Immune System Modeling and Analysis using Bio-PEPA

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Objectives

Analyze the response of the immune system against virus attacks

Membrane computing patterns
 Bio-PEPA

Identify formal conditions for successful immune responses against virus attacks

□ identified and expressed based on Bio-PEPA functional rates

Immune system



Membrane computing

Membrane structure



Bio-PEPA (1)

- Process algebra framework
- Model and analyze the biochemical networks
- Improvement of PEPA

□ Performance analysis of computer systems

Bio-PEPA (2)



Bio-PEPA (3)

General form of an irreversible reaction j



- A_{hj} = reactants
- B_{ij} = products
- E_{vj} = enzymes
- I_{uj} = the inhibitors of the reaction
- k_{hj} and k'_{lj} = stoichiometric coefficients

Bio-PEPA (4)

Bio-PEPA Model

formal and compositional representation of a biological system

□ allows the execution of a series of analyzes

Bio-PEPA Eclipse Plug-in ASCII representation of BIO-PEPA symbols

Immune System Modeling (1)

Immune system model architecture



Immune System Modeling (2)

Virus replication and propagation processes



Immune System Modeling (3)

Virus neutralization process



Experimental results (1)

- Immune System Analysis using Bio-PEPA
 - Stochastic
 - ODE

Experimental results (2)

Stochastic simulation of the successful Bio-PEPA immune response model



ODE simulation of the successful Bio-PEPA immune response model



Experimental results (3)

- Formal conditions for successful immune responses against virus attacks
- Sufficient condition for the system state to be "clean"
 M > 2D

Necessary condition for the system state to be "clean"
 n (t) = n (t-P) + n (t-M) (2)

Future work

Java parallel implementation of the immune system model
 Map each membrane on a core of a multicore computer
 Validate the stochastic and ODE simulations

Investigate the semantics of Bio-PEPA
 operational and denotational semantics
 continuations semantics for concurrency

Conclusions (1)

- Strategy of modeling and analyzing the behavior of the immune system against virus attacks
- Membrane computing patterns
- Bio-PEPA process algebra

Conclusions (2)

The effectiveness of modeling biochemical networks can be significantly improved by providing an intermediate, formal compositional representation of the model on which different kinds of analysis can be carried out