

Neurodata Without Borders – An Ecosystem for Standardizing Diverse Neurophysiology Data

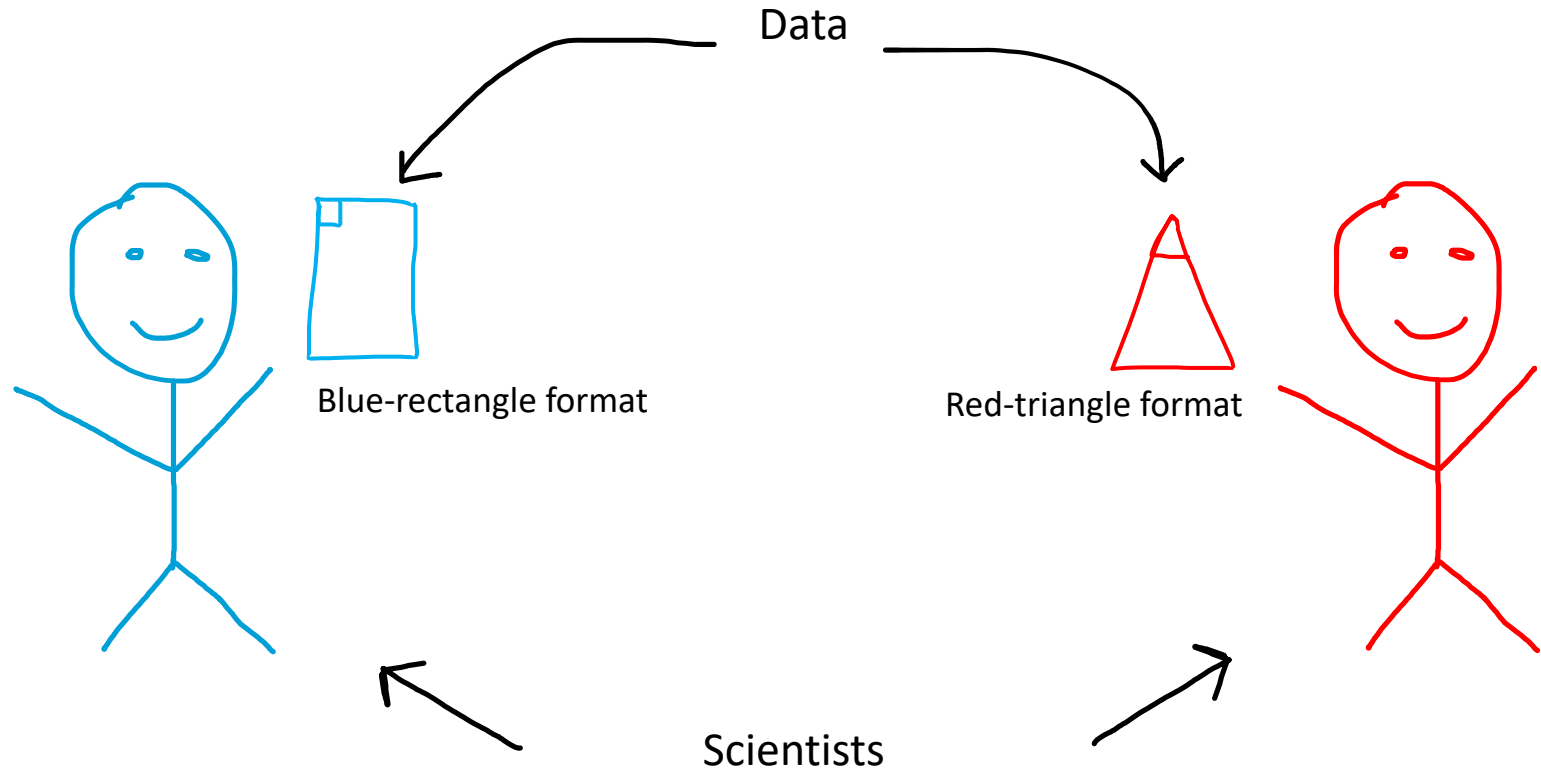
Andrew Tritt

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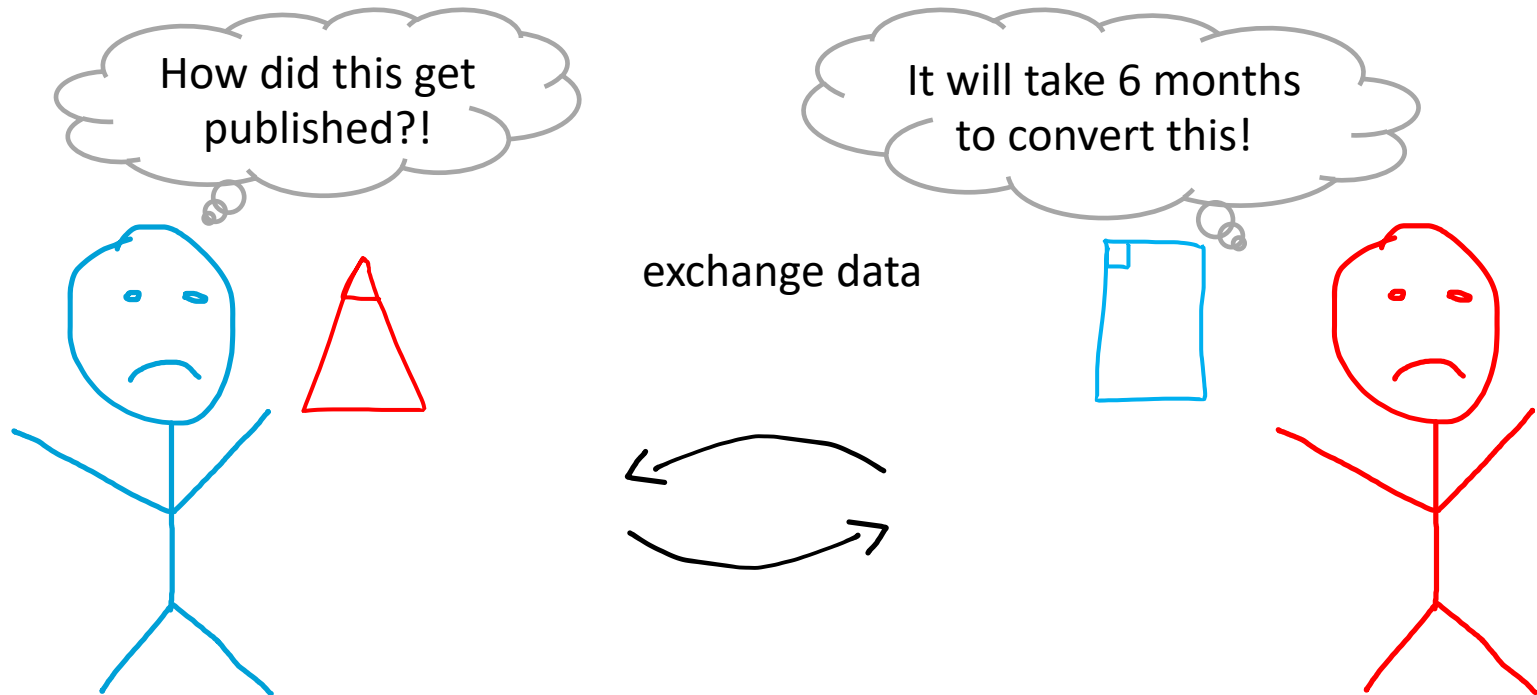
HDF5 Users Group 2020
October 16, 2020

