

Automated Analysis of Mycobacterial Microcolonies Growth on a Chip

Nicolle Ho¹, Maxime Mistretta², Giulia Manina²

1. University of Notre Dame, IN, USA 2. G5 Microbial Individuality and Infection, Institut Pasteur, Paris, France

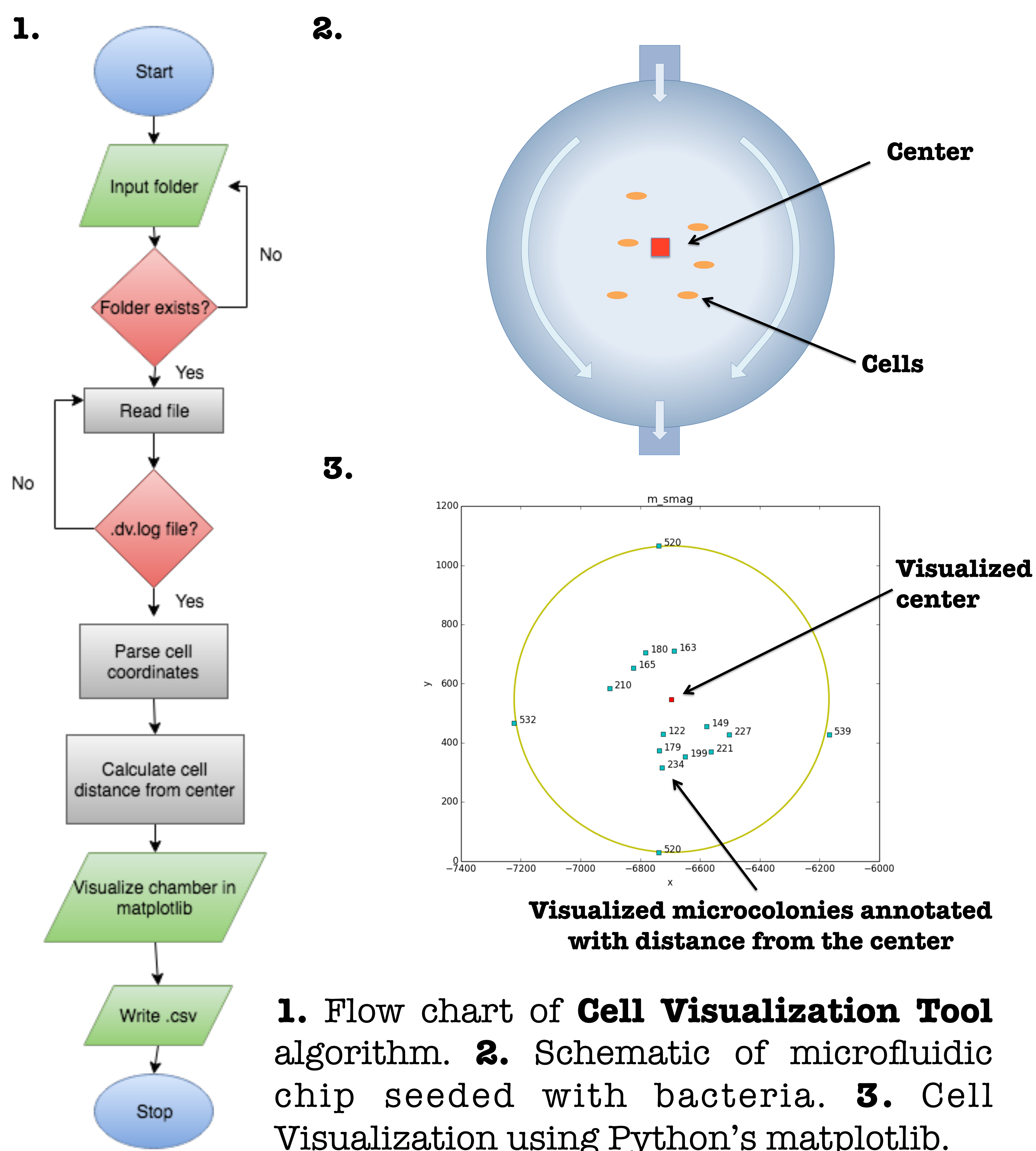
Introduction

Tuberculosis (TB) is a deadly infectious disease caused by *Mycobacterium tuberculosis*. Though curable by lengthy multidrug therapy, drug-resistance spreads ([PMID:2784885](#)). Existence of non-genetic cell-to-cell heterogeneity further exacerbates this problem by making bacilli also phenotypically tolerant to drugs ([PMID:27837741](#)). To elucidate the mechanisms of drug tolerance, we study phenotypic heterogeneity by monitoring the growth and behavior of live bacilli inside a microfluidic chip with live microscope imaging. However, this approach produces vast amounts of data that need robust computational strategies to be analyzed and processed more efficiently, which is the purpose of this summer project.

