INTERNATIONAL DATA WEEK
13-16 October 2025
Brisbane, Australia

RDA
RESEARCH DATA ALLIANCE

RDA 25th Plenary Meeting [part of IDW 2025] Collaborative Notes

Group(s) name(s) / *session title*	Life Science Data Infrastructures IG - *Linking Pixels, Proteins & Populations: Integrating Data Across Life Science Domains*
Session link for more information	https://www.rd-alliance.org/groups/life-science-data-infrastructures-ig/plenary-participation
Session programme time	Wednesday-Thursday, 15-16 October 23:00 – 00:30 UTC / Thursday, 16 October 09:00-10:30 AEST, Breakout 4
Presentation slides	RDA P25 Life Science Data Infrastructures IG.pptx

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Session summary (to be filled by group chairs):

We will use the content in the table below to highlight your work to the RDA community in a report by the Technical Advisory Board (RDA P24 report example). **Please complete ALL fields below by *Friday, 31 October*, to be included in the report** and other communication. We also ask you to update your group webpage with the key takeaways from your post-plenary session.

1. **Describe what your session is about in three sentences maximum:**
This session explored emerging practices and standards for integrating and sharing multi-modal data (imaging, structural, genomic, and other life science data types). Presentations highlighted experiences from national efforts to support multi-modal studies such as BioFAIR UK and Melbourne “PX4 Health”, regional efforts to connect services from across digital infrastructures focusing on overlapping and complementary modalities exemplified by the emerging European Life Science Connect EOSC Node, and global efforts to connect multi-modal data resources exemplified by the foundingGIDE (GIDE - Global Image Data Ecosystem) project.

2. **Highlight a maximum of five key outcomes/actions/takeaways of your session:**
    1. *Tony Burdett, BioFAIR (UK) – introduced three conceptual layers of multimodal integration (assay-based, multi-experiment, and cross-domain) while emphasising the role of persistent identifiers and provenance to link data “from assay to insight.”*
    2. *Bernie Pope, PX4 Health (Australia) – provided examples from a multimodal phenotyping and multi-omics data platform addressing reproducibility and batch effect challenges through dedicated instrumentation and standardised workflows.*
    3. *Maria Mirza, Founding GIDE (Global Image Data Ecosystem) – described efforts*

to harmonise metadata across international bioimaging repositories to enable shared APIs and cross-repository querying for a wide range of imaging modalities.

4. *Aastha Mathur, EOSC Life Science Connect Node (Europe) – shared experiences from developing a federated model connecting ELIXIR, Euro-BioImaging, EMBL, and Instruct-ERIC within the European Open Science Cloud to support interoperable FAIR data and services.*
5. *Nils Hoffmann, MOMSI Working Group (RDA) – outlined the RDA Multi-Omics Metadata Standards Integration (MOMSI) WG's landscape review of existing omics standards, published in FAIRsharing, that can guide harmonisation and identify gaps and priorities for future interoperability work.*

3. What collaborations or synergies did you discover between your group and other RDA group(s) or external (outside of the RDA) organisations?

- *RDA Sample Type Classification WG*
- *RDA Multi-Omics Metadata Standards Integration (MOMSI) WG*
- *HUPO PSI MS Metabolomics Standards Initiative Lipidomics Standards Initiative, https://hupo.org/Proteomics-Standards-Initiative-(PSI)*
- *Science for Life Laboratory (SciLifeLab) Sweden, www.scilifelab.se*
- *foundingGIDE, https://founding-gide.eurobioimaging.eu/*
- *BioFAIR UK, https://biofair.uk/*
- *Life Sciences Connect EOSC Node, https://eosc.eu/building-the-eosc-federation/eosc-node-life-sciences-connect/*

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Attendee Check-in

New to the RDA? Check out where to start **here**

Get involved in the **RDA Community**

This meeting will take place in accordance with the **RDA Code of Conduct**

Please complete this table to indicate your attendance (add rows as needed):

Full Name	**Affiliation**	**Location**	**Email**
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Meeting Aims

This meeting will explore emerging practices and standards for integrating and sharing multi-modal data—including imaging, structural, genomic, and other life science data types. The session will present early experiences from European efforts to bring together services from ELIXIR, EMBL, Euro-BioImaging, and Instruct-ERIC as part of a federated Life Science Research pilot node within the European Open Science Cloud (EOSC). It will also provide an opportunity to connect with global initiatives such as the Global Image Data Ecosystem (GIDE), to identify common challenges and promising approaches that could inform broader data integration efforts across biomolecular disciplines.

