xolotl Documentation

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Nov 08, 2018

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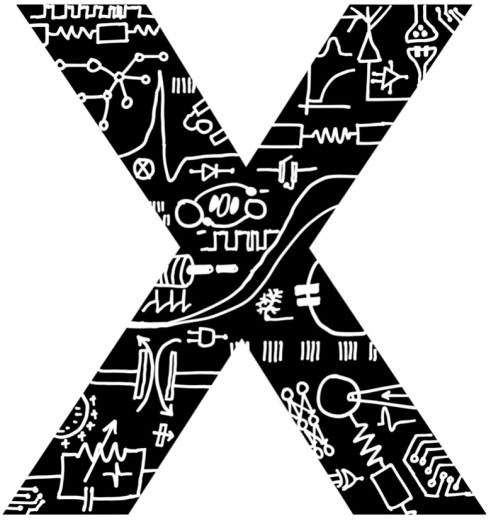

`xolotl` is a fast single-compartment and multi-compartment simulator written in `C++` with a `MATLAB` interface. Designed with a focus on ease-of-use, flexibility and speed, `xolotl` simulates conductance-based neuron models and networks.

CHAPTER 1

Quickstart

This quickstart guide will get you started using `xolotl` right away. It will cover installation and basic usage.

1.1 Installing

The easiest way to get `xolotl` is as a MATLAB toolbox. Click here to download it, and click on the downloaded file to install.

1.2 Creating a Hodgkin-Huxley Model

We will now create a `xolotl` object that describes a single-compartment neuron model with a fast sodium conductance, delayed rectifier potassium conductance, and passive leakage. The compartment has a membrane capacitance `'Cm'` of 10 nF/mm^2 and a surface area of 0.01 mm^2. These conductances come from Liu *et al.* 1998. `'gbar'` is the maximal conductance in uS/mm^2 and `'E'` is the reversal potential in mV.

```
% create the xolotl object
x = xolotl;

% add a compartment
x.add('compartment', 'HH', 'Cm', 10, 'A', 0.01);

% add conductances
x.HH.add('liu/NaV', 'gbar', 1000, 'E', 50);
x.HH.add('liu/Kd', 'gbar', 300, 'E', -80);
x.HH.add('Leak', 'gbar', 1, 'E', -40);
```

1.3 Simulate the Model

We simulate the model using the GUI to manipulate the leak conductance.

```
x.t_end = 1000; % ms
x.manipulate('*Leak*')
```

You should get a GUI that pops up showing the voltage trace, with sliders that allow you to vary parameters for the Leak conductance. Play with the sliders and see what happens!

CHAPTER 2

Frequency Asked Questions (FAQ)

2.1 Who Wrote xolotl?

`xolotl` was designed and written by Srinivas Gorur-Shandilya and Alec Hoyland in Eve Marder's laboratory at Brandeis University.

2.2 How Can I Contribute?

`xolotl` is far from complete and contributions are welcome. Check out our guide on how to report bugs, add conductances and mechanisms, or contribute to the code base.

2.3 Something is Broken, What Do I Do?

As the Hitchiker's Guide to the Galaxy reads, "DON'T PANIC". The most common error we see is an issue between `MATLAB`, the `MEX` compiler, and your computer. In that situation, a first step would be to check our compilers guide which has detailed fixes for some of the most common compiler issues we've seen.

Hint: If `GetMD5` fails, then it's definitely at least a compiler issue.

If it's not a compiler issue and you've checked all the typical programming pitfalls (syntax, spelling, your `MATLAB` path, cleared your workspace, etc...), try the following

```
% erases all the compiled binaries of xolotl networks
x.cleanup
```

If you're still having a problem, we might have fixed it already! Reinstall or update by running the `xolotl.update()` if you installed the toolbox or pulling from the repository if you're using `git`. Remember that if you're using `git` you should be sure to pull all the dependencies as well (`srinivas.gs_mtools`, `cpplab`, `puppeteer`).

2.4 How Do I Cite This?

Thanks for thinking of us! We'll be publishing later this year, and a preprint is available on bioRxiv.

CHAPTER 3

Installing, Updating and Uninstalling

There are multiple ways to install this toolbox, based on your level of expertise and the toolchain on your computer.

