

HemeWeb: Blood flow simulation in the cloud using Docker

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Abstract

In this dissertation, we developed HemeWeb, an alternative interface to HemeLB, a complex computational fluid dynamic tool. This web application is developed to enable domain experts to use HemeLB simulation software without worrying about configurations of the software and the simulation. To measure the system, we run a usability evaluation and a performance benchmark. In the usability evaluation, respondents have to run a HemeLB simulation and reproduce a past simulation, in which after both scenarios, they will be asked to answer some questions. Respondents generally find the system subjectively satisfying to use and usable in doing the tasks given. In the performance benchmark, we compare the performance of the HemeLB simulation on HemeWeb using cloud platforms compared to the dedicated HPC infrastructure. We found out that HemeWeb performs worst and costs more while offering more flexibility in running the simulation.

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Declaration

I declare that this thesis was composed by myself, that the work contained herein is my own except where explicitly stated otherwise in the text, and that this work has not been submitted for any other degree or professional qualification except as specified.

(Steven Steven)

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Chapter 1

Introduction

1.1 Motivation

To study how blood flows in a given vessel, Mazzeo and Coveney [2] developed a fluid dynamic simulation software named HemeLB. Currently, it is actively developed and used by researchers to help their study. For example, Itani et al. [3] used HemeLB for automated ensemble simulation of blood flow for a range of exercise intensities, Bernabeu et al. [4] used it for detecting the difference in retinal hemodynamics with regards to diabetic retinopathy, and recently Franco et al. [5, 6] used it to understand the branching pattern of blood vessel networks.

As I have written in the proposal for this dissertation [1], HemeLB works by calculating fluid flow in parallel with using the Lattice-Boltzmann method [2]. This calculation allows HemeLB to simulate blood flow within a given blood vessel structure. Inevitably, the calculation is only a small part of the workflow to run the simulation. There are multiple pre-processing and post-processing steps needed to run the simulation from start to end. These include preparing the input so HemeLB can work on it, and also processing the output so it is ready to view or further analysis.

These long pipelines of steps needed to run the simulation, coupled with the complexity of the configuration of HemeLB created a high barrier of entry for scientists and doctors to use it. Furthermore, as observed previously [1], an interesting simulation will require parallel computing resources like the ARCHER supercomputer which might be difficult to get access to by interested parties. While smaller simulation instances can run on a typical laptop, most of the problems will require more powerful machines. These facts might prevent usage of the software by domain experts. More importantly, it shows there are still improvements that can be made to lower the barrier

of entry for users to use HemeLB. This is important for HemeLB, especially when it is envisioned to be part of future medical decisions [7].

Another aspect of the HemeLB workflow that can be improved is with regards to its reproducibility and replicability aspect. Chris Drummond [24] make a distinction between these two terms by arguing that reproducibility require changes to the original experiment, while replicability avoid changes to it. Research projects that used HemeLB embraces these concepts as their priority. There are steps that are in place to make sure HemeLB and its simulation result are reproducible. First, the entire code base is publicly available on Github. Second, in running a simulation with HemeLB, a version of the software is automatically recorded. Lastly, in addition to the version used, input files and configurations are also recorded automatically. These facts can be seen from the publications mentioned above [4, 3, 5, 6] that include all this information. This information allows researchers interested to replicate the simulation or tweak the simulation parameters to run their own simulation. Automation of these steps could further improve HemeLB's reproducibility and allow peers to replicate, duplicate, and audit its simulation results quickly and easily.

1.2 Objectives

Based on the need to improve the usability and reproducibility aspects of the HemeLB project, I will develop a prototype web interface for HemeLB. This prototype web interface will lower the barrier of entry in using HemeLB software compared to the current approach of using the Command Line Interface(CLI). Currently, the approach consists of manual installation of HemeLB onto the HPC infrastructure, copying data into it, running simulation, and extracting outputs. These steps require users to be proficient with the CLI and are hard for people without the appropriate skills. By using a web interface, it will allow domain experts to do all these steps in a more-familiar setting of web browser. In addition, it will also allow features to be added to the simulation workflow which might not be essential to the HemeLB core itself. For example, automating packaging, sharing, and reproducing the simulation result. These features are not essential but useful for helping the overall workflow of blood flow simulation.

Using the dynamic capabilities of the cloud computing vendor, the web backend should be able to dynamically scale without much effort. On top of that, these infrastructures are available to everyone for a cost, can be started on demand, and user will

only pay what were used. These benefits allow user to rent computing resources to run HemeLB simulation without having to get access to dedicated HPC infrastructure. The web backend will allow users to run a blood flow simulation without having to deal with the complexity of running each step of the workflow manually.

In addition to the web interface, I will also develop a deployment script so that peers can deploy their own instance of the web interface. This will ease up the deployment process for individuals or organizations intending to use HemeLB for their own purposes. This script will be developed as part of the project.

1.3 Outline

I provide a brief introduction to the topic of this dissertation in this chapter. The rest of the chapters will be organized as follows:

- **Chapter 2, Background.** I will provide background information that is necessary for readers to understand the concepts, technology, and implementation in this dissertation. HemeLB, containerization technology, cloud computing, High-Performance computing infrastructure, and other topics will be discussed in detail in this chapter.
- **Chapter 3, Design and Implementation.** I will discuss the bulk of the work in this chapter. The implementation details and design of the proposed solutions will be provided and discussed in detail.
- **Chapter 4, Evaluation.** In this chapter, I will discuss how the success of this project will be measured. I detail how I conduct a usability survey and use performance benchmarks to measure how the proposed solution performs.
- **Chapter 5, Result and Analysis.** I will discuss my findings from the evaluation of the project.
- **Chapter 6, Conclusion.** I will conclude and summarize the whole project.
- **Chapter 7, Future Work.** Some recommendations on the future of the project in the context of the HemeLB simulation workflow.

Chapter 2

Background

In this chapter, I will discuss various background information that is used as a basis for the work presented in this dissertation. I will discuss how HemeLB currently works, the High-Performance Computing (HPC) infrastructure, and Docker.

2.1 Usability of complex applications

2.1.1 Current HemeLB workflow

Currently, running a blood flow simulation with HemeLB consists of multiple steps that need to be run in sequence. These steps are followed in a variety of interfaces, from the Command Line Interface(CLI) to Graphical User Interface(GUI). Additionally, these steps also require various levels of computing resources to work efficiently. In order to understand how the proposed work will improve the current conditions, I will elaborate on how HemeLB currently works.

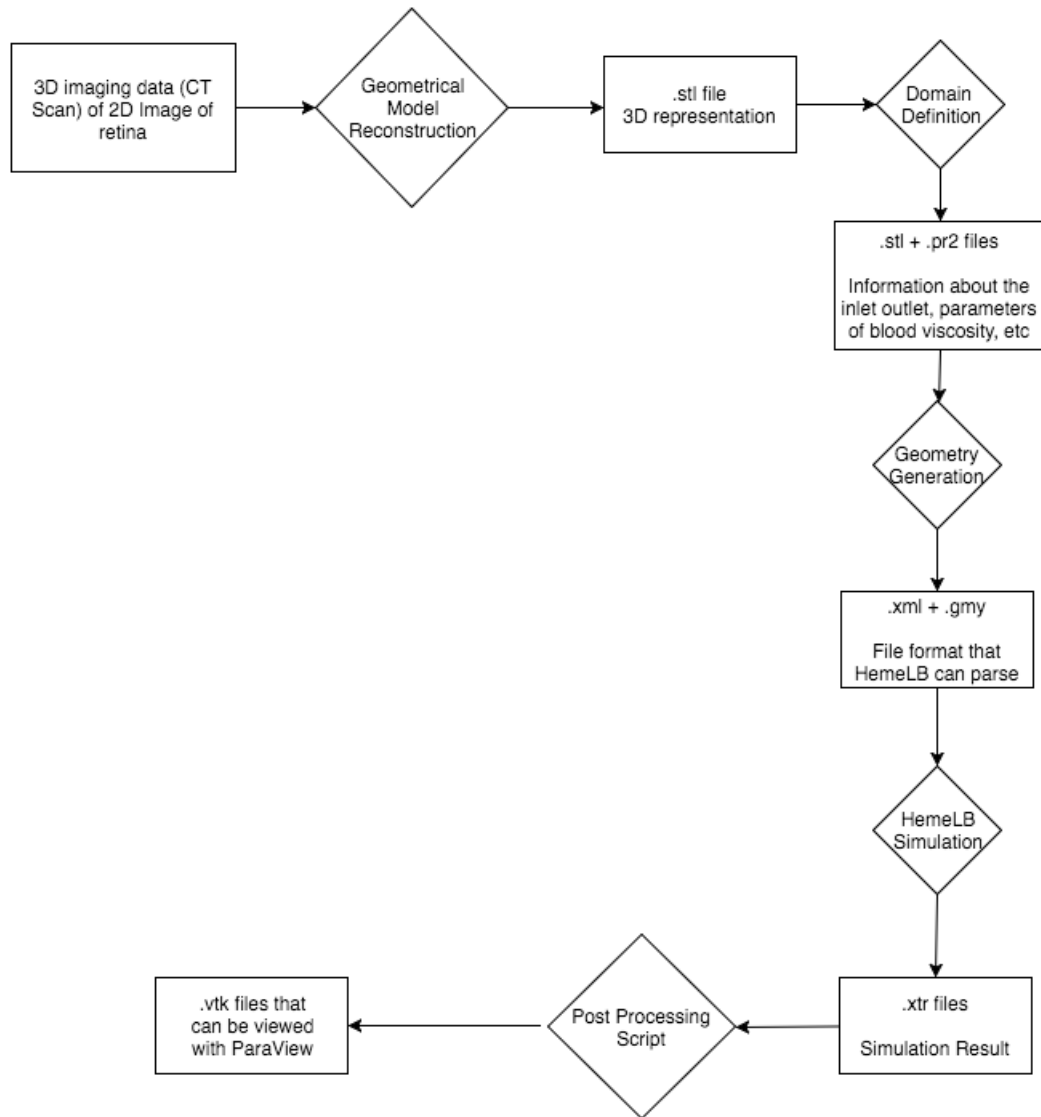


Figure 2.1: Current HemeLB workflow taken from HemeWeb proposal [1]

Figure 2.1 illustrates the steps involved in running the HemeLB workflow. These steps will be discussed in detail below:

1. Geometrical model reconstruction

In this step, a 3D model of a vascular system is constructed from the raw microscopy image of it. Alternatively, the 3D model can also be constructed from a CT scan with its 3D imaging data. From this step, a 3D geometry file is generated in the form of a .STL (STereoLithography) file, a standard file format to describe 3D model object geometry. This process can run in a regular workstation. However, it is highly problem dependent as the tools needed to parse and generate the 3D model are dependent on the problem domain experts try to

simulate.

2. Domain definition

The 3D geometry model generated from the previous step is now used as input for the domain definition step. In this step, a graphical user interface is used to add domain information to the 3D model. Information like blood viscosity, inlet outlet placement, and blood pressure will determine how the simulation will run. The HemeLB setup tool was developed for this particular need. The setup tool provides a graphical user interface for domain experts to add these parameters. All parameters are then saved in a profile file in .pr2 format. This step can run on standalone commodity hardware and should not require highly parallel computing resources.

3. Geometry generation

This step will take the encoded information from the domain definition step and the 3D model of the vascular system to generate files that can be understood by the main HemeLB program. These files contain similar information as the previous 3D model and the profile file. However, both of them are now formatted in a HemeLB parseable format, an XML configuration file and a GMY geometry file. This geometry generation step can also run on a commodity hardware. However, it requires users to use the CLI to convert the files. The process is done by piping the input files into a Python script which is part of the HemeLB setup tools. In scientific computing this step is also known as domain discretisation.

4. HemeLB simulation

The main heavy computations of the workflow are done in this step. Configuration and geometry files that are generated in the previous step are feed into the HemeLB binary as input files. HemeLB will then run calculations that govern how blood will flow inside the provided vascular system for a number of iterative steps. The number of steps is defined in the configuration file that is generated in the domain definition steps.

As observed in the proposal of this work [1], HemeLB can scale up from 1 up to 32,000 cores in running the simulation [8]. This means that a typical problem could run in a commodity hardware with a small number of cores. However, bigger and scientifically challenging problems will require a higher number of

cores that requires high-performance computing resources as portrayed in studies by Franco et al. [6, 5] and Bernabeu et al. [4]. In addition to that, users of HemeLB have to use the CLI to configure, to run the HemeLB simulation, and to interact with the output files.

The output files generated by this step are written in parallel into the output directory which is set when running the simulation. These output files represent the state of blood flow in the vascular system at a given step count. The interval in which HemeLB writes an output is also set from the domain definition step.

5. Post processing

The output files generated by the HemeLB simulations are not easily viewed by domain experts. The files are generated in a fashion that is efficient to write in parallel, however, it will need further conversion to make it easy to interpret. This is where the post-processing step comes in.

In this step, the output files are piped into two python scripts that are included in HemeLB tools to convert them into .VTU files. These .VTU files are viewable in separate software called ParaView¹. With it, domain experts can visualize the result of the simulation in a graphical user interface which ParaView provided. This step can be run on commodity hardware without any problems. However, to do this step, users will need to interact with the command line interface.

All of these steps require users to configure and install the tools required for each step by themselves. However, the target audience of HemeLB are biologists, clinicians, and researchers, who might not have the capabilities and the technical know-how to do it. This is one of the motivating reasons for the proposed work in this thesis.

2.1.2 High performance computing infrastructure

Researchers increasingly use complex mathematical and computational approaches in doing their research. In understanding complex phenomenon, researchers use interdisciplinary approaches to provide insight into the problem [9]. Bioinformatics and computational biology are examples of this interdisciplinary fields.

The problems that these disciplines try to understand require computational approaches that are costly. The smaller sized problems would probably run on a powerful workstation, while more complex ones will often require institutional or regional

¹<http://www.paraview.org>

HPC facility. These resources are often found in the form of a supercomputer like the ARCHER supercomputer. The HemeLB software package is one of many examples of these computational approaches that require highly parallel computing resources.

To tackle problems that require large computing resources, two paradigms of computation are developed. These are High Performance Computing (HPC) and High Throughput Computing (HTC). While both of these disciplines are developed to solve problems that require large computing resources, they are different in the nature of the problems they are trying to solve.

High performance computing uses uniform computing nodes to perform a tightly coupled computation. They are placed in one physical location and are connected to a high bandwidth network amongst them. This network connection allows these nodes to communicate with each other efficiently, thus, allowing them to coordinate computation across the nodes [10]. A message passing interface (MPI) library is often used to perform this type of computation and it allows every process to communicate with each other in parallel. As observed in the proposal, computer clusters, GPUs, and supercomputers are prime examples of computing resources to run this type of computation.

On the other hand, high throughput computing tries to treat computing resources like a utility line. Users should not have to worry about where the computing resources come from, they can just request them and they will be provided. This type of paradigm uses a middleware that allows non-uniform computing resources to communicate and cooperate in order to solve common problems [10]. These differing resources will then do different works that are scheduled independently.

HemeLB uses the MPI library to communicate between processes and runs tightly coupled computations on each of these processes. Based on the definitions outlined above, we can categorize HemeLB as an HPC application that requires an HPC infrastructure to run its computation efficiently.

Running an HPC application like HemeLB requires access to an HPC infrastructure which is often managed by a university or a research facility. These institutions give access to HPC projects by computing hours on the basis of the merit of their proposal. For example, this is how the Partnership for Advanced Computing in Europe (PRACE)² and the Engineering and Physical Science Research Council (EPSRC)³ operate. They conduct a peer-review of proposals that indicate the need for their infrastructure and

²<http://www.prace-project.eu>

³<https://www.epsrc.ac.uk>

give access selectively.

The model of operation of this institute often does not prioritize the reproducibility of a research study or an exploratory one. Experts wishing to reproduce previous simulation have to compete for the limited amount of available computing hours with other projects. Most likely, the reproducibility of past studies is not the top priority of these institutes, causing a barrier for reproducing computational research that relies on this type of infrastructure.

In addition to the above problem, most research that tackles biological and biomedical disciplines often falls outside the scope of these institutions. Also at the time of writing, the equivalent funding bodies for these disciplines do not have access to HPC resources. These problems limit the capabilities of researchers to reproduce past studies easily.

2.1.3 Cloud computing

To answer the huge demand for computation powers from researchers and academics, a concept called grid computing was born in the 1990s [11, 12], in which computing resources are treated like utility grid. Computing resources should be able to be acquired without users knowing how they were provided to them. This model caters mostly to the interest of researchers and academia that usually give CPU hours based on projects proposal [13]. As an example of this is the TeraGrid⁴ project which ended its operations in 2011.

The cloud computing paradigm was then developed by commercial operators based on a similar idea that computing resources should be available to users without them knowing where it came from. However, this is where the similarity ends. Cloud computing caters more to the business aspect of these computing utilities. While grid computing prioritizes the features and functionalities that researchers and academia would like, cloud computing vendors focus on features that business will pay for. Cloud computing vendors are driven by economies of scale and it will not survive if businesses do not use their services [13].

The conditions outlined above have created a tight feedback loop between users and the cloud vendors. This led to the development of features that users need and will pay for. As observed in the proposal, cloud vendors now are massively scalable, allows computing resources abstraction, configurable dynamically, and provisioned

⁴<https://www.xsede.org/tg-archives>

on-demand. This has led to cloud computing vendors being more relevant to common use-cases compared to grid computing.

Cloud vendors continue to grow significantly. In 2013, it was reported that some cloud vendors had a more than 90% growth per annum [14]. This growth enables them to have more incentives for businesses and individuals to buy their services. In a few instances [15, 16, 17], cloud vendors have cut their pricing for their services and reduced price fueled more demands. Renting computing resources is getting cheaper every year and could make more sense both economically and technically than building your own infrastructure.

On top of that, cloud vendors also do not vet projects based on their proposals. Projects could easily start on-demand computing units for their purpose. The business mindset of these cloud vendors allows reproducibility to be a priority in research, unlike requesting resources from research institutes. This scenario is perfect for researchers and institutions that do not own their own HPC infrastructure. Instead of building their own, they can rent them from the cloud vendors and not have to worry about maintenance.

The above conditions are also capitalized by cloud vendors like Amazon by attracting customers that need computing resources for HPC applications [10]. While it is reported that running HPC applications on a cloud platform will incur performance overheads, it is a viable alternative to having your own dedicated infrastructure. This is shown in various studies in the past, for example, the Nekkloud project [18], NASA HPC applications [19], and an HPC application benchmark in the public cloud [20]. In addition, the capabilities to massively scale your computing resources, limited by one's purchasing power, is an attractive feat for an HPC application that needs scalability. This is also why the HemeLB software package can rely on the cloud platform to scale up or down depending on the problems.

2.1.4 How other HPC applications tackle usability issues

In this section, I will discuss how similar HPC applications solve problems like HemeLB faces. Recently, some complex HPC software packages have been deployed to the cloud. Their experience in deploying the software and their approach to solving similar problems will be indispensable for the work I proposed.

The first project that tackles a similar problem to HemeLB is Nekkloud. In this project, Nektar++ faces a usability issue just like HemeLB. It is a complex high-order

finite element code which is mainly operated using command line interface. The original workflow is complex and only a limited number of people can operate it, barring people without computer expertise from actually taking advantage of the software package.

This usability problem coupled with the fact that users have to get access to the HPC infrastructure might not be a viable option for everyone. In order to answer these problems, the Nekkloud project was hatched. Nekkloud was developed to make the software configuration invisible to users. It uses a web application to provide an easy to use and learn interface for the domain experts. This allows people without computing expertise to actually run Nektar++ without having to be troubled with configurations. In addition to solving the usability problems, Nekkloud also uses public cloud vendors, alleviating concerns with regards to having dedicated HPC infrastructures from users.

Galaxy [21] is another project that is trying to tackle similar problems. It describes itself as a web-based reproducible research platform and runs on public cloud infrastructure. With Galaxy, researchers can run various HPC applications that are compatible with an easy to use web interface. Users do not have to worry about the configurations and working in command lines, only about the software executions.

The developers of Galaxy developed a super-resolution spark (SRS) model to illustrate its use case. This model is an example of an HPC application that requires highly parallel computing resources like a supercomputer to run efficiently. However, running the SRS model in the cloud via Galaxy is observed to be a viable alternative. In addition to that, Galaxy provides an easy to use interface to run this model for users, making it easy for them to run their experiments and share them with their peers.

Nekkloud and Galaxy projects illustrate that a web interface is a viable alternative interface for complex HPC applications. With the correct application and design, it will allow domain experts to operate the underlying HPC application with relative ease. However, the change of underlying infrastructure from a dedicated HPC infrastructure to the public cloud has some negative impacts.

One notable drawback is the lower performance of the HPC applications. It has been studied that running HPC applications on the public cloud means performance degradation compared to the dedicated HPC infrastructure. Mehrotra et al. [19] conducted a performance evaluation of the NASA HPC applications on Amazon EC2 and found out that in the worst case using Amazon EC2 as an HPC infrastructure increases runtime by up to a factor of five. The worst case is consistently found in the larger number of cores used, compared to the smaller number of cores. This severe penalty

is largely caused by the inherent difference in the networking capabilities between cloud vendors like Amazon with supercomputers, as the more nodes the more severe the penalty is. Amazon Web Service offers 10GigE(10Gb/s) compared to FDR InfiniBand(54.5Gb/s) on the NASA supercomputer, Pleiades. In addition, Mehrotra et al. also found that there was a small performance penalty on Amazon due to its virtualization layer. This penalty should be carefully considered when running HemeLB in the cloud.

2.2 Reproducibility of software

In this section, I will discuss the problem of reproducibility and how the proposed components try to solve it

2.2.1 Reproducibility problem in computational research

The American Physical Society [22] describes science as "the systematic enterprise of gathering knowledge about the universe and organizing and condensing that knowledge into testable laws and theories". For theories and experiments to be testable, they have to be independently reproducible or replicable by peers. However, a recent study [23] highlights that some published psychology studies are not replicable to the same significance as reported. At machine learning conferences [24], a similar sentiment is being shared. Not being replicable does not necessarily mean that the result of those studies is wrong. However, it suggests that academics may not prioritize the verification of results. The novelty of an idea may be seen as better than verifying what we already know.

With the recent study highlighting a reproducibility problem of a research study, previous pushes [25, 26] for reproducibility in studies become more relevant than ever. This is especially crucial in a discipline like computational research. Computational research disciplines like bioinformatics and computational physics involve complex computations that require huge computational power depending on the problem size. The complexity of the configuration, algorithm, and execution process actually become a barrier for peers to replicate and reproduce the works of studies on this discipline. Making results produced have less weight than it could be

This complexity is also one of the reasons why the Galaxy project came into development [21]. While science values rigorous testing, replicable, and reproducible

results, the complexity of the HPC software package hinders that. Galaxy tries to solve that by producing automatic metadata that record the execution of an analysis done by tools on the Galaxy platform. It records all the input files, configurations, and outputs of an analysis and makes them available for the users to view and copy. This metadata information enables users to share the analysis with their peers, allowing peers to replicate or reproduce the analysis results independent of the original researcher. Galaxy allows ease of reproducibility and replicability for the domain experts.

2.2.2 Containerization technology and HPC application

One of the main problems with replicating or even reproducing the results of studies with a complex software package is configurations. A complex software package like typical HPC applications often requires hands-on configuration by users for it to run correctly. This complex configuration coupled with complex usage becomes a barrier for an independent party to verify the results of a study.

Containerization technology, particularly Docker⁵, can help with the issue above. Docker is a technology that is developed on top of kernel-level technologies like Linux Containers (LXC)⁶ which allow containers to be a sandbox between processes [27]. Containers allow applications to be securely placed in their own environment that shares the kernel with its host. Unlike full virtualization, containerization does not require a full operating system to be installed on the virtual environment so the application can run. Docker is arguably the most popular containerization technology currently. It is built on LXC and added features that allow an application to be deployed easily. It handles container image creation, versioning, sharing and archiving in addition to running the image like LXC does. On top of that, there is also a web application called Docker hub⁷ that allows Dockerfile, a text file that contains the commands to build a container, to be inspected publicly if set correctly. It allows interested peers to audit a container and to make changes to it for their own container.

