SiNAPS Data Pipeline User Guide

(Initial Issue - October, 2025)

PLEXON®
Neurotechnology Research Systems

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Introduction

Plexon has partnered with Corticale SRL, Genoa Italy, to develop high-density “SiNAPS” silicon probes compatible with the OmniPlex data acquisition platform. Together, SiNAPS and OmniPlex enable the recording of extracellular neural activity in unprecedented detail from thousands of tightly packed neural electrode sensors called pixels.

High-density neural probes like SiNAPS require a different method of data acquisition and spike sorting workflow. As increases in inter-pixel density pack pixels more tightly together, signals from a given neuron can register across multiple adjacent pixels. Traditional spike sorters are ill-equipped to handle the resulting data redundancy as they were built with the assumption that adjacent pixels share no common units. This redundancy is compounded by the accompanying increased number and density of pixels on a single probe, up to 1024 pixels on a single shank in two or more columns.

As a leading innovator in neural data acquisition technologies, Plexon has long been committed to providing its users with the tools needed to process data in a seamless, integrated workflow. In this spirit, Plexon has developed the **SiNAPS Data Pipeline (SDP)**, a collection of Plexon- and 3rd-party software tools that enable users to overcome the challenges inherent in sorting and analyzing neural data recorded into Plexon PL2 files with OmniPlex and SiNAPS probes.

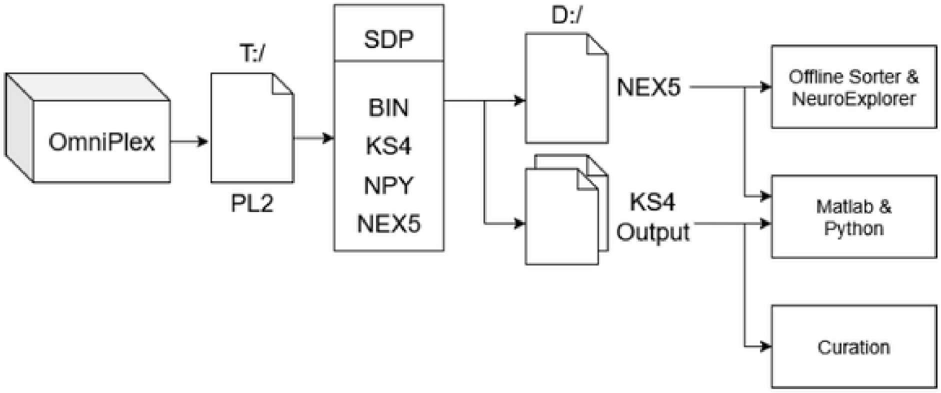
OmniPlex provides two paths for recording neural data and thus two pathways for the SiNAPS Data Pipeline to follow. The first path, *online*, is conventional spike processing that takes advantage of a cutting-edge culling heuristic that eliminates redundancy in the waveforms shared across adjacent pixels and the data is recorded as SPK data type in PL2 files. OmniPlex conventional channel-based visualizations and sorting are supported. The second path is raw, wide band (WB), high-density pixel data from SiNAPS recorded directly to PL2 files for subsequent *offline* processing. OmniPlex supports recording both SPK and WB acquisition paths simultaneously. Experiment related digital, FP, and analog data are also recorded into the PL2 file either way.

The **online** pathway is used primarily for visualization during an experiment. Sorting and analysis can proceed based on the conventional OPX/OFS/NeuroExplorer workflow if desired but is not recommended as this approach *does not* perform corrections for probe drift, overlaps, or jitter, and *does not* provide the exceptional high-quality sorting for which SiNAPS probes are intended. The results are draft quality and in general recommended only for getting started with HD sorting and experimenting with OPX.

The **offline** pathway is the standard method for processing a file of recorded WB raw data. WB data in a PL2 file is extracted and converted to a .bin BINary file in raw-interleaved format. Kilosort is perhaps the most widely used high-density array sorter. Kilosort4 performs operations on the .bin file including high pass filtering, waveform extraction, spike sorting, drift and overlap correction, and stores the spike sorted results in a collection of Python *NumPy* files with the extension *.npy*. A NeuroExplorer .nex5 file is also created containing a simple curation of spike clusters into time stamps, digital events, FP waveforms, and experiment analog data. Spike waveforms are optional but not recommended. See Why Neuroexplorer.

Ref: Marius Pachitariu , Shashwat Sridhar, Jacob Pennington & Carsen Stringer (2024) Spike sorting with Kilosort4

SDP Environment



OmniPlex Offline Pathway

Recordings from SiNAPS HD probes can be quite long, from a few GB up to a few hundred GB, and require substantial processing power for offline array processing and spike sorting. Plexon provides Dell workstations configured with fast storage and a high-performance Nvidia graphics processing unit (GPU) for SiNAPS signal processing and array sorting, but the processing time can still be quite long, depending.

