

NeuroField Reference

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Abstract

NeuroField is a computer program (accompanied with helper scripts) that solves the neural field model of Robinson et al. This document is a reference of **NeuroField** for both users and developers.

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1 Users guide

NeuroField , written by Peter Drysdale with contributions from James Roberts, Felix Fung and Romesh Abeysuriya, is a **C++** program (accompanied with helper scripts) that solves the neural field model of Robinson et al.:

$$\begin{aligned}D_{ab}V_{ab}(\mathbf{r}, t) &= \nu_{ab}\phi_{ab}(\mathbf{r}, t), \\Q_a(\mathbf{r}, t) &= S_a\left[\sum_b V_{ab}(\mathbf{r}, t)\right], \\ \mathcal{D}_{ab}\phi_{ab}(\mathbf{r}, t) &= Q_b(\mathbf{r}, t - \tau_{ab}).\end{aligned}$$

NeuroField generalizes the neural field theory by allowing users to:

1. Specify an arbitrary number of populations and connections between populations;
2. Specify the parameters for any objects, including populations, dendritic responses, firing responses, propagators, synapses, and stimulus pattern;
3. Choose alternative wave propagation types, i.e. choose different forms of \mathcal{D}_{ab} ;
4. Uses plastic synapses, i.e. $\nu_{ab} = \nu_{ab}(\mathbf{r}, t)$.
5. Use different firing responses, i.e. change S_a .

This users guide covers the obtaining and setting up (Sec. 1.1), configuring (Sec. 1.4) and launching of **NeuroField** (Sec. 1.3).

Within this documentation, specific terminology as appeared in the computer is in **typewriter font** . Commands are denoted as

`Command to put in computer`

1.1 Obtaining and setting up **NeuroField**

The code for **NeuroField** is managed by a version control system called **subversion** , which provides a single place to obtain the latest copy of the code, as well as storing the entire history of the program. To access the repository, contact Romesh Abeysuriya (r.abeyasuriya@physics.usyd.edu.au) or Sue Yang (xue.yang@sydney.edu.au).

To set up the latest version of **NeuroField** in the current directory within the School of Physics, execute

```
svn co
  http://silliac.physics.usyd.edu.au:18080/svn/neurofield/trunk
  neurofield --username=<your SVN username>
```

You can also use these steps to obtain a copy of **NeuroField** from a computer which is not connected to the School of Physics network (eg. personal laptops at home). You will require a version of **SVN** higher than 1.6. However, you may need to have your IP address/network domain registered for remote access. If you are unable to access the repository remotely, please contact Sebastian Juraszek to request this (ideally by logging a helpdesk request at <http://physics.usyd.edu.au/itsupport> - only available within the School of Physics).

1.2 Directory layout

The canonical directory is **neurofield/trunk** . Within this directory, the user can find:

<code>*.h, *.cpp</code>	C++ source code.
<code>Configs/</code>	Stores configuration files for <code>NeuroField</code> .
<code>Documentation/</code>	<code>Documentation/doc.tex</code> is the <code>L^AT_EX</code> file for generating this document. Running <code>make doc</code> produces this document in <code>pdf</code> format, and <code>make clean</code> removes all the files <code>L^AT_EX</code> produced (excluding <code>doc.pdf</code> and <code>doc.tex</code>).
<code>Helper_scripts/</code>	Stores helper scripts, including plotting routines and other post-processing of data procedures.
<code>Launch</code>	A launcher script that handles compilation and launching of <code>NeuroField</code> , capable of automating parameter sweeps and submitting jobs in <code>yossarian</code> .
<code>Output/</code>	When using the launcher script to sweep over parameters, the launcher script produces this directory, which stores all output files <code>neurofield.*</code> in independent subdirectories.
<code>Release/</code>	All compiled files, including the object files and the <code>NeuroField</code> executable is stored here. This directory will be deleted by <code>make clean</code> , so user data should not be stored here.
<code>Test/</code>	Directory for unit testing and is irrelevant for users.
<code>neurofield.*</code>	Output files generated by <code>NeuroField</code> .

1.3 Launching NeuroField

The `Launch` script is used to compile and launch the `NeuroField` program. Users are encouraged to use this script rather than calling the `NeuroField` executable directly. To launch `NeuroField`, do:

1. Edit `Makefile`: Identify the platform to run `NeuroField`, and comment/uncomment the appropriate `COMP` directions. Generally, this step is not needed, but users are encouraged to check.
2. To execute with only one set of parameters, edit your configuration file in `./Configs`, then run

```
./Launch Configs/config_file
```

For example,

```
./Launch Configs/cortex.conf
```

The output will be stored in the current directory.¹

3. To ease parameter exploration, the launcher script is capable of doing parameter sweeps. The launcher script supports sweeping over an arbitrary number of objects, parameters and runs. For example, if the user wants to launch `NeuroField` 3 times, with parameters varying according to the following table,

