SpikeNet Documentation

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1 Overview

SpikeNet is a software developed for simulating spiking neuronal networks, of which the design provides the following four main features.

Configurability SpikeNet supports any user-defined structure of synaptic connectivity topologies, coupling strengths and conduction delays. It can be easily extended by developers to support any variations of integrate-and-fire neuron and synapse models. For the models that are currently available, see Neuron and synapse models.

Performance Simulation of spiking neuronal network quickly becomes computationally intensive if the number of neurons N in the network exceeds a few thousand. To achieve superior performance, various measures have been taken at both algorithmic and implementation level. Notably, at the algorithmic level, kinetic models are exclusively chosen for their algorithmic efficiency (e.g., [2, 4, 8, 9]). Furthermore, for such kinetic models, computational cost of the simulation can be dramatically reduced with the commonly used mathematical abstraction that synapses can be simplified into a few groups, within which their dynamics (or more specifically, the time constants) are identical [1]. At the implementation level, C++, a programming language renowned for its high-performance computing, is used.

User-friendly interface In SpikeNet, although, C++ is used for heavy-duty computation, its user-interface is written in a high-level programming language (Matlab) for user-friendliness. This means SpikeNet does not require non-developer users to be familiar with C++. In practise, the typical work-flow of SpikeNet user is as following.

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1. In Matlab, use SpikeNet functions to generate the input files that define the simulation case.
2. Evoke the SpikeNet C++ simulator, which reads the input files, runs the simulation and generates the output files.
3. In Matlab, use SpikeNet functions to parse the output files into Matlab data for post-processing.

Please see Matlab user interface for more detailed descriptions of the workflow. This design essentially makes the SpikeNet C++ simulator a stand-alone software. Based on these protocols, the C++ simulator can easily interface with any other high-level programming languages if Matlab is not prefered. Developer users will be interested to know that SpikeNet supports two types of input/output file formats: plain text and HDF5. Both text-based and HDF5 file formats follow pre-defined protocols (see Input/Output protocols).

Scalability The design of the SpikeNet C++ simulator readily supports parallel computing used Message Passing Interface (MPI). The simulator has two central C++ classes, representing populations of neurons and synaptic connectivities among these populations, respectively. For example, for a recurrent network consisting of an excitatory neuron population (E) and an inhibitory one (I), two neuron population objects will be created together with up to four synaptic connectivity objects including $E \leftarrow E$, $I \leftarrow E$, $E \leftarrow I$ and $I \leftarrow I$. These six objects can be created and simulated in parallel and the amount of message passing among them at each simulation time step is minimal. Additionally, HDF5 is supported for handling large input/output data files.

2 Tech Stack

- C++11 standard is required (GCC 4.2.1 or later; Intel C++ 12.0 or later).
- Matlab (2013a or later) is optional but highly recommended.
- HDF5 C++ and C API are optional but recommended for data-intensive projects.
- Portable Batch System (PBS) is optional.
- Message Passing Interface (MPI) implementation is optional.

3 Quickstart

Following are the steps to set up the SpikeNet C++ simulator.

- Ask for read permission from one of the contributors with admin rights.
- Make a new directory: `mkdir tmp; cd tmp`
- Clone SpikeNet: `git clone git@github.com:BrainDynamicsUSYD/SpikeNet.git` (Method 2: `git clone https://github.com/BrainDynamicsUSYD/SpikeNet`)

- Go into the directory: `cd SpikeNet`
- Make a copy of the makefile: `cp other_scripts/make*bak makefile`
- Build the C++ simulator: `make; make clean`

Now you should see the "simulator" in the current directory, with which you can run simulations by creating input files according to Input/Output protocols. However, it will be much easier to work with the Matlab user interface. If you do not have access to Matlab, try to contact the contributors to request interfaces with other high-level programming languages (Python for example). Following are the steps to use the Matlab user interface.

- Make a new directory for storing data: `cd ..; mkdir tmp_data; ls`
- Start Matlab: `matlab -nodisplay`
- Set up the environment for Matlab: `cd SpikeNet; addpath(genpath(cd));`
- Generate the example input files: `cd ../tmp_data; main_demo;`
- Quit Matlab: `quit`
- Run the simulator with the input files: `cd tmp_data; ../simulator *ygin;`
- Start Matlab: `cd ..; matlab -nodisplay`
- Set up the environment for Matlab: `cd SpikeNet; addpath(genpath(cd));`
- Parse the output files, run some basic post-processing and visualization: `cd ../tmp_data; PostProcessYG()`
- Load the simulation result: `d = dir(`*RYG.mat'); R = load(d(1).name)` (You may need to correct the single quotes in Matlab if you are directly copying the code from here.)