nwb.org

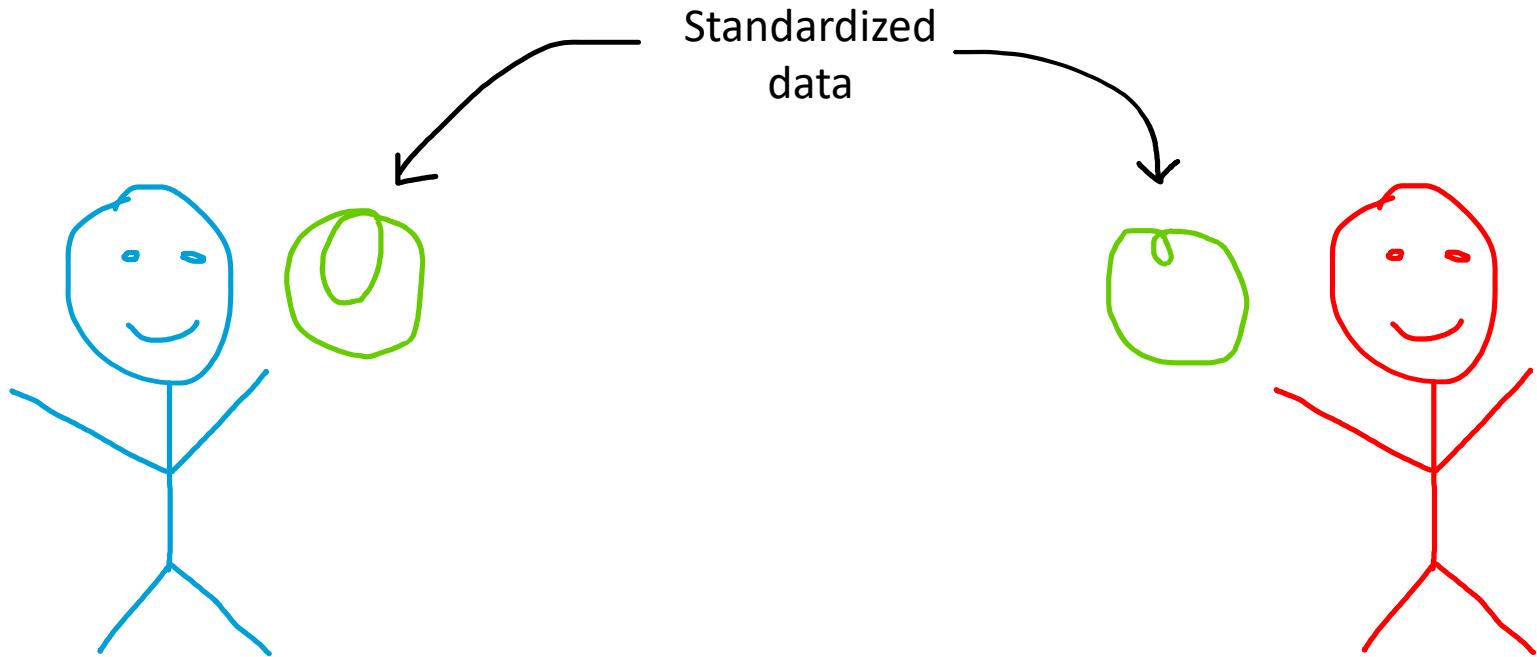
Community science...



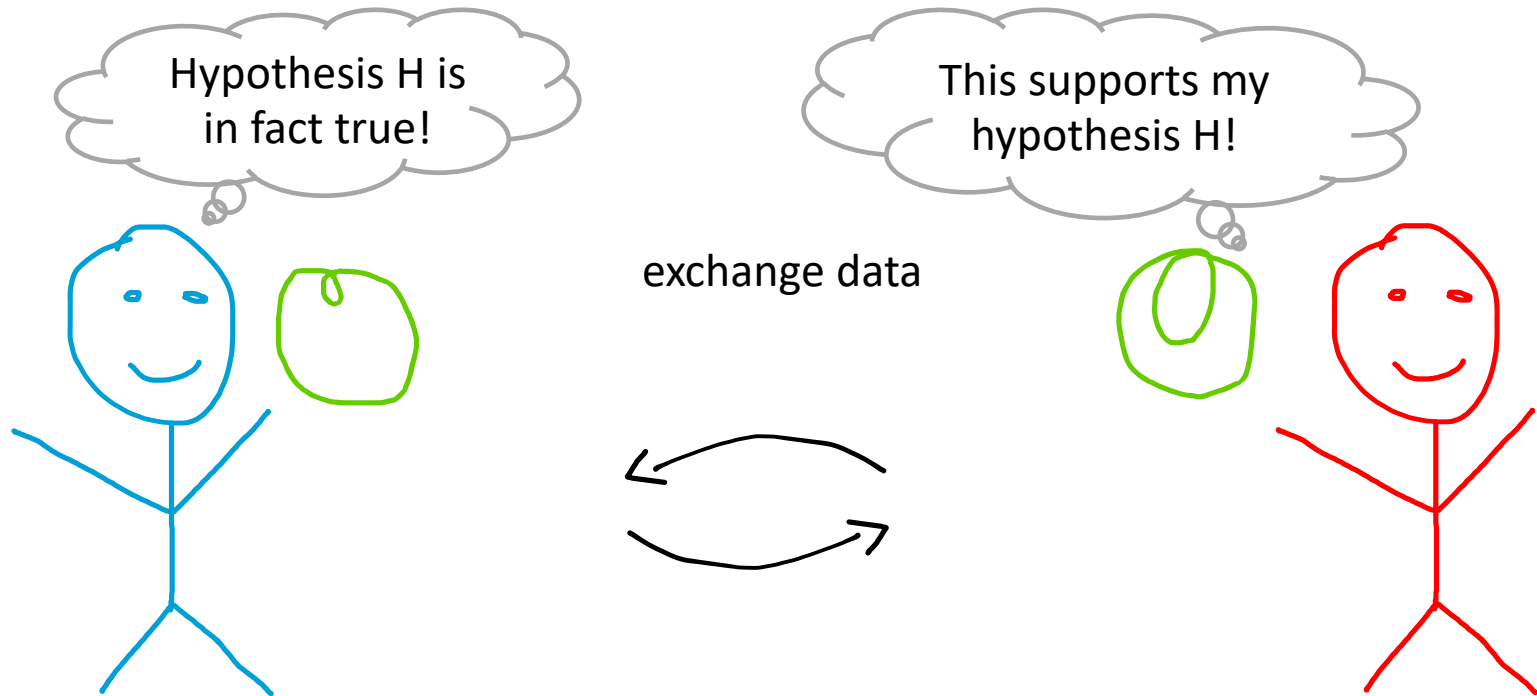
Community science...