Object(s)	Parameter	1 st run	2 nd run	3 rd run
Propag 1, Propag 2	gamma	10	20	30
Couple 1	nu	1	2	3

simply list the above table entries into the argument list:

```
./Launch Configs/cortex.conf 'Propag 1' 'Propag 2' gamma 10 20
30 'Couple 1' nu 1 2 3
```

In terms of syntactic restriction, each row in the table can have an arbitrary number of objects, but only one parameter; every row must have the same number of runs.²

¹Tips for `vi` users: you can launch `NeuroField` in `vi` with `!:./Launch % [optional params]`

²Tips: the UNIX `seq` program allows shortening parameter value listing from `10 20 30 40 50 60` into `'seq 10 10 60'`, e.g. `Launch Configs/cortex.conf 'Propag 1' gamma 'seq 10 10 60'`.

4. Switches are accepted for choosing options. To turn on the switches, put them in the argument list to the launcher script. The following switches are accepted:
 - `--restart` run `NeuroField` in restart mode.
 - `-i` specify an configuration file name.
 - `-o` specify an output dump file name.
 - `-v` prints to standard output rather than to a file.
 - `-h` prints out a list of these switches.
5. In case the script is executed on `yossarian`, the launcher script tries to find a file called `pbs`. If no such file is found, the user would be prompted for a job name, expected computational time and email to generate `pbs`. This file is then submitted to the PBS system.
6. To clean up the directory, delete or store your `neurofield.*` output files and the `Output/` directory and subdirectories. Then run

```
make clean
```

to delete `./Release/` and the files \LaTeX produced in `Documentation/`.

7. This documentation can be generated by running

```
make doc
```

which produces `./Documentation.pdf`. `make clean` deletes the files (excluding `./Documentation.pdf`) created by \LaTeX .

1.4 Writing a configuration file

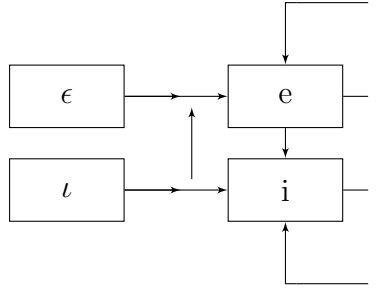
`NeuroField` allows an arbitrary number of populations and connections between them, with all objects taking arbitrary parameter values. These are all configured via a configuration file. This section documents the specifications of configuration files, where we use `Configs/cortex.conf` as an illustrative example.

To write a configuration file, a user can follow these steps:

1. Determine your population model by drawing a schematic diagram, thereby constructing a connection matrix. An example is shown in Fig. 1.
2. Look up existing configuration files in `Configs/`. By checking the comment located at the top of a configuration file, and also the connection matrix, a user should find the most suitable existing file to construct his own. This is less tedious (and less error prone) than writing a new one from scratch.
3. Specify the global parameters and connectivity matrix (Sec. 1.4.1).
4. Specify all populations (Sec. 1.4.2).
5. Specify all propagators (Sec. 1.4.3).
6. Specify all couples (Sec. 1.4.4).
7. Specify all output requests (Sec. 1.4.5).

In general, the entries in configuration file follow the following rules:

1. Each entry generally follows a `Parameter: value` pattern.
2. Most parameters are essential. Failure to provide these parameters would result in `NeuroField` terminating with an error message. A minority of the parameters are optional.
3. The ordering of the parameters are important. Wrong parameter ordering results in `NeuroField` terminating with an error message.



From:	ϵ	l	e	i
To ϵ :	0	0	0	0
To l :	0	0	0	0
To e:	1	0	2	3
To i:	0	4	5	6

Figure 1: Left: schematic diagram of a purely cortical population model comprising excitatory and inhibitory populations, as well as two stimulus populations; each arrow indicates a connection between populations, so that each stimulus connects to a cortical population, and each cortical population connects to all cortical populations. Right: connection matrix indicating the connections between populations; zero indicates no connection, and a connection is indicated by a nonzero number, ordered top to bottom, left to right.

4. With the exception of keywords, the configuration file is white-space independent, e.g., there can be either no spaces, many spaces, or new lines between the colon of **Integration steps:** 10000 and 10000, but you cannot have two spaces between **Integration** and **steps** . For consistency and readability, users are encouraged to follow the existing white space scheme when reasonable.
5. Tip for `vi` users: `./helper_scripts/neurofield.vim` implements syntax highlighting for configuration files in `vi` . See comments within for installation instructions.

1.4.1 Global information

- Purely cortical model with excitatory and inhibitory neurons

Any text before the entry, **Time:** , is disregarded by `NeuroField` and serves as comment.

- **Time:** 10 **Deltat:** 1e-4

Time is the simulation duration in seconds.

