



Beyond Bermuda

Challenges for Open Data from Biology

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Life

OUT OF
SEQUENCE

A DATA-DRIVEN
HISTORY OF
BIOINFORMATICS



- Bermuda and a history of open access
- Reflections from Santa Cruz
- *Gigascience*



HUMAN GENOMIC SEQUENCE GENERATED BY LARGE SCALE CENTRES:

RELEASE

- Automatic release of sequence assemblies >1kb (preferably daily)
- Immediate submission of finished annotated sequence

- ~~_____~~ Aim to have all sequence freely available in the public domain for both research and development, in order to maximise its benefit to society.

POLICY

- The funding agencies are urged to foster these policies

Kathryn Maxson Jones, Robert Cook-Deegan, and Rachel A. Ankeny. "The Bermuda Triangle: The Politics, Principles, and Pragmatics of Data sharing in the History of the Human Genome Project, 1963-2003" *Journal of the History of Biology* (forthcoming).

Bermuda 2.0: Reflections from Santa Cruz

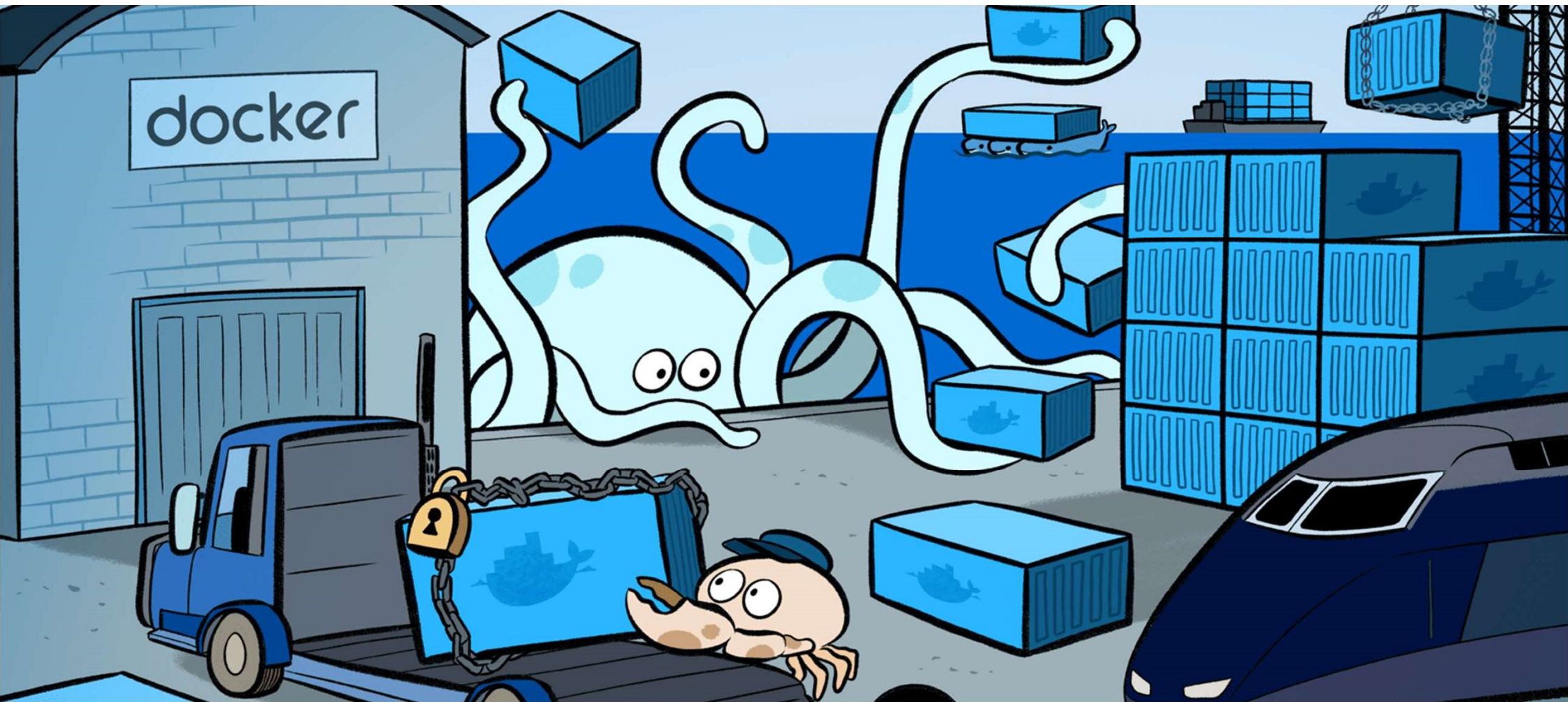


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- Rachel A. Ankeny
- Jenny Bangham
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- Stephen Hilgartner
- Kathryn Maxson Jones
- Beth Shapiro
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- Julie Harris-Wai
- David Haussler
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<https://academic.oup.com/gigascience/article/doi/10.1093/gigascience/giw003/2756884/Bermuda-2-0-reflections-from-Santa-Cruz>

- What is data?
- What is sharing?
- What is the public good?

(GIGA)ⁿ
SCIENCE



“Developers using Docker don’t have to install and configure complex databases nor worry about switching between incompatible language toolchain versions. When an app is dockerized, that complexity is pushed into containers that are easily built, shared and run. Onboarding a co-worker to a new codebase no longer means hours spent installing software and explaining setup procedures. Code that ships with Dockerfiles is simpler to work on: Dependencies are pulled as neatly packaged Docker images and anyone with Docker and an editor installed can build and debug the app in minutes.”