

An agent based model for the light signal transduction in *Neurospora crassa* - (session: Novel Algorithms for Bioinformatics)

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We used the relatively simple multiprotein blue light transduction cascade of a filamentous fungus, *Neurospora crassa*, as subject for the test and development of a formal language able to describe molecular biology dynamic interactions.

The blue light transduction in *N. crassa* is controlled by two proteins White collar-1 and 2 (WC-1 and WC-2) forming a complex (WCC) that functions as a photoreceptor, (Ballario et al., Froehlich et al.). WC proteins are involved not only in light perception (through the LOV domain of WC-1 and the chromophore associated) but also in DNA binding and transcriptional activation (by the GATA Zinc finger domains of both proteins).

Many light induced responses are known at phenotypic and molecular biology level in *N. crassa*. One of the most interesting is the circadian rhythm of conidiation controlled by the protein FRQ that interacts with WCC. Although the blue light signal transduction of *N. crassa* is far from to be completely elucidated it seems a model suitable for testing the biological expressivity of the language we are developing.

In particular, first we introduce a map model (Khon 1998) for the light regulated signal transduction. Then we translate the map in the core molecular language recently introduced by Danos-Laneve, so providing a process algebra approach to the description of the involved molecular interactions. In this way, we prepare the study of emerging behaviour in the dynamics of the biological system by mathematical and computational tools.

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