Deltat is the time increment for each time step.

- **Nodes:** 4 **Longside:** 2

Nodes is the number of grid points in the spatial dimension per population of neurons. The code has been explicitly designed to have equal number of neurons per population.

Longside is an optional parameter, specifying the longside of the rectangular grid. If it is not supplied, it is assumed to be a square.

Both spatial dimensions have periodic boundary conditions, so that populations have the topology of a torus.

- **Glutamate dynamics - fast** **Lambda:** 3e-4 **fast tGlu:** 5e-3
slow Lambda: 3e-4 **slow tGlu:** 5e-3

Parameters governing glutamate dynamics, which is currently useful only for `CaDP` . This block is optional.

Lambda is the glutamate release concentration per presynaptic spike, in moles.

tGlu is the decay timescale of glutamate in seconds.

```

Purely cortical model with excitatory and inhibitory neurons
Time: 10 Deltat: 1e-4
Nodes: 4

Connection matrix:
From: 1 2 3 4
To 1: 0 0 0 0
To 2: 0 0 0 0
To 3: 1 0 2 3
To 4: 0 4 5 6

Population 1: Stimulation
Stimulus: Const - Onset: 0 Mean: 5

Population 2: Stimulation
Stimulus: Const - Onset: 0 Mean: 5

Population 3: Excitatory neurons
Q: 8.87145
Firing: Sigmoid - Theta: 13e-3 Sigma: 3.8e-3 Qmax: 340
Dendrite 1: V: Steady alpha: 83 beta: 769
Dendrite 2: alpha: 83 beta: 769
Dendrite 3: alpha: 83 beta: 769

Population 4: Inhibitory neurons
Q: 8.87145
Firing: Sigmoid - Theta: 13e-3 Sigma: 3.8e-3 Qmax: 340
Dendrite 4: V: Steady alpha: 83 beta: 769
Dendrite 5: alpha: 83 beta: 769
Dendrite 6: alpha: 83 beta: 769

Propag 1: Map - Tau: 0
Propag 2: Wave - Tau: 0 Deltax: 3.5e-3 Range: 80e-3 gamma: 116
Propag 3: Map - Tau: 0
Propag 4: Map - Tau: 0
Propag 5: Wave - Tau: 0 Deltax: 3.5e-3 Range: 80e-3 gamma: 116
Propag 6: Map - Tau: 0

Couple 1: Map - nu: .15e-3
Couple 2: Map - nu: 1.5e-3
Couple 3: Map - nu:-1.8e-3
Couple 4: Map - nu: .15e-3
Couple 5: Map - nu: 1.5e-3
Couple 6: Map - nu:-1.8e-3

Output: Node: All
Population:
Dendrite:
Propag: 3 4
Couple:

```

Figure 2: An example configuration file, which can be found in `Configs/cortex.conf`.

- Connection matrix:

From: 1 2 3 4

To 1: 0 0 0 0

To 2: 0 0 0 0

To 3: 1 0 2 3

To 4: 0 4 5 6

We specify an arbitrarily sized square connection matrix, where each entry is the connection from the column population to the row population.

Zero indicates no connection.

A nonzero number indicates connection. This number must be indexed from top to bottom, left to right.

1.4.2 Population data

This section contains population information sections. There are two types of neural populations: ordinary populations and stimulus populations:

Stimulus populations

NeuroField identifies stimulus populations as populations which have no dendrites, i.e., the row for that population contains no nonzero elements. Each stimulus population information section is as follows.

- Population 1: Stimulation

The identifier **Population 1** is required for cross-checking.

The descriptor **Stimulation** is not parsed by **NeuroField**, but it is strongly recommended for human referencing.

- Stimulus: Const - Onset: 0

The identifier **Stimulus** is required for cross-checking.

This is followed by the type of stimulus, to be further elaborated below.

Optional parameter **Onset** specifies the time onset for the stimulus to begin. If unspecified, stimulus starts at time 0.

Either **Cease** or **Duration** can be an optional parameter to specify the end time of the stimulus. If unspecified, stimulus ends at 1000 seconds.

Possible stimulus patterns:

Constant

Const - Mean: 5

Pulse

Pulse - Amplitude: 1 Width: 2e-2 Frequency: 1 Pulses: 1

White noise stimulus

White - Ranseed: -98716872 Amplitude: 20 Mean: 1

One issue with white noise is that the power spectrum of white noise depends on both the temporal sampling rate and the grid size. For a thorough discussion of this phenomenon, see **noise.pdf** in the **NeuroField** documentation. Therefore, if you change the sampling rate, the number of nodes, or **Deltax** then the power spectrum will change in amplitude. If you know what amplitude the noise should have in Fourier space e.g. $\phi_n(\omega) = 1 \times 10^{-5}$ then specifying **Deltax** in the stimulus population will tell

