

Wrapper for BluePyOpt

Liuyuan He

Run steps

- 1.Edit input files
- 2.Copy wrapper programs to server folder
- 3.Put files to server folder
- 4.Compile mod files
- 5.Run Programs

Edit input files

- Configure Files:
 - main configure file
 - morphology file
 - mechanisms file
 - protocols file
 - features file
 - parameters file
- mod files of ion channel mechanism

File Format of Configure Files

- JSON

- JSON 对象
- 对象可以包含多个名称/值对：
 - { "firstName":"John", "lastName":"Doe" }
- 与这条 JavaScript 语句等价：
 - firstName = "John"
 - lastName = "Doe"
- JSON 数组在方括号中书写：
- 数组可包含多个对象：
 - {
 - "employees": [
 - { "firstName":"John", "lastName":"Doe" },
 - { "firstName":"Anna", "lastName":"Smith" },
 - { "firstName":"Peter", "lastName":"Jones" }
 -]
 - }
- 在上面的例子中，对象 "employees" 是包含三个对象的数组。每个对象代表一条关于某人（有姓和名）的记录。
- see more: http://www.w3school.com.cn/json/json_intro.asp

Main Configure File

sample-configure.json

```
{  
  "cell": {  
    "name": "I5pc"  
  },  

```

```
  "input_file": {  
    "morphology": "morphology_sample.hoc",  
    "mechanisms": "sample-mechanisms.json",  
    "parameters": "sample-parameters.json",  
    "protocols": "sample-protocols.json",  
    "features": "sample-features.json"  
  },  

```

```
  "thresholds": {  
    "soma": -20,  
    "default": -55  
  },  

```

```
  "optimize": {  
    "pool": 24,  
    "offspring": 2,  
    "ngen": 2  
  },  

```

```
  "run": {  
    "best": 3  
  }  
}
```

other input files:

location of morphology file

location of mechanisms json file

location of parameters json file

location of protocols json file

location of features json file

spiking thresholds:

in soma

other

Genetic Algorithm optimization:

number of processes

number of offspring

number of generation

RUNNING

number of best results to display

Main Configure File

- other input files:
 - location must correct direction to files in server
- Spiking thresholds:
 - except 'default', other name of segments in that must be same as **name of segments** in **features json file**
 - value of 'default' is for value of segments if it not appears in other names
- Genetic Algorithm:
 - if value of 'pool' is larger than 'offspring', it run the same time as 'pool' is same as 'offspring'
 - Bigger 'pool' is better, but may need **≤ 200**

Morphology File

- File Format:
 - SWC
 - ASC
 - HOC

HOC Morphology File

morphology_sample.hoc

begintemplate Cell

objref all, basal, somatic, axonal, apical
objref this, CellRef

create soma[1]
public soma
create dendrite[1]
public dendrite

```
proc init() {  
  all = new SectionList()  
  somatic = new SectionList()  
  basal = new SectionList()  
  apical = new SectionList()  
  axonal = new SectionList()  
  forall delete_section()  
  CellRef = this  
}
```

```
{create soma[1]}  
{create dendrite[205]}
```

// section 3d definition

- **template_name**

- **SectionList**

- must be same in your hoc

- **Morphology**

- "SectionList name" ->
"Section Array name"

- "somatic" -> "soma"
- "basal" -> "dendrite"
- "apical" -> "apic"
- "axonal" -> "axon"

- must public your section array
- later is your pt3d & connect definition

HOC Morphology File

morphology_sample.hoc

```
// .... section 3d defination
```

```
soma all.append()  
for i=0, 204 dendrite[i] all.append()  
  
soma somatic.append()  
for i=0, 204 dendrite[i] basal.append()
```

```
}
```

```
proc destroy() {localobj nil  
  CellRef = nil  
}
```

```
endtemplate Cell
```

- Morphology

- **append** all sections to "all"(SectionList)
- **append** every type sections to own SectionList

- **proc destroy**

- must be same in your hoc

- **template_name**

Mechanisms JSON File

sample-mechanisms.json

```
{
  "somatic": [
    "na3",
    "kdr",
    "kap",
    "hd",
    "pas"
  ],
  "apical": [
    "na3",
    "kdr",
    "kap",
    "pas"
  ],
  "axonal": [
    "na3",
    "kdr",
    "kap",
    "pas"
  ],
  "basal": [
    "pas",
    "na3"
  ]
}
```

segment location

- "somatic": soma type in SWC (type value = 1)
- "apical": apical dendrite type in SWC (type value = 4)
- "axonal": axon type in SWC (type value = 2)
- "basal": dendrite type in SWC (type value = 3)

ion channels in those segments

see more in

- parameter json file
- mod file (same as **SUFFIX** in mod)

This file defines the mechanism in segments

```
{ segment-name:
  [have those channels],
}
```

Parameters JSON File

sample-parameters.json

```
[
  {
    "param_name": "celsius",
    "type": "global",
    "value": 22
  },
  {
    "param_name": "Ra",
    "type": "section",
    "location": "all",
    "value": 200
  },
  {
    "param_name": "ena",
    "type": "section",
    "location": "all",
    "value": 40
  },
  {
    "param_name": "gbar_na3",
    "location": "dendrite",
    "type": "range",
    "bounds": [
      0,
      0.5
    ]
  },
  {
    "param_name": "gbar_na3",
    "location": "somatic",
    "type": "range",
    "init": 0.05
  }
]
```

Parameter Type

- "global": Parameter set in the global namespace of NEURON, for example: celsius, v_init
- "section": Parameter of a section, for example: cm, Ra, ena, etc.
- "range": Parameter that has a range over a section for example: gbar_na3