For HDF5, please make relevant changes in the makefile to specify the paths where you have installed your HDF5 API. Each of the matlab interfaces has a corresponding HDF5 version. For a complete list of both types of matlab interfaces,

- `ls SpikeNet/matlab_interfaces/write2ygin`
- `ls SpikeNet/matlab_interfaces/write2HDF5`

For those who have access to a high-performance computing cluster with PBS, SpikeNet also provides bash script that fully automates the above Matlab → C++ → Matlab workflow for PBS job array submission. The script all_in_one.sh has the following features:

- It automatically detects which stage each array job (with a unique 4-digit integer array ID) has reached: pre-processing done, simulation done or post-simulation data parsing done. The script will start each array job from the last unfinished stage instead of the first stage. This feature comes in handy when hundreds of array jobs end prematurely at different stages, say, due to the HPC being shut down unexpectedly, in which case simply a re-submission of the script will clean up the mess.
- It passes the array ID as an input argument to the matlab pre-processing script.
- It automatically saves a copy of the pre-processing Matlab script to the data directory when starting the array job with ID 0001.

Following are the steps to use the PBS script.

- Make sure you have set up your PBS environment correctly (e.g., modelue load HDF5-1.10.0). This can be done by editing shell config file.
- Go to the tmp directory
- Make a copy of the script: `cp SpikeNet/other_scripts/all*bak all_in_one.sh`
- Change it to executable: `chmod +x all_in_one.sh`
- Edit the following variables in the bash script accordingly:
  - MATLAB_SOURCE_PATH_2='your_path'
  - MATLAB_PRE_PROCESS_FUNC='your_functions'
- Make a directory for PBS output: `mkdir PBSout`
- Submit the job: `qsub -t 1-X -q queue_name all_in_one.sh`

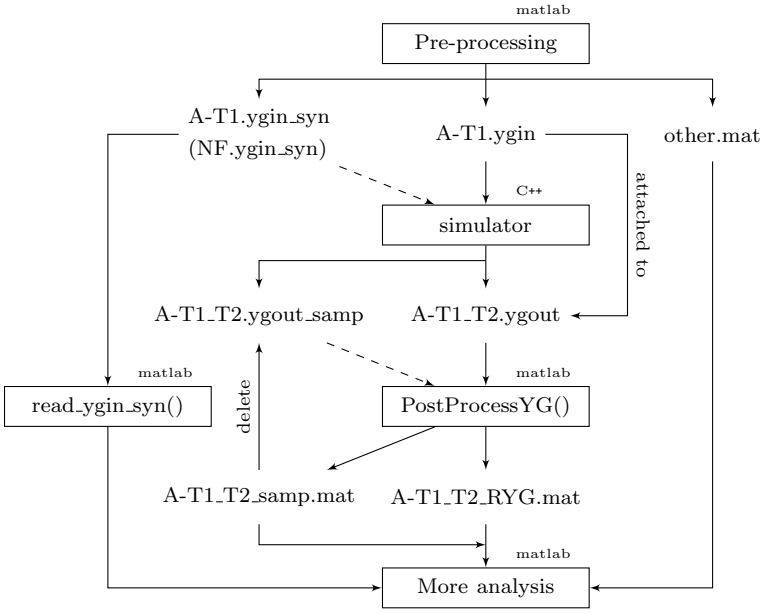
For MPI jobs with SpikeNet, please contact Yifan Gu for more technical details. Here are some basic tips on git.

- To get the most recent version of SpikeNet: `git pull origin master`
- Build the new simulator: `make; make clean`
- Avoid directly modifying any existing files in SpikeNet unless you are a developer. Create another directory alongside SpikeNet and put all of your files there. In summary, your project folder should look like:

```
tmp
├── SpikeNet
│   ├── cpp_sourses
│   ├── matlab_interfaces
│   ├── makefile
│   └── other_scripts
├── simulator
├── tmp_data
├── my_functions
├── PBS_out
└── all_in_one.sh
```

4 Workflow

The typical workflow of SpikeNet with text-based input/output files is as shown in the following flowchart.