3.1 Installing: Download a MATLAB Toolbox

`xolotl` is available as a MATLAB toolbox. Click here to download it, and click on the downloaded file to install.

> **Warning:** If you wish to develop `xolotl` further, you should probably use git (see below).

3.2 Installing: Via Git

If you are comfortable with `git`, you can clone all the code and dependencies yourself:

```
git clone https://github.com/sg-s/srinivas.gs_mtools
git clone https://github.com/sg-s/puppeteer
git clone https://github.com/sg-s/xolotl
git clone https://github.com/sg-s/cpplab
```

You will have to manually set your `MATLAB` paths. Make sure you add the main folder for `puppeteer`, `cpplab`, and `xolotl`, and all subfolders of `srinivas.gs_mtools/src`.

> **Warning:** If you want to develop `xolotl` further, make sure you're running a non-Windows OS, and that you make the *pre-commit* git hook executable: `chmod a+x ./git/hooks/pre-commit`

3.3 Updating

In most cases, `xolotl` can update itself to the latest version using

```
xolotl.update()
```

If you installed using `git`, `xolotl` will attempt to do a `git pull` and update itself. If you installed it as a MATLAB toolbox, `xolotl` will delete the old toolbox, download the new one, and install that.

3.4 Uninstalling

If you installed `xolotl` as a MATLAB toolbox, you can easily uninstall it using

```
xolotl.uninstall()
```

Note that this doesn't do anything if you installed using `git`, or if you manually downloaded the files and linked them.

CHAPTER 4

How do I. . .

4.1 create a empty xolotl object?

```
x = xolotl;
```

This is a prerequisite to doing anything else. (You can name your object whatever you want, but this documentation will assume that you've named it `x`).

4.2 create a new compartment?

You can first create a new compartment using `cpplab`

```
AB = cpplab('compartment','vol',.01);
```

At this point you have created a free-floating object. You can inspect it just like you would any other `MATLAB` object:

```
AB

AB =

 compartment object with:

     hash : 44c3772
       Cm : 10
        A : 0.01
   radius : NaN
      vol : NaN
  Ca_average : NaN
  shell_thickness : NaN
  tree_idx : NaN
        V : -60
```

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```
  neuron_idx : NaN
  Ca_target : NaN
       Ca : NaN
   Ca_out : 3000
      len : NaN
```

and then add it to the `xolotl` object tree:

```
x.add('AB', AB);
```

A handy shortcut for this is:

```
x.add('compartment', 'AB', 'vol', .01)
```

This shortcut syntax will be used for the rest of the documentation, but remember that you can also do things the "long" way.

4.3 add a mechanism to a compartment?

Assuming you have a compartment called `AB` in your `xolotl` object, you can add the mechanism `CalciumMech1` through the `add` function and specify the value of the parameter `f`,

```
x.AB.add('CalciumMech1', 'f', 1.498)
```

4.4 add a conductance to a compartment?

Assuming you have a compartment called `AB` in your `xolotl` object,

```
x.AB.add('liu/NaV');
```

The string `liu/NaV` specifies the path within the `C++` folder that indicates where the header file for the thing that we want to add is.

Once again, you can inspect this object just like you would any other `MATLAB` object:

```
x.AB.NaV

ans =

 NaV object with:

       hash : 49007f5
          E : NaN
          m : NaN
       gbar : NaN
          h : NaN
```

As always, you can set these properties after-the-fact (e.g. `x.gbar = 100`), or when the conductance is added (e.g. `x.add('liu/NaV', 'gbar', 100)`).

4.5 find out what conductances are available?

Look in the folder yourself! All C++ headerfiles are contained in the C++ folder in the xolotl directory. If you are unsure where that is, type this in your MATLAB prompt:

```
fileparts(fileparts(which('xolotl')))
```

4.6 add a custom conductance?

The quickest way is to use the conductance class. The conductance class expects steady-state gating functions for activation and inactivation variables (m_inf and h_inf) and their respective time-constants (tau_m, tau_h). Whether the channel fluxes calcium (is_Ca) and whether it should use approximations for the gating functions rather than integrating (is_approx) can be set. In addition, you can set the default activation and inactivation variable initial conditions (default_m and default_h), and the default reversal potential (default_E). Finally, you should be sure to set the exponential fit parameters (p and q) so that the instantaneous conductance is gbar * m^p * h^q.

