# Advances in the PANDORA Matlab Toolbox for neural database analysis

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Advances in neural database analysis with Pandora

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# Outline

# Introduction to Pandora

- 2 Analyzing voltage trace data
  - Loading a membrane voltage trace
  - Analyzing a membrane voltage trace

#### 3 Database analysis with Pandora

- Creating a database from arbitrary data
- Creating a database from analysis of traces
- Multivariate analysis with database objects

#### 4 Conclusion

Use it if:

- You are already using Matlab
- 2 Python and other environments are too complex or unsustainable in your lab

Use it if:

- You are already using Matlab
- Python and other environments are too complex or unsustainable in your lab Seriously, why would anyone still use Matlab?
  - If you're just starting in computational neuroscience, probably the best option is using Python (Jupyter notebooks, etc)
  - e However, even though Python and its modules have improved considerably, they still require a bit of maintenance
  - Matlab still has its audience in non-programmer, scientist communities (e.g. experimentalists)
  - Solution Also many researchers can't quit Matlab because of inherited legacy code

# Main features of the Pandora toolbox

Has several independent, major features-not limited one type of data or analysis:

- Extracting electrophysiological properties from intracellular recordings
  - Can find spikes from a membrane voltage trace using multiple methods
  - Frequency filtering of data (lowpass, bandpass, highpass)
  - Finding bursts and analyzing their properties
  - You can add any other custom measurement yourself
  - Made to process large number of files and produce uniform database output

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- 2 Analysis of model or experimental data using a *Dataframe*-like objects
  - Creating a database from tabular data for querying and plotting.
  - Putting results from analysis of voltage traces of multiple models into a database.
  - Advanced operations with a database: statistics, multivariate analysis, etc.

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  - Putting results from analysis of voltage traces of multiple models into a database.
  - Advanced operations with a database: statistics, multivariate analysis, etc.
- Improved plotting functions
  - Matlab's plotting functions are augmented
  - Can stack subplots that share same axes
  - Control spacing between subplots
  - Render plots based on export size to produce publication-quality figures

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- Simple model simulation and parameter fitting
  - Can simulate simple neuronal structures such as single ion channels and passive membrane
  - Useful for fitting responses from voltage and current clamp protocols
  - For instance, you can compensate for series resistance artifacts
  - Used in Gunay et al (2015) *PLOS Comp Bio* Gunay et al (2015) PLOS Comp Bio and packaged separately as param-fitter

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- Ø Model simulation parameter optimization
  - Uses the GODLIKE toolbox that can run **multiple optimization algorithms** (multi-objective evolutionary algorithms, swarm, ...)
  - Can control running simulations by calling an external simulator like Neuron, GENESIS, etc)
  - Experimental feature used in Gunay et al (2019) eNeuro and published on Github

Pandora is originally described in Günay et al. (2009) *Neuroinformatics*; and documentation can be found on Github and Mathworks File Exchange pages.

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## The basic Pandora workflow



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# Loading a membrane voltage trace

Pandora can read the file formats from:

- Simulators:
  - Neuron, Genesis, others can be added
- Oata acquisition programs:
  - All NeuroShare-compatible acquisition devices (Alpha Omega, Cambridge Electronic Design, NeuroExplorer, Plexon, R.C. Electronics Inc., Tucker-Davis Technologies, and Cyberkinetics Inc., etc.)
- Other:
  - Simple text file, CSV, Hierarchical data format (HDF5)

#### Tutorial demo on Github

#### Analyzing a membrane voltage trace By extracting electropysiological characteristics

- Measure spike shape and firing rate properties
- Measure sag, spike adaptation and current response properties
- Can be done repetitively for a large number of models
- Can be entered into a Matlab database



annotated spike characteristics



#### Tutorial demo on Github

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What do we mean by database analysis?

- Labeling columns and rows of numerical matrices.
- Makes scripts more readable
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- Labels propagate into plots and reports, reducing human errors.