Although the C++ simulator accepts input files with any names, A-T1 is the recommended and default naming format. A is a 4-digit PBS array ID number. T1 is a timestamp identifying when the ygin file was generated. Similarly, T2 is a timestamp identifying when the ygout file was generated. Note that T2 allows multiple simulations to be run for the same ygin file. The synaptic connectivity definition file ygin_syn is separated from ygin for better memory management, since the connectivity definitions (protocol INIT006) are the single most memory-intensive component. Due to the same reason, the sampled time series data from simulation (protocol SAMP001) are stored separately in ygout_samp and samp.mat. Non-default (NF) ygin_syn file path should be given in ygin using the provided Matlab interface. The dashed lines mean that the C++ simulator and the PostProcessYG() matlab function will automatically look for those auxiliary input files based on the information contained in the main input files.

5 Documentation for the C++ simulator

To view the documentation

- Make sure doxygen and graphviz are installed

- Go to the SpikeNet directory
- Generate the documentation: `doxygen`
- Open the documentation: `open docu*/html/index.html`

6 Neuron and synapse models

6.1 Default model

A description of the neuron and synapse models can also be found in a publication that used SpikeNet [3]. The default neuron model in SpikeNet is leaky integrate-and-fire neuron. The membrane potential V_i^α of the i-th neuron ($i = 1, \cdots, N_\alpha$) from population α evolves according to

$$C_m \frac{dV_i^\alpha}{dt} = -g_L(V_i^\alpha - V_L) + I_{i,syn}^\alpha(t) + I_{i,app}^\alpha(t), \text{ if } V_i^\alpha < V_{th}. \tag{6.1}$$

When neurons reach the threshold V_{th}, a spike is emitted and they are reset to V_{rt} for an absolute refractory period τ_{ref}. The spike times t_i^α are recorded.

The default synapse model in SpikeNet is conductance-based. The synaptic currents received by a neuron are given by

$$I_{i,syn}^\alpha(t) = \sum_{\beta=1}^{P} I_i^{\alpha\beta}(t) \tag{6.2}$$

$$= \sum_{\beta=1}^{P} [-g_i^{\alpha\beta}(V_i^\alpha - V_{rev}^\beta)] \tag{6.3}$$

$$= \sum_{\beta=1}^{P} \{-[\sum_{j=1}^{N_\beta} a_{ij}^{\alpha\beta} g_{ij}^{\alpha\beta} s_{ij}^{\alpha\beta}(t)](V_i^\alpha - V_{rev}^\beta)\} \tag{6.4}$$

where V_{rev}^β is the reversal potential of the corresponding current $I_i^{\alpha\beta}$ induced by pre-synaptic population β. $a_{ij}^{\alpha\beta}$ is a binary variable which determines the existence of synapse from the j-th neuron in population β to the i-th neuron in population α, while $g_{ij}^{\alpha\beta}$ reflects the (maximal) strength of the synaptic conductance. The gating variable $s_{ij}^{\alpha\beta}(t)$ models the instananeous value of synaptic conductance in terms of the fraction of open channels, described by

$$\frac{ds_{ij}^{\alpha\beta}}{dt} = -\frac{s_{ij}^{\alpha\beta}}{\tau_d^\beta} + \sum_{t_j^\beta} h^\beta(t - t_j^\beta - d_{ij}^{\alpha\beta})(1 - s_{ij}^{\alpha\beta}) \tag{6.5}$$

where h models the concentration time-course of the channel-opening neurotransmitters, arrived with a conduction delay $d_{ij}^{\alpha\beta}$ after the pre-synaptic spike time t_j^β. The $(1 - s_{ij}^{\alpha\beta})$ term introduces saturation effect. Following the simplification in [1], a rectangular pulse with unitary area is used for h

$$h(t) = \begin{cases} 1/\tau_r, & \text{if } 0 \le t \le \tau_r \\ 0, & \text{otherwise} \end{cases} \tag{6.6}$$

All numerical values are in consistent units unless mentioned otherwise (ms for time, mV for voltage, nA for current, nF for capacitance and μS for conductance). Default numerical integration is performed using Euler method and the suggested time-step is 0.1 ms [6].

