

Bioconductor on the RosettaHUB community platform

www.rosettahub.com

Karim Chine
RosettaHUB, Inc

karim.chine@rosettahub.com

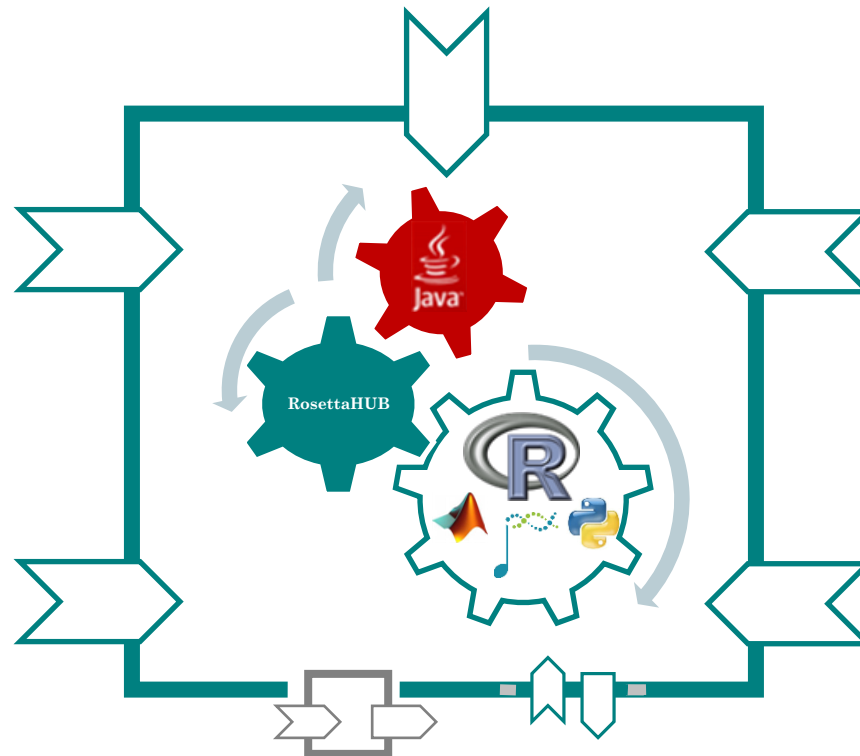
BioC 2016

24th June 2016

A universal open platform for scientific computing and collaboration

Computational Components

R packages, Bioconductor, Wrapped C,C++,Fortran code, Python modules, Matlab Toolkits...
Open source or commercial



Computational Resources

Clusters, grids, private or public clouds
Free or pay-per-use

Computational GUIs

HTML5 and Desktop Workbench
Built-in views /Plugins /Collaborative views
Shiny apps
Open source or commercial

