

# **HemeWeb: Blood flow simulation in the cloud using Docker**

*Steven Steven*



Master of Science  
School of Informatics  
University of Edinburgh  
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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

Software is increasingly complex. Our everyday software is packed with features that make its usage difficult. To people without familiarity with the product, complex usage can be a barrier to use the software even when it can help them tremendously.

This also ties into the complexity of a research that use this software. Open science dictates that research should be reproducible or replicable for it to better validate the research. However, recent findings have shown that not many research in psychology are replicable.

### 1.1 Motivation

To study how blood flow in a given vessel, [1] developed a fluid dynamic simulation software named HemeLB. Currently, it is actively developed and used by researchers to help their study. For example, [2] used HemeLB for automated ensemble simulation of blood flow for a range of exercise intensities, [3] used it for detecting the difference of retinal hemodynamics with regards to diabetic retinopathy, and recently [4, 5] used it to understand branching pattern of blood vessel networks.

As I have written in the proposal for this dissertation [6], HemeLB works by calculating fluid flow in parallel by using lattice-Boltzmann method [1]. This calculation allows HemeLB to simulate blood flow within a given blood vessel structure. Unfortunately, the calculation part 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 the end. These includes of preparing the input so HemeLB can work on it, and also processing the output so it is ready to view.

These long pipelines of steps needed to run the simulation, coupled with the com-

plexity of the configuration of HemeLB created a high barrier of entry for scientists and doctors to use it. Furthermore, as observed previously [6], an interesting simulation will require parallel computing resources like 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 interested parties. More importantly, it shows there are still improvements that can be done to lower the barrier of entry for users to use HemeLB. This is important for HemeLB, especially when it is envisioned to be an integral part of future medical decision [7].

Another aspect that HemeLB workflow can be improved is with regards to its reproducibility aspect. Researches that used HemeLB embrace reproducibility as one of its concern. As observed before [6], 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, 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 [3, 2, 4, 5] that include all these information. This information allow researchers interested to replicate the simulation to do it manually. Automation of these steps could further improve HemeLB's reproducibility and allow peers to replicate, duplicate, and audit its simulation results quickly and easily. This automation will be important, in addition to being usable, for HemeLB to become an integral part of the medical decision in the future.

## 1.2 Objectives

Based on the needs to improve the usability, reproducibility, and auditability aspect of HemeLB project, I will develop a prototype web interface for HemeLB. This prototype web interface will lower barrier of entry in using HemeLB software compared to the current approach of using command line interface. In addition to that, using web interface 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 simulation result. These features are not essential for the HemeLB core, but definitely, help the overall workflow of blood flow simulation.

Using the dynamic capabilities of cloud computing vendor, the web backend should be able to dynamically scale without many efforts. On top of that, these infrastructures

are available to everyone with a cost, allowing its user to access it without having to get access to supercomputers. Its user should be able 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 deployment script so that peer could deploy its own instance of the web interface. This will ease up deployment process for individuals or organizations intending to use HemeLB for its 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 follow:

- **Chapter 2, Background.** I will provide background information that is necessary for readers to understand the concepts, technology, and implementation that are done in this dissertation. HemeLB, containerization technology, cloud computing, High-Performance computing infrastructure, and other topics will be discussed in details in this chapter.
- **Chapter 3, Design and Implementation.** I will discuss the bulk of the work in this chapter. Implementation details and design of the proposed solutions will be provided and discussed in details.
- **Chapter 4, Evaluation.** In this chapter, I will discuss how the success of this project will be measured. I detailed how I conduct an interview and performance benchmark to measure how the proposed solution perform.
- **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 HemeLB simulation workflow.

# Chapter 2

## Background

In this chapter, I will discuss about various background information that are used as a basis for the work presented in this dissertation. I will discuss about how HemeLB currently works, 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 needs to be run in sequence. These steps are done in a variety of interface, from command line to graphical user interface. Additionally, these steps also require various level 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. Also, discussion on computing resources and interface for each steps will be provided.

