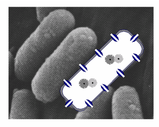
INDIVIDUAL-BASED MODELLING AND SIMULATION: TOWARDS A BETTER UNDERSTANDING OF GROWTH DYNAMICS FROM SMALL INOCULA

Dalmau, R.[1*]; Portell, X.[2]; Prats, C.[1]; Ginovart, M.[3]; Giró, A.[1]

*roger.dalmau.andreu@upc.edu
Campus del Baix Llobregat
ESAB building
Av. Canal Olímpic 15
08860 Castelldefels
Barcelona (Spain)

Universitat Politècnica de Catalunya, Departaments of:
(1) Physics and Nuclear Engineering
(2) Agri-Food Engineering and Biotechnology
(3) Applied Mathematics III



Complex systems. Modelling and computer simulation of biological systems
Escola Superior d'Agricultura de Barcelona
Universitat Politècnica de Catalunya

INTRODUCTION

The lag phase is one of the main aspects to be considered in extending the safe shelf life of foods. It has mostly been investigated with continuous population models, using rather high inoculum levels. However, foods are often contaminated with just a few microorganisms and, therefore, they demand an individual-based approach. The aim of this contribution is to explore the effect of the inoculum size in population and individual lag phases using an Individual-based Model (IbM). Specifically, we have tackled the dynamics of bacterial and yeast cultures separately, due to the importance of these microorganisms in food. INDISIM is an IbM designed for modelling and simulation of microbial growth [1], and it has been already used in the study of different microbial communities with success [2,3].

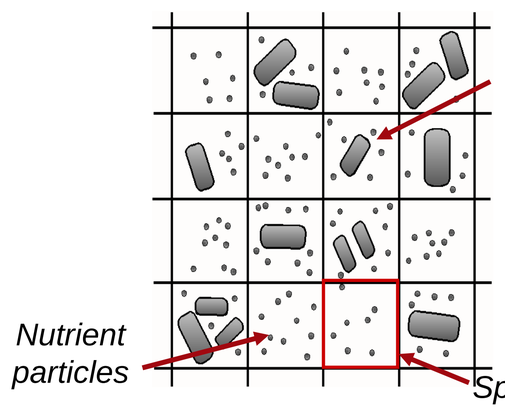
GENERAL FEATURES OF THE MODEL

Low-level entities

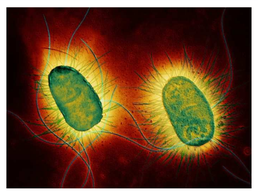
INDISIM: bacterial cells

INDISIM-YEAST: yeast cells

Characteristics:
- Position
- Mass
- Mass to initiate cell division
- Reproduction cycle status