Computational Storage

Local, NFS, FTP, Amazon S3, EBS, HDFS

Computational Scripts

R / Python / Matlab / Groovy

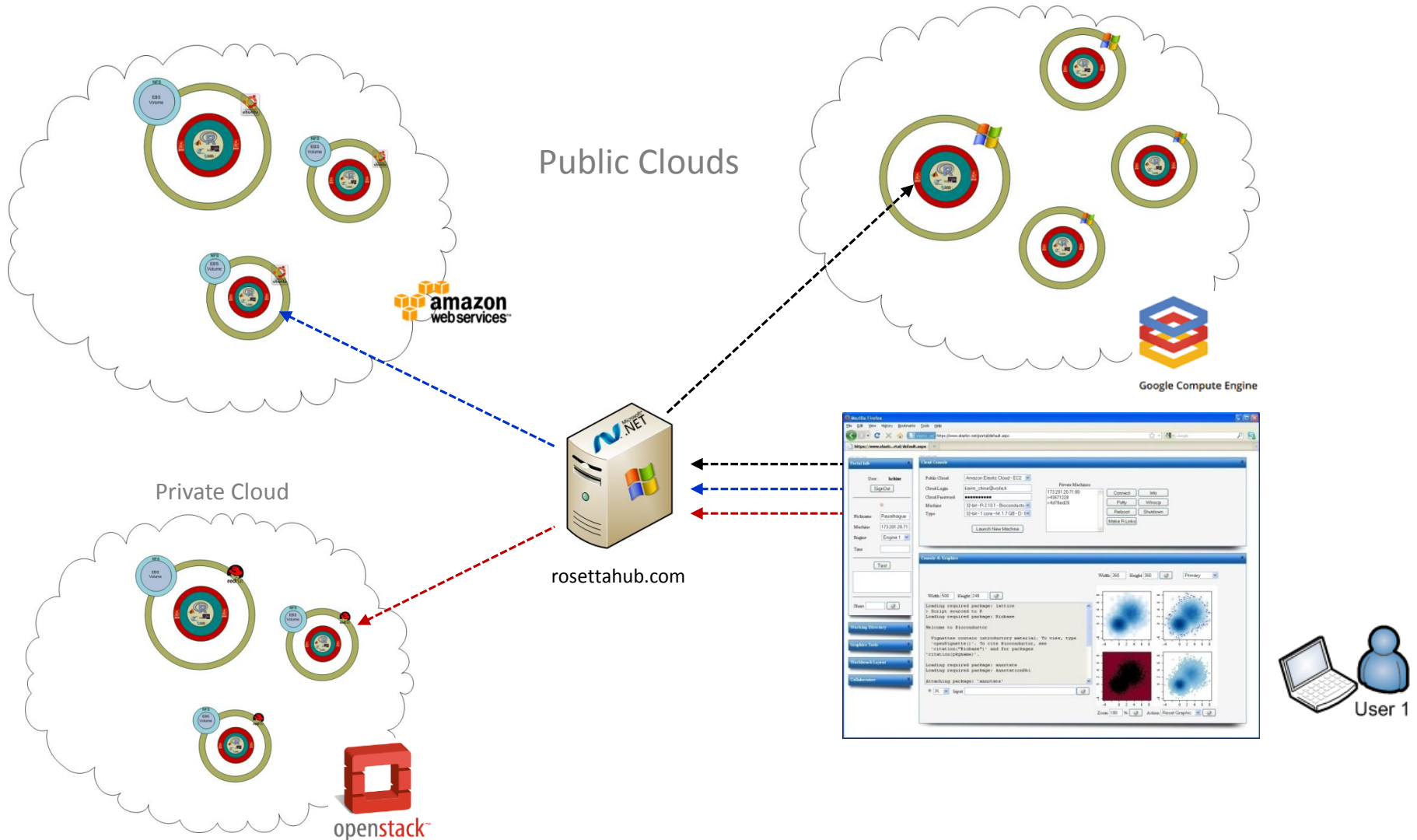