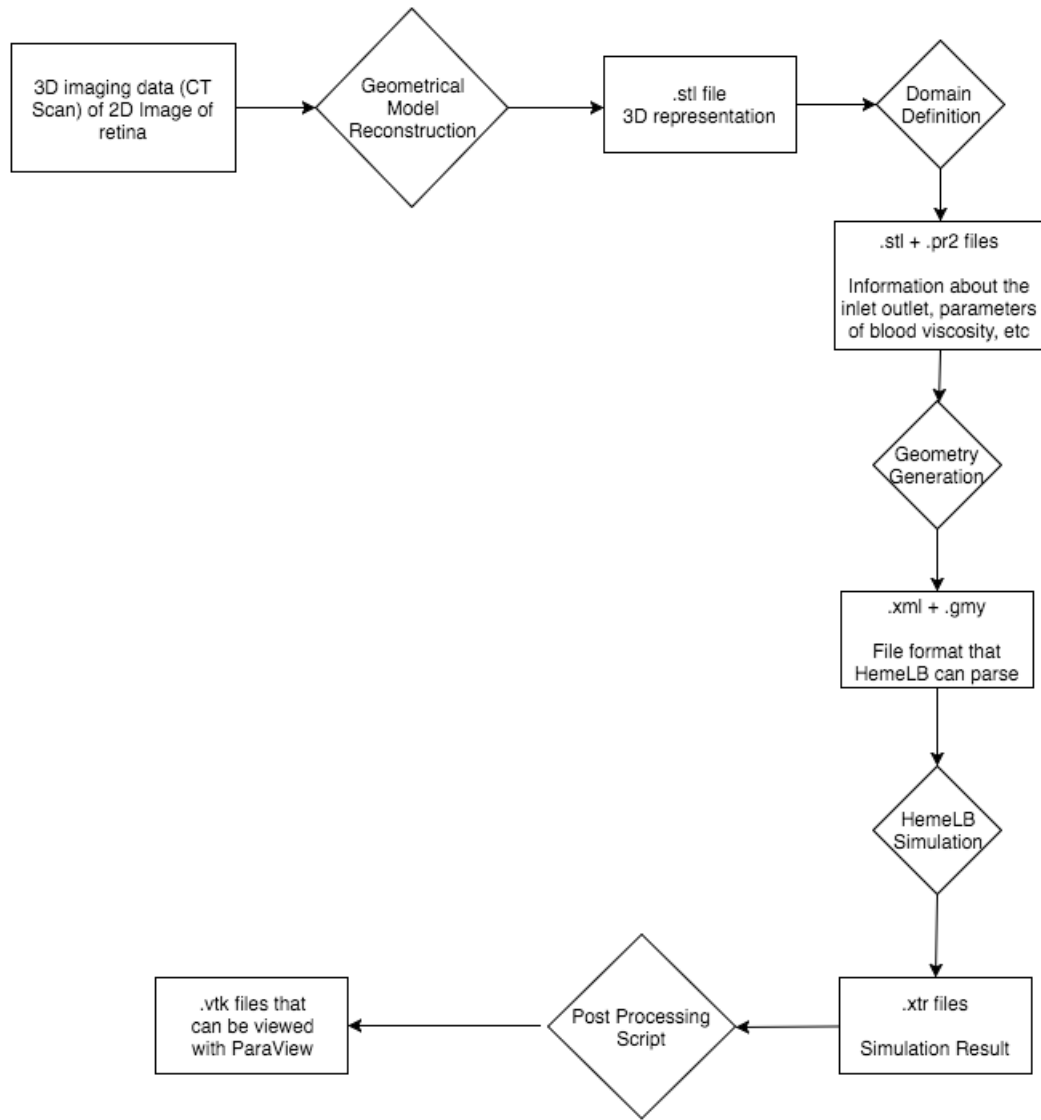


Figure 2.1: Current HemeLB workflow taken from [6]

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

### 1. Geometrical model reconstruction

In this step, a 3D model of vascular system is constructed from the raw microscopy image of it. Alternatively, the 3D model can also be constructed from CT scan with its 3D imaging data. From this step, a 3D geometry file are generated in the form of .stl file. This process can run in a regular workstation just fine. However, it is highly problem dependent as the tools needed to parse and generate the 3D model are dependent to the problem experts try to simulate.

## 2. Domain definition

3D geometry model generated from the previous step is now used as an 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 needs. The setup tool provides a graphical user interface for domain experts to add these parameters. All parameters are then saved in a profile file with .pr2 format. This step can run on standalone commodity hardware and should not require a highly parallel computing resources.

## 3. Geometry generation

This step will take the encoded information from 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 with 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 command line interface to operate with the files. The process is done with piping the input files to a python script which is part of 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 [6], 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 [5, 4]

and [3]. In addition to that, users of HemeLB have to use command line interface to configure, run HemeLB simulation, and interact with the output files.

Output files generated by this step are written in parallel into 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 be interpreted. 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 a .VTU files. These .VTU files are viewable in a separate software called ParaView <sup>1</sup>. With it, domain experts could visualize the result of the simulation in a graphical user interface which ParaView provided. This step can be run on commodity hardware without problems. However, to do this step, users will require to interact with command line interface.

All of these steps requires users to configure and install the tools required for each step by themselves. However, the target audience of HemeLB are biologists, clinician, researchers, and medical professionals, which 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 in providing insight into the problem [9]. Bioinformatics and computational biology are examples of this interdisciplinary discipline.

The problems that these disciplines tries to understand require computational approaches that are not cheap. The smaller size of these problems would probably run on a commodity hardware, more complex one will require highly parallel computing resources. These resources are often found in the form of a supercomputer like

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<sup>1</sup><http://www.paraview.org>

ARCHER supercomputer. HemeLB software package is one of many examples of these computational approach that requires highly parallel computing resources.

To tackle these type of problems that require large computing resources, two paradigms of computation is 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 often placed in one location and connected to 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 the prime example 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 it and it will be given. 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 MPI library to communicate between processes and run 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 HPC application like HemeLB requires access to HPC infrastructure that 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)<sup>2</sup> and Engineering and Physical Science Research Council (EPSRC)<sup>3</sup> operate. They conduct a peer-review of proposals that indicates the need for their infrastructure and give access selectively.

The model of operation of this institute often does not prioritize reproducibility of a

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<sup>2</sup><http://www.prace-project.eu>

<sup>3</sup><https://www.epsrc.ac.uk>



research or an exploratory one. Experts with reproducibility purposes have to compete for the limited amount of available computing hours with other projects. Most likely, 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 discipline often fall 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 by researchers and academics, a concept called grid computing was born in the 1990s [11, 12]. This concept treats computing resources like utility grid. Computing resources should be able to be acquired without users knowing how it was provided to them. This model caters mostly to the interest of researchers and academia that usually give CPU hours based on projects proposal [13]. An example of this is TeraGrid<sup>4</sup> project which ended its operation at 2011 .

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

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 vendor now is massively scalable, allows computing resources abstraction, configurable dynamically, and provisioned on-demand. This has led cloud computing vendors to be more relevant compared to grid computing.

Cloud vendors continue to grow significantly in the recent years. In 2013, it was reported that some cloud vendors reached had more than 90% growth per annum [14].