There are three storage drives; C: is a 1TB for the OS, standard programs, scripts, documentation, scratch files, etc., T: Temp is 2TB for recording and temporary working storage, and D: Data is a selected configuration of HDD for mainline storage. All three are enterprise class high reliability drives; C: and T: are high-bandwidth M.2 NVME SSD drives, D: is a RAID 0 pair of HDDs. Plexon OmniPlex software records to the T: drive. SDP processes and sorts the PL2 file on T: for performance reasons. The resulting files are moved to D:, and then T: is cleared for the next operation. T: is very fast and is used as a temporary transient location. After the first sorting on T: files may be resorted from D: though the process is slower.

There is typically no redundancy in the D: drive configuration as that requires more drives. Many researchers store archived data on departmental or institutional online storage servers, but not everyone has access to such facilities. After the raw data has been processed and sorted, storing PL2 files online may be unnecessary and moving them to offline media is an optional redundant safety move. It can always be brought back online if needed. What and how to do that depends on the volume of storage. The processed and sorted data files suitable for analysis are kept online. Plexon can provide HDD data storage in the computer for up to many tens of TB if requested, or more using the third-party storage options.

The output from KS4 is sorted spikes and additional data items for optional curation. Other experiment data is contained in the NEX5 file; digital events, Field Potentials, experiment analog data. NEX5 files are small and fast. and extracting data with the SDK is straightforward. This permits saving off the large PL2 files to free up disk space.

Installation

System Requirements

The SiNAPS Data Pipeline is intended only for use on a Plexon-provided PC.

Installation and Upgrade Procedure

There are three steps to installing the SDP software (which are detailed in the sections below):
1. Download and run the SDP installer
2. Run the Miniconda installer included with the SDP installation
3. Run the Git installer included with the SDP installation
4. Generate the SDP Conda environment through the SDP user interface

When upgrading an existing SDP installation, only steps 1 and 4 are required.

Download and Run the SDP Installer

The latest SDP installer can be found on the Plexon website.
https://plexon.com/software-downloads/

A version of the software will also be available on the software thumb drive included with your OmniPlex system.

To run the SDP installer, double-click on SDPv1Setup.exe. Follow the prompts to accept the EULA and complete the installation. An icon will be placed on the desktop.

The SDP software will be installed to C:\Program Files (x86)\Plexon Inc\SDP

Run the Miniconda Installer

Use the Windows Explorer to navigate to C:\Program Files (x86)\Plexon Inc\SDP\Common Files
.
Double-click on Miniconda3-latest-Windows-x86_64.exe. Follow the prompts to complete the installation. It is highly recommended that you do not deviate from the default options presented during the installation process. Simply click on “Next” until the installation is complete.

Run the Git Installer

Use the Windows Explorer to navigate to C:\Program Files (x86)\Plexon Inc\SDP\Common Files.

Double-click on Git-2.50.1-64-bit.exe. Follow the prompts to complete the installation. It is highly recommended that you do not deviate from the default options presented during the installation process. Simply click on “Next” until the installation is complete.

Generate the SDP Conda Environment

Run the SDP software by clicking on the SDP icon on the desktop. In the Tools menu, click on “Create Conda Environment”. Click “OK” to create the environment. This requires a connection to the internet, and downloads several gigabytes of data.

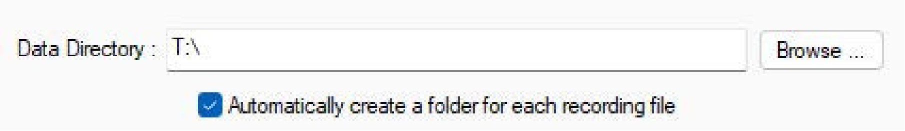
Recording a SiNAPS PL2 in OmniPlex

The SDP only processes SiNAPS PL2 files recorded by OmniPlex. The sorting process generates several folders and files. To avoid confusion the recorded PL2 file will be in its own folder (with the same name as the PL2 file) on the T:. After the SDP is finished processing, the entire folder on T: containing the PL2 file, and folders and files created during sorting, will be moved to D:.

OmniPlex should already be set up to record a PL2 file to its own folder, however, some SiNAPS systems configured for use with other Plexon front-end hardware (such as the DHP for Intan) may not have this option set.

To set up for SiNAPS only (not for other front-end hardware such as DHP or DigiAmp), open PlexControl and in the “Configure” menu select “Global Options”. Select the “Recording Files” tab.

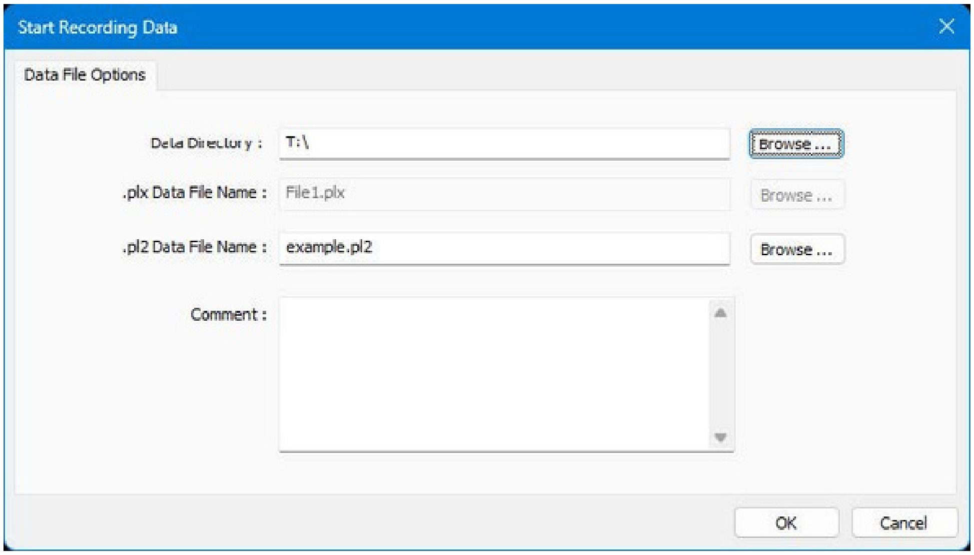
The OmniPlex “Data Directory” should be set to “T:\”, and the “Automatically create a folder for each recording file” option should be enabled, as shown below:



