NWB User Days 2023

NeuroConv

&

GUIDE

NEURODATA WITHOUT BORDERS

CATALYST NEURO

DANDI
dandiarchive.org

We are an international team of neuroscientists

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We use data and software engineering to connect neurophysiology data producers, tool builders, and users

NeuroConv: A Python library for automatic conversions to NWB

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Challenges

- Converting neurophysiology data to NWB is challenging due to
  - **Diversity** - many different proprietary formats
  - **Complexity** - experiments often use multiple data sources (each stream in a unique format)
  - **Volume** - terabyte (TB) scale and growing

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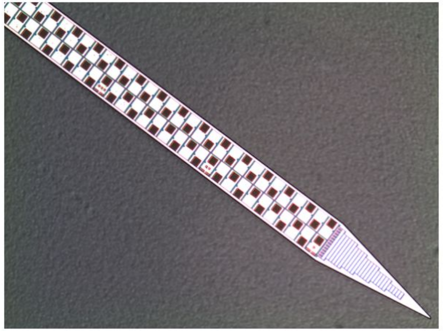
- Cutting edge recording techniques continue to push the boundaries of temporal and spatial resolution

- Starting to see data sharing of…
  - multi-probe Neuropixels (version 1) recordings
    - ~30 kHz sampling rate can yield ~23 MB/s of data per probe
    - That’s ~1 TB of data per probe every 12 hours!
  - whole-brain imaging (example resolution: ~1k x 2k px imaging plane)
    - ~40 scans per plane per second can yield ~160 MB/s of data
    - That’s ~1 TB every 2 hours!



neuropixels.org

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- Reminder: DANDI is happy to store all that raw data **for free**!

Challenges

NeuroConv is an open-source software package developed to simplify these challenges for converting neurophysiology data to NWB

- Currently supports 40+ common neurophysiology data formats
- Automatically extracts format-specific metadata
- Seamlessly integrated data engineering
  - Converts on the TB scale
  - Can reduce file size by ~35%
  - Optimizes chunking for streaming from DANDI
- Allows easy combinations from multiple input sources

Installation

- Minimal installation (no extra ‘frills’)

```
pip install neuroconv
```

- Format-specific installation

```
pip install neuroconv[<format name>]
```

E.g., `pip install neuroconv[spikeglx]`

- Full installation (if you plan to use EVERY format… mostly for developers)

```
pip install neuroconv[full]
```

- Can always specify more than one

```
pip install neuroconv[tiff,extract,sleap]
```

