

# University of Applied Sciences Western Switzerland MSE - Software Engineering

## Projet d'approfondissement Inphinity

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# 1 Introduction

TODO: phages Vs bacteria

## 2 State of the art

#### 2.1 Biology

TODO: genome

#### 2.2 Bio-informatic

**TODO:** sequence alignment

### 3 Methods

- 3.1 Docker
- 3.1.1 Docker-machine installation
- 3.1.2 Docker commands
- 3.1.3 Inphinity, build & run
- 3.2 Phamerator
- 3.2.1 Installation

**TODO:** install on GUI machine

3.2.2 How it's works

 $\frac{\text{TODO: screens}}{\text{screens}} + \text{explain}$ 

- 3.3 PhamDB
- 3.3.1 Installation & Run
- 3.3.2 Utilisation
- 3.4 Database & Dataset
- 3.5 Phamily
- 3.5.1 Alignment
- 3.5.2 Phages selection
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## 4 Results & Analyse

- 4.1 First result
- 4.1.1 Tree
- 4.1.2 Hosts
- 4.2 Database
- 4.2.1 SEA
- 4.2.2 Phages list integration

#### 5 Conclusion

#### 5.1 Problems encountered

- 5.1.1 Phamerator Installation
- 5.1.2 SEA database
- 5.1.3 PhamDB Limitation jobs
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