FAIR Sequencing Data Repository based on iRODS

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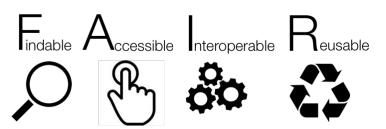
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Silvia D. Olabarriaga

Problem

- Inadequate RDM (Research Data Management) solution for NGS data (Next Generation Sequencing):
 - Individual storage and backup
 - Dispersed datasets
 - Disconnected from metadata
 - Not FAIR



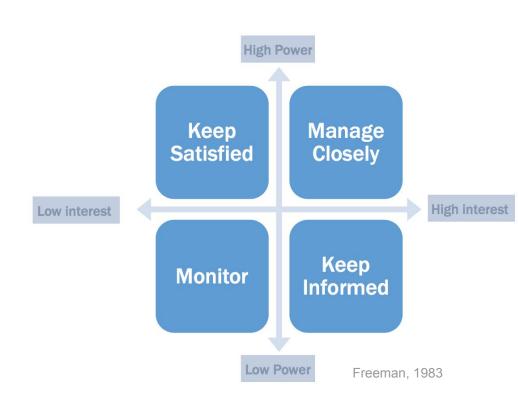
Considerations

Fit within organization

- ICT culture
- Research culture
- Sustainability vision

Adhere to international community best practices

Reuse and extend existing solutions

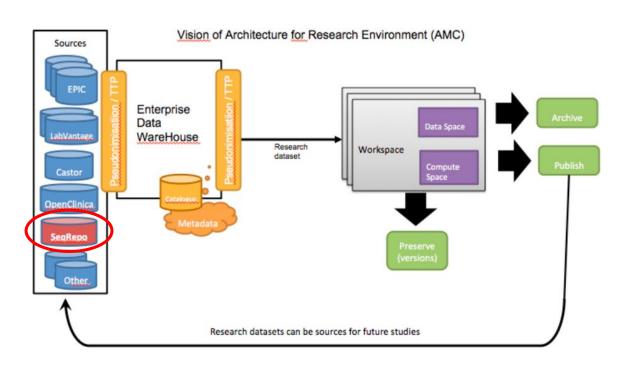


Fit into AMC Vision for RDM

Based on NFU Data4Lifesciences WP2

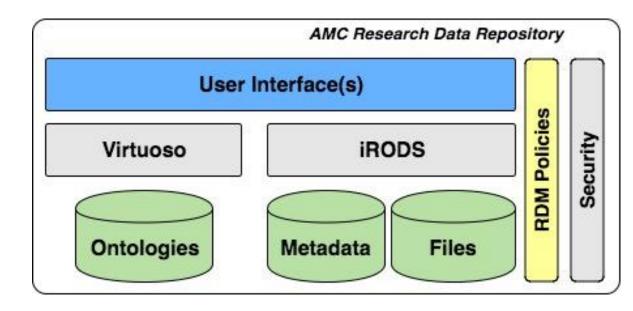
An NGS repository that is:

- Part of an ecosystem
- Controlled by AMC
- Distributed
- Scalable
- FAIR compliant
- Easy to use

