INTRODUCTION

Biological switches drive changes in the functional state of a system in an all-or-none fashion. These switch-like behaviours have been observed in different biological processes, like the transitions between phases of the cell cycle, the epigenetic changes, the regulation of polarity, or the septation initiation. A simple model able to capture the dynamics of these complex processes is a population protocol, Approximate Majority (AM), widely used in distributed computing. This algorithm describes how to drive a population of agents (molecules), initially in two different states, into a final population where all agents (molecules) are in the same state.

We investigate if this type of system could have been the ancestor of a class of biological switches, where the transitions between functional states should happen in a fast, reliable and robust way.

RESULTS

Accumulation of variants

Allosteric changes

Introduction of a new conformation (OP).

The system is faster. Bistability is kept. $k_1 k_2 k_3 k_4 > 1$

Accumulation of variants

Allosteric changes

Allosteric changes in the catalytic conformations.

Bistability is kept. It restores AM’s dynamics. $k_1 k_2 k_3 k_4 > 1$

Allosteric changes in the intermediary conformations.

- OO cannot dephosphorylate buried sites (PO)
- OO reduces its activity over OP ($k_1 = k_2 = 0.5$)
- Allosteric changes in PP block the dephosphorylation by OO and allow the autodephosphorylation ($k_1 = k_2 = 0.1$)
- PP cannot phosphorylate buried sites (OP)

Lose of catalytic activity due to accumulation of variants.

- Each species have one catalytic state and another inactive state.
- The system resembles a mutual inhibition (MI) system.
- OO active state autodephosphorylates and activates itself.
- OO active state dephosphorylates PP and inhibit it.
- PP active state autophosphorylates and activates itself.
- PP active state phosphorylates OO and inhibit it.

REFERENCES