6.2 Currently available models

1. Exponential leaky integrate-and-fire neuron model
2. Double-exponential synapse model: see [5]
3. Inhibitory plasticity: see [9]
4. Spike frequency adaptation: see [7]

7 Matlab user interface

See main_demo.m for a list of the basic case-building matlab functions and their usages. Each such function implements one particular input protocol.

```
function main_demo()
% Use coherent units (msec+mV+nF+miuS+nA) unless otherwise stated


%%%% Seed the Matlab random number generator
seed = 1;

%%%% Open new (uniquely time-stamped) input files for the SpikeNet C++
% simulator.
% FID is the main input file, FID_syn is the input file with the
% synaptic connectivity definitions (could be very large).
[FID, FID_syn] = new_ygin_files_and_randseed(seed);
% If no FID_syn is needed, use FID = new_ygin_files_and_randseed(seed,0)


%%%% Define some basic parameters
% Time step (ms)
dt = 0.1; % 0.1 is usually small enough
% Total number of simulation steps
step_tot = 10^2;
% Create two neuron populations with 50 neurons in the 1st population
% and 10 neurons in the 2nd population.
N = [40, 10];
% Write the above basic parameters to the input file
writeBasicPara(FID, dt, step_tot, N);


%%%% Define non-parameters for the neuorn model
```

```
% For demo purpose, the values used as following are the still the
% default ones.
% If default values are to be used, there is no need to re-define them.
Cm = 0.25; % (nF) membrane capacitance
tau_ref = 2.0; % (ms) absolute refractory time
V_rt = -60.0;   % (mV) reset potential
V_lk = -70.0;   % (mV) leaky reversal potential
V_th = -50.0;   % (mV) firing threshold
g_lk = 0.0167;   % (miuS) leaky conductance (note that Cm/gL=15 ms)
for pop_ind = 1:2
    writePopPara(FID, pop_ind,'Cm',Cm,'tau_ref',tau_ref,'V_rt',V_rt,...
        'V_lk',V_lk,'V_th',V_th,'g_lk',g_lk);
end

%%%% Add spike-frequency adaptation to the 1st population
pop = 1;
writeSpikeFreqAdpt(FID, pop);


% % Use Adam 2016 synapse model
% model_choice = 2;
% writeSynapseModelChoice(FID, model_choice)


%%%% Define the initial condition
p_fire = [0.1 0.1]; % initial firing probabilities for both populations
% set initial V distribution to be [V_rt, V_rt + (V_th-V_rt)*r_V0]
r_V0 = [0.5 0.5];
writeInitCond(FID, r_V0, p_fire)

%%%% Add external Poissonian spike trains into the 1st population
pop = 1;
type_ext = 1; % 1 for AMPA-like syanpses
g_ext = 2*10^-3; % synaptic coupling strength (miuS)
N_ext = 1000; % No. of independent external connections onto each neuron
rate_ext = 2*ones(1, step_tot); % Poisson rate for each time step (Hz)
neurons_recv = zeros(1, N(pop));
neurons_recv(1:10) = 1; % only neurons #1-10 receive such external input
writeExtSpikeSettings(FID, pop, type_ext, g_ext,  N_ext, rate_ext,...
    neurons_recv );


%%%% Add external currents (Gaussian white noise) to the 2nd population
pop = 2;
I_ext_mean = 0.5*ones(1,N(2)); % defined for each neuron (nA)
I_ext_std = 0.2*ones(1,N(2)); % defined for each neuron (nA)
writeExtCurrentSettings(FID, pop, I_ext_mean, I_ext_std)

%%%% Add external conductances (Gaussian white noise) to the 2nd population
% The default reveral potential is V_ext = 0.0 mV.
pop = 2;
g_ext_mean = 50*10^-3*ones(1,N(2)); % defined for each neuron (muS)
g_ext_std = 0.0*ones(1,N(2)); % defined for each neuron (muS)
writeExtConductanceSettings(FID, pop, g_ext_mean, g_ext_std)


%%%% Define runaway killer
% The computational cost of the simulation is directly proportional to
```

```
% the avearage firing rate of the network. Very often, your parameters
% may lead to biologically unrealistically high firing rate or even
% runaway activity (the highest rate possible ~1/tau_ref). To save the
% computational resources for more interesting simulation cases, it is
% advised to define the runawary killer.
% Note that the simulator will still output all the relevant data before
% the kill.
min_ms = 500; % the min simulation duration that should be guaranteed
runaway_Hz = 40; % the threshold above which the simu should be killed
Hz_ms = 200; % the window length over which the firing rate is averaged
pop = 1; % the population to be monitored by the runaway killer
writeRunawayKiller(FID, pop, min_ms, runaway_Hz, Hz_ms);


%%%% Record the basic statistics for the 1st neuron population
pop = 1;
writePopStatsRecord(FID, pop);

%%%%%%%%%%%%%%%%%%%% Chemical Connections %%%%%%%%%%%%%%%%%%%%%%%
% type(1:AMAP, 2:GABAa, 3:NMDA)
% Define AMAP-like excitatory synaptic connection wtihin the 1st pop
pop_pre = 1;
pop_post = 1;
syn_type = 1; % 1 for AMPA-like synapse
g_EE = 10*10^-3; % synaptic coupling strength (miuS)
% random adjacency matrix with a wiring probability of 0.2
A = rand(N(1), N(1)) < 0.2;
[I_EE, J_EE] = find(A);
K_EE = g_EE*ones(size(I_EE)); % identical coupling strength
