GUIDOCK

Using **Docker Containers** with a Common Graphics User Interface **to Address the Reproducibility of Research**

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MS - COMPUTER SCIENCE

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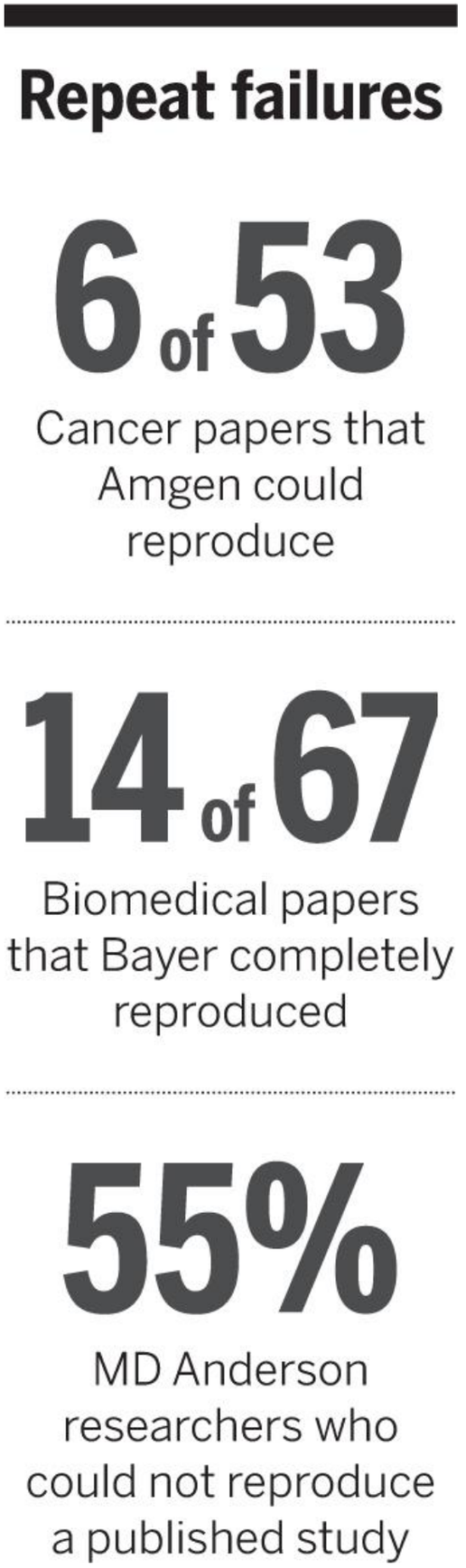
Motivation

The cancer test, Jocelyn Kaiser

Science **26 Jun 2015**: Vol. 348, Issue 6242, pp. 1411-1413 DOI: 10.1126/science.348.6242.1411



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Last Week Tonight with John Oliver: Scientific Studies (HBO)
Published on May 8, 2016

[https://youtu.be/0Rnq1NpHdmw]

Challenges

Computational Biology:

- Involve complicated pipelines with many tools,
  multiple OS’es
- Software versioning
- Dependency and configuration constraints

[google images]

Our Solution

We distribute the entire computing environment —not just the codes.

[Icon made by Freepik from www.flaticon.com]

Virtual Machines

[OSes runing inside OS]

- Bundle everything as a single machine

Docker Containers

Similar to VM, but with additional advantages:

- Smaller, easy to distribute
- Straightforward pipelines
- Easier to deploy
- Open source
- Build on top of other containers

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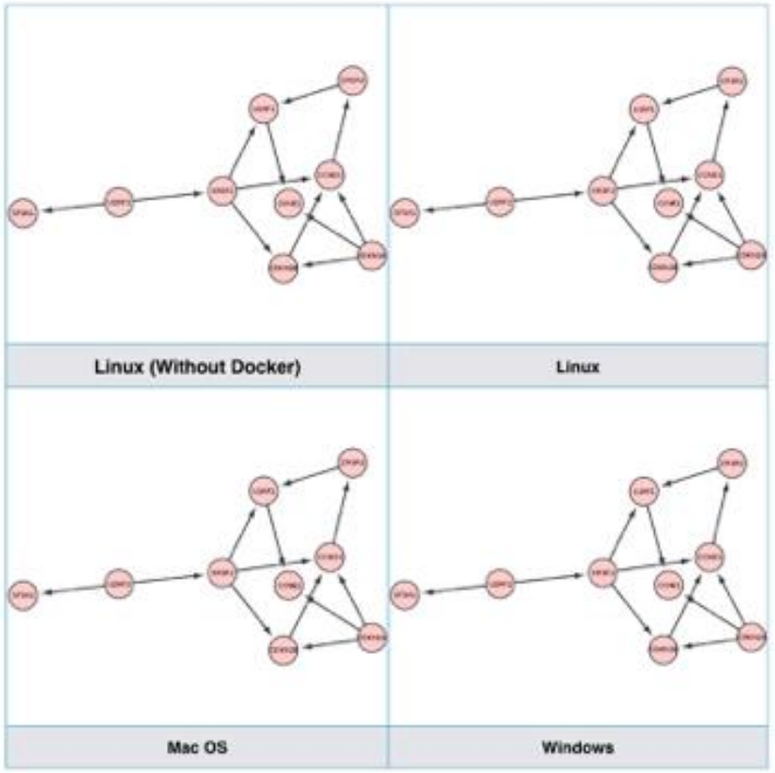
Proof of concept: **Gene Network Inference**