Community science...



Community science...

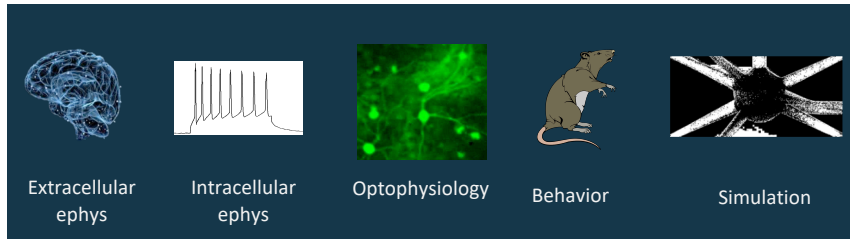


Neurodata Without Borders

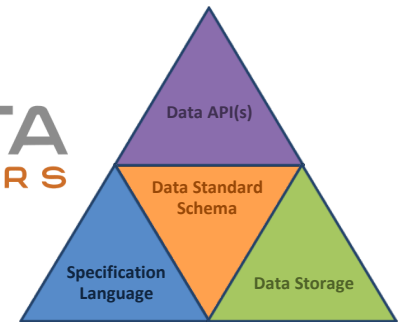
Motivation: community science needs a stable target for data

NWB – An Ecosystem for Neurophysiology Data Standardization

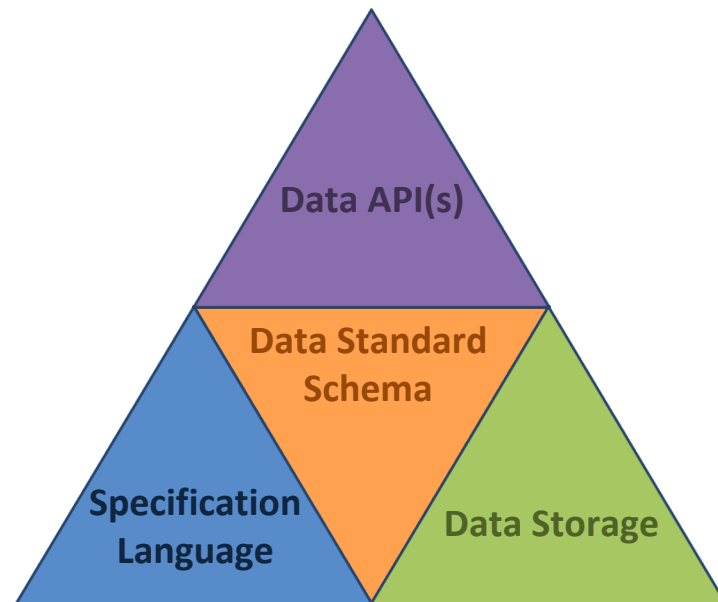
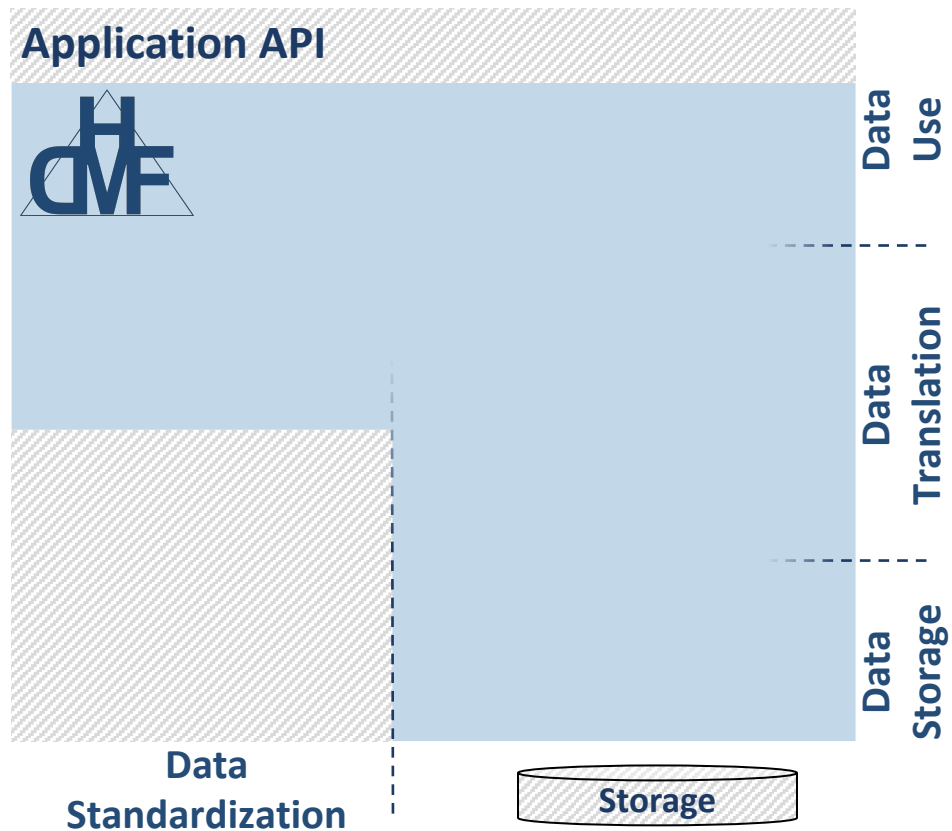
- Defines a unified format for neurophysiology data
→ focus on dynamics of groups of neurons
- More than just a file format
 - tools, methods, and standards for storing, sharing, and analyzing complex neurophysiology data



