1 Multiscale modelling

```
Program structure is following.
```

```
 \begin{array}{l} \langle \ ^{*} \rangle \equiv \\ \langle Import \rangle \\ \langle main.py \rangle \end{array}
```

Dependencies and import We need lxml.etree for XML parsing. To print error and warning messages, I wrote a small module DebugModule by myself. This module is in file debug.nw. We'd be needing these modules in almost every python file. Lets keep them in one chunck Import.

Imports Lets just import the minimal required. We'll try import cElement tree first and then some other implementation of etree. Then we'll add a command line parser to get filepaths of XML. And why not, let parse these models too.

2 Parser

Let's include the parser here.

elemDict = dict()

3 XML parser

This document deals with parser of XML models.

```
(parser.py)
import debug
import os

def getModels(models) :

"""

Parses given xml models. We can pass either one or two models; one described
in neuroML and the other in sbml.

Notes: Document is properly. See

http://www.biomedcentral.com/1752-0509/7/88/abstract

sent by Aditya Girla. It a online composition tool for SBML. In its
references, some other tools are mentioned.

Args :

Raises :

Return
return a list of elementTree of given models.

"""
```

```
if models.nml :
    # Get the schema
    with open(models.nml, "r") as nmlFile :
        elemDict['nml'] = models.nml

if models.sbml :
    elemDict['sbml'] = models.sbml
return elemDict
```

 ${\bf Parse~xml~~Let's~write~a~function~to~parse~xml~and~return~the~root~element}.$

```
\langle parser.py \rangle + \equiv def parseModel(modelPath): if not os.path.exists(modelPath): pass
```

```
Print debugging messages
   Different type of messages are printed in different colors.
\langle debuq.py \rangle \equiv
  HEADER = '\033[95m'
  OKBLUE = '\033[94m']
  OKGREEN = '\033[92m'
  WARNING = '\033[93m'
  ERR = '\033[91m']
  ENDC = '\033[Om'
  RED = ERR
  WARN = WARNING
  INFO = OKGREEN
  TODO = OKBLUE
  DEBUG = HEADER
  prefix = dict(
      ERR = ERR
       , WARN = WARN
       , FATAL = ERR
      , INFO = INFO
       , TODO = TODO
       , NOTE = HEADER
       , DEBUG = DEBUG
       )
  def colored(msg, label) :
      Return a colored string. Formatting is optional.
      global prefix
       if label in prefix :
           color = prefix[label]
       else :
           color = ""
      return "[{0}] {1} {2}".format(label, color+msg, ENDC)
  def printDebug(label, msg):
      print(colored(msg, label))
\langle main.py \rangle \equiv
  \langle Import \rangle
  \langle functions \ in \ main \rangle
  \langle argument \ parser \rangle
  \langle parse\ models \rangle
```

We prefer cElementTree for its speed. If it is not available then go for something else. $\langle Import \rangle \equiv$ import logging import debug logger = logging.getLogger('multiscale') try: import cElementTree as etree debug.printDebug("DEBUG", "running with lxml.etree") except ImportError: try: # Python 2.5 import xml.etree.cElementTree as etree debug.printDebug("DEBUG", "running with cElementTree") except ImportError: try: # Python 2.5 import xml.etree.cElementTree as etree debug.printDebug("DEBUG", "running with ElementTree") except ImportError: try: # normal cElementTree install import cElementTree as etree debug.printDebug("DEBUG", "running with cElementTree") except ImportError: try: # normal ElementTree install import elementtree.ElementTree as etree debug.printDebug("DEBUG", "running with ElementTree") except ImportError: try: import lxml.etree as etree except ImportError : debug.prefix("FATAL", "Failed to import ElementTree")

os._exit(1)

Agrument parser Paths of models files are to be passed from the command line. More than one xml file can be passed. We use **argparse** library to build a command-line interface.

```
(argument parser) =
  import argparse

# This section build the command line parser
  argParser = argparse.ArgumentParser(description= 'Mutiscale modelling of neurons')
  argParser.add_argument('--nml', metavar='nmlpath'
       , help = 'File having neuron described in neuroML'
    )
  argParser.add_argument('--sbml', metavar='sbmlpath'
       , help = 'File having neuron described in SBML'
       , required = False
    )
  args = argParser.parse_args()
```

Parse xml models We pass two kind of models from command line to this application, sbml and neuroML. Parse them and we'll think of next step. We need at least one model to start with (neuroML?).

But before we parse, we need a helper function to check if given paths are correct.

```
def ifPathsAreValid(paths) :
    ''' Verify if path exists and are valid. '''
    if paths.nml :
        if os.path.isfile(paths.nml) : pass
        else :
            debug.printDebug("ERROR", "Filepath {0} is not valid".format(paths.nml))
            return False
    if paths.sbml :
        if os.path.isfile(paths.sbml) : pass
        else :
            debug.printDebug("ERROR", "Filepath {0} is not valid".format(paths.sbml))
            return False
    return True
```

```
Parse xml files.
\langle parse\ models \rangle \equiv
 # There must be at least one model present
 import parser
 if args.nml or args.sbml :
   if ifPathsAreValid(args) :
      logger.info("Started parsing XML models")
      debug.printDebug("INFO", "Started parsing XML models")
     etreeList = parser.parseModels(args)
   else :
      debug.printDebug("FATAL", "One or more model file does not exists.")
      sys.exit()
 else :
   debug.printDebug("FATAL", "Please provide at least one model. None given.")
   sys.exit()
 debug.printDebug("INFO", "Parsing of models is done")
```