Challenges of a Sustainable Software Platform for Predictive Biology: Lessons Learned on the KBase Project

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What is KBase?



Open software and data platform for addressing the grand challenge of systems biology:

Predicting and designing biological function



Unified system that integrates data and analytical tools for comparative functional genomics of microbes, plants, and their communities

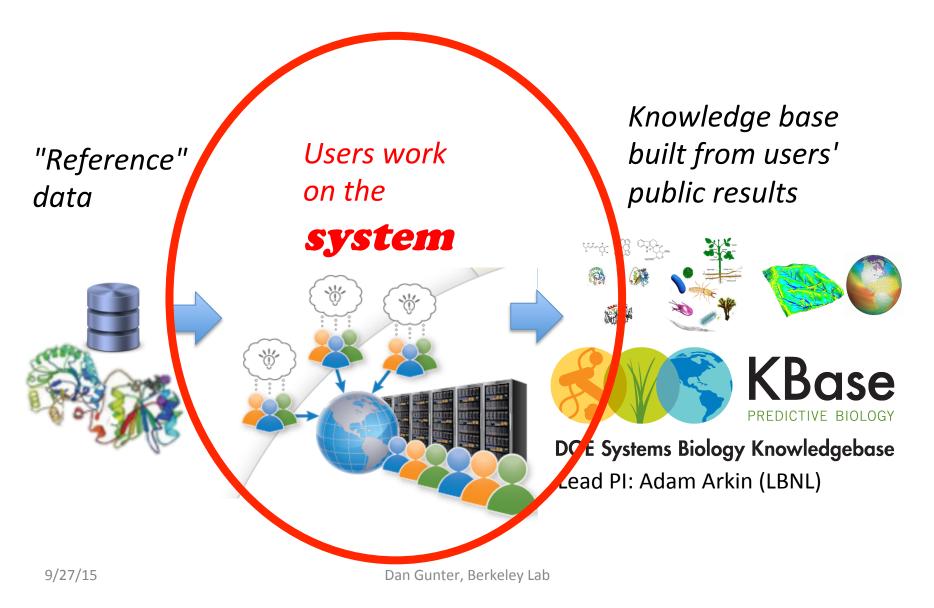


Collaborative environment for sharing methods and results and placing those results in the context of knowledge in the field

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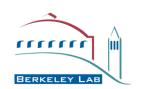


What do we need to build?





Multi-institutional project



Lawrence Berkeley National Laboratory

Lead institution



Argonne National Laboratory



Brookhaven National Laboratory



Oak Ridge National Laboratory

Cold Spring Harbor Laboratory of California, Davis

Hope College University of Illinois at Urbana-Champaign

Yale University University of Tennessee



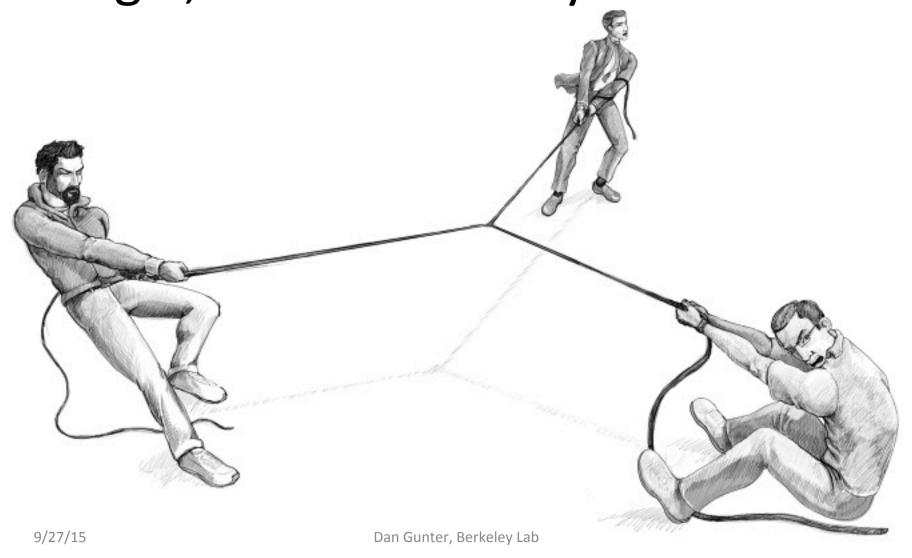


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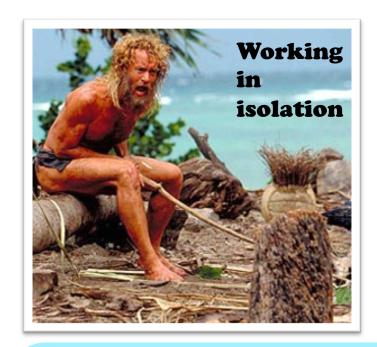


Challenge: pull together to make a single, maintainable system

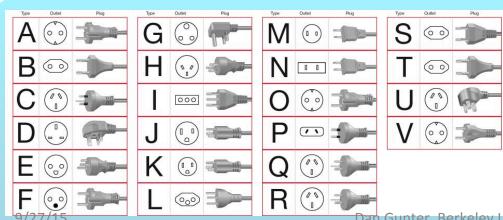




What doesn't work







No standards for software engineering

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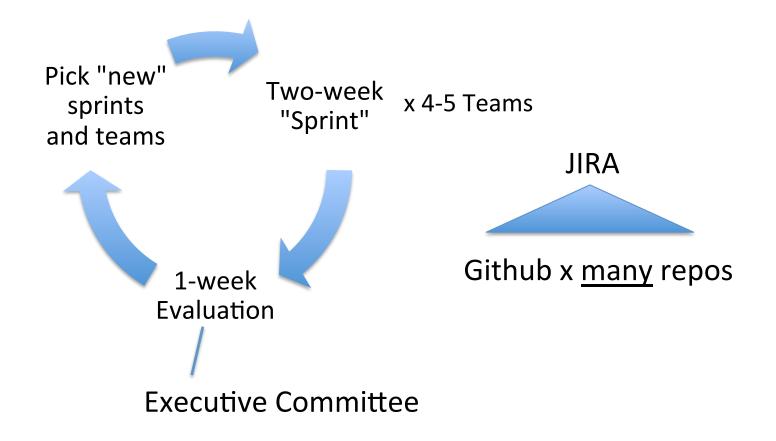
Umm.. why think that would work?

- It (mostly) works for C.S. research
 - avoiding long design cycles, not standardizing save time for the highly rewarded activities like publishing, doing performance studies, graduating students. Isolation can help "protect" ideas before they are published.
- Going from research groups to a cohesive software team is a deep shift



What we are trying:

(1) "Agile" for large, distributed science teams





(2) Openness of process

https://github.com/kbase/project_guides

Index of documents:

- Process guide
- Acknowledgment guidelines
- External data sources
- How to add a method
- How to add a new data type
- Developer deployment
- Setting up Travis CI and Coveralls
- ThirdPartyDevelopmentProtocol
- Towards a Social Platform
- Feature requests
- Help Desk Process