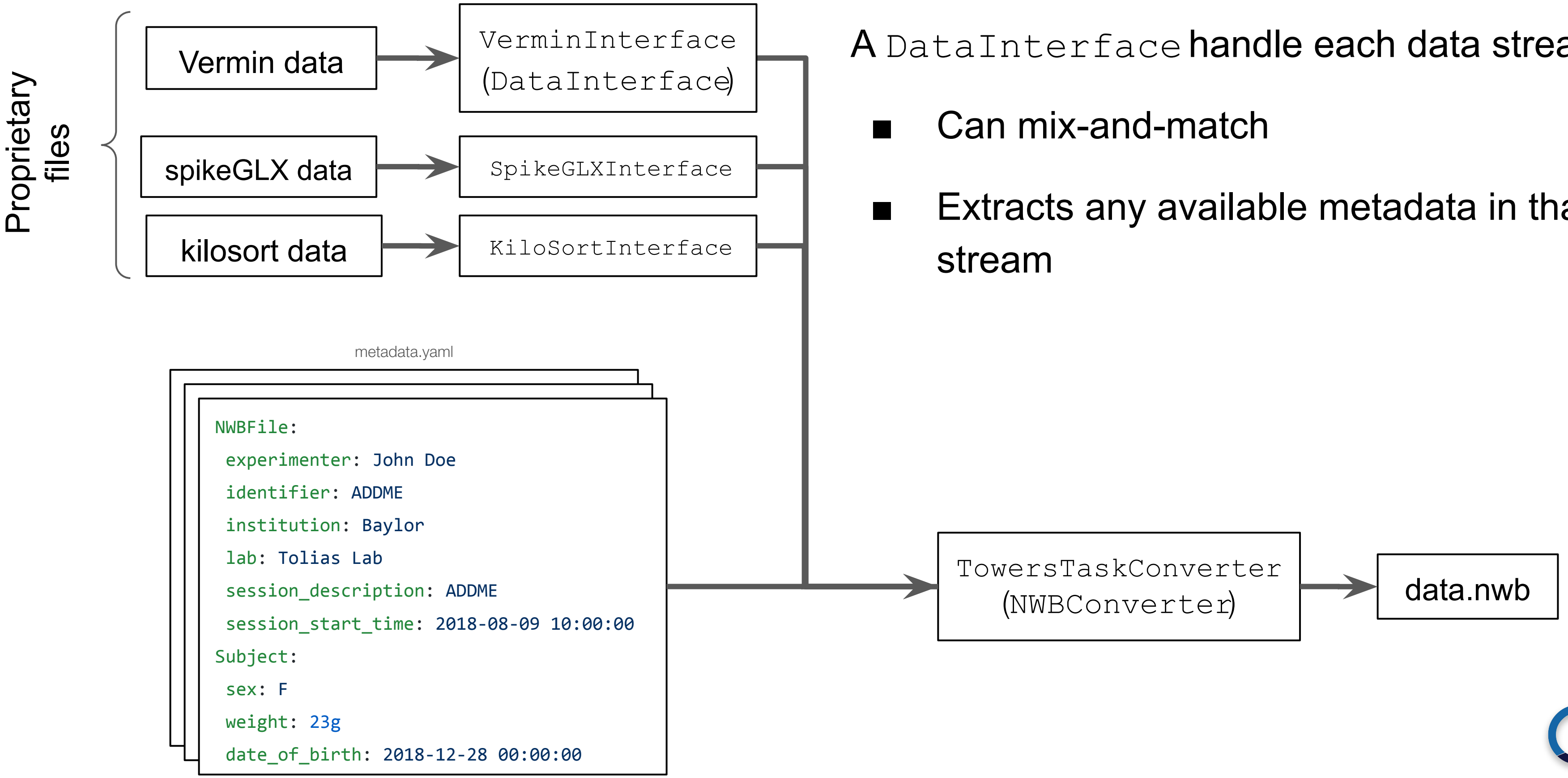
- Mac Users: must wrap in quotes when using extra requirements

```
pip install "neuroconv[full]"
```

Strategy: Modularize by data stream

A `DataInterface` handle each data stream

- Can mix-and-match
- Extracts any available metadata in that stream

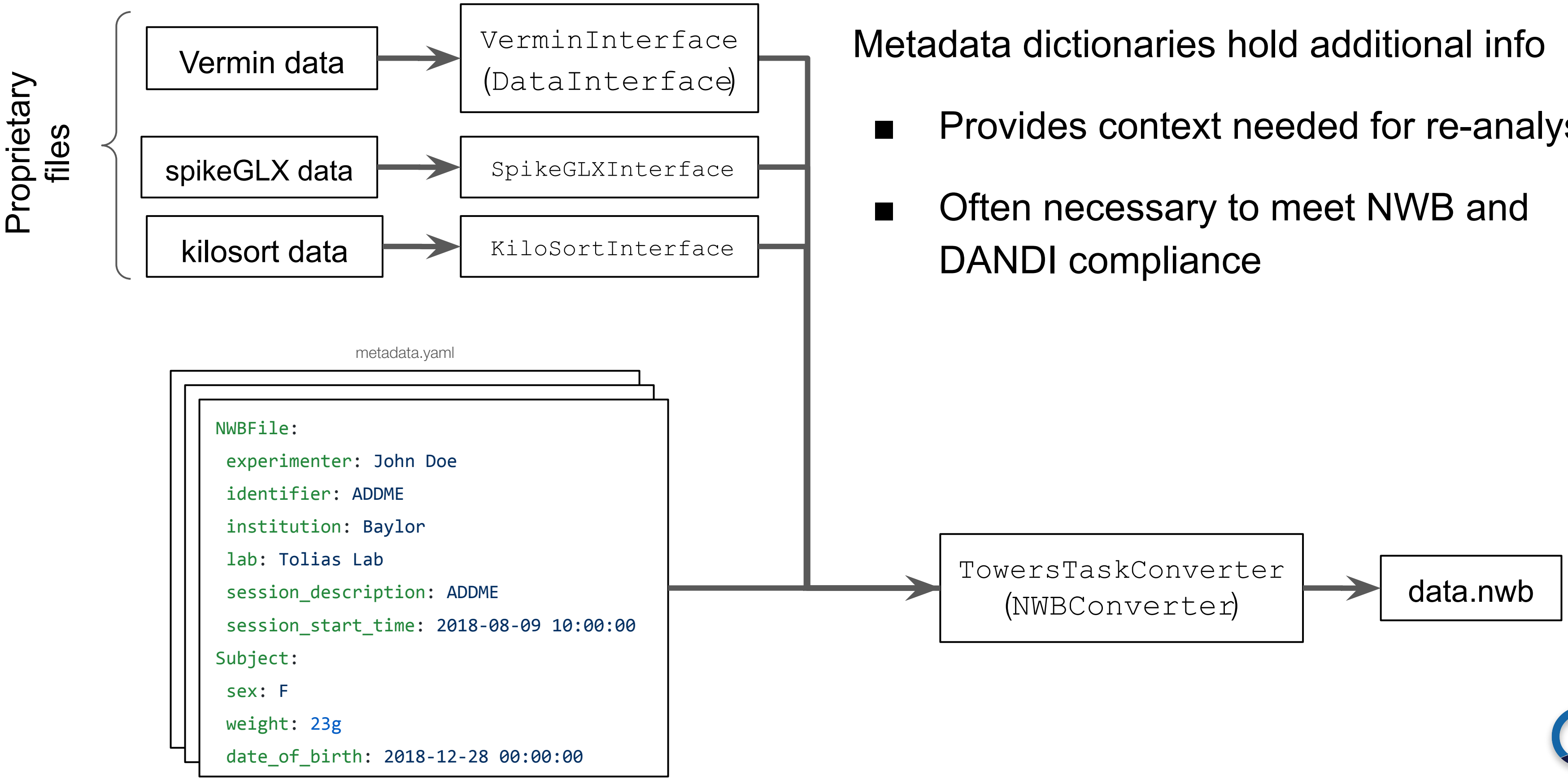


```
NWBFile:
 experimenter: John Doe
 identifier: ADDME
 institution: Baylor
 lab: Tolias Lab
 session_description: ADDME
 session_start_time: 2018-08-09 10:00:00
Subject:
 sex: F
 weight: 23g
 date_of_birth: 2018-12-28 00:00:00
```

