

bio**boxes**

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What is Bioboxes?

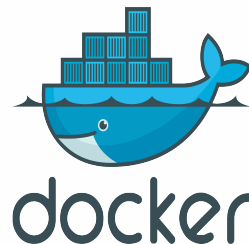
- Motivated by CAMI & Nucleotid.es



- Reproducibility
- Easy to use
- Continuous Evaluation

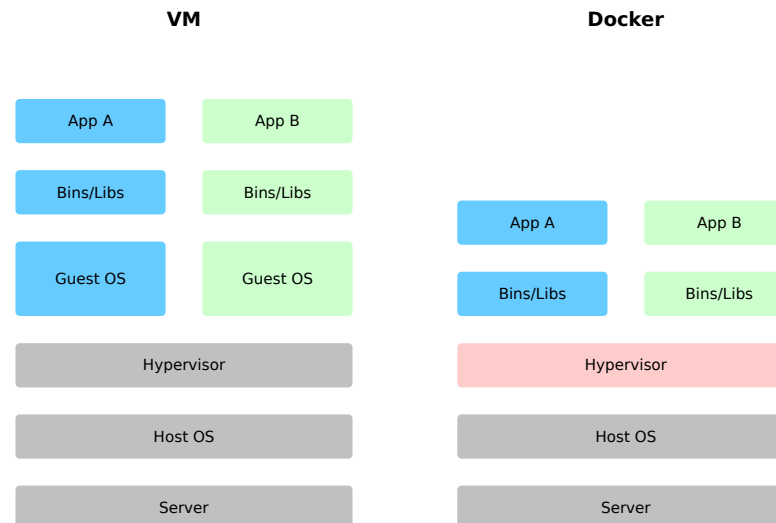


- A standard for creating interchangeable bioinformatics software containers
- Community standard
- Based on Docker



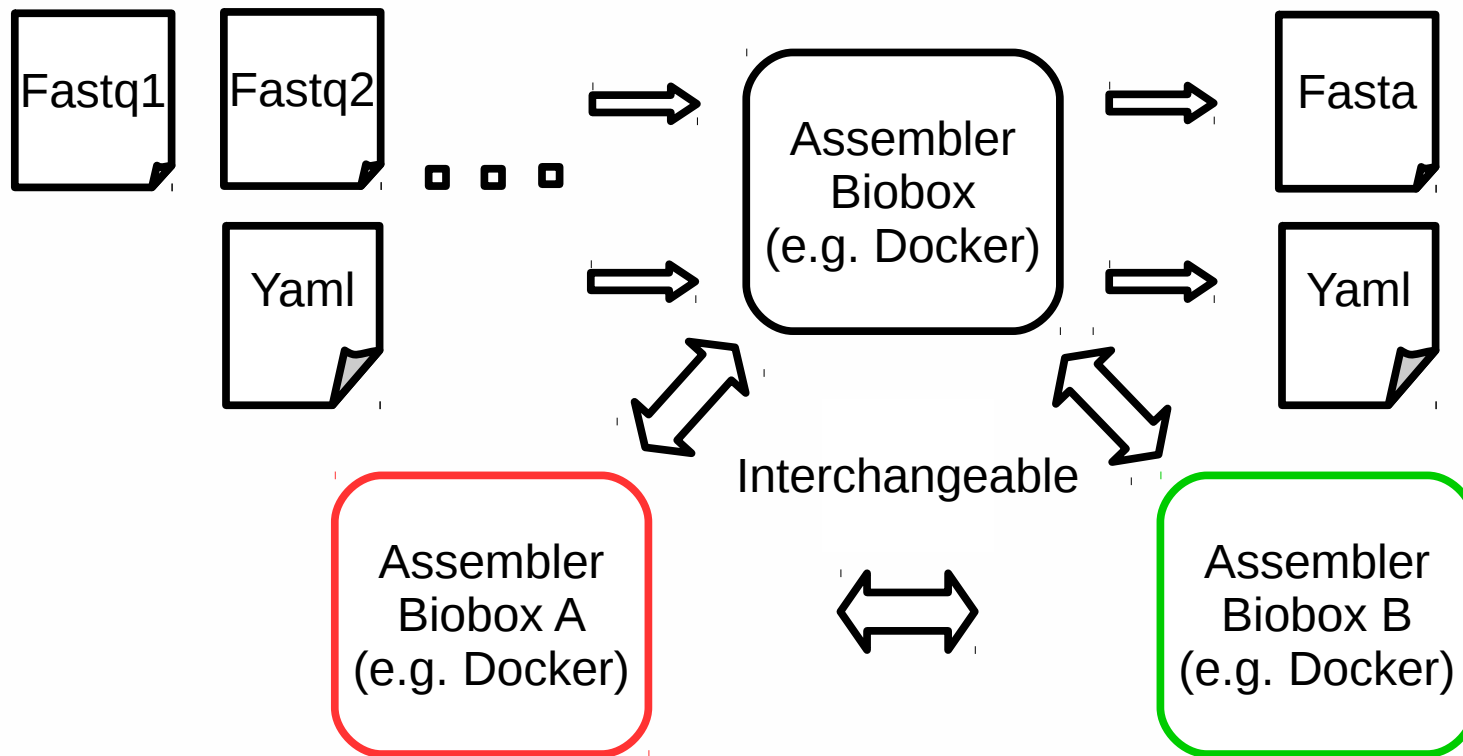
What is Docker?

- Platform for creating encapsulated environments

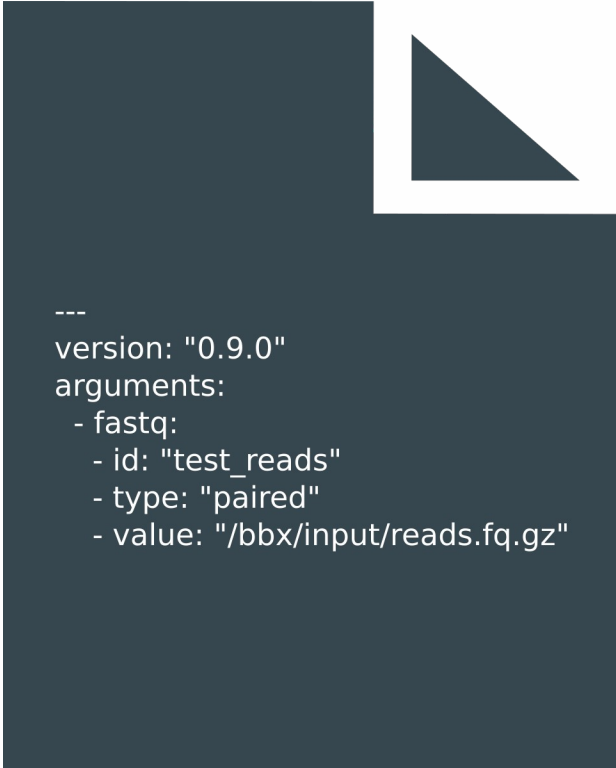


- Portable, lightweight runtime
- Solves Development vs. Production problem

How does Bioboxes work?



Example YAML



```
---  
version: "0.9.0"  
arguments:  
  - fastq:  
    - id: "test_reads"  
    - type: "paired"  
    - value: "/bbx/input/reads.fq.gz"
```

Community Driven



- Github
- User & Developer Guide
- Conferences
- Collaborations

Thank you for your attention!

Visit bioboxes.org and shape with us the future of
bioboxes.