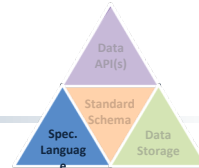
NEURODATA
WITHOUT BORDERS



HDMF Software Stack



Specification language



Goal:

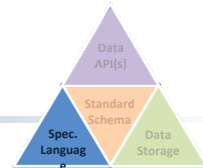
- Enable the formal definition of data standards that is *machine and human* readable

Format specification language

- Schema for defining hierarchical data schemas

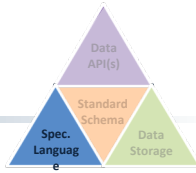
Main primitives of the specification language:

- Object primitives
- Data type specifications
- Namespace specification



Object primitives:

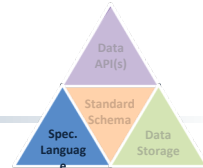
- **Group:** collection of objects i.e. subgroups, datasets, links
- **Dataset:** n-dimensional array with associated data type, dimensions, etc.
- **Attribute:** metadata attached to a Group or Dataset
- **Link:** a soft link to given target data_type



Data type specifications

- **Basic data types:** strings and numeric types
- **Compound data types:** complex data types
- **isodatetime:** ISO8061 date-time string
 - e.g. 2018-09-28T14:43:54.123+02:00
- **Object reference:** a link that can be as a value
- **Region reference:** a link to a dataset that also stores slice

Defining reusable data types



data_type: Defines reusable type

- Similar to a class in OOP
- All objects must have either a unique name or data_type

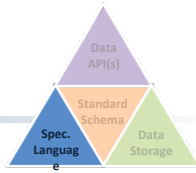
Enables reuse of types through inheritance and:

- **data_type_inc:** include an existing type
- **data_type_def:** defines a new type

A schema is a collection of reusable data_types

- Extend by:
 - defining new data_types
 - extending existing data_types

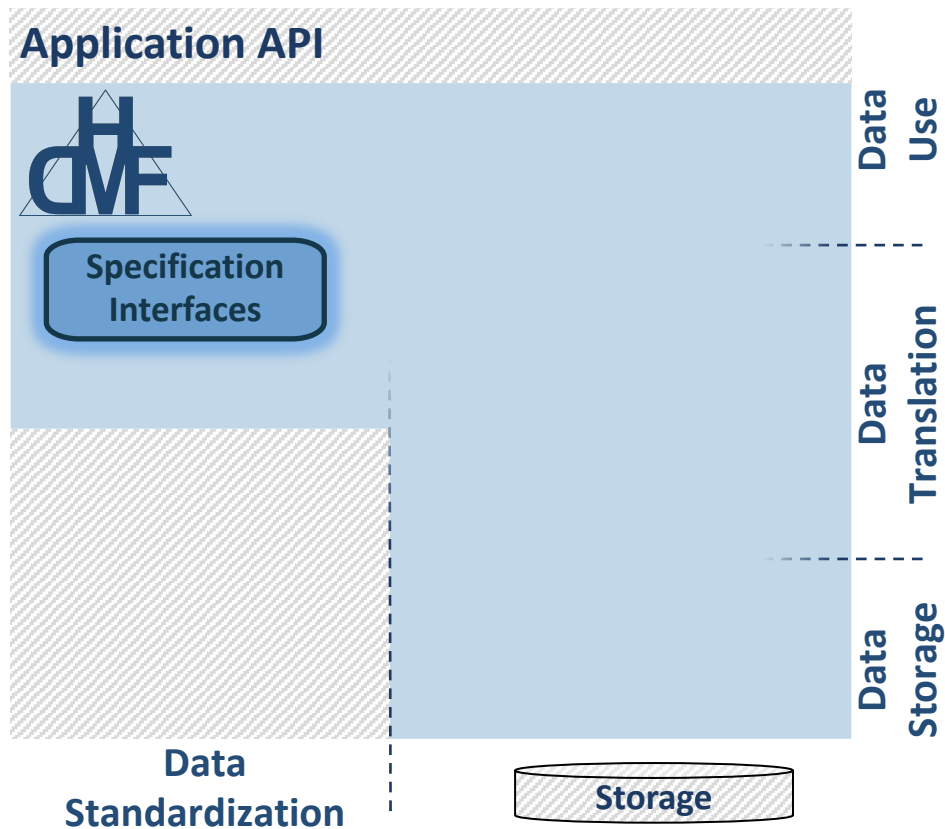
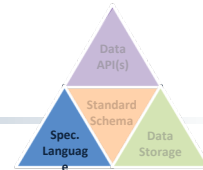
Specification language



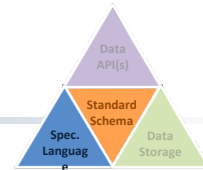
Namespace specification:

- define a standard
- insulate extensions from each other
- enable the creation of new data standards
- extensions shared in the form of a namespace

