OSB Automated Model Validation

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Status

Note: this table is still in development!

These status values are currently based on a manual curation process, scoring the models on the completeness of the translation of the model from the original format to NeuroML (or PyNN).

For simulators, the score represents how well the model translates to the specific simulator from the simulator independent format, NOT the availability of original scripts in that simulator.

| | Curation | NeuroML v1.x | NeuroML v2.x | PyNN | NEURON | GENESIS 2 | MOOSE | PSICS | NEST | Brian | OSB Model Validation |
|-----------------------------------------------|----------|-----------------|-----------------|------|-------------|--------------|-------|-------|------|------------|----------------------------|
| vogelsetal2011 | ** | | 0 | (XX) | CITA | | | | • | • | |
| blender-to-neuroml | * | | (11) | | | | | | | | |
| osa bluehive-showcase | | | • | | | | | | | | |
| osb brianshowcase | - | | • | • | | | | | | (### | |
| OSB nc_ca1 | * | • | 0 | | • | 0 | 0 | 0 | | | |
| User nc_superdeep | | 0 | 0 | | 0 | 0 | 0 | | | | |
| osb catmaidshowcase | * | | 612 | | | | | | | | |
| osb cnoshowcase | ** | | | | | | | | | | |
| osb dbdflymodel | | 0 | 0 | | | | | | | | |
| OSB dentategyrus2005 | * | • | 0 | | 611 | • | • | | | | |
| OSB dentate | * | • | 0 | | • | 0 | 0 | | | | |
| oss drosophila-acc-l3-motoneuron-gunay-et-al- | * | • | • | | • | 0 | 0 | | | | |
| osB fitzhugh-nagumo-fitzhugh-1969 | * | | • | | • | | | | | 633 | build passing |
| OSB fpgashowcase | | 0 | 0 | | | | | | | | build passing |

- Manual curation / Subjective star rating
- Some form of "quality control" for OSB models
- Concrete example: how accurate are NeuroML translations?
- ► The danger of blindly using software



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Retraction

We wish to retract our research article "structure of MsbA from E. coli: A homolog of the multidrug resistance ATP binding cassette (ABC) transporters" and both of our Reports "Structure of the ABC transporter MsbA in complex with ADP-vanadate and lipopolysaccharide" and "X-ray structure of the EmrE multidrug transporter in complex with a substrate" (1-3).

The recently reported structure of Say1866 (4) indicated that our MsbA structures (1, 2, 5) were incorrect in both the hand of the structure and the topology. Thus, our biological interpretations based on these inverted models for MsbA are invalid.

An in-house data reduction program introduced a change in sign for anomalous differences. This program, which was not part of a conventional data processing package, converted the anomalous pairs (I+ and I-) to (F- and F+), thereby introducing a sign change. As the diffraction data collected for each set of MsbA crystals and for the EmrE crystals were processed with the same program, the structures reported in (1-3, 5, 6) had the wrong hand.

The error in the topology of the original MsbA structure was a consequence of the low resolution of the data as well as breaks in the electron density for the connecting loop regions. Unfortunately, the use of the multicopy refinement procedure still allowed us to obtain reasonable refinement values for the wrong structures.

OSB projects are dynamic

- Does a new model version behave as "expected"?
- Back our claims: does the code really produce figure 7?
- ▶ Will the model behave the same in different environments?
 - ▶ tabula rasa environment for testing
 - (another approach: Andrew Davison's sumatra)



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Zeroth order validation:

- Is the model doing what we claim it to do?
- Sanity checking
 - activation variables, concentrations, temperatures....
- ▶ Are different implementations producing the same results?
- Comparing distinct models is a "higher order" goal
 - Richard Gerkin's neurounit / sciunit



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Guidelines

- ▶ Simple to use and setup. Declarative format, no logic
- Automated testing for new commits (continuous integration)
- Extensible (adding new tests/backends)



How does it look like

proof-of-concept implementation! expect changes!

- https://github.com/borismarin/hh-testing
- https://travis-ci.org/borismarin/hh-testing



How to enable it for a project

1. Dry-run test file (*omt* extension)

engine: NEURON

target: NEURON/script.hoc

2. Add our .travis.yaml file to the repo

OR

- 1. Install our python package
- 2. Follow the wizard: omv_autogen



Model Emergent Properties [mep] files

```
system: Classical HH model
experiments:
  experiment 1, autonomous activity:
    expected:
    resting: -64.9
    morphology:
    total area: 157080
    number of cells: 1
    temperature: 6.3
```

- We need to specify our expectations
- Information that comes from the model after computations
- Can be used to generate visual summary



OSB Model **T**est

```
target: hhnostim.hoc
engine: NEURON
implements:
 mep: ../hh.mep
  experiment: experiment 1, autonomous activity
  observables:
    resting:
      file:
        path: /tmp/nrnhhnostim.dat
        columns: [0,1]
        average last: 100
      tolerance: 1e-2
    morphology:
      base section: soma
```

- ► Given a *mep* file, specify mappings to implementation
 - how to "run"
 - how/where info is stored



- More tests!
 - ▶ BTW, what should we test for?
- ▶ More backends!
- ► Coupling to NeuroML exporters:
 - "download as..." available if test passes
- ▶ Unit handling



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