```
newCond = conductance;
newCond.m_inf = @m_inf;
newCond.h_inf = @h_inf;
...
newCond.generateCPPFile('name_of_conductance');
```

Alternatively, you can make your own custom conductances by editing a copy of the conductance templates found in ../xolotl/conductances/templates/. If you think it should be added to xolotl as a permanent feature, send us a message.

4.7 inspect the object I have created?

You can inspect any object by outputting it in the command window. For example, to inspect the whole xolotl object

```
>> xolotl object with
----------------------
+ HH
  > NaV (g=NaN, E=NaN)
----------------------
```

You can click on the linked (blue) text to inspect those properties, or reference them directly (e.g. x.AB.NaV).

4.8 connect two compartments using a synapse?

Connect two compartments with an electrical synapse

```
x.connect('AB', 'PD')
```

Connect two compartments with an electrical synapse and specify properties

```
x.connect('AB' 'PD', 'gbar', 100)
```

Connect two compartments with a glutamatergic synapse

```
x.connect('AB', 'LP', 'prinz/Glut')
```

Connect two compartments with a glutmatergic synapse and specify properties

```
x.connect('AB', 'LP', 'prinz/Glut', 'gbar', 100)
```

4.9 find out what synapse types are available?

Look in the folder yourself! All C++ headerfiles are contained in the `c++/synapses` folder in the `xolotl` directory. If you are unsure where that is, type this in your MATLAB prompt:

```
fileparts(fileparts(which('xolotl')))
```

4.10 inject current into a compartment?

Add a scalar, vector, or matrix to `x.I_ext`. This is interpreted as an injected current in nanoamperes.

Inject a constant current into all compartments

```
x.I_ext = 0.2;
```

Inject a constant current into one of two compartments

```
x.I_ext = [0.2 0];
```

Inject a variable current into one of two compartments

```
nSteps = x.t_end / x.dt;
I_ext  = zeros(nSteps, 2);
I_ext(:,1) = 0.2 * rand(nSteps, 1);
x.I_ext = I_ext;
```

4.11 voltage clamp a compartment?

Add a matrix to `x.V_clamp`. This is interpreted as an `nSteps x nComps` matrix of clamped voltage, where `nSteps` is the number of time-steps in the simulation, and `nComps` is the number of compartments.

Clamp the voltage and step it from -50 mV to 50 mV and back

```
nSteps = x.t_end / x.dt;
V_clamp = -50 * ones(nSteps, 1);
V_clamp(ceil(nSteps/2), 1) = 50;
V_clamp(ceil(nSteps*3/4), 1) = -50;
x.V_clamp = V_clamp;
```

4.12 specify simulation time step and other integration parameters?

Specify the time step by setting `x.dt` in milliseconds. Specify the simulation time by setting `x.t_end` in milliseconds. Injected current and voltage clamp are determined by setting `x.I_ext` and `x.V_clamp`.

Set the simulation time to 5000 ms

```
x.t_end = 5000
```

Set the time step to 0.1 ms

```
x.dt = 0.1
```

4.13 integrate the model and obtain outputs?

Integrate the model

```
[V, Ca, cont_states, currents, syn_currents] = x.integrate
```

`V` is the voltage trace as a matrix `nSteps x nComps`. `Ca` is the intracellular calcium concentration trace. `cont_states` is the controller states and controlled parameters as time series. `currents` and `syn_currents` are the time traces of all the currents and synaptic currents, in the order that they are displayed in the serialized `xolotl` object (e.g. how `x` displays them in the command window).

4.14 debug a model or simulation?

`xolotl` has a debug mode that can be turned on using

```
x.verbosity = 1;
```

CHAPTER 5

Methods

This page lists the methods of the `xolotl` class in `MATLAB`. This can serve as a reference for advanced usage.

In the rest of this documentation we will assume a `xolotl` object named `x` that can be created using

```
x = xolotl;
```

Hint: You can list all the methods of `xolotl` object `x` by

```
x.methods;
```

5.1 show

shows activation functions and timescales of any conductance. Usage

```
x.show('cond_name')
```

'cond_name' must be a string that resolves to a valid C++ file that describes a conductance.

5.1.1 Example