Specification Language API



Specification

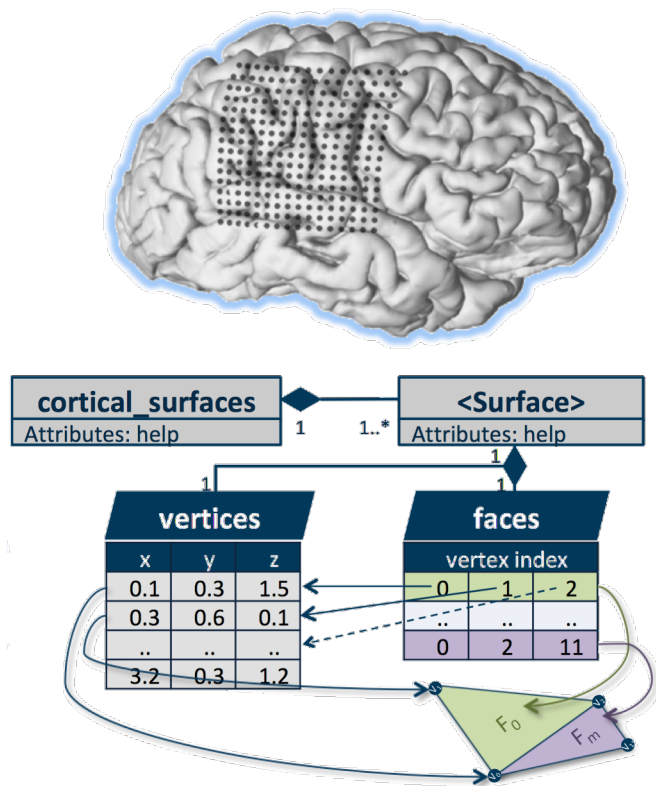


Creating the extension

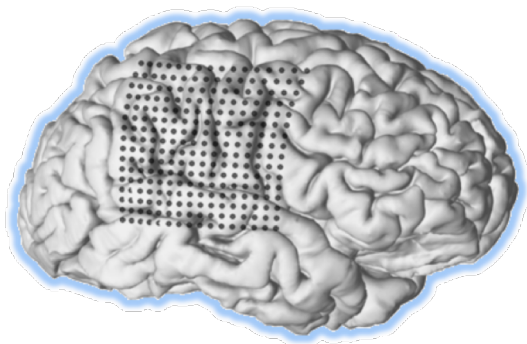
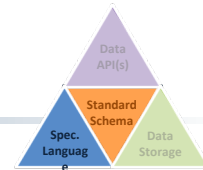
```
from pynwb.spec import NWBDatasetSpec, NWBNamespaceBuilder,
                    NWBGroupSpec, NWBAttributeSpec

surface = NWBGroupSpec(neurodata_type_def='Surface',
                       neurodata_type_inc='NWBDataInterface',
                       quantity='+', doc='brain cortical surface')
surface.add_dataset(NWBDatasetSpec(
    doc='...', shape=(None, 3),
    name='faces', dtype='uint', dims=...))
surface.add_dataset(NWBDatasetSpec(
    doc='...', shape=(None, 3),
    name='vertices', dtype='float', dims=...))
surface.add_attribute(...)

ns_builder = NWBNamespaceBuilder(doc=..., name='ecog',
                                  version='1.0', author='Ben Dichter', ...)
ns_builder.add_spec('ecog.extensions.yaml', surface)
ns_builder.export('ecog.namespace.yaml')
```



Specification



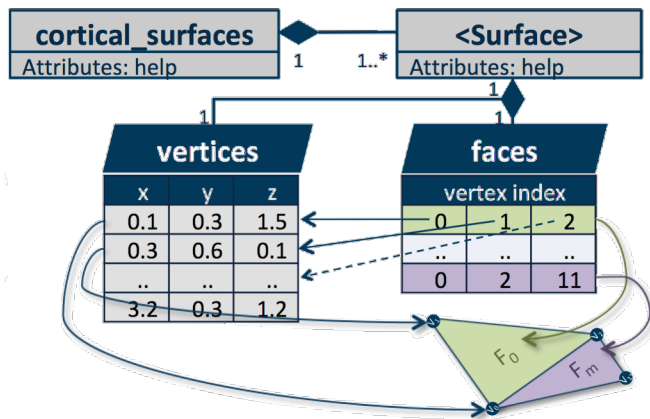
Write data

```
from pynwb import load_namespaces, get_class,
                  NWBHDF5IO, NWBFile ...

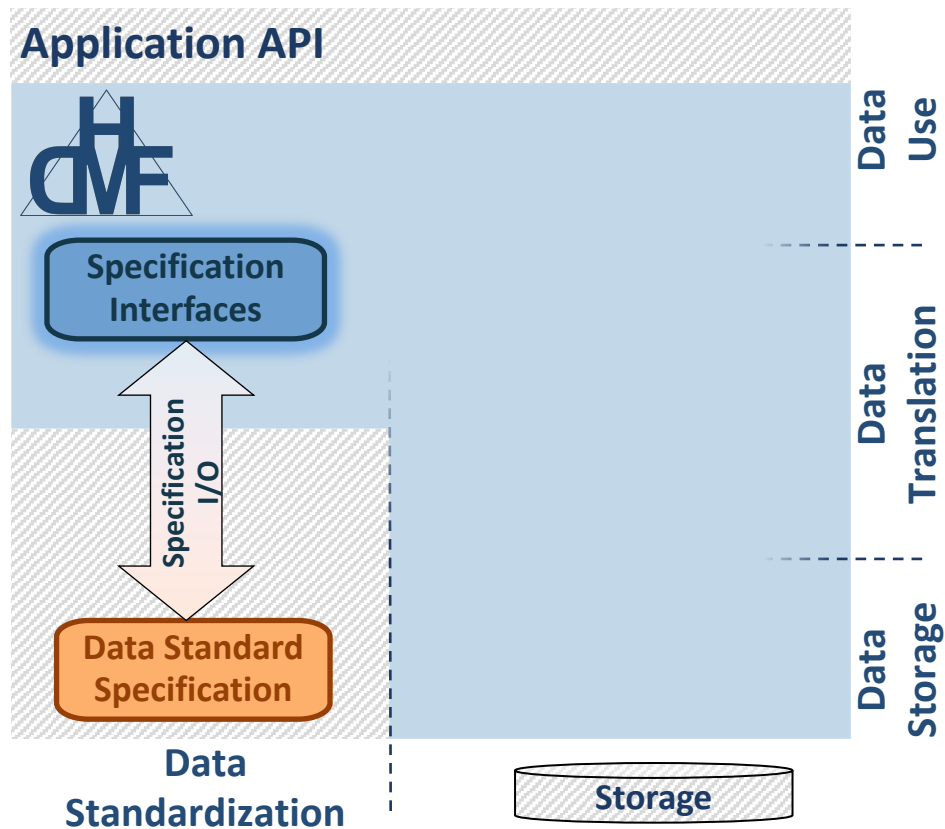
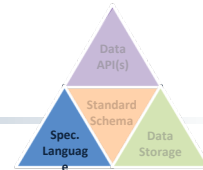
nwbfile = NWBFile(...)
load_namespaces('ecog.namespace.yaml')
Surface = get_class('Surface', 'ecog')
surf = Surface(faces=... , vertices=..., name='Surface_1')
nwbfile.add_acquisition(surf)
with NWBHDF5IO('surface_example.nwb', 'w') as io:
    io.write(nwbfile)
```