NeuroField that the amplitude has been specified in Fourier space, and it will be rescaled accordingly. In this representation, the mean of the distribution corresponds to the zero-frequency component of the noise.

```
White - Amplitude: 0.00001 Mean: 1 Deltax: 0.025
```

To superimpose 2 or more stimuli, begin with the keyword **Superimpose** , followed by the number of stimuli. Then list all the stimulus patterns and their parameters, with each stimulus pattern preceded by the keyword **Stimulus** .

```
Stimulus: Superimpose: 2
Stimulus: White - Amplitude: 1 Mean: 1
Stimulus: Pulse - Onset: 0.5 Width: 2e-2 Frequency 1
Pulses: 1
```

Ordinary populations

Any non-stimulus population is an ordinary population.

- Population 3: Excitatory neurons

The identifier **Population 3** is required for cross-checking.

The descriptor **Excitatory neurons** is not parsed by **NeuroField** , but it is strongly recommended for human referencing.

- Q: 8.87145

The initial firing rate.

- Firing: Sigmoid - Theta: 13e-3 Sigma: 3.8e-3 Qmax: 340

Specify the sigmoidal firing response of the population.

Sigma is sometimes known as $\tilde{\sigma}$. It is already scaled by $\pi/\sqrt{3}$.

Alternatively, you can specify a linear firing response by using

```
Firing: Linear - Gradient: 1 Intercept: 1
```

- Dendrite 1: V: Steady alpha: 83 beta: 769

The identifier **Dendrite 1** , where 1 is the presynaptic connection index, is required for cross-checking. Users should find that these indices are simply ordered as 1, 2, 3, 4, ...

V is the initial depolarization contribution from presynaptic activity. It can be a numerical value with units of V, or set at **Steady** , so that **NeuroField** calculates the initial value by $V_{ab} = \nu_{ab}\phi_{ab}$.

alpha and **beta** are the parameters for the depolarization response.

1.4.3 Propagation data

```
Propag 1:
```

This identifier is required for cross-checking.

A propagator type is required at this point. Choices are **Map** , **Wave** , and **Harmonic** .

Map

```
Map - Tau: 0
```


This propagator is the mapping propagator where spatial spreading is negligible. Its form is given by

$$\phi_{ab}(\mathbf{r}, t) = Q_b(\mathbf{r}, t - \tau_{ab}).$$

Its only one parameter, τ_{ab} , is the delay term. It is specified below.

Wave

This propagator is the wave equation propagator governed by the equation

$$\left[\frac{1}{\gamma_{ab}^2} \frac{d^2}{dt^2} + \frac{2}{\gamma_{ab}} \frac{d}{dt} + 1 \right] \phi_{ab}(\mathbf{r}, t) = Q_b(\mathbf{r}, t - \tau_{ab}).$$

Its input is given by

```
Wave - phi: Steady Deltax: 0.0035 Tau: 0 Range: 0.08 gamma: 116
```

`phi` is the initial value for ϕ_{ab} in the wave equation. Inputting `Steady` gives $\phi_{ab} = Q_b$.

`Deltax` is the length of a node in mm. This must satisfy the Courant condition,

$$\Delta t / \Delta x < \sqrt{2} / r_e \gamma_e.$$

`Range` is r_{ab} in the wave equation.

The final parameter can be `gamma` or `velocity` in the wave equation.

In case there is only one node, this degenerates into a `Harmonic` propagator.

Harmonic This is a harmonic oscillator implementation of the damped wave equation. If there is no spatial variation, use `Harmonic` instead of `WaveEqn`. The input form is given by

```
Harmonic - phi: Steady Tau: 0 gamma: 116
```

Tau

The axonal time delay between populations. If it is spatially homogeneous, then it is a number with units of seconds. If it is spatially inhomogeneous, then input n numbers, where $n = \text{Nodes}$.

1.4.4 Coupling data

-

```
Couple 1:
```

Identifier for cross-checking.

- A couple type is required at this point. Choices are `Map`, `CaDP`, `BCM` and `Matrix`.

Map

Nonplastic synaptic coupling with a single constant parameter `nu`,

```
Map - nu: 0.0012
```

`nu` is the synaptic coupling parameter. It corresponds to the product of the mean synaptic strength s_{ab} and N_{ab} , the mean number of connections from cells of type b to cells of type a .