Strategy: Modularize by data stream

Metadata dictionaries hold additional info

- Provides context needed for re-analysis
- Often necessary to meet NWB and DANDI compliance



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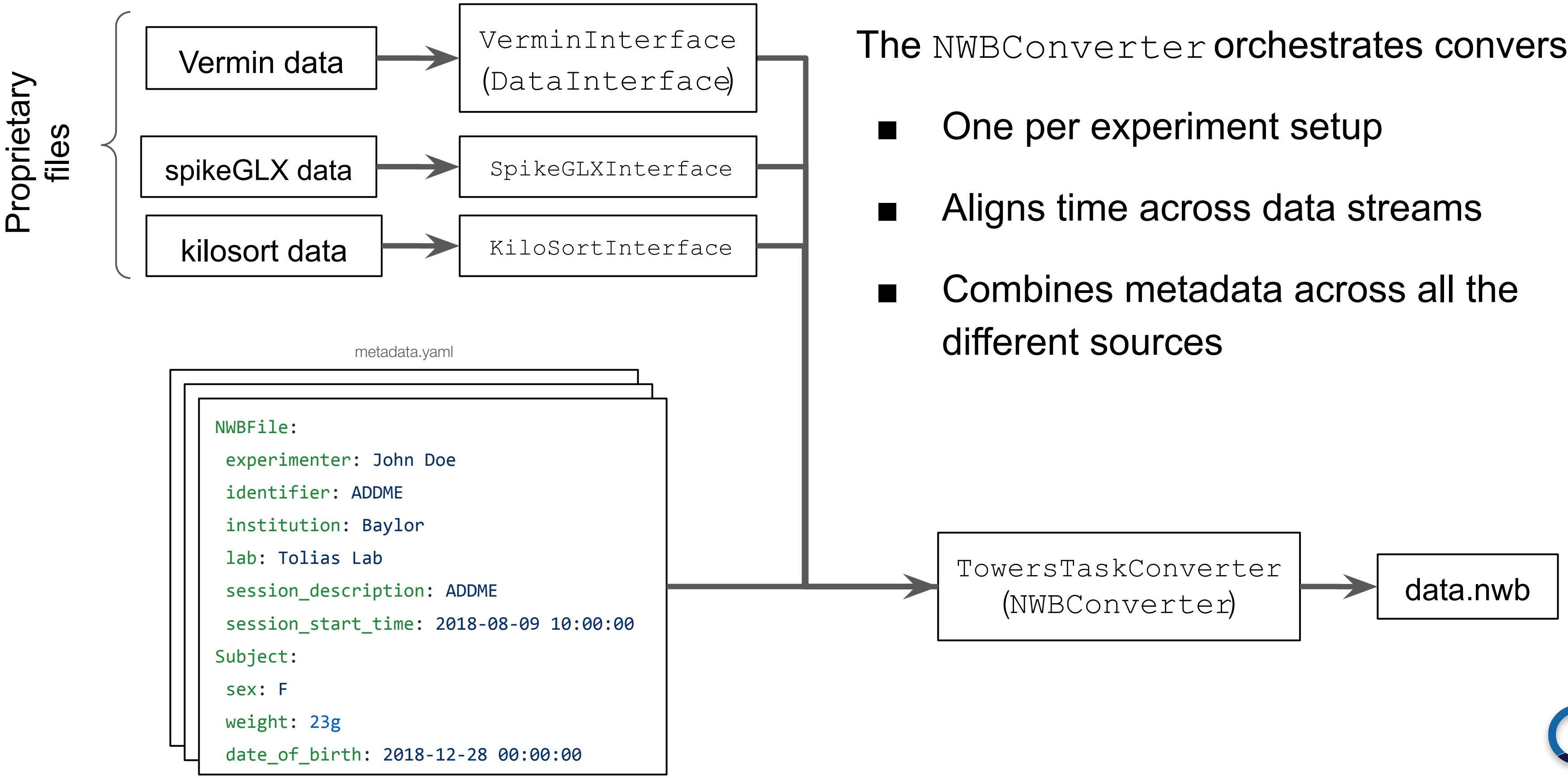