The examples presented will provide a starting point for discussion with the wider RDA community to identify opportunities for adoption of standards, future work, and new collaborations, emphasizing practical considerations for designing interoperable, cross-domain data services and supporting FAIR data sharing practices. The meeting outcome will be a short report summarising the approaches discussed, highlighting shared challenges and potential areas for collaboration, and outlining next steps for engaging interested participants in ongoing or new initiatives.

The meeting will focus on examples from the biomolecular life sciences but is open to and will provide context for anyone interested in disciplinary challenges related to combining different types of research data.

Agenda

Time	Topic	Format	Speakers / Facilitators

(AEST)			
09:00	Welcome & Introduction (10min)	Brief introduction to the RDA group(s) hosting the session followed by an interactive icebreaker to the topic where all participants are invited to engage.	Wolmar Nyberg Åkerström Jeff Christiansen
09:10	Setting the scene: Linking Pixels, Proteins & Populations (30min)	coordinated flash talks providing different perspectives on integration and sharing multi-modal data followed by Q&A	Tony Burdett Bernie Pope Maria Mirza Aastha Mathur
09:40	Discussion: Practices and standards for integrating and sharing multi-modal data (25min)	Guided discussions in smaller groups with reporting supported by Mentimeter and collaborative notes.	Wolmar Nyberg Åkerström
10:05	Synthesis: State of the art and opportunities for future collaborations (20min)	Reporting from the smaller groups and open plenary discussion moderated by the session chairs	Wolmar Nyberg Åkerström Nils Hoffmann
10:25	Wrap-Up & Next Steps (5min)	Summary of today and where next	Wolmar Nyberg Åkerström
10:30	END		

Collaborative Session Notes *(To be used by participants and chairs during the session)*

4 presentations:

Tony Burdett BioFAIR.
3 conceptual layers of multimodal integration:

- Multimodal assays (one expt, several different techniques) - e.g. spatial omics (webAtlas from HCA, wheat atlas)
- Multimodal Experiments (several coordinated experiments to probe one phenomenon) - e.g. conducting molecular (multi-omics) and cellular phenotyping to create a holistic feature of a single perturbation (MorPhiC)
- Cross-domain analysis - combining and resign data of multiple modalities for exploration or hypothesis testing - e.g. HoloFood (gut microbiome of framed animals + genomics from hosts). Farm Scale Digital twinning from Rothamsted - drone, climate

Combine / linking data at Sample level (e.g. BioSample)
BioFAIR BioCOmmons - Data COmmons + Methods COmmons + People COmmons.

Qs for Tony:

- Any reflections on what are the common focal points for integration? E.g. molecule, cell, tissue, organism, population? UniProt, BioSamples, … where is there global consensus?
    - A: Not yet a consensus. Can model things explicitly with a detailed knowledge graph, but can be very difficult to tease apart later. Very use case dependent. Think about anticipated reuse of the data. E.g. plant cross breeding - very complex breeding program (20 generations) - consider the last generation + passport info on how the last generation was produced could be sufficient.
- Where do you see the greatest practical challenge in making multi-modal data integration possible? Are formats and repositories often too specialised for one modality?
- What strategies have proven effective in motivating people to invest the effort required to add comprehensive metadata on platforms such as BioSamples?

Bernie Pope, Australian BioCommons
PX4 Heath initiative UoM.
Assay based multi-modal approach
Phenotyping clinic - variety of tests (BMI, clinical tests, wearables etc)
Integrated multimodal omics (genomics, epigenetics, metabolomics, lipidomics, etc)
Dedicated equipment to assist in consistency.

Multimodal data = combo of data of multiple modalities about the same individual and groups of individuals.

Challenges:

- Batch effects - especially relevant for longitudinal studies
- Highly dimensional data, so dimension reduction will be necessary
- Interoperability - with external studies (e.g. UK BioBanks, Precise SIngapore)

Qs for Bernie:

- Is there a difference in what you do to enable effective primary use of the data and what is later asked for to enable reuse of it? How did you approach harmonising data/metadata?
- using dedicated mass spec instrument does not sound very scalable. Do you consider implementing some calibration approach?
- Who should drive the work on methodology for multi-modal data integration?

