



INCF virtual training weeks 2021 – NIX Neo workshop –

Michael Denker, Jan Grewe, Julia Sprenger, & Michael Sonntag

German Neuroinformatics Node

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Reuse of public genome-wide

“ *The authors replicated two studies ‘in principle’ and six ‘partially’, whereas ten were not reproduced. [...] The main reason for the lack of reproducibility was the unavailability of all relevant data or metadata.* — Rung & Brazma, 2012

... databases process, analyse and annotate these data further to make them accessible to every biologist. In this Review, we discuss the utility of the gene expression data that are in the public domain and how researchers are making use of these data. Reuse of public data can be very powerful, but there are many obstacles in data preparation and analysis and in the interpretation of the results. We will discuss these challenges and provide recommendations that we believe can improve the utility of such data.

Sorting Out the FACS: A Devil in the Details

William C. Hines,^{1,5,*} Ying Su,^{2,3,4,5,*} Irene Kuhn,¹ Kornelia Polyak,^{2,3,4,5} and Mina J. Bissell^{1,5}

¹Life Sciences Division, Lawrence Berkeley National Laboratory, Mailstop 977R225A, 1 Cyclotron Road, Berkeley, CA 94720, USA

²Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, MA 02215, USA

³Department of Medicine, Brigham and Women's Hospital, Boston, MA 02115, USA

⁴Department of Medicine, Harvard Medical School, Boston, MA 02115, USA

⁵These authors contributed equally to this work

*Correspondence: chines@lbl.gov (W.C.H.), ying_su@dfci.harvard.edu (Y.S.)

“ ... our two laboratories quite reproducibly were unable to replicate each other's fluorescence-activated cell sorting (FACS) profiles of primary breast cells. — Hines et al., 2014

of the United States, decided to collaborate on a problem of mutual interest—namely, the heterogeneity of the human breast. Despite using seemingly identical methods, reagents, and specimens, our two laboratories quite reproducibly were unable to replicate each other's fluorescence-activated cell sorting (FACS) profiles of primary breast cells. Frustration mounted, given that we had not found the correct answer(s), even after a year.

most suitable for distinguishing diversity among different cell populations in the mammary gland. Flow instruments have evolved from being able to detect only a few parameters to those now capable of measuring up to—and beyond—an astonishing 50 individual markers per cell (Cheung and Utz, 2011). As with any exponential increase in data complexity, the importance of developing robust preparation and analytical protocols that

initial analysis of separated cell populations grown in 3D matrices was to take place in Berkeley (M.J.B.'s laboratory, Lawrence Berkeley National Lab, University of California, Berkeley). Both our laboratories have decades of experience and established protocols for isolating cells from primary normal breast tissues as well as the capabilities required for flow sorting primary cells from mice and women.

Reproducibility crisis

"Challenges in irreproducible research", Nature special, 06.07.2018, ISSN 1476-4687 <https://www.nature.com/collections/prbfkwmwvz>

“ *More than 70% of researchers have tried and failed to reproduce another scientist's experiments, and more than half have failed to reproduce their own experiments. Those are some of the telling figures that emerged from Nature's survey of 1,576 researchers who took a brief online questionnaire on reproducibility in research.*”

Reproducibility crisis

What factors contribute to irreproducible research?

- › Selective reporting
- › Pressure to publish
- › Low statistical power or poor analysis
- › Not replicated enough in original lab
- › Insufficient oversight/mentoring
- › Methods & code unavailable
- › Poor experimental design
- › Raw data not available from original lab
- › Fraud
- › Insufficient peer review
- › Problems with reproduction efforts
- › Technical expertise required for reproduction
- › Variability of standard reagents
- › Bad luck
- › Insufficient metadata

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Reproducibility crisis also in the Neurosciences

There is a lack of standardization

- › Earlier (roughly 2007/2008) this was also identified as one problem in neuroscience.

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- › Earlier (roughly 2007/2008) this was also identified as one problem in neuroscience.
- › We need standards and tools to help doing good neuroscience.
- › The INCF task force on **Standardization in electrophysiology** was the starting point of the NIX project.

