**Intro to Metadata Episode Notebook**

Part of FAIR in (bio) practice, <https://carpentries-incubator.github.io/fair-bio-practice>

**Attendance**

Please sign in here: your name/ pronoun (if you prefer to share it) / institution / country.

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**Exercise 1. Identify types of metadata**

Here we have an excel spreadsheet that contains project metadata for a made-up experiment of plant metabolites: <https://carpentries-incubator.github.io/fair-bio-practice/fig/04-metadatafull_spreadsheet.png>

In groups, identify different types of metadata (administrative, descriptive, structural) present in this example.

**Just as a reminder:**

Administrative: relevant to managing it e.g. Experimental code, PI

Descriptive/citation: assists with discovery/identity e.g. Authors, persistent identifier

Structural: how the data came about and is structured e.g. Collection method, folder structures

**Minimal Information Standards**

<https://fairsharing.org/collection/MIBBI>

<https://fairsharing.org/standards/>

**Exercise 2. Minimal Information Standard**

Look at Minimum Information about Neuroscience Investigation (MINI) Electrophysiology

<https://www.nature.com/articles/npre.2008.1720.1.pdf>

which contains recommendations for reporting the use of electrophysiology in a neuroscience study. (Neuroscience, or neurobiology, is the scientific study of the nervous system)

Scroll to \*Reporting requirement\* and decide which of the points 1-8 are:

a) important for understanding and reuse of data:

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b) important for technical replication:

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c) could be applied to other experiments in neuroscience:

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**Exercise 3. What to include – discussion**

Think of the data you generate in your projects and imagine you are going to share them.

What information would another researcher need to understand or reproduce your data (the structural metadata)?

Think as a consumer of your data not the producer!

For example, we believe that any dataset should have:

* A name/title
* Experiment purpose or experimental hypothesis

Write down your proposals:

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