Generated Computational Web Services

Stateful or stateless, mapping of R objects/functions

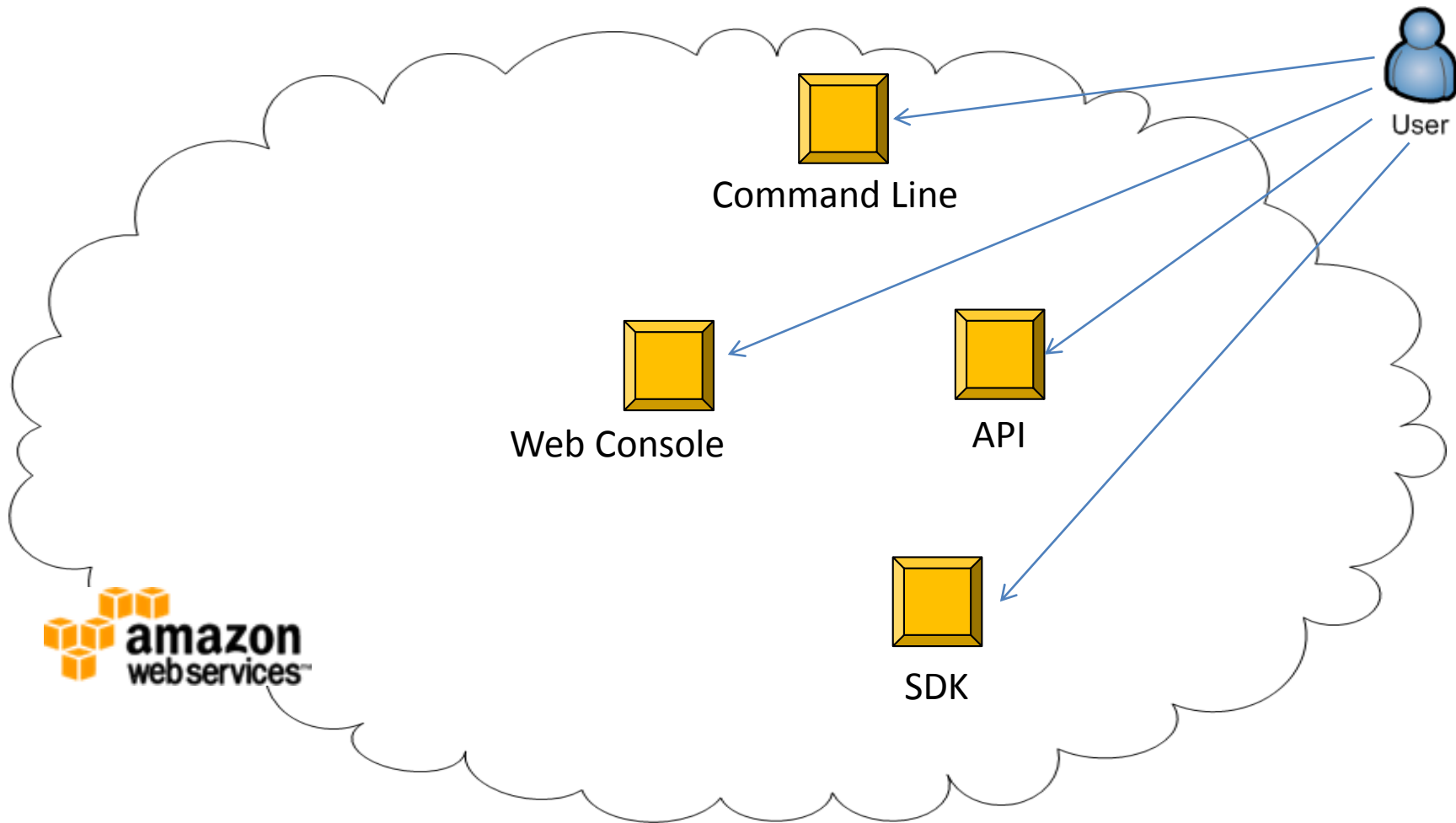