Maria Mirza - EuroBioImaging
FoundingGIDE - increasing coordination among global bioimage data resources. Image file sizes are ever increasing, >160 file formats. Aiming to bring together DBs across Europe, Japan, Australia. Can 3 repositories identify shared info, and arise at an API to query across. Metadata was harmonised.
Once the foundations are built, aiming to link bioimaging data to other data types - e.g. Same study - imaging data (in BioImag Archive) + Proteomics data (in PRIDE), Transcriptomics data (ArrayExpress), and Data Analysis code (GitHub)

Qs for Maria:

- Are the descriptive models for the Global Image Data Ecosystem aligned with those of Omics and other modalities? E.g. for samples, molecules, cells …

    - The approach is to describe the images using sufficient metadata and to be able to iteratively add more metadata as needed. The metadata model is developed iteratively using feedback from the community and it is aligned with the imaging community needs.

Aastha Mathur - EuroBioImaging

A life Science Node in EOSC
EuroBioImaging + ELIXIR, Instruct ERIC, EMBL
The vision of a web of FAIR Data and Services to enable horizontal analysis
EOSC - sharing infrastructure, data software practices in an interoperable way.
The life science node - a dedicated

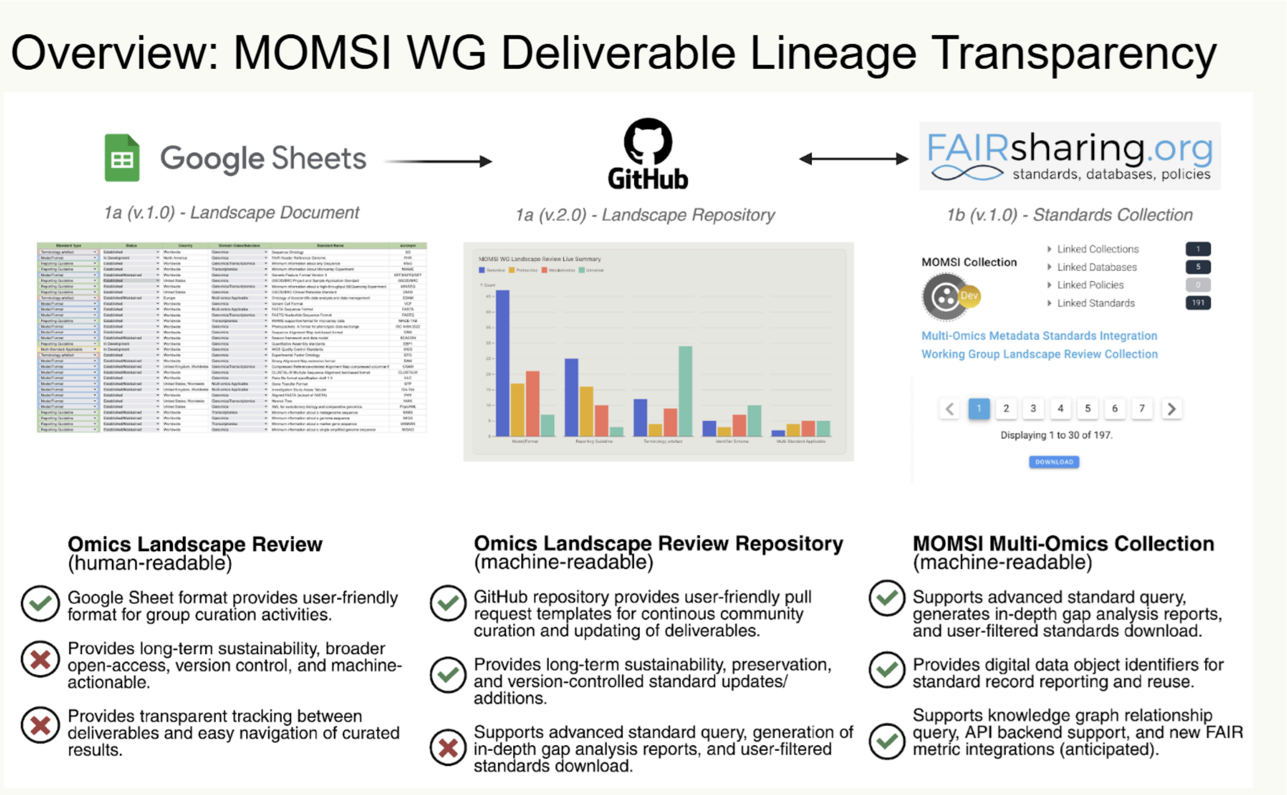
Qs for Aastha:

- Who decides which (meta)data models to use for the joint services? Are you already aligned where the partners have services for the same modalities?
- What obstacles do you expect concerning semantic data interoperability within and between EOSC nodes? Will EOSC favor a few centralized repositories to reduce complexities of Interop?
    - EOSC wants to preserve richness of existing repositories and resources - aim for linking across these. EOSC is not just for life science - the discipline nodes are aiming for a more meaningful inroad to the services though for people what are associated with that discipline
- are there examples of practice to integrate multimodal data in other disciplines in EOSC (eg physics etc) that we in life science might learn from?

