

# Signal processing and data analysis in Matlab

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EMORY  
UNIVERSITY

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- 1 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

# Why should I use a Matlab toolbox?

Use it if:

- ① You are already using Matlab
- ② Python and other environments are too complex or unsustainable in your lab

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Seriously, why would anyone still use Matlab?

- ① If you're just starting in computational neuroscience, probably the best option is using Python (Jupyter notebooks, etc)
- ② However, even though Python and its modules have improved considerably, they still require a bit of maintenance
- ③ Matlab still has its audience in non-programmer, scientist communities (e.g. experimentalists)
- ④ 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:

- ① 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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- ③ 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

## ① 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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## ① Simple model simulation and parameter fitting

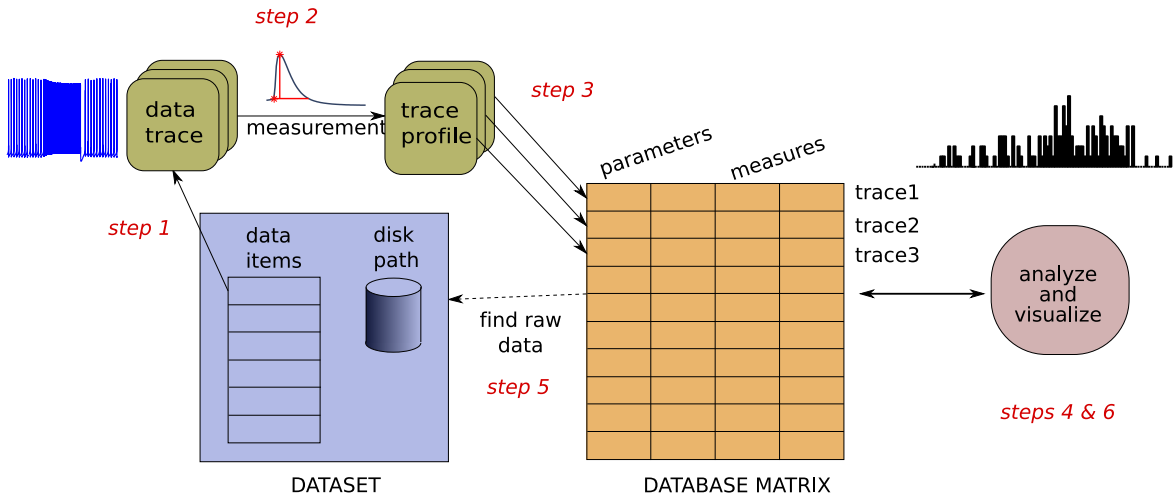
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- Useful for fitting responses from **voltage and current clamp protocols**
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## ② Model simulation parameter optimization

- 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.

# The basic Pandora workflow



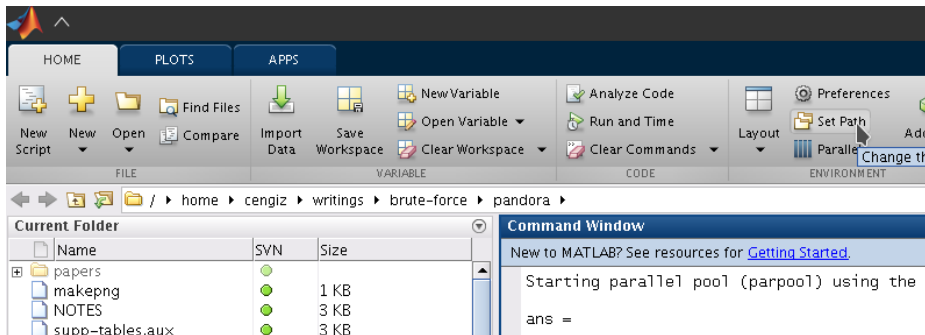
# Installing the Pandora toolbox

Download from:

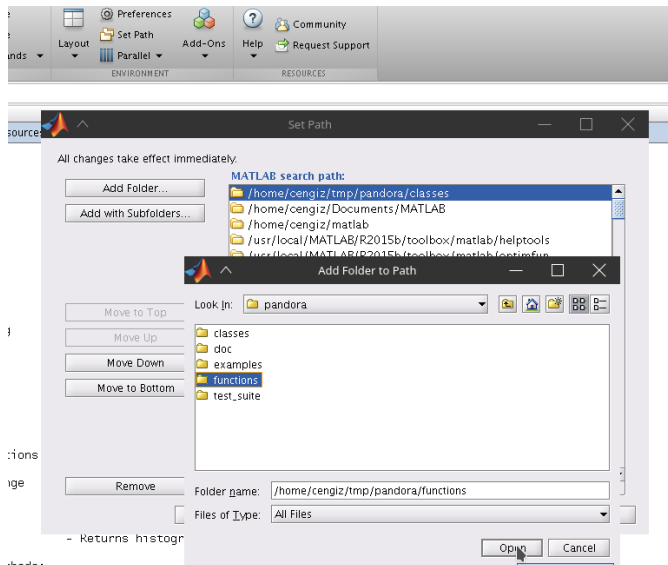
- [Mathworks File Exchange](#) (see below if you don't want to create an account)