Using containerization technology like Docker can help with reproducing the results of studies. A complex configuration process can be recorded and encapsulated in the form of Docker container; hiding complexity to the casual users. Studies can package the complete software package in a Docker container to be shared with peers for independent replication and reproduction of an analysis. In addition to that, the

⁵<https://www.docker.com/>

⁶<https://linuxcontainers.org>

⁷<https://hub.docker.com>

versioning feature of Docker also allows the software package to be continuously developed and for an analysis to be tied down to an older version of the package. As an analysis can be replicated even if the software is currently way ahead compared to the time an analysis is made. It also creates a good opportunity for the study to be reproduced, an analysis could have different results if it is running with the new version of the package. Hence, containerization technology enables reproducibility of results.

This is also the reason why the Galaxy project supports Docker in its toolsets. The galaxy ecosystem uses Docker to create a secure, isolated environment for the tools and its dependencies [28]. Tools are versioned, archived, and shared with Docker containers so peers can download and audit all the tools. This openness is also important for the tools to be trusted.

HemeLB as a complex HPC application is also actively developed. While development is ongoing, it is often used as part of a research study. Docker can help with the recording of the version used for a study with its versioning feature. In addition to that, configuration work is also taken out of the hands of the peer because it is done initially during the packaging of the application. Containerization technology sounds appropriate to be used for HemeWeb to enable easy reproduction, replication, and audit for HemeLB simulation.

Chapter 3

Design & Implementation

In this chapter, I will discuss HemeWeb's development and implementation. This will consist on how the HemeLB core Docker container is developed, how it is deployed, and how the web application is developed.

3.1 Development phases

The development process is divided into 5 phases. The planned phases are as follow:

1. Separate HemeLB core into its own container
2. Orchestrate the deployment of HemeLB cluster / infrastructure
3. Develop HemeWeb to accept user input
4. Extends HemeWeb to handle geometry generation workflow
5. Extends HemeWeb to handle domain definition step or Viewing of HemeLB simulation result

The development process loosely follows the agile method in which I regularly meet with the stakeholders every week to give an update and gather feedback on the project. The phases are designed in such a way to minimize the risk of having nothing at all during the end of the project phase. This is due to that HemeWeb can work on its own after finishing step 3. The HemeLB simulation can be done on its own. The rest of the steps are there to extend the functionalities of the HemeWeb to cover more functionalities.

3.2 HemeLB core Docker container

HemeLB core is a Docker container that consists of essential software and services needed to run HemeLB simulation. It is the main component that runs the HemeLB simulation on the cloud. Calculations will be done on the container which will be started on the compute nodes of the HemeWeb architecture.

Previously, there was an effort to make HemeLB software package portable by creating its own container package¹. It has all the necessary tools for HemeLB simulation workflows such as setup tools, HemeLB binary, and post-processing scripts. Moreover, it also includes a Virtual Network Computing(VNC) capability that allows users to access the container's headless graphical user interface via HTML5 capable browser. All of these are necessary to make HemeLB more portable. Independent peers can replicate and reproduce simulation without having to configure all above tools. However, users will still need to configure Docker on their workstation to be able to run the container. HemeWeb will take this effort a step further. With HemeWeb, users will not be required to install any tools to run simulation workflows. Only web browser, which is normally installed by default, is needed.

In this phase, I took the previous container and modify the Dockerfile, the instructions file to build the container. The original Dockerfile uses a base image of Ubuntu², a popular open source operating system, that is provided by Docker. This image by Docker incorrectly handle Ubuntu's init system, Upstart³, that results in some system services cannot be started correctly. One of this service is Secure Shell daemon(sshd)⁴. This daemon is responsible for allowing remote users to get secure encrypted access to the host, in this case, a Docker container. Without sshd, HemeLB, which is a Message Passing Interface(MPI) application, cannot run a multi-host simulation because communication cannot be done between hosts. To solve this issue, I switched the base image to base ubuntu provided by Phusion⁵, a company in Netherland that released their version of Ubuntu container that solves above problem.

After switching the base image of the Docker container with Phusion's Ubuntu (See Appendix A), I added commands to correctly start the ssh service, and configure the access keys. It is currently configured to use a shared insecure key that is committed to the repository. Ideally, this should be automatically generated at each container

¹<https://github.com/mobernabeu/docker-hemelb>

²<http://www.ubuntu.com>

³<http://upstart.ubuntu.com>

⁴<http://www.openssh.com>

⁵<https://github.com/phusion/baseimage-docker#>

build, however, due to the time limit of this project, this is not done yet. The next step is to strip out tools which will not be needed by the compute nodes to run HemeLB simulation. I added commands to purge the packages that are not essentials to the compute nodes. The resulting container is a minimal container that contains only the HemeLB binary and SSH service running. With these changes, the size of the container is also halved from originally 948MB⁶ to 430 MB⁷.

The modification of the Dockerfile of the container is the initial part to make HemeLB core container. To create the container correctly, this Dockerfile needs to be integrated into the development workflow of HemeLB. Currently, the modified Dockerfile still lives under the HemeWeb codebase⁸. HemeLB development should trigger an automated build of HemeLB core containers with each version of the software it pushes to the public GitHub repositories. In addition, the development team also needs to create a consistent tag naming in order for the HemeLB core containers to be created correctly.

3.3 Deployment scripts

The next step of the implementation is to develop deployment scripts to configure the overall software architecture. Due to the nature of the architecture that consists of many moving parts, manual configuration is not considered a manageable solution. I decided to create deployment scripts that facilitates the pain of deployment by provisioning and configuring the architecture with minimal manual intervention. The scripts are created using a configuration management and orchestration tool called Ansible⁹.

Ansible is arguably the most popular tools in IT infrastructure automation space[29]. It is an open source tool that is used for provisioning, configuring, and orchestration of IT infrastructure. Moreover, it is an agentless software that allows it to work without installing client-side software on the hosts it manages. I decided to use Ansible for deploying HemeWeb's infrastructure because it is developed in Python[29]. In addition, Ansible being an agentless software is really useful because there is one less moving part that HemeWeb have to worry about. Another reason is because it uses YAML(YAML Ain't Markup Language¹⁰) syntax for the configuration management

⁶<https://hub.docker.com/r/mobernabeu/hemelb/tags/>

⁷<https://hub.docker.com/r/seiryuz/hemelb-core/tags/>

⁸https://github.com/SeiryuZ/HemeWeb/tree/master/hemelb_docker

⁹<https://www.ansible.com>

¹⁰<http://yaml.org>

language which is described by the team as "easier for humans to read and write than other common data formats like XML or JSON"¹¹. I find YAML is easy to work with in developing the scripts and also used extensively in HemeLB software package. Finally, there are a lot of community contributed components that are included with Ansible that makes developing the deployment scripts much faster. For example, there are modules that enable a script to provision instances from cloud vendors like Amazon Web Service, Google Cloud Platform, and Digital Ocean.

At the current time of writing, the deployment process consists of multiple files, templates, and configuration scripts that are modularly assembled to be run as a set of instructions to build the infrastructure. These deployment scripts can be divided into two separate distinct functions, which are:

1. Provision instances and configure cloud vendor specific settings
2. Configure the provisioned instances to produce correctly set architecture

I will discuss the deployment script in details in the following sections.

3.3.1 Provision instances and configure cloud vendor specific settings

In this phase, the scripts are mainly responsible for provisioning master and compute instances for the infrastructure. The script will request instances from the cloud vendors based on the number and type of instances set in the script. Because cloud vendors have their own interface to interact with their platform, I decided to separate the scripts into their own directories for each cloud vendors. This is due to the fact that in Ansible, to interact with each vendor, it needs to use a different module.

At the time of writing, I developed the provisioning script for three different cloud vendors (See Appendix B, section B.1). They are Digital Ocean, Amazon Web Service, and Google Cloud Platform. Each script has slightly different YAML syntax due to the difference in the module that is used. In addition, there is a different model of provisioning that needs to be adhered to by the scripts. The most notable one is the Amazon Web Service one. The script has to be able to create a correct security settings for each instances or it will not allow the instances to be connected remotely. Without this ability, the deployment script will not be able to configure the instances correctly for the infrastructure.

¹¹<http://docs.ansible.com/ansible/YAMLSyntax.html>

To run the provisioning script, each cloud providers require authentication. Because this authentication is in the form of keys that need to be provided to the script, I decided that it should not be hard-coded in the script. The authentication credentials are to be set in the environment variable of the workstation that the script will be run from. The script will then look up the credentials from the environment and use it to authenticate with the cloud providers. This is done to prevent the credentials being publicly shown because the repository for the source code is public.

3.3.2 Configure the provisioned instances to produce correctly set architecture

After developing the script for instances provisioning, I developed the deployment scripts (See Appendix B, section B.2 and B.3). This deployment scripts will require addresses of the hosts to configure. However, because provisioning the instances will create new instances with new addresses every time it is run, it is not convenient to write a static list of addresses every time deployment script is run. Therefore, I find a community-contributed script¹² that allows addresses to be dynamically queried to the respective cloud providers. Each of this script lives in the same folder as the provisioning script and has a different configuration that needs to be set once. After entering the credentials in the configuration file for this dynamic addresses script, deployment script can now target the correct hosts every time.

For each cloud providers, there are different deployment scripts. However, these different deployment scripts are setting up the variable that will be used in the main deployment script that lives outside this cloud vendor specific folder. After setting variables like instance tag that varies between the vendors, it calls the main deployment script. In the main deployment script, it handles 3 separate tasks. First, to configure every host with common configurations. Second, configure the master instance. And finally, to configure the worker instances.

These configuration tasks are separated into its own Ansible "roles", modular component of tasks that live in its own directory. In each role, I defined tasks that are relevant to that specific roles. For example, in the "common" roles, I defined tasks to configure SSH service, update the instance's packages, and update the `/etc/hosts` file on each instance. These tasks are common to every type of instances so I put it into its own role. Another example of the role is the database role that I called "post-

¹²<https://github.com/ansible/ansible/tree/devel/contrib/inventory>

gresql” that is only applied to the master instance. In it, I defined tasks that download and configure the database correctly so it is ready for HemeWeb uses. With these roles defined, I can include the roles in the main deployment script so it is included in the execution of the deployment script.

3.4 HemeWeb web application

In this section, I will discuss the bulk of the work of this project which is developing the web application component. The web application component will be the interface for users to interface with HemeLB simulation workflow and is an essential part of this project. It is developed using Python 2.7 and Django web framework¹³. I chose Django web framework due to my previous experience with the web framework and also the existing HemeLB codebase has other tools written in python. Using Django web framework is to make sure that the codebase in HemeLB software package is done mostly consistent with Python.

All the source code for HemeWeb web application is available online at my GitHub’s public repository¹⁴.

¹³<https://www.djangoproject.com>

¹⁴<https://github.com/SeiryuZ/HemeWeb/tree/master/src>

3.4.1 Architecture

3.4.1.1 Web application components

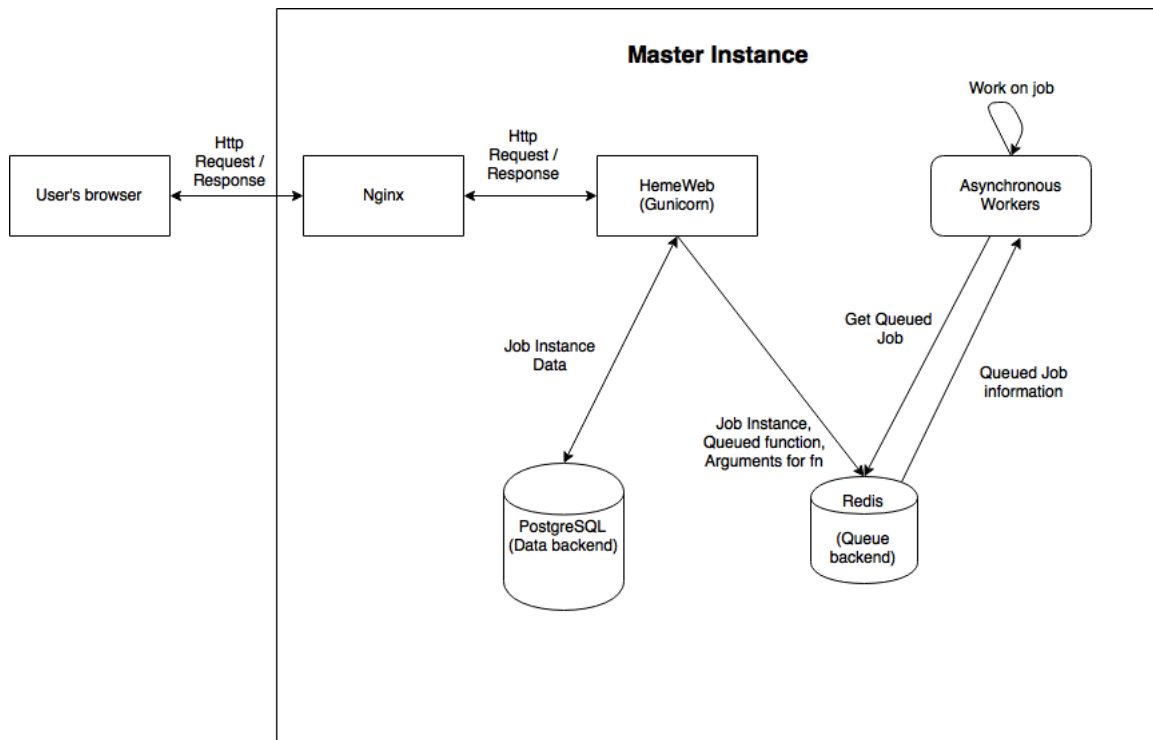


Figure 3.1: HemeWeb architecture

Figure 3.1 above illustrates how HemeWeb application process interacts with the other components inside the master instance. It also illustrates how user's HTTP request starts a chain of events inside the master instance that will eventually return a response to the user's browser.

To start, user's browser will send an HTTP request to the master instance. This request will be captured by Nginx process, a HTTP processing engine, that will act as a reverse proxy. Nginx¹⁵ will proxy the HTTP request towards the correct web application server process or serve static files depending on the requested URL. If the request is routed to the web application, HemeWeb web application which is handled by Green Unicorn¹⁶ HTTP server will accept the request. This library will run the HemeWeb python code to process the HTTP request by the user. Depending on the type and path of the request, the web application will serve a static HTML as a

¹⁵<https://www.nginx.com>

¹⁶<http://gunicorn.org>

response, or handle job-related logic that might interact with another part of the system. One of the components the web application might interact with is the PostgreSQL database¹⁷. The database will persist job information locally on the instance to provide persistent information between HTTP request. However, it will be wiped out when the master instance is terminated and is not shared between HemeWeb instances.

Another part of the master instance the HemeWeb application can interact is with the queuing system. HemeWeb can submit a job into the queue which uses Redis datastore¹⁸ as the queue backend. HemeWeb uses third party library called `django-rq`¹⁹ that handles asynchronous background tasks handling using Redis backend. It uses Redis to store job information on a queue that will be processed by lightweight background job workers. HemeWeb process will store the function to be executed, the job instance and parameters to used by the function into the Redis backend. A background worker will look at the queue at an interval and work on a job if there's any in the queue. The worker will execute the function and update the instance with relevant job execution result. Finally, the worker will go back to being idle waiting for next job to be executed.

¹⁷<https://www.postgresql.org>

¹⁸<http://redis.io>

¹⁹<https://github.com/ui/django-rq>

3.4.1.2 Docker components

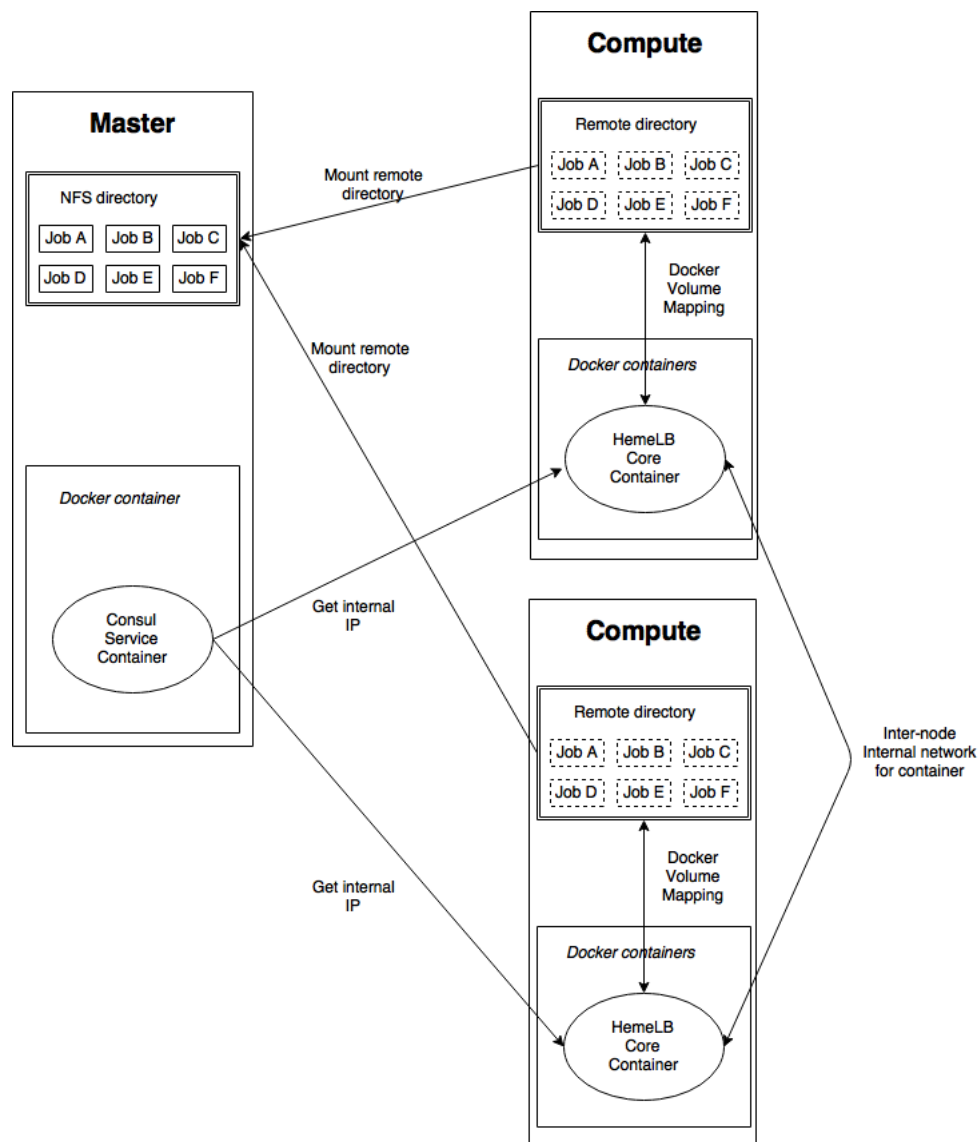


Figure 3.2: HemeWeb Docker component

In this section, I will discuss the interaction between Docker components and a master instance or compute instance. As illustrated on figure 3.2, each host will run Docker service to run specific Docker container depending on their purpose.

In the master instance, a Consul²⁰ container is constantly running to provide the inter-container communication mechanism. Consul is used by the Docker containers to coordinate the internal networking communication between them. In a host, multiple

²⁰<https://www.consul.io>

containers can be started without conflicting IP because they can communicate via the host. However, in HemeWeb the communication between containers will go beyond single hosts. Containers will need to communicate with other containers living on other hosts. Consul service is needed to coordinate this communication.

On the other hand, on the compute nodes, only the HemeLB core container is run. The compute nodes will be started by a job submission to HemeWeb. After the nodes are started, HemeWeb process will instruct the compute nodes to pull the specified HemeLB core container version from Docker hub. If the specified version is locally cached on the compute nodes, no network activity will be triggered. HemeLB core container is then started to accept simulation command.

To start the simulation, the HemeLB core containers require the job directories to be exported via Networked File System interface. HemeWeb process in the master node will prepare the job directories with the correct folder and files locally in the master node. Every job submission to HemeWeb will create a specific folder for storing submitted job-related files. The exported job directories will then be mounted by the compute nodes provisioned for the simulation. Finally, HemeLB simulation can use the mounted job directories to read input from and write output to.

3.4.1.3 Job instance structure

As mentioned above, HemeWeb uses Django web framework to handle web functionalities. Django framework follows the object-oriented principle where everything is modeled as an object. Job information that is handled by HemeWeb is also modeled as an object that is derived from object class of Django. Literally named **Job**, is a class that represents simulation information. Each instance of this class will contains information specific to a simulation instance. **Job** class inherits from *django.db.models.Model* class that is included within Django framework. HemeWeb **Job** class extends this basic class and add functionalities specifically related to job information.

HemeWeb's Job class has the following attributes:

- **id**: This is a Uniquely Universal Identifier (UUID) field that represents the Job ID. UUID field was chosen because it is appropriate for the possibility of sharing the job simulation files between different deployment of HemeWeb. UUID can prevent clashes of job ID between these instances.
- **input_file**, **stl_file**, **profile_file**, **output_file**, **configuration_file**: These attributes keep track of the files that are used by the job. It is stored as the path to the

file in the local filesystem, but with Django functionalities, HemeWeb can work with the file as an object.

- `container_image`: This attribute determines which container of HemeLB core will be used in the simulation. Currently, the choice of the field's value is set manually in the codebase.
- `instance_type`: This determines which compute node type will be started for the simulation.
- `instance_count`: This attribute determines how many compute node will be started for the simulation. Currently, this is also set manually in the source code.
- `status`: The attribute to determine Job's status, whether it is *queued*, *added*, *done*, *failed*, etc
- `created`: Attribute to keep track when the job is created
- `updated`: Attribute to keep track when the job is updated

3.4.1.4 Job directory structure

Each simulation done with HemeWeb have its own job directory. These directories are located in the master instance and are shared with the compute node. To provide a clearer picture how the application package and work with the job's files, I will discuss how HemeWeb structure each job's files.

```
<UPLOAD_FOLDER_DIR>/<JOB_ID>  
<UPLOAD_FOLDER_DIR>/<JOB_ID>/inputs/*  
<UPLOAD_FOLDER_DIR>/<JOB_ID>/logs/*  
<UPLOAD_FOLDER_DIR>/<JOB_ID>/outputs/*  
<UPLOAD_FOLDER_DIR>/<JOB_ID>/metadata
```

Listing above illustrates the structure of a job instance's directory structure. The first component of all job instance's directory is the `UPLOAD_FOLDER_DIR`. This is the path to a directory in which HemeWeb will upload all files. To change this parameter, one should change the path in the HemeWeb settings file and restart the web application so the changes took place.

The next part of the directory structure is the job folder named with its ID. The ID will be generated by HemeWeb using Universally Unique Identifier (UUID) scheme.

More specifically, UUID Version 4 that depends on the random number. Using UUID is important for HemeWeb because it is accurately approximated to have a really low chance of producing duplicate ID. Hence, HemeWeb does not have to take care of the possibility of jobs having duplicate ID.

Next, we have the inputs folder inside the job folder. This is where all the inputs and configurations are stored by the web application. There's also logs folder, where the job stdout, stderr, and HemeLB logs are stored. The web application will read from this folder and make it available on the web interface. Outputs folder will be used by the HemeLB simulation to write output files in this folder. One final file is the metadata file. This file is used by the web application to store the state of the job. The job is serialized into this metadata file using python pickle protocol so when it is downloaded, the web application can unserialize the state of the job instance and it is preserved, ready to be used for another simulation.

A Job instance is preserved with this job directory structure. This allows job information to be preserved in an external storage that can be used for backup. HemeWeb currently supports uploading job directory to Amazon simple storage service (S3). However, backup is not the only purpose for this functionalities. By making job directory files available to the public, independent peers can download these files and run the simulation with correct files and configurations. It allows peers to replicate a simulation exactly or with modifications.

