[REP-42] how to read synaptic report when projection is included
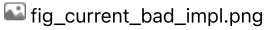Created: 03/Jul/19 Updated: 05/Dec/24 Resolved: 05/Dec/24

Status:	Archived
Project:	ReportingLib
Component/s:	None
Affects Version/s:	None
Fix Version/s:	None

Type:	Support request	**Priority:**	Medium
Reporter:	Oren Amsalem	**Assignee:**	Jorge Blanco Alonso
Resolution:	Expired	**Votes:**	0
Labels:	None		
Remaining Estimate:	Not Specified		
Time Spent:	Not Specified		
Original Estimate:	Not Specified		

Attachments:	BlueConfig_6666_106746 fig_current_bad_impl.png fig_proposal.png launchScript_bg_6666_106746.sh replay_one_neruon.out
Epic Link:	General Support
Team:	cellular
CC:	Fernando Pereira, Giuseppe Chindemi [X] (Inactive), Ioannis Magkanaris [X] (Inactive), Jorge Blanco Alonso, Pramod Kumbhar, Weina Ji

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Description

Hi,

I'm having difficulty in understanding how to read SynapseReport.

I have a simple simulation with one neuron in this path:

```
/gpfs/bbp.cscs.ch/project/proj2/simulations/ThlInput/AudInput23_09_18/SSA_No_SK_E2/Ca1p23_K4p15/EE1_EI1_IE1_II1_TM0/test_synaptic_report
```

I have thalamic projections with spikeReplay and also a spikeReplay from one other neuron

SpontMinis are disabled

After the simulation finish, I try to examine the SynapseReport like this:

```
base_path =
'/gpfs/bbp.cscs.ch/project/proj2/simulations/ThlInput/AudInput23_09_18/SSA_No_SK_E2/Ca1p23_K4p15/EE1_EI1_IE1_II1_TM0/test_synaptic_report/'blue_con
= base_path + '/BlueConfig_6666_106746'
sim = bluepy.Simulation(blue_config)
rep = sim.v2.report('g_AMPANMDA')
rep.get().sort_index('columns').sum().sort_values()
```

```
        65      0.013854
        63      0.017666
  0     0       0.018801
66446   78      0.021558
        66      0.026596
  0     0       0.046272
```

My first assumption was that the 0,0 are the report for the thalamic synaptic activations and the [66446,x] are the reports for the cortico-cortical activations. No
not so sure. what are the 0,0 locations refer to ?

Also as I activated only cell 65376 which correspond to synapse (66446,112). I do not understand how did I get all of the other synaptic activations. If they refer
the thalamic activation how can I know which is thalam-cortical and which is cortico-cortical?

If I disable the thalamic projections and examine the synaptic activation again I get this:

```
      159     0.000000
      171     0.000000
      710     0.000000
      112     0.018801
```

Can I please get instructions on how to read this report?

Thanks.

Comments

Comment by Jean-Denis Courcol [24/Nov/21]

👍

Comment by James Gonzalo King [24/Nov/21]

I think we agree in that yes, when data is read from a synapse report, that data will come from one edge population. The configuration file spec will need to be up
details in order to clearly identify which edge population is selected for a report file.

Comment by Jean-Denis Courcol [24/Nov/21]

Should we then consider to group by edge population name in the case of synapse report ?
In the case of compartment report, we group by node population name in the h5 SONATA report which makes sense as it is a neuron specific information.
Here we are talking about synapses, we should therefore use the same pattern and group by edge population in that case.

Comment by James Gonzalo King [24/Nov/21]
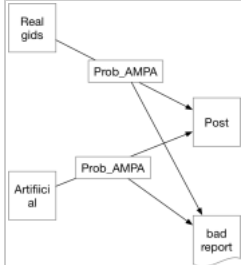
Had meeting to sync on this issue. The difficulty is that the current implementation tries to put all synapses from multiple populations into single report.
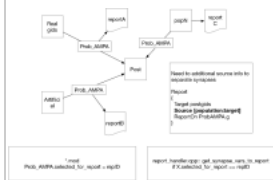
One solution is that synapses from different edge populations will go into different report files. Since CoreNEURON currently only has an on/off flag indicating wh
indicate a reportID.

This solution has limitations since a synapse could not go into multiple reports. For a more long term solution, we need to look again at how CoreNEURON can ad

Comment by Jean-Denis Courcol [23/Oct/20]

I don't recall if we have that documented somewhere in the case of the multipopulation. I don't know if we have multiple files (one per population, or dataset) and

I guess it is not addressed as we have only virtual neurons in the case of 'multipopulation'.

Anyway, I think we should have a link here to some documentation that answers to the initial question.

Comment by Pramod Kumbhar [23/Oct/20]

As SONATA reports are now supported, does that addresses this issue? If so, this ticket can be closed?