Installation: Follow instructions on [Github](#)

- Extract ZIP
- Add **classes** and **functions** folders to the Matlab search path:



# Matlab path should look like this



# Testing the installation

In Matlab type:

```
>> help tests_db
```

Your installation is **successful** if you see:

```
tests_db - Construct a numeric database organized in a matrix format.
```

```
Usage:
```

```
obj = tests_db(test_results, col_names, row_names, id, props)
```

```
[and a lot more here]
```

```
...
```

Otherwise, it is **broken** if you see:

```
>> help tests_db
```

```
tests_db not found.
```

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# Loading a membrane voltage trace

Pandora can read the file formats from:

① Simulators:

- Neuron, Genesis, others can be added

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.)

③ Other:

- Simple text file, CSV, Hierarchical data format (HDF5)
- 

Tutorial demo on Github

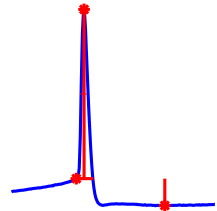
# Analyzing a membrane voltage trace

By extracting electrophysiological characteristics

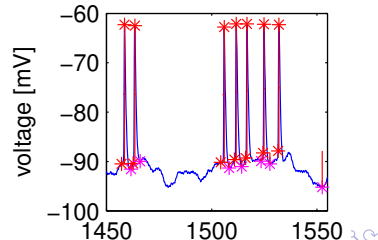
- Measure spike shape and firing rate properties
- Measure sag, spike adaptation and current response properties
- Can be done repetitively for a large number of models
- Can be entered into a Matlab database

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Tutorial demo on Github



annotated spike characteristics





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# Database analysis in Pandora

What do we mean by database analysis?

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

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- Makes scripts more readable
- 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:

	col1	col2
row1	1	2
row2	3	4

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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).

# Creating a database from analysis of traces

Using a dataset:

```
>> my_dataset_obj =  
    my_dataset_class('data/*.bin', arguments...)
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>> 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_obj2 =  
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    db_obj(db_obj(:, 'neuron_index') == 46, :)  
>> db_obj2 =  
    db_obj(anyRows(db_obj(:, 'neuron_index'),  
                    [46; 56; 12])), :)
```

# Database analysis: Querying

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>> db_obj2 =  
    db_obj(anyRows(db_obj(:, 'neuron_index'),  
                   [46; 56; 12])), :)  
>> db_obj2 =  
    db_obj(db_obj(:, 'neuron_index') ~= 46 &  
           (db_obj(:, 'CIP') > 100 |  
            db_obj(:, 'rate') <= 50 ), :)
```

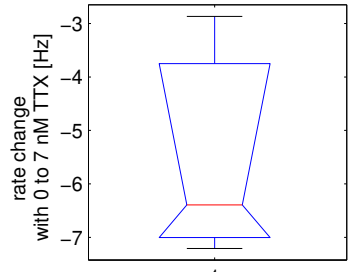
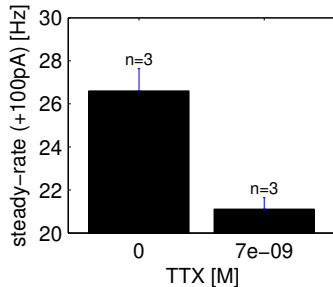
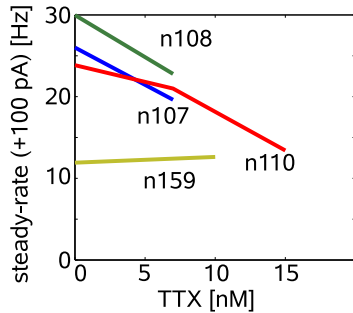
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>> db_obj2 =  
    db_obj(db_obj(:, 'neuron_index') ~= 46 &  
            (db_obj(:, 'CIP') > 100 |  
             db_obj(:, 'rate') <= 50 ), :)  
  
>> db_obj2 =  
    model_db_obj(anyRows(model_db_obj(:, 'rate'),  
                           neuron_db_obj(:, 'rate'))), :)
```

Tutorial demo on Github

# 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	$7e-09$	0	$7e-09$	0	$7e-09$
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:

	Page 1		Page 2		Page 3	
TTX	0	$7e-09$	0	$7e-09$	0	$7e-09$
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:

d1_2	-6.3926	-7.2045	-2.8699
PageIndex	1	2	3

Regrouping to find average values for each TTX level:

	Page 1			Page 2		
TTX	0	0	0	$7e-09$	$7e-09$	$7e-09$
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](mailto:cgunay AT ggc.edu)
- Fill [our survey](#) please!

Credits goes to:

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