

HemeWeb survey

Hi there,

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

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

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

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

Steven

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

***Required**

About the tools

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

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

Demographic

Some questions to know you better

1. **Age? ***

.....

2. **Gender ***

Mark only one oval.

☐

Male

☐

Female

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

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

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

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

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

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

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

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

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

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

Running a blood flow simulation

Scenario

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

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

Instructions

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

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

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

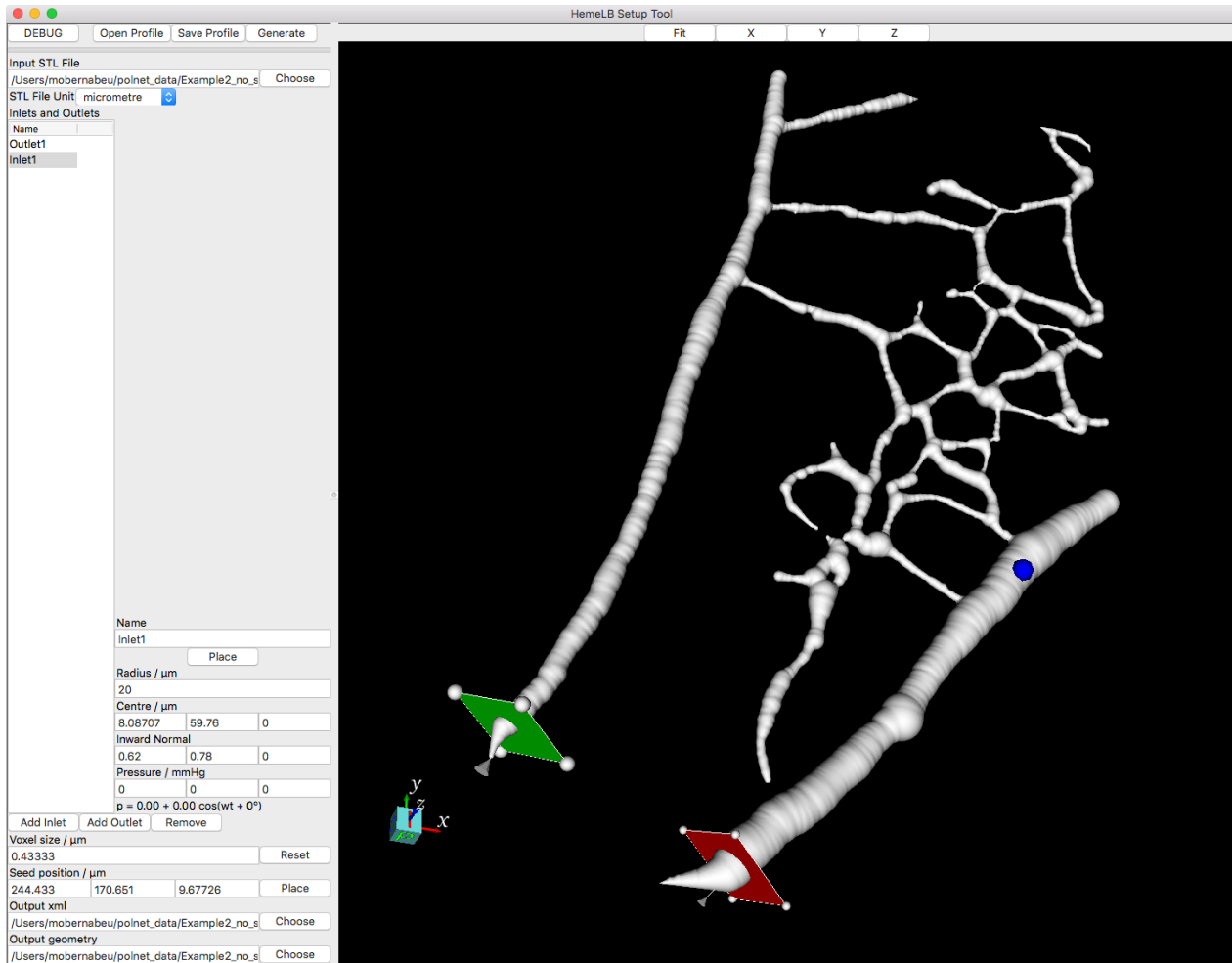
https://s3-eu-west-1.amazonaws.com/hemeweb-evaluation/990_Example2-skeleton_corrected_tubed_smoothed.gmy (43 MB)

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

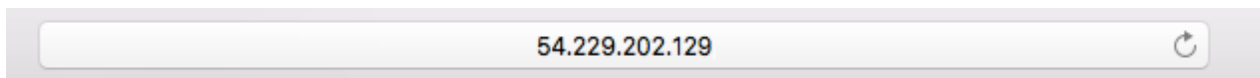
<https://drive.google.com/open?id=0B9-H3nR0aNncR3NqZnQ5ck5mQUU> (2.5 KB)

<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 (.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-xxxx-xxxx-xxxx-xxxx):

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 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.

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

Save (Ctrl+S)

Next step >

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

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

HemeLB 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

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

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

Job Overview We're almost done

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

```
1 - <hemelbsettings version="3">  
2 -   <simulation>  
3 -     <step_length units="s" value="9.62e-10" />  
4 -     <step_units "1attice" 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>

Submit

Questions

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

Mark only one oval.

- ☐ Yes
- ☐ No

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

Mark only one oval per row.

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

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

.....

.....

.....

.....

.....

Running a simulation using command line

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

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

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

Mark only one oval.

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

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

Mark only one oval.

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

Reproducing past blood flow simulation

Scenario

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

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

Instructions

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

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

↻
54.229.202.129

2. Click add new job

HemeWeb: HemeLB in the cloud

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

+ Add new job

HemeWeb Job Index		
Job ID	Submission time	Status

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

HemeWeb: HemeLB in the cloud

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

Create new job from unprocessed inputs

STL geometry file (.stl):
 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-xxxx-xxxx-xxxx-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 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_tubes_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

GMY 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        <center units="mm" 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
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 *

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

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