Searching the DANDI Archive

Support

NIH The BRAIN Initiative®

NIH National Institute of Mental Health

1R24MH117295
AWS Public dataset program

BICCN

Dandiset. n.

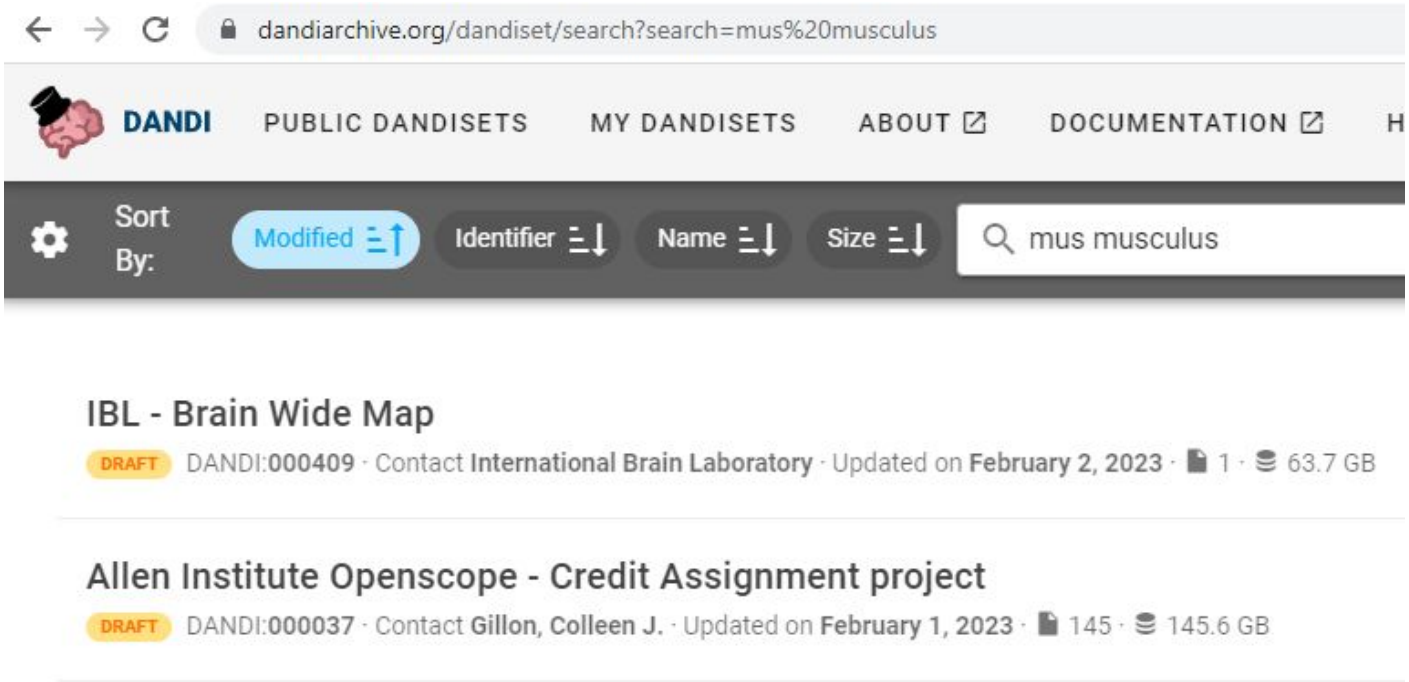
An organized collection of assets (files) with both file level and dataset level metadata generated from an experiment or a project.