3.4.2 Simulation workflow

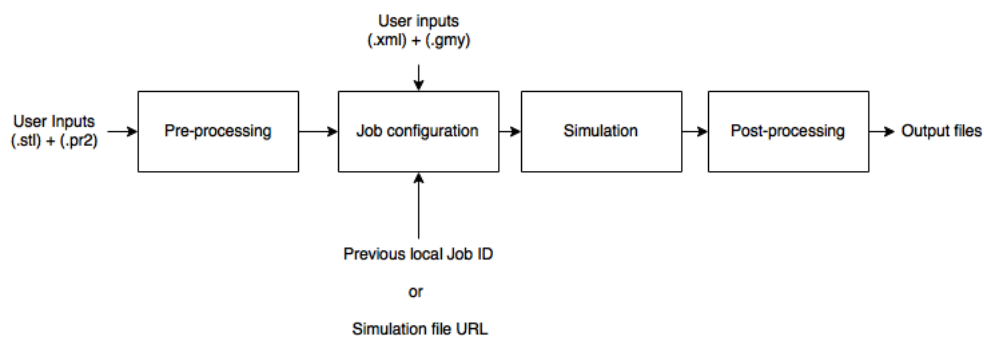


Figure 3.3: HemeWeb flow

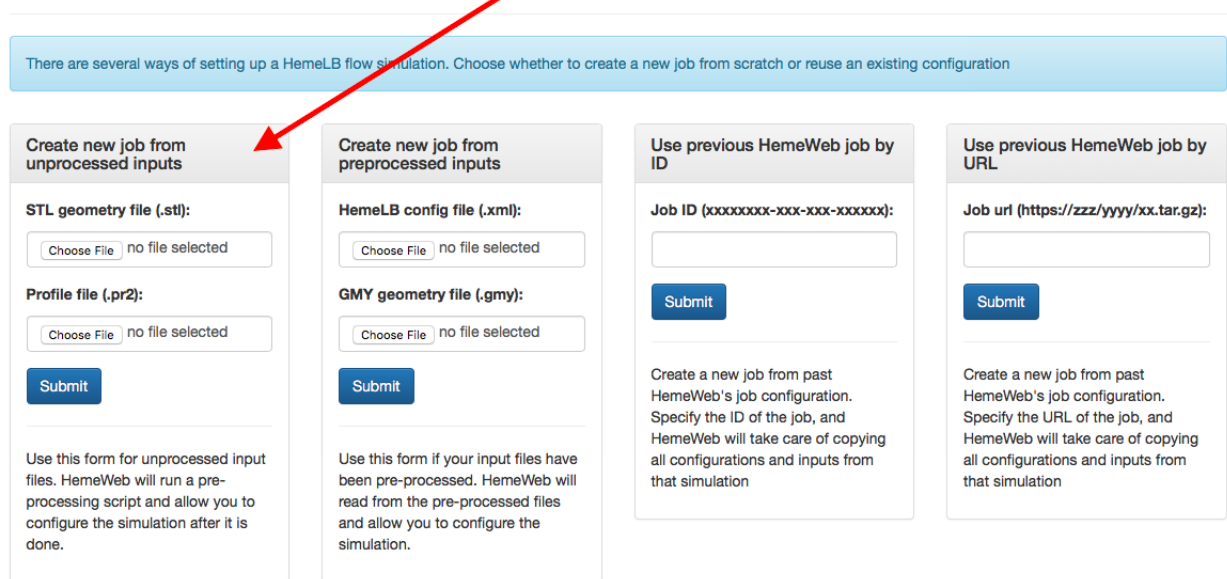
Figure 3.3 illustrates how the HemeWeb web application works. HemeWeb currently consists of 4 core activities that will be discussed in details in the following

section.

3.4.2.1 Geometric Pre-processing

In this step, HemeWeb take the description of the flow domain and the configuration of the inlets/outlets, and generates a domain discretisation suitable to be used by the underlying numerical solver. This step is only required to be run once and the user can change many of the parameters directly in the .XML file without requiring pre-processing again.

HemeWeb: HemeLB in the cloud



There are several ways of setting up a HemeLB flow simulation. Choose whether to create a new job from scratch or reuse an existing configuration

Create new job from unprocessed inputs

STL geometry file (.stl):

no file selected

Profile file (.pr2):

no file selected

Use this form for unprocessed input files. HemeWeb will run a pre-processing script and allow you to configure the simulation after it is done.

Create new job from preprocessed inputs

HemeLB config file (.xml):

no file selected

GMV geometry file (.gmv):

no file selected

Use this form if your input files have been pre-processed. HemeWeb will read from the pre-processed files and allow you to configure the simulation.

Use previous HemeWeb job by ID

Job ID (xxxxxxxx-xxx-xxx-xxxxxx):

Create a new job from past HemeWeb's job configuration. Specify the ID of the job, and HemeWeb will take care of copying all configurations and inputs from that simulation

Use previous HemeWeb job by URL

Job url (https://zzz/yyyy/xx.tar.gz):

Create a new job from past HemeWeb's job configuration. Specify the URL of the job, and HemeWeb will take care of copying all configurations and inputs from that simulation

Figure 3.4: HemeWeb pre-processing form

Figure 3.4 shows HemeWeb user interface to upload the files. After submission of both files and job being queued, the asynchronous worker on the master instance will work on the job whenever they are free. It will run the pre-processing python script to generate the geometry files and HemeLB configuration file. These files will then be saved to the master instance, and HemeWeb will track these files by recording the path to these files on the job instance. Now the job instance is ready for the next step. of the workflow.

3.4.2.2 Job configuration

In this step, HemeWeb application will take a job instance with valid geometry file (.gmy) and HemeLB configuration (.xml). However, there are multiple ways that HemeWeb can get this job instance. As illustrated on Figure 3.3, there are 4 possible entry points for this step. The web interface for these 4 entry points are also shown on Figure 3.4 They are:

- **From the post-processing step.** These files are generated from the previous pre-processing step. The job instance is directly used in this step
- **User's provided geometry and configuration file.** User have pre-processed their own file locally, or have their own geometry and configuration files available. HemeWeb will create a new job instance, save both files and keep them tracked with the job instance.
- **User's provided previous job ID.** There are two possible case when user specify previous job ID. First, the previous job is available locally on the HemeWeb instance. Second, the previous job is cached on the persistent storage on the cloud vendor and are not available locally. HemeWeb will download the previous file from the persistent storage if it is not available locally. It will then create a new job instance that copy the previous job's geometry file and configuration file to be used for further configuration.
- **User's provided simulation file URL.** The last alternative is for user to provide the simulation file URL. Simulation files are uploaded to a persistent storage at the end of the workflow. These files, if made public, can be used by other instance of HemeWeb to download the simulation files and use it as a basis to create a new job instance. The way the system work is the same as using previous job ID, but its source is not its own persistent storage, but other people's simulation files.

After the job instance is created from one of the four way possible discussed above, HemeWeb will then ask users for the job configuration.

Job 64d894d8-d7e9-4d64-8cd1-f6bc6abbd0a4

HemeLB Config Job config Overview

Configure HemeLB execution

```

1 <hemeLBsettings version="3">
2 <simulation>
3 <step_length units="s" value="9.62e-10" />
4 <steps units="lattice" value="18000" />
5 <stresstype value="1" />
6 <voxel_size units="m" value="3.333e-07" />
7 <origin units="m" value="(-1.56566857229e-07,-3.5224964629e-07,-1.14997991702e-05)" />
8 </simulation>
9 <geometry>
10 <datafile path="990_Example2-skeleton_corrected_tubed_smoothed.gmy" />
11 </geometry>
12 <inlets>
13 <inlet>
14 <condition subtype="cosine" type="pressure">
15 <amplitude units="mmHg" value="45.0" />
16 <mean units="mmHg" value="0.0" />
17 <phase units="rad" value="0.0" />
18 <period units="s" value="1" />
19 </condition>
20 <normal units="dimensionless" value="(0.574837835699,0.818267354816,-2.08425869156e-15)" />
21 <position units="m" value="(8.45432716982e-06,6.07165744613e-05,0.0)" />
22 </inlet>
23 </inlets>
24 <outlets>
25 <outlet>
26 <condition subtype="cosine" type="pressure">
27 <amplitude units="mmHg" value="0.0" />
28 <mean units="mmHg" value="0.0" />
29 <phase units="rad" value="0.0" />
30 <period units="s" value="1" />
31 </condition>

```

Save (Ctrl+S) Next step >

Figure 3.5: HemeWeb HemeLB configuration form

Figure 3.5 shows the interface where users are offered to make further adjustment to the HemeLB simulation parameter. In this page, an online XML editor will be provided for the user to directly edit the .xml file that is provided by the users or from the pre-processing step. This XML editor allow users to edit many simulation parameters on the web interface without changing the .GMY file. Users can directly edit values that affect simulation execution like inlet pressure, outlet pressure, blood viscosity, and etc. After configuring the simulation parameter it will then be redirected to job configuration page.

Configure Job execution

Instance count:

Instance type:

Container image:

Save

Figure 3.6: HemeWeb Job configuration form

Figure 3.6 shows the job configuration page. This page asks users about the pa-

parameter in which the simulation will be run with. These parameters are instance count, instance type, and HemeLB core container version. Instance count will determine how many compute node will be provisioned for this simulation by HemeWeb. Instance type will determine what type of compute node will be started, and the HemeLB core container version will determine what version of the container the compute node will use to run HemeLB simulation. After all of these parameters are set, users will be asked to confirm the job execution in the overview page. In the page, the user can then finally queue the job into the queue system.

3.4.2.3 HemeLB simulation

Once job instance is queued into the simulation queue, a free asynchronous worker will pop the queue and run the job. The worker will start up the configured amount and type of server instance from the cloud provider. These instances will then be further reconfigured by an Ansible script so that it points to the correct master instance address. Next, input files are shared via Networked File System (NFS), the compute units will mount the input folders to their instance.

The correct HemeLB core container version will be pulled from Docker hub in the next step. This step will skip the download if the container requested is already cached in the image for compute units which are prepared on the deployment part. After all of these are done, then the simulation can finally begin. Master node will issue an MPI command to be run by the leader of compute nodes. The leader of compute node then will run this MPI command in the Docker container. This command will be run on multiple compute node if it is configured as such in the previous steps.

The HemeLB simulation will run until outputs are produced. The output will be written back to the correct output folder in the shared folder. This means that the master instance will have access to the outputs file and can do further processing. This step ends with the termination of the instances.


```

TASK [Terminate instances that were previously launched] *****
changed: [localhost]

PLAY RECAP *****
172.31.23.149      : ok=11  changed=6  unreachable=0  failed=0
localhost         : ok=4    changed=3  unreachable=0  failed=0

```

Stderr

```

[WARNING]: Host file not found: /etc/ansible/hosts
[WARNING]: provided hosts list is empty, only localhost is available

```

HemeLB output

```

! [188.6s]time step 800 render_network_stream 0 write_image_to_disk 0 rendering 0
! [188.6s]time step 800, tau 0.603898, max_relative_press_diff 0.000, Ma 0.000, max_vel_phys 4.664540e-02
! [209.6s]time step 900 render_network_stream 0 write_image_to_disk 0 rendering 0
! [209.6s]time step 900, tau 0.603898, max_relative_press_diff 0.000, Ma 0.000, max_vel_phys 4.739036e-02
! [230.7s]time step 1000 render_network_stream 0 write_image_to_disk 0 rendering 0
! [230.7s]time step 1000, tau 0.603898, max_relative_press_diff 0.000, Ma 0.000, max_vel_phys 4.739036e-02
! [251.8s]time step 1100 render_network_stream 0 write_image_to_disk 0 rendering 0
! [251.8s]time step 1100, tau 0.603898, max_relative_press_diff 0.000, Ma 0.000, max_vel_phys 4.739036e-02
! [272.9s]time step 1200 render_network_stream 0 write_image_to_disk 0 rendering 0
! [272.9s]time step 1200, tau 0.603898, max_relative_press_diff 0.000, Ma 0.000, max_vel_phys 4.739036e-02
! [294.0s]time step 1300 render_network_stream 0 write_image_to_disk 0 rendering 0
! [294.0s]time step 1300, tau 0.603898, max_relative_press_diff 0.000, Ma 0.000, max_vel_phys 4.739036e-02
! [315.1s]time step 1400 render_network_stream 0 write_image_to_disk 0 rendering 0
! [315.1s]time step 1400, tau 0.603898, max_relative_press_diff 0.000, Ma 0.000, max_vel_phys 4.739036e-02
! [336.2s]time step 1500 render_network_stream 0 write_image_to_disk 0 rendering 0
! [336.2s]time step 1500, tau 0.603898, max_relative_press_diff 0.000, Ma 0.000, max_vel_phys 4.739036e-02
! [349.8s]Finish running simulation.

```

Figure 3.7: HemeWeb Job logs

Figure 3.7 shows how the Job execution will produce logs that can be viewed on HemeWeb web application. During simulation, logs are written to the respective job folder and are served to the browser by the HemeWeb app. Showing the logs allows users to easily view the progress of the job or even debug failed job.

3.4.2.4 Post-processing

After a HemeLB simulation is finished, the HemeWeb web app will do some post-processing steps to make sure the output files can be viewed easily. The outputs from HemeLB simulation are structured in such a way that makes it efficient to write in parallel. However, these outputs cannot be viewed by visualization system like Paraview. What HemeWeb will do is to pipe the output files to two python scripts that will format the output into a format that can be understood by ParaView.

There are further steps that HemeWeb took to make sure that the simulation files, configurations, and results are preserved externally. HemeWeb will package the job directory, compress it, and upload it into persistent storage that cloud vendors provide. As the time of writing, HemeWeb only supports amazon simple storage service. The simulation files are uploaded to this storage and made accessible to the public so other HemeWeb instance can use them. Also, with the job files persisted on persistent storage, the next HemeWeb instance deployed can take advantage of these files that it can use it as previous jobs to be used on current deployment

3.4.3 Implementation Challenges

In this section, I will outline and discuss the challenges in implementing this project, and if any, the solution that I choose.

3.4.3.1 Cloud vendors features and API difference

The challenge in developing the deployment script is the difference of cloud vendors' API and features. This has led to some problems when trying to create a common API to do a certain task. One notable problem is that the absence of image creation from running instance feature from one of the cloud vendors. Image creation feature is not an essential requirement of the project. However, with an image creation, the compute nodes that will be requested by the web application can be configured much quicker because all the pre-configuration that are done during the deployment phase. However, one of the cloud vendors, Digital Ocean, does not have this feature. This creates a situation where there is no elegant way to create image with the deployment script and users are asked to manually created the image on the web interface

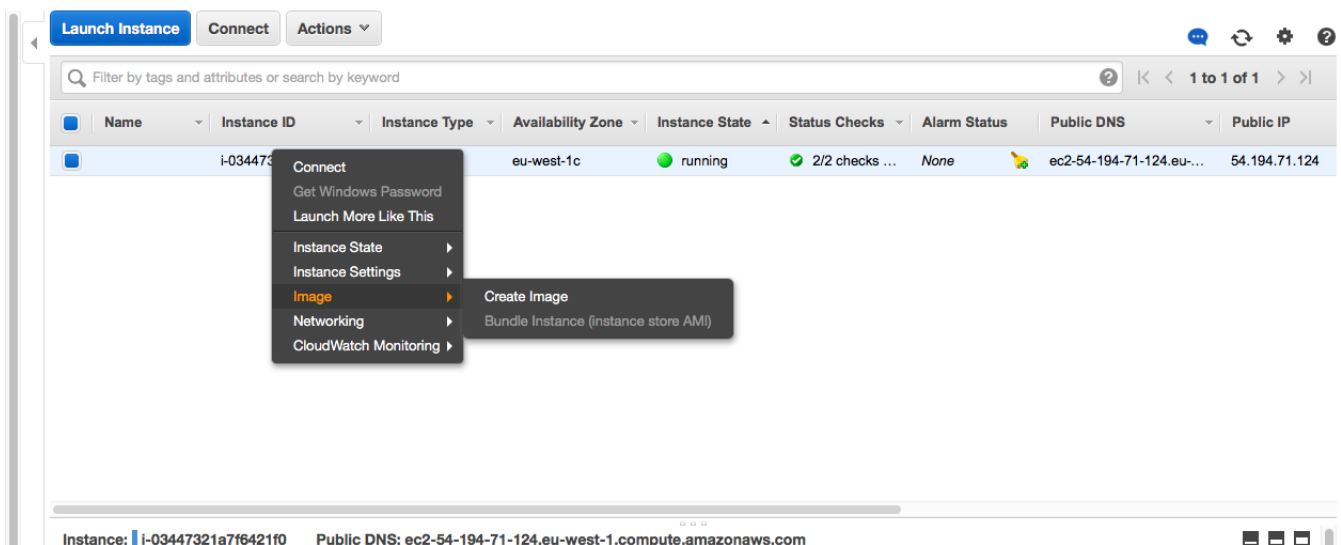


Figure 3.8: Manual image creation instead of automatic

Figure 3.8 shows how users are instructed to manually create an image from running instance. Users have to go the web interface of specific cloud vendors, right-click on the running instance, and create the image from it. This is a simple workaround which is less complicated compared to accommodating different or missing features

and API from different cloud vendors.

Another problem is the different storage API across cloud vendors. Due to the time constraint, I can only prioritize one vendor, Amazon Web Service. However, this means that the codebase is currently tied to one cloud vendors. Features like automatically reading past simulation files from cloud storage and uploading simulation files are tied to Amazon's infrastructure. It is possible to refactor these functionalities out to become more generic, however due to the time limit, I decided not to.

3.4.3.2 Security

Another challenge that I face during the development of HemeWeb is to handle the security of the application. However, security is not the main focus of this work and is apparent in the development of HemeWeb. I will still discuss the security issues so that I can give an objective assessment of the application.

The first security issues that I found is with regards to the compute node security in some cloud vendors. Digital Ocean, for example, does not provide private networking options that blocks other people's node to communicate with our compute node with the private network. Theoretically, this allow other people access to your private compute node if they have the credentials. In this case, I made sure that all the compute nodes have a sensible access policy to deter unauthorized access to the nodes. I only allow SSH access with a public key and disabled password access to SSH. Also, it is also much better to choose cloud vendors that have sensible setting for private networking like Amazon Web Service. On AWS, compute nodes are not accessible to other nodes that are not part of your own private network. This is much more secure and sensible.

"real" private networking option within compute nodes. They have a "shared" private networking options that allow other compute nodes, which are not even on your account have network connectivity to your node.

Another security issue is on how compute and master node share simulation job's files. It currently uses Network File System without any security measures towards the nodes that try to mount it via the private network. There is an opportunity to secure this communication by encrypting the job files, but it is not currently done.

Chapter 4

Evaluation

In this chapter, I will discuss on the system's evaluation. Success will be measured by answering these questions:

- Can users run a simulation using our system ?
- Can users reproduce past simulations using our system ?
- Are users satisfied in using our system ?
- Are users more likely to run a simulation using our system compared to the command line ?
- How does it perform compared to the existing infrastructure ?

In answering questions above, I conduct two sets of evaluations. First, an online questionnaire was conducted to measure user's experience and system's usability. And secondly, a performance analysis comparing the performance of HemeLB between dedicated hardware against cloud vendors. The questionnaire will answer most of the questions related to user experience and usability above, while the performance benchmark will be the basis for performance evaluation and justification in using HemeWeb.

4.1 Questionnaire

In measuring user's experience, I created a questionnaire for HemeWeb using google form. The questionnaire was live for 10 days, from 3rd of August 2016 until 12th of August 2016.

At the start of the questionnaire, respondents are asked about their background information. This information will be used to provide demographic insight on the respondents and how it affect the type of answers the respondents will most likely give. Respondents will be asked to fill out their age, gender, job, discipline, and level of familiarity with various software tools. From their responses, I can determine whether the sample population is representative of the target audience.

The questionnaire is set to make tester run specific scenarios that HemeWeb is developed for. These scenarios are running a simulation using the web interface and reproducing past simulation with it. Testers running the scenario are given an option to skip the scenario and go straight to the questions below it to measure their experience if they find it too difficult.

The first scenario asks testers to run a simulation with given inputs. The questionnaires list two input files, a geometry file and a HemeLB configuration file that testers will need to download to their computers. After downloading the input files, testers are asked to open their browser and go to a specific URL where HemeWeb was deployed for the evaluation purposes. In that URL, testers will then add a new simulation job with the downloaded files, configure the job, and submit the job to the queue. The scenario ends when the job is submitted.

The second scenario asks testers to reproduce past simulation with a given URL that contains past simulation files. It asks testers to create a new job from the given URL instead of using files that are downloaded in the past scenario. After creating a new job, testers then will change some configuration and parameters from the past scenario and submit the job. The scenario also ends when the job is submitted.

Following each scenario are questions to measure whether users skip the scenario and an after-scenario questionnaires that users have to answer. The after-scenario questionnaire is based on the usability measurement at IBM developed by James R Lewis [30]. It measures users' usability satisfaction with the system with regards to given scenario. The questionnaire give 3 statements which testers should agree or disagree, they are:

- Overall, I am satisfied with the ease of completing the tasks in this scenario
- Overall, I am satisfied with the amount of time it took to complete the tasks in this scenario
- Overall, I am satisfied with the support information (online-line help, messages, documentation) when completing the tasks

In addition to above questions, there are some questions about the tester's willingness to do exactly the same tasks as the scenario, but with the command line. This question will measure user's willingness in using the command line interface compared to the web interface.

After running both scenarios, testers are then redirected to the final questionnaire. The Post Study System Usability Questionnaire which is based on the same work by James R Lewis [30]. In this questionnaire, testers are given 19 statements where they should agree or disagree, they are:

- Overall, I am satisfied with how easy it is to use this system
- It was simple to use this system
- I can effectively complete my work using this system
- I am able to complete my work quickly using this system
- I am able to efficiently complete my work using this system
- I feel comfortable using this system
- It was easy to learn to use this system
- I believe I became productive quickly using this system
- The system gives error messages that clearly tell me how to fix problems
- Whenever I make a mistake using the system, I recover easily and quickly
- The information (such as online help, on-screen messages, and other documentation) provided with this system is clear
- It is easy to find the information I needed
- The information provided for the system is easy to understand
- The information is effective in helping me complete the tasks and scenarios
- The organization of information on the system screens is clear
- The interface of this system is pleasant
- I like using the interface of this system

- This system has all the functions and capabilities I expect it to have
- Overall, I am satisfied with this system

In addition to the above questions, testers also will be asked to list the most negative aspects and positive aspects of the system if they have any. These questions will measure users satisfaction with the overall system, whether it is useful, whether the information given by the system is any good, and the interface quality.

4.2 Performance benchmarks

The second part of the evaluation is the performance benchmark. HemeWeb is running HemeLB simulation outside its original scope of being used on a highly parallel computing resources like a supercomputer. This could have an interesting impact on the performance of the system because cloud vendors, while being easily accessible and provisioned, have an underlying infrastructure difference with the stand-alone infrastructure. This performance benchmarks will then measure whether the impact on the performance justify the claimed usability benefit that we measure on the first half of the evaluation.

The performance benchmark will be done by the internal tooling that is available inside HemeLB. Every HemeLB simulation will produce a report file that measures the performance of said simulation. On this evaluation, I will compare the performance of HemeLB simulation on three different infrastructure to measure the performance impact on having HemeLB simulation on the cloud with Docker containers.

They are:

- ARCHER supercomputer
- INDY2 HPC Cluster
- Cloud computing infrastructure with AWS EC2

On these three infrastructure, ARCHER supercomputer has the oldest processor architecture. It use a three-year old 2.7 GHz, 12-core E5-2697 v2 Ivy Bridge processor as the basis of its compute node. Each compute node consist of this two processors. INDY2 is a newly installed HPC infrastructure on EPCC that is currently in early-access testing. It has the newer Broadwell-based 18-core Intel Xeon CPU E5-2695 v4 @ 2.10GHz. Lastly, for AWS-EC2, we use Amazon's c4.8xlarge EC2 instance

which has Haswell-based E5-2666 v3 processor that has 18 virtual cores¹ or 36 vCPU with hyperthreading². Essentially, we will be using 18 core on AWS-EC2 instance for the simulation, because HemeLB is a compute bound task that do not benefit from hyperthreading.

Next, the three different architecture also have different networking interface that could contribute to the performance difference. While AWS-EC2 offer 10 Gigabit per second interface, ARCHER use a Cray Aries router interconnectivity that provides higher network throughput (ranging from 12.5 Gigabit per second to 14 Gigabit per second) throughout the infrastructure. Finally, INDY2 has FDR InfiniBand network interface connected to each compute node that provides 54.5 Gigabit per second.

