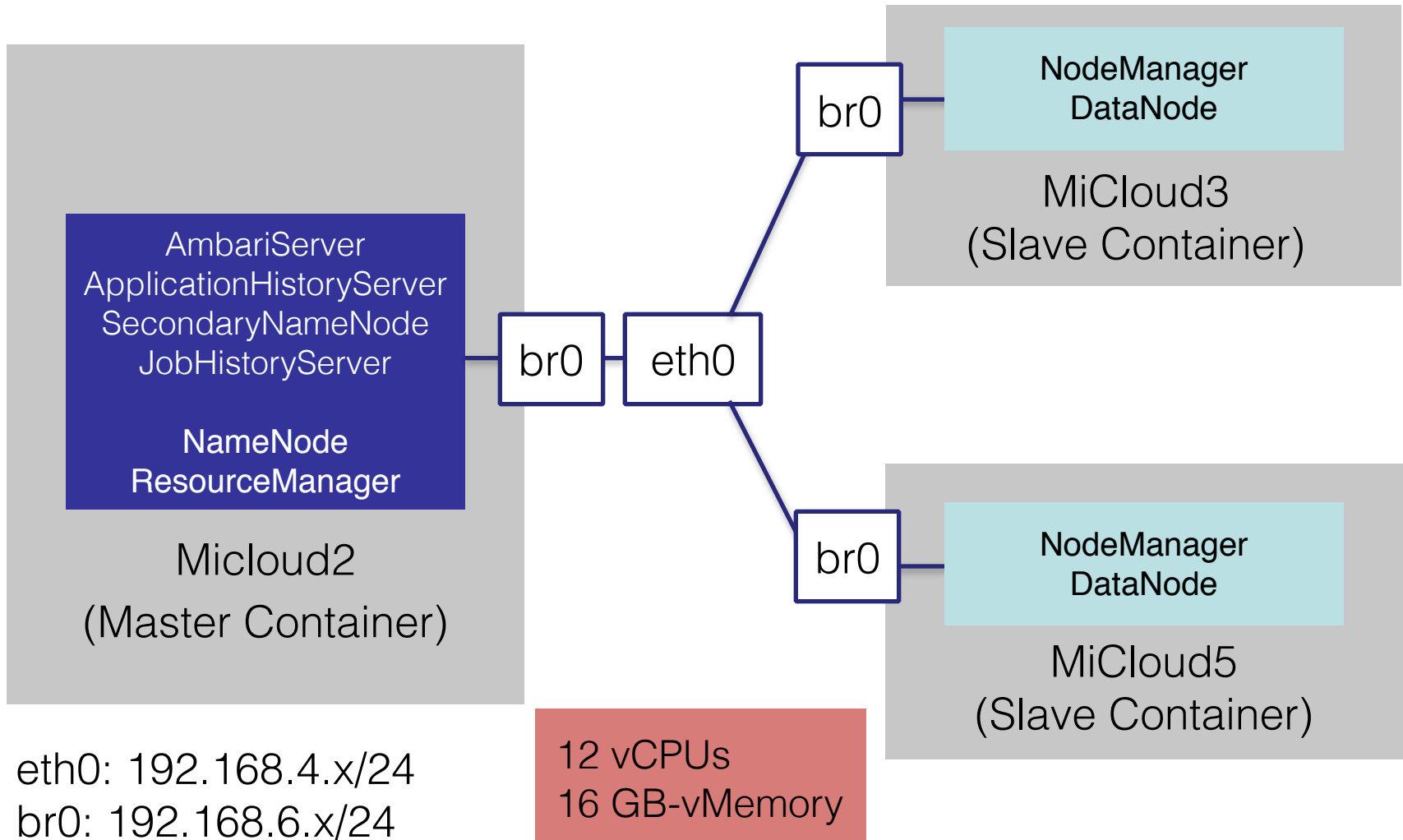
Experiment: Hadoop on Bare Metal Environment



