# GUIDOCK

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

DANIEL KRISTIYANTO MS - COMPUTER SCIENCE

@kristiyanto\_

### Motivation

#### The cancer test, Jocelyn Kaiser

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

UNIVERSITY of WASHINGTON

### Repeat failures



Cancer papers that Amgen could reproduce

14 of 67

Biomedical papers that Bayer completely reproduced

55%

MD Anderson researchers who could not reproduce a published study

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

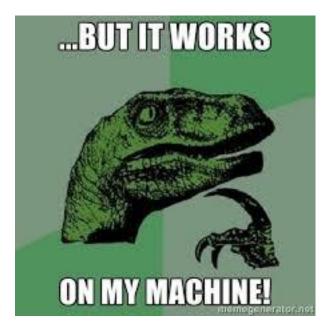


[https://youtu.be/0Rnq1NpHdmw]

## 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.





### Virtual Machines

### 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

[ OSes runing inside OS ]

 Bundle everything as a single machine



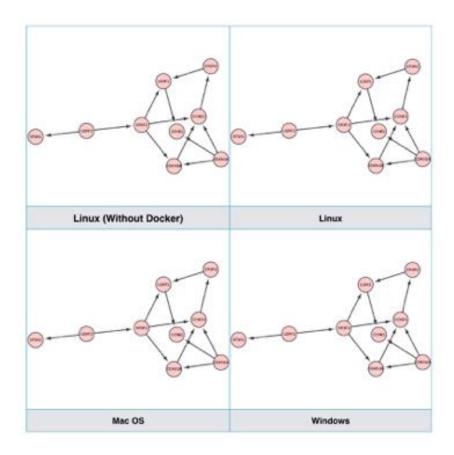
#### Proof of concept: Gene Network Inference

#### Maciej Fronczuk | UWTacoma

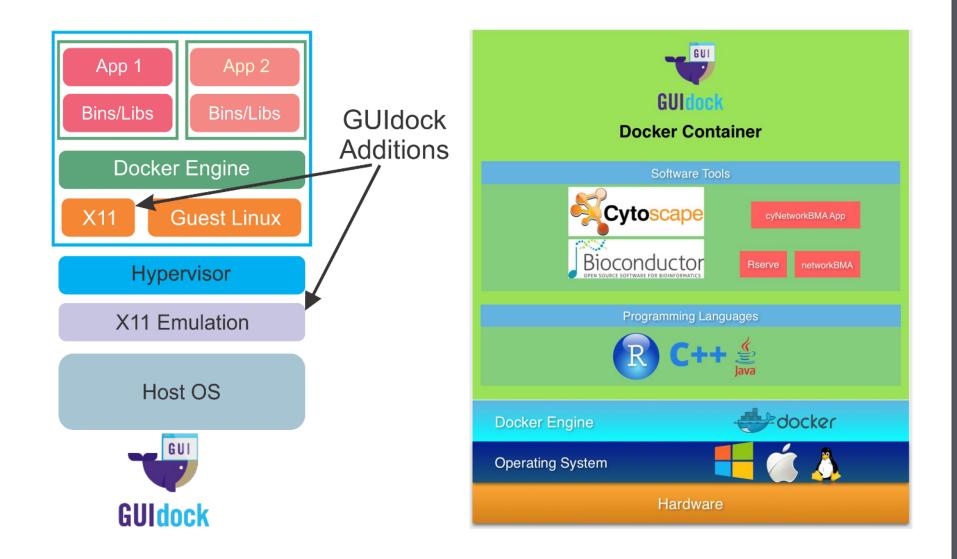
Source Code for Biology and Medicine 2015 10:11 DOI: 10.1186/s13029-015-0043-5

#### Chad Young | UWSeattle

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











RESEARCH ARTICLE

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

Ling-Hong Hung<sup>e</sup>, Daniel Kristiyanto<sup>e</sup>, Sung Bong Lee<sup>e</sup>, Ka Yee Yeung\*

Institute of Technology, University of Washington, Tacoma, WA 98402, United States of America

These authors contributed equally to this work.
\* kayee@uw.edu

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

Repository: http://github.com/biodepot

### Acknowledgement



Dr. Ling-Hong Hung, Sung Lee, Dr. Ka Yee Yeung





DATA COORDINATION AND INTEGRATION CENTER





## Further Works

### Varun Mittal | UWT

#### noVNC:

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

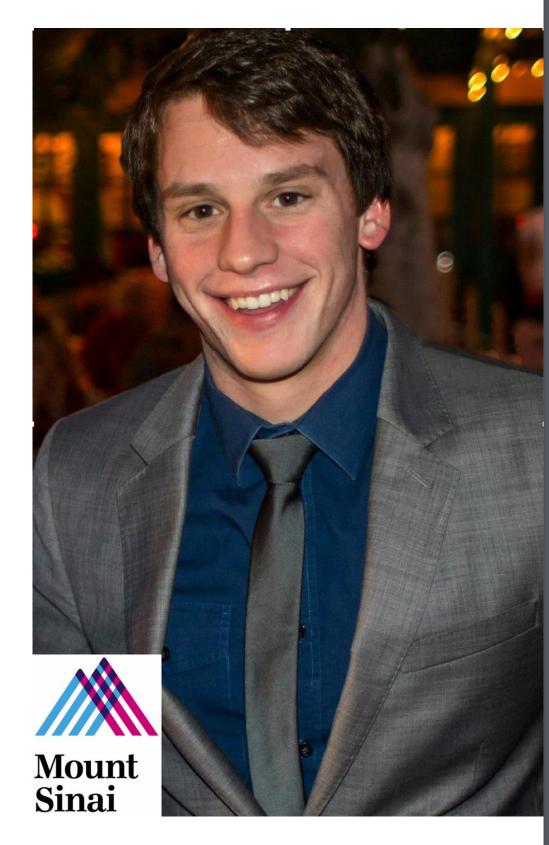


### Further Works Trevor Meiss

UWT

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

DNA Alignment and differentially expressed genes identification



## BioDepot

#### http://tacoma.uw.edu/bi oinformatics

Repository of containerized bioinformatics pipelines





[google images]