It's not new:

- R had similar concept of Dataframe earlier
- Python acquired Dataframes with the pandas package, around the same time as Pandora :)
- Matlab introduced the table command recently, with similar functionality
- Pandora still offers some benefits as an integrated environment

## Creating a database from arbitrary data

Create a  $2 \times 2$  database matrix:



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# Creating a database from arbitrary data

Create a  $2 \times 2$  database matrix:



```
With Matlab code:
>> db_obj =
      tests_db([1 2; 3 4],
      {'col1', 'col2'},
      {'row1', 'row2'}, 'a 2x2 DB')
```

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```

Can also import text files as database (e.g., Excel export).

Using a dataset:

```
>> my_dataset_obj =
    my_dataset_class('data/*.bin', arguments...)
```

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>> my_dataset_obj =
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    param_tests_db(my_dataset_obj)
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Using a dataset:
```

```
>> my_dataset_obj =
    my_dataset_class('data/*.bin', arguments...)
>> my_database_obj =
    param_tests_db(my_dataset_obj)
>> sorted_obj =
    sortrows(my_database_obj, 'AP_amplitude')
```

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```
>> db_obj2 =
    db_obj(1:10, {'neuron_index', 'fire_rate'})
>> db_obj2 =
    db_obj(db_obj(:, 'neuron_index') == 46, :)
```

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    db_obj(anyRows(db_obj(:, 'neuron_index'),
        [46; 56; 12]), :)
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     db_obj(anyRows(db_obj(:, 'neuron_index'),
                    [46: 56: 12]), :)
>> db_obi2 =
     db_obj(db_obj(:, 'neuron_index') ~= 46 &
            (db_obj(:, 'CIP') > 100 |
             db_obj(:, 'rate') <= 50 ), :)
```

```
>> db_obj2 =
     db obj(1:10, {'neuron index', 'fire rate'})
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     db_obj(db_obj(:, 'neuron_index') ~= 46 &
            (db_obj(:, 'CIP') > 100 |
             db_obj(:, 'rate') <= 50 ), :)
>> db_obj2 =
     model_db_obj(anyRows(model_db_obj(:, 'rate'),
                  neuron_db_obj(:, 'rate')), :)
                         Tutorial demo on Github
```

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# Multivariate analysis with non-grid data

Tetrodotoxin block effects on firing rate of globus pallidus neurons with current injection



#### Multivariate analysis (I) Sifting the database to find effects of parameters

#### Sample with 3 Neurons:

PicroTx	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
KynAcid	0.001	0.001	0.001	0.001	0.001	0.001
TTX	0	7 <i>e</i> – 09	0	7 <i>e</i> – 09	0	7 <i>e</i> – 09
Apamin	0	0	0	0	0	0
drug 4AP	0	0	0	0	0	0
NeuronId	107	107	108	108	110	110
D100pA steady rate	25.9982	19.6056	29.9673	22.7628	23.8443	20.9744

Focus on changes with TTX:

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## Multivariate analysis (II) Processing database contents

Change in rate ( $\Delta$ ) between successive TTX levels:

Regrouping to find average values for each TTX level:

	Page 1			Page 2		
TTX	0	0	0	7e - 09	7 <i>e</i> – 09	7 <i>e</i> – 09
D100pA steady rate	25.9982	29.9673	23.8443	19.6056	22.7628	20.9744
RowIndex	1	3	5	2	4	6

#### DEMO

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# Try it out and share your feedback

How to access Pandora:

- Main publication: Günay et al. (2009) Neuroinformatics
- Downloads and documentation on Github and Mathworks File Exchange pages

How to give feedback/ask questions:

- Open issues and "star" project on Github
- Also looking for developers to improve it
- Email: cgunay AT ggc.edu
- Fill our survey please!

Credits goes to:

• Supervisors who supported development, Dieter Jaeger and Astrid Prinz, from Emory Univ.

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- Several other contributors, see full list at our Github page
- Cite our paper above and the RRID if you use Pandora, and send us a message!

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