Data Directory : T:\

☑ Automatically create a folder for each recording file

When you click “Start Recording”, PlexControl will present a dialog that allows you do set the .pl2 Data File Name:



Start Recording Data

Data File Options

Data Directory : T:\

.plx Data File Name : File1.plx

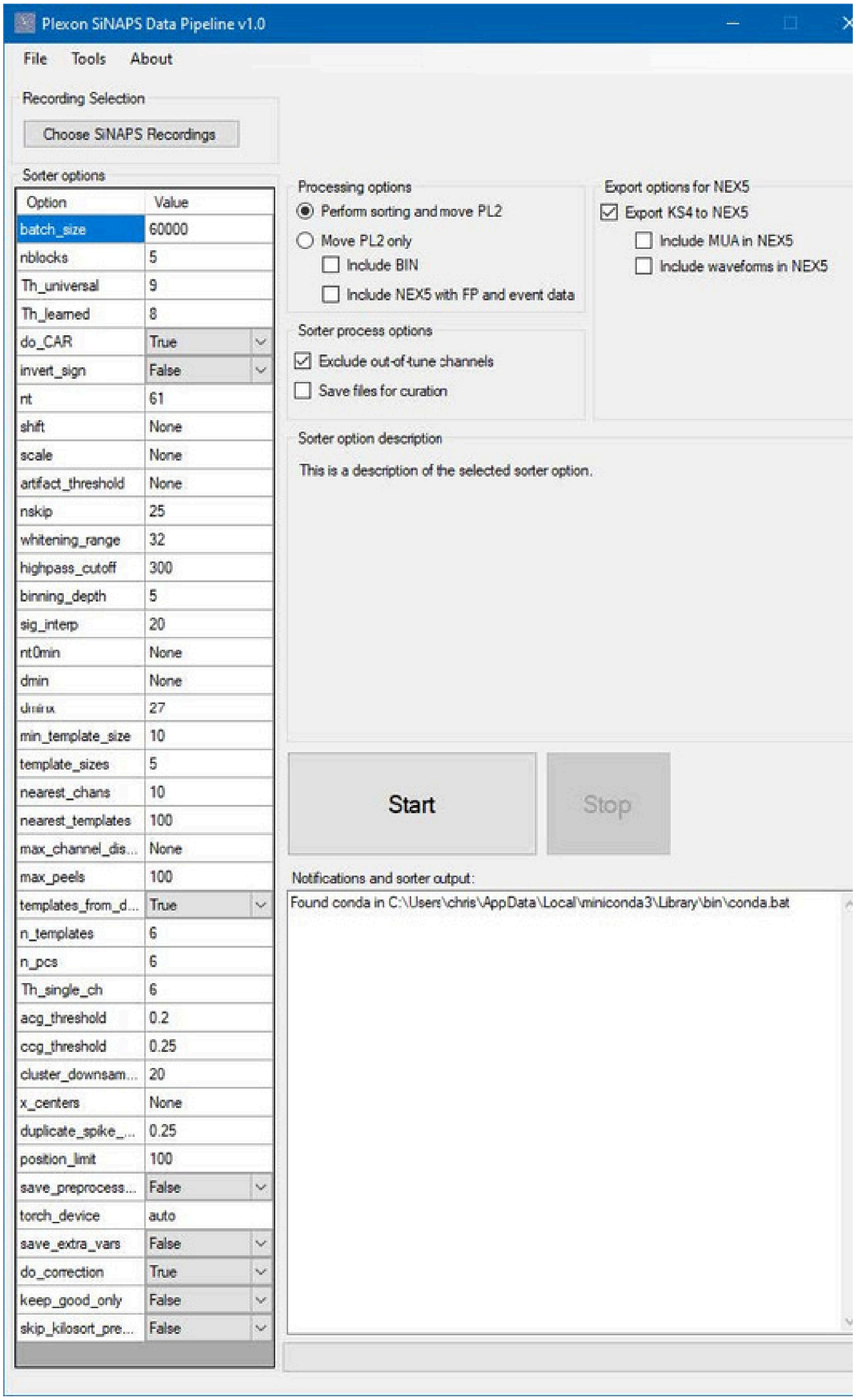
.pl2 Data File Name : example.pl2

Comment :

The file “example.pl2” will be recorded to “T:\example\example.pl2”.

SDP User Interface

The SDP user interface is a program that controls several separate underlying programs to achieve a simplified operational environment.