D_EE = rand(size(I_EE))*5; % uniformly random conduction delay [0, 5] ms
writeChemicalConnection(FID_syn, syn_type,  pop_pre, pop_post, ...
    I_EE, J_EE, K_EE, D_EE);

% Define AMAP-like excitatory synaptic connection from pop 1 to pop 2
pop_pre = 1;
pop_post = 2;
syn_type = 1; % 1 for AMPA-like synapse
g_IE = 10*10^-3; % synaptic coupling strength (miuS)
% random adjaceny matrix with a wiring probability of 0.5
A = rand(N(1), N(2)) < 0.5;
[I_IE, J_IE] = find(A);
K_IE = g_IE*ones(size(I_IE)); % identical coupling strength
D_IE = rand(size(I_IE))*5; % uniformly random conduction delay [0, 5] ms
writeChemicalConnection(FID_syn, syn_type,  pop_pre, pop_post, ...
    I_IE, J_IE, K_IE, D_IE);

% Define GABA-like excitatory synaptic connection from pop 2 to pop 1
pop_pre = 2;
pop_post = 1;
syn_type = 2; % 2 for GABA-like synapse
g_EI = 10*10^-3; % synaptic coupling strength (miuS)
% random adjaceny matrix with a wiring probability of 0.5
A = rand(N(2), N(1)) < 0.5;
[I_EI, J_EI] = find(A);
K_EI = g_EI*ones(size(I_EI)); % identical coupling strength
D_EI = rand(size(I_EI))*5; % uniformly random conduction delay [0, 5] ms
writeChemicalConnection(FID_syn, syn_type,  pop_pre, pop_post, ...
    I_EI, J_EI, K_EI, D_EI);
```

```
145
146 % Define GABA-like excitatory synaptic connection within pop 2
147 pop_pre = 2;
148 pop_post = 2;
149 syn_type = 2; % 2 for GABA-like synapse
150 g_II = 20*10^-3; % synaptic coupling strength (miuS)
151 % random adjaceny matrix with a wiring probability of 0.5
152 A = rand(N(2), N(2)) < 0.5;
153 [I_II, J_II] = find(A);
154 K_II = g_II*ones(size(I_II)); % identical coupling strength
155 D_II = rand(size(I_II))*5; % uniformly random conduction delay [0, 5] ms
156 writeChemicalConnection(FID_syn, syn_type,  pop_pre, pop_post, ...
157     I_II, J_II, K_II, D_II);
158 %%%%%%%%%%%%%%%%%%%% Chemical Connections Done %%%%%%%%%%%%%%%%%%%%%%
159
160
161 %%%% Use an existing synapse connectivity definition file instead of
162 % generating a new one:
163 % writeSynFilename(FID, 'path/to/existing/XXX.ygin_syn')
164 % In this case, you should use
165 % "FID = new_ygin_files_and_randseed(seed, 0)"
166 % to avoid creating an empty ygin_syn file.
167
168
169
170 %%%% Define non-default synapse parameters
171 writeSynPara(FID, 'tau_decay_GABA', 3);
172 % "help writeSynPara" to see all the parameter names and default values
173
174 %%%% Add short-term depression to the synapses with the 1st population
175 pop_pre = 1;
176 pop_post = 1;
177 step_start = round(step_tot/3); % Turn on STD at this time step
178 writeSTD(FID, pop_pre, pop_post, step_start);
179
180
181 %%%% Add inhibitory STDP to the synapses from pop 2 to pop 1
182 pop_pre = 2;
183 pop_post = 1;
184 % Turn on inhibitory STDP at a certain time step
185 step_start = round(step_tot/3*2);
186 writeInhSTDP(FID, pop_pre, pop_post, step_start);
187
188 %%%% Record the basic statistics for the excitatory synapses within
189 % the 1st neuron population
190 pop_pre = 1;
191 pop_post = 1;
192 syn_type = 1; % 1 for AMPA-like synapse
193 writeSynStatsRecord(FID, pop_pre, pop_post, syn_type);
194
195 %%%% Sample detailed time serious data from the 1st population
196 pop = 1;
197 sample_neuron = 1:10:N(1); % sample every 10th neuron
198 sample_steps = 1:2:step_tot; % sample every 2nd time step
199 sample_data_type = logical([1,1,1,1,0,0,1,0]);
200 % The logical vector above corresponds to
201 % [V,I_leak,I_AMPA,I_GABA,I_NMDA,I_GJ,I_ext, I_K]
202 writeNeuronSampling(FID, pop, sample_data_type, ...
```

```
    sample_neuron, sample_steps)

%%%% Optional: record explanatory variables (scalars only)
% They will also be used in pro-processsing for auto-generated comments
discard_transient = 0; % transient period data to be discarded (ms)
writeExplVar(FID, 'discard_transient', discard_transient, ...
    'g_EE', g_EE, ...
    'g_EI', g_EI, ...
    'g_IE', g_IE, ...
    'g_II', g_II, ...
    'g_ext', g_ext, ...
    'N_ext', N_ext, ...
    'rate_ext', rate_ext);


%%%% Additional comments to be passed to the post-processing stage
comment1 = 'This is a demo.';
comment2 = ['If you have any question regarding SpikeNet,'...
    'please contact Yifan Gu (yigu8115@gmail.com).'];
writeExplVar(FID, 'comment1', comment1, 'comment2', comment2);

%%%% append this matlab file to the input file for future reference
appendThisMatlabFile(FID)

end



function appendThisMatlabFile(FID)
breaker = ['>',repmat('#',1,80)];
fprintf(FID, '%s\n', breaker);
fprintf(FID, '%s\n', '> MATLAB script generating this file: ');
fprintf(FID, '%s\n', breaker);
Fself = fopen([mfilename('fullpath'),'.m'],'r');
while ~feof(Fself)
    tline = fgetl(Fself);
    fprintf(FID, '%s\n', tline);
end
fprintf(FID, '%s\n', breaker);
fprintf(FID, '%s\n', breaker);
fprintf(FID, '%s\n', breaker);
end
```