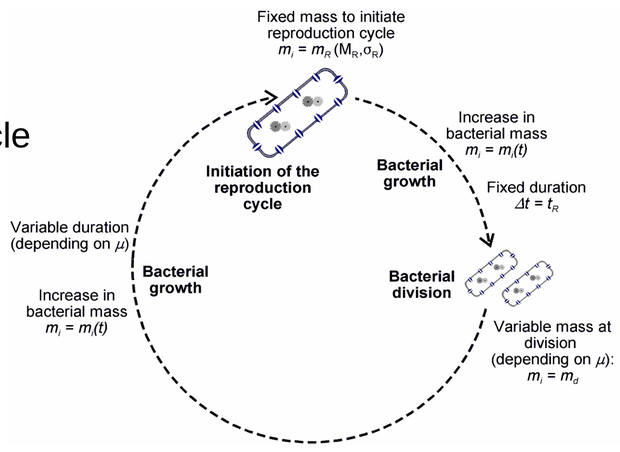


Rules:
- Motion
- Nutrient uptake
- Metabolism
- Reproduction cycle
- Viability



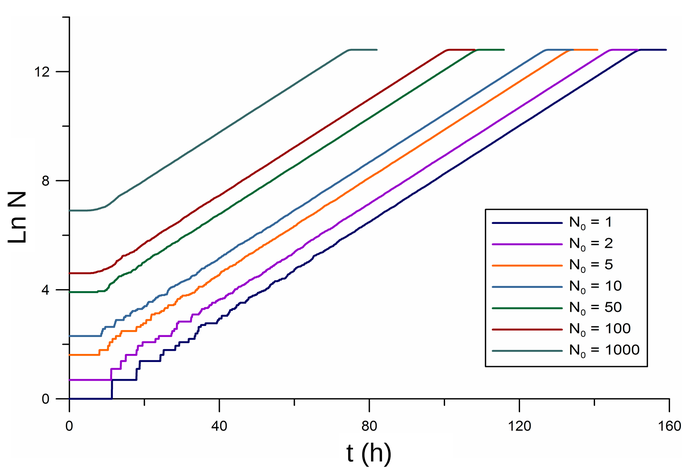
INDISIM

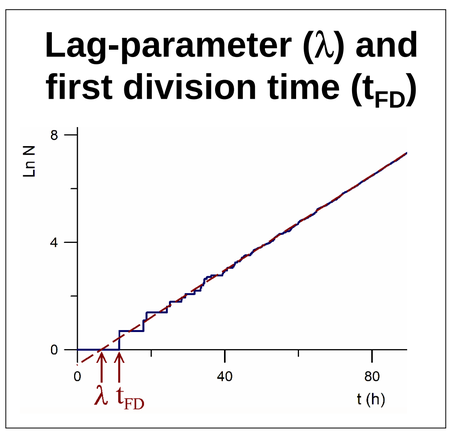
A different rule:
Reproduction cycle



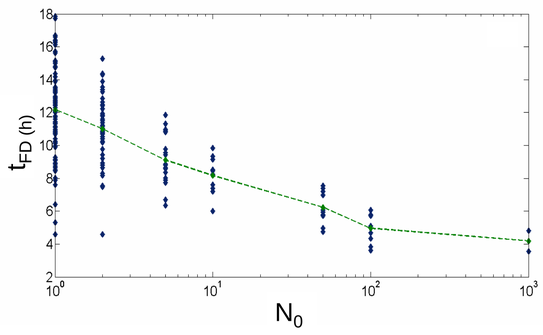
RESULTS

Several simulations changing the initial inoculum size were carried out with INDISIM, covering inocula levels from 1 cell/ml to 1000 cell/ml.



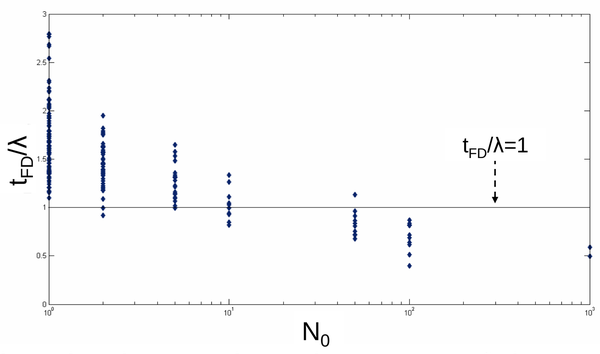


Different simulations show that there is no influence of inoculum size in the population lag-parameter, λ, but the first division time (t_{FD}) changes.

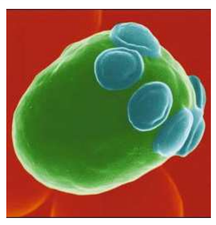


The t_{FD} dispersion is much greater for small inocula and also changes its mean value. Each dot represents an independent simulation.

Different simulations show that for small inocula the t_{FD} is greater than λ, indicating that the lag phase ends before any bacteria has reproduced. This is due to an imprecise definition of the lag parameter.

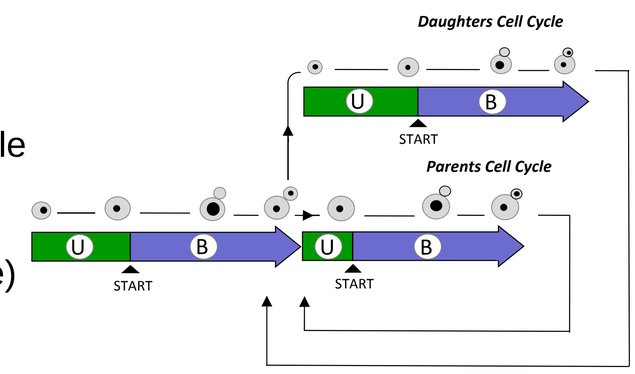


We also observed that the culture lag time is shorter than the mean of the single cell lags, as has been stated previously in the literature.