Computational APIs

Java / SOAP / REST, Stateless and stateful

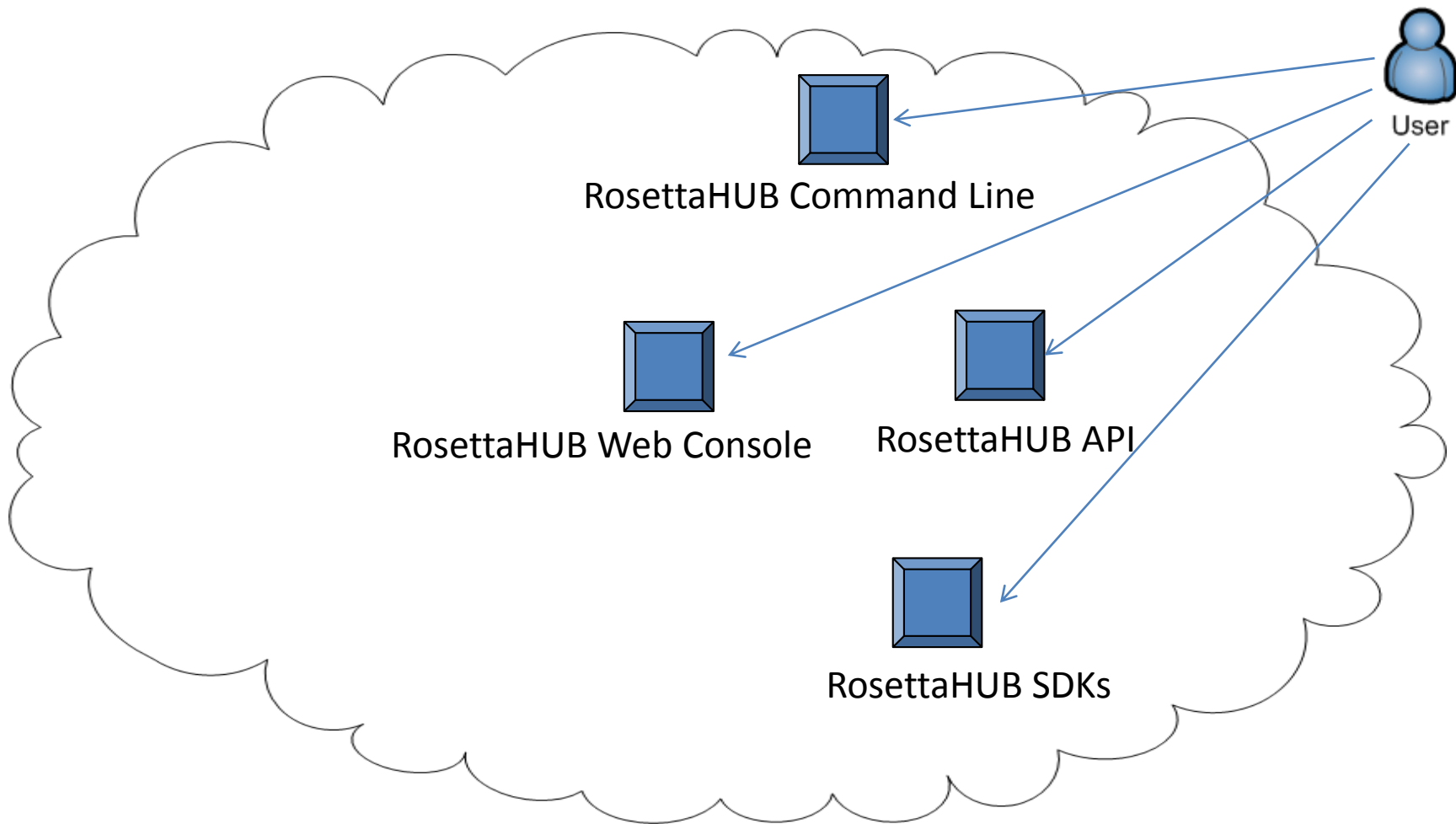
Infrastructures federation: RosettaHUB cloud