*A dandiset is a **FAIR** collection.*

***F**indable* ***A**ccessible* ***I**nteroperable* ***R**eusable*

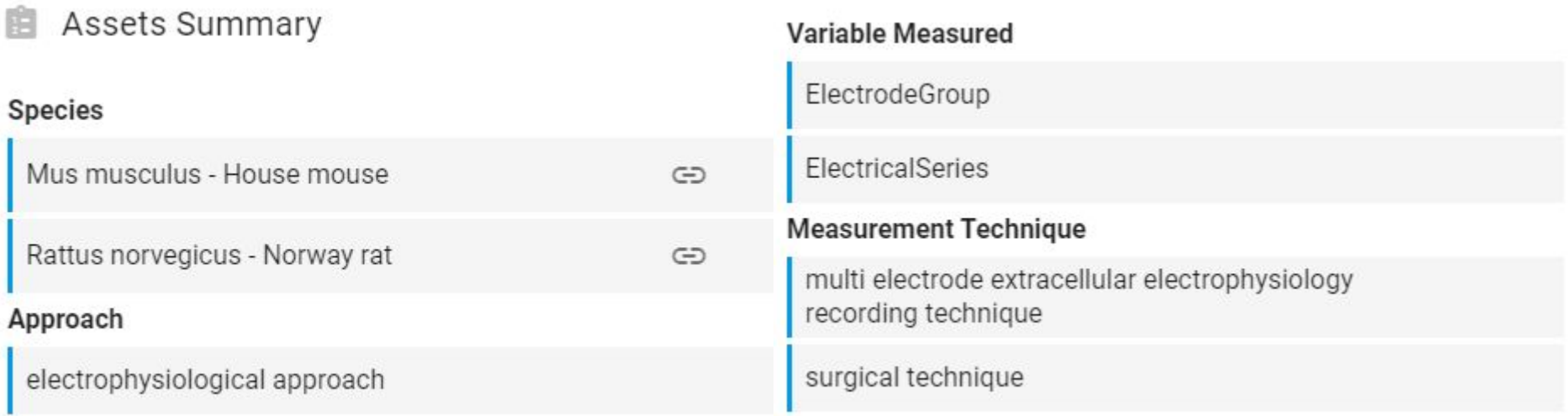
From the Web Interface

- From the main page https://dandiarchive.org/dandiset, type a query in the search bar



Web Interface

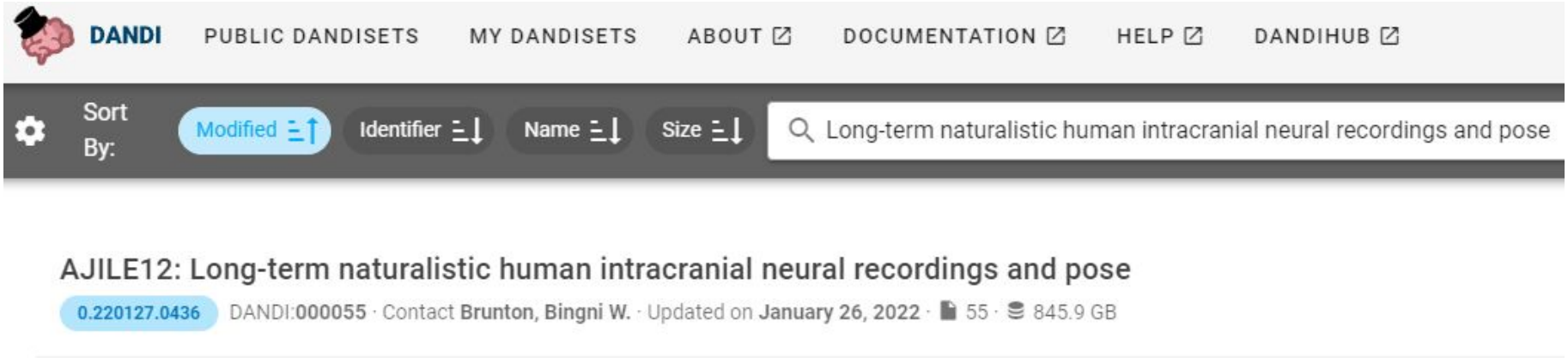
- These top-level queries look at the highest level of dandiset metadata
  - Titles, keywords, dandiset description
  - Automatically extracted subject species, modality, and techniques
  - You can see these fields listed at the bottom of the main page of any dandiset



github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Web Interface

- Good for…
  - A quick glance or casual browsing of general content
  - Finding the dandiset corresponding to a publication
    - ➢ usually the title, or linked as a Related Resource (‘IsDescribedBy’)



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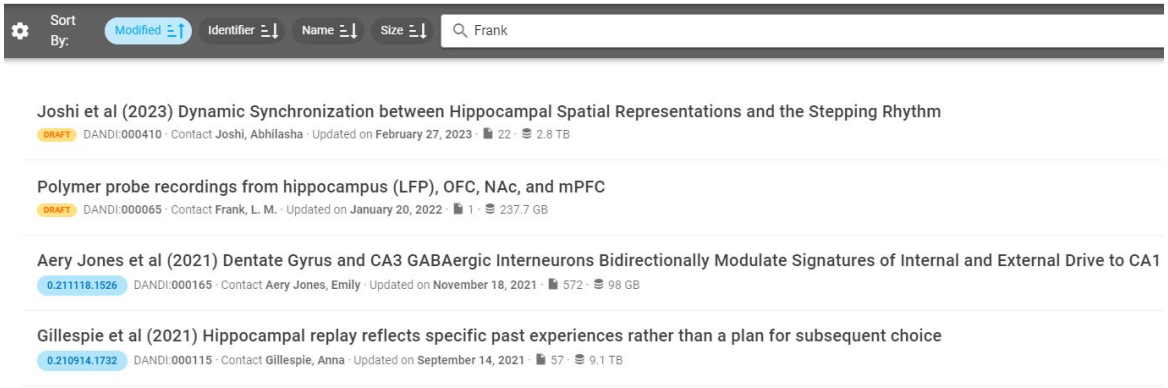
  - Finding all the dandisets belonging to a particular lab
    - ➢ search by name of a ‘Contributor’



