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Histological Data Sharing Guide

Introduction

This guide provides instructions for sharing histology data across labs. Following these guidelines will ensure your histology datasets are findable, accessible, interoperable, and reusable (FAIR principles), maximizing their scientific value and impact.

Repositories

Repository Links:

- **Zenodo**: https://zenodo.org (50 GB of storage per file)
- **Figshare**: https://figshare.com (5 GB of storage per file up to 20 GB, in the free plan)
- **MorphoSource**: https://www.morphosource.org (No hard storage limit)

For 2D data, **Zenodo**, run by CERN, is a free and open-source platform known for its long-term preservation and support for a wide range of file formats.

Another 2D option is **Figshare**, a for-profit company, offers features like data usage metrics and private sharing options, with storage options dependent on subscription tiers.

Repository Selection Guidelines:

Choose Zenodo or Figshare when:

- You have traditional 2D histology images.
- You need simple, straightforward data sharing.
- Your data consists primarily of standard image formats.
- You want guaranteed DOI assignment and long-term preservation.

Choose MorphoSource when:

- You have 3D morphological data (CT scans, serial sections).
- You want specialized tools for 3D data visualization.
- You might need project-based organization with multiple collaborators.
- Your data includes complex imaging workflows with multiple file types.

Aim to ensure that your histology data is properly documented, easily discoverable, and maximally useful to the research community. The choice of repository should align with your data type, intended audience, and long-term preservation goals.

Data Types and File Formats

Data Types:

Histology, 3D morphological data, serial section imagery

File Formats:

Traditional histology images: .tiff, .png, .jpg, .svs (whole slide images)

3D and volumetric data:

- STL files (3D surface models)
- PLY files (3D point clouds)
- NRRD files (volumetric data)

Serial section data:

- Sequential histological section images
- Image stacks for 3D reconstruction

Annotations or metadata: .csv, .json, .xml .txt

README.txt or **description file** (required)

Best Practices for File Organization:

1. Use consistent, descriptive file naming conventions.
2. Prioritize open, non-proprietary file formats when possible.
3. Include sufficient documentation to understand and reuse the data (species name, type of tissue, staining type, section thickness, magnification).
4. Consider including both raw and processed data.
5. Organize files logically in directories with clear names.
6. Keep individual file sizes under repository limits (**50GB for Zenodo, 20GB for free in Figshare**; larger files supported by MorphoSource).
7. For 3D data, include both raw volumetric data and derived surface models when applicable.

How to Access Data in the Repositories

Zenodo

1. Search for datasets using keywords, authors, or titles on the Zenodo search page

2. Filter results by community, resource type, or file type
3. Download files directly from the dataset page
4. Cite the data using the provided DOI and citation information

Figshare

1. Navigate to figshare.com and use the search function
2. Browse by category or filter by file type, license, or institution
3. Download files from the dataset page
4. Use the provided citation information to properly attribute the data

MorphoSource

1. **Registration required**: Create a free account to access download features
2. **Browse and search**: Use keywords, taxonomic names, or institution filters to find datasets
3. **Project-based organization**: Data is organized into research projects with multiple specimens and media files
4. **In-browser viewing**: Preview 3D models directly in your web browser
5. **Batch downloads**: Download multiple files or entire projects at once
6. **Access levels**: Some data may be immediately available, while others require permission from contributors
7. **Citation**: Each dataset has a unique identifier and DOI for proper citation