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<sup>4</sup><https://www.xsede.org/tg-archives>

This growth enables them to keep more incentives for businesses and individuals to buy their services. In few instances [15, 16, 17], cloud vendors have cut their pricing for their service and fueled more demands. Renting computing resources is getting cheaper every year and could make more sense than building your own infrastructure.

On top of that, cloud vendors also do not vet projects based on their proposals. Projects could easily get access to computing resources as long as they can pay for it. The business mindset of this 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 from the cloud vendors and does not have to worry about maintenance.

Conditions above 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 cloud platform will incur performance overhead, it is a viable alternative to having your own dedicated infrastructure. This is shown in various studies in the past, for example, Nekkloud project [18], NASA HPC applications [19], and an HPC application benchmark in public cloud [20]. In addition to that, the capabilities to massively scale your computing resources, limited by one's purchasing power, is an attractive feat for HPC application that needs scalability. This is also why 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 that I proposed.

The first project that tackles a similar problem like HemeLB is Nekkloud. In this project, Nektar++ faces usability issue just like HemeLB. It is a complex high-order finite element code which mainly is operated using command line interface. The original workflow is complex and only limited number of people can operate it, barring people without computer expertise into actually taking advantage of the software package.

This usability problem coupled with the fact that users have to get access to HPC infrastructure, might not be a viable option for everyone. In order to answer these prob-

lems, Nekkloud project was hatched. Nekkloud was developed to make the software configuration invisible to the 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 described itself as a web-based reproducible research platform and ran 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 worry about the software executions.

Developers of Galaxy developed a super-resolution spark (SRS) model to illustrate its use case. This model is an example of HPC application that requires a 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 the users. Making it easy for them to run their experiments and share it with their peers.

Nekkloud and Galaxy projects illustrate that 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 the underlying infrastructure from dedicated HPC infrastructure to the public cloud have 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 increase runtime 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, the more nodes the severe the penalty is. Amazon web service offers 10GigE compared to InfiniBand on NASA supercomputer, Pleiades. In addition, Mehrotra et al. also find out 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 and Auditability of software

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

### 2.2.1 Reproducibility problem in computational research

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, it has 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. In machine learning conferences [24], a similar sentiment is being shared. Being not replicable does not necessarily mean that the result of those studies is wrong. However, it shows how much the academia do not prioritize verification of results. The novelty of idea is seen as better than verifying what we already know.

With the recent study highlighting a reproducibility problem of a research, 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 discipline like bioinformatics and computational physics involves complex computation that requires huge computational power depending on the problem size. The complexity of configuration, algorithm, and execution process actually become a barrier for peers to replicate and reproduce works of studies of this discipline. Making results produced have less weight than it could be

This complexity is also one of the reasons why Galaxy project came into development [21]. While science values rigorous testing, replicable, and reproducible results, the complexity of 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 Galaxy platform. It records all the input files, configurations, and outputs of an analysis and makes it 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's. Galaxy allows the 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 results of studies with complex software package is configurations. A complex software package like HPC application often requires hands-on configuration by the users for it to run correctly. This complex configuration coupled with complex usage become barriers for an independent party to verify results of a study.

Containerization technology, particularly Docker<sup>5</sup>, can help with the issue above. Docker is a technology that is developed on top of kernel-level technologies like Linux Containers (LXC)<sup>6</sup> which allow containers to be a sandbox between processes [27]. Containers, allow applications to be securely placed in its own environment that shares the kernel with its host. Unlike full virtualization, containerization does not require a full operating system installed on the virtual environment so the application could 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 hub<sup>7</sup> 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 make changes to it for their own container.

Using containerization technology like Docker can help with reproducing results of studies. Complex configuration process can be hidden with the containerization technology. 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 versioning feature of Docker also allows the software package to continuously developed and for an analysis tied down to an older version of the package. 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 enabling reproducibility of results.

This is also the reason why Galaxy project supports Docker in its toolsets. Galaxy ecosystem uses Docker to create a secure, isolated environment for the tools and its

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<sup>5</sup><https://www.docker.com/>

<sup>6</sup><https://linuxcontainers.org>

<sup>7</sup><https://hub.docker.com>

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. Docker can help with the recording of the version used for a study by 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 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 package<sup>1</sup>. 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 instruc-

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

tions file to build the container. The original Dockerfile uses a base image of Ubuntu<sup>2</sup>, a popular open source operating system, that is provided by Docker. This image by Docker incorrectly handle Ubuntu's init system, Upstart<sup>3</sup>, that results in some system services cannot be started correctly. One of this service is Secure Shell daemon(sshd)<sup>4</sup>. 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 Phusion<sup>5</sup>, a company in Netherland that open-sourced their version of Ubuntu container that solves above problem.

After switching the base image of the Docker container with Phusion's Ubuntu (Line 8 listing A.1), 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 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 948MB<sup>6</sup> to 430 MB<sup>7</sup>.

The modification of the Dockerfile of the container is the initial part to make HemeLB core container created correctly. To correctly create the HemeLB container, this Dockerfile needs to be integrated into the development workflow of HemeLB. Currently, the modified Dockerfile still live under the HemeWeb codebase<sup>8</sup>. 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.

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<sup>2</sup><http://www.ubuntu.com>

<sup>3</sup><http://upstart.ubuntu.com>

<sup>4</sup><http://www.openssh.com>

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

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

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

<sup>8</sup>[https://github.com/SeiryuZ/HemeWeb/tree/master/hemelb\\_docker](https://github.com/SeiryuZ/HemeWeb/tree/master/hemelb_docker)



## 3.2 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 alleviate the pain of deployment by provisioning and configuring the architecture with minimal manual intervention. The scripts are created using a configuration management and orchestration tools called Ansible<sup>9</sup>.