Read data

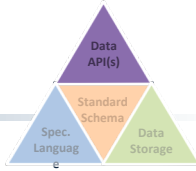
```
load_namespaces('ecog.namespace.yaml' )
io = NWBHDF5IO('surface_example.nwb', 'r')
nwbfile = io.read()
nwbfile.get_acquisition('Surface 1').vertices
```



Specification Language API



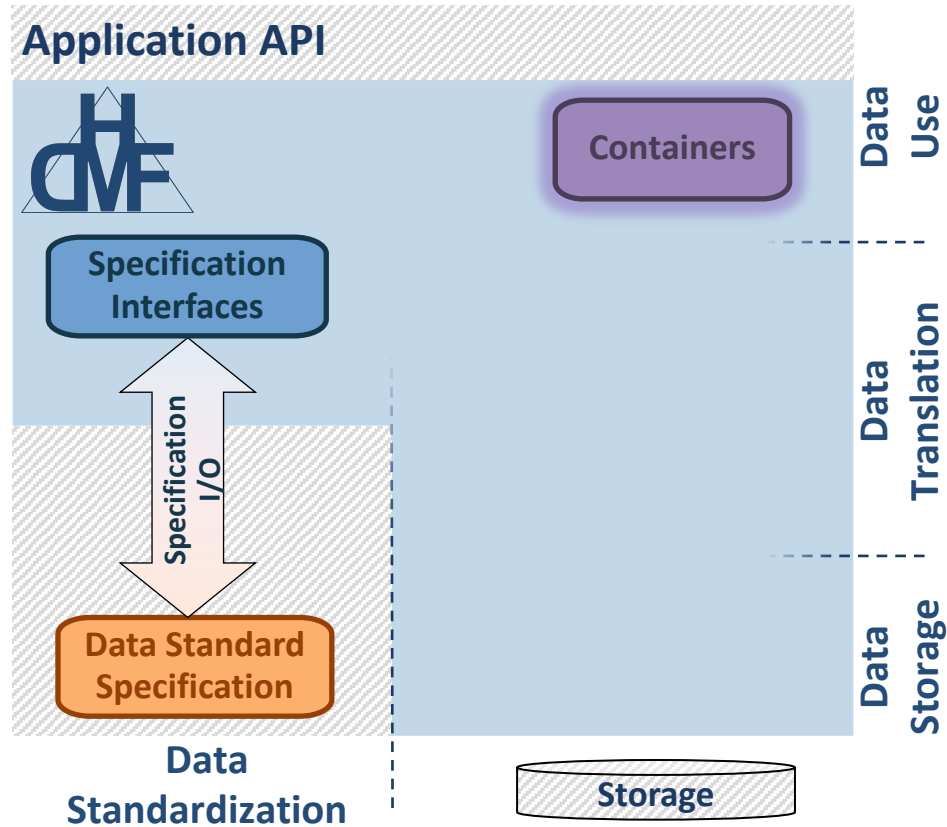
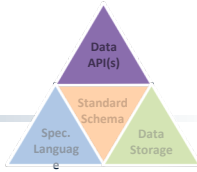
Data API



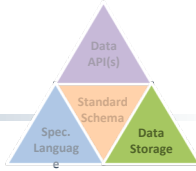
Container: Main in-memory data interface for applications

- One for each `data_type` in the standard schema
 - Class dynamically generated if one does not exist
- HDMF provides base classes and decorators to facilitate the implementation of new Container classes
- Containers hold handles to on-disk data → data lazily loaded
 - backend dependent

Data API



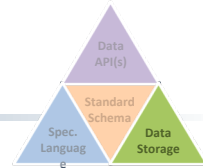
Data storage



Primary function:

- Map primitives to storage
- Decouple backend from specification and in-memory data structures
- **Builders:** Intermediary objects for I/O representing data primitives
 - GroupBuilder, DatasetBuilder, LinkBuilder, ReferenceBuilder, RegionBuilder
- **HDMFIO:** I/O Interface for reading/writing builders
 - Need to define: read_builder, write_builder, open, close, and __init__ functions
 - HDF5IO and ZarrIO

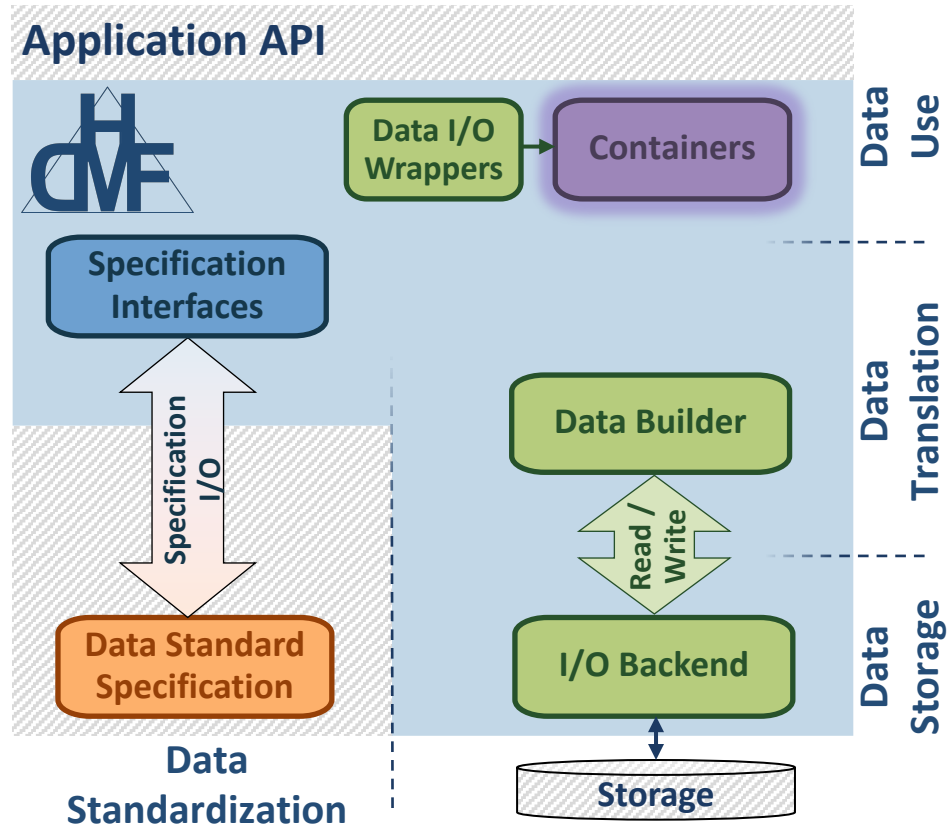
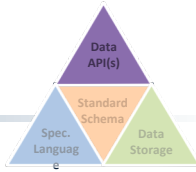
Data storage