(More need to be added on the available post-processing Matlab functions. SpikeNet has a variety of statistical analysis and visualization tools for spiking networks.)

++Add descriptions of CollectVectorYG and CollectCellYG.

8 Input/Output protocols

8.1 Text-based input protocols

The default filename for text-based input file is "filename.ygin". It is advised that synapse definitions always be given in a separate file. The default synapse definition filename is "filename.ygin_syn". Non-default synapse definition file path and name can be specified by "SYNF001" protocol. Following is the complete list of the input

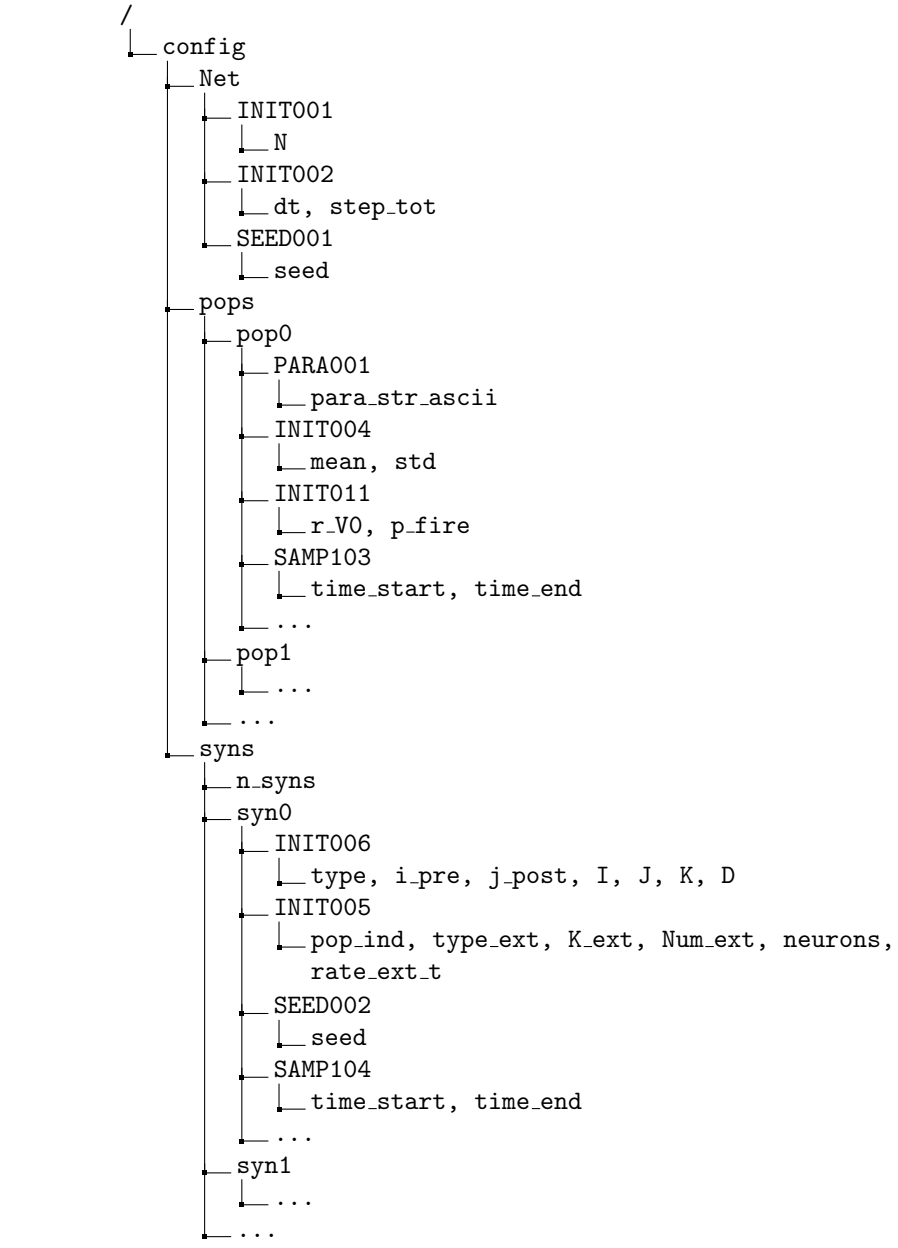
data protocols. Note that the protocols use three special characters, including ">" for starting a new protocol, "#" for commenting and "," for delimiting.

```
1
2  > INIT001 # number of neurons in each population
3      N1, N2, ...,
4
5  > INIT002 # time step length and total number of steps
6      dt (ms), step_tot,
7
8  > INIT003 # random initial distributions for V (deprecated)
9      p_fire_pop1 (range (−∞,1]), ..., p_fire_popN,
10
11 > INIT004 # external Gaussian currents
12     pop_ind,
13     mean_1 (nA), mean_2, ..., mean_N, (for each neuron)
14     std_1 (nA), std_2, ..., std_N,
15
16 > INIT005 # external Poissonian spikes
17     pop_ind, type_ext, K_ext (μS), Num_ext,
18     1, 1, 0, 0, ..., (1-by-N_pop logical values)
19     rate_1 (Hz), rate_2, ..., rate_step_tot
20
21 > INIT006 # chemical connection definition
22     type, pop_ind_pre, pop_ind_post,
23     I (row vector),
24     J (row vector),
25     K (row vector),
26     D (row vector),
27
28 > INIT007 # set perturbation (remove one spike)
29     pop_ind, step_perturb,
30
31 > INIT008 # add short-term depression
32     pop_ind_pre, pop_ind_post, STD_on_step,
33
34 > INIT009 # add inhibitory STDP
35     pop_ind_pre, pop_ind_post, STDP_on_step,
36