Matrix

Coupling becomes connection matrix, where connection strength does *not* change with time. The format of the `nu` matrix is the same as the population connection matrix, each row is to the same node, each column is from the same node. When outputting, each specified outputting node output the indexed row.

```
nu :
  13e-6  0
  0  13e-6
```

CaDP

Calcium dependent plasticity according to Fung and Robinson.

```
CaDP - nu: 13e-6 nu_max: 80e-6 Dth: .25e-6 Pth: .45e-6
      xyth: 1e-4 x: 2.3e-2 y: 2e-2 B: 30e3 glu_0: 200e-6
      gNMDA: 2e-3
```

BCM

BCM plasticity according to Fung and Robinson. Based on `CaDP`, it has an additional parameter `t_BCM`.

```
CaDP - nu: 13e-6 nu_max: 80e-6 Dth: .25e-6 Pth: .45e-6
      xyth: 1e-4 x: 2.3e-2 y: 2e-2 B: 30e3 glu_0: 200e-6
      gNMDA: 2e-3 t_BCM: 7
```

1.4.5 Output data

NeuroField outputs field quantities (i.e. a neurodynamic quantity which takes a value for each node) with respect to nodes and time. By default, the output file is `neurofield.output`, which can be changed by launching the program with the `-o` switch.

- Output:

Begin with the `Output` declaration.
- Node: 1 2

Enumerate all nodes to be outputted. If outputting all nodes, use shorthand `All`.
- Start: 0 Interval: 1e-3

Optional parameters for the time to start output, and optional parameter for time interval between outputs.
If undefined, defaults, to 0 and `Deltat`, respectively.
- Population: 2.V
Dendrite:
Propag: 1 2.phi
Couple: 3.nu

Specifying desired objects and fields to output. Enter the appropriate object indices after the labels. For each entry, a field name may be appended after the index with a `.`, so that only that field of the object is outputted. If no field name is specified for that entry, then all fields of that object is outputted.

1.5 Postprocessing

NeuroField produces 3 files:

- | | |
|--------------------------------|--|
| <code>neurofield.conf</code> | When using the launcher script, this file is created to store the running configuration file. |
| <code>neurofield.output</code> | The result of the simulation is stored here for postprocessing. |
| <code>neurofield.pbs</code> | If NeuroField is run in <code>yossarian</code> , then this file stores the output of the queueing system. |

When the launcher script runs with only one set of parameters, all output files are also in the present working directory. However, if the launcher script sweeps over parameters, each parameter set has its own subdirectory inside `Output/`, and each set of `neurofield.*` files are stored in its subdirectory.

Example content in `neurofield.output` is

Time		Propag.2.phi
		0
1.0000000000000000e-04		8.871450000000000e+00

Each column is a time series with its name indicated in the first line. The first column is always time, and in this example, the second column is `Propag.2.phi`, indicating that it is ϕ_{ee} (when checked against connection matrix). The delimiter `|` indicates that the two columns are different fields, rather than different nodes of the same field. The node number is indicated in the second line.

It is also worth noting that traces will be written in the order that they are specified. For example, if you write `Population: 3 1` then the columns in the output file will be arranged in this order.

1.5.1 Quickplot

The data in `neurofield.output` may be plotted by `./Helper_script/quickplot.pl` or in MatLab via the matlab scripts within `./Helper_script/`.

To use `./Helper_script/quickplot.pl`, execute

```
./Helper_script/quickplot.pl [output.file] [field] [node index]
```

where an example is

```
./Helper_script/quickplot.pl neurofield.output Propag.2.phi 1
```

or a shorthand to plot all fields and nodes is

```
./Helper_script/quickplot.pl all
```

All these commands launches `gnuplot` plotting sessions.

1.5.2 Matlab

A number of Matlab functions are provided to make it easy to manipulate `NeuroField` data from within Matlab. The functions are generally self-documenting with comments at the start of the file.

Essentially, an output file from `NeuroField` is read into a `nf` struct object in Matlab which simply contains all of the output from `NeuroField` in memory for easy access. Here is an example of a `nf` object:

```
fields: {'Propag.1.phi' 'Propag.3.phi'}
nodes: {[1] [1]}
data: {[300000x1 double] [300000x1 double]}
time: [300000x1 double]
deltat: 1.0000e-04
npoints: 300000
```

- `fields` stores a record of which traces from `NeuroField` are present in the output file
- `nodes` is a cell with the same size as `fields`, and records for each field present, the number of the node in the output.
- `data` is a matrix storing the actual values of the traces
- `time` is a vector of time values, so that you can plot any of the data traces directly again `nf.time`
- `deltat` stores the temporal sampling rate

- `npoints` stores the total number of points in the output. The total duration is `nf.deltat*nf.npoints` (or `nf.time(end)`)

There are two ways to create the `nf` object. You can read the output file directly after executing `NeuroField` elsewhere

```
nf = nf_read('neurofield.output')
```

or you can use the `nf_run` helper script to run the config file using `NeuroField` and automatically parse the output

```
nf = nf_run('neurofield.conf')
```

Using `nf_run` means you will need to add `NeuroField` to your shell search path.