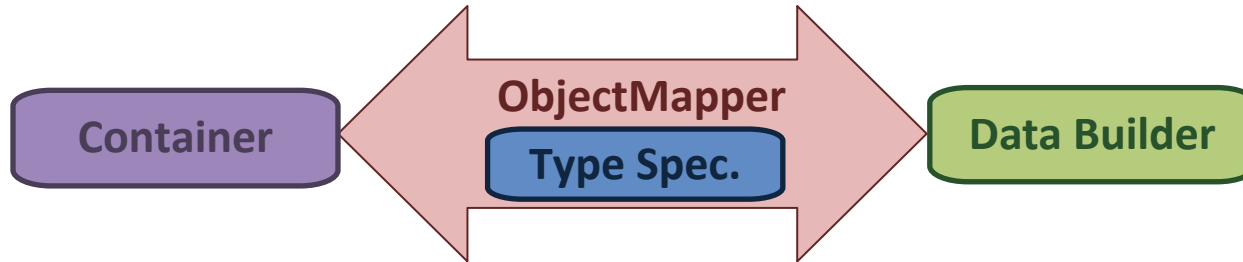
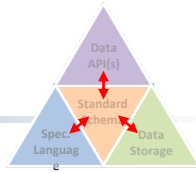
Primary function:

- Map primitives to storage
- Decouple backend from specification and in-memory data structures
- **Data I/O wrappers:**
 - **DataIO:** Define chunking, compression, linking, modular storage etc. to optimize storage and I/O
 - **DataChunkIterator:** Iterator to produce data chunks for iterative data write (e.g., for data streaming or large data import)

Data API

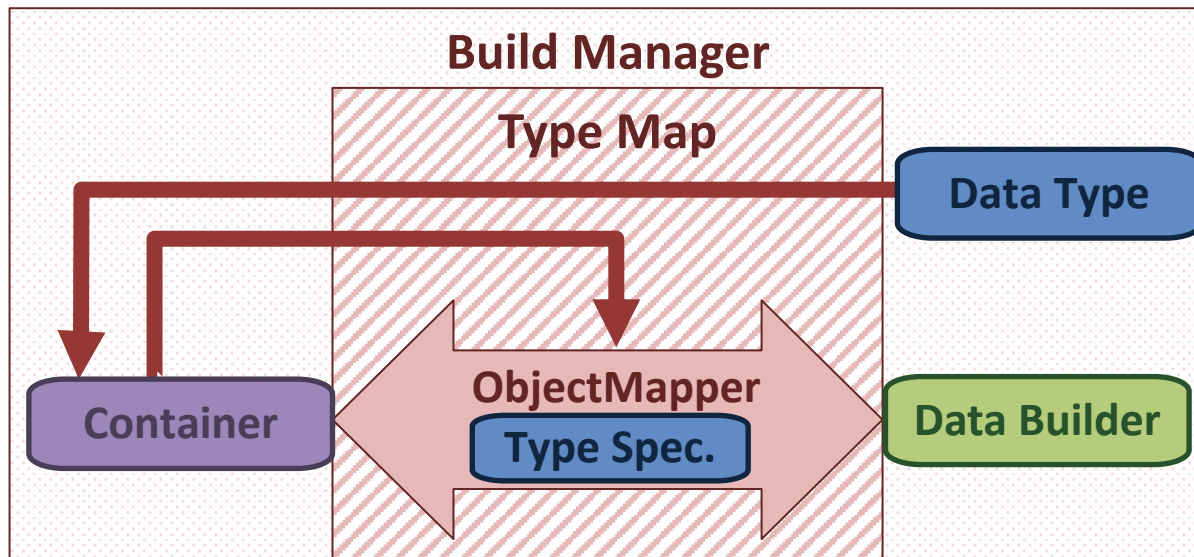
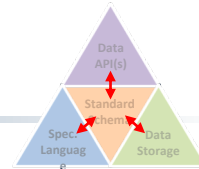


ObjectMapper



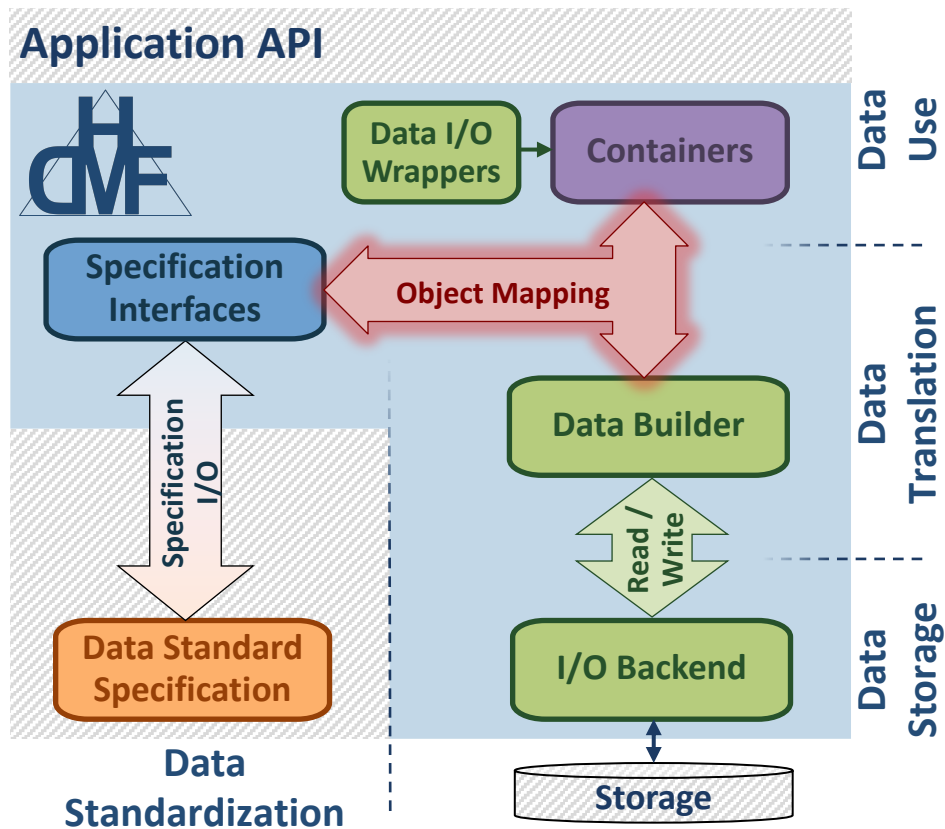
- Maintains mapping between *Container attributes* and *specification components*
- Constructed from a `data_type` specification
- One for each `data_type`
 - base functionality or provided by user