Option	Value
batch_size	60000
nblocks	5
Th_universal	9
Th_learned	8
do_CAR	True
invert_sign	False
nt	61
shift	None
scale	None
artifact_threshold	None
nskip	25
whitening_range	32
highpass_cutoff	300
binning_depth	5
sig_interp	20
nt0min	None
dmin	None
dmax	27
min_template_size	10
template_sizes	5
nearest_chans	10
nearest_templates	100
max_channel_dis...	None
max_peels	100
templates_from_d...	True
n_templates	6
n_pcs	6
Th_single_ch	6
acg_threshold	0.2
ccg_threshold	0.25
cluster_downsam...	20
x_centers	None
duplicate_spike_...	0.25
position_limit	100
save_preprocess...	False
torch_device	auto
save_extra_vars	False
do_correction	True
keep_good_only	False
skip_kilosort_pre...	False

Processing options

● Perform sorting and move PL2

○ Move PL2 only

□ Include BIN

□ Include NEX5 with FP and event data

Export options for NEX5

☑ Export KS4 to NEX5

□ Include MUA in NEX5

□ Include waveforms in NEX5

Sorter process options

☑ Exclude out-of-tune channels

□ Save files for curation

Sorter option description

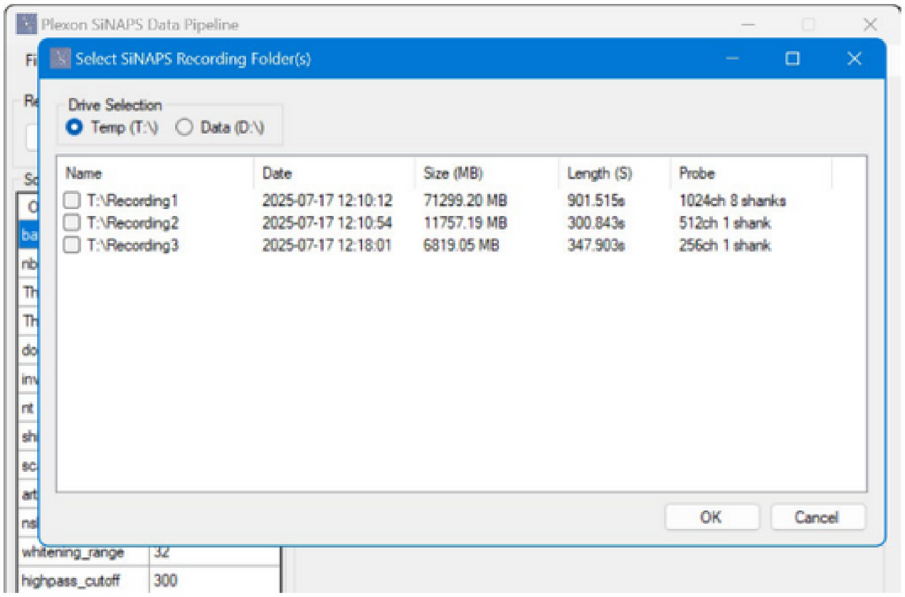
This is a description of the selected sorter option.

Notifications and sorter output:

```
Found conda in C:\Users\chris\AppData\Local\miniconda3\Library\bin\conda.bat
```

SDP User Interface Operation

Selecting SiNAPS Recording Folders


Plexon SiNAPS Data Pipeline
Select SiNAPS Recording Folder(s)
OK
Cancel

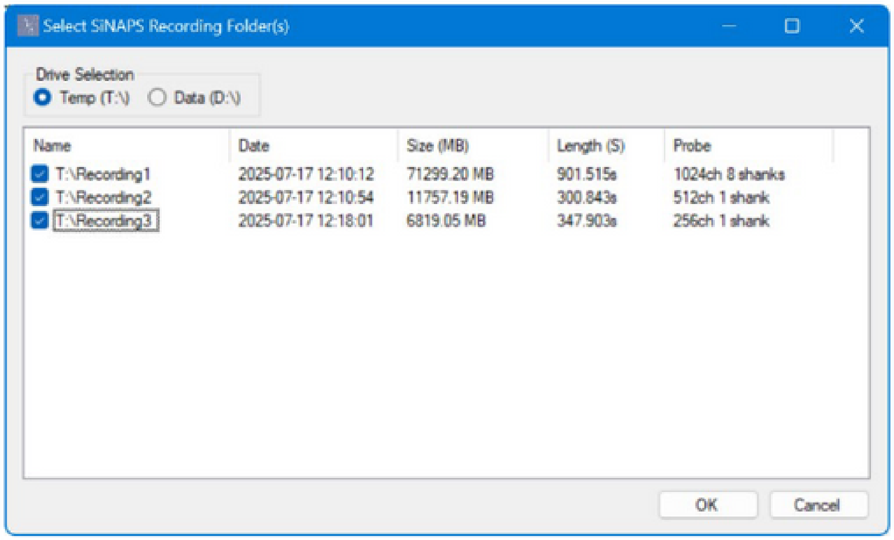
Drive Selection
● Temp (T:\) ○ Data (D:\)

Name	Date	Size (MB)	Length (S)	Probe
□ T:\Recording1	2025-07-17 12:10:12	71299.20 MB	901.515s	1024ch 8 shanks
□ T:\Recording2	2025-07-17 12:10:54	11757.19 MB	300.843s	512ch 1 shank
□ T:\Recording3	2025-07-17 12:18:01	6819.05 MB	347.903s	256ch 1 shank

whitening_range	32
highpass_cutoff	300

When the SDP software is opened, a dialog box is shown that displays the SiNAPS recordings available on the T: for sorting. If there are no recordings on the T: the recordings on the D: are displayed, instead (for possible re-sorting).