Parameter Name

- must can be used in NEURON
- "gbar_na3":
 - "gbar": range name (RANGE in mod)
 - "na3": channel name (SUFFIX in mod)

rgc_na3n.mod

```
TITLE na3
: Na current
: modified from Jeff Magee. M.Migliore may97
: added sh to account for higher threshold M.Migliore, Apr.2002
```

```
NEURON {
```

```
  SUFFIX na3
```

```
  USEION na READ ena WRITE ina
```

```
  RANGE gbar, ar, sh
```

```
  GLOBAL minf, hinf, mtau, htau, sinf, taus,qinf, thinf
```

```
}
```

Parameters JSON File

sample-parameters.json

```
[
  {
    "param_name": "celsius",
    "type": "global",
    "value": 22
  },
  {
    "param_name": "Ra",
    "type": "section",
    "location": "all",
    "value": 200
  },
  {
    "param_name": "ena",
    "type": "section",
    "location": "all",
    "value": 40
  },
  {
    "param_name": "gbar_na3",
    "location": "dendrite",
    "type": "range",
    "bounds": [
      0,
      0.5
    ]
  },
  {
    "param_name": "gbar_na3",
    "location": "somatic",
    "type": "range",
    "init": 0.05
  }
]
```

Parameter (Section) Location

• "location"

- "somatic"; "basal"; "apical"; "axonal": same as segment location in mechanisms json file
- "dendrite" = "basal" + "apical"
- "all" = all sections, (**default** value)
- when type == "global", it's no need for "location"

Parameter (Fixed) Value

- please set "value" in lines

Parameter (Unfixed) Value

- "bounds": [lower_bound, upper_bound]
- "init": lower_bound = "init"/10., upper_bound = "init"*10
that = {"bounds": [0.005, 0.5]}

Parameters JSON File

- Parameters-file must **match** Mechanisms-file, for instance:
 - if type of parameter "gbar_na3" is "somatic"
 - "somatic" in mechanisms-file must have "na3"
 - otherwise this program will raise exception

Specific Global Parameters

- **dt**
 - The integration interval for fadvance ().
 - **default: 0.025 (ms)**
- **secondorder**
 - specifies the time integration method
 - **0: default** fully implicit backward euler.
 - **1: crank-nicholson** Can give large numerical error oscillations.
 - **2: crank-nicholson** like 1 but in addition Ion currents are fixed up so that they are second order correct when plotted at $t-dt/2$
- See more:
 - <http://www.neuron.yale.edu/neuron/static/docs/help/neuron/1nnr.html>

Protocols JSON File

sample-protocols.json

```
{
  "Step1": {
    "stimuli": [
      {
        "delay": 300,
        "amp": 0.04,
        "duration": 400,
        "totduration": 1000
      }
    ]
  },
  "Step2": {
    "stimuli": [
      {
        "delay": 300,
        "amp": 0.07,
        "duration": 400,
        "totduration": 1000
      }
    ]
  }
}
```

Stimulation Name

Stimulation information
(unit: neuron default)

- "delay": stimuli begin time (ms)
- "amp": stimuli current amp (nA)
- "duration": stimuli duration (ms)
- "totduration": total simulation time (ms)

Features JSON File

sample-features.json

```
{
  "Step1": {
    "soma": {
      "Spikecount": [
        3,
        0.01
      ],
      "time_to_first_spike": [
        100,
        10
      ]
    }
  },
  "Step2": {
    "soma": {
      "Spikecount": [
        6,
        0.01
      ]
    }
  }
}
```

Stimulation Name

Feature Location

- **now only somatic recording**
- **"soma" == "soma[0]"**
- **MUST BE "soma"**

Features

feature-name: [
 mean-value,
 standard-deviation
]

more features:

web:

<http://bluebrain.github.io/eFEL/eFeatures.html>

documents:

[\(attachments\) efeature-documentation.pdf](#)

Features JSON File

page from documents:

2.10 time to first spike

2 ELEMENTARY FEATURES

2.10 time to first spike

Time from the start of the stimulus to the maximum of the first peak

namespace / identifier	LibV1:time_to_first_spike
unit	ms
required features	peak time
required trace data	stim start
required parameters	none

```
pt0, ..., ptn-1 = peak.time
IF  $n < 1$  THEN
  FAIL "One spike required for time_to_first_spike."
ENDIF
APPEND pt0 - stim_start TO time_to_first_spike
```

"param_name":
"time_to_first_spike",

pseudocode

Mod Files of NEURON Mechanisms

- *.mod file for every mechanisms
- Must make sure name of mechanisms are correct
- Must make sure parameter names are correct

RUN

- **(ssh)**

- ` [redacted] /neuron/nrn/x86_64/bin/nrnivmodl
*.mod`

- **NOW**

≤ 24

[redacted] python27/bin/python
wrapper.py sample-configure.json

[sample-configure.json] is the main configure file

Results

No.3

param_name.location

```
BEST      Parameter      Value:
3         gbar_na3.dendrite    0.381887
3         gbar_na3.somatic     0.131259
BEST      Feature Name    Fitness value:
3         Step2.soma.Spikecount 600.000000
3         Step1.soma.Spikecount 300.000000
3         Step1.soma.time_to_first_spike 250.000000
```

protocol_name.recording_location.feature_name

Less is Better

Running Log

Genetic Algorithm Log

generation	number of offsprings	fitness value mean	fitness value std	fitness value min	fitness value max
Optimize Log					
gen	nevals	avg	std	min	max
1	2	1150	0	1150	1150
2	2	1150	0	1150	1150

Running Time

```
BEGIN: 2016-08-23 19:51:37.289727
END: 2016-08-23 19:51:46.590388
TOTAL TIME: 0:00:09.300661
```