Tools and Techniques for Discrete Systems Analysis

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C.elegans Modelling Workshop Cambridge, 2008-07-07

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Engineering Method



Direct Engineering

Scientific Method



Reverse Engineering









2008-07-08



The Program and the State Space

The "program":



Finite



Potentially infinite

Chemistry vs. Process Algebra



These diagrams commute via appropriate maps.

L. Cardelli: "On Process Rate Semantics" (TCS)

L. Cardelli: "A Process Algebra Master Equation" (QEST'07)

Simulation

- Run "the program" through a walk in states space.
- Basic stochastic algorithm: Gillespie
 - Exact (i.e. based on physics) stochastic simulation of chemical kinetics.
 - Can compute concentrations and reaction times for biochemical networks.
- Stochastic Process Calculi
 - Now may [BioSPi, SPiM, BioPEPA, BetaBinders, ...]
- Hybrid approaches
 - Continuous + discrete/stochastic switching



Control Flow Analysis

- Who called who?
 - Overapproximation of behavior used to answer questions about what "cannot happen".

What event may (or may not) have been involved in reaching this state?



Causality Analysis

- What event caused what other event or state to happen?
- Need a different level of representation (the "event space")
 - Petri Nets
 - Event Structures



What event "caused"



Abstract Interpretation

• Precisely relating abstract views to more concrete views of the system



Modelchecking

- Asking questions (in Temporal Logic) about structure of a (finite) state space.
- Various flavors of modelchecking:
 - Temporal
 - About paths through state space
 - Quantitative
 - About quantitative measures of states
 - Probabilistyc/Stochastic
 - About probabilities of reaching states.

Is this state a necessary checkpoint to reach this state?

Model Maintenance

- Biology (unlike much of chemistry) is combinatorial
 - Biochemical systems have many regular repeated components
 - Components interact and combine in complex combinatorial ways
 - Components have local state
 - A biochemical system is vastly more compact that its potential state space
- One may expand the state space during analysis, but must not do it during description
- There is a good way:
 - Describe biochemical systems compositionally
 - Each component with its own state and interactions
 - ... as Nature intended...







Or ...

Conclusions

- Connections between modeling approaches
 - Connecting the discrete/concurrent/stochastic/molecular approach
 - to the continuous/sequential/deterministic/population approach
- Connecting syntax with semantics
 - Syntax = model presentation (equations/programs/diagrams/blobs etc.)
 - Semantics = state space (generated by the syntax)
- Ultimately, connections between analysis techniques
 - We need (and sometimes have) good semantic techniques to analyze state spaces (e.g. calculus, but also increasingly modelchecking)
 - But we need equally good syntactic techniques to structure complex models (e.g. compositionality) and analyze them