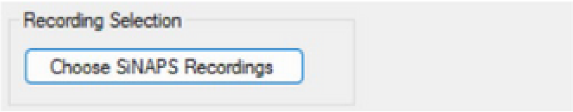
One or more SiNAPS recordings can be selected for processing.



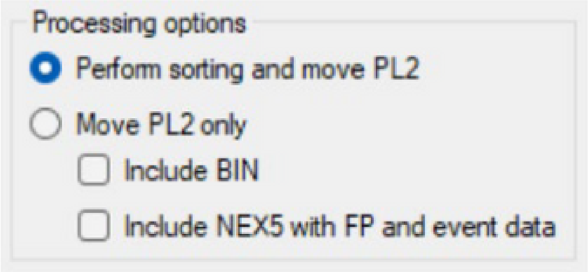
Drive Selection
● Temp (T:\) ○ Data (D:\)

Name	Date	Size (MB)	Length (S)	Probe
☑ T:\Recording1	2025-07-17 12:10:12	71299.20 MB	901.515s	1024ch 8 shanks
☑ T:\Recording2	2025-07-17 12:10:54	11757.19 MB	300.843s	512ch 1 shank
☑ T:\Recording3	2025-07-17 12:18:01	6819.05 MB	347.903s	256ch 1 shank

Select one or more recordings and click OK. The Select SiNAPS Recording Folder(s) dialog box can be re-opened to change the selected recordings by clicking on “Choose SiNAPS Recordings” in the main user interface.



Processing Options



Processing options

● Perform sorting and move PL2

○ Move PL2 only

□ Include BIN

□ Include NEX5 with FP and event data

The processing options represent two processing paths:

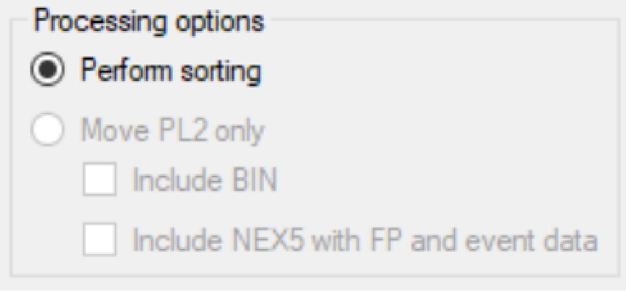
Perform sorting and move PL2 – This is the *default* processing path that will sort the selected PL2 file with Kilosort 4 and then move the PL2 and sorting results to the D: output folder location.

Move PL2 only – This option does not do any sorting. As a convenience it moves the PL2 file to the D: output folder location for other user-selected processing operations. Other options in the user interface (except for the following two below) are ignored.

Include BIN – If selected, a BIN file will be generated and included in the D: output folder location. This file will be nearly as large as the original PL2. This is a convenience to support other sorting operations that take BIN files as input.

Include NEX5 with FP and event data – If selected, a NEX5 file with the non-wideband data (excluding spike data) from the original PL2 (events, FP, AuxAI) will be generated in the D: output folder location. This is to provide this data in an easy-to-use API where other user sorting is performed.

The Processing Options section of the user interface will have some options disabled if the recording(s) selected are on the D:.



Processing options

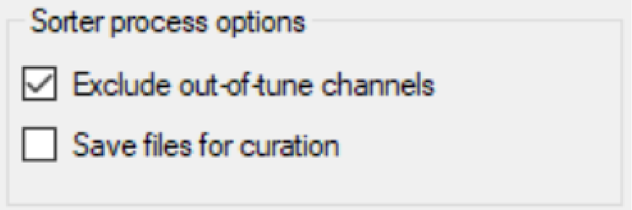
● Perform sorting

○ Move PL2 only

□ Include BIN

□ Include NEX5 with FP and event data

Selecting SiNAPS Recording Folders



Sorter process options

☑ Exclude out-of-tune channels

□ Save files for curation

Exclude out-of-tune channels – Before, and even during recording, SiNAPS probe pixels may become “out-of-tune”, which means they have fallen out of calibration. These channels are likely to be noisy or have unstable data. This option excludes these out-of-tune channels from the sorting process.

Save files for curation – When selected, a copy of the filtered and whitened wideband data will be stored with the sorter output. This file will be called “temp_wh.dat”. It is used with curation programs, or with the SDP NEX5 export tool, if spike waveforms are required. This file will be nearly the same size as the original PL2.

