Public repositories Episode Notebook

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

Type your name and institution:

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**E1. Public general record**

Have a look at the following record for data set in Zenodo repository:

<https://doi.org/10.5281/zenodo.5045374>

1. What elements make it FAIR?

FINDABLE (persistent identifiers, easy to find data and metadata):

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ACCESSIBLE (The (meta)data retrievable by their identifier using a standard web protocols):

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INTEROPERABLE (The format of the data should be open and interpretable for various tools):

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REUSABLE (data should be well-described so that they can be replicated and/or combined in different settings, reuse states with a clear licence):

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1. Skim through the data set description (HINT there is also a README), try to judge using marks from 0 to 5 (5 best) if

* It is clear what the content of the data set is:
* It is clear why (what for) the data could be used:
* Is is well described
* How confident will you be to work with this data set:
* How easy it is to access the data set content:

1. Give +1 to the statement that the best describes your latest public dataset or a current project folder:

* It does not have readme like description:
* It description has only one/two paragraph(s), I have not thought of adding so many details:
* My data set description is similar in details:
* My data /project description is much richer or formalised:

**E2. Dataset discovery**

Try to find either:

- similar data sets in Zenodo

- data sets interesting for you

Judge using marks from 0 to 5 (5 best)

- how easy is to find similar or interesting dataset:

- It is clear what the content of the data set is:

- It is clear why (what for) the data could be used:

- They are well described :

**E3. Domain specific repositories.**

Select one of the following repositories based on your expertise/interests:

Have a look at mRNAseq accession 'E-MTAB-7933' in [ArrayExpress](https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-7933/)

* What makes it better than Zenodo:
* What domain specific features can you see:
* What makes its metadata interoperable/reusable:
* Searching:

> - Have a look at microscopy 'project-1101' in [IDR](https://idr.openmicroscopy.org/webclient/?show=project-1101)

* What makes it better than Zenodo:
* What domain specific features can you see:
* What makes its metadata interoperable/reusable:
* Searching:

> - Have a look at the synthethic part record 'SubtilinReceiver\_spaRK\_separated' within the 'bsu' collection in [SynBioHub](https://synbiohub.org/public/bsu/SubtilinReceiver\_spaRK\_separated/1)

* What makes it better than Zenodo:
* What domain specific features can you see:
* What makes its metadata interoperable/reusable:
* Searching:

> - Have a look at the proteomics record 'PXD013039' in [PRIDE](https://www.ebi.ac.uk/pride/archive/projects/PXD013039)

* What makes it better than Zenodo:
* What domain specific features can you see:
* What makes its metadata interoperable/reusable:
* Searching:

> - Have a look at the metabolomics record 'MTBLS2289' in [Metabolights](https://www.ebi.ac.uk/metabolights/MTBLS2289/descriptors)

* What makes it better than Zenodo:
* What domain specific features can you see:
* What makes its metadata interoperable/reusable:
* Searching:

**E4. Finding repository**

1. Find and type a repo for genomics data:
2. Find and type repo for microscopy data:
3. Your favourite/chosen data type and recommended repo:

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1. List repositories you have used (either to download or to share your data):  
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