```
    % compare some channels from the Prinz et al. paper
xolotl.show('prinz/NaV')
xolotl.show('prinz/Kd')
xolotl.show('prinz/KCa')
```

5.1.2 See Also

- plot
- getGatingFunctions

5.1.3 Test coverage

`show` is tested in:

5.2 compile

compiles a executable binary form a transpiled `C++` file. These are stored in your `xolotl` directory. `xolotl` automatically compiles when t needs to. You can turn this functionality off by setting

```
x.skip_hash = true;
```

In addition, creating a `xolotl` object through a function call does not utomatically hash and compile. In this case, you should use `x.md5hash`.

If you turn hashing off, `xolotl` might not compile

5.2.1 See Also:

- transpile
- cleanup

5.2.2 Test coverage

`compile` is tested in:

5.3 contributingCurrents

This static method calculates the contributions of each current at every point in a voltage race. This is used internally in `xolotl.plot` to color voltage traces. The syntax is

```
curr_index = xolotl.contributingCurrents(V, I)
```

where V is a vector of voltages, I is the corresponding matrix of currents

5.3.1 See Also

- plot
- manipulate

5.3.2 Test coverage

`contributingCurrents` is tested in:

5.4 matrixCost

a static method to compute the distance between two LeMasson matrices. This is a useful way to determine how similar two voltage traces are.

Usage

```
C = matrixCost(M1,M2)
```

where `M1` and `M2` are two matrices returned by xolotl.V2matrix() and represent discretized probability distributions of a derivative-embedded attractor of the voltage trace.

5.4.1 See Also

LeMasson G, Maex R (2001) Introduction to equation solving and parameter fitting. In: De Schutter E (ed) Computational Neuroscience: Realistic Modeling for Experimentalists. CRC Press, London pp 1–21

- V2matrix

5.4.2 Test coverage

`matrixCost` is tested in:

5.5 checkCompartmentName

is used internally by `xolotl` to verify that the compartment name you are using is valid and legal. This method is called every time you add a compartment to a `xolotl` object. Usage

```
ok = checkCompartmentName(self,comp_name)
```

5.5.1 See Also

- add

5.5.2 Test coverage

`checkCompartmentName` is tested in:

5.6 benchmark

performs a quick benchmarking of a given `xolotl` model. `benchmark` first varies the simulation time step, and measures how quickly the model integrates. It then varies `t_end`, and measures how fast it integrates at a fixed `sim_dt`. Usage

```
x.benchmark;
```

5.6.1 Test coverage

`benchmark` is tested in:

5.7 V2matrix

a static method that converts a voltage trace into a LeMasson matrix. Usage

```
[M, V_lim, dV_lim] = V2matrix(V, V_lim, dV_lim)
```

where V is a vector (a voltage time series), and `V_lim` and `dV_lim` are two-element vectors that specify the lower and upper bounds of `V` and `dV`

This static method allows you to create a delay-embedding of a voltage trace, and then discretize the space and count the number of points in each bin. The resultant matrix is sometimes called a LeMasson matrix. `M` is the LeMasson matrix, which is always of size `101x101`.

If you do not specify `V_lim` and `dV_lim`, they will be computed automatically and returned.

5.7.1 See Also

LeMasson G, Maex R (2001) Introduction to equation solving and parameter fitting. In: De Schutter E (ed) Computational Neuroscience: Realistic Modeling for Experimentalists. CRC Press, London pp 1–21

- matrixCost

5.7.2 Test coverage

`V2matrix` is tested in:

5.8 uninstall

A static method that uninstalls your installation of xolotl in place. If you installed using git, `xolotl` will attempt to use git to uninstall itself. Usage

```
xolotl.uninstall
x.uninstall
```

5.8.1 Test coverage

`uninstall` is tested in:

5.9 plotgbars

makes a stem plot of conductance densities in a given compartment. Usage

```
x.plotgbars('compartment_name');
x.plotgbars(axes_handle,'compartment_name');
```

5.9.1 Test coverage

`plotgbars` is tested in:

5.10 update

A static method that updates your installation of xolotl in place. If you installed using git, `xolotl` will attempt to use git to update itself. Usage

```
xolotl.update
x.update
```

5.10.1 Test coverage

`update` is tested in:

5.11 copy

copies a xolotl object. `copy` creates an identical copy of a xolotl object that can be manipulated seperately. Both copies will use the same binary to integrate, unless you add a new component to one of them. Syntax