Ansible is arguably the most popular tools in IT infrastructure automation space[29]. It is a python-based 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 and also an agentless software[29]. 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 Language<sup>10</sup>) syntax for the configuration management language which is described by the team as "easier for humans to read and write than other common data formats like XML or JSON"<sup>11</sup>. I find YAML is easy to work with in developing the scripts. 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.

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<sup>9</sup><https://www.ansible.com>

<sup>10</sup><http://yaml.org>

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

### 3.2.1 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 3 different cloud vendors. 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.

To run the provisioning script, each cloud providers require authentication. Because this authentication is in the form of keys that needs 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 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.

### 3.2.2 Configure the provisioned instances to produce correctly set architecture

After developing the script for instances provisioning, I developed the deployment scripts. 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 script 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 configura-

tion 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 "postgresql" 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.

### 3.3 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 framework<sup>12</sup>. I chose Django web framework due to my previous experience with the web framework and also the existing codebase have 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. Additionally, using Django also allow me to focus on the development instead of learning the framework due to my past experience with it.

All the source code for HemeWeb web application is available online at my GitHub's

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<sup>12</sup><https://www.djangoproject.com>

public repository<sup>13</sup>.

### 3.3.1 Architecture

#### 3.3.1.1 Web application components

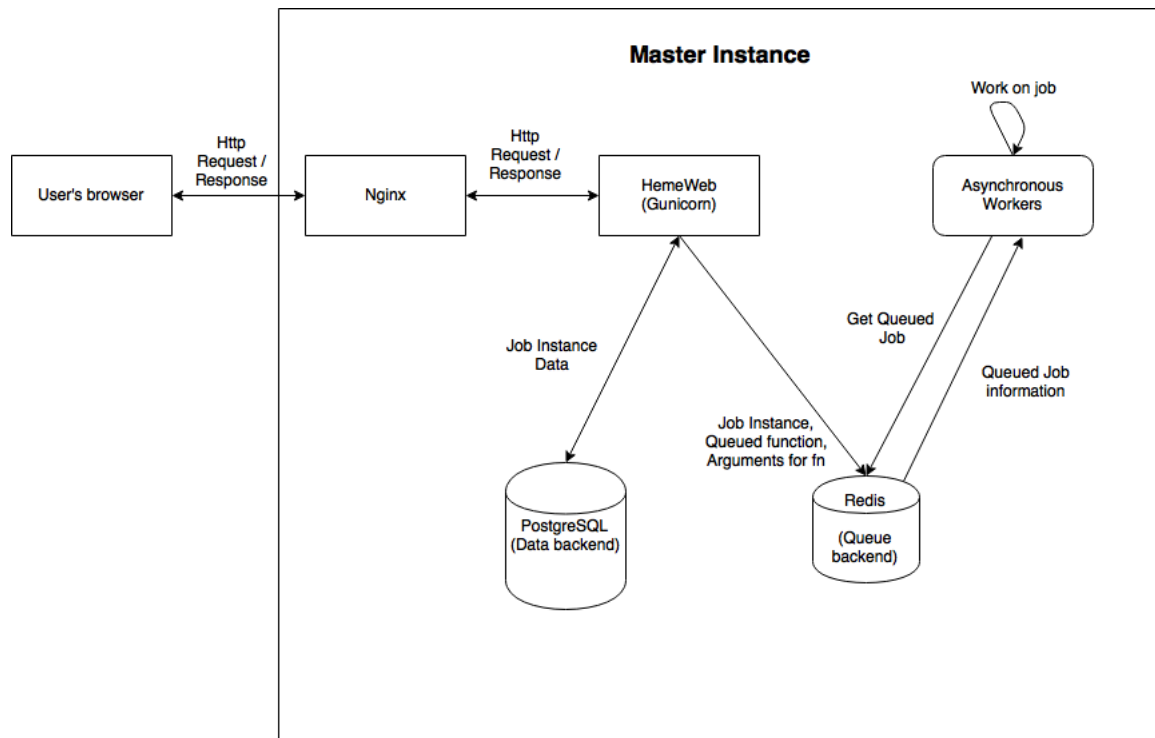


Figure 3.1: HemeWeb architecture

Figure 3.1 above illustrate how HemeWeb application process interacts with the other components inside the master instance. It also illustrates how user's HTTP request start a chain of events inside the master 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 that will act as a reverse proxy. Nginx<sup>14</sup> 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 unicorn<sup>15</sup> HTTP server

<sup>13</sup><https://github.com/SeiryuZ/HemeWeb/tree/master/src>

<sup>14</sup><https://www.nginx.com>

<sup>15</sup><http://gunicorn.org>

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 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 database<sup>16</sup>. 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 data-store<sup>17</sup> as the queue backend. HemeWeb uses third party library called Django-rq that handles asynchronous background tasks handling using Redis backend. It uses the pub / sub mechanism of Redis to create a 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.