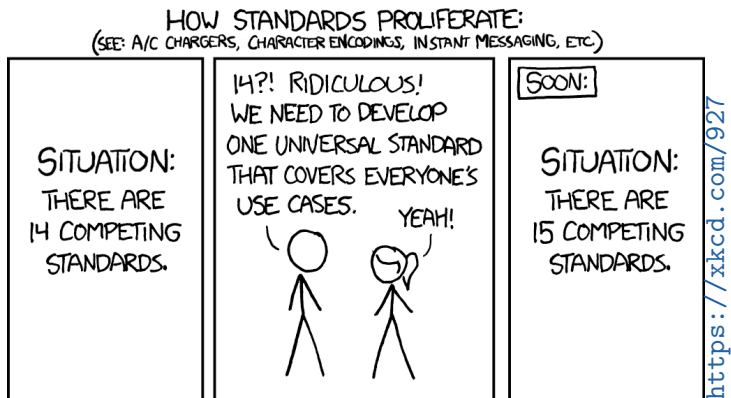
Reproducibility crisis also in the Neurosciences

HOW STANDARDS PROLIFERATE:
(SEE: A/C CHARGERS, CHARACTER ENCODINGS, INSTANT MESSAGING, ETC.)



<https://xkcd.com/927>

Reproducibility crisis also in the Neurosciences



... but at least some of these are **open-source!**



Neuroscience Information Exchange

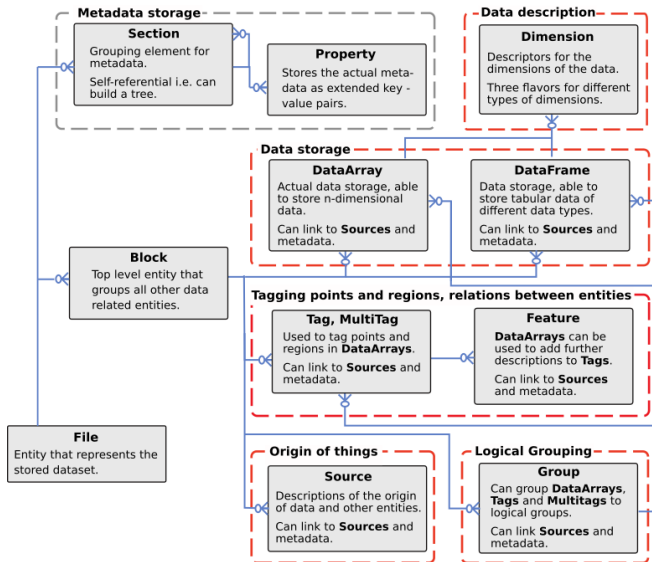
Originates from the neuroscience ...
but is not limited to it.

NIX concept

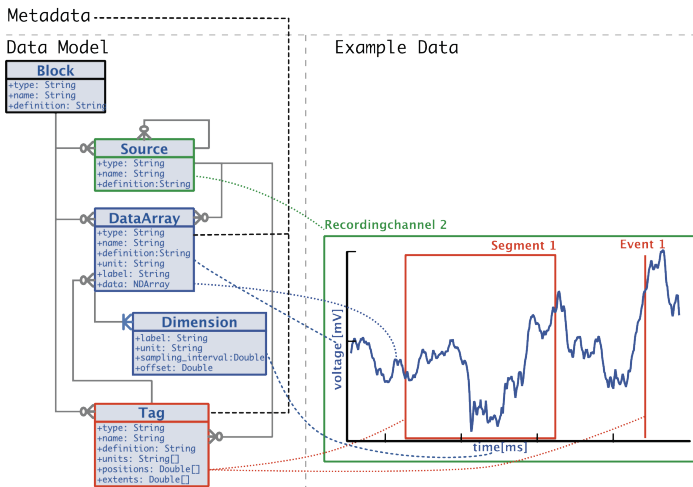
NIX aims at:

1. One data model for storing data and metadata within the same container.
2. Flexible enough to support a high variety of data types.
3. Store n-dimensional data.
4. Allow in-depth annotations.
5. Data entities are self describing.
6. Support standardization in data and metadata storing.
7. Of course, open source.