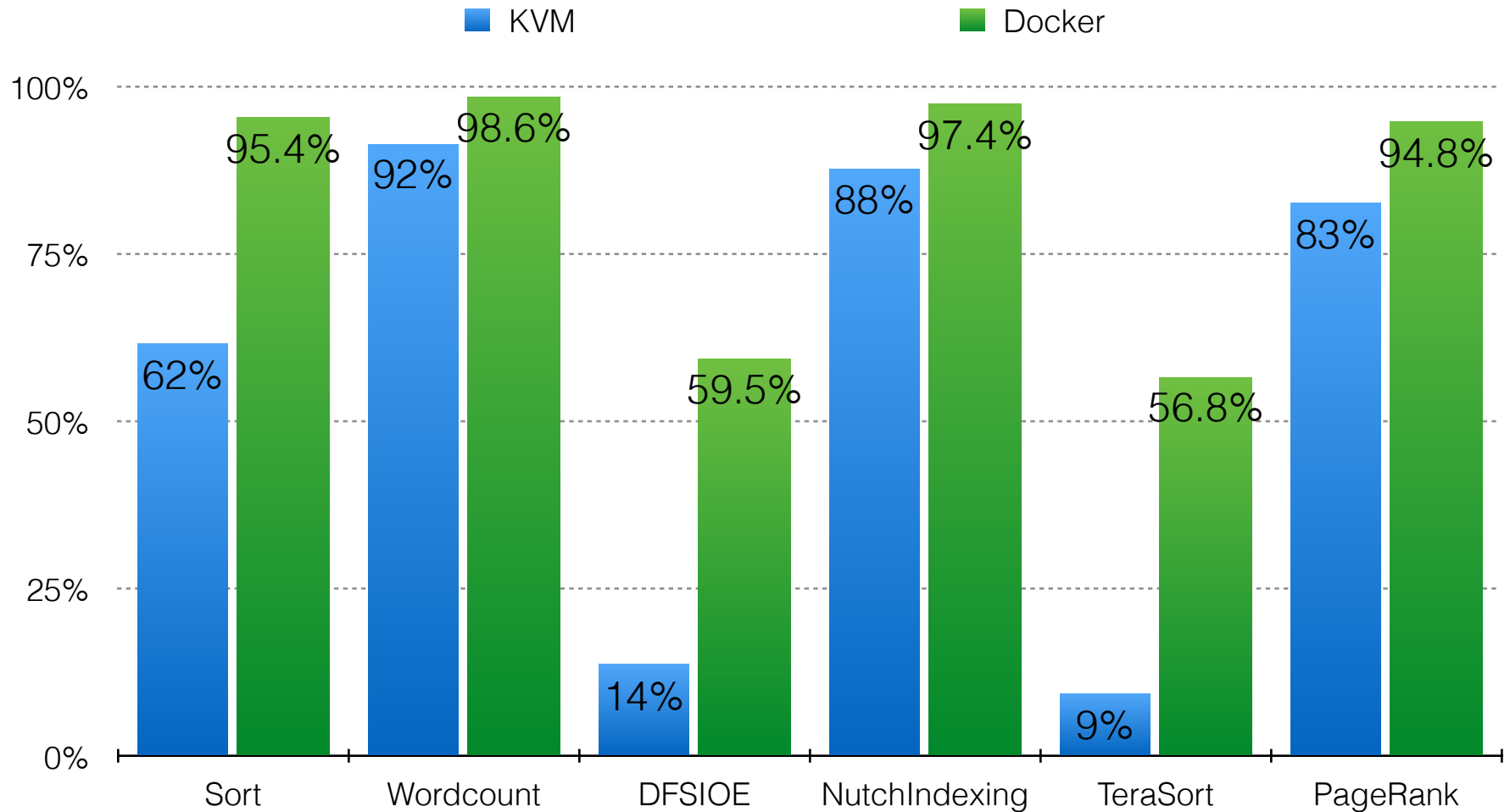
Experiment: Hadoop on Virtual Machine Environment



