**SVAI - NF Hackathon** 

September 2019





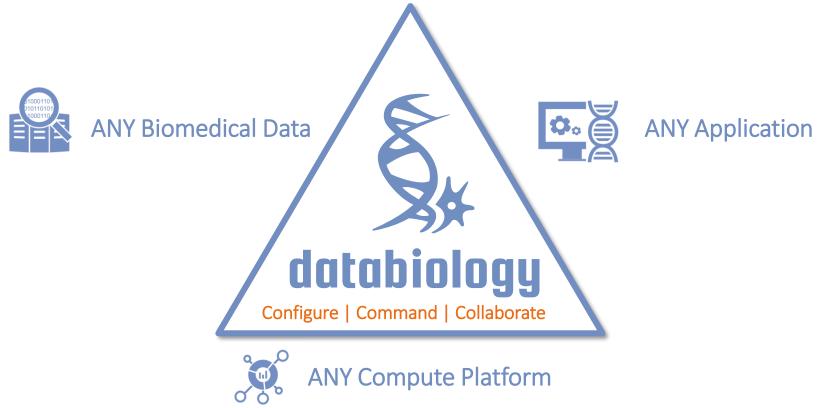
#### **Databiology Company Overview**

- Global software and services company
- Providing specialist solutions for global life sciences sector
- Business hubs in Oxford, San Francisco, Hong Kong and Mexico
- Databiology's mission is to be the enterprise platform for globally distributed biomedical data, applications and infrastructure





#### **Our Solution: Biomedical Information Management & Process Orchestration**





#### **NF Hackathon**

# **Objectives**

- Demonstrate data and metadata import and management
- Demonstrate FAIR principles applied in Data and Analysis (APPs)

# Main participant

Juan Caballero, CSO (remotely from Mexico)

# **NEUROFIBROMATOSIS**

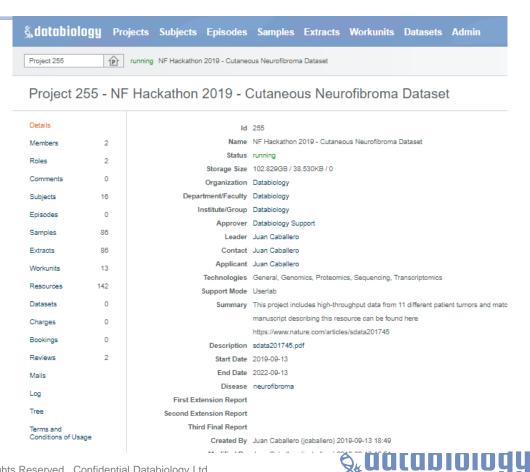
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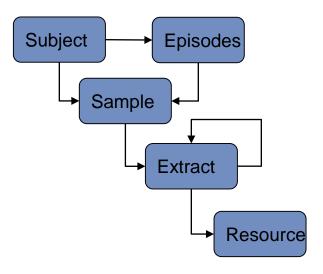
#### **Data import**

- After registration in Synapse, data was imported into our public instance
  - https://www.lab.databiology.net/
    into a private project
- Access is restricted and data is secured all the time



#### Data and metadata

Data was modeled in our data schema

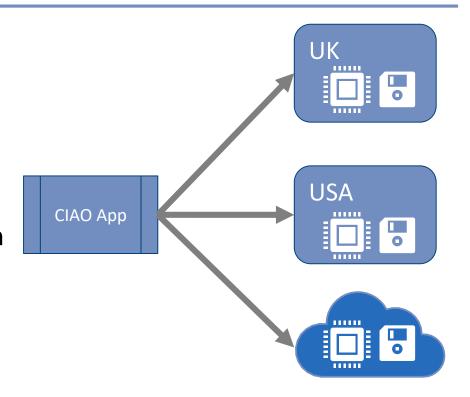


- The data model is flexible and FAIRcomplete
- Data is indexed after import, enabling search immediately



#### Real portable apps

- Analysis are performed with our CIAO apps (based on Docker)
- Any developer can create Apps with minimal requirements
- Apps are portable (can be run in diverse infrastructures)
- Apps are also FAIR-complete