For the simulation, we used an input file which has 4,520,681 fluid sites³ ⁴. With these files, we are going to do a strong scaling analysis, where we keep the problem size the same while we increase the core count. According to the performance analysis by Groen et al. [8], HemeLB scales up near-linearly up to 32,768 cores. It also performs near its maximum efficiency when using 5,000 to 500,000 sites per core. This means that for the problem size we use, HemeLB should perform near maximum efficiency when using 9 cores up to 900 cores. Above that core counts, HemeLB simulation will incur a performance penalty.

The benchmark on ARCHER supercomputer will be the gold standard of the performance. It's a gold standard because the infrastructure has a clear purpose of being used for the HPC application. It has the necessary resources and components that are tailored for it. It should be the ideal performance scenario. Next, the INDY2 as the locally installed and managed HPC infrastructure. INDY2's performance will paints a picture if how HemeLB will perform on a private local infrastructure which is built to run highly parallel jobs. Based on all these infrastructure difference, our hypothesis is that AWS-EC2 will provide slower performance compared to INDY2 and ARCHER.

In running the simulation, I had help from Dr. Rupert Nash to run HemeLB simulation on ARCHER and INDY2. I need help because I did not have access to both of these infrastructures. On AWS-EC2 infrastructure, however, I run the HemeLB scenario myself. HemeLB simulation was run using the HemeWeb interface on AWS.

¹<https://aws.amazon.com/ec2/virtualcores/>

²<https://aws.amazon.com/ec2/instance-types/>

³Available online at https://github.com/SeiryuZ/HemeWeb/blob/master/deployment/roles/hemeweb_master/files/990_Example2-skeleton_corrected_tubed_smoothed.gmy

⁴Config for the simulation can be found online at <https://github.com/SeiryuZ/HemeWeb/blob/master/documents/resources/evaluation/performance/config.xml>

Chapter 5

Analysis

5.1 Usability result and analysis

In evaluating HemeWeb's usability and capability to run and reproduce simulation, I conducted a usability evaluation via an online survey hosted by Google Form¹. Respondents are given 2 tasks to complete, which are to run a simulation and reproduce a past simulation. After the tasks, they are given statements to respond to. Based on the answers, I can make an analysis about HemeWeb's usability.

5.1.1 Demography

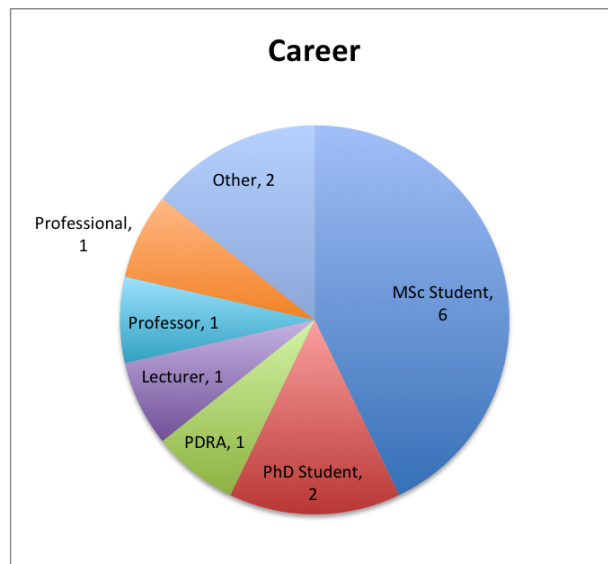


Figure 5.1: Career stage distribution

¹<https://goo.gl/forms/toYsRwnGIGumMBUD2>



Figure 5.2: Career discipline

The survey was filled by 16 respondents over the period of 10 days (3rd August 2016 - 12th August 2016)²See Appendix D)³. From all the responses, one of the respondent was unable to run both of the tasks, citing errors preventing him to run the scenarios which we cannot reproduce. Another respondent also skip the second scenario without specifying reasons or contacting the author. Due to this problem, we have to remove these two responses from our analysis because it will not add meaningful information about the usability of the system when the scenarios are not run. In total, we got 14 valid responses out of the questionnaire period.

Figure 5.1 and 5.2 illustrates the distribution of career stage and discipline of our participants. Based on this distribution, we can further analyze the response we get on the survey questions based on their background. One meaningful comparison we can make is when we classify respondents based on their informatics-related discipline. 10 of our respondents are related to informatics background, while 4 of the respondents can be considered as domain experts which consists of Biologist, Clinician, and Biophysicist.

²(

³Raw and compiled responses can be found at <https://github.com/SeiryuZ/HemeWeb/tree/master/documents/resources/evaluation/usability>

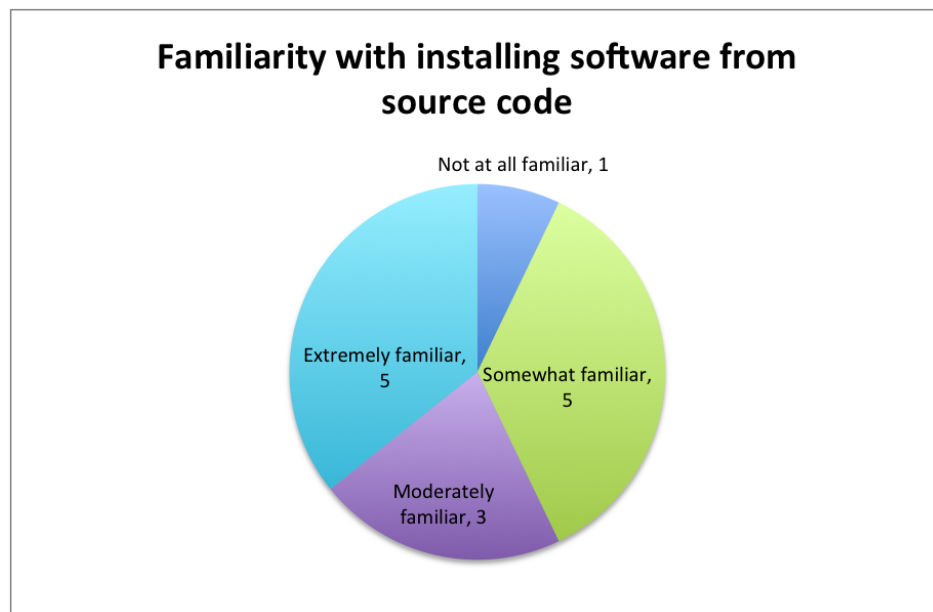


Figure 5.3: Familiarity with installing software from source code

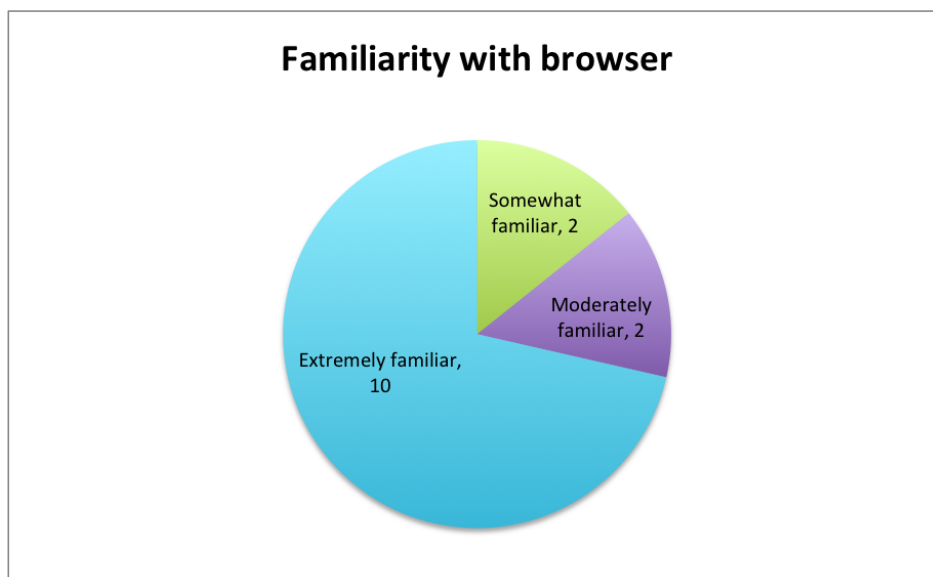


Figure 5.4: Familiarity with web browser

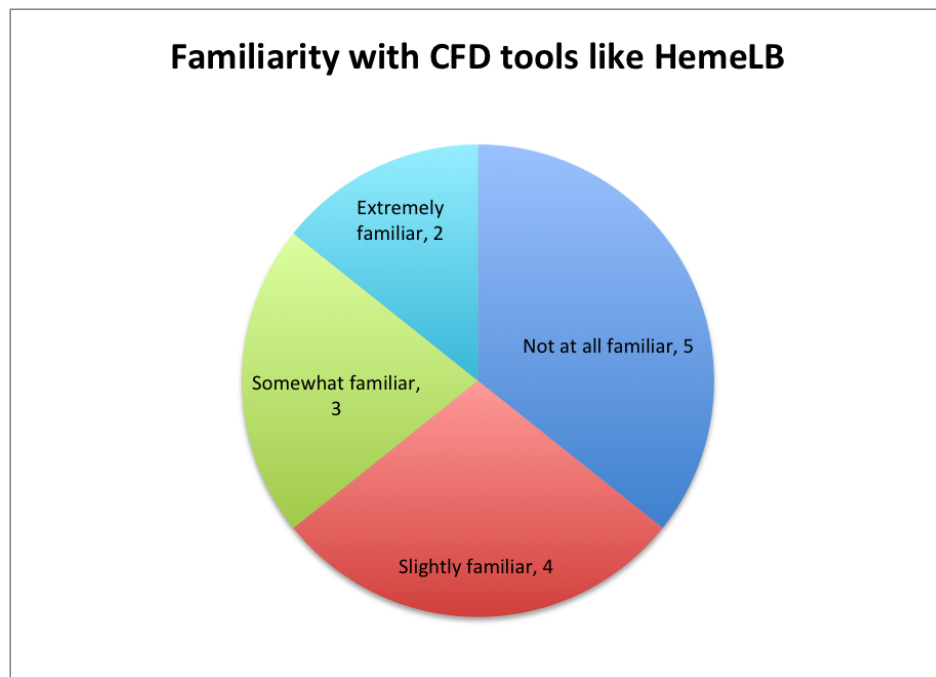


Figure 5.5: Familiarity with CFD tools like HemeLB

We can also further classify analyze the respondents' response based on the familiarity with browsers, computational fluid dynamic tools, and installing software from source code. All of this are shown in Figure 5.3, 5.4, and 5.5.

5.1.2 Scenario 1: Run a HemeLB simulation

In this scenario, respondents are provided with two input files necessary for running a simulation. Respondents are asked to download the files beforehand and follow the instructions provided in the online questionnaire to run a HemeLB simulation using HemeWeb. After running the simulation, Respondents are then asked to state agreement with three positive statements about HemeWeb that will measure their satisfaction with HemeWeb in running a HemeLB simulation scenario.

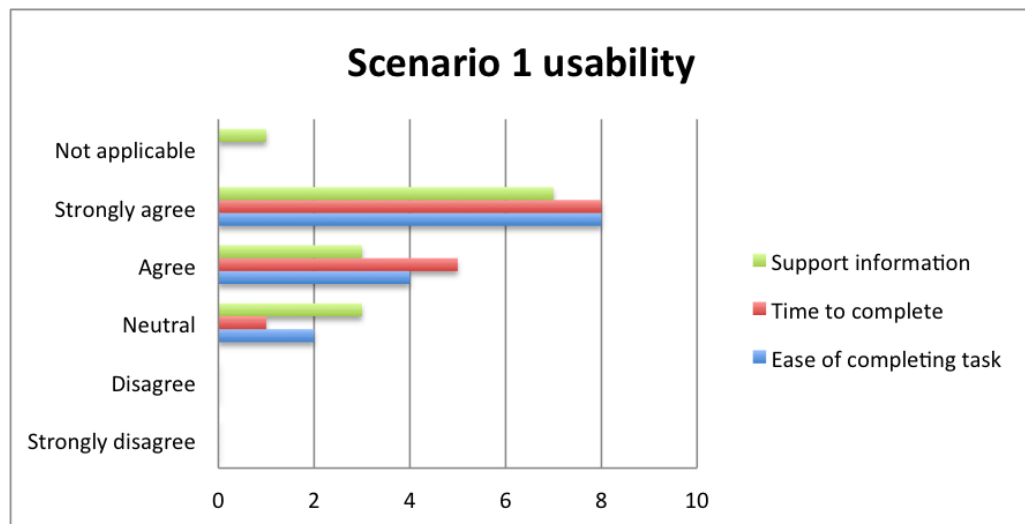


Figure 5.6: Scenario 1 usability

Figure 5.6 show the responses for the three positive statements about HemeWeb. From the 14 valid responses we get, all of them did not skip the instructions to run the simulation. From the responses, respondents tend to agree that they are satisfied with HemeWeb in running a HemeLB simulation. Respondents tend to equally agree on the three positive statements about the ease of completing a task, time to complete, and supporting information available to help complete the task. However, one respondent fills out "Not Applicable" towards the statement about HemeWeb giving them enough support information.

In addition to the general sentiment of the respondents, we can also put a number value to the responses to further measure the satisfaction objectively. We can calculate the After Scenario Questionnaire(ASQ) score. To do this, we assign an integer value for each response; 1 for "Strongly disagree", 2 for "Disagree", 3 for "Neutral", 4 for "Agree", and 5 for "Strongly agree". With this value, we can take the mean of the response for each question as a single ASQ score for the respondent. If a respondent skips a question, we can take the average of the remaining responses as the score. With this mechanism, we can calculate the respondent's average ASQ score, which is 4.4 when rounded. This score falls between "Agree" and "Strongly agree", therefore, we can conclude that in general respondents are satisfied with HemeWeb with regards to running a HemeLB simulation.

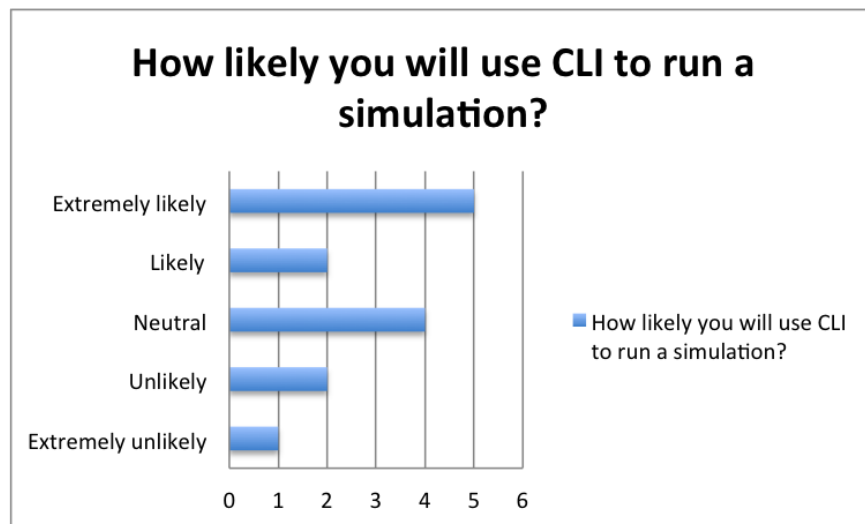


Figure 5.7: Scenario 1 command line preference

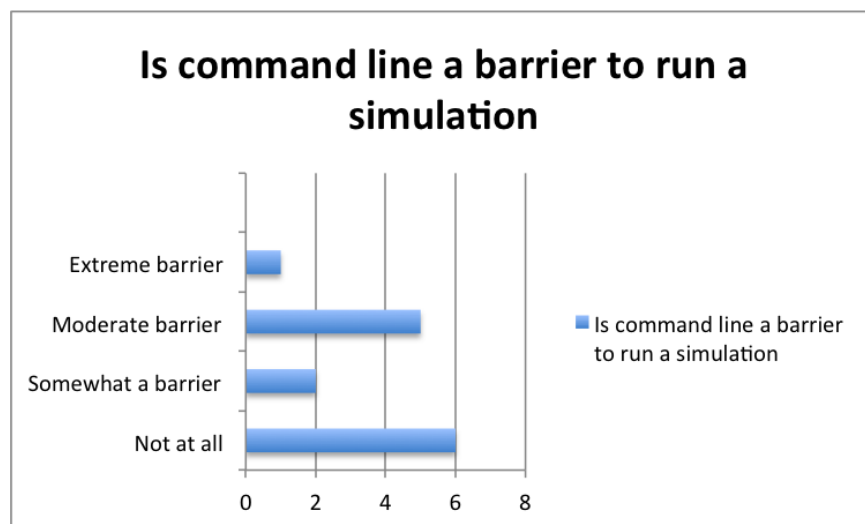


Figure 5.8: Scenario 1 barrier in using command line

After the above sentiments about using HemeWeb to run a HemeLB simulation, respondents were asked about their sentiment about using Command Line Interface(CLI) to do the same activity. Figure 5.7 and 5.8 shows the respondent's responses. Respondents are generally open to the likelihood of them running a simulation using CLI. If we quantify the results like we did with the ASQ score, we get 3.6, which is between neutral and likely.

The distribution of the responses also is quite spread out, that respondents fill out all possible responses with the highest frequency being "Extremely Likely" with 5 responses. However, we have to keep it mind the general background of the respondents that may explain the highest frequency answer being "Extremely Likely", which is

about familiarity with installing software with source code. To build software with source code, one will interact with the command line interface quite often. Thirteen of our respondents answered at least somewhat familiar with building software from source code, that can explain that our respondents are mostly quite competent in operating command line interface and would not shy away in using the command line interface. In addition to that, two out of three respondents has backgrounds in informatics and computational science. This could in effect explains why the respondents feel they are likely and extremely likely to do the same in CLI.

However, not all respondents who are at least somewhat familiar with building software from source code skew towards to the likely side of using CLI. There are respondents that, while familiar with the interface, running a HemeLB simulation using CLI is unlikely to be done by them. These responses might be explained by respondents' sentiment in using command line interface. This is further supported by the response of CLI being a barrier for the respondents. While six of the respondents think it is not a barrier at all to use CLI, eight of the respondents answered at least it is somewhat a barrier. With five of the nine respondents, feel it is a moderate barrier, and one of the nine feel it as an Extreme barrier. From these results, we can safely say that using command line interface is a form of a barrier to run HemeLB for almost 60% of the respondents, with this figure going up to 75% when only the answers of the domain experts are considered.

5.1.3 Scenario 2: Reproduce a past simulation

In the second scenario, respondents are asked to reproduce past simulation with HemeWeb. They are given instructions in the online questionnaire to create a HemeLB simulation job from past simulation. They have to enter a URL that contains past simulation job and modifies the simulation parameters to avoid only replicating the past simulation without changes. After reproducing past simulation, respondents are then asked to state agreement with the same questions like they had in the first scenario. These questions will also measure their satisfaction with HemeLB in reproducing past simulation.

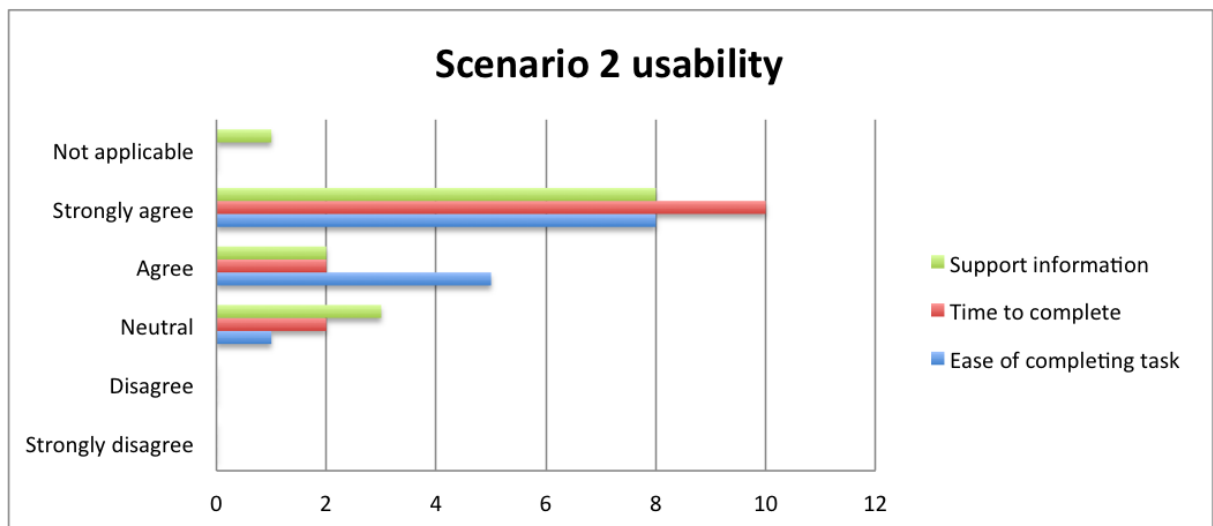


Figure 5.9: Scenario 2 usability

Figure 5.9 shows the general sentiment to the three statements that we provided. Generally, the response tends to skew towards agreeing that respondents are satisfied with HemeWeb with regards to reproducing past simulation. However, it has to be noted that 1 of the respondent skipped the instructions. This particular respondent did not give out any comments about encountering any problems, so we cannot deduce whether his skipping the instruction is due to usability problems or he just wants to skip it. Without further information, we cannot deduce why he skips the instructions and his response is one of the two taken out from the overall responses.

Also, similar to the first scenario, one respondent fills out "Not Applicable" to support information statement. In a nutshell, respondents tend to agree that HemeWeb is satisfying to use for the purpose of reproducing past simulation. If we convert the responses to a numerical value, we will get 4.5 of ASQ score. Which is in line with the sentiment that I described. The ASQ score falls between agreeing and strongly agree towards the positive statements we provided.

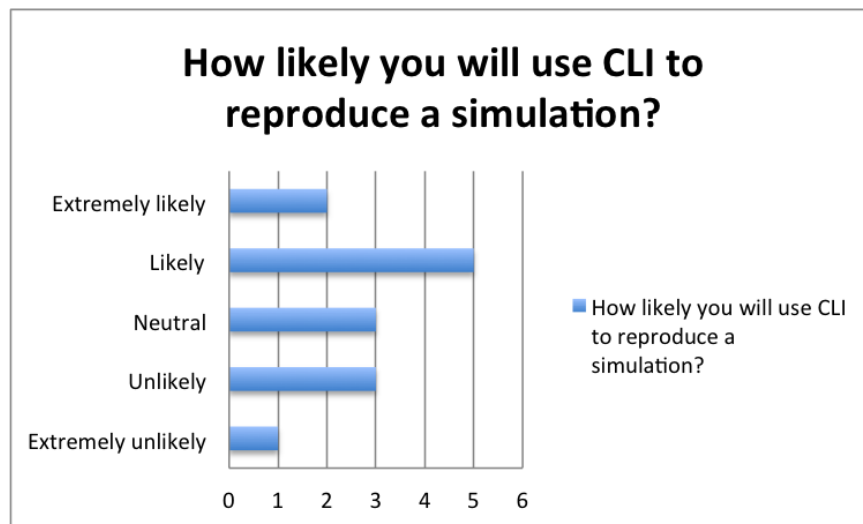


Figure 5.10: Scenario 2 command line preference

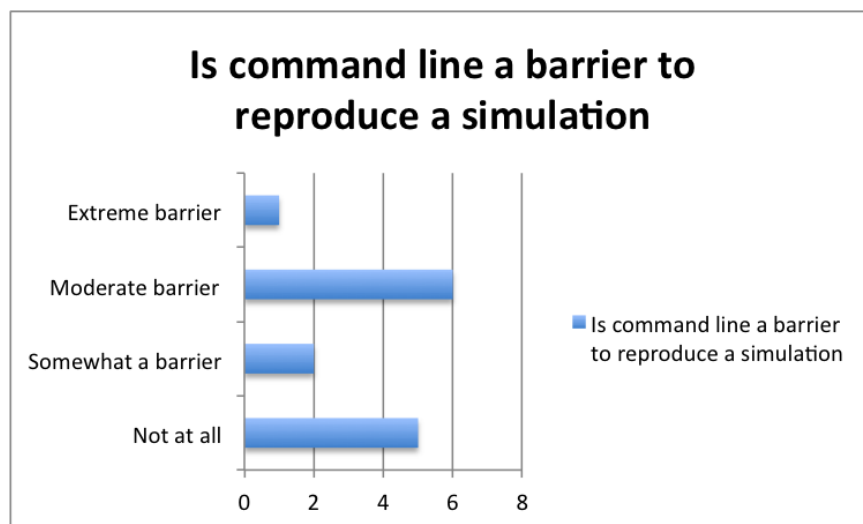


Figure 5.11: Scenario 2 barrier in using command line

Respondents are then given high-level steps to reproduce past simulation using the command line interface. Figure 5.10 and 5.11 shows the respondent's response. Similar to the first scenario, the respondents are generally open to the idea of operating command line interface to do their tasks. However, the scenario to reproduce past simulation provides a bit difference in the distribution of the answers. While in the first scenario the highest frequency of the answer is "Extremely likely", the highest frequency response in this scenario is "Likely".