How to Upload: Step-by-Step Guide

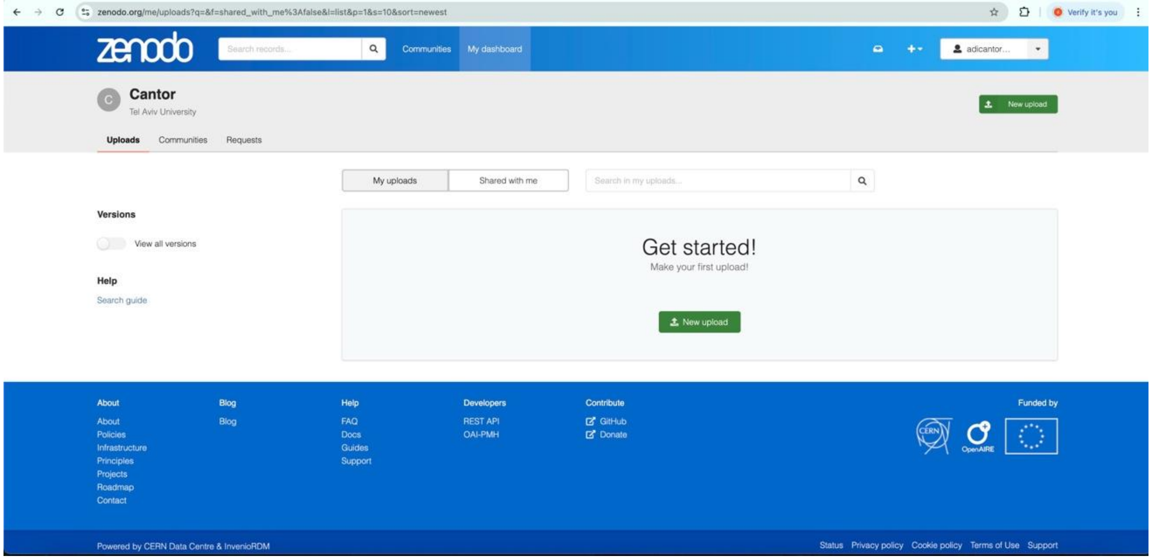
Preparing Your Data

1. **Organize your files** into a logical structure
2. **Create a README file** that includes:
    - Dataset description and context
    - Methods used to generate the data
    - File descriptions and formats
    - Software or tools needed to view/analyze the data
    - Any processing applied to the images
    - For 3D data: scanning parameters, resolution, and reconstruction methods
    - Contact information for questions
3. **Check for sensitive information** and ensure data is de-identified as needed
4. **Verify file formats** are appropriate for your chosen repository

Uploading to Zenodo

1. **Create an account**
    - Register using your institutional email or ORCID
    - Login to your account

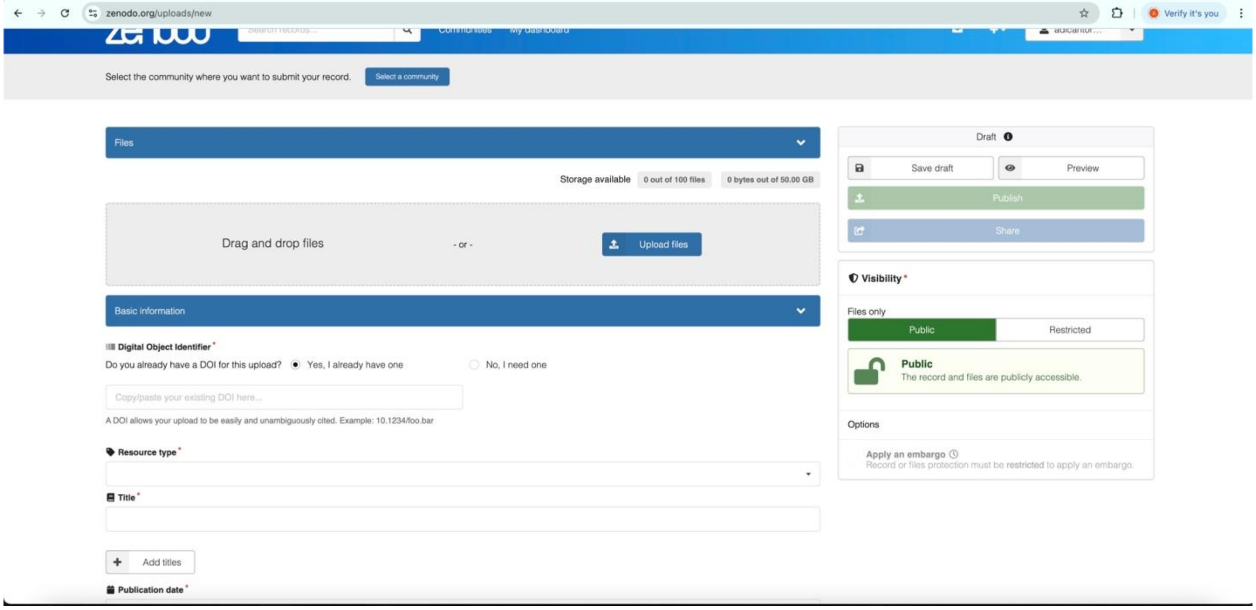
2. **Start a new upload**
    - Click the "New upload" button on your dashboard
    - You can save a draft at any point in the process