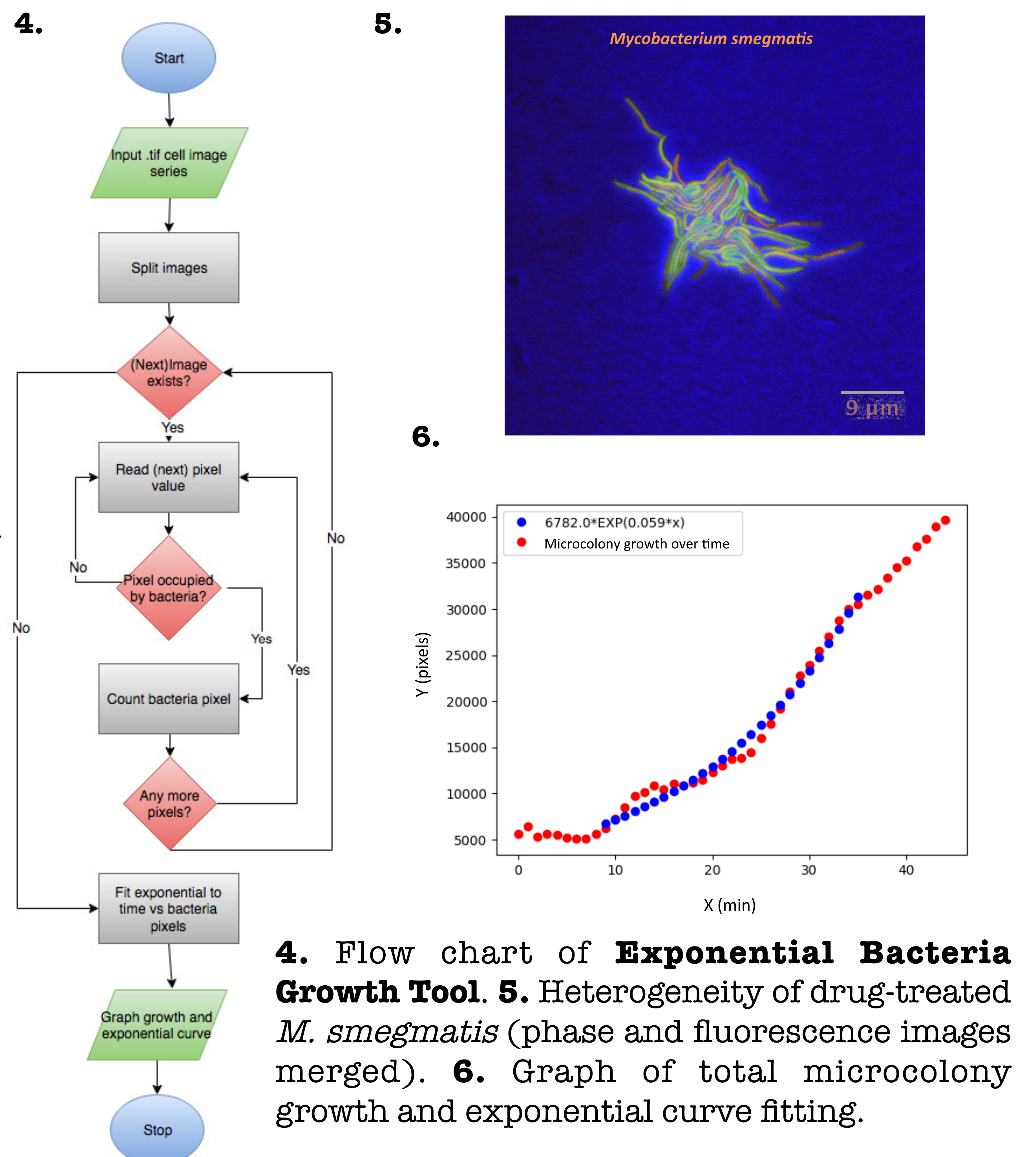
Objectives

- ❖ Track the growth and division of microcolonies of *Mycobacterium smegmatis*, a TB model
- ❖ Create a map of the microfluidic cell microchamber
- ❖ Organize the microcolony growth data automatically in Python
- ❖ Fit exponential curves to microcolony growth data to calculate the growth rate

Cell Visualization Tool



Exponential Bacteria Growth Tool



Conclusions

Cell Visualization tool reads a folder of data files, maps the chamber, and writes a .csv with file name, cell location, and distance from center. Exponential Bacteria Growth tool reads bacterial movies, estimates exponential fit, and graphs total growth and rate. The Python tools automate and accelerate analysis, and can be applied to other TB research.

Perspectives

- ❖ Validate accuracy
- ❖ Visualize chip array
- ❖ Include a 3D interface
- ❖ Enhance program robustness to read unclear images
- ❖ Write documentation

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