

A CmePy Tutorial

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1 Overview

CmePy computes numerical solutions of the Chemical Master Equation (CME).

CmePy is a Python package, employing the SciPy and NumPy packages.

2 Installation

2.1 Dependencies

CmePy was developed with Python 2.5.2, SciPy 0.7.0, & NumPy 1.2.1 . In addition, matplotlib is used to display graphical output in some examples, but is not otherwise a dependency.

2.2 Testing & Installation

Once CmePy has been obtained, the package can be tested and installed by running the `setup.py` script via Python as follows:

```
python setup.py test
python setup.py install
```

2.2.1 Local package installation (Linux)

If it is not possible to install CmePy to the Python's global `site-packages` directory, CmePy may be installed locally to a user's `${HOME}` directory. First, ensure the path `${HOME}/lib/python` exists, and that the `${PYTHONPATH}` environment variable includes `${HOME}/lib/python`. Then, CmePy may be installed locally via

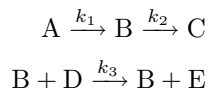
```
python setup.py install --home=${HOME}
```

A (possibly better) alternative to this method of local installation is to use the `virtualenv` package to establish isolated (local) Python environments. See <http://pypi.python.org/pypi/virtualenv>.

3 Tutorial: Catalytic Reaction

3.1 Introducing a Catalytic Reaction example

Consider the following example of a ‘catalytic reaction’ system, modified slightly from [MHR07]:



The rate constants are $k_1 = 1$, $k_2 = 1000$ and $k_3 = 100$, while the initial copy counts are 15 copies of the species A, 20 copies of D, and 0 copies of both B and C.

3.2 Solving the CME for the Catalytic Reaction with CmePy

Suppose we wish to solve the Chemical Master Equation for this catalytic reaction model, and determine the expected copy count of the species E at the time $t = 0.5$. Using **CmePy**, an *almost* complete script to perform this task is the following:

```
import numpy
import cme.py.recorder
import cme.py.solver

def create_catalytic_model():
    """
    creates a model for the catalytic reaction example
    """
    pass # TODO CREATE MODEL HERE

m = create_catalytic_model()
solver = cme.py.solver.create(
    model = m,
    sink = False
)

recorder = cme.py.recorder.create(
    (m.species, m.species_counts)
)

time_steps = numpy.linspace(0.0, 0.5, 101)
for t in time_steps:
    solver.step(t)
    recorder.write(t, solver.y)

e_ev = recorder['E'].expected_value[-1]
print 'expected copy count of species E at final time: %g' % e_ev
```

1. The model `m`, as returned by the `create_catalytic_model()` function, defines the system of reactions for this ‘catalytic reaction’ example. We will define this function during the next section.
2. The `solver` object:
 - is initialised via `cme.py.solver.create`, passing the model `m` as an argument. Setting the flag `sink` to `False` indicates that the state space of the model is complete – no states are missing – so a ‘sink’ state to track lost probability is unnecessary;
 - can be advanced to the time `t` by `solver.step(t)`;
 - computes `solver.y`, the solution to the Chemical Master Equation for the given model.

3. The `recorder` object is used to store the solutions produced by the `solver` object, and then compute derived statistics:

- the `recorder` is initialised with information about the species involved in the catalytic reaction contained in the model `m`;
- the solution `solver.y` of the Chemical Master Equation is stored inside the `recorder` via `recorder.write(t, solver.y)` after each time step;
- when all the time steps are complete, the most recently recorded expected value of the copy count of the species E is computed via `recorder['E'].expected_value[-1]`.

3.3 Defining the Catalytic Reaction model

3.3.1 Defining the state space initial state and shape

We shall use a reaction count state space for this model. We represent states as triples of non-negative integers, and shall use the variable `x` to denote an arbitrary state. Let `x[0]`, `x[1]` and `x[2]` denote the counts of the first, second, and third reactions, respectively.

