

REACTIVE TRANSITION MODELS TO BIOLOGICAL SYSTEMS

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Reactive frames have been study by Gabbay and his collaborators (see [1]) and are those frames whose structure is not fixed, *i.e.*, can vary according to the path chosen. Informally, a reactive frame can be seen as a digraph (V, E) where the set of edges can be altered whenever an edge is crossed. Some particular cases of these kind of structures have been proposed by authors like Areces and van Benthem (see [2], [3]) that proposed swap and sabotage logics.

We used this kind of model to describe biochemical events which usually are not naturally modeled or that require the consideration of additional components in order to be correctly described. In particular, we show that this approach can lead to more intuitive models for many biochemical systems. In particular, we focus our attention in biological regulatory networks.

We conclude with some ideas about how fuzziness/probability can be introduced in these models and how it can be useful to describe biological phenomena. In particular, we present some examples of how this would more detailedly describe the referred biological regulatory networks.

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