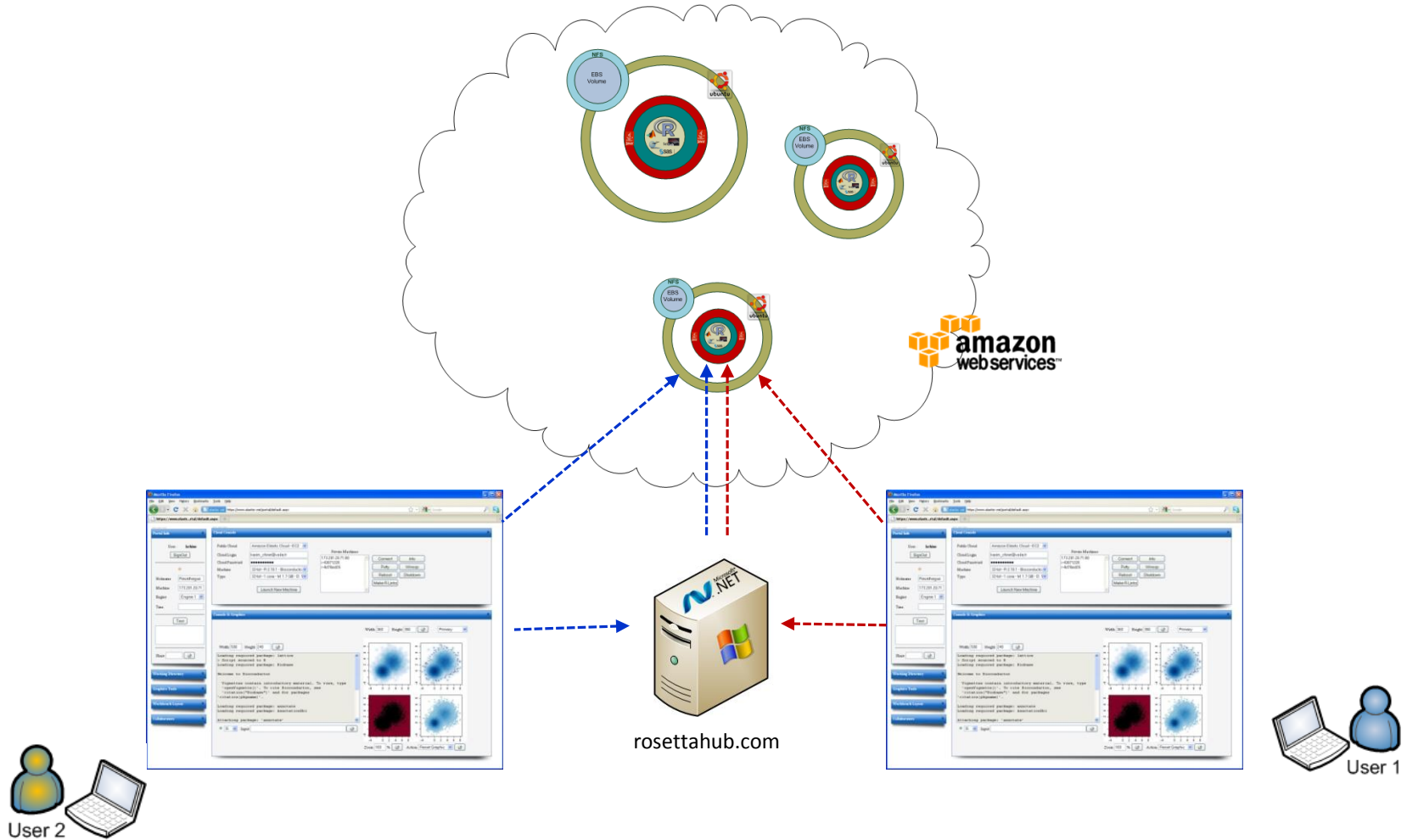
AWS: programmable infrastructure