Get started!

Make your first upload!

3. **Upload your files**
    - Drag and drop files or use the file browser
    - Maximum file size is 50GB per file
    - For larger datasets, consider splitting into multiple uploads



Select the community where you want to submit your record.

Do you already have a DOI for this upload? ● Yes, I already have one ○ No, I need one

A DOI allows your upload to be easily and unambiguously cited. Example: 10.1234/foo.bar

Files only: Public

Public

The record and files are publicly accessible.

Record or files protection must be restricted to apply an embargo.

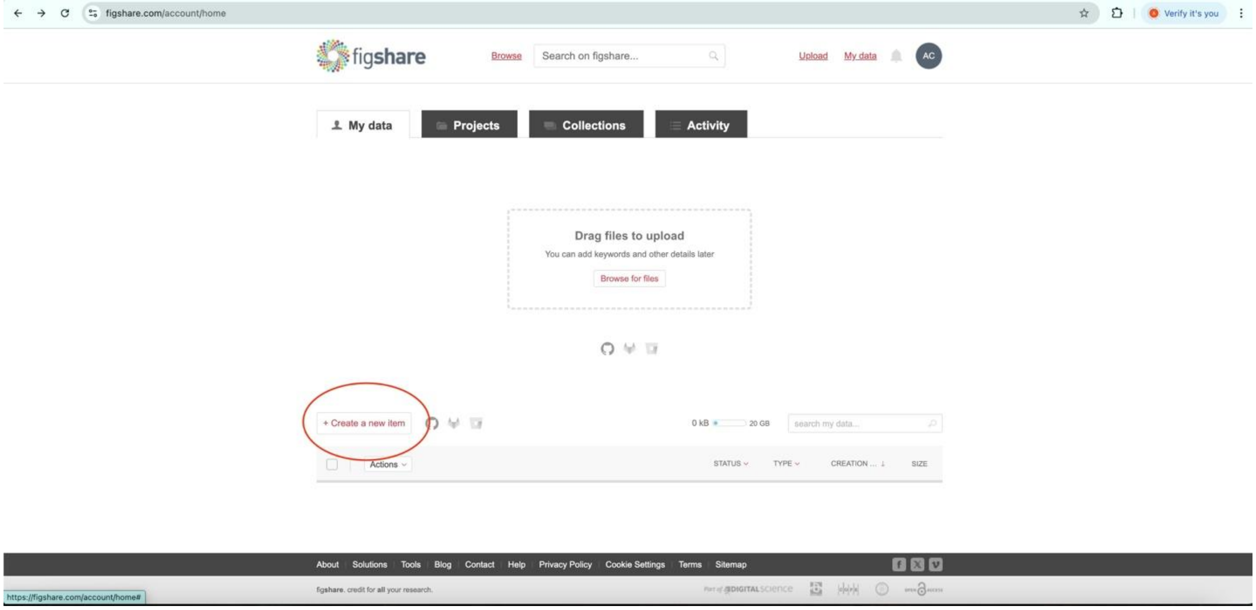
4. **Add Metadata**
    - All meta-data information is should be added in the same page as uploading your files - just keep scrolling.