```
x2 = copy(x);
```

Some read-only properties in a xolotl object may not be copied over.

Warning: Do not make vectors of `xolotl` objects, as it may lead to undefined behavior.

5.11.1 Test coverage

`copy` is tested in:

5.12 reset

Resets a xolotl object to some default state. Usage

```
x.reset()
x.reset('snap_name')
```

reset called without any arguments resets the model as best as it can – voltages are set to -60 mV, Calcium in every compartment is set to the internal value, and the gating variables of every conductance are reset.

`reset` can also be called with a string argument, which is the name of a snapshot previously stored in the model object. Then, `reset` reconfigures the parameters of the model to match that snapshot. This is useful for working with a model, changing parameters, evolving it, and then coming back to where you started off from.

5.12.1 Example

```
% assuming a xolotl object is set up
x.integrate;
x.snapshot('base');
x.set('*gbar') = 1e-3; % turn off all conductances
x.integrate;
% now go back to original state
x.reset('base')
```

5.12.2 See Also

- snapshot

5.12.3 Test coverage

`reset` is tested in:

5.13 snapshot

Saves the current state of a `xolotl` object for future use. Usage

```
x.snapshot('snap_name')
```

Creating two snapshots with the same name will overwrite the first.

5.13.1 Example

```
% assuming a xolotl object is set up
x.integrate;
x.snapshot('base');
x.set('*gbar') = 1e-3; % turn off all conductances
x.integrate;
% now go back to original state
x.reset('base')
```

5.13.2 See Also

- reset

5.13.3 Test coverage

`snapshot` is tested in:

5.14 setup

A static method that allows you to set up compilers on some operating systems. You need to run this only once. If xolotl works, there is no need to run this.

Usage

```
xolotl.setup
x.setup
```

5.14.1 Test coverage

`setup` is tested in:

5.15 plot

Makes a plot of voltage and calcium time series of all compartments. The default option is to color the voltage traces by the dominant current at that point using `contributingCurrents` and to also show the Calcium concentration on the same plot. Usage

```
x.plot()
```

If you want to turn off the colouring, or to hide the Calcium concentration, change your preference using

```
setpref('xolotl','plot_color',false)
setpref('xolotl','show_Ca',false)
```

5.15.1 See Also

- manipulate
- contributingCurrents

5.15.2 Test coverage

`plot` is tested in:

5.16 getGatingFunctions

static method of `xolotl` that returns function handles that represent the gating and activation functions of a particular conductance. Example use

```
[m_inf, h_inf, tau_m, tau_h] =  getGatingFunctions(conductance)
```

where `conductance` is a string that specifies a conductance C++ header file. The outputs are function handles that can be evaluated independently. This method is used internally in `xolotl.show()`

5.16.1 See Also

- show

5.16.2 Test coverage

`getGatingFunctions` is tested in:

5.17 cleanup

A static method that cleans up all transpiled `C++` and compiled binary files. Usage

```
xolotl.cleanup
x.cleanup
```

Use of this method will trigger a warning every time it is called. You do not need to use this in normal use, but can call this to force a recompile, or to delete old and unused binaries.

5.17.1 Test coverage

`cleanup` is tested in:

5.18 integrate

integrates a `xolotl` model. Usage

```
V = x.integrate;
I_clamp = x.integrate;
[V, Ca] = x.integrate;
[V, Ca, mech_state] = x.integrate;
[V, Ca, mech_state, I] = x.integrate;
[V, Ca, mech_state, I, syn_state] = x.integrate;
```

`integrate` will return different outputs as shown above. Unless you need every output, it is recommended to skip it, as it makes the integration faster (and reduces the memory footprint).

5.18.1 Explanation of outputs

- `V` Voltage trace of every compartment. A matrix of size (nsteps, n_comps)
- `I_clamp` also returned in the first argument, this is the clamping current when a compartment is being voltage clamped. This can be inter-leaved with the voltage of other, non-clamped compartments.

- `Ca` Calcium concentration in every cell and the corresponding `E_Ca` (reversal potential of Calcium). A matrix of size (nsteps, n_comps)
- `mech_state` a matrix representing every dimension of every mechanism in the tree. This matrix has size (nsteps, NC), where NC depends on the precise controllers used, and is automatically determined.
- `I` the currents of every ion channel type in the model. This is a matrix of size (nsteps, n_cond)

5.18.2 Test coverage

`integrate` is tested in:

5.19 transpile

Generate a C++ file that constructs the model, integrates it, and moves parameters and data from MATLAB to C++ and back. Usage