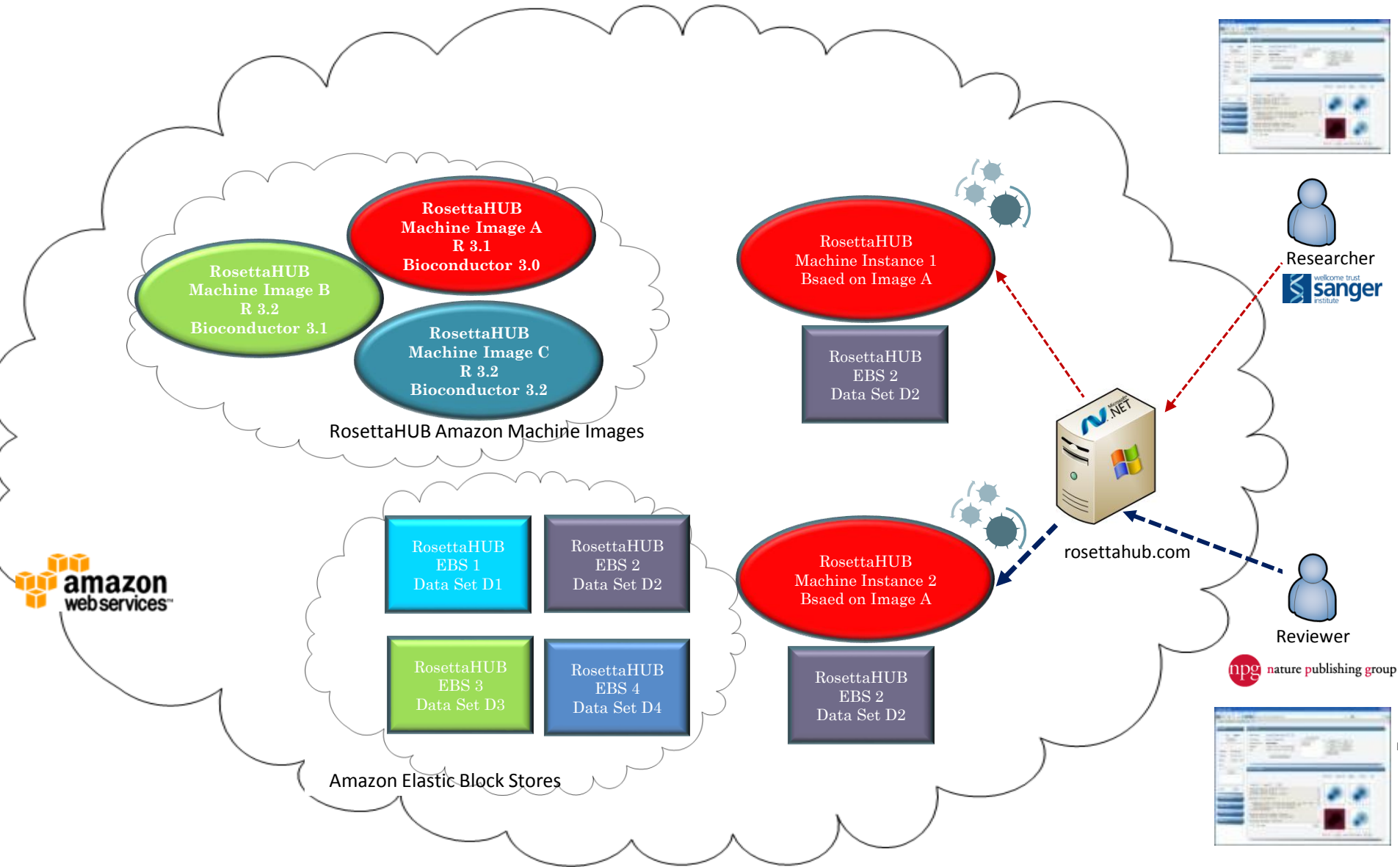
RosettaHUB: programming with data and infrastructure