GENERAL DISCUSSION:

Tony - BioFAIR is thinking about data journeys as opposed to only data repositories (which are specialist, siloed) - a set of transformations from assay to insight, with bridges to describe transformations (using PIDs etc) in a robust way.

MOMSI WG



Overview: MOMSI WG Deliverable Lineage Transparency

Omics Landscape Review (human-readable)

✓ Google Sheet format provides user-friendly format for group curation activities.

✗ Provides long-term sustainability, broader open-access, version control, and machine-actionable.

✗ Provides transparent tracking between deliverables and easy navigation of curated results.

Omics Landscape Review Repository (machine-readable)

✓ GitHub repository provides user-friendly pull request templates for continous community curation and updating of deliverables.

✓ Provides long-term sustainability, preservation, and version-controlled standard updates/ additions.

✗ Supports advanced standard query, generation of in-depth gap analysis reports, and user-filtered standards download.

MOMSI Multi-Omics Collection (machine-readable)

✓ Supports advanced standard query, generates in-depth gap analysis reports, and user-filtered standards download.

✓ Provides digital data object identifiers for standard record reporting and reuse.

✓ Supports knowledge graph relationship query, API backend support, and new FAIR metric integrations (anticipated).

- Omics Standard Landscape Review Curation Workflow & Interactive Web-based Dashboard Tool (10.15497/RDA00133)
- https://rda-momsi.github.io/Dashboard/

Summary

Welcome & Introduction

Wolmar: Welcome and introduction to the session.

- Focus on exploring what “multi-modal” means across different research and infrastructure contexts,
- Aim to identify relevant standards and starting points for continued discussions.
- Participants were invited to use Mentimeter for Q&A and the collaborative notes for check-in, follow-up and documenting possible collaborations.

Tony: BioFAIR use cases for life sciences multi-modal data integration.

- BioFAIR is a UK federated digital research infrastructure focused on FAIR research data management, service coordination, data access, skills and reuse.
- Three conceptual layers of multi-modal integration: assay-level integration, coordinated multi-experiment integration, and cross-domain data analysis.
- Assay-level integration examples: spatial transcriptomics and single-cell RNA sequencing in Human Cell Atlas / WebAtlas contexts and wheat studies.

- Multi-experiment integration example: MorPhiC, combining molecular and cellular phenotyping to understand gene function.
- Cross-domain integration examples: HoloFood and Rothamsted Research digital twinning, combining microbiome, host genomics, phenotyping, imaging, crop yield and environmental data.
- Practical linking points: shared sample provenance and persistent sample identifiers.
- Main challenge: culture change and early use of shared identifiers so that data are linkable later.

Bernie: Melbourne “PX4 Health” Initiative — Predictive, Preventative, Personalised and Participatory.

- PX4 Health combines deep phenotyping, biobanking, multi-omics assays and data commons infrastructure around individuals and cohorts.
- Modalities include proteomics, metabolomics, lipidomics, blood genome sequencing, clinical measures, questionnaires and potential links to population health and medical records.
- Data are being brought together in a Gen3-based data commons.
- Pilot status: around 160 volunteers through the phenotyping platform, with samples being sequenced.
- Dedicated mass spectrometry equipment is used to reduce batch effects and improve comparability.
- Key challenges: batch effects, longitudinal calibration, high dimensionality, interpretability, privacy, consent, re-identifiability and interoperability with external studies such as UK Biobank and PRECISE Singapore.

Maria: Founding a Global Image Data Ecosystem.

- foundingGIDE is a global initiative with partners in Europe, Australia and Japan, focused on coordination among image data resources.
- Imaging challenges: increasing image file sizes, more than 160 image file formats and fragmented standards for image experiment metadata.
- Repositories in scope include SSBD, BioImage Archive and IDR for bioimaging, with additional preclinical imaging partners.
- Aim: shared metadata across repositories without replacing existing repository data models.
- Outputs include metadata harmonisation, ontology recommendations and future metadata packaging recommendations for APIs and applications.
- Example linkages in BioImage Archive: imaging data connected to transcriptomics in ArrayExpress, proteomics data and GitHub analysis code.
- Main challenge: community consensus around metadata, not only technical representation.