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Web Interface

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  - Finding the dandiset corresponding to a publication
    - ➢ usually the title, or linked as a Related Resource (‘IsDescribedBy’)
  - Finding all the dandisets belonging to a particular lab
    - ➢ search by name of a ‘Contributor’
  - Finding all the dandisets that use a particular species
    - ➢ Latin binomial, *e.g.*: *Mus musculus*, *Rattus norvegicus*, *Danio rerio*, etc.

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Web Interface

- Doesn’t help with…
  - Presence or absence of raw, pre-processed, or post-processed data
  - Presence or absence of identified brain regions
    - ➢ unless the creator of the dandiset set these as keywords or ‘subject matter’
  - Presence or absence of exact brain coordinates (like Allen CCFv3)
  - The huge variety of behavioral techniques
    - ➢ open exploration vs. maze task
    - ➢ virtual reality vs. simple stimulus presentation
    - ➢ trialized tasks or spontaneous events
    - ➢ and many, many more…

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Using the DANDI API in Python

- For finer-grain searchability, we can use the **A**pplied **P**rogramming **I**nterface (API) for DANDI to scan the `metadata.yml` files to programmatically obtain information

- Installation - preferably in a new conda environment

```
pip install dandi jupyter
jupyter notebook
```

Or use the DANDI Hub

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

How to use the **FREE** DANDI Hub computing resources

- Step 1: Make an account on the DANDI Archive
  - 1a: Requires a GitHub account
  - 1b: Wait for account approval (~1 day, faster during special events)
- Step 2: Go to https://hub.dandiarchive.org/
  - 2a: Sign in

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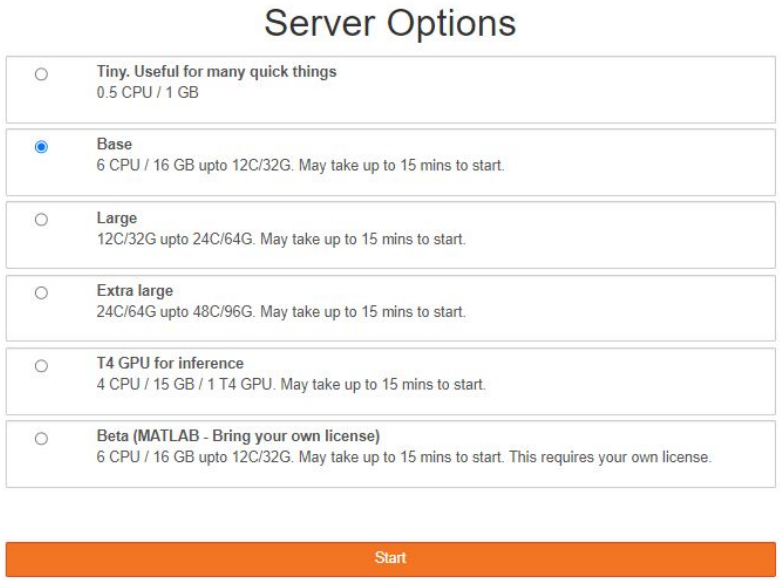

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- Step 2: Go to https://hub.dandiarchive.org/
  - 2a: Sign in
  - 2b: Select instance size (amount of resources)
  - 2c: Wait a few minutes
- Step 3: …. No more steps

You're in!