Maciej Fronczuk | UWTacoma

Source Code for Biology and Medicine 2015 10:11
DOI: 10.1186/s13029-015-0043-5

Chad Young | UWSeattle

Fast Bayesian inference for gene regulatory networks using ScanBMA. BMC Syst Biol. 2014; 8(1):47.

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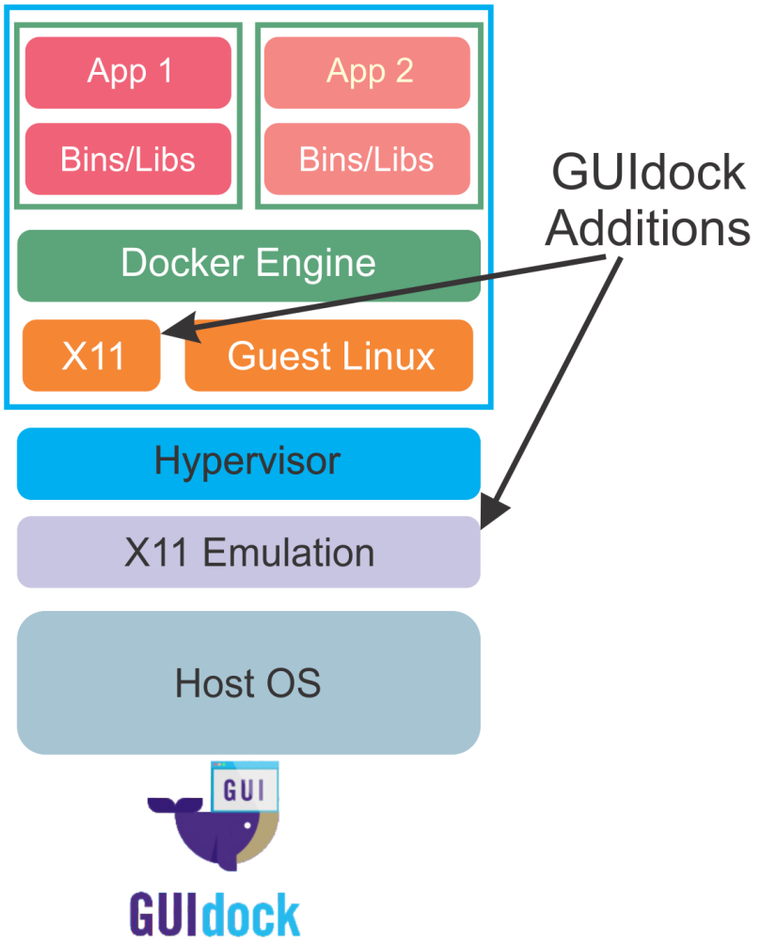