Comment by Jean-Denis Courcol [14/Nov/19]

The SONATA support is still partial at the moment. We support nodes & edges per the SONATA specification, however, multipopulation and others element of the

Comment by Oren Amsalem [12/Nov/19]

SONATA is now supported with neurodamus (and CoreNEURON) ? if so should I try to use it to get the correct synaptic reports?

Comment by Jean-Denis Courcol [10/Jul/19]

> Giuseppe Chindemi [X] Pramod Kumbhar we should sync on how synapse ids are handled for multiple projections (or is there already a plan Jean-Denis Co

It is addressed by the SONATA specification. I imagine you will start working on that with the integration of SONATA in the simulator. Please ping us when you sta

Comment by Thomas Delemontex [X] (Inactive) [09/Jul/19]

I have corrected some of my comments that were incorrect. Now it should be ok. Sorry about that.

Comment by James Gonzalo King [09/Jul/19]

Thomas Delemontex [X] thanks for the info. I think the duplicate synapse ids is causing the issue. As I understand, Oren Amsalem will split simulations so that ea
are present and then BluePy can operate as normal. If that fixes the results, then let's close the ticket.

Regarding the over-arching synapse ids across projections issue, we can make a ticket, but I think it will take some discussion and sub tasks to finish 🙂

Comment by Thomas Delemontex [X] (Inactive) [09/Jul/19]

> That said, how is BluePy is retrieving pre gid info?

In bluepy, we can retrieve the post synaptic cell using the `CompartmentReport.gids` function and then retrieve the pre synaptic cell from the projection files.
Maybe it can be useful so I give this snippet for Oren Amsalem:

```
import bluepy
from bluepy.v2 import Synapse, Circuit

base_path = '/gpfs/bbp.cscs.ch/project/proj2/simulations/ThlInput/AudInput23_09_18/SSA_No_SK_E2/Ca1p23_K4p15/EE1_EI1_IE1_II1_TM0/test_synaptic_repo
blue_config = base_path + '/BlueConfig_6666_106746'
sim = bluepy.Simulation(blue_config)
rep = sim.v2.report('g_AMPANMDA')
circuit = Circuit(blue_config)
proj = circuit.projection('Thalamocortical_input_VPM')
gids = rep.gids
values = proj.pathway_synapses(None, gids, properties=[Synapse.PRE_GID])
```

This works actually.

But we should be able to retrieve pre synaptic cells via something close to that:

```
view = CompartmentReport.create_view(gids)
times, data = view.load(t_start, t_end, t_step)
synapse_ids = list(map(tuple, view.mapping.index))
values = proj.synapse_properties(synapse_ids, properties=[Synapse.PRE_GID])
```

but right now in synapse_ids you will have something like this:

```
print(synapse_ids)
[(66446, 307) (66446, 311) (66446, 310) (66446, 673) (66446, 682) (66446, 681) (66446, 693) (0, 0) (0, 0) (0, 0) ...]
```

The (0, 0) should not be there I guess.

Comment by Oren Amsalem [09/Jul/19]

Yes, thanks! for regular synapses and the projection.

I actually started to split the simulation into two different simulations, one with only thalamic connections and one with only the cortical connection. In this way, I
folders.
For now, as I am doing spike replay, I am ok and I do not think I need a workaround.

Thanks.

Should we close the ticket and open a new one titled: "synapse report- add the ability to report multi-projection simulation" or something like that?

Comment by James Gonzalo King [09/Jul/19]

You want to report values for both the regular synapses and the projections? I'm thinking in that case maybe we can add a way for the simulator to spit out 2 repo

Comment by Oren Amsalem [09/Jul/19]

Thanks, James Gonzalo King as far as I can see bluepy use this line:

```
zz =
brain.CompartmentReport('/gpfs/bbp.cscs.ch/project/proj2/simulations/ThlInput/AudInput23_09_18/SSA_No_SK_E2/Ca1p23_K4p15/EE1_EI1_IE1_II1_TM0/test_s
ll =zz.create_view([66446])
etc..
```

to load the synapses.

I'll try to find a workaround in the mean time.

Comment by James Gonzalo King [09/Jul/19]

Giuseppe Chindemi [X] Pramod Kumbhar we should sync on how synapse ids are handled for multiple projections (or is there already a plan Jean-Denis Courcol?

meanwhile, for Oren Amsalem, maybe we can do a short term solution to avoid duplicate synapse ids in the report.