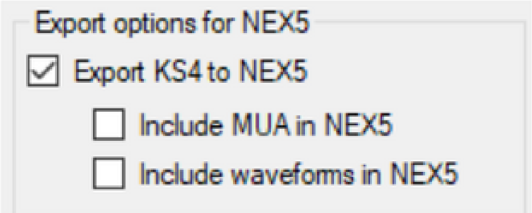
Export Options

After sorting, SDP provides three offline processing options:

1) Create a .nex5 file using the NumPy files from sorting, combined with field potential, analog, and digital event data from the original Pl2 file.

2) For user-selected analysis methods, the spike data in the NumPy files may be curated using Bombcell, Phy, or other curations methods, or the NumPy files used directly.

3) The Phylib library or npy-matlab packages can be used to import the NumPy file data directly into Python or Matlab.



Export options for NEX5

☑ Export KS4 to NEX5

□ Include MUA in NEX5

□ Include waveforms in NEX5

Export KS4 to NEX5 – When enabled, a NeuroExplorer 5 file (.nex5) with the Kilosort 4 results and non-wideband data (events, FP, AuxAI) from the PL2 will be generated.

Include MUA in NEX5 – Clusters that KS4 labeled as “good” will always be included. Enable this option to also include clusters labeled as “MUA”.

Include waveforms in NEX5 – Includes the spike waveforms in the NeuroExplorer 5 file.

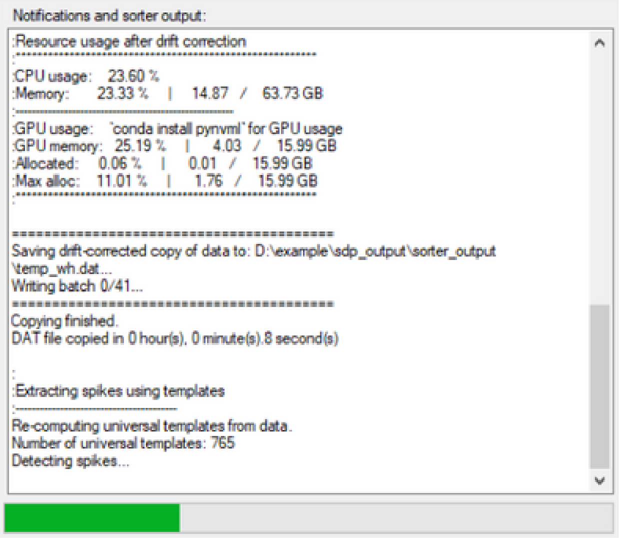
Sorter Options

This spreadsheet view contains nearly all the options that Kilosort 4 uses for sorting. These options have been set with values that are known to work well with SiNAPS data. Do not change these options unless you are very familiar with the internal operation of Kilosort 4. Click on an option name in the list to get a brief description.

Start and Stop

Processing is started with the “Start” button. To stop prematurely stop processing, click “Stop”.

Notifications and Sorter Output



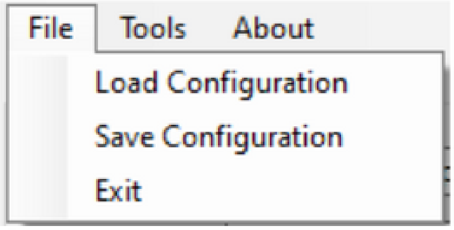
Notifications and sorter output:

```
:Resource usage after drift correction
:**************************************************
:
:CPU usage:    23.60 %
:Memory:      23.33 %    |    14.87  /    63.73 GB
:------------------------------------------------
:GPU usage:    `conda install pynvml` for GPU usage
:GPU memory:   25.19 %    |     4.03  /    15.99 GB
:Allocated:    0.06 %    |     0.01  /    15.99 GB
:Max alloc:   11.01 %    |     1.76  /    15.99 GB
:**************************************************
:

========================================
Saving drift-corrected copy of data to: D:\example\sdp_output\sorter_output
\temp_wh.dat...
Writing batch 0/41...
========================================
Copying finished.
DAT file copied in 0 hour(s), 0 minute(s).8 second(s)

:
:Extracting spikes using templates
:------------------------------------
Re-computing universal templates from data.
Number of universal templates: 765
Detecting spikes...
```

This view shows output from the SDP processing scripts, as well as the console output generated by Kilosort 4. A log file will be generated in the output folder that contains this text.

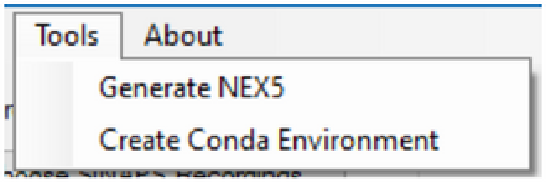
The progress bar indicates the progress of each Kilosort 4 processing phase.