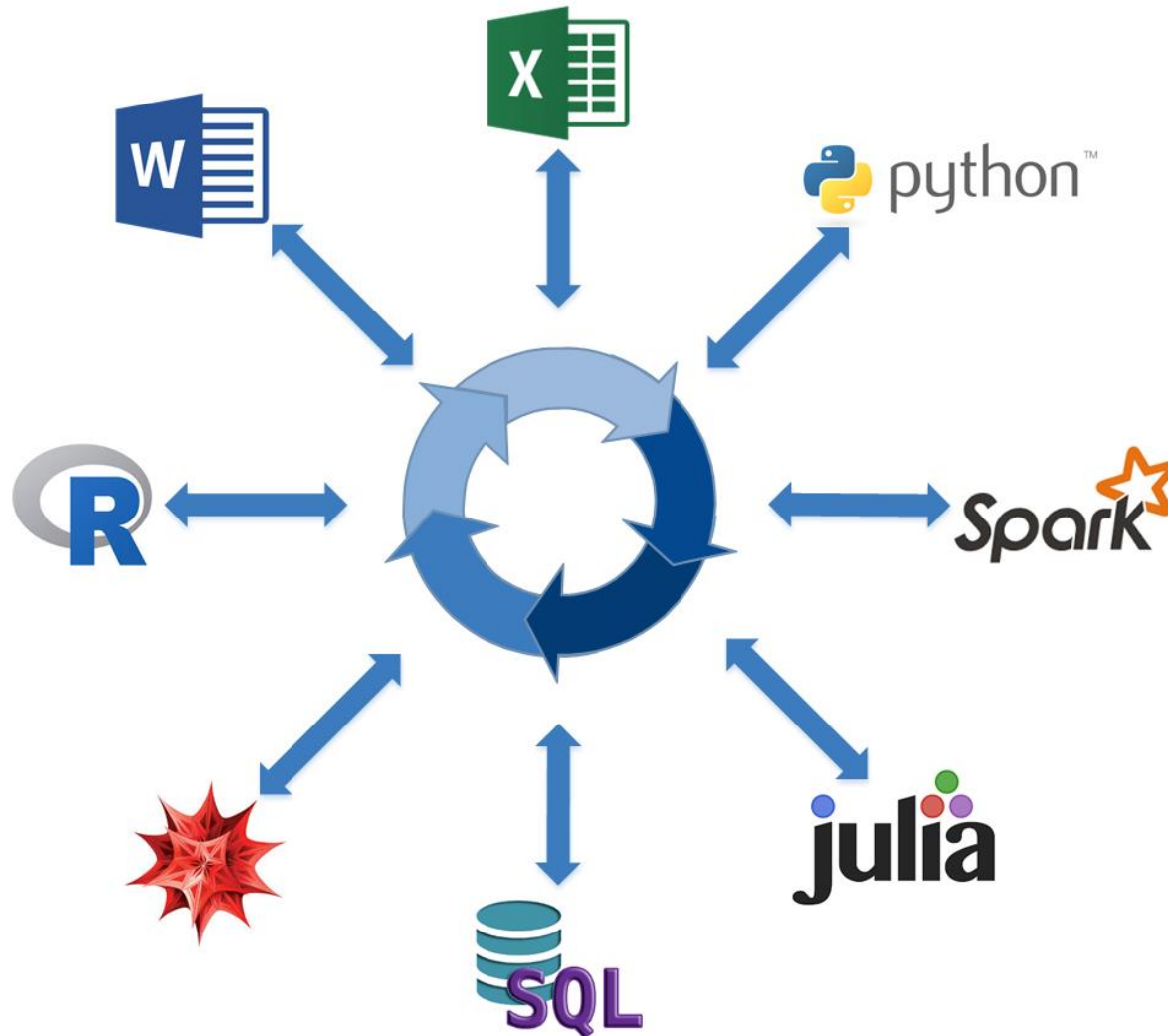
Google Docs-like real time collaboration