```
x.transpile;
```

Warning: `transpile` assumes that your `xolotl` object has a valid hash. Empty hashes will throw an error.

5.19.1 Example

```
% assuming a xolotl object is set up
x.transpile;

% now view the transpiled code
x.viewCode;
```

Warning: You should generally never use `transpile` since `xolotl` will automatically transpile and compile code for you. Manually transpiling will hinder performance.

5.19.2 See Also

- compile
- viewCode

5.19.3 Test coverage

`transpile` is tested in:

5.20 viewCode

view the C++ code generated by xolotl.transpile that constructs the model and integrates it

```
x.viewCode;
```

5.20.1 See Also:

- transpile

5.20.2 Test coverage

`viewCode` is tested in:

5.21 add

adds a `cpplab` object to a `xolotl` object.

The add method is the most important way you construct models. Usage

```
x.add(compartment,'comp_name')
x.add('compartment','comp_name')
x.add('compartment','comp_name',...)
```

There are two primary ways of using `add`. The first is to first construct a `cpplab` object (here called AB), and then add it to the `xolotl` object using `x.add(AB,'AB')`. `xolotl` requires that every compartment is named, and the name has to be specified as a string argument.

5.21.1 Test coverage

`add` is tested in:

5.22 findNSpikes

static method of `xolotl` that computes the number of spikes in a voltage trace. Example use

```
N = xolotl.findNSpikes(V);
N = xolotl.findNSpikes(V, on_off_thresh)
```

`V` is a vector of voltages, and `on_off_thresh` is an optional argument that determines the threshold above which a voltage fluctuation is considered a spikes. The default is 0 mV.

5.22.1 See Also

- findNSpikeTimes

5.22.2 Test coverage

`findNSpikes` is tested in:

5.23 manipulateEvaluate

This method is used to update the `xolotl` object every time a slider is moved in the manipulate window. This is used internally in `xolotl.manipulate`. You should not need to use this by itself.

5.23.1 See Also

- manipulate

5.23.2 Test coverage

`manipulateEvaluate` is tested in:

5.24 connect

Connects two compartments with a synapse. The basic syntax is

```
x.connect('Comp1', 'Comp2', 'SynapseType', ...)
```

The first two arguments are the presynaptic and postsynaptic compartment names. For example

```
% connects two different neurons with an electrical synapse
x.connect('AB', 'LP')
```

Axial synapses are a special type of electrical synapse that are created between spatially-discrete compartments in a morphological structure. Electrical and axial synapses differ in how they are integrated (see Dayan & Abbott 2001, Ch. 5-6).

`connect` defaults to an axial synapse when the type of synapse is not specified and either compartment has a defined `tree_idx` (which identifies the compartment as a part of a multi-compartment neuron model). Otherwise, the created synapse is electrical.

```
% create an (electrical or axial) synapse between AB and LP with gbar f NaN
x.connect('AB', 'LP')
% create an (electrical or axial) synapse between AB and LP with gbar f 10
x.connect('AB', 'LP', 10)
```

The most common way to produce a synapse is to pass the synapse type and hen any properties. This is used to create chemical synapses. For example, o add a glutamatergic synapse (from Prinz *et al.* 2004) between `AB` and `LP` with a maximal conductance of 100:

```
x.connect('AB', 'LP', 'prinz/Glut', 'gbar', 100)
```

Synapses can also be connected by passing a `cpplab` object to the `connect` method

```
% create a synapse using the cpplab object 'syn_cpplab'
x.connect('AB', 'LP', syn_cpplab)
```

The following properties can be specified

Name	PropertyName
Maximal conductance	`gbar`
Reversal potential	`E`
Activation variable	`s`

5.24.1 Test coverage

`connect` is tested in:

5.25 slice

`slice` partitions a cylindrical compartment into N slices. Usage

```
x.slice('comp_name',N)
```

The compartment to be sliced must explicitly be a cylindrical section, i.e., it must have a defined length and radius. `slice` cuts the cylinder along the axis, and connects each slice with `Axial` synapses. This object can then be treated as a multi-compartment model, and `xolotl` will integrate it using the Crank-Nicholson scheme reserved for multi-compartment models.

5.25.1 Example