This change of the highest frequency might be because there are extra step which might complicate the scenario to reproduce past simulation. respondents are more hesitant to answer "Extremely likely". However, the general nuance of the answer is

still the same, respondents are generally not afraid of using command line interface to do this task. If we convert the answers into a numerical form like we did before, we got 3.3, which is between neutral and likely.

In addition, same observation as the first scenario can be made. While some respondents are likely to reproduce past simulations, there are those who are not likely to reproduce past simulations even with their background that have dealt with building software from source code. This can be explained by Figure 5.11 where only five of the respondents did not feel that using CLI is a barrier at all. 2 of the respondents feel using CLI is somewhat a barrier, six feel it as a moderate barrier, and one feels it as an extreme barrier. This means that this nine respondents agree that CLI is a form of barrier to them, however small it is.

5.1.4 Overall usability

Here, I will discuss the overall usability of the system using the Post Study System Usability Questionnaire(PSSUQ) as the basis. This part of the questionnaire consists of 19 questions that can be divided into measuring three different component of the systems. These are system usefulness, information quality, and the interface quality. I will discuss each of them in details.

Table 5.1: System usefulness

	Strongly disagree	Disagree	Neutral	Agree	Strongly agree	Not applicable
Overall, I am satisfied with how easy it is to use this system	0	0	0	7	7	0
It was simple to use this system	0	0	0	1	13	0
I can effectively complete my work using this system	1	1	1	3	4	4
I am able to complete my work quickly using this system	0	1	2	3	6	2
I am able to efficiently complete my work using this system	0	1	2	4	5	2
I feel comfortable using this system	1	0	0	3	10	0
It was easy to learn to use this system	0	0	1	0	13	0
I believe I became productive quickly using this system	0	0	2	3	5	4

Table 5.1 shows the respondents sentiment towards positive statements about the system usefulness. Generally, we can see the distribution of respondents mostly agreeing with the statements presented. Ignoring the respondents that answered with "Not

applicable”, we can find the distribution is skewed to the agreeing side of the statements. There are respondents that disagree or even strongly disagree with some questions. However, the frequency is much lower compared towards the frequency of people agreeing to the statements.

Converting the response into a numerical value, we can get the score of 4.4 of system usefulness, which is quite high. However, there are still some improvements that can be made, and it is apparent in the feedbacks⁴ of the system we got. For example, one respondent find the job configuration inflexible, another respondent find Firefox does not render the interface correctly. All of these can be addressed in the next iteration of HemeWeb development. In addition to these sentiments, there are respondents that respond to the statement by answering Not applicable. It is mostly on the framing of the simulation as a 'work'. Respondents might have no point of reference whether using the HemeLb via HemeWeb is quicker or efficiently because they are new to the system. This is apparent from their background that they don't have familiarity with HemeLB.

Table 5.2: Information quality

	Strongly disagree	Disagree	Neutral	Agree	Strongly agree	Not applicable
The system gives error messages that clearly tell me how to fix problems	0	1	1	4	2	6
Whenever I make a mistake using the system, I recover easily and quickly	0	0	4	1	3	6
The information (such as online help, on-screen messages, and other documentation) provided with this system is clear	0	0	3	3	5	3
It is easy to find the information I needed	0	0	2	3	6	3
The information (such as online help, on-screen messages, and other documentation) provided for the system is easy to understand	0	0	2	5	6	1
The information is effective in helping me complete the tasks and scenarios	0	1	3	2	7	1
The organization of information on the system screens is clear	0	0	2	8	4	0

Table 5.2 gives more insight on the respondents sentiment on HemeWeb's information quality. This includes information like error messages, documentation, the organization of this information, and etc. From seven positive statements that we presented.

⁴See Appendix D - Figure D.4

most respondents tend to agree that the information quality is good. The overall sentiment is more towards agreeing compared to disagreeing. If we convert the sentiment into a score, it will get 4.1 average score, Which falls under "Agree" and "Strongly agree" sentiment.

However, there are more respondents answering "Not applicable" in this part of the questionnaire. This led to the remaining answer having more contribution towards the average sentiment because many of the answers are not counted. For example, there are 6 ignored responses on the first statement about error messages. This is likely because the scenario given to the respondents will not give out an error message if they are correct the first time. In the end, however, respondents tend to agree that information quality of HemeWeb is good.

Table 5.3: Interface quality

	Strongly disagree	Disagree	Neutral	Agree	Strongly agree	Not applicable
The interface of this system is pleasant	1	0	1	7	5	0
I like using the interface of this system	0	1	1	8	4	0
This system has all the functions and capabilities I expect it to have	1	1	1	4	4	3

Table 5.3 shows the respondents sentiment with regards to HemeWeb's interface quality. In it, we see respondents strongly disagree and disagree with positive statements about the interface. While in general, most respondents tend to agree that the interface is good, some disagree. When we see this particular response, it seemed that the respondent had trouble with the interface not rendering correctly in firefox. This feedback means that the browser compatibility of HemeWeb should be improved. There are parts of the interface which are broken if it is viewed on firefox. There are other respondents who dislike the XML editor based on their feedbacks. However, all this are subjective in nature and further testing of the interface is needed.

However, if we convert the respondents answer to a numerical value, we got 4.0, which is "agree". It shows that while some respondents find the interface quality is not up to their standards, some find it good enough although a lot can be improved. Browser compatibility, web form choice, user experience, and etc should be improved on the next iteration of HemeWeb.

Table 5.4: Overall user satisfaction quality

	Strongly disagree	Disagree	Neutral	Agree	Strongly agree	Not applicable
Overall, I am satisfied with this system	0	0	1	7	6	0

The last part of the question is the overall perceived satisfaction that the user has in using the system. The distribution of the response can be found in Table 5.4. Most of the respondents gravitate towards agreeing and strongly agreeing that they are satisfied with the system. When we convert it into a numerical mean, it is 4.4, which is between "Agree" and "Strongly agree". To get the overall user satisfaction score of the study, we average the numerical score between the 19 questions and we got 4.2. This means that the respondents mostly agree that they are satisfied with how the system performs, inform, and looks like.

5.2 Performance result and analysis

In this section, I will discuss the performance benchmark of HemeLB simulation done in three infrastructure, ARCHER supercomputer, INDY2 HPC cluster, and AWS EC2. Understanding the difference in performance is essential for HemeWeb project to justify the flexibility that cloud vendors provide.

In this benchmark, we are going to rely on the report file that HemeLB produced. It is produced after each simulation is done and contains performance metric of each simulation like how many seconds are spent on communication, initializations, reading input files, and most importantly total simulation time. We are going to take a look at the total simulation time because it is the metric that captures the difference in the infrastructure better. We ran the exact same simulation scenario on all three infrastructure. On each infrastructure, the simulations were done with an increasing number of compute node to measure the scalability of HemeLB. From the produced output, then we can measure the performance difference between architecture.

Table 5.5: HemeLB performance on INDY2 vs ARCHER vs AWS EC2. Results for ARCHER and INDY2 run provided by Dr. Rupert Nash

# Compute node(s)	INDY2		ARCHER		AWS-EC2	
	Core	Time / s	Core	Time / s	Core	Time / s
1	36	24.7	24	33.6	18	35.3
2	72	12.7	48	22.1	36	24.6
4	144	7.08	96	13.4	72	16.8
8	288	3.44	192	9.81	144	11.5
16	576	1.81	384	9.94	288	10.3
32	1152	1.58	768	9.64	N/A	N/A

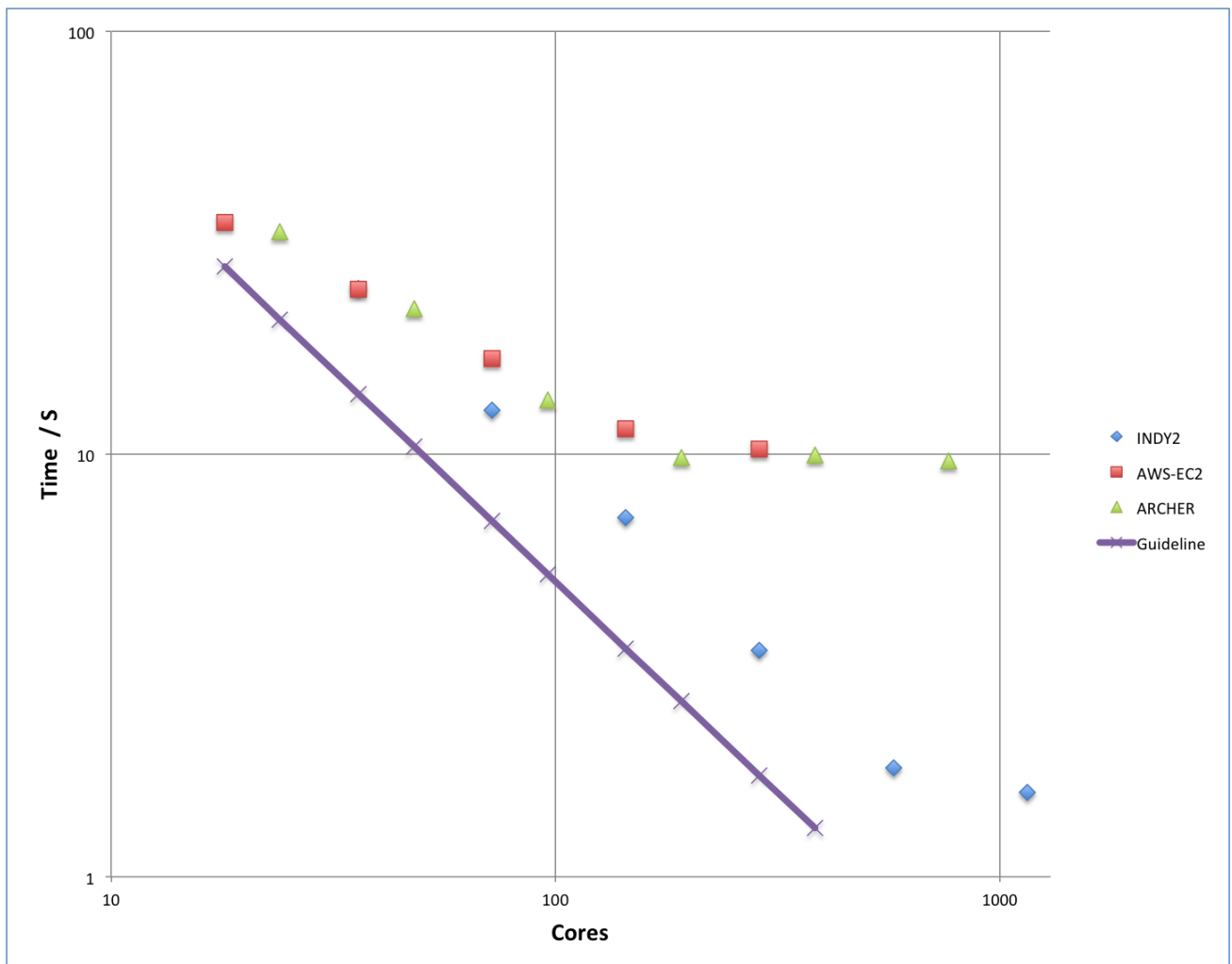


Figure 5.12: HemeLB performance comparison. Results for ARCHER and INDY2 run provided by Dr. Rupert Nash

Table 5.5 shows the performance comparison between HemeLB total simulation time between AWS-EC2, INDY2, and ARCHER. It shows that AWS-EC2 perform relatively well in lower amount of cores used. At 36 cores, AWS-EC2 perform even

slightly better compared to INDY2. It has to be noted that AWS-EC2 has lower core count in a single compute node compared to ARCHER that makes direct comparison impossible. However, we can see from the simulation time that AWS-EC2 perform relatively well compared to ARCHER's performance because it has small difference of the performance despite the lower core count.

Another observation that can be made from the performance information, is that AWS-EC2 performance experienced a bigger performance degradation on increased core counts compared to the other two infrastructures. This shows that while the raw performance of the compute cores are very respectable, the parallel scalability of AWS EC2 is not as good as the other two infrastructures.

Figure 5.12 also shows the difference in performance between the three infrastructure. INDY2 performed much faster than the other infrastructures. In addition, its performance also scales almost linearly up to 576 cores and had a performance degradation on 1152 cores. This closely follows the performance analysis by Groen et al. [8].

Next, ARCHER perform better than AWS-EC2. While it is still slower than INDY2, ARCHER provide more performance per compute nodes when we compare it to AWS-EC2. However, on 192 cores up to 768 cores, the performance became stagnant. It didn't achieve a better improvement as we scale. The performance difference between INDY2 and ARCHER can be explained by the different load on each system at the time of benchmark. INDY2 is on the early-access testing phase where at the time of execution, Dr. Rupert Nash was the only person using the infrastructure. On the other hand, when Dr. Rupert Nash executed HemeLB on ARCHER, the utilization was very high, which means that the HemeLB job potentially has to share network interconnectivity with other jobs.

Finally, AWS-EC2 perform slower on each compute nodes count we tested. The performance improved on increased the core count. However, this improvement is not nearly linear as modeled by Groen et al. [8]. This result could have many causes, but generally still in line with the benchmark that Mehrotra et al. did on NASA's HPC application [19]. The performance degradation comes from the network and the virtualization overhead that this cloud platform has. In addition, we do not have control over how the compute node are arranged on the cloud platform. We could have nodes with varying degree of interconnectivity on each simulation. A simulation might have started compute nodes near each other in the Amazon's data center, the next simulation might start compute nodes which need longer network interconnectivity.

Table 5.6: HemeLB parallel efficiency table of INDY2 vs ARCHER vs AWS EC2. ARCHER and INDY2 result is based on the data provided by Dr. Rupert Nash

INDY2			ARCHER			AWS-EC2		
Core	Speedup	Efficiency	Core	Speedup	Efficiency	Core	Speedup	Efficiency
36	1	1	24	1	1	18	1	1
72	1.94488189	0.972440945	48	1.520361991	0.760180995	36	1.43495935	0.717479675
144	3.488700565	0.872175141	96	2.507462687	0.626865672	72	2.101190476	0.525297619
288	7.180232558	0.89752907	192	3.425076453	0.428134557	144	3.069565217	0.383695652
576	13.64640884	0.852900552	384	3.38028169	0.211267606	288	3.427184466	0.214199029
1152	15.63291139	0.488528481	768	3.485477178	0.108921162	N/A	N/A	N/A

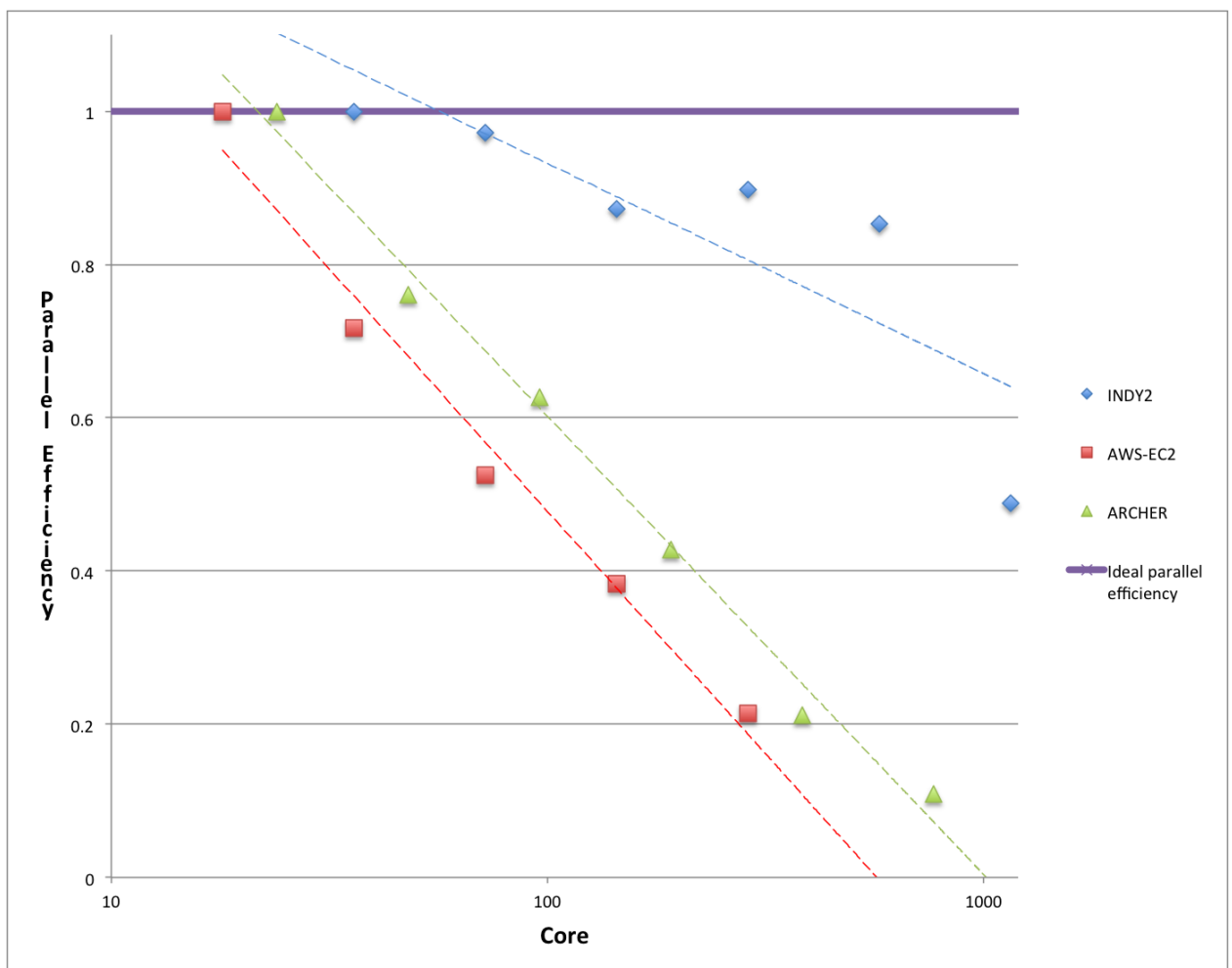


Figure 5.13: HemeLB parallel efficiency plot. ARCHER and INDY2 result is based on the data provided by Dr. Rupert Nash

From the raw performance information above, we can calculate the parallel scal-

ability of HemeLB on all three infrastructure. Table 5.6 and Figure 5.13 shows the difference of the parallel scalability on the three infrastructures with the basis of the smallest number of core used on each infrastructure. INDY2 has the best parallel scalability that it has the efficiency nearest to the ideal parallel scalability. However, the last data point produces a much slower speedup compared to other points that reduce its efficiency at 1,152 cores.

ARCHER also perform better than AWS-EC2 in this evaluation. However, the parallel efficiency is still far below the level of INDY2 because of the utilization of the system. AWS-EC2 has the lowest parallel scalability as expected. This shows that running HemeLB on Amazon's infrastructure might not scale as well as using dedicated HPC infrastructure. However, on lower compute node count, AWS-EC2 provide a comparable parallel scalability (5% difference) and performance compared to ARCHER under very high utilization.

From the observations above, we can conclude that that AWS-EC2 perform comparably to dedicated HPC infrastructure, especially on lower core count. However AWS-EC2 infrastructure does not scale as well as the dedicated HPC infrastructure. Based on this finding, we can further conclude that a small problem size that can be run on lower core count is an ideal use-case for HemeWeb because it will run with comparable performance with dedicated HPC infrastructure with the flexibility of cloud vendors.

5.2.1 Simulation cost analysis

In addition to performance analysis, we can further analyze the notional cost of a simulation job. For this, we need to come up with the way to calculate the simulation cost. This can be done by multiplying simulation time with cost per unit of time on that infrastructure.

$$\text{Simulation cost} = \text{simulation time} \times \text{cost per unit of time} \times \text{number of nodes}$$

In running the simulation for the benchmark, we used "c4.8xlarge" Linux instances on EU Ireland region which at the time of writing costs GBP 1.51⁵ per hour⁶. Phase 2 XC30 ARCHER supercomputer give access to screened projects by compute hour unit which has the price of GBP 0.20 per compute node for research councils which are partnered and GBP 0.48 per compute node for non-partnered research council⁷.

⁵USD 1.96 converted to GBP on <https://www.oanda.com/currency/converter/> at 13th August 2016

⁶<https://aws.amazon.com/ec2/pricing/>

⁷Calculated on <http://archer.ac.uk/access/au-calculator/>

INDY2, however, have no public pricing released by the EPCC yet and cannot be included in this analysis.

Calculating simulation time can be done by taking the performance of compute nodes on each infrastructure divided by the base time. The base time will be chosen from the fastest performance of the smallest compute node count on each infrastructure. In this evaluation, we ignore INDY2 because of missing pricing, so the base time is ARCHER with one compute node that runs for 33.6s. This will make sure that the simulation time across infrastructure shrinks relative to the performance of that time. With this information, we can finally calculate the simulation cost of using various compute nodes on each infrastructure.

$$\text{Simulation time ratio} = \text{simulation time} / \text{base time}$$

Table 5.7: HemeLB simulation cost on AWS-EC2 vs ARCHER. ARCHER and INDY2 result is based on the data provided by Dr. Rupert Nash

Compute node	ARCHER time difference ratio	ARCHER-partner simulation cost	ARCHER-nonpartner simulation cost	AWS-EC2 time difference ratio	AWS-EC2 simulation cost
1	1	0.2	0.48	1.05	1.59
2	0.66	0.26	0.63	0.73	2.2
4	0.40	0.32	0.77	0.5	3.02
8	0.30	0.47	1.12	0.34	4.13
16	0.30	0.95	2.27	0.31	7.41
32	0.29	1.84	4.41	N/A	N/A

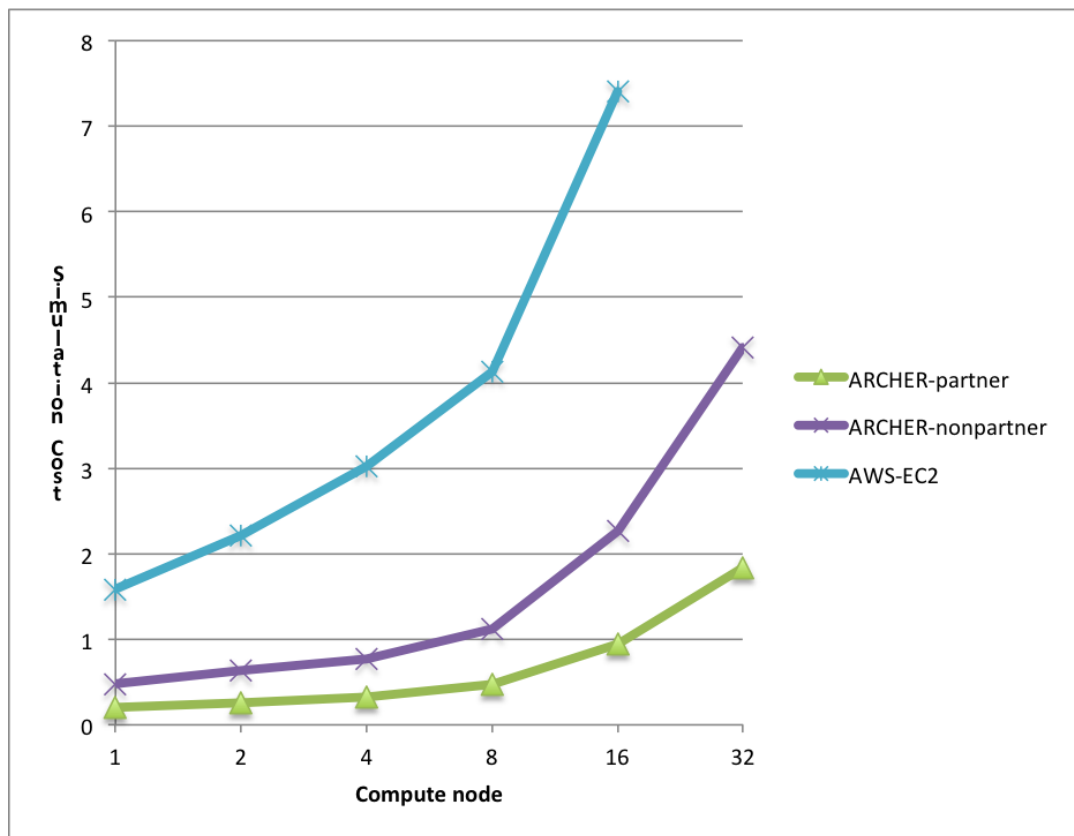


Figure 5.14: HemeLB simulation cost difference. ARCHER and INDY2 result is based on the data provided by Dr. Rupert Nash

Table 5.7 shows the breakdown of simulation cost between AWS-EC2 with ARCHER with partner institutions and non-partner. From the calculation, AWS-EC2 is 680% up to 850% more costly compared to ARCHER with partner pricing. When we compare to the price of a non-research partner, we get 230% to 290% more cost to run a simulation.