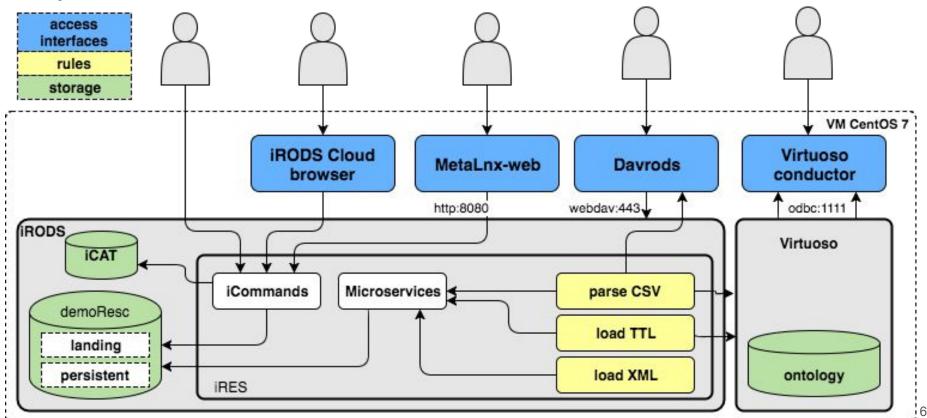


System Design

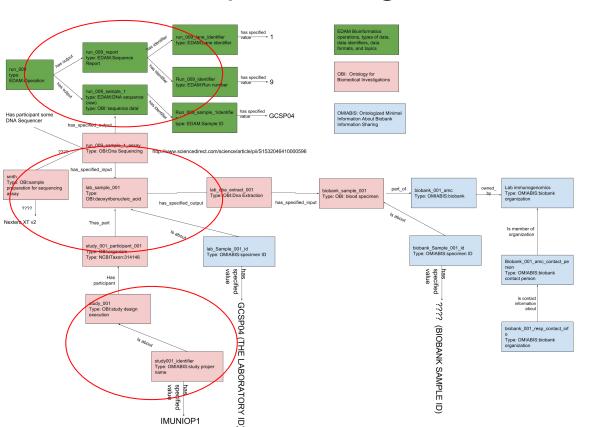
- iRODS 4.1.10
 - Middleware
 - Data virtualization
- Virtuoso 7.2
 - Triplestore
 - Supports ontologies
- User interfaces:
 - Metalnx web
 - Davrods 4.1
 - iCommands



System Architecture

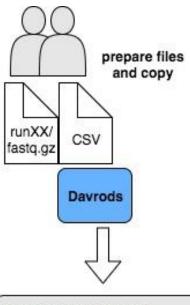


Stewardship: Ontologies



- EDAM
 - Ontology for bioinformatics operations, types of data, data identifiers, data formats, and topics
- OMIABIS
 Ontologized Minimum Information About Biobank data Sharing (MIABIS)
- OBI
 Ontology for Biomedical Investigations
- EFOExperimental Factor Ontology