We define the initial state and the shape of the state space:

```
a_initial = 15
d_initial = 20

initial_state = (0, )*3
shape = (a_initial + 1, )*2 + (d_initial + 1, )
```

Observe how we have defined the initial state of the system as `(0,)*3`, that is, `(0, 0, 0)`, where the count of all three reactions is zero. The shape of the state space is defined as `shape`, with the value `(a_initial + 1,)*2 + (d_initial + 1,)`. This specifies that the first two reaction counts range over `0, 1, ..., a_initial`, while the third reaction count ranges over `0, 1, ..., d_initial`.

By default, the state space $\Omega \subset \mathbf{N}^d$ is defined from the `shape` variable $(s_0, \dots, s_{d-1}) \in \mathbf{N}^d$ to be a dense ‘rectangular’ lattice of integer points, that is,

$$\Omega = \{(x_0, \dots, x_{d-1}) : x_i \in \mathbf{N}, 0 \leq x_i < s_i \text{ for all } i = 0, \dots, d-1\}.$$

In our case, this means that the state space will contain $(a_initial + 1)^2(d_initial + 1) = 16^2 \cdot 21$ distinct states. This state space is actually quite wasteful, as states with $x_1 > x_0$ are not reachable using this catalytic reaction model. XXX TODO more on that later

3.3.2 Defining the species counts and names

We must define the species count functions. The i -th species count function maps a reaction count state `x` to the copy count of the i -th species. We define functions `s_1`, `s_2`, `s_3`, `s_4` and `s_5` to give the copy counts of the species A, `...`, E as follows:

```
s_1 = lambda *x : a_initial - x[0]
s_2 = lambda *x : x[0] - x[1]
s_3 = lambda *x : x[1]
s_4 = lambda *x : d_initial - x[2]
s_5 = lambda *x : x[2]

species = ('A', 'B', 'C', 'D', 'E')
species_counts = (s_1, s_2, s_3, s_4, s_5)
```

Note how we have placed the species count functions inside the tuple `species_counts`, and defined a second tuple, `species`, containing the corresponding species names.

3.3.3 Defining the reaction propensities, transitions, and names

We define each reaction in the system by providing a name, a propensity function, and a state transition:

```
reactions = ('A->B', 'B->C', 'B+D->B+E')

propensities = (
    lambda *x : 1.0 * s_1(*x),
    lambda *x : 1000.0 * s_2(*x),
    lambda *x : 100.0 * s_4(*x) * s_2(*x)
)

transitions = ((1, 0, 0), (0, 1, 0), (0, 0, 1))
```

For example, these definitions specify that the third reaction has the name 'B+D->B+E', occurs with a propensity equal to 100 times the product of the species counts of the second (B) and fourth (D) species for the current state x , and corresponds to a transition from the state $(x[0], x[1], x[2])$ to the state $(x[0], x[1], x[2] + 1)$.

3.3.4 The complete model definition

We may combine the above definitions into one complete model definition for this catalytic reaction example, use it to fill out the body of the function `create_catalytic_model()` from the initial script:

```
def create_catalytic_model():
    """
    creates a model for the catalytic reaction example
    """
    import cmepy.model

    a_initial = 15
    d_initial = 20

    s_1 = lambda *x : a_initial - x[0]
    s_2 = lambda *x : x[0] - x[1]
    s_3 = lambda *x : x[1]
    s_4 = lambda *x : d_initial - x[2]
    s_5 = lambda *x : x[2]

    return cmepy.model.create(
        name = 'catalytic reaction',
        initial_state = (0, ) * 3,
        shape = (a_initial + 1, ) * 2 + (d_initial + 1, ),
        species = ('A', 'B', 'C', 'D', 'E'),
        species_counts = (s_1, s_2, s_3, s_4, s_5),
        reactions = ('A->B', 'B->C', 'B+D->B+E'),
        propensities = (
            lambda *x : 1.0 * s_1(*x),
            lambda *x : 1000.0 * s_2(*x),
            lambda *x : 100.0 * s_4(*x) * s_2(*x)
        ),
        transitions = ((1, 0, 0), (0, 1, 0), (0, 0, 1))
    )
```

References

- [MHR07] E.A. Mastny, E.L. Haseltine, and J.B. Rawlings. Two classes of quasi-steady-state model reductions for stochastic kinetics. *The Journal of Chemical Physics*, 127:094106, 2007.