# Two-dimensional Modeling on PopZ Bipolarization in Caulobacter Cell Cycle

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***Short Abstract* — The asymmetric location of proteins is crucial to the *Caulobacter* cell cycle. The landmark protein PopZ determines the location of the key cell cycle regulators and tethers the replicated chromosome. Experiments demonstrate a self-assembly mechanism for the PopZ polarization. Here, we proposed a two-dimensional model based on Turing mechanism to explain PopZ bipolarization. We explore the parameter set and cell shapes that generate patterns with polar activator. Both deterministic and stochastic simulations capture the observed variations in cell length and time when PopZ becomes bipolar.**

***Keywords* — *Cauoubacter* cell cycle, PopZ polarization, Turing pattern.**

## I. INTRODUCTION

Experiments on the bacterium *Caulobacter crescentus* reveal that the bacterial cytoplasm is elaborately organized on space and evolves during the cell cycle [1]. The localizations of proteins determine the cell shape, chromosome segregation event and differentiation [1]. In *Caulobacter crescentus*, the protein PopZ was identified as a potential landmark protein [2]. PopZ locates at the old pole of the swarmer cell and begins to accumulate at the new pole when the gene segregation is initiated in the stalked cell.

While the dynamic localization pattern of PopZ is clearly observed, the mechanism behind PopZ localization is still being revised and debated. This abstract demonstrates our two-dimensional model to explain the reaction mechanism behind the PopZ localization and illustrates the spatiotemporal properties of the cell cycle.

## II. MATHEMATICAL MODEL

Experiments show that overexpression of PopZ can lead to cell division defects [3]. PopZ is able to maintain its population level by forming polymers under a self-organization mechanism. The PopZ polymerization is responsible for the PopZ polarization [3]. In order to explain the mechanism behind the polarization, we proposed a Turing pattern mechanism in coordination with the chromosome segregation [4]. Our model can reproduce the bipolarization behavior of PopZ in two-dimensional cell shapes, as well as the stochastic variation on the bipolar time. Figure 1 shows the deterministic PopZ distribution at the end of cell cycle. Figure 2 is a snapshot of an animation that shows the stochastic results during the cell cycle.

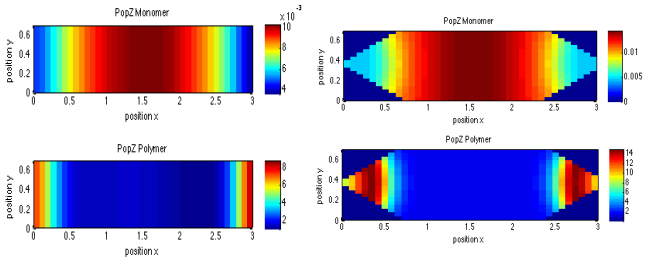


Figure 1: The distribution of PopZ with rectangular cell shape (left) and triangle-end shape (right).

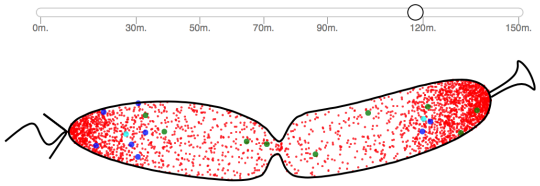


Figure 2: A snapshot of an animation that showing the stochastic results during the cell cycle. PopZ Polymer (red), Monomer (dark green), Gene (light green), mRNA (blue)

## III. CONCLUSION

We propose a two-dimensional model for the PopZ localization based on Turing pattern. Under this mechanism, PopZ drives its own spatiotemporal distribution by a self-assembly process. Furthermore, the statistics shows the variant of the timing for chromosome segregation as well as the timing for the PopZ becomes bipolar.

## REFERENCES

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