How restrictive is the current action decomposition property for compression bisimulation?

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Bio-PEPA is a stochastic process algebra for modelling biological systems. Semantic equivalences such as bisimulation are defined for process algebras and allow for the comparison of different models with respect to their behaviour. A question of interest is what semantic equivalences are useful in systems biology modelling. There are three approaches that can be taken in answering this question. First, one can consider the existing equivalences used in computer science and second, one can develop equivalences based on what biologists view as equivalent behaviour. The third approach involves considering two systems that we expect to have the same behaviour and use that as the basis for an equivalence. This approach has been successfully applied to Bio-PEPA to define compression bisimulation.

Bio-PEPA avoids the state space explosion in two ways: by allowing analysis based on ordinary differential equations and by discretising the concentrations of species. In the second case, we can use different step sizes to obtain different discretisations of the same Bio-PEPA model. Even though these models have different discretisations, we expect them to have the same behaviour and it is possible to construct an equivalence that identifies two different discretisations of the same model. This equivalence is called compression bisimulation (Galpin and Hillston, Discretisation and equivalence in Bio-PEPA, to appear in Proceedings of CMSB 2009) and is qualitative in that it only considers reaction names and not reaction rates.

Compression bisimulation involves equivalence classes of states in the labelled transition system obtained from the Bio-PEPA model. States are considered equivalent if they have the same reactions available. Transitions are then generated between classes of states from the transitions of the labelled transition system, creating a new transition system. Classical bisimulation as defined by Milner is then used to determine if the new transitions systems obtained for each discretisation have the same behaviour.

It is possible to show that two discretisations of a single species are compression bisimilar without any restrictive conditions. However, when showing that compression bisimulation is a congruence with respect to the synchronisation operator, a condition called the current action decomposition property (CADP) is currently required. This property requires that if we have two Bio-PEPA models $P_1 \underset{L}{\bowtie} Q_1$ and $P_2 \underset{L}{\bowtie} Q_2$ that are both derived from the same Bio-PEPA model $P \underset{L}{\bowtie} Q$ and which both have the same reactions available, that P_1 and P_2 have the same reactions available and Q_1 and Q_2 have the same reactions available.

The investigations of this property have shown so far that for a reaction $\alpha \notin L$ there are two basic cases where CADP does not hold and for $\alpha \in L$ there are two basic cases where CADP does not hold. The first two cases are easy to exclude from consideration since they are not reasonable Bio-PEPA models. In these cases, we can show that α appears in P and in Q but we know that $\alpha \notin L$. For $P \underset{L}{\bowtie} Q$ to be a reasonable representation of a biological system, any shared reaction should be in L. For the cases with $\alpha \in L$, there are a number of avenues to consider including the role of creation and degradation reactions, and whether a Bio-PEPA model is fully expressible. These points will be elucidated during the presentation. This is work in progress.