```
% assuming there is a compartment called 'Dendrite'
xolotl.slice('Dendrite',10)
```

5.25.2 See Also

- connect

5.25.3 Test coverage

`slice` is tested in:

5.26 findNSpikeTimes

static method of `xolotl` that returns a vector of spike times from a voltage trace. Spikes are defined as voltage crossings across a threshold. Example use

```
spiketimes = xolotl.findNSpikeTimes(V,n_spikes,on_off_thresh);
```

`V` is a vector of voltages, and `on_off_thresh` is an optional argument that determines the threshold above which a voltage fluctuation is considered a spikes. The default is 0. `n_spikes` is the number of spikes it should look for, and `spiketimes` will always be a vector `n_spikes` elments long.

5.26.1 See Also

- findNSpikes

5.26.2 Test coverage

`findNSpikeTimes` is tested in:

5.27 manipulate

method that allows you to manipulate some or all parameters in a model hile visualizing its behaviour. Usage

```
x.manipulate();
x.manipulate('some*pattern')
x.manipulate({'parameter1','parameter2'})
```

The simplest way to use `manipulate` is to simply call it with no arguments. By default, all the parameters are linked to sliders that you can play with. In models with a large number of parameters, this can get messy. You can selectively only manipualte some parameters whose names match a pattern using `x.manipulate('some*pattern')`

5.27.1 Test coverage

`manipulate` is tested in:

5.28 rebase

Configures some internal house-keeping settings. This is called every time a new object is created. You probably don't ever have to use this, unless you copy `xolotl` objects across computers with different file systems or operating systems. Usage

```
x.rebase()
```

5.28.1 Test coverage

`rebase` is tested in:

CHAPTER 6

Compiler Support

`xolotl` simulates models by running compiled `C++` code in ``MATLAB``. This process requires a `C++` compiler that is linked to the `MATLAB` executable (`mex`) system.

6.1 Compiling on Microsoft Windows

For Windows systems, it is best to use the `MinGW-w64` compiler, which uses the GNU `gcc` toolchain. You should get this from the Add-Ons menu in `MATLAB` if possible, and the file exchange if not. More details can be found **here_**.

6.2 Compiling on MacOS & Linux

Compilers for which `xolotl` has been known to work (or not). Note that this has nothing to do with `xolotl`, but rather reflects whether `mex` works with these compilers on these OSes.

OS	Compiler	Version	Works
macOS 10.13.6	clang	Apple LLVM version 9.1.0	✓
macOS 10.12.6	clang	Apple LLVM version 9.0.0	✓
Ubuntu 18.04 LTS	g++	8.1	✓
Ubuntu 18.04 LTS	g++	7.3	✓
Ubuntu 17.10	g++	7.3	
Ubuntu 17.04	g++	7.0.1	
Ubuntu 17.10	g++	6.4	
Ubuntu 17.04	g++	6.3	
Ubuntu 17.04	g++	4.8.5	✓
Ubuntu 17.10	g++	4.8	✓
Ubuntu 16.04.3 LTS	g++	6.3	✓
Manjaro Linux	g++	8.1	✓
Manjaro Linux	g++	7.3	✓

6.3 Compiling on Linux

There are a couple of quirks specific to using the MEX compiler on Linux machines. First, make sure that you have a C++ compiler installed. We recommend g++, which is part of the GCC software project.

To get the requisite compiler on Debian/Ubuntu systems, do something similar to

```
sudo apt-get install g++
```

On Arch-based systems such as Manjaro, do something similar to

```
sudo pacman -Syu gcc6
```

Hint: MATLAB can be particular about which version of g++ it works with. For best results, use the compiler version recommended by MATLAB. In addition, it's best to point MATLAB towards the system compiler, rather than one installed through distributions like Anaconda.

On certain Linux distributions (Arch-based in particular), MEX cannot identify the installed g++ compiler, even when it exists on your path. The error looks something like this:

Even though the compiler exists on your path,

```
>> !which g++
/bin/g++
>> !g++ -dumpversion
8.1.0
```

MATLAB cannot find the intended C++ compiler.

