

Creating an Open Source Infrastructure for Image Phenotyping in Clinical Research

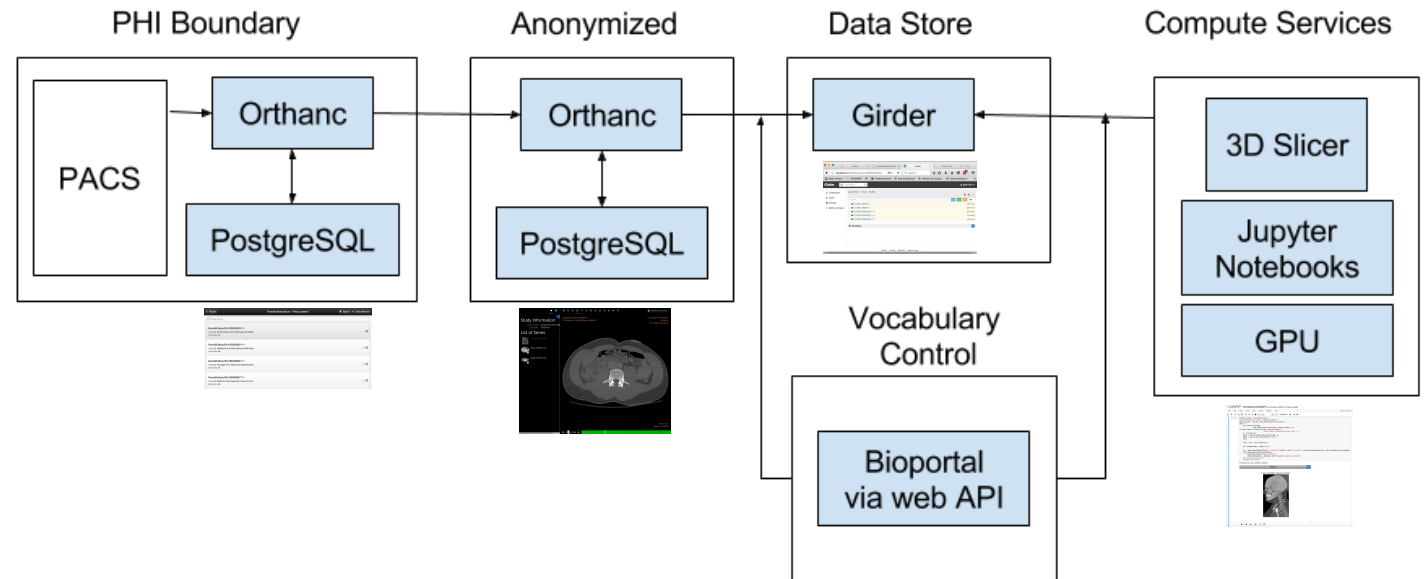
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Overview

We are building a lightweight, shareable image phenotyping environment

- Virtualization to isolate components
- Docker/docker-compose for ease of distribution
- Focus on internal “cloud computing” architecture (infrastructure entirely within an institution, but accessed primarily through web browsers)
- Also support traditional desktop computing with tools such as 3D Slicer, ITK Snap, etc.



Why Orthanc?

- Open source
- Actively maintained
- RESTful API
- Highly configurable d—identification schemas via Lua scripts

Why Girder?

- Content agnostic with support for DICOM
- Actively developed/maintained
- RESTful API
- Rich metadata support via JSON

Why Jupyter?

- Allows for centralized computing/minimizing software distribution challenges in highly regulated environments
- Supports multiple languages, including Python (with rich image processing support) and R
- Facilitates “literate science”
- Easy to create interactive programming environments requiring minimal programming skill to use.