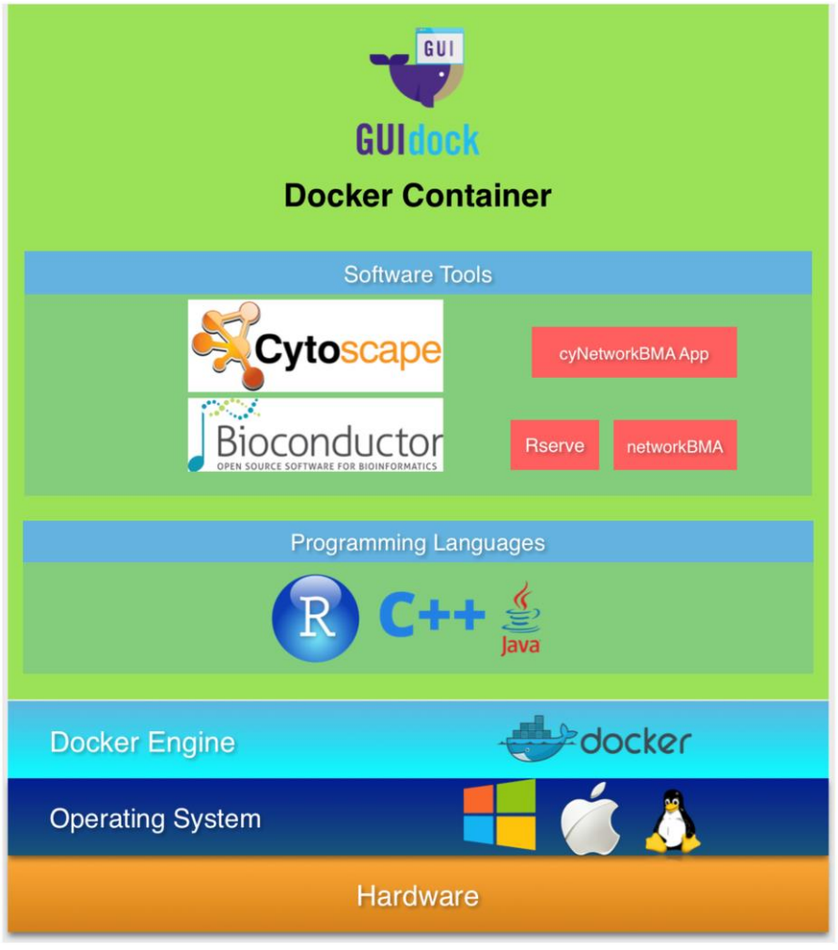

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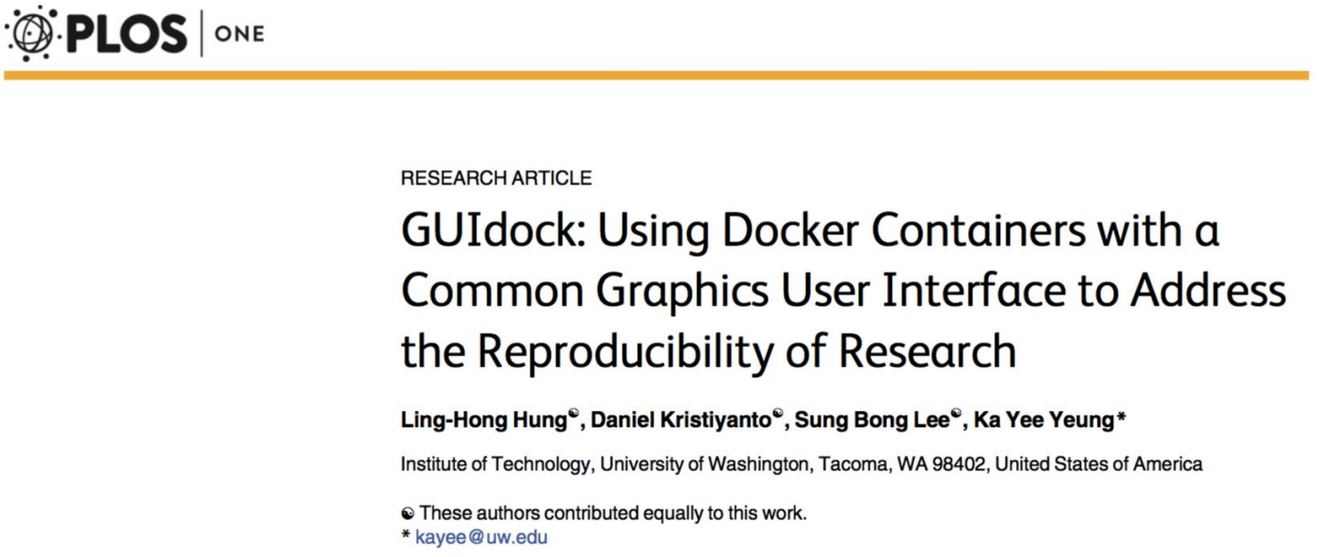

RESEARCH ARTICLE

GUIdock: Using Docker Containers with a Common Graphics User Interface to Address the Reproducibility of Research

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Paper:
http://dx.doi.org/10.1371/journal.pone.0152686

Repository: http://github.com/biodepot

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DATA COORDINATION AND INTEGRATION CENTER

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Further Works

Varun Mittal | UWT

noVNC:

- Works better in the cloud
- More robust graphic and for more complex pipelines

Further Works

Trevor Meiss | UWT

DToxS: Reproducibility of RNAseq analyses
(in collaboration with Mount Sinai, NYC)

DNA Alignment and differentially expressed genes identification

Mount Sinai

BioDepot

http://tacoma.uw.edu/bioinformatics

Repository of containerized bioinformatics pipelines

[google images]