Abstract

Simulation of Different Age Distributions for the Analysis of the Aging Curve of a Population of "*S. cerevisiae*" †

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Abstract: Newly developed microfluidic devices ("Mother Machines") have improved data gathering for the study of aging in unicellular models, and thereby the understanding of this process. Each device has different features that cause them to have certain advantages or disadvantages. This has the advantage of not using mechanical pressure to trap the cells, but as it starts with a mixed age population it does not guarantee that the cells studied are virgin. One of the basic outputs in these studies is the aging curve, which shows how the fraction of viable cells varies with respect to time. From this it can be deduced how fast or slow the population ages. For devices where it is not possible to work with virgin cells, the age distribution is assumed, but changes in this distribution could affect the analysis of the data. Therefore, the present work seeks to carry out a series of simulations to find the different age distributions that could be present and determine the corresponding changes in the aging curve. We propose two population growth models, synchronous and asynchronous. For each model we will start with the possible age distributions and determine the various curves that can be obtained and then compare these computational results with the experimental data to propose a better interpretation of the data obtained from mother machine devices.

Keywords: age distribution; simulation; analysis of data; aging curve; microfluidic devices

Supplementary Materials: The following are available online at https://www.mdpi.com/article/10.3390/Micromachines2021-09577/s1.

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Data Availability Statement: In the following link you can find the simulations used to carry out this study https://github.com/Ivonne-Rojas/Simulation-of-Different-Age-Distributions-for-the-Analysis-of-the-Aging-Curve-of-a-Population-of-S.