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```

The `NWBConverter` orchestrates conversion

- One per experiment setup
- Aligns time across data streams
- Combines metadata across all the different sources

So what does it look like in practice?

Simple Snippet

```python
from datetime import datetime
from neuroconv.datainterfaces import TiffImagingInterface

file_path = … / "imaging_datasets" / "Tif" / "demoMovie.tif"
session_start_time = datetime(2020, 1, 1, 12, 30, 0)

interface = TiffImagingInterface(
    file_path=".../imaging_datasets/Tif/demoMovie.tif",
    sampling_frequency=15.0
)
metadata = interface.get_metadata()
metadata["NWBFile"].update(session_start_time=session_start_time)
interface.run_conversion(
    nwbfile_path=".../my_nwbfile.nwb", metadata=metadata
)
```

Demos

https://neuroconv.readthedocs.io

- “Conversion Gallery”
- “Catalogue”

Don’t see your format listed? Request support for it

https://github.com/catalystneuro/neuroconv/issues

- Need a small snippet of example data for our testing repository
- Helps if you know of a Python library for reading the format

No-code Specification File

For users less familiar with coding in Python, we have developed a text-only YAML language for specifying a full NWB conversion

- Only requires specification of file/folder paths and metadata not within the sources
- Example: GIN_conversion_specification.yml
- Run conversion from the command line

```
neuroconv my_conversion_specification.yml
```

Note: Behavior Types

Most representations of behavior used by labs is ad-hoc (not proprietary or widespread)…

- NeuroConv supports video, audio, spreadsheet tables, and DeepLabCut + SLEAP for pose estimation
- Open to supporting more, possibly including arbitrary objects from `.mat`, `.pkl`, or `.npy` files, but we would have to work with you to ensure it meets your needs
- Usually this is the most custom part of the conversion and will require a little bit of actual PyNWB or MatNWB code…
- …so be sure to check out the tutorial sessions for those after lunch

New Feature: Multi-stream Converters

A `DataInterface` represents the lowest level of connection between a single data stream and its corresponding NWB representation

Many formats have multiple streams, even some that are cross-modal (simultaneous behavior + neural recording)

So we have made two ‘subconverters’ (converters that can also be combined within another `NWBConverter` and act much like an interface)

```
from neuroconv.converters import MiniscopeConverter

miniscope_converter = MiniscopeConverter(
    folder_path= … / "miniscope_folder"
)  # Includes the behavior camera as well!

miniscope_converter.run_conversion()
```

```
from neuroconv.converters import SpikeGLXConverterPipe

spikeglx_converter = SpikeGLXConverterPipe(
    folder_path= … / "spikeglx_folder"
)

spikeglx_converter.run_conversion()
```

