# Advances in the PANDORA Matlab Toolbox for neural database analysis

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#### Outline

- Introduction to Pandora
- Analyzing voltage trace data
  - Loading a membrane voltage trace
  - Analyzing a membrane voltage trace
- Oatabase analysis with Pandora
  - Creating a database from arbitrary data
  - Creating a database from analysis of traces
  - Multivariate analysis with database objects
- 4 Links



# Why should I use the Pandora toolbox?

#### Use it if:

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

# Why should I use the Pandora toolbox?

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#### 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)
- Output
  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)
- Also many researchers can't quit Matlab because of inherited legacy code



#### Main features of the Pandora toolbox

Pandora has several independent features, which also work well together:

- 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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- Analysis of model or experimental data using a Dataframe-like objects
  - Creating a database from any 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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  - 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**

#### Newer features of the Pandora toolbox

- Simple model simulation and parameter fitting
  - Can simulate simple neuronal structures such as single ion channels, passive membrane, etc
  - Useful for fitting responses from voltage and current clamp protocols
  - For instance, you can compensate for series resistance artifacts
  - Packaged separately as param-fitter, but depends on Pandora objects

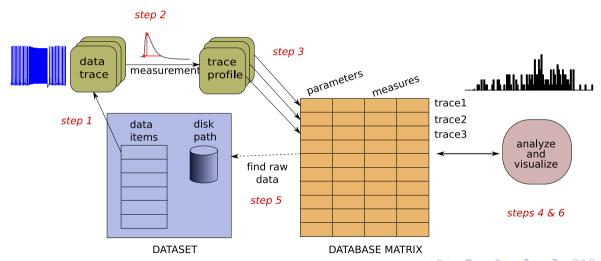
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  - Packaged separately as param-fitter, but depends on Pandora objects
- Model simulation parameter optimization
  - Uses the GODLIKE toolbox that can run multiple optimization algorithms (multi-objective evolutionary algorithms, swarm, ...)
  - Can control running simulations by calling an external simulator like Neuron, GENESIS, etc)
  - Experimental feature, not included in main Pandora package

See Günay et al. (2009) Neuroinformatics; also Github and Mathworks File Exchange pages.



### The basic Pandora workflow



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## Loading a membrane voltage trace

#### Pandora can read the file formats from:

- Simulators:
  - Neuron
  - Genesis
- ② Data 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:
  - Hierarchical data format (HDF5)

#### Tutorial demo on Github

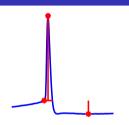


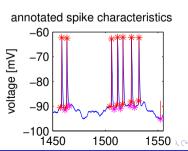
## Analyzing a membrane voltage trace

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

Tutorial demo on Github





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## Creating a database from arbitrary data

Create a  $2 \times 2$  database matrix:

	col1	col2
row1	1	2
row2	3	4

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With Matlab code:

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With Matlab code:

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

# Creating a database from analysis of traces

## Creating a database from analysis of traces

```
Using a dataset:
```

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

# Creating a database from analysis of traces

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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')
```

# Database analysis: Querying

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

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```
>> db_obj2 =
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    db_obj(db_obj(:, 'neuron_index') == 46, :)
```

## Database analysis: Querving

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>> db_obj2 =
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>> db_obj2 =
     db_obj(db_obj(:, 'neuron_index') == 46, :)
>> db_obj2 =
     db_obj(anyRows(db_obj(:, 'neuron_index'),
                    [46; 56; 12]).:)
```

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## Database analysis: Querving

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>> db_obj2 =
     db_obj(1:10, {'neuron_index', 'fire_rate'})
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     db_obj(db_obj(:, 'neuron_index') == 46, :)
>> db_obj2 =
     db_obj(anyRows(db_obj(:, 'neuron_index'),
                    [46: 56: 12]). :)
>> db_obi2 =
     db_obj(db_obj(:, 'neuron_index') ~= 46 &
            (db_obj(:, 'CIP') > 100 |
             db_obi(:, 'rate') <= 50 ), :)
```

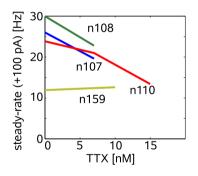
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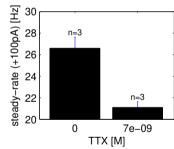
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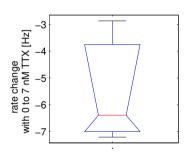
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>> db_obi2 =
     model_db_obj(anyRows(model_db_obj(:, 'rate'),
                  neuron_db_obj(:, 'rate')), :)
```

## 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
Neuronld	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:

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

# 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	7 <i>e</i> – 09	7e - 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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## Testing and 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 on Github
- Email: cgunay AT ggc.edu
- Fill survey (TBA)

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