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<sup>16</sup><https://www.postgresql.org>

<sup>17</sup><http://redis.io>

### 3.3.1.2 Docker components

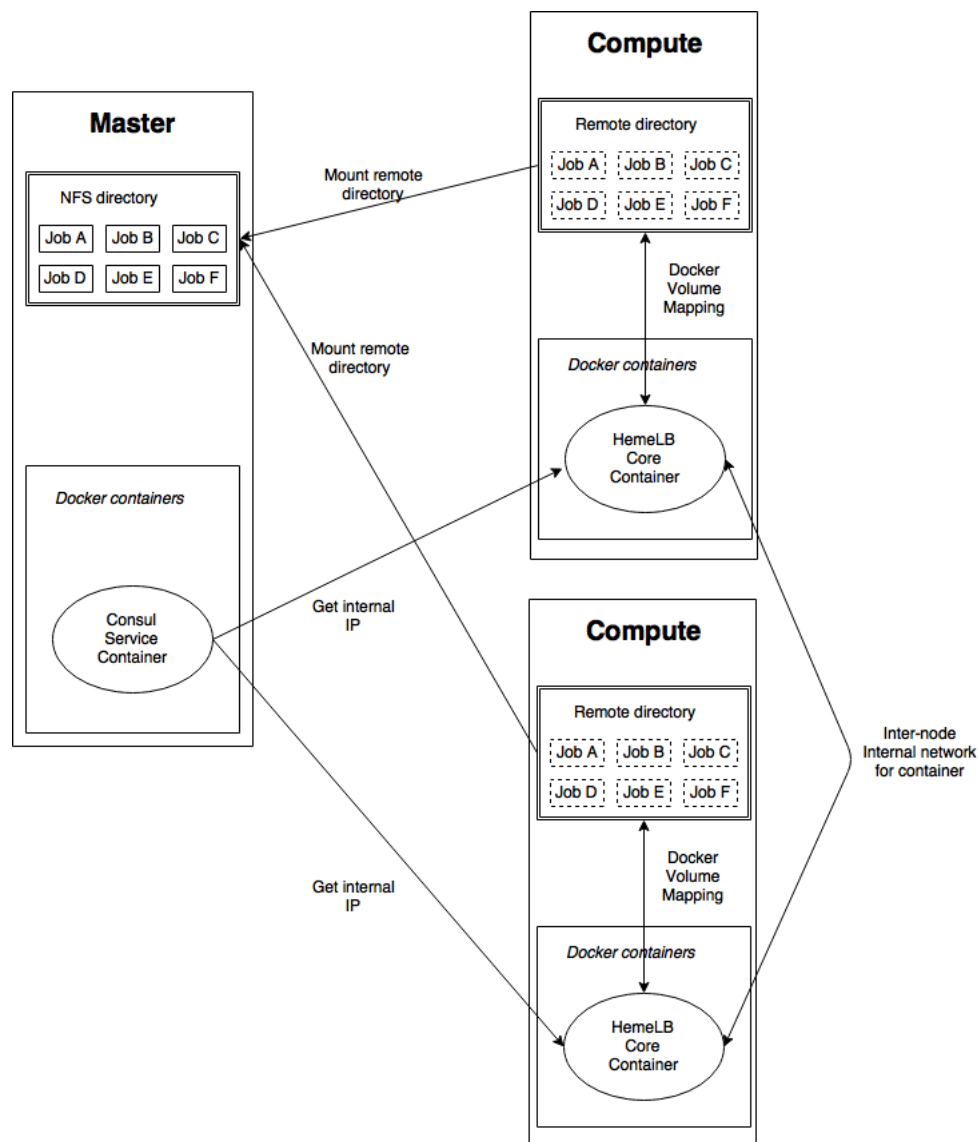


Figure 3.2: HemeWeb Docker component

In this section, I will discuss the interaction between Docker components and the hosts. 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 consul container is constantly running to provide inter-container communication mechanism. Consul<sup>18</sup> is used by the Docker containers to coordinate the internal networking communication between them. In a host, multiple

<sup>18</sup><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 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 made. HemeLB core container is then started to accept simulation command.

To start the simulation, the HemeLB core containers requires 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.

### 3.3.1.3 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 unique 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