Several helper files are provided to manipulate the `nf` object. The two most important helpers are `nf_extract` and `nf_grid`. Often you want to extract a particular field from the `nf` object, for example, to examine the output from `Propag.3.phi`. To do this directly with the `nf` object, you would need to check the `fields` variable to find the index of the trace you wanted, and then extract it from the `data` field. In the previous example, `Propag.3.phi` is the second trace. These expressions are identical:

```
trace = nf.data{2};
trace = nf_extract(nf, 'Propag.3.phi')
```

`nf_extract` quickly becomes useful when there are many different fields. It is not case sensitive (so `propag.3.phi` works as well). You can also specify using additional arguments to extract only a portion of the time series, and also to select a subset of nodes. Finally, you can also provide multiple traces to concatenate them into a single matrix. For example,

```
trace = nf_extract(nf, 'propag.1.phi', 'propag.3.phi');
```

will create a 300000x2 matrix with both of the traces.

Finally, if you run `NeuroField` with multiple nodes, it typically solves the system of equations on a square grid. Therefore, if you have output for nodes 1-400, this corresponds to a 20x20 grid. `nf_grid` allows you to request a trace from the `nf` object and have it reshaped into a square grid. This lets you easily make surface plots of the data, or perform tasks that are spatially dependent.

One important task is computing the power spectrum as predicted by the linearized analytic equations. This can be achieved using `nf_spatial_spectrum` which takes in an `nf` object and computes the power spectrum integrated over k taking into account volume conduction.

2 Developers guide

NeuroField is coded in **ANSI C++** . This guide assumes readers have basic knowledge of **C++** , including object oriented programming, usage of template, and standard template library (STL).

NeuroField solves each equation within the Robinson et al. model with an object:

$$\begin{array}{ll}
 P = \nu_{ab}\phi_{ab}, & \text{Couple} \\
 D_{ab}V_{ab} = P, & \text{Dendrite} \\
 Q_a = S_a \left[\sum_b V_{ab} \right], & \text{QResponse} \\
 \mathcal{D}_{ab}\phi_{ab} = Q_b. & \text{Propag}
 \end{array}$$

Each object class may be overloaded for more sophisticated behaviour; for example, **Couple** may be overloaded for synaptic plasticity (see Sec. 2.7.2).

2.1 Coding style

Within the C++ source files, developers should stick to this conventions for consistency:

Tabs: two spaces.
 Braces: the K&R style is strongly encouraged.
 Class names: UpperCamelCase
 Function names: lowerCamelCase
 Variable names: lowercase