NIX Data Model



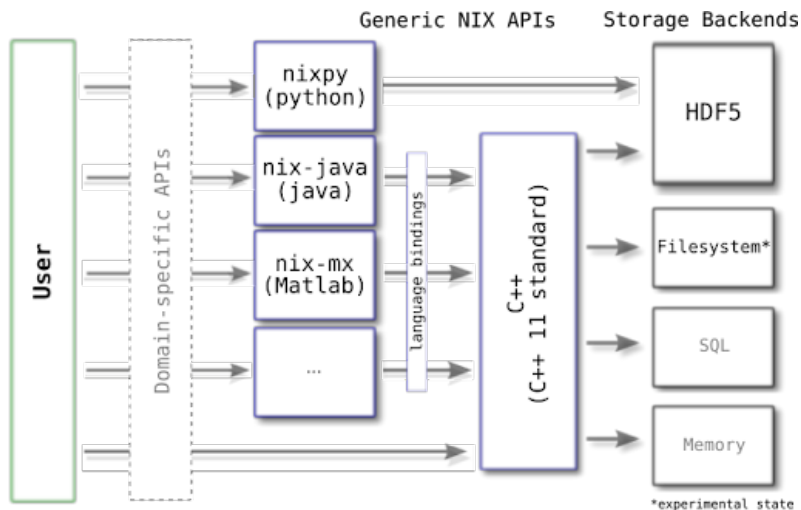
NIX Data Model



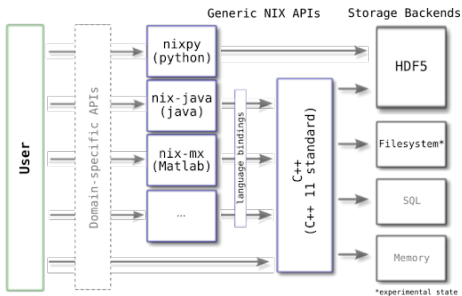
NIX Data Model

- › The NIX data model is not a file format.
- › It can be implemented in many backends.
- › So far, we use the HDF5 file format as storage backend.

NIX Implementations

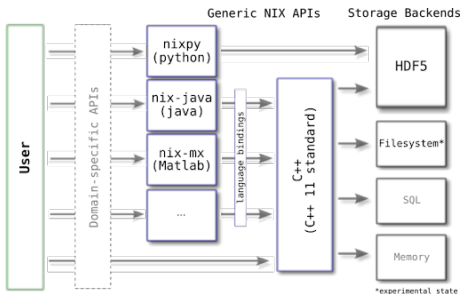


Generic APIs



- › There are two native APIs: `nixpy` (python) and `nixio` (C++) and two that use language bindings to write NIX files to HDF5 files.
- › In principle, we can support several different backends.

Domain specific APIs

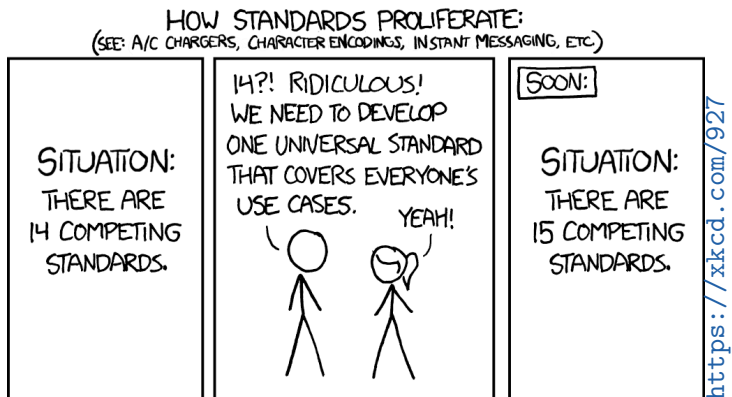


- › Domain specific APIs use the generic ones to ease access to data from one domain, e.g. Electrophysiology.
- › They provide a way to adapt and standardize storing data.
- › This does not hinder to read the data with the generic libraries.

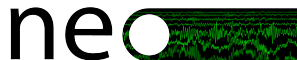
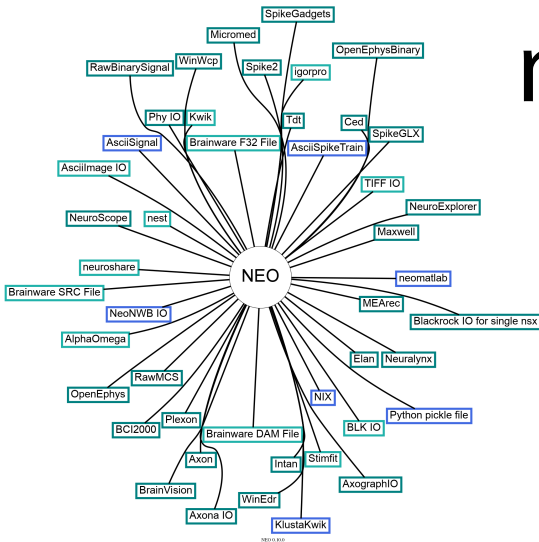
⇒ Neo-nixio stores Neo electrophysiology data using NIX as storage backend.