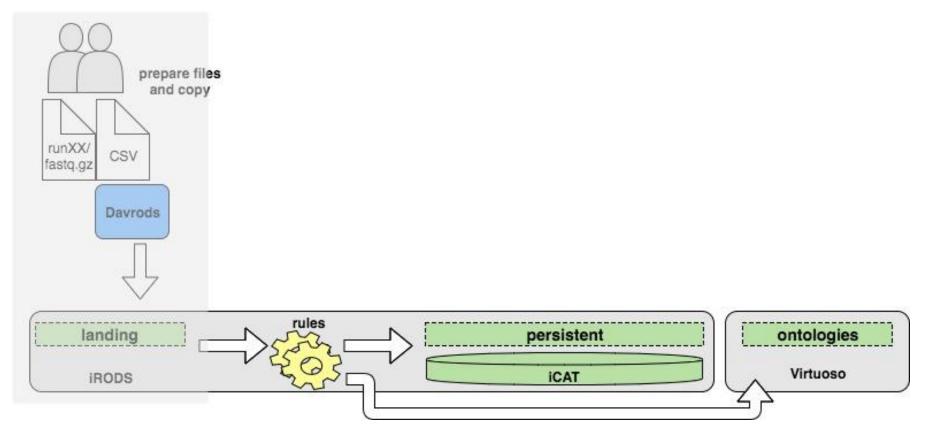
Workflow: Data Ingestion



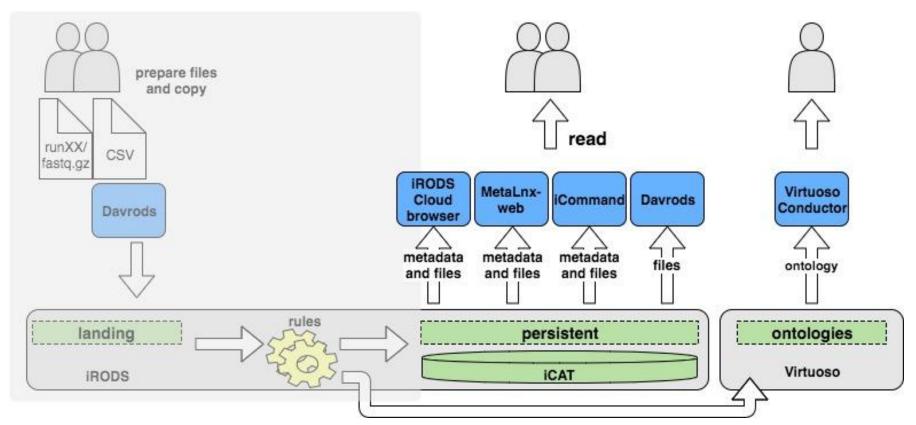




Workflow: (meta)data Registration

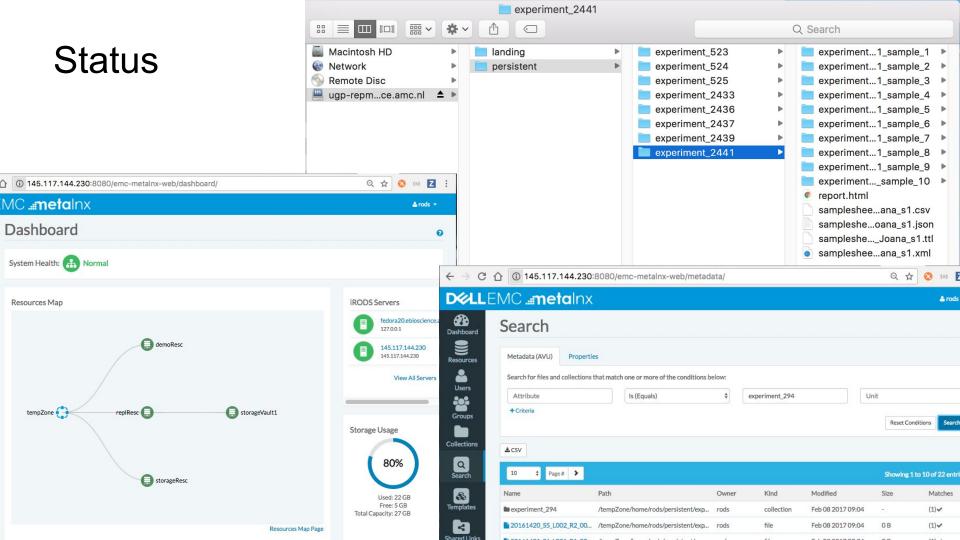


Workflow: (meta)data Retrieval

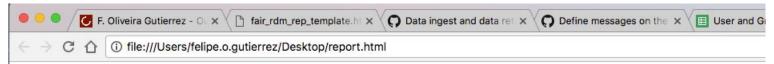


Access and Security

	iRODS roles					
functions	Davrods	iRODS Cloud Browser	Metalnx web	iCommand	Virtuoso	
Data management	user	user	user	user	user	
Metadata management	user *	user	user	user	user	
User/Group management			PI	PI		
Access control			PI	PI		
(meta)data curation		Data steward	Data steward	Data steward		
Policies and rules			Admin	Admin		
Security			Admin	Admin		



Report file

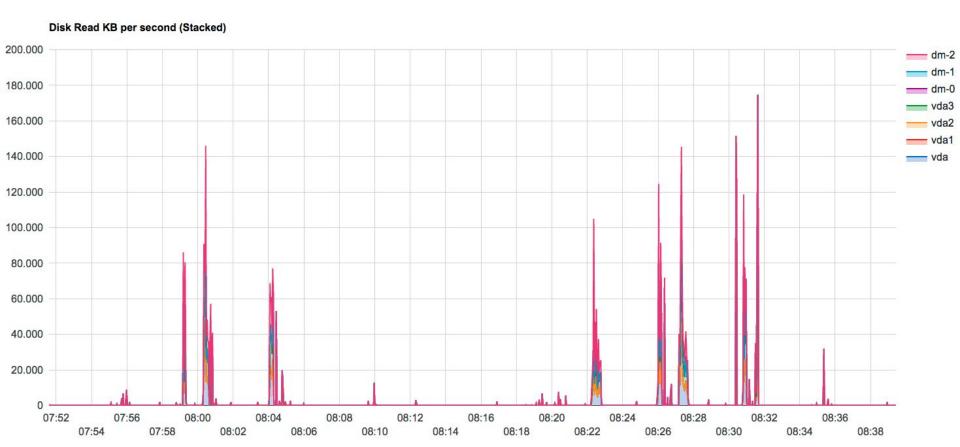


Report file of the FAIR-RDM workflow

Sample sheet	Final status	Date
samplesheet_2016_12_20_Joana_s1.csv	Workflow process completed successfully	2017-04-11