2.2 Class diagram

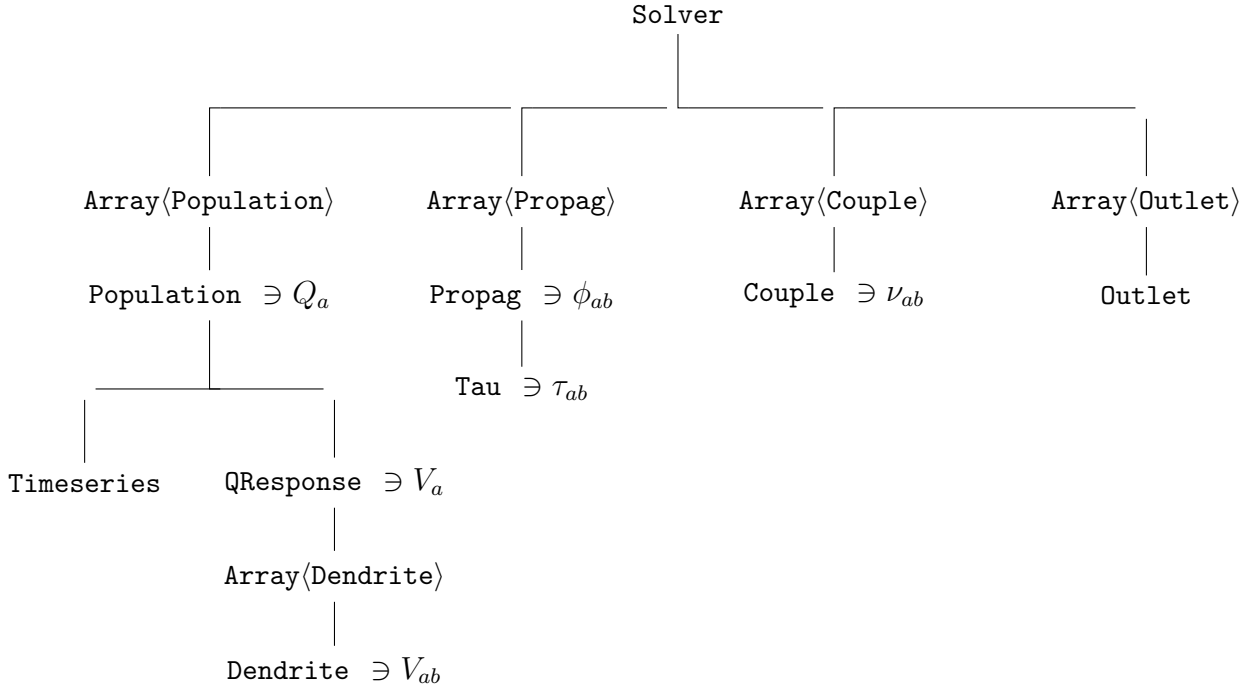


Figure 3: Schematic of the main class structures in **NeuroField** . Each line indicates that the bottom class is a member of the top class. The $a \ni b$ symbol indicates that the dynamical field $b(\mathbf{r}, t)$ is a member of the class **a** . Inheritance structures are NOT illustrated.

2.3 Class NF

ALL classes that requires the configuration file should derive from the `NF` object. This abstract base class contains 3 member variables, and 5 interface methods:

Variable

<code>nodes</code>	The number of nodes as specified from the configuration file.
<code>deltat</code>	The time increment per timestep in units of seconds.
<code>index</code>	The index associated with the object.

Methods

<code>init(Configf& configf)</code>	Initializes the object with the config file.
<code>dump(Dumpf& dumpf) const</code>	When the program terminates, all objects dump information into a dump file (<code>dumpf</code>) for later restart. <code>Dumpf</code> is an <code>ofstream</code> .
<code>restart(Restartf& restartf)</code>	Restarts the object in restart mode, <i>in addition</i> to <code>init()</code> . The developer should have dumped all relevant information in dump, then reads it here.
<code>step(void)</code>	At each timestep, this function is called.
<code>output(Output& output) const</code>	Specifies which fields to output.

All `NF` classes automatically handles the `ofstream::<<` and `ifstream::>>` operators.

2.4 Class Array

`Array` is a container array to store objects that supports the `ofstream::<<` and `ifstream::>>` operators, as well as a `step(void)` function. This object typically is, but not necessarily has to be an `NF` object.

The `step(void)` function is equivalent to a `foreach(element).step()` in pseudocode. This function is encouraged over the use of `empty()` , `size()` , and `operator[]()` , which are discouraged to be used.

2.5 Class Population

Models a neural population, which may be either a stimulus or normal population. If it has any dendrites, i.e. it has presynaptic connections, then it is a normal population, and it is a stimulus if it does not have dendrites.

In the former case, it contains the `QResponse` class and have a soma potential; in the latter case it contains the `Timeseries` class, and does not have a soma potential. See Fig. 3 for reference.

In either cases, the `Population` class has a keyring storing the firing rate history, coded as a 2D array plus an integer key.

A population is “settled” after `Population::init()` is called, after which no dendrites can be added, and the firing rate history cannot grow.

2.6 Input/Output

Input via the configuration file is implemented in the `init()` function, via `Configf` , which provides the following functions:

1. `next`: go to the next keyword
2. `param`: go to the next keyword and reads in a variable. If the keyword is not found, barks and exits.
3. `optional`: same as `param`, but does not bark nor exit.
4. `find`: search a keyword and return the next variable as string.

In restart mode, `init()` is called, followed by `restart()`. `Restartf` is identical to `Configf`.

There are two modes of output. One is outputting the solution in `Population::output()`, `Dendrite::output()`, `Propag::output()`, and `Couple::output()`, and the other is the dumping of data for restart implemented in `dump()`.

To output field solutions, overload `NF::output()` to write

```
output.prefix("Object Name",index+1);
output("field1",field1);
output("field2",field2);
output("field3",field3);
subobject1.output(output);
subobject2.output(output);
```

or for a single output field,

```
output("Object Name",index+1,"field1",field1);
```

`dumpf()` provides a `Dumpf` object, which is essentially an `ofstream`. Dump all data here, so that it can be read in `restart()`.

2.7 Writing a new class

In extending `NeuroField` it is likely new classes needs to be written. When doing this, it would be useful to keep in mind:

1. When appropriate, the default constructor, copy constructor, and `operator=` should be made inaccessible by declaring them to be private.
2. If the configuration file is used, the `NF` class **MUST** be inherited.
3. The `init()`, `restart()`, `dump()`, `step()` functions should be overloaded appropriately. Keep in mind that `restart()` internally calls `init()` at the beginning.
4. `Population`, `Propag`, and `Couple` has the `output()` function to specify which field(s) to output. Overload this if appropriate.
5. When in doubt, read existing class implementations for examples.

2.7.1 Class Propag

The `Propag` class implements the axonal propagation as an identity map, i.e.

$$\mathcal{D}_{ab} = 1.$$

To introduce more sophisticated axonal propagation, this class is inherited and overloaded.

The `Propag` class provides a constant references to both presynaptic and postsynaptic populations.

