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# **HML Blast tutorial documentation**

***Release 0.1***

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<b>1</b>	<b>Getting started</b>	<b>1</b>
1.1	Installation . . . . .	1
1.2	Overview . . . . .	1
1.3	Running the Tutorial . . . . .	2
<b>2</b>	<b>Developers</b>	<b>3</b>
2.1	Contributing . . . . .	3



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## Getting started

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### 1.1 Installation

#### 1.1.1 Git

Install nextflow by running the following command.

```
apt-get install git
```

For further documentation on git [click here](#).

#### 1.1.2 Nextflow

Install nextflow by running the following command.

```
curl -fsSL get.nextflow.io | bash
```

For further documentation on nextflow [click here](#).

#### 1.1.3 Docker

[Click here](#) for instructions on how to install docker. After you have docker installed run the following commands to start the docker daemon on your machine.

```
docker-machine start default  
eval $(docker-machine env default)
```

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**Note:** If you're using a VPN the docker-machine will not work.

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### 1.2 Overview

#### 1.2.1 Parameters

**--hml**

- HML file
- Required parameter

<b>--output</b>	<ul style="list-style-type: none"><li>• Output directory</li><li>• Required parameter</li></ul>
<b>--imgtdir</b>	<ul style="list-style-type: none"><li>• Location of where the BLAST IMGT database is located</li><li>• Default location is /opt/html on the docker container</li></ul>
<b>--imgt</b>	<ul style="list-style-type: none"><li>• IMGT database version</li><li>• Default is 3200</li></ul>
<b>--report</b>	<ul style="list-style-type: none"><li>• Binary flag for generating HTML validation report</li><li>• default is 1</li></ul>

### 1.2.2 Executing

```
./nextflow run nmdp-bioinformatics/flow-blast-hml -with-docker \  
  nmdpbioinformatics/docker-blast-hml \  
  --hml test_file.html --outdir /path/to/output/dir
```

After running this command you should find a report and a validated file in the output directory you specified.

## 1.3 Running the Tutorial

### 1.3.1 Clone github repository

```
git clone https://github.com/nmdp-bioinformatics/flow-blast-hml  
cd flow-blast-hml
```

### 1.3.2 Install nextflow

```
curl -fsSL get.nextflow.io | bash
```

### 1.3.3 Start docker machine

```
docker-machine start default  
eval $(docker-machine env default)
```

### 1.3.4 Execute

```
./nextflow run nmdp-bioinformatics/flow-blast-hml -with-docker \  
  nmdpbioinformatics/docker-blast-hml \  
  --hml tutorial/ex00_ngsp_expected.xml \  
  --outdir tutorial/output --report 0
```

## 2.1 Contributing

1. Log into Github web interface with your username-nmdp account
2. Browse to the repo at <https://github.com/nmdp-bioinformatics/flow-blast-hml>, hit the Fork button.
3. Copy the clone URL from the Github web page for the fork (something like <https://github.com/username-nmdp/pipeline.git>)
- 4) Clone the fork .. code-block:: shell

```
git clone https://github.com/username-nmdp/flow-blast-hml.git cd flow-blast-hml
```
- 5) Add upstream as remote .. code-block:: shell

```
git remote add upstream https://github.com/nmdp-bioinformatics/flow-blast-hml
```
- 6) Pull and merge latest changes from upstream master to your local master branch .. code-block:: shell

```
git checkout master git pull upstream master git push
```
- 7) Create a new local feature branch .. code-block:: shell

```
git checkout -b new-feature-branch
```
8. Edit files locally
- 9) Commit changes to local feature branch .. code-block:: shell

```
git commit -m "made changes"
```
- 10) Push changes from local feature branch to remote feature branch on your fork .. code-block:: shell

```
git push origin new-feature-branch
```
11. Browse to the Github web page for your fork repo (something like <https://github.com/username-nmdp/flow-blast-hml>) and hit the new pull request button.
12. Edit the pull request description and hit create new pull request button.
13. Other contributors will review the changes in the pull request.
14. When the pull request looks good, it will be merged into the master branch.
15. Hit the delete branch button to delete your remote feature branch (the commits have been merge upstream, so it is no longer necessary).
- 16) Delete your local feature branch .. code-block:: shell

`git branch -d new-feature-branch`