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## Tutorial: How to set up and use the Mule Docker image?

In this tutorial we describe how to set up and execute the model checker Mule using Docker. The **steps** considered throughout the tutorial are:

1. [Install Docker](#);
2. [Download Mule Docker image](#);
3. [Create and run Mule Docker container](#);
4. [Run model checker Mule](#);
5. [Case study: Acute inflammation of the gut and lung](#).

### 1. Install Docker

Tutorials on how to install Docker on most operating systems are provided on its [official website](#) and will not be explicitly restated here.

For your convenience a **direct link** to these tutorials for Windows, Linux and Mac OS X users are given below:

- Linux: [Install Docker](#);
- Mac OS X: [Install Docker Mac OS X](#);
- Windows: [Install Docker for Windows](#).

After installing Docker you should be able to run the following command from a **regular terminal** on Linux, respectively from a **Docker terminal** on Mac OS X and Windows:

```
docker --help
```

In the following the word **terminal** will refer to the regular terminal for Linux users, respectively the Docker terminal for Mac OS X and Windows users.

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### 2. Download Mule Docker image

The Mule Docker image is made **freely available online** in the [Docker Hub Registry](#). It can be **downloaded** using the following command in the terminal:

```
docker pull icerage/mule
```

where "icerage" is the username of Ovidiu Parvu and "mule" is the name of the Docker Hub repository.

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### 3. Create and run Mule Docker container

To **create** and **run** a **Docker container** using the Docker image downloaded at the previous step execute the following command in the terminal:

```
docker run -ti icerage/mule
```

where the command line arguments "-ti" are used to ensure that commands can be executed in the Docker container using standard input; see the documentation of the Docker *run* command for more details.

After executing the immediately above command the **last line** in your **terminal** should look similar to:

```
root@d4t8fa168dk3:/home/user/software#
```

This is an indication that the container was successfully created and commands can be executed inside it.

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### 4. Run model checker Mule

To display the **help page** of Mule execute the following command in the terminal:

```
Mule --help
```

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## 5. Case study: Acute inflammation of the gut and lung

We illustrate how to use Mule for the **verification of a computational model** based on the [acute inflammation of the gut and lung](#) case study.

#### 5.1. Download model simulation traces

First of all an **archive** will be downloaded containing the **model simulation traces** previously generated for the acute inflammation of the gut and lung case study:

```
wget http://oviduparvu.com/data/software/mule/case_studies/
acute_inflammation_of_gut_and_lung
acute_inflammation_of_gut_and_lung_mstm1_dataset.zip
```

**Remark:** Alternatively it is possible to download the computational model and generate simulation traces on demand but this requires additionally installing the corresponding model simulator.

Next a **folder is created** in which the contents of the model simulation traces archive are **extracted**. The archive is then removed. This can be done by executing the following command in the terminal:

```
mkdir traces && unzip acute_inflammation_of_gut_and_lung_mstm1_dataset.zip -d
```

```
traces && rm acute_inflammation_of_gut_and_lung_mstml_dataset.zip
```

## 5.2. Download formal PBLMSTL specification

Afterwards the **formal PBLMSTL specification** is downloaded by executing the following command in the terminal:

```
wget http://ovidiparvu.com/data/software/mule/case_studies  
/acute_inflammation_of_gut_and_lung  
/specification_pblmstl_acute_inflammation_of_gut_and_lung.in
```

## 5.3. Download multiscale architecture graph

The **multiscale architecture graph** is downloaded using the following command:

```
wget http://ovidiparvu.com/data/software/mule/case_studies  
/acute_inflammation_of_gut_and_lung  
/multiscale_architecture_graph_acute_inflammation_of_gut_and_lung.xml
```

## 5.4. Execute model checker

Finally the model checker **Mule** can be **executed** considering the model simulation traces, the formal PBLMSTL specification and the multiscale architecture graph using a **statistical model checking algorithm** with the probabilities of **type I** and **type II errors** set to 5% using the following command:

```
Mule -v -q specification_pblmstl_acute_inflammation_of_gut_and_lung.in -t traces  
-a multiscale_architecture_graph_acute_inflammation_of_gut_and_lung.xml -m 1 -e 0  
--type-I-error 0.05 --type-II-error 0.05
```

where the command line argument:

- "-v" specifies that the model checker should be executed in "verbose" mode;
- "-q" specifies the path to the logic queries or formal PBLMSTL specification;
- "-t" specifies the path to the folder containing the model simulation traces;
- "-a" specifies the path to the multiscale architecture graph;
- "-m" specifies which model checking algorithm should be employed (e.g. 1 = frequentist statistical);
- "-e" specifies the extra evaluation time i.e. if there are insufficient model simulation traces available how many minutes should Mule wait for new model simulation traces to be potentially provided;
- "--type-I-error" specifies the probability of type I errors;
- "--type-II-error" specifies the probability of type II errors.

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