# List of attendees

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# Episode 4. Notebooks to speed up work

## Exercise 1.

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## Exercise 2.

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## Exercise 3.

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# Episode 5. Public repositories

### Exercise 1: Public general record

Have a look at the following record for a 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):

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

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

REUSABLE (data should be well-described so that they can be replicated and/or combined in different settings, and any conditions on reuse stated clearly with a licence):

2. Skim through the data set description (HINT there is also a README), try to judge the following, and indicate your evaluation using marks from 0 to 5 (5 best) as to whether:

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

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

• It is well described:

• How confident will you be to work with this data set:

• How easy it is to access the data set content:

DONE:

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## Exercise 2: Dataset discovery

Try to find:

- similar data sets in Zenodo

Judge the following, indicating your assessment using marks from 0 to 5 (5 best)

• how easy it is to find similar or interesting data sets:

• It is clear what the content of the other data sets are:

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

• They are well described:

DONE:

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Exercise 3: 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:

• Searching:

Have a look at microscopy 'project-1101' in [IDR]

(https://idr.openmicroscopy.org/webclient/?show=project-1101)

• What makes it better than Zenodo:

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• What domain specific features can you see:

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• Searching:

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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:

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• What domain specific features can you see:

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• Searching:

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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:

• 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:

• Searching:

DONE:

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Exercise 4: Finding a repository

Using [Fairsharing](<https://fairsharing.org/>) or [Registry of repositories re3data](https://www.re3data.org/)

a) Find and type a repo for flow cytometry data:

b) Find a recommended repo for Your favourite/chosen data type (write both repo and data type):

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

d) What’s your favourite research data repository? Why?

DONE:

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Exercise 5: Wrap up discussion

Discuss the following questions:

• Why is choosing a domain specific repositories over zenodo more FAIR?

• How can selecting a repository for your data as soon as you do an experiment (or even before!) can benefit your research and help your data become FAIR?

• What to do if your publication contains multiple data types?

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DONE:

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