37 > INIT010 # add spike-frequency adaptation
38     pop_ind,
39
40 > INIT011 # random initial conditions for V and firing prob
41     r_V0_pop1 (range (0,1]), ...,r_V0_popN,
42     p_fire_pop1 (range (0,1]), ..., p_fire_popN,
43
44 > INIT012 # external Gaussian conductance
45     pop_ind,
46     mean_1 (μS), mean_2, ..., mean_N, (for each neuron)
```

```
47      std_1 (μS), std_2, ..., std_N,
48
49  > INIT013 # synapse model choice
50      synapse_model_number,
51
52  > SYNF001 # non-default synapse definition file name
53      path/to/file_name (no comma!)
54
55  > KILL001 # runaway killer setting
56      pop_ind, min_ms, runaway_Hz, Hz_ms,
57
58  > PARA001 # non-default neuron population parameter
59      pop_ind, number_of_parameters,
60      parameter_name1, value1,
61      parameter_name2, value2,
62      ...
63
64  > PARA002 # non-default synapse parameter
65      number_of_parameters,
66      parameter_name1, value1,
67      parameter_name2, value2,
68      ...
69
70  > SAMP001 # neuron data sampling
71      pop_ind,
72      data_type (logical vector),
73      ind1, ind2, ..., indX, (sample neuron indices)
74      1, 1, 0, 0, ..., (1-by-step_tot logical values)
75      # Note that data_type specifies sample data types
76      # and it must correspond to
77      # [V,I_leak,I_AMPA,I_GABA,I_NMDA,I_GJ,I_ext]
78
79  > SAMP002 # synapse data sampling
80      pop_ind_pre, pop_ind_post, syn_type,
81      ind1, ..., indX, (post-synaptic sample neuron indices)
82      1, 1, 0, 0, ..., (1-by-step_tot logical values)
83
84  > SAMP003 # neuron population statistical data record
85      pop_ind,
86
87  > SAMP004 # synaptic currents  statistical data record
88      pop_ind_pre, pop_ind_post, syn_type,
89
90  > SAMP005 # local field potential data record
91      pop_ind, No_of_measures
92      1, 0, 0, 1, ...,
93      ...
94      0, 0, 1, 1, ..., (No_of_measures-by-N logical values)
```