#### 3.3.1.4 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.

```

1 <UPLOAD_FOLDER_DIR>/<JOB_ID>
2 <UPLOAD_FOLDER_DIR>/<JOB_ID>/inputs/*
3 <UPLOAD_FOLDER_DIR>/<JOB_ID>/logs/*
4 <UPLOAD_FOLDER_DIR>/<JOB_ID>/outputs/*
5 <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 pickled into this metadata file so when it is downloaded, the web application can unpickle 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.

### 3.3.2 Simulation workflow

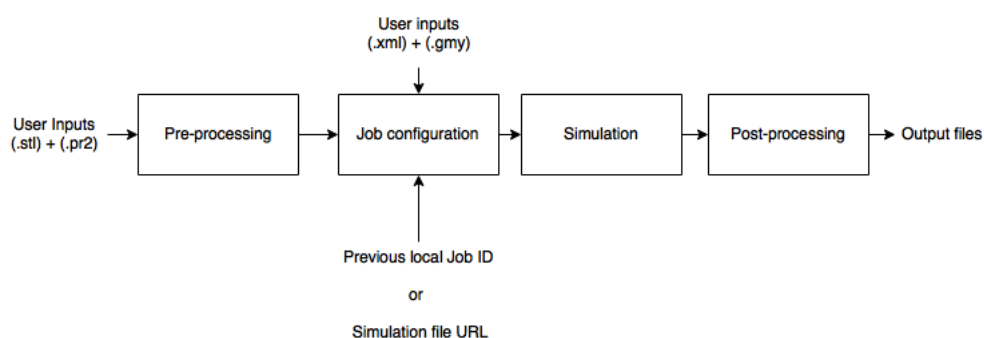


Figure 3.3: HemeWeb flow

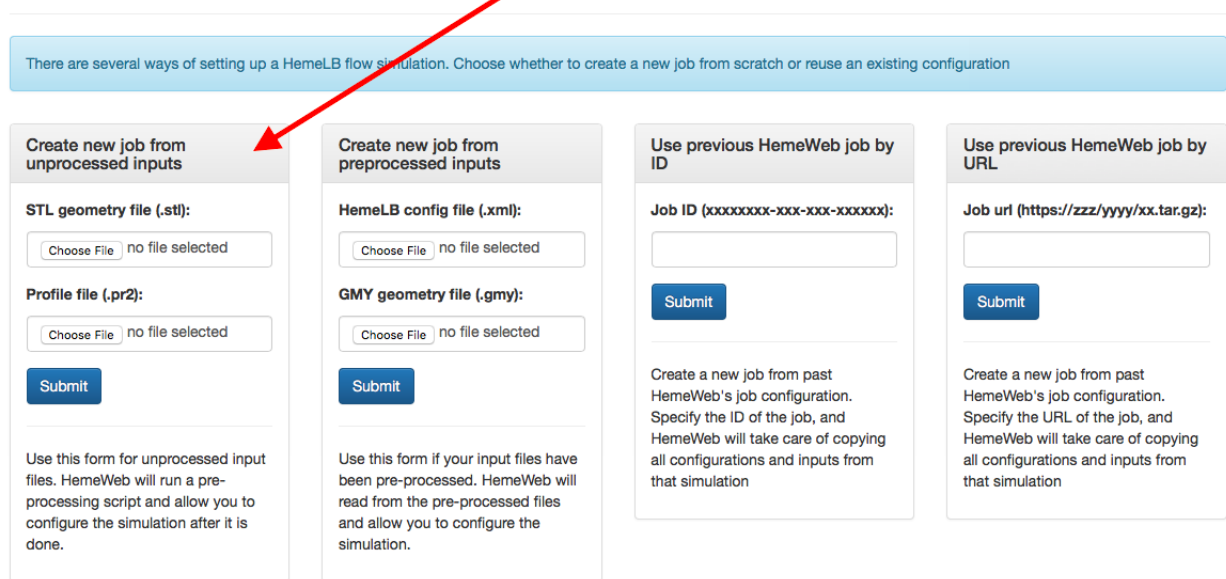
Figure 3.3 illustrates how the HemeWeb web application works. HemeWeb currently consists of 4 core activities that will be discussed in details in the following

section.

### 3.3.2.1 Pre-processing

In this step, HemeWeb handles pre-processing of inputs that are needed so that HemeLB simulation can parse the files. The user provides a geometry file (.stl) and a profile file (.pr2) to the web application for processing. HemeWeb will then create a job instance with these two files, save them locally on master instances and queue the pre-processing job.

#### 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 (.gmy):

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 unprocessed 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.

### 3.3.2.2 Job configuration

In this step, HemeWeb application will take a job instance with correctly set geometry file (.gmy) and HemeLB configuration (.xml). However, there are multiple ways that HemeWeb can get this correctly set 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     <stress units="lattice" value="180018" />
5     <stress_type 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="(0.574837835699,0.818267354016,-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>

```

Save (Ctrl+S) Next step >

Figure 3.5: HemeWeb HemeLB configuration form

Figure 3.5 shows the interface where users are asked to configure 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. 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 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.

### **3.3.2.3 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 asked are 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.

### 3.3.2.4 Post-processing

After HemeLB simulation is finished, 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.

However, the post-processing steps are not done yet. 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, compressed 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 pre-

vious jobs to be used on current deployment

### 3.3.3 Implementation Challenge

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

#### 3.3.3.1 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 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

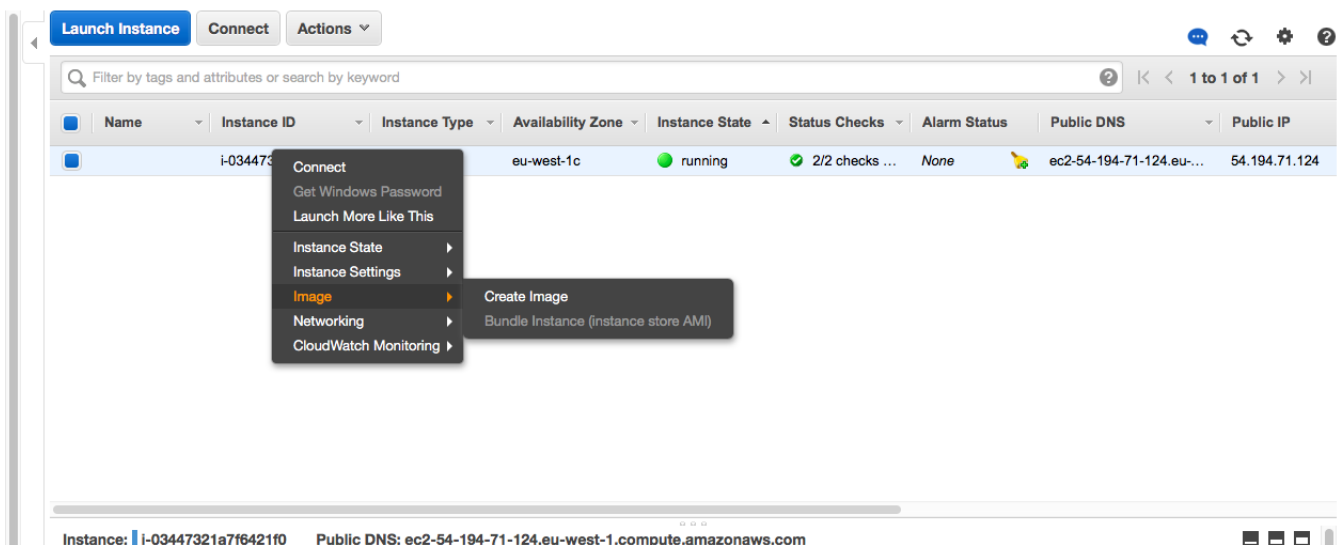


Figure 3.8: Manual image creation instead of automatic

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 time constraint. Due to the time constraint, I cannot achieve full compatibility with all cloud vendors. The development time is mainly focused on amazon web service because it has all the features HemeWeb need. 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 infrastructure. It is possible to refactor these functionalities out to become more generic, however for the interest of time, I decided not to.