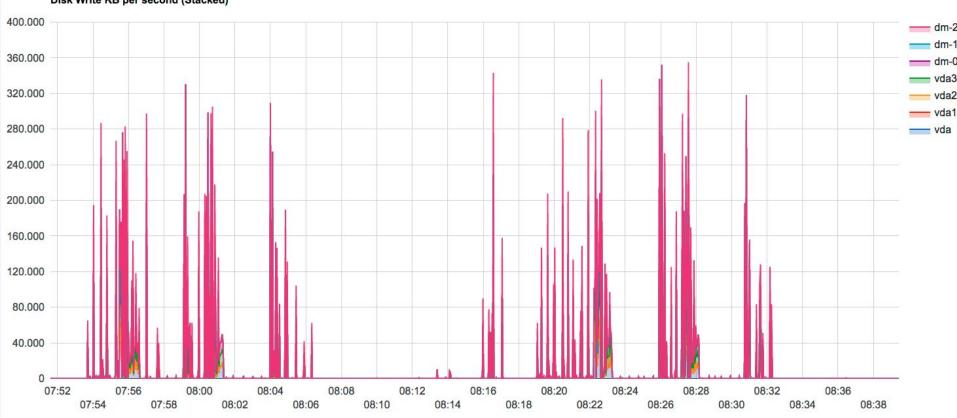
Step	Status	Code	Timestamp	Description
010	Process on going	010	2017-04-11:11:02:44	Workflow started successfuly.
010	OK	011	2017-04-11:11:02:45	Changed the permission of the landing directory to read-write successfuly.
012	OK	014	2017-04-11:11:03:05	The number of fastq files matches with the [samplesheet_2016_12_20_Joana_s1.csv] file.
011	OK	012	2017-04-11:11:03:05	The [samplesheet_2016_12_20_Joana_s1.csv] file name matches with regex expression (sa
013	OK	016	2017-04-11:11:03:05	The experiment from the [samplesheet_2016_12_20_Joana_s1.csv] file is new.
020	OK	020	2017-04-11:11:03:05	Connected to Virtuoso and get unique ID.
021	OK	022	2017-04-11:11:03:05	Created new experiment directory.
021	OK	027	2017-04-11:11:03:20	Fastq files restructured inside the experiment.
021	OK	024	2017-04-11:11:04:04	Created XML file successfuly.
021	OK	023	2017-04-11:11:06:39	Created TTL file successfuly.
021	OK	028	2017-04-11:11:06:39	Experiment [experiment_51] copied to the persistent directory.
040	OK	040	2017-04-11:11:07:30	A XML [samplesheet_2016_12_20_Joana_s1.xml] was upload.
041	OK	041	2017-04-11:11:07:32	XSD for XML [samplesheet_2016_12_20_Joana_s1.xml] exists.
042	OK	043	2017-04-11:11:07:33	XML [samplesheet_2016_12_20_Joana_s1.xml] validate by XSD schema.
043	OK	045	2017-04-11:11:08:12	XML [samplesheet_2016_12_20_Joana_s1.xml] load process OK.
046	OK	047	2017-04-11:11:08:14	Changing the permission of the persistent directory to read-only. This is the last operation o

nmon read KB/s



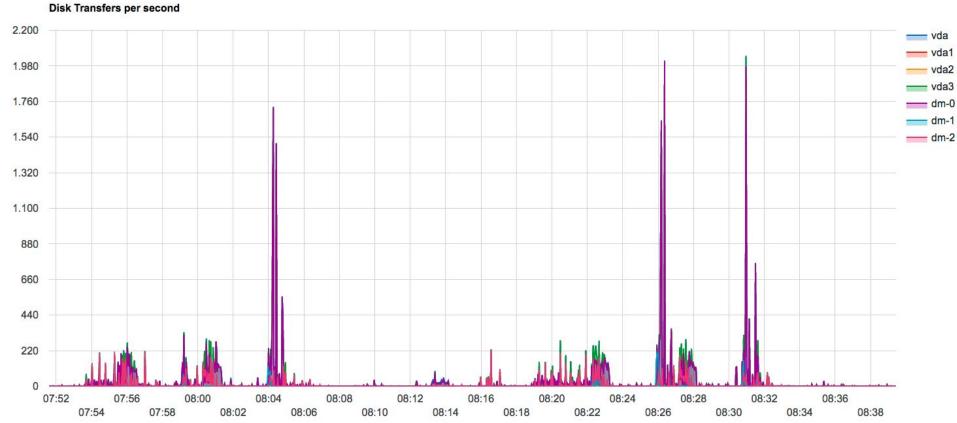
nmon write KB/s





nmon IOPs





Qualitative & Quantitative questions

- (meta)data preparation? Clear, doable, easy, ...
- (meta)data upload? Type, size, quantity, integrity, ...
- Rule processing? Report file clear and easy, system delay feedback, ...
- (meta)data retrieval? Findable, Accessible, Organized, Interoperable, Reusable, ...
- Concurrent users, variation on the number and size of files.

Acknowledgements

KEBB:

- Barbera van Schaik
- Allard van Altena

ADICT: Hans van den Berg UvA ICTS: Joyce Nijkamp

Medical Library: Lieuwe Kool
Clinical Research Unit: Rudy Scholte

Reproductive medicine: Sjoerd Repping Genetic Metabolic Diseases: Frédéric Vaz

Immunogenomics: Niek de Vries