8.2 HDF5-based input protocols

HDF5-based input protocols basically follow the text-based protocols (with a few exceptions!).



8.3 Notes on RNG control

To fully control the RNG in C++ simulator, you need to pass the seed via this two functions.

1. writeExtSpikeSettingsHDF5(..., Seed)
2. writePopSeedHDF5

8.4 Text-based output protocols

The default filename of text-based output file is "filename-X.ygout", where X is a time-stamp that uniquely marks the output file so that multiple simulations can be run for the same input files. For data completeness, the corresponding input file will be attached to the output file. Following is the complete list of the output data protocols.

```
1
2  > KILL002 # step at which runaway activity is killed
3      step_killed,
4
5  > POPD001 # spike history of neuron population
6      pop_ind,
7      spike_neuron_ind (row vector),
8      num_spikes_t (1-by-step_tot row vector),
9      num_ref_t (1-by-step_tot row vector),
10
11 > POPD002 # neuron parameters in the population
12     pop_ind, number_of_parameters,
13     parameter_name1, value1,
14     parameter_name2, value2,
15     ...
16
17 > POPD003 # neuron population statistical data
18     pop_ind,
19     V_mean_t1, V_mean_t2, ... (1-by-step_tot)
20     V_std_t1, V_std_t2, ... (1-by-step_tot)
21     I_input_mean_t1, I_input_mean_t2, ... (1-by-step_tot)
22     I_input_std_t1, I_input_std_t2, ... (1-by-step_tot)
23
24 > POPD004 # sampled neuron data (deprecated)
25     pop_ind, number_of_sample_neurons,
26     data_name1, ..., data_nameX,
27     data_1 (sampled_neurons-by-sampled_steps matrix),
28     data_2 (sampled_neurons-by-sampled_steps matrix),
29     ...
30     data_X (sampled_neurons-by-sampled_steps matrix),
31
32
33 > POPD005 # E-I ratio for each neuron
```

```
    pop_ind,
    EI_ratio_1, EI_ratio_2, ... (1-by-N),

> SAMF001 # sampled data file name
    path/to/file_name (no comma!)

> POPD006 # sampled neuron data
    pop_ind, number_of_neurons, number_of_steps
    data_name1, ..., data_nameX,
    step_1 (sampled_neurons-by-data_types matrix),
    step_2 (sampled_neurons-by-data_types matrix),
    ...
    step_X (sampled_neurons-by-data_types matrix),

> POPD007 # local field potential data
    pop_ind,  No_of_measures,
    LFP_1, LFP_2, ..., LFP_step_tot, (measure 1)
    ...

> SYND001 # synaptic connection parameters
    number_of_parameters,
    parameter_name1, value1,
    parameter_name2, value2,
    ...

> SYND002 # sampled synapse  data
    pop_ind_pre, pop_ind_post, syn_type, no_of_sample_neurons,
    data (sampled_neurons-by-sampled_steps matrix),

> SYND003 # synapse statistical data
    pop_ind_pre, pop_ind_post, syn_type,
    I_mean_t1, I_mean_t2, ... (1-by-step_tot)
    I_std_t1, I_std_t2, ... (1-by-step_tot)
```

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