Experiment: Hadoop on Docker

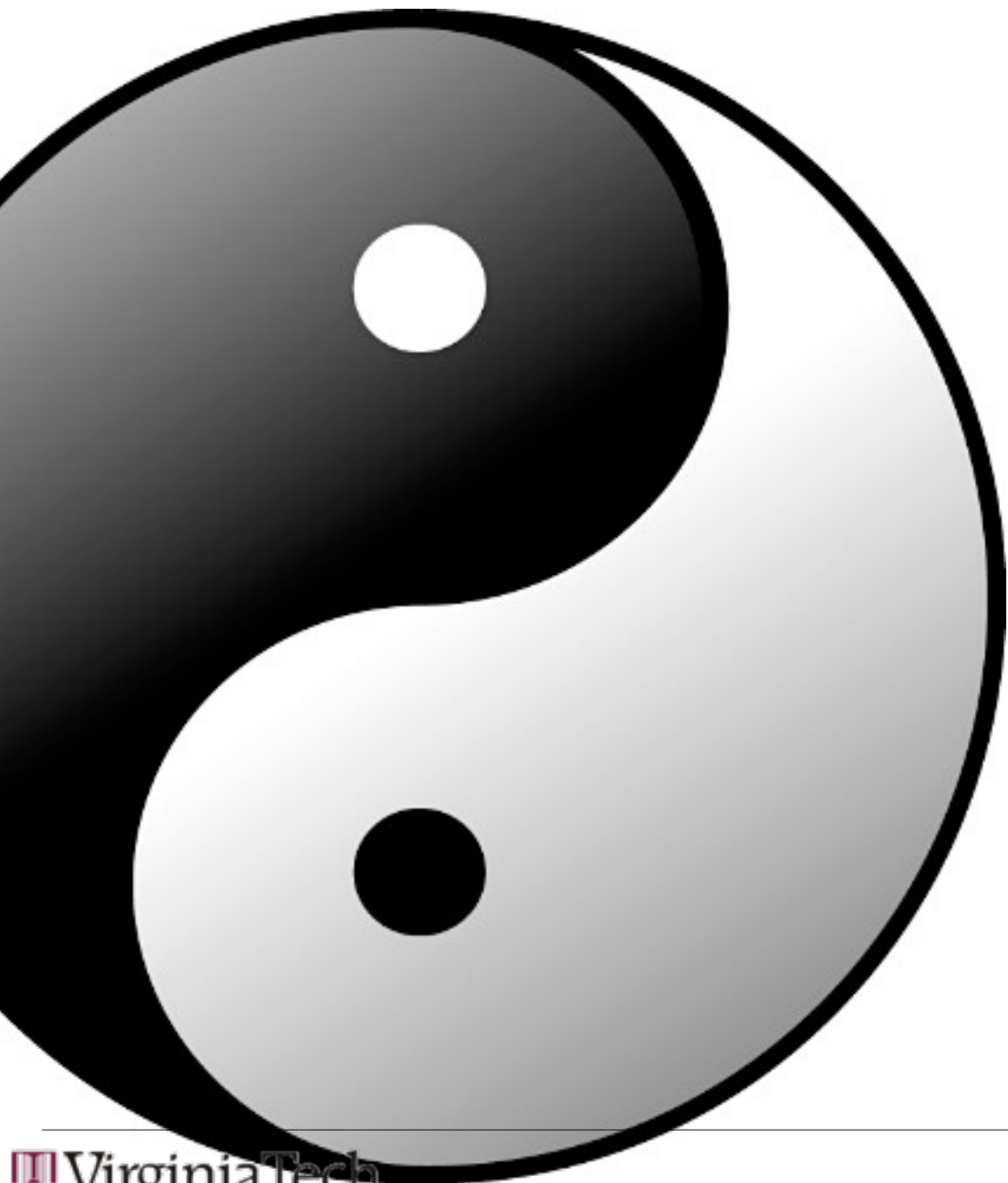


Initial Results: Slow Down



Future Work

- Automatic resources provisioning
 - Determining the number of computing nodes needed for each stage
 - Based on the scalability of each stage
 - Based on user's constraints (budget/expected response time)
- Automatic task scheduling
 - Determining the optimal execution location for each stage (either client or cloud)



Thank you