Comment by James Gonzalo King [09/Jul/19]

If I use reporting lib's fullDump tool, at the last timestep I see 6 synapses with non-zero values. Going back to the mapping, those correspond to synids:

63
65
66
67
78
112

(provided I didn't make a mistake as this was a manual process)

Comment by James Gonzalo King [09/Jul/19]

Synapse reports do not have pre gids written. They only contain the synid in the mapping portion of the report. In the past, we only had the single nrn.h5 file, so different projections) is currently not handled by the simulator/reportinglib. That said, how is BluePy is retrieving pre gid info?

Comment by Jean-Denis Courcol [08/Jul/19]

James Gonzalo King I forward that ticket to you. From what Thomas Delemontex [X] wrote, it seems that the pre gids are all '0' in the report.

Comment by Thomas Delemontex [X] (Inactive) [08/Jul/19]

Is there any new informations about this ticket ?
Since this is not proven that the problem is bluepy related can we close it ?
(we can reopen if we realise that the problem does not come from the report creation)

Comment by Thomas Delemontex [X] (Inactive) [05/Jul/19]

Yes this is post synaptic sorry.

Comment by Oren Amsalem [04/Jul/19]

Thanks, Thomas Delemontex [X].

You mean post-synaptic and not pre-synaptic, right?

I have in the simulation a single neuron a66446, meaning that I only have synapse on this neuron.

```
Target Cell one
{
  a66446
}
```

Anyway, I run the simulation using the latest neurodamus module

```
module load neurodamus-neocortex/0.1/python3
srun  special -mpi -c "{strdef configFile configFile=\"BlueConfig_6666_106746\"}" -NFRAME 256 $HOC_LIBRARY_PATH/init.hoc
```

James Gonzalo King Fernando Pereira maybe you can help with this issue?

Thanks,
Oren

Comment by Thomas Delemontex [X] (Inactive) [04/Jul/19]

It appears that you only have 2 pre synaptic "cells" in the report. One virtual the 66446 and the 0 one that does not exists.
The problem is that all nrn offset are set to 0. So we have

```
d = rep.get()
print(d[0])
          0    0    0    0
 time
0.0     0.0  0.0  0.0  0.0
0.1     0.0  0.0  0.0  0.0
0.2     0.0  0.0  0.0  0.0
0.3     0.0  0.0  0.0  0.0
```

when we should have something like:

```
          1    5   89   26
 time
0.0     0.0  0.0  0.0  0.0
0.1     0.0  0.0  0.0  0.0
0.2     0.0  0.0  0.0  0.0
0.3     0.0  0.0  0.0  0.0
```

Are you sure that your bbp file has been correctly created ? It looks like we have post synaptic cell that should be there and duplicate in synapse_ids (0,0)
And it looks good for the projection.

Comment by Oren Amsalem [04/Jul/19]

Thanks, Thomas Delemontex [X] can you try to load the synapses again and see what you get?
It seems that the data that was in the folder was without thalamic synapse, I re-run the simulation with thalamic synapses.

Comment by Thomas Delemontex [X] (Inactive) [04/Jul/19]

Ok so for this kind of reports the indexing is done by time/synapse_id. So when you call a .get you will have:

synapse id	(66446,307)	(66446,311)

time			
0.0		V1,1	V2,1
0.1		V 1,2	V2,2

To have the voltage as a function of time for one or multiple synapses just do:
rep.get_synapses([[(66446, 307), (66446, 311)])

If you do:

```
print(rep.get().columns)
```

you will have that:

```
levels=[[66446], [0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, ...]]
```

it means that you only have (66446, x) synapses in the report.

If I do :

```
rep.get().sort_index('columns').sum().sort_values()

66446  0      0.000000
       397    0.000000
       ......
       112    0.018801
```

only the 112 is firing which is what you expect I guess.

For your case where :

```
       65     0.013854
       63     0.017666
0      0      0.018801
66446  78     0.021558
       66     0.026596
0      0      0.046272
```

The left number is the post synaptic GID and right are the nrn offset.
The (66446, 78) (66446, 66) are synapses from Thalamocortical_input_VPM projection.
Others should be from the cortical only synapses (I guess).

Do you have only 0 0 or something else for cortico-cortical synapses ?

Comment by Thomas Delemontex [X] (Inactive) [04/Jul/19]

Yes ! I will have a look now

Comment by Oren Amsalem [04/Jul/19]

Hi Thomas Delemontex [X] did you get the permission?

Comment by Thomas Delemontex [X] (Inactive) [03/Jul/19]

Thx, It can take up to one day for the sync to be effective.
I will let you know when I have access.

Comment by Oren Amsalem [03/Jul/19]

Thomas Delemontex [X] I've just added you, thanks.

Comment by Thomas Delemontex [X] (Inactive) [03/Jul/19]

Hi Oren,
Can you add me to the proj2 group so I can have access to the report files ?

Comment by Oren Amsalem [03/Jul/19]

Giuseppe Chindemi [X]

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