Aastha: A Life Science Node in EOSC.

- The Life Science Node in EOSC involves Euro-BioImaging ERIC, ELIXIR, Instruct-ERIC and EMBL.

- EOSC aims to support FAIR data and services for storing, sharing, processing, analysing and reusing research outputs across disciplines and borders.
- The Life Science Node is intended as a dedicated space for life science researchers to discover, access and reuse FAIR research objects and services.
- Data types include imaging, structural biology, biomolecular and multi-omics data, and correlative or multi-modal datasets.
- Services include consultation, data acquisition support, metadata support, deposition services, ELIXIR Core Data Resources and infrastructure databases from EMBL.
- OSCARS FIESTA example: reusable image analysis workflows across bioimaging, astronomy and environmental sciences.

Discussion: Practices and standards for integrating and sharing multi-modal data

Tony: Common focal points for integration.
- No single global consensus on whether integration should centre on molecule, cell, tissue, organism, population or another level.
- Appropriate modelling depth depends on anticipated reuse rather than complete representation of the data collection process.
- Practical approach: use sufficient identifiers and provenance to enable later interpretation, without over-modelling every relationship.

Aastha: Depth of interoperability.
- Planned atlas-style projects can support deeper interoperability through shared procedures and coordinated data generation.
- Existing databases may only support shallower interoperability, but this can still improve integrability.

Bernie: Calibration and scalability in PX4 Health.
- Dedicated mass spectrometry equipment is used for consistency within the PX4 Health platform.
- Absolute quantification and calibration are important strategies for reducing batch effects when platforms change over time.
- Main scaling constraint for PX4 Health: cost rather than mass spectrometry throughput.

Maria: Alignment of foundingGIDE with omics and other modalities.
- foundingGIDE metadata schema items are associated with ontology references.
- RO-Crate packaging is intended to support bridges to ontologies and metadata from other domains.
- The model is iterative and can be extended as community needs develop.

Tony: Data journeys rather than repositories.
- Multi-modal integration should be considered as a journey from assay to insight rather than as a problem of aligning repository schemas alone.
- Persistent identifiers and provenance are bridge points between transformations along that journey.
- Specialist repositories can remain useful if data can be exported, linked and transformed robustly.

Maria: Metadata export rather than new repositories.
- foundingGIDE exports metadata from existing repositories rather than creating another database.

- Exported metadata can be indexed into APIs and applications while data remain in their original repositories.

Aastha: Semantic interoperability within and between EOSC nodes.

- EOSC does not aim to replace existing repositories with a small number of centralised repositories.
- EOSC aims to preserve existing resources and methods while enabling common communication between them.
- Key obstacles include cross-domain semantic diversity, legal and political issues, and organisational coordination.
- Discipline-specific nodes can provide more meaningful entry points while still connecting to the wider EOSC landscape.

Synthesis: State of the art and opportunities for future collaborations

Nils: Multi-Omics Metadata Standards Integration Working Group.

- MOMSI WG supports standard selection and harmonisation for multi-omics metadata integration.
- Existing output: Omics Standard Landscape Review Curation Workflow and Interactive Web-based Dashboard Tool, DOI: 10.15497/RDA00133.
- Dashboard: https://rda-momsi.github.io/Dashboard/.
- Planned outputs include a Multi-Omics Metadata Integration Checklist Template, use-case gap analyses and final recommendations.

Participants: Standards and collaboration opportunities.

- Possible need for a short document describing different types of multi-modal data sharing and reuse scenarios.
- Possible need for data stewardship practice to support multi-modal data sharing and effective integration.
- Potential collaborations or synergies: HUPO PSI MS, Metabolomics Standards Initiative, Lipidomics Standards Initiative, SciLifeLab, RDA Sample Type Classification WG and MOMSI WG.
- Possible alignment with curated resources and atlases such as UniProt and the Human Protein Atlas.

Wrap-up and next steps

Wolmar: Closing and follow-up.

- Participants were invited to add links, groups and organisations to the collaborative notes for follow-up.
- Organisers will use Mentimeter input, collaborative notes and the recording to complement the session notes.
- Follow-up may include contacting participants who shared details in the collaborative notes and continuing the discussion through the RDA Life Science Data Infrastructures IG.