INTRODUCTION

Biological switches drive changes in the functional state of a system in an all-or-none fashion. These switch-like behaviors have been observed in different biological processes, like the transitions between phases of the cell cycle\(^1\), the epigenetic changes\(^2\), the regulation of polarity\(^3\), or the septation initiation\(^4\). A simple model able to capture the dynamics of these complex processes is a population protocol, Approximate Majority\(^5\) (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**

- Introduction of a new conformation (OP)
  - The system is faster. Bistability is kept. \(k_4 = k_5 = k_6 = 1\)
- Allosteric changes
- Allosteric changes in the catalytic conformations
  - Bistability is kept. It restores AM’s dynamics. \(k_4 = k_5 = k_6 = 1\)
- Loss 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 dephosphorylates and activates itself.
  - PP active state dephosphorylates PP and inhibit it.
  - PP active state autophosphorylates and activates itself.
  - PP active state phosphorylates OO and inhibit it.

**Gene Duplication**

- Double amount of protein
- Faster system. Bistability is kept.

**Gene Duplication. Double amount of protein**

- Loss of catalytic activity due to accumulation of variants
  - Bistability is kept but it is unbalanced. Once state is a better attractor.

REFERENCES