

FORMALIZING THE LOW-DENSITY LIPOPROTEIN DEGRADATION

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*Dedicated to the 85th anniversary
of Professor Solomon Marcus*

The biological degradation of low-density lipoprotein is described using a rule-based formalism involving explicit resources, parallelism and mobility. Turing completeness of this formalism is proved by using matrix grammars.

1. Introduction

Systems biology is an emerging field which arises from the interaction of biology, mathematics and computer science. In order to cope with ensembles and quantities in biology, new approaches using mathematics and software tools are required. The biologists increasingly recognize that computational methods became powerful enough to model the complexity of biological entities and systems. In this sense, “mathematics is biology's next microscope, only better” [6]. In biology, new ensemble behaviours emerge from the interactions of biological elements, and new formalisms are required to cope with these properties. In this sense, “biology is mathematics' next physics, only better”[6].

Formal models are used for many purposes, and the purpose influences the degree of system detail that is represented. If we provide greater detail, the number of systems to which our model applies will decrease. A model should usually have three properties, and each of these properties trades off against the other two [9]:

- *Realism*: the degree to which the model mimics the real world;
- *Power and Precision*: collection of revealed properties, and the accuracy of the model predictions;
- *Generality*: the number of systems and situations to which the model correctly applies.

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