This result is as expected because, with slower performance, we are going to use compute nodes for longer. Longer usage means more cost to be paid by the users. In addition, cloud platform on AWS-EC2 rent out their services with a premium that allows a certain flexibility that dedicated HPC infrastructure like ARCHER cannot afford. This flexibility like the amount of time needed to first start running a simulation or running an exploratory experiments.

While being slower in running simulation, cloud vendors like Amazon web service allow domain experts to run simulation on-demand. On the contrary, running a simulation, even a small exploratory one, on dedicated HPC infrastructure like ARCHER, require users to apply for a spot, write a proposal, and wait for the next application de-

cision. This is the time of doing simulation that cannot be measured by this evaluation and should be used as one of the basis of using HemeWeb on cloud vendors compared to dedicated HPC infrastructure.

This result means that if you are an existing scientists with access to HPC infrastructure like ARCHER, using HemeWeb might not be the best way to run your HemeLB simulation because of the costs. However, if you are a scientists with no access to HPC infrastructure like ARCHER or INDY2 and does not have a constant demand for compute hour for your simulation, HemeWeb may worth the cost compared to applying for a spot on these HPC infrastructures. In addition, the on-demand nature of HemeWeb fits perfectly with exploratory studies type of job which usually needs a one-off job with relatively small problem size. With HemeWeb, users can start running the simulation on-demand.

5.3 Limitation of the evaluations

5.3.1 Usability evaluation

When observing the evaluation, one might argue that 5 point scale used in the questionnaire is not enough as pointed out by Kraig Finstad [32]. In his research, he argued that 5 point scale for a questionnaire allows more room for respondents to interpolate their response. He compared the same version of usability study but with five-point and seven-point scale and found out that 3% of the respondents answer to five point scale actually are interpolation, while the seven point scale have no interpolation. He concluded that administering usability study using seven point scale will achieve greater accuracy. However, I decided to use the five point scale of the questionnaire because of the limitation of google survey platform.

Indicate whether you agree or disagree with the following statements? *

	Strongly disagree	Disagree	Somewhat disagree	Neutral	Somewhat agree	Agree
Overall, I am satisfied with the ease of completing the tasks in this scenario	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Overall, I am satisfied with the amount of time it took to complete the tasks in this scenario	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Overall, I am satisfied with the support information (online-line help, messages, documentation) when completing the tasks	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Figure 5.15: Google form hiding some options on 7 point scale

Indicate whether you agree or disagree with the following statements? *

	Strongly disagree	Disagree	Neutral	Agree	Strongly agree	Not Applicable
Overall, I am satisfied with the ease of completing the tasks in this scenario	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Overall, I am satisfied with the amount of time it took to complete the tasks in this scenario	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Overall, I am satisfied with the support information (online-line help, messages, documentation) when completing the tasks	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Figure 5.16: Google form render 5 point scale rating better

Figure 5.15 show the limitation of the platform. The response options are not rendered in complete, as in some are hidden in a scrolling element of the page. This leads to respondents have to scroll left and right to see the options and answers. I find this is a detriment to the respondents to do more work in answering the question so I decided to use 5 point scale to make sure everything is rendered better like shown in Figure 5.16.

Another limitation of the study is the way the study compare the experience of doing the scenarios in the questionnaire between using web browser and using command line. When measuring the usability of HemeWeb, respondents are asked to do the task

in the web browser, compared to the task in command line where it is just described in an overview. This decision is made because we cannot make sure the respondents have the necessary tools to run or reproduce a simulation in their computers. In addition, in order to run the scenario in command line interface, respondents have to install tools on their computer which are timely and prone to errors. I believe this will affect their sentiment in answering the survey questionnaire and decided against it.

5.3.2 Performance evaluation

On running the HemeLB simulation on the three systems compared, we cannot fully isolate the infrastructure from various system loads the infrastructure is handling. The performance might be affected by other jobs running in the system, which is apparent in the case of ARCHER supercomputer where many jobs are executing at the same moment. The same case with INDY2. The performance benchmark might be not as accurate as a completely isolated environment, however, it paints a pretty good picture of performance you get when using cloud vendors compared to the dedicated infrastructure.

Also, another limitation on the performance evaluation is that we cannot get more than 20 instances of c4.8xlarge instances on AWS. This causes the evaluation for AWS-EC2 cannot be done for the 6 compute nodes to compare it directly with INDY2 and ARCHER. Another limitation is that each infrastructure has different core counts in their compute nodes. ARCHER has 24, INDY2 has 36, and AWS-EC2 has 18. Ideally, we want exact core count so we can make a direct comparison between each infrastructure, but this is not the case. However, it could help in painting the general trend of the scaling capabilities and performance measure based on the compute node count.

Chapter 6

Conclusion

Computational fluid dynamics simulation platforms like HemeLB are inherently complex. Domain experts, whose knowledge in the subject is invaluable, often face difficulties in using the software package. This complexity creates a barrier for them to run a study or even an exploratory use of the software. In addition to that, this barrier is also detrimental towards the replicable and reproducible aspect of the discipline. In this project, I tried to solve this problem by providing an alternative interface for HemeLB.

With HemeWeb, I provide another example to the likes of Nekkcloud and Galaxy projects on how a web application can be used as an alternative interface to complex application. In addition, this web application coupled with Docker enables it to provide a reproducible research platform for complex applications which is valuable to science in general. I believe using web application and cloud platform is the trend forward for complex applications like HemeLB. For example, at 10th August 2016, The VMTK Lab team announced that they will release a "Computational Fluid Dynamic on the Cloud" tools for their cardiovascular modeling application, VMTKLab, at 20th September 2016. The tools they add to the application allow users to run on-demand simulation using cloud infrastructure[33]. This is in line with what this project is about and shows that there is a company solving similar demands of on-demand computational platform beyond the academia sector.

In this project, I designed and implemented HemeWeb, a web-based interface to interact with the HemeLB simulation workflow. It is developed to answer the problems above. Originally, users are required to use command line interface, but HemeWeb allows them to use a web browser to configure and run HemeLB simulation.

In developing HemeWeb, I managed to produce three software outputs. These are

HemeLB core Docker container, HemeWeb deployment scripts, and HemeWeb web application. All of these components are developed openly and are publicly available on the public repository of this project¹. In addition, HemeLB core Docker container is also published on the Docker hub. All of these enables an interested party to get their hands on the project to experiment or work with it.

The deployment scripts can configure HemeLB ready infrastructure on three cloud vendors. They are Digital Ocean, Amazon Web Service, and Google Cloud Platform. With it, users can configure cloud platform's instances to handle multi-host HemeLB simulation via command line interface. However, currently, the HemeWeb web application can only be deployed with Amazon Web Service. This is caused by an abstraction layer that currently only supports Amazon Web Service for a certain feature like simulation files persistence.

The HemeWeb web application itself allows domain experts to use the familiar interface of clicking on a web form to configure and run HemeLB simulation. Users can provide pre-processed input files or even unprocessed input files to the web app, and it will allow users to configure the job and run it within few clicks. In addition to that, HemeWeb also allows users to use past simulation information, both owned locally or remotely, to create a new simulation. This capability allows users to either replicate or reproduce a simulation.

From the survey, we found that the respondents are considerably satisfied with the system. HemeWeb allows the respondents to run a simulation and reproduce a simulation with the exception of two respondents which skip the scenarios. In doing both of these tasks, the respondents are considerably satisfied with the ease of doing it, the time it takes, and the support HemeWeb give them. In addition, some of the respondents find using command line interface is a barrier, so this provides a nice alternatives for them to run a HemeLB simulation. In Chapter 7, I will outline potential improvements for HemeWeb that includes feedback from this survey.

Performance wise, HemeWeb perform respectably, especially in lower core count, when compared against dedicated infrastructure for HPC application like INDY2 and ARCHER supercomputer. AWS-EC2 even perform slightly better than INDY2 machine at one instance during our evaluation. However, AWS-EC2 do not scale as well as the dedicated HPC infrastructure.

Next, we calculated the notional cost of running a simulation job on AWS-EC2 and ARCHER with two different pricing. Running HemeLB simulation on AWS-EC2

¹<https://github.com/SeiryuZ/HemeWeb>

is 230-290% more expensive when compared to ARCHER without partner pricing, and 682-846% more expensive with partner pricing. The cost of simulation grows with regards to the increase of compute nodes used for the simulation.

Based on the performance analysis done on Chapter 5, we identified the ideal use-case that benefits from a cloud-enabled solution. This ideal type of job is a one-off job that is usually an exploratory type of simulation. Being a one-off job, means that users do not need constant compute units. This use-case benefits from the flexibility that cloud platform like Amazon provide compared to going through a grant application to gain access to institutional or regional HPC infrastructure.

With regards to costs, while it is currently more expensive, companies have known to cut prices of their services in the pasts[15, 16, 17], making it potentially more cheaper to use their service in the near future. This makes HemeWeb an attractive alternative interface to run HemeLB simulation for scientists, especially those who does not have access to dedicated HPC infrastructures.

Chapter 7

Future Work

To better support HemeLB simulation workflow, HemeWeb can be further improved. I suggest the following areas to be further developed in the future:

1. Handle geometry generation step of HemeLB simulation workflow

There are some steps which are not included in this project due to time constraints. One of them is the profile generation step. In this step, the domain experts should generate a profile file by pointing out how the simulation will run. They need to point where the blood will flow into the 3D model of the vascular system, where it will flow out, the blood viscosity, and other various parameters that will affect the simulation result. This process will most likely require a graphical user interface for the domain experts to interact with.

2. Viewing simulation result on the browser.

HemeLB simulation outputs are in a format that is viewable by a third party tool, ParaView. It will be ideal if HemeWeb can be one stop solution for HemeLB simulation that domain experts do not have to bother with all other tools to view the output of it. This is in line with the feedback that respondents leave with regards to HemeWeb (See Appendix D, Figure D.4). A ParaView integration can be done in the next step of the development so that simulation result can be directly viewed on the browser so users do not have to bother with an extra tool to configure and install.

3. HemeLB simulation security

As outlined in the implementation challenge of the project, security was not the main focus of this project. However, if this project is to be an essential part of

the future medical decision, security will need to be addressed seriously. After all, the patient's private health information will be used for the simulation. A system using such highly private information should be better secured.

Also, in line with the simulation security. HemeWeb instance should be better protected. Currently, HemeWeb does not have protected user area. Individuals without correct credentials can just run the simulation by entering the address of the application on their browser. This is not ideal because this simulation costs money. It should be better protected by having appropriate security measures against unauthorized access.

4. HemeWeb notification

Currently, users are asked to wait until simulation is done to get the output. The user had to keep the page open or checking back in an interval to see whether it is finished. It would be a better experience for users to be notified when a simulation is finished. The user can leave the web application and get back to it when notification is sent.

5. Better interface to configure HemeLB parameters.

Echoing the suggestions that are collected during the evaluation of HemeWeb, there should be a better interface to configure HemeLB parameters. Currently, HemeWeb provides an online XML editor for users to update the HemeLB parameter directly. However, this process is prone to error and might not be the best interface for new users to configure HemeLB simulation. A better solution can be in the form of an automatic web form building from the XML file which some respondents of the usability survey suggests (See Appendix D, Figure D.4). With it, users can use the easier web form to select and specify the parameters for HemeLB simulation. This is currently not done because the active development cycle of HemeLB means that the format of XML is also actively developed and could create complications in the building in the form if the format is changed.

6. Cloud vendor abstraction on web application

One challenge of the project was the difference between cloud vendors. Due to the time constraint, the developed web application is tied down to amazon web services only. It would be ideal if HemeWeb could work on any cloud vendors with minimal changes. This is going to be more of a reconciling the difference

between cloud vendors and make an abstraction layer that HemeWeb will need to call whenever it needs to interact with the cloud vendors' feature.

The project did achieve cloud vendor abstraction for the deployment scripts. The infrastructure can be deployed to three different cloud vendors easily. They are google cloud platform, amazon web service, and digital ocean. However, the web application needs more work to achieve the similar feat. Infrastructure can be deployed on these infrastructures, but HemeWeb still cannot work on those infrastructure.

To further improve the deployment, the abstraction layer should be able to handle deployment on dedicated HPC clusters. This will improve the flexibility of deployment even further that HemeWeb can be run not only on various cloud platforms, but also dedicated infrastructure that an institution built.

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Appendix A

Appendix: Dockerfile

A.1 Cloud vendor specific provisioning scripts

Listing A.1: Stripped down version of the Dockerfile

```
1 # Taken from Miguels docker file for the docker-hemelb
   vnc
2 # https://github.com/mobernabeu/docker-hemelb/blob/master
   /Dockerfile
3
4
5
6 # Use phusion/baseimage as base image. See
7 # http://phusion.github.io/baseimage-docker/
8 FROM phusion/baseimage:0.9.18
9
10 # Use baseimage-docker's init system.
11 CMD ["/sbin/my_init"]
12
13 # ...put your own build instructions here...
14
15
16
17
18 ##
```

```
19 # Dependencies
20 ##
21 # Ubuntu's VMTK package is in the Multiverse repository ,
    OpenMPI in Universe
22 RUN apt-get update && \
23     apt-get install -y software-properties-common && \
24     add-apt-repository "deb http://us.archive.ubuntu.com/
        ubuntu/ trusty universe" && \
25     apt-get update
26
27 # CppUnit fails to compile if downloaded by HemeLB's
    CMake, install it system-wide
28 RUN apt-get install -y \
29     git \
30     cmake \
31     libcppunit-dev \
32     build-essential \
33     libopenmpi-dev \
34     libctemplate-dev \
35     openmpi-bin
36
37 ##
38 # Download and install HemeLB
39 ##
40 WORKDIR /tmp
41 RUN git clone https://github.com/UCL/hemelb.git
42 RUN mkdir hemelb/build && \
43     cd hemelb/build && \
44     cmake .. -DHEMELB_STEERING_LIB=none -DHEMELB_USE_SSE3
        =ON && \
45     make
46
47 VOLUME /data
48
49
```

```
50 # Enable SSH
51 RUN rm -f /etc/service/sshd/down
52
53 # Regenerate SSH host keys. baseimage-docker does not
    contain any, so you
54 # have to do that yourself. You may also comment out this
    instruction; the
55 # init system will auto-generate one during boot.
56 RUN /etc/my_init.d/00_regen_ssh_host_keys.sh
57
58 # TODO: Change this to real ssh keys distribution stuff
59 # Enable insecure key
60 RUN /usr/sbin/enable_insecure_key
61
62 COPY container_key /root/.ssh/id_rsa
63 COPY ssh_config /root/.ssh/config
64
65 RUN chmod 400 /root/.ssh/id_rsa
66
67 # Set root password
68 RUN echo "root:Docke!" | chpasswd
69
70 # Clean up packages, except libctemplate-dev and openmpi-
    bin
71 RUN apt-get purge -y \
72     git \
73     build-essential \
74     cmake \
75     libcppunit-dev
76
77 # Clean up APT when done.
78 RUN apt-get clean && rm -rf /var/lib/apt/lists/* /tmp/* /
    var/tmp/*
```

Appendix B

Appendix: Deployment Script

B.1 Cloud vendor specific provisioning scripts

Listing B.1: Amazon web service specific provisioning script

```
1
2 - hosts: localhost
3   connection: local
4   gather_facts: false
5   vars:
6     - region: eu-west-1
7     - master_node_count: 1
8     - worker_node_count: 0
9     - master_instance_type: m3.large
10    - worker_instance_type: c4.xlarge
11
12   tasks:
13
14     - name: Create ssh security group
15       ec2_group:
16         name: ssh
17         description: HemeWeb - Security group that allow
18                     SSH from public IP
19         region: "{{_region_}}"
20         rules:
```

```
20         - proto: tcp
21           from_port: 22
22           to_port: 22
23           cidr_ip: 0.0.0.0/0
24
25     - name: Create web security group
26       ec2_group:
27         name: web
28         description: HemeWeb - Security group that allow
29                     web traffic
30         region: "{{_region_}}"
31         rules:
32           - proto: tcp
33             from_port: 80
34             to_port: 80
35             cidr_ip: 0.0.0.0/0
36
37     - name: Provision master node
38       ec2:
39         region: "{{_region_}}"
40         image: ami-f95ef58a
41         instance_type: "{{_master_instance_type_}}"
42         key_name: hemeweb
43         groups:
44           - default
45           - ssh
46           - web
47         wait: true
48         count_tag:
49           name: master
50         exact_count: "{{_master_node_count_}}"
51         instance_tags:
52           name: master
53
54     - name: Provision worker nodes
```

```

54     ec2:
55         region: "{{_region_}}"
56         image: ami-f95ef58a
57         instance_type: "{{_worker_instance_type_}}"
58         key_name: hemeweb
59         groups:
60             - default
61             - ssh
62         wait: true
63         count_tag:
64             name: worker
65         exact_count: "{{_worker_node_count_}}"
66         instance_tags:
67             name: worker

```

Listing B.2: Digital ocean specific provisioning script

```

1
2 - hosts: localhost
3     connection: local
4     gather_facts: false
5     vars:
6         - image_slug: ubuntu-14-04-x64
7         - droplet_size: 8gb
8         - region_id: lon1
9         - ssh_key_id: 1732394 # Enter your ssh key id from
                                digital ocean API
10
11
12     tasks:
13
14         - name: Provision master node
15           digital_ocean:
16             id: 9999
17             name: master
18             unique_name: true

```

```
19     state: present
20     command: droplet
21     size_id: "{{_droplet_size_}}"
22     region_id: "{{_region_id_}}"
23     image_id: "{{_image_slug_}}"
24     private_networking: yes
25     wait: false
26     ssh_key_ids: "{{_ssh_key_id_}}"
27
28
29 # TODO: Loop these
30 - name: Provision worker nodes
31   digital_ocean:
32     id: 1
33     name: worker1
34     unique_name: true
35     state: present
36     command: droplet
37     region_id: "{{_region_id_}}"
38     size_id: "{{_droplet_size_}}"
39     image_id: "{{_image_slug_}}"
40     private_networking: yes
41     wait: false
42     ssh_key_ids: "{{_ssh_key_id_}}"
43
44 - name: Provision worker nodes
45   digital_ocean:
46     id: 2
47     name: worker2
48     unique_name: true
49     state: present
50     command: droplet
51     region_id: "{{_region_id_}}"
52     size_id: "{{_droplet_size_}}"
53     image_id: "{{_image_slug_}}"
```

```

54     private_networking: yes
55     wait: false
56     ssh_key_ids: "{{_ssh_key_id_}}"

```

Listing B.3: Google cloud platform specific provisioning script

```

1
2 - hosts: localhost
3     connection: local
4     gather_facts: false
5     vars:
6         - hemeweb_project_id: 127280593056
7         - image: "ubuntu-1404-trusty-v20160610" # https://
            console.cloud.google.com/compute/images?_ga
            =1.221098584.1390118076.1465823354&project=hemeweb&
            filter=name:ubuntu*
8         - region: "europe-west1-b"
9         - master_node_count: 1
10        - worker_node_count: 2
11        # https://cloud.google.com/compute/docs/machine-types
            #standard_machine_types
12        - master_instance_type: n1-standard-1
13        - worker_instance_type: n1-standard-1
14
15    tasks:
16
17
18    - name: Provision master node
19      gce:
20        image: "{{_image_}}"
21        machine_type: "{{_master_instance_type_}}"
22        instance_names: master
23        project_id: "{{_hemeweb_project_id_}}"
24        state: active
25        tags: master , http
26        zone: "{{_region_}}"

```



```

27
28   - name: Provision worker nodes
29     gce:
30       image: "hemeweb-worker-node"
31       machine_type: "{{_worker_instance_type_}}"
32       instance_names: worker1
33       project_id: "{{_hemeweb_project_id_}}"
34       state: active
35       tags: workers
36       zone: "{{_region_}}"

```

B.2 Cloud vendor specific deployment scripts

Listing B.4: Amazon web service specific deployment script

```

1 ---
2
3 - include: ../deploy.yml
4   vars:
5     master_hosts_group: "tag_name_master"
6     worker_hosts_group: "tag_name_worker"
7     preferred_network_interface: "eth0"
8     preferred_ansible_interface: "ansible_default_ipv4"

```

Listing B.5: Digital ocean specific deployment script

```

1 ---
2
3 - include: ../deploy.yml
4   vars:
5     master_hosts_group: "master"
6     worker_hosts_group: "workers"
7     preferred_network_interface: "eth1"
8     preferred_ansible_interface: "ansible_default_ipv4"

```

Listing B.6: Google cloud platform specific deployment script

```

1 ---

```

```

2
3 - include: ../deploy.yml
4   vars:
5     master_hosts_group: "tag_master"
6     worker_hosts_group: "tag_workers"
7     preferred_network_interface: "eth0"
8     preferred_ansible_interface: "ansible_default_ipv4"

```

B.3 Common deployment script

Listing B.7: deploy.yml

```

1 ---
2 # Configure all nodes
3 - hosts: all
4   become: true # allow privilege escalation
5   roles:
6     - common
7
8
9 # Specific to master node
10 - hosts: "{{_master_hosts_group_}}"
11   become: true
12   roles:
13     - nginx
14     - redis
15     - postgresql
16     - hemeweb_master
17
18
19 # Specific to worker nodes
20 - hosts: "{{_worker_hosts_group_}}"
21   become: true
22   vars:
23     master_ip: "{{_hostvars[groups[master_hosts_group]
24                               ][0]][_preferred_ansible_interface]['address']_}}"

```

```
24  roles:
25    - hemeweb_worker
```

B.3.1 Common role

Listing B.8: roles/common/tasks/main.yml

```
1  #
2  # Common tasks to be run on the entire architecture
3  # Configuration tasks
4  #
5
6  ---
7
8  - include: ssh.yml
9  - include: apt.yml
10 - include: hosts.yml
11
12 - name: Create shared Folder
13   file: path=/shared state=directory owner={{
        ansible_ssh_user }} group={{ ansible_ssh_user }}
```

B.3.1.1 SSH specific common role

Listing B.9: roles/common/tasks/ssh.yml

```
1  #
2  # Configure SSH config and keys on nodes
3  #
4
5  ---
6
7  - name: Copy hosts private key
8    copy: src=insecure_key dest=~/.ssh/id_rsa force=yes
          mode=0600
9    become: false
10
```

```

11 - name: Copy containers private key
12   copy: src=container_key dest=~/.ssh/container_key force
      =yes mode=0600
13   become: false
14
15 - name: Copy insecure key pub to authorized key
16   become: false
17   authorized_key: user={{ ansible_ssh_user }} key={{
      lookup('file', 'insecure_key.pub') }}
18
19 - name: Configure SSH hosts config
20   become: false
21   template: src=ssh_config.j2 dest=~/.ssh/config force=
      yes