    - **Title**: Create a clear, descriptive title (e.g., "Annotated H&E Histology Images of Mouse Liver Tissue")
    - **Authors**: Add all contributors with ORCID IDs where available
    - **Description**: Provide a comprehensive description including:
        - What the dataset contains
        - Sample types and preparation methods
        - Imaging devices/microscopes used
        - Staining protocols
        - Image acquisition parameters
        - Analysis methods (if applicable)
    - **Keywords**: Include relevant terms like:
        - Tissue type (e.g., "liver", "brain", "kidney")
        - Staining method (e.g., "H&E", "immunohistochemistry")
        - Specific markers or structures
        - "histology", "digital pathology", "whole slide imaging"
    - **Publication date**: Set the date of data publication
    - **Resource type**: Select "Dataset"
    - **License**: Choose an appropriate license (e.g., CC-BY 4.0)
    - **Related/alternate identifiers**: Link to associated publications, protocols, or code
    - **Funding**: Add grant information if applicable
5. **Publish**
    - Review all information for accuracy
    - Click "Publish" to make your dataset public and obtain a DOI
    - Note: Files cannot be modified after publication, only metadata

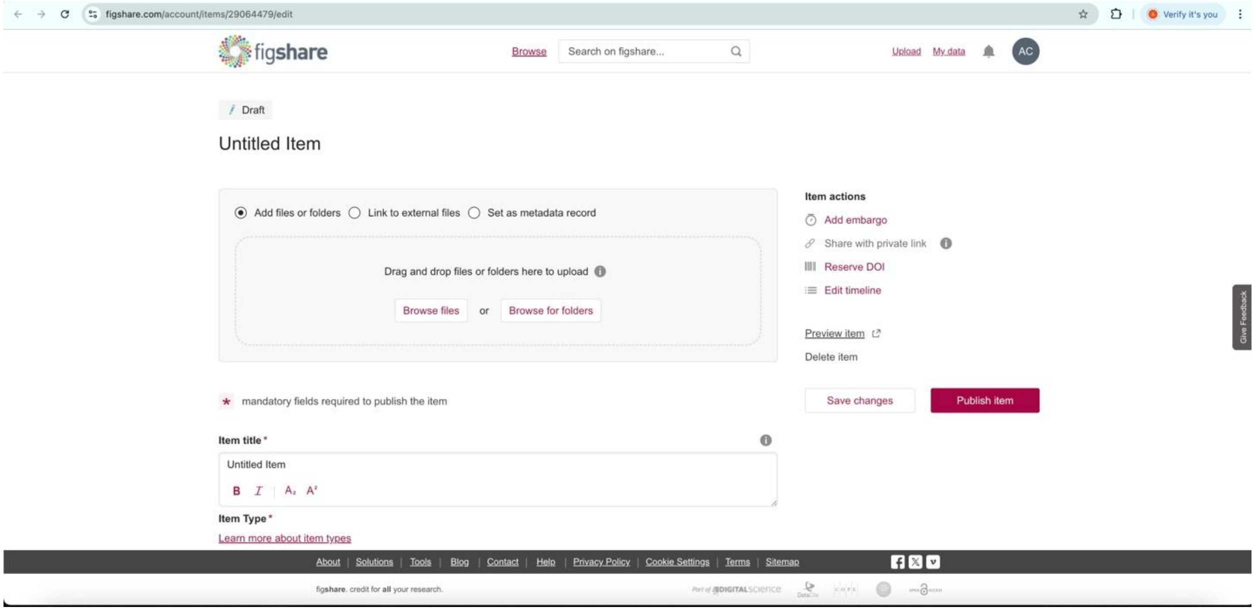
Uploading to Figshare

1. **Create an account**
    - Register using your institutional email or ORCID
    - Login to your account
2. **Start a new item**
    - Click the "Create a new item" button

- Select appropriate item type (Dataset)



3. **Upload your files**
    - Drag and drop files or use the file browser
    - Standard account file size limit is 5GB per file (20GB total)
    - Figshare+ can accommodate larger datasets (up to several TB)



4. **Add Metadata**
    - All meta-data information is in the same page as uploading your files, just keep scrolling.