### 3.3.3.2 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 the application. 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 a "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. 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 with a public key and disabled password access to ssh. Also, it is also much better to choose cloud vendors that have real private networking like AWS. In which, the compute nodes are not accessible to other nodes that are not part of your own private network. This is much more secure and sensible.

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.



### 3.4 Development process

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.

During the first week of the development, I focused more on stripping the HemeLB core container into its own. I researched on how Docker and Dockerfile work, and finding out what are the issues with the current container. After identifying the issues, which are ssh service and full of functionalities which are not essential, I stripped down the image and changed the base image so that the container could avoid the mentioned problems. I end up with smaller container size and it is available online on <https://hub.docker.com>.

However, one particular issue with what I have currently is that the Dockerfile is published as a part of the HemeWeb source code. It should be tied down to the HemeLB development instead of HemeWeb. Currently, the development model of HemeLB is that there is an internal private repository where the less than stable build is pushed to it, and there are public repositories where only stable builds are pushed into. The release process should include adding the Dockerfile towards the core HemeLB source code repository and tagging the release correctly. HemeLB core containers should then be built automatically on Docker hub with regards to additional tags being pushed to the public repository.

After the development of HemeLB core container, I then focused on how the architecture could be primed for the HemeLB simulation. It involves on configuring the servers and all supporting infrastructures on cloud vendors to be ready for HemeLB simulation. Network configuration, security configuration, Docker configuration, and other should be handled automatically. I elect to choose ansible orchestration software because it is closely related to python language that I used.

In this phase, I successfully achieve the provision and deployment process that with the correct credentials and authorization, the script could provision and configure the architecture correctly so it is ready for HemeLB simulation. In addition to that, I successfully created the script so that it will be cloud vendors agnostic. I can deploy the architecture to google cloud vendors, amazon web service, and digital ocean.

However, it is to be noted that the deployment process that I achieve can only run HemeLB simulation from the command line. I have not considered the web application installation and configuration at this point of the deployment. I only considered the infrastructure being built and configured for HemeLB simulation.

Next, I started developing HemeWeb web application. I choose Django web application framework due to my experience with it. I created a basic interface, where job simulation is listed on the index page on the home interface. After that, I added a basic interface to add new job with a geometry file and HemeLB configuration file. The web application will then add those input files into a newly created job instance and configure the job instance in the job configuration step. The job will then be submitted.

Here I developed a separate ansible script that will be called when a queued job is being worked at. The ansible script is responsible for starting up compute nodes needed by the job and executing HemeLB simulation. After the simulation is done, the script is also responsible for correctly terminating the compute node.

After the basic HemeWeb web application is achieved, I extend it to handle pre-processing. I added an extra form in the adding new job form to handle a profile file and geometry file. These two files will be converted into a geometry file and HemeLb configuration file that the job configuration steps expect. In addition to adding the interface, I also added a new function on the job instance that will run this pre-processing step on the background.

Lastly, due to the limited time, I can only manage to run a small post-processing step on HemeWeb. What I did was adding post-processing step that converts the Extracted results from HemeLB output into a format that can be viewed by third party software, ParaView. The results are piped into two scripts that will output a .vtu that is

compatible with ParaView. This is done during the background activity after simulation result is outputted. However, currently, this is done on the master node.

In addition to that, I also managed to add persistence capability to HemeWeb application. What I did was to package the job simulation folder into a compressed archive and upload it to persistent storage service of cloud vendors. These archives can be queried by another instance of HemeWeb to get previous job IDs available for the particular cloud vendor account used to deploy HemeWeb. Also, the job simulation file URL is also showed on the web interface. Making it easy for the users to share the simulation file with their peers.

# 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 evaluation. 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 a week, from 3rd of August 2016 until 10th 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, being much more 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 baked 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 four different scenarios to measure the performance impact on having HemeLB simulation on the cloud with Docker containers. They are:

- ARCHER supercomputer
- Highly parallel computing resources
- Cloud computing with Docker
- Cloud computing without Docker

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 local computing infrastructure. This paints a picture if how HemeLB will perform on a private local

infrastructure which is built to run highly parallel jobs. This will be the measure that can be used if HemeLB is to run on private infrastructure.

The next two benchmark will be done to measure the performance of HemeLB simulation compared to the local infrastructure. Cloud computing vendors have an underlying difference with regards towards how the infrastructures are structured and connected together. This could have an inherent performance different with a standalone infrastructure. However, an analysis will be made with regards to running HemeLB simulation with another overhead, which is Docker. While Docker is used for easily swapping of the HemeLB version, it might affect the performance of HemeLB simulation. With this benchmark, we can answer whether the flexibility of Docker container can justify the performance that we get. It is also interesting to see whether there are performance penalties that we incur when using Docker.