```

B.3.1.2 Package manager specific common role

Listing B.10: roles/common/tasks/apt.yml

```

1 #####
2 # Configure APT, install packages and upgrade all
   packages
3 #####
4
5 ---
6
7 - name: Configure apt repository
8   apt_repository: repo={{ item.name }} state=present
9   with_items:
10     - name: "deb_http://us.archive.ubuntu.com/ubuntu/_
      trusty_universe"
11     - name: "deb_http://us.archive.ubuntu.com/ubuntu/_
      trusty_multiverse"
12
13 - name: Add docker keyserver to apt
14   command: apt-key adv --keyserver hkp://p80.pool.sks-
      keyservers.net:80 --recv-keys 58118

```

```

E89F3A912897C070ADBF76221572C52609D
15
16 - name: Add docker repository to apt
17   shell: sh -c "echo 'deb https://apt.dockerproject.org/
      repo_ubuntu-$(lsb_release -sc)_main' | cat > /etc/
      apt/sources.list.d/docker.list"
18
19 - name: Update apt cache
20   apt: update_cache=yes
21
22
23 #####
24 # Update kernel and restart if necessary
25 #####
26 - name: Update kernel
27   apt: name=linux-image-generic-lts-vivid
28   register: kernel_install
29
30 - name: Restart all nodes
31   shell: sleep 2 && shutdown -r now "Ansible updates
      triggered"
32   async: 1
33   poll: 0
34   ignore_errors: true
35   when: kernel_install.changed
36
37 - name: Waiting for all nodes to come back
38   local_action: wait_for host={{ inventory_hostname }}
      port=22 state=started delay=5 timeout=300
39   become: false
40   when: kernel_install.changed
41
42
43 #####
44 # Install softwares

```

```

45 #####
46 - name: Install needed software
47   apt: name={{ item.name }} state=latest
48   with_items:
49     - name: python
50     - name: openmpi-bin
51     - name: docker-engine
52     - name: libffi-dev
53
54 - name: Upgrade packages
55   apt: upgrade=yes

```

B.3.1.3 Host specific common role

Listing B.11: roles/common/tasks/hosts.yml

```

1 #####
2 # Update /etc/hosts file
3 # We need separate task for this, because this task
4 # can be run independently of configuration tasks
5 #####
6
7 ---
8 # From https://gist.github.com/rothgar/8793800
9 - name: Update /etc/hosts file
10   template: src=hosts.j2 dest=/etc/hosts

```

Listing B.12: roles/common/templates/hosts.j2

```

1 # {{ ansible_managed }}
2 127.0.0.1    localhost localhost.localdomain localhost4
3             localhost4.localdomain4
4
5 ::1         localhost localhost.localdomain localhost6
6             localhost6.localdomain6
7
8
9
10 {{ hostvars[groups[ master_hosts_group ]][0]][
11     preferred_ansible_interface ][ 'address' ] }} master

```

```

7
8
9 {% if worker_hosts_group in groups %}
10     {% for host in groups[ worker_hosts_group ] %}
11         {{ hostvars[host][ preferred_ansible_interface ][ '
            address ' ] }} hemelb-node-{{ loop.index }}
12     {% endfor %}
13 {% endif %}

```

B.3.2 Redis role

Listing B.13: roles/redis/tasks/main.yml

```

1 #
2 # Configuration specific for Redis
3 #
4
5 ---
6
7 - name: Add redis ppa
8   apt_repository: repo='ppa:chris-lea/redis-server'
9
10 - name: Update apt cache
11   apt: update_cache=yes
12
13 - name: Install redis-server
14   apt: name=redis-server state=latest
15   register: install_result
16
17 - name: Restart redis
18   service: name=redis-server state=restarted
19   when: install_result.changed

```

B.3.3 Nginx role

Listing B.14: roles/nginx/tasks/main.yml

```

1 #

```

```

2  # Configuration specific for Nginx
3  #
4
5  ---
6
7  - name: Add nginx ppa
8    apt_repository: repo='ppa:nginx/stable'
9
10 - name: Update apt cache
11   apt: update_cache=yes
12
13 - name: Install nginx
14   apt: name=nginx state=latest
15   register: install_result
16
17 - name: Configure nginx
18   template: src=nginx.j2 dest=/etc/nginx/nginx.conf force
              =True
19   register: nginx_configuration
20
21 - name: Configure reverse proxy for HemeWeb
22   template: src=default.j2 dest=/etc/nginx/sites-
              available/default force=True
23   register: sites_available
24
25 - name: Restart nginx
26   service: name=nginx state=restarted
27   when: install_result.changed or nginx_configuration.
         changed or sites_available.changed

```

Listing B.15: roles/nginx/templates/default.j2

```

1  server {
2      listen 80;
3      server_name default_server ;
4

```



```
5      root /var/www/hemeweb/src ;
6
7      location / {
8          try_files $uri @proxy_to_app;
9      }
10
11     location /shared {
12         root /;
13
14         try_files $uri @proxy_to_app;
15     }
16
17     location @proxy_to_app {
18         proxy_set_header X-Forwarded-For
19             $proxy_add_x_forwarded_for;
20         proxy_set_header Host $http_host;
21         proxy_redirect off;
22         proxy_pass http://127.0.0.1:8000;
23     }
24 }
```

Listing B.16: roles/nginx/templates/nginx.j2

```
1 user www-data;
2 worker_processes auto;
3 pid /run/nginx.pid;
4
5 events {
6     worker_connections 768;
7     # multi_accept on;
8 }
9
10 http {
11
12     ##
13     # Basic Settings
14     ##
```

```
15
16     sendfile on;
17     tcp_nopush on;
18     tcp_nodelay on;
19     keepalive_timeout 65;
20     types_hash_max_size 2048;
21     # server_tokens off;
22
23 client_body_timeout 6000s;
24 client_max_body_size 5G;
25
26     # server_names_hash_bucket_size 64;
27     # server_name_in_redirect off;
28
29     include /etc/nginx/mime.types;
30     default_type application/octet-stream;
31
32     ##
33     # SSL Settings
34     ##
35
36     ssl_protocols TLSv1 TLSv1.1 TLSv1.2; # Dropping
37     SSLv3, ref: POODLE
38
39     ssl_prefer_server_ciphers on;
40
41     ##
42     # Logging Settings
43     ##
44
45     log_format upstreamlog '[ $time_local ] $remote_addr -
46     $remote_user - $server_name to: $upstream_addr:
47     $request upstream_response_time
48     $upstream_response_time msec $msec request_time
49     $request_time ';
```

```
45     access_log /var/log/nginx/access.log upstreamlog;
46     error_log /var/log/nginx/error.log;
47
48     ##
49     # Gzip Settings
50     ##
51
52     gzip on;
53     gzip_disable "msie6";
54
55     # gzip_vary on;
56     # gzip_proxied any;
57     # gzip_comp_level 6;
58     # gzip_buffers 16 8k;
59     # gzip_http_version 1.1;
60     # gzip_types text/plain text/css application/json
        application/javascript text/xml application/
        xml application/xml+rss text/javascript;
61
62     ##
63     # Virtual Host Configs
64     ##
65
66     include /etc/nginx/conf.d/*.conf;
67     include /etc/nginx/sites-enabled/*;
68 }
69
70
71 #mail {
72 #     # See sample authentication script at:
73 #     # http://wiki.nginx.org/
        ImapAuthenticateWithApachePhpScript
74 #
75 #     # auth_http localhost/auth.php;
76 #     # pop3_capabilities "TOP" "USER";
```

```

77 #         # imap_capabilities "IMAP4rev1" "UIDPLUS";
78 #
79 #         server {
80 #             listen      localhost:110;
81 #             protocol    pop3;
82 #             proxy        on;
83 #         }
84 #
85 #         server {
86 #             listen      localhost:143;
87 #             protocol    imap;
88 #             proxy        on;
89 #         }
90 #}

```

B.3.4 Postgresql role

Listing B.17: roles/postgresql/tasks/main.yml

```

1 #
2 # Configuration specific for PostgreSQL
3 #
4
5 ---
6
7 - name: Install postgresql
8   apt: name={{ item.name }} state=latest
9   with_items:
10     - name: postgresql
11     - name: postgresql-contrib
12     - name: postgresql-server-dev-all
13   register: install_result
14
15 - name: Allow postgresql to trust 127.0.0.1
16   template: src=pg_hba.j2 dest=/etc/postgresql/9.3/main/pg_hba.conf force=True

```

```

17   register: config_update
18
19 - name: Restart postgresql
20   service: name=postgresql state=restarted
21   when: install_result.changed or config_update.changed
22
23 # This is ugly because becoming an unprivileged user '
    postgres' is problematic
24 # http://docs.ansible.com/ansible/become.html
25 - name: Create superuser
26   command: sudo -u postgres createuser --superuser {{
        ansible_ssh_user }}
27   ignore_errors: true
28
29 - name: Create database
30   become: false
31   command: createdb hemeweb
32   ignore_errors: true

```

Listing B.18: roles/postgresql/templates/pg_hba.j2

```

1 # PostgreSQL Client Authentication Configuration File
2 # =====
3 #
4 # Refer to the "Client Authentication" section in the
    PostgreSQL
5 # documentation for a complete description of this file.
    A short
6 # synopsis follows.
7 #
8 # This file controls: which hosts are allowed to connect,
    how clients
9 # are authenticated, which PostgreSQL user names they can
    use, which
10 # databases they can access. Records take one of these
    forms:

```

```
11 #
12 # local      DATABASE USER METHOD [OPTIONS]
13 # host       DATABASE USER ADDRESS METHOD [OPTIONS]
14 # hostssl    DATABASE USER ADDRESS METHOD [OPTIONS]
15 # hostnssl   DATABASE USER ADDRESS METHOD [OPTIONS]
16 #
17 # (The uppercase items must be replaced by actual values
18 # .)
19 #
20 # The first field is the connection type: "local" is a
21 # Unix-domain
22 # socket, "host" is either a plain or SSL-encrypted TCP/
23 # IP socket,
24 # "hostssl" is an SSL-encrypted TCP/IP socket, and "
25 # hostnssl" is a
26 # plain TCP/IP socket.
27 #
28 # DATABASE can be "all", "sameuser", "samerole", "
29 # replication", a
30 # database name, or a comma-separated list thereof. The "
31 # all"
32 # keyword does not match "replication". Access to
33 # replication
34 # must be enabled in a separate record (see example below
35 # ).
36 #
37 # USER can be "all", a user name, a group name prefixed
38 # with "+", or a
39 # comma-separated list thereof. In both the DATABASE and
40 # USER fields
41 # you can also write a file name prefixed with "@" to
42 # include names
43 # from a separate file.
44 #
45 # ADDRESS specifies the set of hosts the record matches.
```

```
    It can be a
35 # host name, or it is made up of an IP address and a CIDR
    mask that is
36 # an integer (between 0 and 32 (IPv4) or 128 (IPv6)
    inclusive) that
37 # specifies the number of significant bits in the mask.
    A host name
38 # that starts with a dot (.) matches a suffix of the
    actual host name.
39 # Alternatively, you can write an IP address and netmask
    in separate
40 # columns to specify the set of hosts. Instead of a CIDR
    -address, you
41 # can write "samehost" to match any of the server's own
    IP addresses,
42 # or "samenet" to match any address in any subnet that
    the server is
43 # directly connected to.
44 #
45 # METHOD can be "trust", "reject", "md5", "password", "
    gss", "sspi",
46 # "krb5", "ident", "peer", "pam", "ldap", "radius" or "
    cert". Note that
47 # "password" sends passwords in clear text; "md5" is
    preferred since
48 # it sends encrypted passwords.
49 #
50 # OPTIONS are a set of options for the authentication in
    the format
51 # NAME=VALUE. The available options depend on the
    different
52 # authentication methods — refer to the "Client
    Authentication"
53 # section in the documentation for a list of which
    options are
```

```
54 # available for which authentication methods.
55 #
56 # Database and user names containing spaces, commas,
    quotes and other
57 # special characters must be quoted. Quoting one of the
    keywords
58 # "all", "sameuser", "samerole" or "replication" makes
    the name lose
59 # its special character, and just match a database or
    username with
60 # that name.
61 #
62 # This file is read on server startup and when the
    postmaster receives
63 # a SIGHUP signal. If you edit the file on a running
    system, you have
64 # to SIGHUP the postmaster for the changes to take effect
    . You can
65 # use "pg_ctl reload" to do that.
66
67 # Put your actual configuration here
68 # _____
69 #
70 # If you want to allow non-local connections, you need to
    add more
71 # "host" records. In that case you will also need to
    make PostgreSQL
72 # listen on a non-local interface via the
    listen_addresses
73 # configuration parameter, or via the -i or -h command
    line switches.
74
75
76
77
```



```

78 # DO NOT DISABLE!
79 # If you change this first entry you will need to make
    sure that the
80 # database superuser can access the database using some
    other method.
81 # Noninteractive access to all databases is required
    during automatic
82 # maintenance (custom daily cronjobs, replication, and
    similar tasks).
83 #
84 # Database administrative login by Unix domain socket
85 local    all                postgres
                                peer
86
87 # TYPE  DATABASE      USER      ADDRESS
                                METHOD
88
89 # "local" is for Unix domain socket connections only
90 local    all                all
                                peer
91 # IPv4 local connections:
92 host     all          all          127.0.0.1/32
                                trust
93 # IPv6 local connections:
94 host     all          all          ::1/128
                                md5
95 # Allow replication connections from localhost, by a user
    with the
96 # replication privilege.
97 #local    replication    postgres
                                peer
98 #host     replication    postgres    127.0.0.1/32
                                md5
99 #host     replication    postgres    ::1/128
                                md5

```

Appendix C

Appendix: Survey

HemeWeb survey

Hi there,

My name is Steven and I am currently writing my MSc dissertation titled "HemeWeb: Blood flow simulation on the cloud". Today, I will be conducting a usability testing for the project's evaluation with your help.

In this evaluation, I will ask you to run two scenarios in the simulation workflow. First, You are going to configure and run a simulation. Secondly, you are going to reproduce previous simulation with modification to simulation parameters. Following each scenario, I will ask few questions to measure your experience. At the end, there are final set of questions to measure the overall experience in using the system.

This session should last around 20 minutes and if you have any questions or problems, I can be reached via email at s1561690@sms.ed.ac.uk.

Once again, thank you for helping me with my work.

Steven

* This survey will be closed at 11:59PM Friday, 12th August 2016

*Required

About the tools

HemeWeb is an alternative interface to use a computational fluid dynamic software called HemeLB. Traditionally, to use HemeLB to run a simulation, command line interface is used. HemeWeb tries to make it easier for domain experts to run HemeLB and use it for their study.

In addition to being an alternative interface, HemeWeb also add features that might not fit in HemeLB's scope, one such example is convenience in reproducing past simulation.

Demographic

Some questions to know you better

1. Age? *

.....

2. Gender *

Mark only one oval.

- ☐ Male
☐ Female

3. Career Stage **Mark only one oval.*

- ☐ MSc student
- ☐ PhD student
- ☐ PDRA
- ☐ Lecturer
- ☐ Professor
- ☐ Researcher
- ☐ Professional
- ☐ Other:

4. Career discipline **Mark only one oval.*

- ☐ Informatics / Computer Science
- ☐ Computational Scientists
- ☐ Biologist
- ☐ Clinician
- ☐ Other:

5. Level of familiarity with installing software from source code? **Mark only one oval.*

	1	2	3	4	5	
Not at all familiar	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Extremely familiar

6. Level of familiarity with operating web browser (Safari / Firefox / Chrome / IE / Opera) ? **Mark only one oval.*

	1	2	3	4	5	
Not at all familiar	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Extremely familiar

7. Your level of familiarity with computational fluid dynamic tools like HemeLB ? **Mark only one oval.*

	1	2	3	4	5	
Not at all familiar	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Extremely familiar

Running a blood flow simulation

Scenario

Imagine that you are a computational researcher. You are trying to understand how haemodynamic and structural changes relate in the context of vascular remodelling. HemeLB, a computational fluid dynamic solver, can help you to simulate different scenarios and find interesting correlations.

Coincidentally, computing support have just deployed HemeWeb to the division's computing resource. You open up your browser and access HemeWeb, the web application that allows you to run HemeLB simulation from the web browser.

Instructions

Try to run a blood flow simulation from your browser. If you find it too difficult, you can skip these instructions and go straight to the questions below

Before we start, you need to download these input files first

<https://s3-eu-west-1.amazonaws.com/hemeweb-evaluation/input.xml> (2.5 KB)

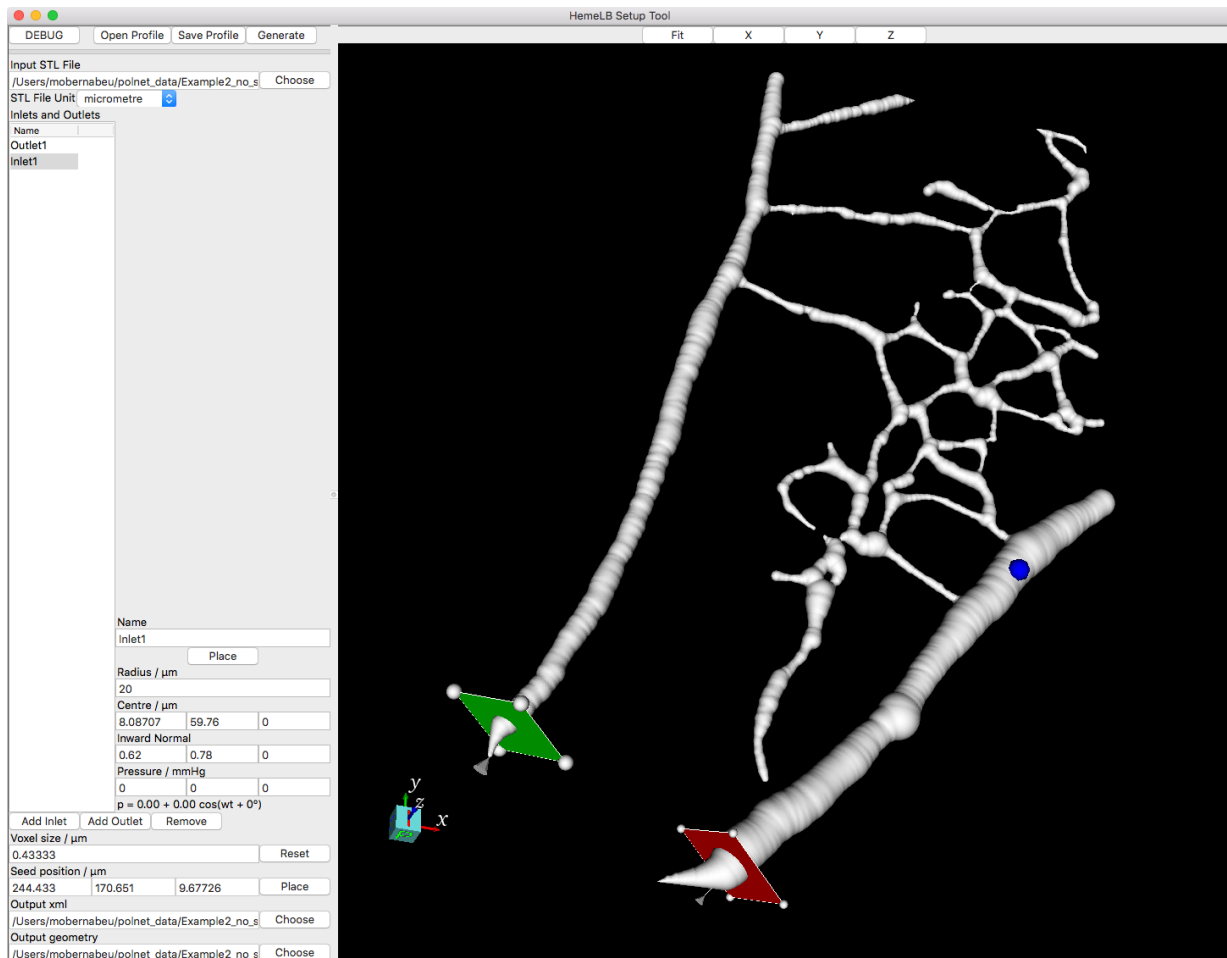
https://s3-eu-west-1.amazonaws.com/hemeweb-evaluation/990_Example2-skeleton_corrected_tubed_smoothed.gmy (43 MB)

or if the links above does not work, here's an alternative link

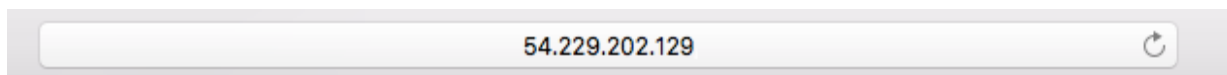
<https://drive.google.com/open?id=0B9-H3nR0aNncR3NgZnQ5ck5mQUU> (2.5 KB)

<https://drive.google.com/open?id=0B9-H3nR0aNncTkM1SFhfUE9BRIE> (43 MB)

These input files were generated with the HemeLB Setup Tool based on a confocal microscopy image of a mouse retinal vascular plexus. The HemeLB Setup Tool can be run standalone on commodity hardware and provides a graphical interface for HemeLB simulation definition. See image below.



1. To start, open up your browser and access <http://54.229.202.129>



2. This is HemeWeb homepage, click on "Add new job" button

HemeWeb: HemeLB in the cloud

Welcome to HemeWeb homepage! HemeWeb aim to allow users to run blood flow simulation using HemeLB from web browser. To create a new simulation job, please press the Add new job button. To view past simulation's overview please click on one of the Job IDs below.

[+ Add new job](#)

HemeWeb Job Index		
Job ID	Submission time	Status

3. Use the input file downloaded above to create a new job from preprocessed inputs

HemeWeb: HemeLB in the cloud

There are several ways of setting up a HemeLB flow simulation. Choose whether to create a new job from scratch or reuse an existing configuration

Create new job from unprocessed inputs

STL geometry file (.stl):

no file selected

Profile file (.pr2):

no file selected

Use this form for unprocessed input files. HemeWeb will run a pre-processing script and allow you to configure the simulation after it is done.

Create new job from preprocessed inputs

HemeLB config file (.xml):

no file selected

GMV geometry file (.gmv):

no file selected

Use this form if your input files have been pre-processed. HemeWeb will read from the pre-processed files and allow you to configure the simulation.

Use previous HemeWeb job by ID


Job ID (xxxxxxxx-xxx-xxx-xxxxxx):

Create a new job from past HemeWeb's job configuration. Specify the ID of the job, and HemeWeb will take care of copying all configurations and inputs from that simulation

Use previous HemeWeb job by URL

Job url (https://zzz/yyyy/xx.tar.gz):

Create a new job from past HemeWeb's job configuration. Specify the URL of the job, and HemeWeb will take care of copying all configurations and inputs from that simulation



4. You will be redirected to HemeLB configuration page (Which is read from the .xml file you uploaded). You can change the configuration here before submitting a job, but we will not make any changes now

Job 234533e3-fa63-40fb-94cf-23eb5352a3b1

HemeLB ConfigJob configOverview

Configure HemeLB execution

The panel below contains content from the HemeLB configuration file you provided. You can modify the content of the file and save it back before proceeding to the next step.

```
36 <visualisation>
37 <centre units="m" value="(0.0,0.0,0.0)" />
38 <orientation>
39 <longitude units="deg" value="45.0" />
40 <latitude units="deg" value="45.0" />
41 </orientation>
42 <display brightness="0.03" zoom="1.0" />
43 <range>
44 <maxvelocity units="m/s" value="0.1" />
45 <maxstress units="Pa" value="0.1" />
46 </range>
47 </visualisation>
48 <initialconditions>
49 <pressure>
50 <uniform units="mmHg" value="0.0" />
51 </pressure>
52 </initialconditions>
53 <monitoring>
54 <incompressibility />
55 <steady_flow_convergence terminate="false" tolerance="1e-5">
56 < criterion type="velocity" units="m/s" value="0.001" />
57 </steady_flow_convergence>
58 </monitoring>
59 <properties>
60 <propertyoutput file="surface-pressure.xtr" period="5000">
61 < geometry type="surface" />
62 < field type="pressure" />
63 </propertyoutput>
64 </properties>
65 </hemeLBsettings>
66
```

Save (Ctrl+S)

Next step >

5. In the Job config page, configure the job execution with the parameters specified below (Number of Machine: 5, Type of Machine: 4 Core, HemeLB container Version: 0.0.3) and click save.