```
>> mex -setup C++
Error using mex
No supported compiler was found.
```

MATLAB recommends changing your PATH so that you default to an older version of g++. This is not strictly necessary; MATLAB can still compile using MEX with newer versions of g++ in most cases. Generally, downgrading to an older version of g++ doesn't solve this problem.

There is a relatively simple fix however. Credit goes to github user bonanza123 for figuring it out.

- First download the proper version of gcc/g++. If you use a package manager there are generally legacy versions under gcc-VERSION, where VERSION is the version number (e.g. 6). You can also find them **here_**.
- Second change the mex_LANG_glnxa64.xml specification file, where LANG is either C or C++. This is typically found at ~/.matlab/R2018a/mex_C_glnxa64.xml where R2018a is the version of MATLAB and C is the name of the language.
- Replace all references to $GCC with the path to the soft link to your gcc compiler (e.g. /usr/bin/gcc-6). If you don't have a soft link to your compiler set up (i.e. which gcc doesn't tell you the path to the link), then you have to set one up.
- Repeat this process for the mex_C++_glnxa64.xml file. It should be in the same location as the C-specific file.
- Sometimes MATLAB doesn't generate the C++ .xml file, causing a lot of errors. If it doesn't exist, copy the C version of the file, rename it to mex_C++_glnxa64.xml, and replace all references to gcc with g++, so that MATLAB knows to use the right compiler.

The problem is fixed if you see something like this in MATLAB

```
>> mex.getCompilerConfigurations('C++')
ans =

CompilerConfiguration with properties:

           Name: 'g++'
   Manufacturer: 'GNU'
       Language: 'C++'
        Version: ''
       Location: '/usr/bin/g++-6'
      ShortName: 'g++'
       Priority: 'A'
        Details: [1×1 mex.CompilerConfigurationDetails]
     LinkerName: ''
  LinkerVersion: ''
        MexOpt: '/home/alec/.matlab/R2018a/mex_C++_glnxa64.xml'
```

CHAPTER 7

Units

`xolotl` doesn't come with a automatic unit handling system like in `NEURON`, `BRIAN`, or in `Julia`, so you have to pay attention and make sure your parameters are in the right units. The following are default units for various parameters.

Variable	**Units**
Length of cell	mm
Surface area of cell	mm^2
Volume of cell	mm^3
Voltage	mV
Specific capacitance of membrane	nF/mm^2
Specific conductance of channel	μS/mm^2
Synaptic strength	nS
Current injected into cell	nA
Axial resistivity	MΩ mm
Calcium concentration	μM
temperature	K

CHAPTER 8

Contributing to xolotl

`xolotl` is far from feature complete, and your contributions are welcome.

8.1 Reporting Bugs

- Is it a bug? Are you sure the bug persists after you run `transpile` and `compile` and `xolotl.cleanup`?
- Describe what the expected behavior is, and what the actual behavior was

8.2 Requesting Features

- Describe what you want
- Describe why you want it
- List papers that describe this mechanism, or original research that describes the feature you want

8.3 Adding New Conductances/Synapses/Controllers

- Look at existing conductances/synapses/controllers and use them as a guideline
- If you're making a new conductance, put them in `c++/conductances/<first_author_name>`
- Make sure you add a reference to the paper you're getting the conductance details from in a comment at the top of the file
- Send us a pull request

CHAPTER 9

Troubleshooting

9.1 On macOS, I get an annoying warning saying "xcrun: error: SDK "macosx10.13.4" cannot be located"

Run the following in your shell (not the MATLAB prompt):

```
sudo xcode-select -s /Applications/Xcode.app
```

9.2 On macOS, I get a warning saying that "Warning: Xcode is installed, but its license has not been accepted."

First, make sure you have XCode installed (not just the Command Line Tools – the whole thing). You can get this from the Mac App Store. Then, open XCode and accept the license. You will have to do this only once.

9.3 I ran the quickstart, but I don't see anything

Are you using a tiny screen? Some UI elements may go out of the frame on very small screens. To fix this, acquire the handle to the figure and change the position property. For example

```
x.manipulate;
manip = gcf;
manip.Position = [100 100 34 56];
```

9.4 I get an error saying I don't have a compiler

You need a C/C++ compiler. You need to follow MATLAB's instructions on how to get one, how to install one, and how to configure one. It may be helpful to also see our advice on compilers.

CHAPTER 10

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CHAPTER 11

Indices and tables

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