Models and Languages for Computational Systems Biology

Ian Stark

School of Informatics
The University of Edinburgh

MLCSB runs in Semester 2, starting January 2010
Timing: MLCSB runs during Semester 2, starting January 2009

Lecturer: Ian Stark

Bioinformatics, Systems & Synthetic Biology

*Computational Systems Biology* (Semester 2)
*Synthetic Biology: Modelling* (Semester 1)

Theoretical Computer Science

*Communication and Concurrency* (Semester 1)
*Performance Modelling* (Semester 1)

Course web page: http://www.inf.ed.ac.uk/teaching/courses/mlcsb/
Biology is the study of living organisms; Systems Biology is the study of the dynamic processes that take place within those organisms.

In particular:

- Interaction between processes;
- Behaviour emerging from such interaction; and
- Integration of component behaviours.
Biology is the study of living organisms; Systems Biology is the study of the dynamic processes that take place within those organisms.
Scope of Study

Processes

- Metabolic networks
- Regulatory systems: promotion, inhibition
- Signalling pathways
- Gene expression: translation, transcription

Models

- Discrete time, continuous time
- Discrete space, continuous space
- Deterministic, nondeterministic, probabilistic
- Qualitative, quantitative
This course explores a variety of mathematical models for biological pathways, and introduces formally precise languages to describe and reason about biological processes.

- **Petri Nets**: Dynamic system behaviour; analysis of network properties.
- **Temporal Logics**: Linear time and branching time; model checking.
- **Markov Systems**: Probabilistic behaviour in continuous time.
- **Stochastic Simulation**: Gillespie algorithm; reaction kinetics.
- **Qualitative vs. Quantitative Analyses**: Differential equations.
- **Biological Process Algebras**: Modularity and compositional reasoning.
Example: Petri Nets

http://genome.ib.sci.yamaguchi-u.ac.jp/~pnp/
Example: BioPEPA

Biochemical networks (SBML, KEGG, ...) → Bio-PEPA systems

- ODEs
- Stochastic simulation (Gillespie's algorithm)
- CTMC with levels
- PRISM (model checking)

http://biopepa.org/
Example Process: Enzyme Catalysis

\[ S = s(x, y). (x.S + y.(P|P')) \]
\[ E = \nu M.e\langle u, r\rangle.t.E \]
\[ P = P' = \tau@k_{\text{degrade}}.0 \]
\[ c_S \cdot S \parallel c_E \cdot E \]
Example Process: Enzyme Catalysis

\[
S = s(x, y).(x.S + y.(P|P'))
\]

\[
E = \nu M.e\langle u, r \rangle.t.E
\]

\[
P = P' = \tau@k_{\text{degrade}}.0
\]

\[
c_S \cdot S \parallel c_E \cdot E
\]

```
enzyme.cpi
...

species E() = {
    site t, u, r;
...
```
Example Process: Enzyme Catalysis

\[ S = s(x, y).(x.S + y.(P|P')) \]
\[ E = \nu M.e\langle u, r\rangle.t.E \]
\[ P = P' = \tau@k_{degrade}\cdot 0 \]
\[ c_S \cdot S \parallel c_E \cdot E \]

Cpi tool

```
enzyme.cpi
...
species E() = {
    site t, u, r;
...
```

ODEs

\[ x'_2 = -k_1x_4x_2 + \ldots \]
\[ : \]
Example Process: Enzyme Catalysis

\[ S = s(x, y). (x.S + y.(P|P')) \]
\[ E = \nu M.e(\langle u, r \rangle).t.E \]
\[ P = P' = \tau@k_{\text{degrade}}.0 \]
\[ c_S \cdot S \parallel c_E \cdot E \]

enzyme.cpi
...

species E() = {
  site t, u, r;
  ...
}

Cpi tool

Octave

ODEs
\[ x_2' = -k_1x_4x_2 + \ldots \]
\[ : \]
Vital Statistics

Timing: MLCSB runs during Semester 2, starting January 2009

Lecturer: Ian Stark

Bioinformatics, Systems & Synthetic Biology

*Computational Systems Biology* (Semester 2)
*Synthetic Biology: Modelling* (Semester 1)

Theoretical Computer Science

*Communication and Concurrency* (Semester 1)
*Performance Modelling* (Semester 1)

Course web page: http://www.inf.ed.ac.uk/teaching/courses/mlcsb/