Using the DANDI API in Python

- For finer-grain searchability, we can use the **A**pplied **P**rogramming **I**nterface (API) for DANDI to scan the `metadata.yml` files to programmatically obtain information

- Relevant methods
  - The `client` initiates communication with the archive

```
from dandi.dandiapi import DandiAPIClient

client = DandiAPIClient()
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Using the DANDI API in Python

- For finer-grain searchability, we can use the **A**pplied **P**rogramming **I**nterface (API) for DANDI to scan the `metadata.yml` files to programmatically obtain information

- Relevant methods
  - The `client` can be queried to return currently public dandisets

```
dandisets = list(client.get_dandisets())
dandiset = dandisets[0]
dandiset
> dandi.dandiapi.RemoteDandiset
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Using the DANDI API in Python

- For finer-grain searchability, we can use the **A**pplied **P**rogramming **I**nterface (API) for DANDI to scan the `metadata.yml` files to programmatically obtain information

- Relevant methods
  - A `dandi.dandiapi.RemoteDandiset` can return its pre-parsed metadata

```
raw_metadata = dandiset.get_raw_metadata()
raw_metadata
> { < kind of messy > }
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Using the DANDI API in Python

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- Relevant methods
  - A `dandi.dandiapi.RemoteDandiset` can return its pre-parsed metadata

```
import json

print(json.dumps(raw_metadata, indent=4))
> {
        < A lot more readable >
  }
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Using the DANDI API in Python

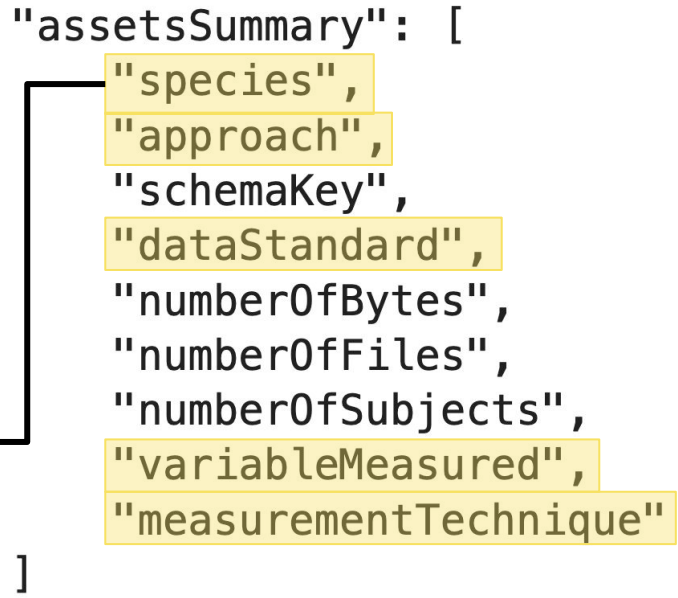
```
['id',
 'doi',
 'url',
 'name',
 'about',
 'access',
 'license',
 'version',
 '@context',
 'citation',
 'keywords',
 'protocol',
 'schemaKey',
 'identifier',
 'repository',
 'contributor',
 'description',
 'publishedBy',
 'studyTarget',
 'assetsSummary',
 'datePublished',
 'schemaVersion',
 'ethicsApproval',
 'wasGeneratedBy',
 'relatedResource',
 'manifestLocation']
```

```
"assetsSummary": [
    "species",
    "approach",
    "schemaKey",
    "dataStandard",
    "numberOfBytes",
    "numberOfFiles",
    "numberOfSubjects",
    "variableMeasured",
    "measurementTechnique"
]
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Using the DANDI API in Python


```
{
    "age": {
        "value": "P209DT55274S",
        "unitText": "ISO-8601 duration",
        "schemaKey": "PropertyValue",
        "valueReference": {
            "value": "dandi:BirthReference",
            "schemaKey": "PropertyValue"
        }
    },
    "sex": {
        "name": "Male",
        "schemaKey": "SexType",
        "identifier": "http://purl.obolibrary.org/obo/PATO_0000384"
    },
    "species": {
        "name": "Mus musculus - House mouse",
        "schemaKey": "SpeciesType",
        "identifier": "http://purl.obolibrary.org/obo/NCBITaxon_100
    },
    "genotype": "Emx1-Cre[tg/wt];Ai32[tg/wt]",
    "schemaKey": "Participant",
    "identifier": "San4"
}
```

Using the DANDI API in Python

- For finer-grain searchability, we can use the **A**pplied **P**rogramming **I**nterface (API) for DANDI to scan the `metadata.yml` files to programmatically obtain information

- Relevant methods
  - Each file from `dandiset.get_asset(...)` can return its pre-parsed metadata

```
all_assets = dandiset.get_assets()
first_asset_raw_metadata = all_assets[0].get_raw_metadata()

print(json.dumps(first_asset_raw_metadata, indent=4))
> {
        < A lot of information >
  }
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Using the DANDI API in Python