File Menu



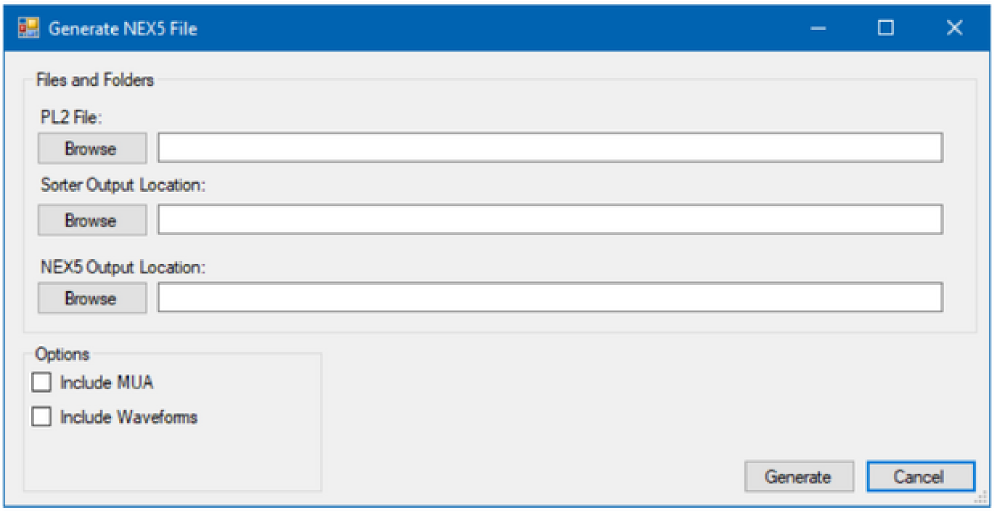
The File menu has selections for loading or saving SDP configuration files and exiting the SDP software.

Tools Menu



Generate NEX5

If a NEX5 file that contains the sorted spike timestamps, as well as the non-wideband data (events, FP, and AuxIO) from the PL2, isn't created at the time of processing, one can be created at a later time using this tool.



There are three paths that need to be set:

PL2 File – Location of the original SiNAPS PL2 file on D: used to generate sorting through the SDP

Sorter Output Location – Location of the set of NumPy (.npy) and other files generated by the SDP

NEX5 Output Location – Location where the NEX5 file will be created

When the PL2 file location is selected, the sorter output location and final NEX5 output location will automatically be populated.

The “Include MUA” and “Include Waveforms” options are the same as documented in “Curation and Export Options”.

Create Conda Environment

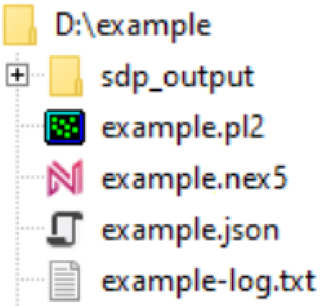
This will delete the existing Conda environment that the SDP depends on, and creates a new one. This should be done after a new install or upgrading.

SDP Output Files

Once processing is complete, files generated by the SDP and Kilosort will be available in the output folder location. This section of the user guide describes which files are generated, and how to access the data within them.

This section of the document uses a PL2 file called “example.pl2” originally recorded to “T:\example\” to demonstrate the output files generated into the output folder “D:\example\” by the SDP software.

Output Folder



```
D:\example
  sdp_output
  example.pl2
  example.nex5
  example.json
  example-log.txt
```

example.pl2 – The original PL2 file.

example.nex5 – If “Export KS4 to NEX5” is selected in the “Curation and export options” section of the SDP interface, a NeuroExplorer file with the sorting results and non-wideband in the original PL2 is created.

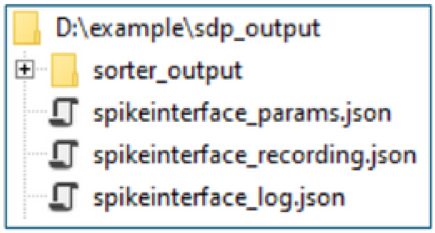
example.json – A JSON with the PL2 file properties normally only accessible by the PL2 API, such as the time of recording, number of channels, digitization rate, number of samples, etc.

example-log.txt – This log file contains the messages displayed in the “Notifications and sorter output” window in the SDP interface.

sdp_output – This folder is detailed in the next section.

sdp_output Folder

The sdp_output folder stores JSON files created by SpikeInterface (the library used by the SDP to invoke Kilosort 4), and the folder containing the Kilosort 4 output.



```
D:\example\sdp_output
  sorter_output
  spikeinterface_params.json
  spikeinterface_recording.json
  spikeinterface_log.json
```

spikeinterface_params.json – Kilosort 4 options used for sorting.

spikeinterface_recording.json – Information about the recording, such as channel numbers, digitization rate, and the probe map.

spikeinterface_log.json – A brief log containing the Kilosort 4 version, date of processing, and run time.
sorter_output – This folder is detailed in the next section.

sorter_output – This folder is detailed in the next section.

sorter_output Folder

The sorter_output folder contains files generated by Kilosort 4. The Kilosort 4 results are stored in a set of NumPy (.npy), tab-separated (.tsv), and Python (.py) files.

Only a small subset of these files is necessary to further analyze sorting results.