    - **Title**: Create a clear, descriptive title (e.g., "Immunohistochemical Analysis of PCNA Expression in Rat Kidney Tissue")
    - **Authors**: Add all contributors (ORCID links supported)
    - **Categories**: Select relevant categories like "Histology", "Pathology", or "Neuroscience"
    - **Keywords**: Include terms like:
        - Specific techniques used
        - Tissue types
        - Disease models
        - "histology", "whole slide image", "digital pathology"
    - **Description**: Explain:
        - What's included in the dataset
        - Sample types and preparation methods
        - Imaging methods and equipment
        - Software used for image acquisition
        - Analysis steps or annotations
    - **License**: Select an appropriate license (CC-BY recommended)
    - **References**: Add citations to related publications
    - **Funding information**: Link dataset to grants/projects
5. **Publish**
    - Review all information for accuracy
    - Click "Publish" to make your dataset public and obtain a DOI
    - You can update metadata after publication, but file changes require a new version

Uploading to MorphoSource

Note: MorphoSource specializes in 3D morphological data and is ideal for CT scans, serial sections, and 3D reconstructions of histological specimens.

1. **Request Access**
    - Register for a free account at morphosource.org
    - Request permission from a site administrator to begin contributing data
    - Approval is typically granted for legitimate research purposes
2. **Create a Project**
    - Once approved, start a new "data project"
    - Projects organize related specimens and media files
    - Add project title, description, and collaborators
3. **Add Specimens**
    - Click "New Specimen" to create specimen records
    - Enter catalog numbers to check if specimens already exist in the database
    - Fill in specimen information including:
        - Institution and catalog number
        - Taxonomic information
        - Collection details
        - Physical specimen location

4. **Upload Media Files**
    - **Supported formats**: DICOM stacks, TIFF stacks, STL files, PLY files, videos, and 2D images
    - **File organization**: Group related files (e.g., raw CT data + derived 3D models)
    - **Large file support**: No strict size limits; can handle multi-GB datasets
    - **File compression**: Use ZIP64 format (7zip or WinZip) for files >4GB
5. **Add Media Metadata**
    - **Title**: Descriptive name for the media group
    - **Facility information**: Scanning facility and equipment details
    - **Technical parameters**: Resolution, scanning parameters, reconstruction settings
    - **Copyright and licensing**: Specify usage permissions and Creative Commons licensing
    - **Citation information**: How others should cite your data
6. **Publish or Restrict Access**
    - **Open access**: Make data immediately downloadable by all registered users
    - **Restricted access**: Require permission requests for downloads
    - **Project management**: Control who can view, download, and manage your data

Resources and Best Practices

More Data Sharing Guides:

- Zenodo Guides
- Figshare Knowledge Portal
- MorphoSource Documentation
- FAIR Data Principles

Best Practices for Histology Data Sharing:

1. **Use standardized file formats** that are widely used in the field – depending on your software, such as .tiff for ImageJ.
2. **Include comprehensive metadata** describing both the biological samples and the imaging process.
3. **Provide both raw and processed data** when possible.
4. **Link datasets to related publications** to provide context.
5. **Choose open licenses** that allow maximum reuse.
6. **Include protocols and methods** used to generate the data.
7. **Consider data size limitations** and split large datasets logically if needed.
8. **De-identify any patient/subject data** according to institutional requirements.
9. **Document any quality control** measures applied to the data.
10. **Update datasets** with new versions when significant changes are made.

11. **For 3D data**: Include both volumetric data and derived models to serve different user needs.
12. **Plan for long-term preservation** by choosing repositories with sustainable funding models.