Data mapping API

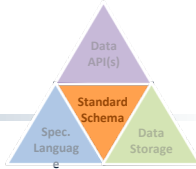


- **TypeMap:** Map between: `data_types` , Container classes and ObjectMapper classes
 - Given `data_type`, return Container class
 - Given Container class, return ObjectMapper
- **BuildManager:** Responsible for memoizing Builders and Containers
 - Given a Builder, return a Container and vice versa

HDMF Software Stack



Neurodata Without Borders

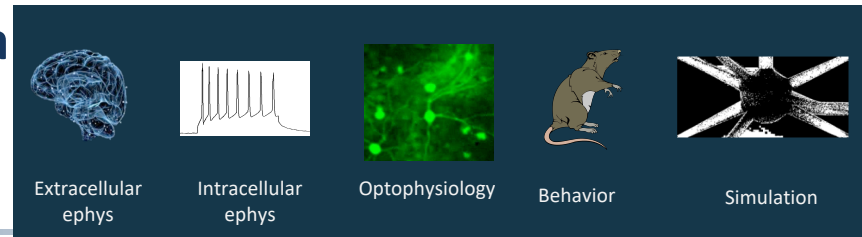
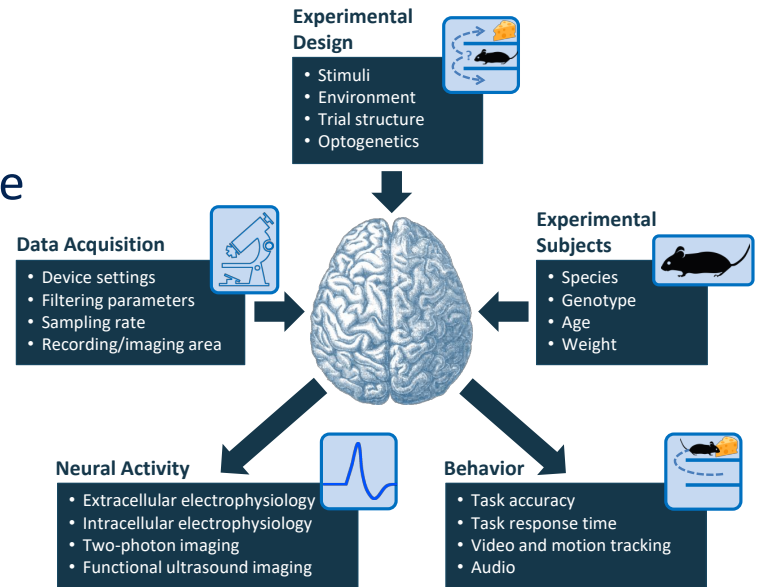


A format schema (a.k.a. specification)

- a collection of YAML files that formally describes the organization of data
- covers data types throughout data life cycle

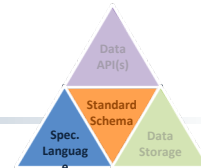
The **NWB data standard** defines:

- **A catalog of neurodata_types**
 - 20 different TimeSeries data types
 - 22+ analysis data types
- **Base hierarchy to logically group data**
 - acquisition, data processing, experimental metadata





NDX Catalog



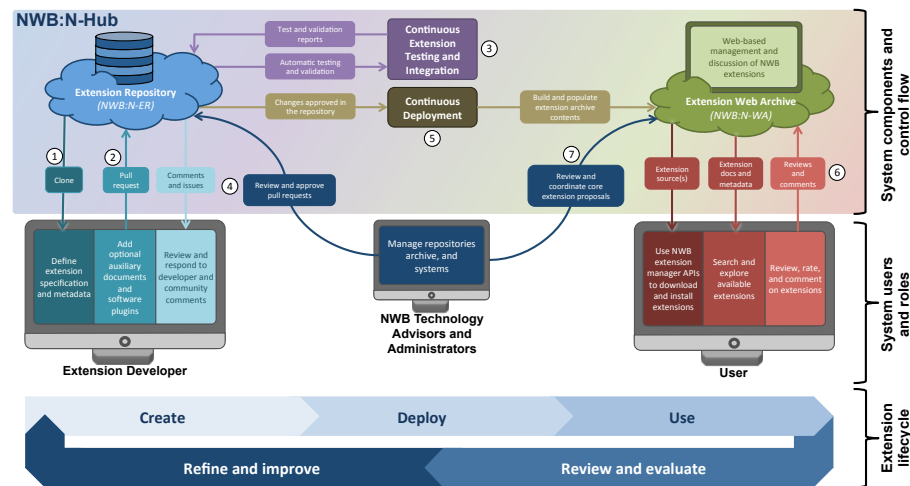
Goal: Enable community adoption, extension, and curation of NWB and integration of new use cases

**Neurodata
Extensions
Catalog**

Approach:

- Tools for creating extensions (PyNWB, nwb-docutils, git template)
- Recipe for deploying extension
- Online catalog for sharing
- Guidelines for versioning, sharing, and review of extension

Resources: <https://nwb-extensions.github.io/>



Online resources

Visit us online at

neurodatawithoutborders.github.io

and

nwb.org

Contribute

Create issues for bugs, feature request and pull requests on GitHub for schema, PyNWB and MatNWB. For details see: neurodatawithoutborders.github.io/contributing