

# Semi-declarative model specification in Python

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# Declarative model specifications

NeuroML, NineML, and similar initiatives allow (XML-based) declarative specifications for models:

“there exists an  $X$  of type  $Y$  with parameters  $P_1, P_2, \dots, P_n$ ” (Goddard et al. 2001)

The obvious converse of a declarative specification is imperative computer code:

```
do A; do B; do C
```

(either domain-specific (hoc, SLI, etc.) or domain-general (Matlab, C++))

# Declarative == good

Declarative specifications are extremely important for:

**Sharing:** Same model running on different simulators

**Comparing:** How do these models differ?

**Maintaining:** Extend/fix/improve code, same spec

**Evolving:** Simple declarative specs can cover a wide range of different models using same codebase

**Communicating:** What is this model, in terms of building blocks we already know about?

“there exists an X of type Y with parameters P1, P2, ... Pn”

# So, everyone's models are always declarative, right?

Well...

Why not?

- Models are actually made of code; new models (usually? often?) need new code.
- Very often you want to mess with the existing code a bit, try out some new ideas, etc.
- Fully declarative specifications can be extremely verbose – no problem for an XML parser, but no good for people.
- Sometimes (**only sometimes!**) code is just clearer.

# Alternative approach

*One approach to meeting these requirements would be to use any common object-oriented programming language (interpreted or compiled) augmented by an extensive set of object classes which provide the high-level constructs. These classes would thereby extend the base language to turn it into a particular set of language elements. The clarity requirement suggests that a simple interpreted language (e.g. Python) would be more appropriate than a compiled language such as C++ or Java. But...*

— Goddard et al. (2001)

# Python code as (semi-) declarative specification

**text:** *there exists an X of type Y with parameters P1, P2, ... Pn*

**XML:** `<Y name="X" P1="2.6" P2="true" P3="Z">`

**Python:** `Y(name="X", P1=2.6, P2=True, P3="Z")`

I.e., Python can be used as a declarative specification by instantiating an object of class Y with attributes P1, P2, ...

OK, but...

# code == bad, right?

Right:

- Code can freely mix imperative and declarative bits
- Imperative bits get hard to understand, compare, etc.
- Cannot generate XML version for arbitrary code
- External parser needs to be very elaborate to parse all of Python

Can we ensure that code is (mostly) declarative, getting some or all of the advantages without the limitations?

# Use Parameters

Python attributes are poor substitutes for declarative parameters in XML, with no:

- types, • descriptions,
- range checking, • units, • dynamic values
- inheritance • automatic extraction . . .

. . . unless you use Python **Parameters** ([topographica.org](http://topographica.org)) or **Traits** ([enthought.org](http://enthought.org)).

Python+Parameters allows fully declarative specifications (in principle with output to XML), imperative specifications, and anything in between – allows smooth transition to declarative spec as model matures, with benefits from every step.



# Code without full Parameters

```
class Connector(object):  
  
    def __init__(self, weights=0.0, delays=None,  
                 space=Space(), safe=True,  
                 verbose=False):  
        self.weights = weights  
        self.space    = space  
        self.safe     = safe  
        self.verbose  = verbose  
        ... self.delays ...
```

**From the 15 Mar 2012 version of PyNN**

**<https://neuralensemble.org/svn/PyNN/trunk/src/connectors.py>**

```
class AllToAllConnector(Connector):
    parameter_names = ('allow_self_connections',)

    def __init__(self, allow_self_connections=True,
                 weights=0.0, delays=None, space=Space(),
                 safe=True, verbose=False):
        """
        Create a new connector.

        `allow_self_connections` -- if the connector is ...
        `weights` -- may either be a float, a
                    RandomDistribution object, a list/...
        `delays` -- as `weights`. If `None`, all synaptic
                    delays will be set to the global...
        `space` -- a `Space` object, needed if you wish to
                    specify distance-dependent...

        """
        Connector.__init__(self, weights, delays, space,
                           safe, verbose)
        assert isinstance(allow_self_connections, bool)
        self.allow_self_connections = allow_self_connections
```

```

class FixedProbabilityConnector(Connector):
    parameter_names = ('allow_self_connections', 'p_connect'

def __init__(self, p_connect, allow_self_connections=True,
              weights=0.0, delays=None, space=Space(),
              safe=True, verbose=False):
    """
    Create a new connector.
    `p_connect` -- a float between zero and one. Each ...
    `allow_self_connections` -- if the connector is ...
    `weights` -- may either be a float, a
                  RandomDistribution object, a list/...
    `delays` -- as `weights`. If `None`, all synaptic
                delays will be set to the global...
    `space` -- a `Space` object, needed if you wish to
                specify distance-dependent...
    """
    Connector.__init__(self, weights, delays, space,
                      safe, verbose)
    assert isinstance(allow_self_connections, bool)
    self.allow_self_connections = allow_self_connections
    self.p_connect = float(p_connect)
    assert 0 <= self.p_connect

```

# Code with Parameters

```
class Connector(param.Parameterized):
    weights = param.Parameter(0.0, doc="""
        May either be a float, a RandomDistribution...
    """)
    delays = param.Parameter(None, doc="""
        May either be a float, a RandomDistribution...
    """)
    space = param.ObjectSelector(Space(), class_=Space,
        doc="""Allows you to specify distance-...
    """)
    safe = param.Boolean(True)
    verbose = param.Boolean(False)
    def __init__(self, **params): ... self.delays ...

class ProbabilisticConnector(Connector):
    allow_self_connections = param.Boolean(True, doc="""
        If the connector is used to connect...
    """)

class AllToAllConnector(ProbabilisticConnector):...

class FixedProbabilityConnector(ProbabilisticConnector):
    p_connect = param.Number(0.5, bounds=(0, 1), doc="""
        Probability with which each potential...
    """)
```

# Parameters: Declarative *code*

- Ranges, types, etc. declared, not imperatively checked
- Much less duplication – most param specs inherited
- Much less code: no checking code (assertions), usually no `__init__` needed
- Makes assumptions explicit
- Type, default value, doc, range specified together – always match
- Rest of code never needs to check any of these
- Automatic help, generated documentation
- Yet Parameters are just Python attributes – rest of your code can stay the same

# Provides a clear path to declarative model

- Model specification file can be purely declarative
- Or semi-declarative (add `for` loops and variables for repetitive structure)
- Or imperative (full Python code all over the place)

But at least in the first two cases it is easy to iterate over a bunch of nested Parameterized objects after instantiation and spit out matching purely declarative XML, Python code, JSON, neuroTools ParameterSets – whatever you like.

# Summary

- Declarative specification is such a good idea it should be applied to code too
- Declarative model spec then almost comes for free
- Parameters is a completely general (not even science specific) pure-Python module for declarative code, with no external dependencies.

- Documentation:

[http://topographica.org/Reference\\_Manual/param-module.html](http://topographica.org/Reference_Manual/param-module.html)

- Download (until we build a separate package):

`svn co https://topographica.svn.sf.net/svnroot/topographica/trunk/topographica/param`

- Traits package almost identical except for GUI packages supported

# References

Goddard, N. H., Hucka, M., Howell, F., Cornelis, H., Shankar, K., & Beeman, D. (2001). Towards NeuroML: Model description methods for collaborative modelling in neuroscience. *Philosophical Transactions: Biological Sciences*, 356 (1412), 1209–1228.