⇒ Storing to NIX can be embedded into the recording software
<http://relacs.sourceforge.net>.

Reproducibility crisis also in the Neurosciences



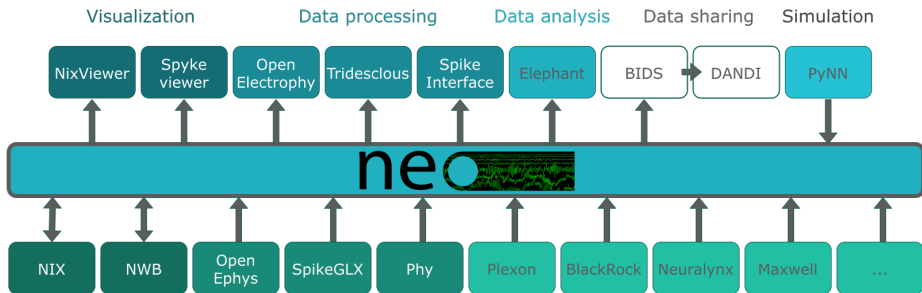
...and the other 40+ ephys data standards?

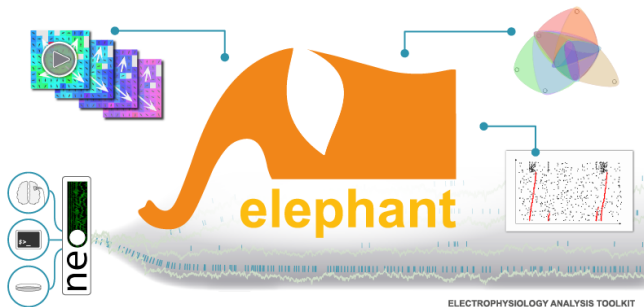


- › interfaces to 40+ ephys proprietary & open formats in various versions
- › provides a standardized ephys data **representation**, it is not a file format.
- › reads all formats, but provides writing capability only for selected open formats.

A basis for

- > format conversion
- > custom data analysis
- > diverse tools dealing with ephys data





Electrophysiology Analysis Toolkit

- › analysis of brain activity (spike trains, local field potentials, . . .)
- › builds on the Neo framework (input, output)
- › focus on population measures from experiment and simulation



Quick visualizations

- › of Neo representations of electrophysiology data
- › of Elephant analysis results

In this workshop we will ...

- › introduce the ideas and concepts of the NIX data model.
- › show how various data types can be represented with it.
- › show how to use and find data in NIX files.
- › become familiar with the Neo representation of electrophysiology data.
- › learn how to use Elephant and Viziphant for data analysis and visualizations.
- › use a lot of hands-on exercises.

NIX-Neo Workshop

Day 1: NIX Basics

- › Introduction
- › File & data handling
- › Tagging
- › Annotations

Day 2: Deeper dive

- › Adding *Features*
- › Finding stuff
- › Advanced features

Day 3: Neo&Elephant

- › Introduction
- › Working with Neo data
- › Elephant toolbox

NIX-Neo Workshop - Requirements

- › We run the workshop using the python version of the NIX library (called nixio while the project is called nixpy...) and you should have some basic knowledge of the python programming language.
- › You need a running python environment (≥ 3.6).
- › Installed libraries:
 - jupyter
 - matplotlib
 - nixio
 - neo
 - elephant
 - viziphant
- › Alternatively we can use Binder (see the README file in the course repository). <https://gin.g-node.org/INCF-workshop-2021/NIX-Neo-workshop>

NIX-Neo Workshop - Requirements

Installing the requirements locally

```
>pip3 install -r requirements.txt
```

NIX-Neo Workshop - Requirements

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```

Please make sure you have the latest nixio version.

We will rely on nixio version 1.5.1 In case of doubt run:

```
pip3 install nixio --upgrade
```

NIX-Neo Workshop - Resources

Course material:

- › <https://gin.g-node.org/INCF-workshop-2021/NIX-Neo-workshop>

Source code:

- › <https://github.com/g-node/nix>
- › <https://github.com/g-node/nixpy>
- › <https://github.com/g-node/nix-mx>

Documentation & tutorials:

- › <https://nixpy.readthedocs.io/>
- › <https://nixio.readthedocs.io/>
- › <https://neuralensemble.org/neo/>
- › <https://python-elephant.org>

NIXPY documentation

The screenshot shows a web browser displaying the NIXPY Python library documentation. The browser's address bar shows the URL `nixpy.readthedocs.io`. The page has a dark blue sidebar on the left with the NIX logo and a search bar. The main content area is white and features a navigation bar with "Docs" and "Edit on GitHub" links. The title of the page is "NIXIO Python library documentation". Below the title, there are several status badges: "NIXPY tests and linting passing", "build passing", "coverage 80%", "codecov 81%", "code quality: python 3.1", and "docs passing". The main text of the page includes an introduction to the NIXIO module, its purpose, and its use in scientific data storage. It also mentions the current implementation using HDF5 and the program's history with the INCF Datasharing Program. The page is structured with sections for Introduction, Support, and Citing.