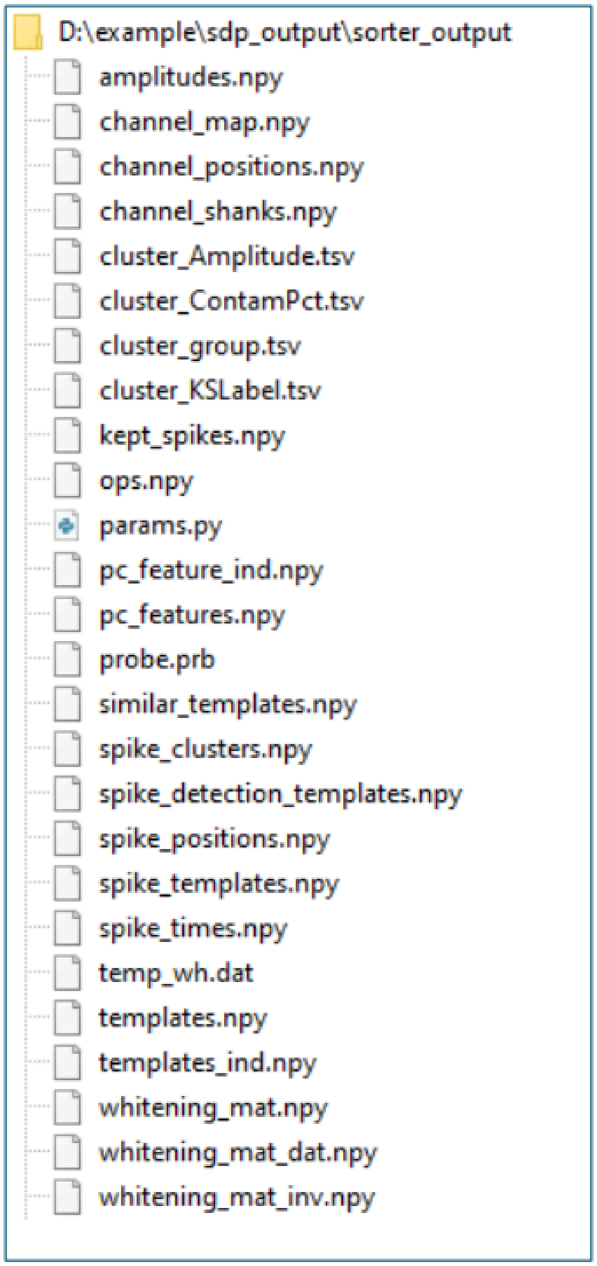
spike_times.npy – contains the time (in units of samples) at the peak of every spike across all clusters. Multiply these values by .000025 (25 microseconds) to convert to seconds.

spike_clusters.npy – contains the cluster assignment of every spike.

temp_wh.dat – This is a copy of the wideband data that has been filtered and whitened by processing in Kilosort 4. This is kept if “Keep copy of filtered data for curation” is enabled in “Sorter process options”. Since this file is nearly as large as the original PL2 file, it is recommended that you delete it if no further curation is required.

These and other files are generated by Kilosort 4 to be compatible with curation procedures. This link to the Phy documentation provides more information.

https://phy.readthedocs.io/en/latest/sorting_user_guide/



D:\example\sdp_output\sorter_output
- amplitudes.npy
- channel_map.npy
- channel_positions.npy
- channel_shanks.npy
- cluster_Amplitude.tsv
- cluster_ContamPct.tsv
- cluster_group.tsv
- cluster_KSLabel.tsv
- kept_spikes.npy
- ops.npy
- params.py
- pc_feature_ind.npy
- pc_features.npy
- probe.prb
- similar_templates.npy
- spike_clusters.npy
- spike_detection_templates.npy
- spike_positions.npy
- spike_templates.npy
- spike_times.npy
- temp_wh.dat
- templates.npy
- templates_ind.npy
- whitening_mat.npy
- whitening_mat_dat.npy
- whitening_mat_inv.npy

Why NeuroExplorer?

NeuroExplorer (Nex) is a data viewing and analysis package widely used by the non-HD community, typically Intan based recording systems. It is very comprehensive with many features of data conditioning and analysis functions. Nex can also be used for viewing and analyzing the output from KS4. Nex does not process, sort, or curate HD cluster oriented data, but as a convenience to the user, the SDP package can process clusters in the NumPy files after KS4 sorting and select the highest amplitude spike in each cluster, assign that spike to the nearest pixel and create a nex5 file with all the recorded data types. Not curation as such but it makes the KS4 sorted output immediately available for viewing and any of the Nex analysis functions can be applied for overview or preliminary analysis.

Nex includes spike snippets, field potentials, digital events, analog experiment data, and limited continuous wide-band data type. Data is stored in .nex5 (5th gen) files and in memory in a vectorized format instead of a blocks-of-data as recorded format. All data types adhere to a rigid time-stamp protocol. Nex requires that an entire file be loaded into ram, which can put a limit on file size depending on the ram size of the computer and the length of the file. Continuous wide-band takes the most space but is rarely used by Nex for analysis.

Nex is not freeware as it is based on many years of continuing development and doesn't suffer the frailties of academic software. Nex is installed on all OmniPlex systems, and a license is included if purchased with the system. Unlicensed Nex supports two out of the many functions, including a one-dimensional viewer which is useful as an overview tool. Full Nex licenses are available from Plexon.

However, even without full Nex as a tool, the nex5 file structure is very fast and easy to access compared to the OmniPlex PL2 file format. The Nex SDK is freely available and supports C++, C#, Python, and Matlab. After sorting, creation of a nex5 file enables any of the SDKs to extract any data type for immediate use.

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