For finite differences integration, `Stencil` provides a 9-point stencil. To use, initialize it with a `vector<double>`, then access the Moore grid with `nw`, `n`, Loop over the stencil with the operator `++`.

To “register” your propagator, look for the

```
// PUT YOUR PROPAGATORS HERE
```

section in `solver.cpp`.

2.7.2 Class Couple

The `Couple` class manages ν_{ab} , which is constant in space and time.

To introduce synaptic plasticity, derive from this class.

The `Couple` class provides a constant references to both presynaptic and postsynaptic populations. Glutamate concentration is also provided. `pos` is +1 or -1, depending on the sign of ν_{ab} .

To “register” your couple, look for the

```
// PUT YOUR COUPLES HERE
```

section in `solver.cpp`.

2.7.3 Stimulus

To implement new stimulus pattern, inherit from class `Timeseries`, where `init()` and `fire()` should be overloaded.

To “register” your stimulus, look for the

```
// PUT YOUR TIMEFUNCTION HERE
```

section in `timeseries.cpp`.

2.8 Program flow

Essentially, the program flow can be read from Fig. 3, so that objects take priority from top to bottom, left to right, both in terms of initialization and stepping through each timestep. A more detailed description is given below, and the reader is referred to the source code for complete description.

We use the semicolon to denote a succession of functions/procedures, and $a() \Rightarrow b()$ symbol to denote function `b()` as content of function `a()`.

<code>main()</code>	\Rightarrow	Initialize the config file, dump file and output file; <code>Solver::init()</code> ; <code>Solver::solve()</code> ;
<code>Solver::init()</code>	\Rightarrow	read in global parameters; Read in <code>CntMat</code> ; Construct <code>Population</code> ; construct <code>Propag</code> ; construct <code>Couple</code> ; <code>Population::add2Dendrite()</code> ; Read configurations for <code>Population</code> , <code>Propag</code> , <code>Couple</code> , and Output .
<code>Solver::solve()</code>	\Rightarrow	<code>for(...)</code> { <code>Solver::step()</code> ; <code>Output::step()</code> ; }
<code>Solver::step()</code>	\Rightarrow	<code>Population::step()</code> ; <code>Propag::step()</code> ; <code>Couple::step()</code> ;
<code>Population::step()</code>	\Rightarrow	<code>QResponse::step()</code> if neural population; <code>Timeseries::step()</code> if stimulus
<code>QResponse::step()</code>	\Rightarrow	<code>Dendrite::step()</code> ; sum over V_{ab}

- One integration step of the model implements the following stages: 1) Dendritic response 2) Afferent summation. 3) Firing response/stimulus response. 4) Wave equation integration step which includes Q delay processing 5) Coupling response.
- Most of the computational load comes from integrating wave equations and harmonic oscillators within the dendritic responses. Most computational time is probably on outputting.

- Wave equations are integrated by explicit finite differences integration. A nine point spatial stencil is used to reduce high frequency spatial instabilities when driven by random noise. Other parts of code are unaffected by spatial geometry so this can be switched to irregular gridding easily.
- Harmonic oscillators with dendritic response are integrated using a heavily strength reduced explicit direct integration assuming constant drive. This was more efficient than a constant drive RK4 algorithm which would not be fourth order in any case due to the constant drive. Rennie used a constant drive RK4 for his 1997 code.

2.9 Tools for solving differential equations

Classes `DE` and `Integrator` (currently RK4 is implemented) are used to solve generic systems of ODEs, where the dynamical variables are homogeneous fields. For inhomogeneous DEs and spatial dependency, a 9-point stencil is provided in `Stencil`.

DE To solve ODEs of homogeneous fields, inherit `DE` and define the purely virtual `rhs()` function. Instantiate a `DE` object and an integrator, then step through it with `integrator.step()`. `STP` is an example using classes `DE` and `RK4`.

Stencil Use `operator=` to apply a `Stencil` to a `vector<double>`, Then increment the stencil with `operator++`. The 9 stencil points can be read with `nw()` ... `se()`.

2.10 Submission to SVN

The SVN repository is a standard installation, so any tutorials on usage of SVN apply here. For developers, we suggest obtaining a copy of the entire repository with

```
svn co http://silliac.physics.usyd.edu.au:18080/svn/neurofield/
neurofield --username=<your SVN username>
```

The following folders are present:

branches Folders for users to make changes to the program.
tags Previous versions of the program.
trunk Latest stable version of the program.

To make changes to the program, it is recommended to copy the trunk into a new subfolder within branches

```
cp -r trunk ./branches/my_branch
```

You can then freely modify the code in the branch with the benefit of version control, and other users can obtain your code through the branch. If your modifications are accepted for the main program, your branch will then be merged into the trunk subject to appropriate testing.

2.11 TODO

1. check numerical entry of connection matrix
2. restart mode has never been used. Leave it that way.