Advanced Feature: Metadata Customization

All metadata that goes into the NWB file can be controlled via the NeuroConv `metadata` dictionary structure

No need to call `.update(key=value)` - fields can be referenced directly

```python
from neuroconv.datainterfaces import TiffImagingInterface

interface = TiffImagingInterface(
    file_path= … / "demoMovie.tif",
    sampling_frequency=15.0
)
metadata = interface.get_metadata()
```

```python
metadata["NWBFile"]["session_start_time"] = datetime(2020, 1, 1, 12, 30, 0)

metadata["NWBFile"]["Subject"]["id"] = "MySubjectID001"
metadata["NWBFile"]["Subject"]["species"] = "Mus musculus"  # Latin binomial
metadata["NWBFile"]["Subject"]["sex"] = "U"  # Must be M, F, U, or O
metadata["NWBFile"]["Subject"]["age"] = "P1W3D"  # Must be in ISO 8601

# Modality-specific structures are mostly auto-filled, can be viewed with
metadata["Ecephys"]
metadata["Ophys"]
metadata["Behavior"]
```

Advanced Feature: Metadata Schema

For those familiar with reading JSON, all NWB metadata in **NeuroConv** have a schema representation

When calling `.run_conversion()` on an `NWBConverter` the metadata structure you pass in will be validated against this schema

The **NWB GUIDE** interactively validates each entry as it is modified

```python
from neuroconv.datainterfaces import TiffImagingInterface

interface = TiffImagingInterface(
    file_path= ... / "demoMovie.tif",
    sampling_frequency=15.0
)
metadata_schema = interface.get_metadata_schema()
```

```json
"required": [
    "Device",
    "ImagingPlane",
    "TwoPhotonSeries"
],
"properties": {
    "Device": {
        "type": "array",
        "minItems": 1,
        "items": {
            "$ref": "#/properties/Ophys/properties/definitions/Device"
        },
        "default": [
            {
                "name": "Microscope"
            }
        ]
    },
    "ImagingPlane": {
        "type": "array",
        "minItems": 1,
        "items": {
            "$ref": "#/properties/Ophys/properties/definitions/ImagingPlane"
        },
...
```

New Advanced Feature: Temporal Alignment

All temporal data in NWB files must be aligned to the `session_start_time`, but there are several different synchronization strategies used to achieve this

Check out the full documentation of methods for all the details, but in a conversion script it might look something like this…

```
from datetime import datetime
from neuroconv.datainterfaces import SpikeGLXNIDQInterface, PhyInterface

nidq_interface = SpikeGLXNIDQInterface(file_path= … / "some_spikeglx_session.nidq.ap.bin")
ttl_times = nidq_interface.get_event_times_from_ttl(channel_name="AUX1")

dlc_interface = DeepLabCutInterface(folder_path=... / "phy_session")
dlc_interface.align_starting_time(starting_time=ttl_times[0])


...
```

GUIDE

NWB GUIDE: A **G**raphical **U**ser **I**nterface for **D**ata **E**ntry

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Summary

NWB GUIDE is an open-source graphical interface developed around NeuroConv to remove the necessity of knowing how to program in Python

- Drag-and-drop data from local folders
- Interactive forms for attaching metadata
- Automated validation and upload to the DANDI Archive
- Currently only supports SpikeGLX and Phy formats
- Beta release at SFN 2023 will include all 40+ NeuroConv supported formats

Tutorial

NWB GUIDE has a built-in tutorial using some NeuroPixels (SpikeGLX) data with Phy-curated KiloSort output

To complete the entire workflow from start-to-finish

- Make an account on https://dandiarchive.org
  - Requires an account on https://github.com
- Download the ‘ephy_testing_data’ folder from this Google Drive
- Installation instructions

Strategy for Hackathon

If you have SpikeGLX or Phy data, then the recommended method would be to try out the **NWB GUIDE** to create some base files to which you can add behavioral data to later

If you have any other formats supported by **NeuroConv**, then start by ensuring it is able to convert your files without error

- If any errors do occur, please report them on the NeuroConv GitHub issues
- I'll be floating around the room, just raise your hand if you have any questions

If your proprietary format is not supported, then please submit a request for it on NeuroConv

- If you do not yet know how to read it in Python, take this time to sit down with one of our expert developers to see if we can help