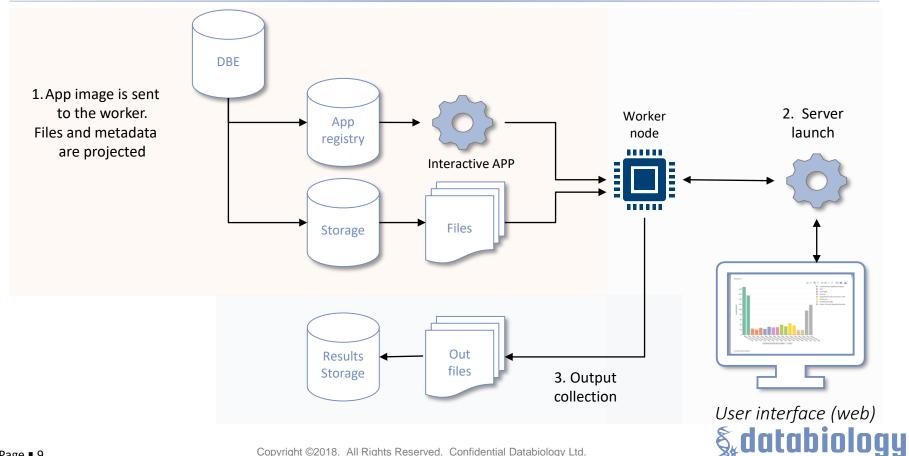




#### **Workunits**

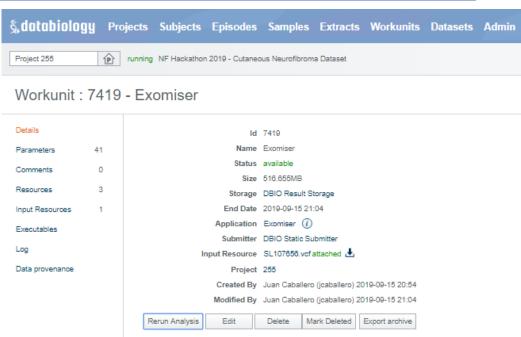
2. Computing server 1. App are run as Workunits, the container image is sent DBE to the workers. Files and Worker 1 metadata are projected App configuring the app registry automatically APP Worker 2 WU Input Files Storage Worker 3 App RefSet RefSet Worker N Storage 3. Output collection Output Results files Storage **&** databiology Copyright ©2018. All Rights Reserved. Confidential Databiology Ltd.

## **Interactive App**



#### WGS data analysis

- VCFs were analyzed with Exomiser, prioritizing genes related to HP:0001067 (Neurofibromas)
- All analysis were performed in a Workunit, keeping record of data inputs, parameters, app version, infrastructure, etc., making the analysis FAIR and reproducible.





## **Example output**

#### Prioritised Genes

NF1 Exomiser Score: 0.998 Phenotype Score: 1.000 Variant Score: 1.000 Phenotype matches: Phenotypic similarity 0.890 to Watson syndrome associated with NF1. Best Phenotype Matches: HP:0001067, Neurofibromas - HP:0001067, Neurofibromas Phenotypic similarity 1.000 to mouse mutant involving NF1. Best Phenotype Matches: HP:0001067, Neurofibromas - MP:0010314, increased neurofibroma incidence Proximity score 0.508 in interactome to NF2 and phenotypic similarity 0.883 to Neurofibromatosis type 2 associated with NF2. Best Phenotype Matches: HP:0001067, Neurofibromas - HP:0009595, Occasional neurofibromas Proximity score 0.508 in interactome to NF2 and phenotypic similarity 0.810 to mouse mutant of NF2. Best Phenotype Matches: HP:0001067, Neurofibromas - MP:0010314, increased neurofibroma incidence Known diseases: OMIM:162200 Neurofibromatosis, type 1 - autosomal dominant OMIM:162210 Neurofibromatosis, familial spinal - autosomal dominant OMIM:193520 Watson syndrome - autosomal dominant OMIM:601321 Neurofibromatosis-Noonan syndrome - autosomal dominant OMIM:607785 Leukemia, juvenile myelomonocytic - autosomal dominant ORPHA: 139474 17g11.2 microduplication syndrome ORPHA:638 Neurofibromatosis-Noonan syndrome Gene scores under compatible inheritance modes: AUTOSOMAL DOMINANT Exomiser Score: 0.998 Phenotype Score: 1.000 Variant Score: 1.000 Variants contributing to score: STOPGAIN chr17:g.29588751C>T [0/1] rs760703505 (variation viewer) Variant score: 1.000 CONTRIBUTING VARIANT Pathogenicity Data: Frequency Data: No frequency data Transcripts: No pathogenicity data



#### Metadata is projected

 Besides data transfer, metadata is also projected into the running container, facilitating complex analysis

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Jupyter resources. Json ✓ hace un minuto



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