

# RO-Crates for BioImaging

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## Abstract

Bioimaging research increasingly relies on complex, high-volume microscopy data that is still rarely shared in a FAIR and interoperable way. While formats such as OME-Zarr address modern, cloud-native data storage and access, the bioimaging community continues to lack Linked Data-ready metadata standards that capture experimental context and relationships between research artefacts. Research Object Crates (RO-Crates) provide a promising, JSON-LD-based mechanism to package data together with rich, standardized metadata. In this work, we explore how RO-Crates can complement existing Open Microscopy Environment standards, with a focus on OME-Zarr. We present recent practical experiences, including the use of RO-Crates in the OME 2024 NGFF Challenge, and discuss ongoing efforts toward formal RO-Crate profiles and metadata pipelines for major bioimaging repositories. Together, these efforts highlight RO-Crate as a valuable addition to the modern bioimaging metadata toolkit.

## Keywords

bioimaging, RO-Crate, OME-Zarr, JSON-LD

## 1. Introduction

Bioimaging has been core to the life sciences for the last two centuries. Today, an immeasurable number of research projects rely on (often expensive) microscopy equipment to gain detailed insight into the living world. While there are solid examples of curated databases, e.g., the Image Data Resource (IDR), BioImage Archive (BIA), and SSBD [7, 2, 3], this wealth of data is rarely shared in a FAIR (Findable, Accessible, Interoperable and Reproducible) way.

The Open Microscopy Environment (OME) initiative has been developing open standards to bridge the gaps in metadata representation for microscopy images, with a particular focus on light microscopy. The original infrastructures designed in the early 2000s by the OME consortium relied on an XML model and the TIFF data formats, and are still valuable to this day. Nevertheless, with the development of new technologies, research software engineers have been developing ways to support the modern needs of bioimaging [4].

On the data side, projects like OME-Zarr provide cloud-native, AI-ready ways to store and share bioimaging data [5]. However, on the metadata side, the world is still in need of FAIR, Linked Data-ready standards for bioimaging. An exciting and promising recent development is the Research Object Crates (RO-Crates) project, which provide infrastructure to pack research artifacts alongside metadata in JSON-LD in standardized, FAIR formats [6].

The value of RO-Crates shines in complex research setups, where rich metadata is essential or where multimodal data from distributed systems needs to be containerized, like in bioimaging. In this poster, we describe progress, perspectives and challenges related to enabling RO-Crates benefits in the context of the Open Microscopy Environment, OME-Zarr and bioimaging data management.

For example, we describe the use of RO-Crate to enrich OME-Zarr in the OME 2024 NGFF Challenge. The data submitted was required to host a top-level `ro-crate-metadata.json` file with metadata minimally containing terms for the specimen (NCBI taxon identifiers) and imaging modality (Biological

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Imaging Methods Ontology terms). While the `ro-crate-metadata.json` file is not part of the OME-Zarr v0.5 specification, the NGFF validator tool detects and validates RO-Crate metadata, demonstrating the interoperability of Zarr objects with RO-Crate.

Other lines under study include (1) an update and formalization of a RO-Crate 1.2 profile for extending OME-Zarr data, covering minimal standardized metadata and a mechanism for extensibility, both for attached and detached RO-Crates; (2) an evaluation of RO-Crate for inclusion in the OME-Zarr specification, not only for contextual entities like licenses and descriptions, but potentially for representing relations between research artifacts; and (3) the development of pipelines to normalize and export metadata from IDR, BIA and SSBD in RO-Crate, so as to generate high-quality RDF representations of the data in the context of the FoundingGIDE project [1].

Successfully combining bioimaging workflows with robust FAIR data management practices presents a substantial hurdle. A variety of equipment and experimental settings, with complex physics, chemistry and biology on one side, and terabyte to petabyte scale, heterogeneous datasets to be harmonized, distributed and analyzed on the other. While Linked Open Data technologies offer a promising framework for integration of all these components, they also introduce their own challenges.

It is precisely that complexity that makes interoperable bioimaging metadata a bottleneck in global life sciences research. We believe that RO-Crate may prove itself a valuable addition to the modern bioimaging metadata toolkit, contributing to the integration of outputs across multiple settings.

## Declaration on Generative AI

During the preparation of this work, the authors used GPT 5.2 in order to: abstract drafting and formatting assistance. After using this tool/service, the authors reviewed and edited the content as needed and take full responsibility for the publication's content.

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