# Chapter 5

## Analysis

### 5.1 Usability result and analysis

### 5.2 Performance result and analysis

Table 5.1: Performance comparison HemeLB on Indy2 vs AWS EC2

	Performance in seconds	
# of Cores	Indy2	AWS EC2
36	24.7	36.3
72	12.7	29.9
144	7.08	
288	3.44	
576	1.81	
1152	1.58	

# Chapter 6

## Conclusion

Computational bioinformatic applications like HemeLB is complex. Domain experts, whose knowledge in the subject is invaluable, often face difficulties in using the software package. This creates a barrier for them to run a study or even an exploratory one with it. In this project, I alleviate this pain by providing an alternative interface for HemeLB. With it, 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 when coupled with Docker enables it to provide a reproducible research platform for complex applications which is valuable to science in general.

I design and implemented HemeWeb, a web-based interface to interact with 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 3 results. These results are HemeLB core Docker container, HemeWeb deployment scripts, and HemeWeb web application. In the spirit of being open, all of these components are open-sourced and publicly available on the public repository of this project. 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, 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.

# 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. 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. 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.

# Appendix A

## 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

## 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**

## **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](mailto: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)

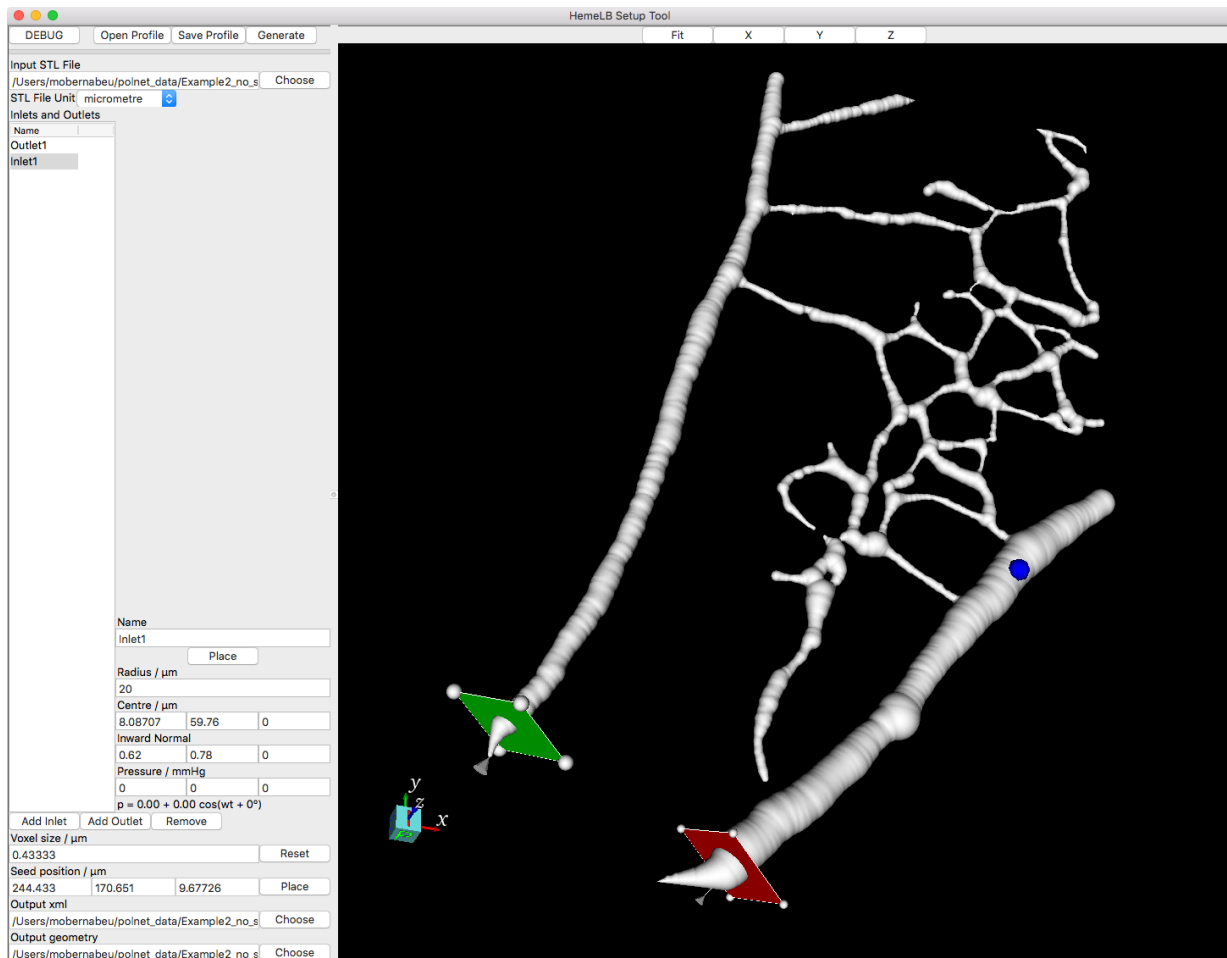
[https://s3-eu-west-1.amazonaws.com/hemeweb-evaluation/990\\_Example2-skeleton\\_corrected\\_tubed\\_smoothed.gmy](https://s3-eu-west-1.amazonaws.com/hemeweb-evaluation/990_Example2-skeleton_corrected_tubed_smoothed.gmy) (43 MB)

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

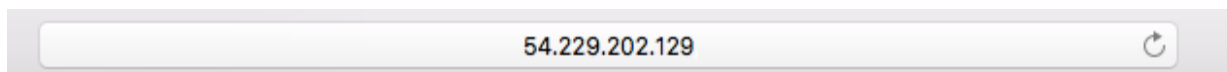
<https://drive.google.com/open?id=0B9-H3nR0aNncR3NgZnQ5ck5mQUU> (2.5 KB)

<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.

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**

GMV 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](http://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

Submit

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](http://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 \*





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