Job 234533e3-fa63-40fb-94cf-23eb5352a3b1

HemeLB ConfigJob configOverview

Configure HemeWeb job execution

Here, you can configure how the simulation will run. Configure the type of compute node and how many of it HemeWeb should start for the simulation. Also, specify the HemeLB container version to use.

How many machine:

5

Machine type:

4 Cores

HemeLB container Version:

seiryuz/hemeLB-core:0.0.3

Save

6. In the overview page, make sure that the parameters are correctly set

Job 234533e3-fa63-40fb-94cf-23eb5352a3b1

[HemeLB Config](#) [Job config](#) [Overview](#)

Job Overview We're almost done

HemeLB config
GMY geometry file(gmy): /shared/234533e3fa6340fb94cf23eb5352a3b1/inputs/990_Example2-skeleton_corrected_tubed_smoothed.gmy (43.1MiB)
HemeLB configuration file(xml): /shared/234533e3fa6340fb94cf23eb5352a3b1/inputs/input.xml

```
1 <hemeLBsettings version="3">
2   <simulation>
3     <step_length units="s" value="9.62e-10" />
4     <steps units="lattice" value="5000" />
```

7. Click on "All good! queue job" If all parameters are set correctly. Your job are queued and will run when the workers are ready. (In the job execution page, there might be low level errors on stdout output that can be safely ignored)

Job config
Machine type: 4 Cores
How many machine: 5
HemeLB version: seiryuz/hemeLB-core:0.0.3

All good! Queue job

(Optional) If you are willing to wait, the job will run and finish in around 45 minutes if there are no other jobs queued. A finished job will show a link to download output file. This file is a compressed folder of output directory that contains a .VTK file viewable with ParaView. In addition, a simulation file URL is also shown for sharing simulation files with other HemeWeb installation

Job status: Done

Output file

/shared/ea24198f97f24b2496841920abaf6eb5/result/ea24198f-97f2-4b24-9684-1920abaf6eb5.tar.gz (156.7MiB)

Simulation file URL

https://s3-eu-west-1.amazonaws.com/hemeweb-jobs/ea24198f-97f2-4b24-9684-1920abaf6eb5.tar.gz

Student

Questions

8. Did you skip the above instructions (Step 1 -7)? *

Mark only one oval.

- ☐ Yes
- ☐ No

9. Indicate whether you agree or disagree with the following statements? *

Mark only one oval per row.

	Strongly disagree	Disagree	Neutral	Agree	Strongly agree	Not Applicable
Overall, I am satisfied with the ease of completing the tasks in this scenario	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Overall, I am satisfied with the amount of time it took to complete the tasks in this scenario	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Overall, I am satisfied with the support information (online-line help, messages, documentation) when completing the tasks	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

10. Do you have suggestions to improve the experience in using the web interface to run the simulation? (Optional)

.....

.....

.....

.....

.....

Running a simulation using command line

Alternatively, one can run the above scenario with these high-level steps on command line (you don't have to do this scenario):

1. Install and configure docker tools
2. Download the HemeLB core docker container from hub.docker.com
3. Run docker container in your machine
4. Find out the internal IP of your running container
5. Run HemeLB on the running docker container

11. How likely are you to run a simulation command line interface? *

Mark only one oval.

	1	2	3	4	5	
Extremely unlikely	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Extremely likely

12. Do you think using command line interface to run the simulation is a barrier to run a simulation? *

Mark only one oval.

	1	2	3	4	
Not a barrier	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Extreme Barrier

Reproducing past blood flow simulation

Scenario

You came across a paper that uses HemeLB to study how haemodynamic and structural changes relate in the context of vascular remodelling. In that paper, the authors include a link that can be used to rerun their simulations on their HemeWeb infrastructure. You want to reproduce those simulation with your own infrastructure and tweak the parameters a bit to see how it affects simulation.

Once again, You open up your browser and access your division's internally deployed HemeWeb and try to reproduce the result with some modifications.

Instructions

Try to run previous blood flow simulation that is ran by your peer in their infrastructure. If you find it too difficult, you can skip these instructions and go straight to the questions below

1. Open the browser and go to <http://54.229.202.129>

↻
54.229.202.129

2. Click add new job

HemeWeb: HemeLB in the cloud

Welcome to HemeWeb homepage! HemeWeb aim to allow users to run blood flow simulation using HemeLB from web browser. To create a new simulation job, please press the Add new job button. To view past simulation's overview please click on one of the Job IDs below.

[+ Add new job](#)

HemeWeb Job Index		
Job ID	Submission time	Status

3. Enter your peer's simulation file URL <https://s3-eu-west-1.amazonaws.com/hemeweb-jobs/234533e3-fa63-40fb-94cf-23eb5352a3b1.tar.gz>

HemeWeb: HemeLB in the cloud

There are several ways of setting up a HemeLB flow simulation. Choose whether to create a new job from scratch or reuse an existing configuration

Create new job from unprocessed inputs

STL geometry file (.stl):

[Choose File](#) no file selected

Profile file (.pr2):

[Choose File](#) no file selected

[Submit](#)

Use this form for unprocessed input files. HemeWeb will run a pre-processing script and allow you to configure the simulation after it is done.

Create new job from preprocessed inputs

HemeLB config file (.xml):

[Choose File](#) no file selected

GMV geometry file (.gmv):

[Choose File](#) no file selected

[Submit](#)

Use this form if your input files have been pre-processed. HemeWeb will read from the pre-processed files and allow you to configure the simulation.

Use previous HemeWeb job by ID

Job ID (xxxxxxxx-xxxx-xxxx-xxxx-xxxxxx):

[Submit](#)

Create a new job from past HemeWeb's job configuration. Specify the ID of the job, and HemeWeb will take care of copying all configurations and inputs from that simulation

Use previous HemeWeb job by URL

Job url (https://zzz/yyyy/xx.tar.gz):

[Submit](#)

Create a new job from past HemeWeb's job configuration. Specify the URL of the job, and HemeWeb will take care of copying all configurations and inputs from that simulation

4. You noticed in the past simulation that the inlet pressure is set to 45. You decided to change inlet amplitude from 45 to 30 because you think it will run better. Click save, and then click next step

HemeLB Config Job config Overview

Configure HemeLB execution

The panel below contains content from the HemeLB configuration file you provided. You can modify the content of the file and save it back before proceeding to the next step.

```

1 <hemelbsettings version="3">
2 <simulation>
3 <step_length units="s" value="9.62e-10" />
4 <steps units="lattice" value="5000" />
5 <stresstype value="1" />
6 <voxel_size units="m" value="3.3333e-07" />
7 <origin units="m" value="(-1.56566857229e-07,-3.5224964629e-07,-1.14997991702e-05)" />
8 </simulation>
9 <geometry>
10 <datafile path="990_Example2-skeleton_corrected_tube_smoothed.gmy" />
11 </geometry>
12 <inlets>
13 <inlet>
14 <condition subtype="cosine" type="pressure">
15 <amplitude units="mmHg" value="45.0" />
16 <mean units="mmHg" value="0.0" />
17 <phase units="rad" value="0.0" />
18 <period units="s" value="1" />
19 </condition>
20 <normal units="dimensionless" value="(0.574837835699,0.818267354016,-2.08425869156e-15)" />
21 <position units="m" value="(8.45432716902e-06,6.07165744613e-05,0.0)" />
22 </inlet>
23 </inlets>
24 <outlets>
25 <outlet>
26 <condition subtype="cosine" type="pressure">
27 <amplitude units="mmHg" value="0.0" />
28 <mean units="mmHg" value="0.0" />
29 <phase units="rad" value="0.0" />
30 <period units="s" value="1" />
31 </condition>

```

1. Change to 30

2. Click Save

3. Next step

Save (Ctrl+S) Next step >

5. Change the job configuration with our own configuration. (Machine type: 4 core, How many machine: 5, and use HemeLB container version 0.0.3)

Job 234533e3-fa63-40fb-94cf-23eb5352a3b1

HemeLB Config Job config Overview

Configure HemeWeb job execution

Here, you can configure how the simulation will run. Configure the type of compute node and how many of it HemeWeb should start for the simulation. Also, specify the HemeLB container version to use.

How many machine:

5

Machine type:

4 Cores

HemeLB container Version:

seiryuz/hemelb-core:0.0.3

Save

6. In the overview page, make sure that the parameters are correctly set

HemeLB Config Job config Overview

Job Overview We're almost done

HemeLB config

GMV geometry file(gmy): /shared/c6cb2920e85a4d96974663dfbc2917a1/inputs/990_Example2-skeleton_corrected_tubed_smoothed.gmy (43.1MiB)

HemeLB configuration file(xml): /shared/c6cb2920e85a4d96974663dfbc2917a1/inputs/input.xml

```

1 - <hemeLBsettings version="3">
2 -   <simulation>
3 -     <step_length units="s" value="9.62e-10" />
4 -     <steps units="lattice" value="5000" />
5 -     <stresstype value="1" />
6 -     <voxel_size units="m" value="3.3333e-07" />
7 -     <origin units="m" value="(-1.56566857229e-07,-3.5224964629e-07,-1.14997991702e-05)" />
8 -   </simulation>
9 -   <geometry>
10 -    <datafile path="990_Example2-skeleton_corrected_tubed_smoothed.gmy" />
11 -   </geometry>
12 -   <inlets>
13 -     <inlet>
14 -       <condition subtype="cosine" type="pressure">
15 -         <amplitude units="mmHg" value="30.0" />
16 -         <clear units="mmHg" value="0.0" />
17 -         <phase units="rad" value="0.0" />
18 -         <period units="s" value="1" />
19 -       </condition>
20 -     <normal units="dimensionless" value="(0.574837835699,0.818267354016,-2.08425869156e-15)" />

```

Confirm value has been updated

7. Click on "All good! queue job" If all parameters are set correctly. Your job are queued and will run when the workers are ready. (In the job execution page, there might be low level errors on stdout output that can be safely ignored)

Job config

Instance type: 4 Cores

Instance count: 2

Container Image: seiryuz/hemeLB-core:0.0.3

All good! Queue job

(Optional) If you are willing to wait, the job will run and finish in around 45 minutes if there are no other jobs queued. A finished job will show a link to download output file. This file is a compressed folder of output directory that contains a .VTK file viewable with ParaView. In addition, a simulation file URL is also shown for sharing simulation files with other HemeWeb installation

Job status: Done

Output file

/shared/ea24198f97f24b2496841920abaf6eb5/result/ea24198f-97f2-4b24-9684-1920abaf6eb5.tar.gz (156.7MiB)

Simulation file URL

https://s3-eu-west-1.amazonaws.com/hemeweb-jobs/ea24198f-97f2-4b24-9684-1920abaf6eb5.tar.gz

Student

Questions

13. Do you skip the instructions (Step 1 - 7)? *

Mark only one oval.

- ☐ Yes
- ☐ No

14. Indicate whether you agree or disagree with the following statements? *

Mark only one oval per row.

	Strongly disagree	Disagree	Neutral	Agree	Strongly agree	Not Applicable
Overall, I am satisfied with how easy it is to use this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Overall, I am satisfied with the amount of time it took to complete the tasks in this scenario	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Overall, I am satisfied with the support information (online-line help, messages, documentation) when completing the tasks	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

15. Do you have suggestions to improve the experience in using the web interface to reproduce a simulation? (Optional)

Reproducing past simulation using command line

Alternatively, one can run the above scenario with these high-level steps on command line (you don't have to do this scenario):

1. Install and configure docker tools
2. Find out the input and configuration of past experiments
3. Download the correct HemeLB core docker container from hub.docker.com
3. Run docker containers in your machine
4. Find out the internal IP of your running containers
5. Run HemeLB on the running docker container with the correct input and parameters

16. How likely are you to reproduce simulations in command line interface? *

Mark only one oval.

	1	2	3	4	5	
Extremely unlikely	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Extremely likely

17. Do you think using command line interface to reproduce the simulation is a barrier? *

Mark only one oval.

	1	2	3	4	
Not a barrier	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Extreme Barrier

Overall evaluation

18. Indicate whether you agree or disagree with the following statements ? *

Mark only one oval per row.

	Strongly disagree	Disagree	Neutral	Agree	Strongly Agree	Not Applicable
Overall, I am satisfied with how easy it is to use this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
It was simple to use this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I can effectively complete my work using this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I am able to complete my work quickly using this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I am able to efficiently complete my work using this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I feel comfortable using this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

It was easy to learn to use this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I believe I became productive quickly using this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The system gives error messages that clearly tell me how to fix problems	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Whenever I make a mistake using the system, I recover easily and quickly	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The information (such as online help, on-screen messages, and other documentation) provided with this system is clear	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
It is easy to find the information I needed	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The information (such as online help, on-screen messages, and other documentation) provided for the system is easy to understand	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The information is effective in helping me complete the tasks and scenarios	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The organization of information on the system screens is clear	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
The interface of this system is pleasant	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I like using the interface of this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
This system has all the functions and capabilities I expect it to have	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
Overall, I am satisfied with this system	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

19. List most negative aspect(s) of the system *

.....

.....

.....

.....

.....

20. List most positive aspect(s) of the system *



Appendix D

Appendix: Survey Response

D1	Age?
D2	Gender
D3	Career Stage
D4	Career discipline
D5	Level of familiarity with installing software from source code?
D6	Level of familiarity with operating web browser (Safari / Firefox / Chrome / IE / Opera) ?
D7	Your level of familiarity with computational fluid dynamic tools like HemeLB ?
S1_1	Overall, I am satisfied with the ease of completing the tasks in this scenario
S1_2	Overall, I am satisfied with the amount of time it took to complete the tasks in this scenario
S1_3	Overall, I am satisfied with the support information (online-line help, messages, documentation) when completing the tasks
S1_4	How likely are you to run a simulation command line interface?
S1_5	Do you think using command line interface to run the simulation is a barrier to run a simulation?
S2_1	Overall, I am satisfied with the ease of completing the tasks in this scenario
S2_2	Overall, I am satisfied with the amount of time it took to complete the tasks in this scenario
S2_3	Overall, I am satisfied with the support information (online-line help, messages, documentation) when completing the tasks
S2_4	How likely are you to reproduce simulations in command line interface?
S2_5	Do you think using command line interface to reproduce the simulation is a barrier?
O1	Overall, I am satisfied with how easy it is to use this system
O2	It was simple to use this system
O3	I can effectively complete my work using this system
O4	I am able to complete my work quickly using this system
O5	I am able to efficiently complete my work using this system
O6	I feel comfortable using this system
O7	It was easy to learn to use this system
O8	I believe I became productive quickly using this system
O9	The system gives error messages that clearly tell me how to fix problems
O10	Whenever I make a mistake using the system, I recover easily and quickly
O11	The information (such as online help, on-screen messages, and other documentation) provided with this system is clear
O12	It is easy to find the information I needed
O13	The information (such as online help, on-screen messages, and other documentation) provided for the system is easy to understand
O14	The information is effective in helping me complete the tasks and scenarios
O15	The organization of information on the system screens is clear
O16	The interface of this system is pleasant
O17	I like using the interface of this system
O18	This system has all the functions and capabilities I expect it to have
O19	Overall, I am satisfied with this system

Figure D.1: Survey response Question code

	R1	R2	R3	R4	R5	R7	R9	R10
D1	39	34	23	39	34	26	45	28
D2	Male	Male	Male	Male	Female	Male	Male	Male
D3	Professor	Lecturer	PhD student	Project Manager	PDRA	Professional	Software Architect	PhD student
D4	Computational Sc	Informatics / Com	Informatics / Cc	Computational	physics/Biophy	Clinician	Informatics / Cc	Biologist
D5	5	5	4	4	3	1	5	3
D6	5	4	3	5	5	3	5	5
D7	5	5	3	2	3	1	1	3
S1_1	Neutral	Strongly agree	Agree	Strongly agree	Strongly agree	Neutral	Strongly agree	Strongly agree
S1_2	Neutral	Strongly agree	Strongly agree	Strongly agree	Agree	Agree	Strongly agree	Strongly agree
S1_3	Neutral	Strongly agree	Neutral	Agree	Strongly agree	Strongly agree	Strongly agree	Strongly agree
S1_4	5	5	5	5	3	2	1	4
S1_5	1	3	1	3	2	3	3	1
S2_1	Agree	Agree	Agree	Strongly agree	Strongly agree	Agree	Strongly agree	Agree
S2_2	Neutral	Strongly agree	Strongly agree	Strongly agree	Strongly agree	Strongly agree	Strongly agree	Agree
S2_3	Neutral	Strongly agree	Neutral	Strongly agree	Strongly agree	Strongly agree	Strongly agree	Agree
S2_4	5	4	4	5	2	4	1	4
S2_5	1	3	2	3	1	3	3	1
O1	Agree	Strongly Agree	Agree	Agree	Agree	Strongly Agree	Strongly Agree	Agree
O2	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree
O3	Neutral	Strongly disagree	Agree	Not Applicable	Disagree	Strongly Agree	Not Applicable	Strongly Agree
O4	Neutral	Disagree	Agree	Not Applicable	Neutral	Strongly Agree	Strongly Agree	Strongly Agree
O5	Neutral	Disagree	Agree	Not Applicable	Neutral	Strongly Agree	Strongly Agree	Strongly Agree
O6	Strongly disagree	Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Agree
O7	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree
O8	Not Applicable	Neutral	Strongly Agree	Not Applicable	Not Applicable	Strongly Agree	Strongly Agree	Agree
O9	Neutral	Not Applicable	Agree	Agree	Disagree	Strongly Agree	Not Applicable	Agree
O10	Neutral	Not Applicable	Neutral	Agree	Neutral	Strongly Agree	Not Applicable	Neutral
O11	Neutral	Strongly Agree	Agree	Agree	Neutral	Strongly Agree	Strongly Agree	Agree
O12	Neutral	Strongly Agree	Neutral	Not Applicable	Agree	Strongly Agree	Strongly Agree	Agree
O13	Agree	Strongly Agree	Neutral	Agree	Agree	Strongly Agree	Strongly Agree	Strongly Agree
O14	Neutral	Strongly Agree	Neutral	Agree	Disagree	Strongly Agree	Strongly Agree	Strongly Agree
O15	Agree	Agree	Neutral	Agree	Strongly Agree	Strongly Agree	Agree	Agree
O16	Strongly disagree	Agree	Strongly Agree	Agree	Strongly Agree	Strongly Agree	Strongly Agree	Agree
O17	Disagree	Agree	Strongly Agree	Agree	Agree	Strongly Agree	Strongly Agree	Agree
O18	Strongly disagree	Disagree	Strongly Agree	Not Applicable	Agree	Strongly Agree	Not Applicable	Agree
O19	Neutral	Agree	Strongly Agree	Agree	Agree	Strongly Agree	Strongly Agree	Agree

Figure D.2: Survey response part 1

	R11	R12	R13	R14	R15	R16
D1	26	24	25	26	24	22
D2	Male	Male	Male	Male	Male	Male
D3	MSc student	MSc student	MSc student	MSc student	MSc student	MSc student
D4	Informatics / Cc	Informatics / Cc	Informatics / Cc	Informatics / Co	Informatics / Co	Biologist
D5	5	4	5	3	3	3
D6	5	5	5	4	5	5
D7	2	2	1	1	2	1
S1_1	Agree	Agree	Strongly agree	Strongly agree	Agree	Strongly agree
S1_2	Agree	Agree	Agree	Strongly agree	Strongly agree	Strongly agree
S1_3	Strongly agree	Agree	Strongly agree	Not Applicable	Neutral	Agree
S1_4	4	3	5	2	3	3
S1_5	1	1	2	3	1	4
S2_1	Strongly agree	Strongly agree	Strongly agree	Strongly agree	Neutral	Strongly agree
S2_2	Agree	Strongly agree	Strongly agree	Strongly agree	Neutral	Strongly agree
S2_3	Strongly agree	Strongly agree	Strongly agree	Not Applicable	Neutral	Agree
S2_4	4	3	3	2	2	3
S2_5	1	1	2	3	3	4
O1	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Agree	Agree
O2	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Agree	Strongly Agree
O3	Strongly Agree	Agree	Strongly Agree	Not Applicable	Not Applicable	Agree
O4	Agree	Strongly Agree	Strongly Agree	Strongly Agree	Not Applicable	Agree
O5	Agree	Agree	Strongly Agree	Strongly Agree	Not Applicable	Agree
O6	Strongly Agree	Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree
O7	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Strongly Agree	Neutral
O8	Agree	Agree	Strongly Agree	Strongly Agree	Not Applicable	Neutral
O9	Not Applicable	Not Applicable	Strongly Agree	Agree	Not Applicable	Not Applicable
O10	Not Applicable	Not Applicable	Strongly Agree	Strongly Agree	Not Applicable	Not Applicable
O11	Strongly Agree	Not Applicable	Strongly Agree	Not Applicable	Not Applicable	Neutral
O12	Strongly Agree	Agree	Strongly Agree	Strongly Agree	Not Applicable	Not Applicable
O13	Strongly Agree	Agree	Strongly Agree	Not Applicable	Agree	Neutral
O14	Strongly Agree	Agree	Strongly Agree	Strongly Agree	Not Applicable	Neutral
O15	Agree	Agree	Strongly Agree	Strongly Agree	Agree	Neutral
O16	Agree	Neutral	Strongly Agree	Agree	Agree	Agree
O17	Agree	Neutral	Strongly Agree	Agree	Agree	Agree
O18	Agree	Agree	Strongly Agree	Strongly Agree	Not Applicable	Neutral
O19	Strongly Agree	Agree	Strongly Agree	Strongly Agree	Agree	Agree

Figure D.3: Survey response part 2

List most negative aspect(s) of the system	List most positive aspect(s) of the system
Firefox does not seem to render web interface as intended.	Helps to make simulations reproducible.
It's too inflexible in the configuration stage, with only one code version and only changes possible in the XML or GMY file (e.g., not in inlet files).	It is extremely easy to use, the interface is very well designed, and it enables people to quickly run pressure-based simulations with default code settings. Definitely a major step ahead compared to the command-line solutions for many users.
Not clear how I can now use this to create my own reproducible experiments to give to someone else (which is something that you might want to do).	Good display of information all in one place (e.g the config file and geometry files etc are all displayed).
It would be nice to be able to view the VTK files without having to have a local ParaView install.	Nice separation of stdout/stderr on the output (again avoiding two separate log files as you potentially need on command line).
Not clear where output files end up	Simplicity to use and requires no command line training (for example you didn't even need to know how to untar the files in the second example. This is very useful for non-expert users).
The simulation failed and it did not provide a useful error message nor I could find instructions on how to fix the problem.	Flexible
nothing	It is easy to use and great for researchers who don't have much computational power themselves. A reference to a paper which explains the method and the results and how to interpret them could help.
The need to edit raw XML.	easy to use
potential (but needed) slow-learning curve, requires a detailed troubleshooting documents	No need to install software or run at the command-line which makes it easy for novices.
Cannot find something to say as a negative part.	Online-based, easier to use to low-computational skills scientists, efficient
just neutral interface, overall is good!	How easy it is to use.
The result takes time to out	easy and fast
Maybe should avoid the users to see the code	It is easy to use and the instruction guide is clear enough.
Necessity to edit XML directly on a webpage. I think it would be good to have links like "Help me choose machine type. Help me choose number of machines." in case the user is not sure what to do.	If just download and upload sth then I can receive the result, it will be good
The job overview page may be confusing for someone who's doing it the for first time	In general, HemeWeb is a much more user-friendly interface compared to a command line. It is very easy to re-run simulations.
	The interface and the possibility of easily reproduce someone else's simulation

Figure D.4: Survey response feedback