Docs • NIXIO Python library documentation [Edit on GitHub](#)

[Next](#)

NIXIO Python library documentation

[NIXPY tests and linting](#) passing [build](#) passing [coverage](#) 80% [codecov](#) 81% [code quality: python 3.1](#) [docs](#) passing

The NIXIO module is the native python re-implementation of the [NIX C++ library](#) for the NIX data model.

The NIX data model allows to store fully annotated scientific datasets, i.e. the data together with its metadata within the same container. Our aim is to achieve standardization by providing a common/generic data structure for a multitude of data types. See the [wiki](#) or the [introduction](#) for more information.

The current implementations store the actual data using the [HDF5](#) file format as a storage backend.

NIX emerged from the activities of the Electrophysiology Task Force of the [INCF](#) Datasharing Program (2010-2015). It is a registered research resource with the [RRID:SCR_016196](#).

Introduction

We have assembled [introductory material](#) that illustrates using nix. The tutorials contain several code examples. The [use_cases](#) explain in more detail how nix is used in real world situations.

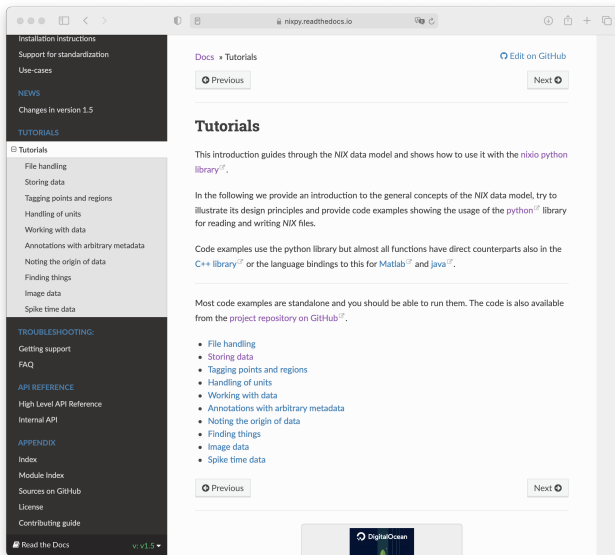
Support

If you need help, want to get in touch, or have any other request [these](#) are your options.

Citing

If you use NIX, it would be much appreciated if you would cite it in publications with its identifier [RRID:SCR_016196](#) and/or the reference:

NIXPY documentation



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Navigation Sidebar (Left):

- Installation instructions
- Support for standardization
- Use-cases
- NEWS
- Changes in version 1.5
- TUTORIALS**
- Tutorials
 - File handling
 - Storing data
 - Tagging points and regions
 - Handling of units
 - Working with data
 - Annotations with arbitrary metadata
 - Noting the origin of data
 - Finding things
 - Image data
 - Spike time data
- TROUBLESHOOTING:
 - Getting support
 - FAQ
- API REFERENCE
 - High Level API Reference
 - Internal API
- APPENDIX
 - Index
 - Module Index
 - Sources on GitHub
 - License
 - Contributing guide
- Read the Docs v.1.5

Main Content Area:

Docs » Tutorials [Edit on GitHub](#)

[Previous](#) [Next](#)

Tutorials

This introduction guides through the NIX data model and shows how to use it with the [nixio python library](#).

In the following we provide an introduction to the general concepts of the NIX data model, try to illustrate its design principles and provide code examples showing the usage of the [python](#) library for reading and writing NIX files.

Code examples use the python library but almost all functions have direct counterparts also in the [C++ library](#) or the language bindings to this for [Matlab](#) and [java](#).

Most code examples are standalone and you should be able to run them. The code is also available from the [project repository on GitHub](#).

- [File handling](#)
- [Storing data](#)
- [Tagging points and regions](#)
- [Handling of units](#)
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- [Annotations with arbitrary metadata](#)
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- [Spike time data](#)

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