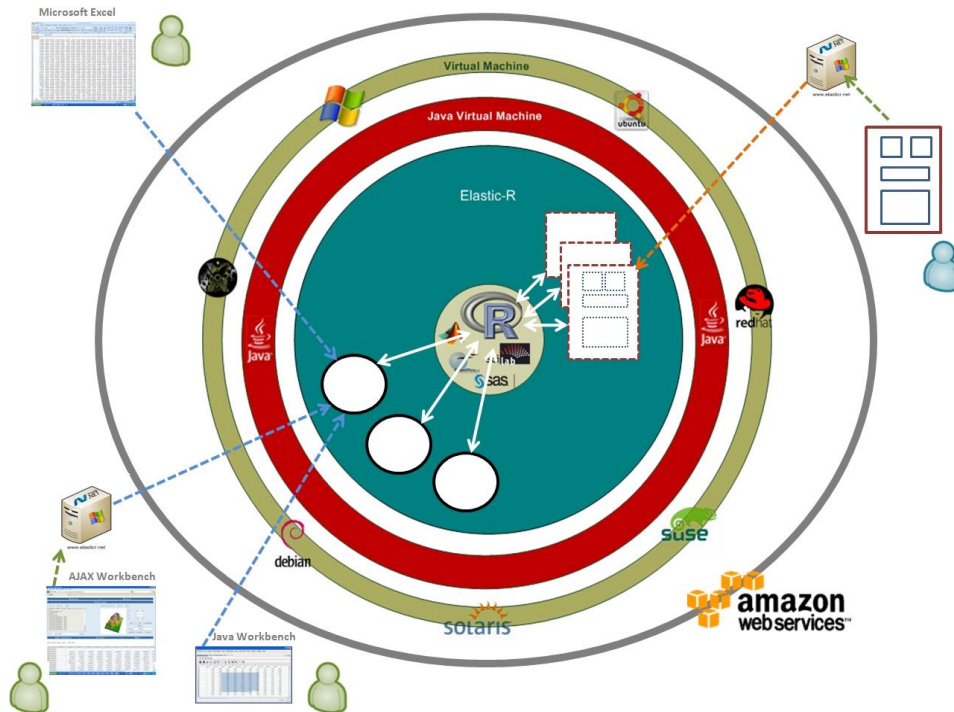
Traceable and reproducible data science



A multi-language framework

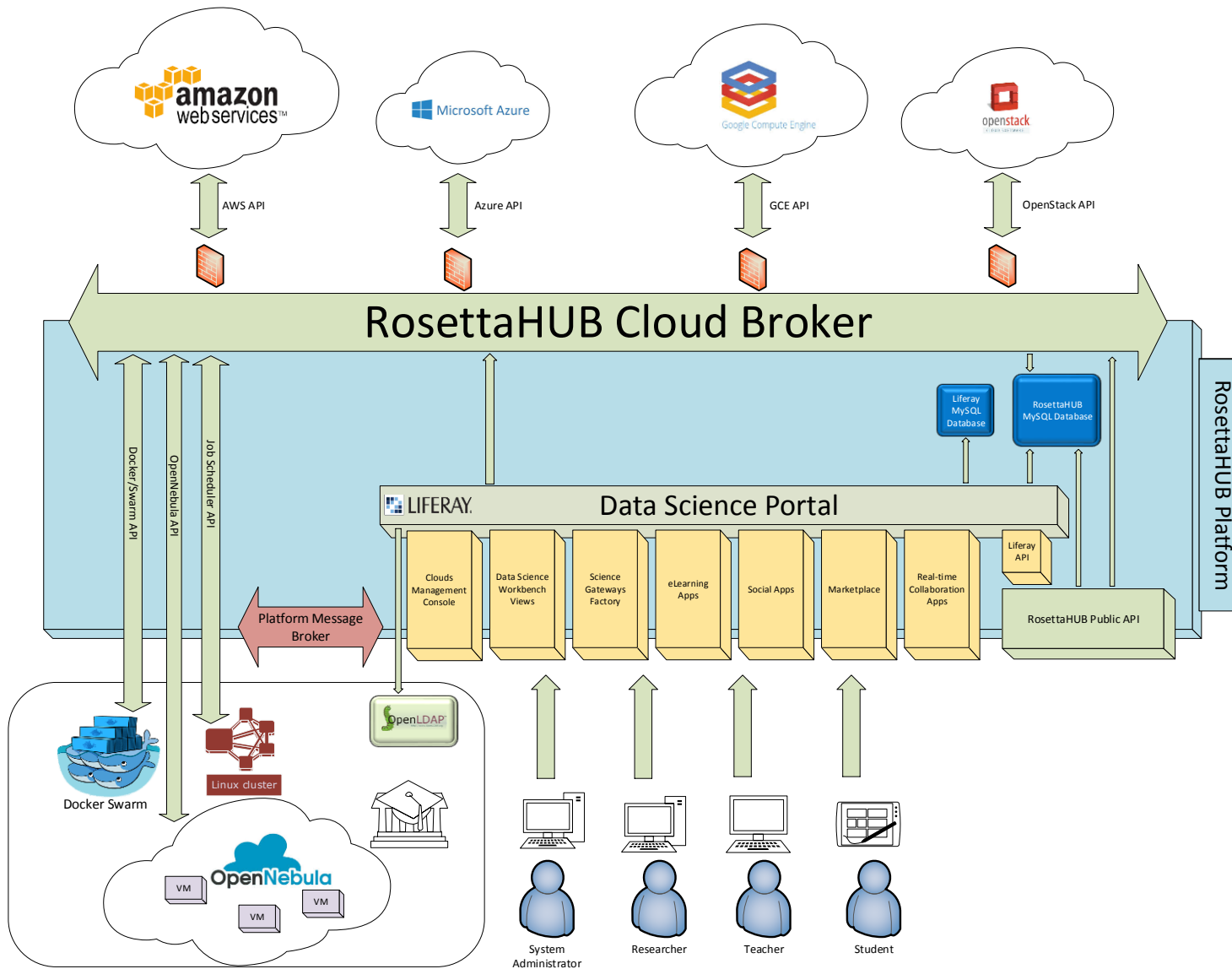


A universal data science engine



- **Reactive data science micro services platform**
- Based on Java/R/Python processes
- Events-driven remote objects/engines
- Fully Dockerized
- Collaborative spreadsheets
- Collaborative scientific graphics canvas
- Collaborative dashboards
- Collaborative widgets

The platform architecture



Inside the containers and engines