- Simple dandiset-level examples

  https://github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023/tutorials/simple_dandiset_search.ipynb

- Advanced asset-level examples

  https://github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023/tutorials/advanced_asset_search.ipynb

Investigating an Individual NWB File on DANDI

- The dandi-api metadata aggregates information over the contents of the dandiset
- To investigate the contents of a single file, a good place to start is to try the NWB Widgets

```
pip install -U pynwb dandi jupyter nwbwidgets

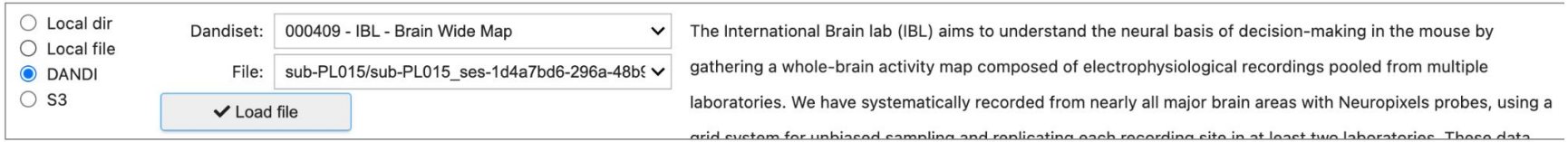
jupyter notebook
```

And in the notebook…

```
from nwbwidgets import Panel

Panel()
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023



session_description:	The full description of the session/task protocol can be found in Appendix 2 of Inte
identifier:	c33e2740-5475-463e-bd16-d1c38da37463
session_start_time:	2022-07-21 16:08:53.428769+01:00
timestamps_reference_time:	2022-07-21 16:08:53.428769+01:00
related_publications:	https://doi.org/10.6084/m9.figshare.21400815.v6, https://doi.org/10.1101/2020.01.17.909838
experiment_description:	IBL aims to understand the neural basis of decision-making in the mouse by gather
session_id:	1d4a7bd6-296a-48b9-b20e-bd0ac80750a5
lab:	Hausser
institution:	University College London
protocol:	_iblrig_tasks_ephysChoiceWorld6.6.1

- **file_create_date**
- **acquisition**
- **processing**
- **electrodes: metadata about extracellular electrodes**
- **electrode_groups**
- **devices**

Reading directly from an identified file

- Once you have concluded your investigation and found some NWB files of interest, you can either…
  - download them locally via command-line terminal

```
dandi download DANDI:<six-digit-ID>  # Will download all files
```

Or

```
dandi download <copy and paste individual file URL>
```

Then in Python (script or notebook)...

```
from pynwb import NWBHDF5IO


io = NWBHDF5IO(path="../path_to_single_file.nwb", load_namespaces=True)

nwbfile = io.read()
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

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```

Or

```
dandi download <copy and paste individual file URL>
```

Then in MATLAB…

```
%% With MatNWB downloaded and added to your MATLAB session path…
nwbfile = nwbRead('.../path_to_single_file.nwb')
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Streaming directly from an identified file

- Or stream from the cloud (most recommended for one-off analyses or quick calculations)

  In Python, there are two methods: ros3 and fsspec

```
import h5py
import fsspec
from fsspec.implementations.cached import CachingFileSystem
from nwbinspector.tools import get_s3_urls_and_dandi_paths
from pynwb import NWBHDF5IO

S3_urls_to_dandi_paths = get_s3_urls_and_dandi_paths(dandiset_id="<sig-digit ID>")
dandi_paths_to_s3_urls = {dandi_path: s3_url for s3_url, dandi_path in s3_urls_to_dandi_paths.items()}
s3_url = dandi_paths_to_s3_urls["<file path on DANDI>.nwb"]

cache = CachingFileSystem(fs=fsspec.filesystem("http"), cache_storage="some/temporary/folder")
file_system = cache.open(s3_url, "rb")
file = h5py.File(file_system)

io = NWBHDF5IO(file=file, load_namespaces=True)
nwbfile = io.read()
```

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023

Streaming directly from an identified file

- Or stream from the cloud (most recommended for one-off analyses or quick calculations)

  In MATLAB*…

```
%% The S3 path must be copy/pasted manually

s3_url = 's3://dandiarchive/blobs/7ee/415/7ee41580-9b0b-44ca-8675-6959ddd8dc33'

nwbfile = nwbRead(s3_url)
```

* streaming speeds are much slower than in Python

github.com/NeurodataWithoutBorders/nwb_hackathons/tree/main/Cosyne_2023