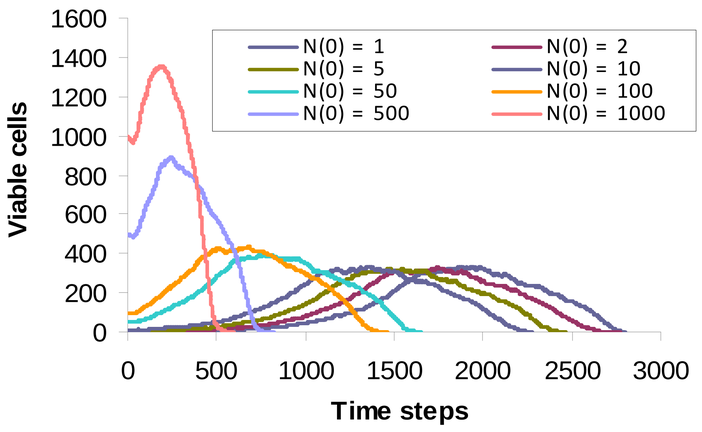


INDISIM-YEAST

A different rule:
Reproduction cycle
A new characteristic:
Number of scars (genealogical age)

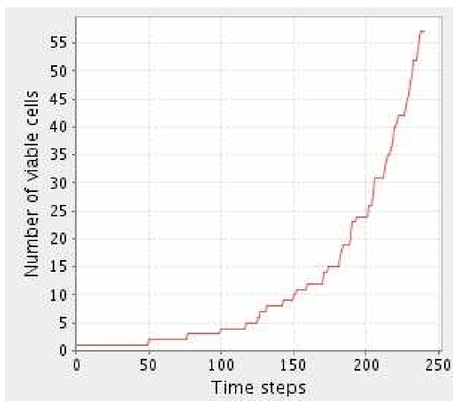


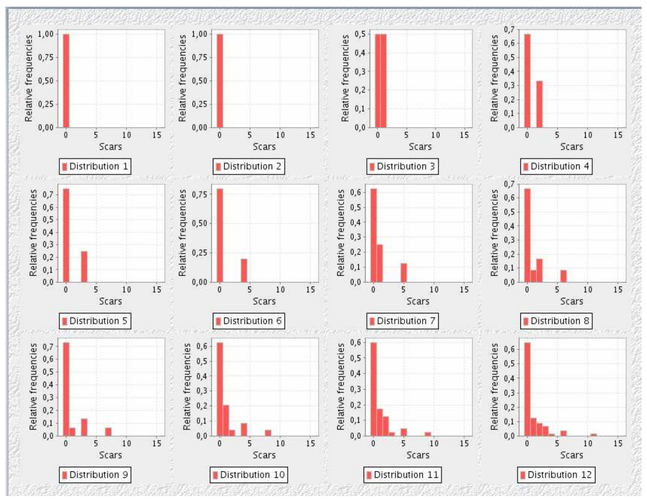
RESULTS



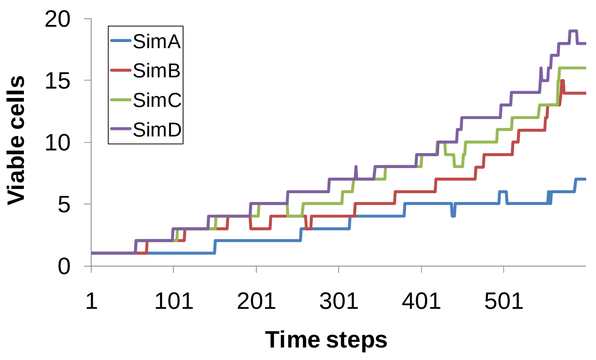
Several simulations changing the initial inoculum size were carried out with INDISIM-YEAST, covering inocula levels from 1 cell/ml to 1000 cell/ml.

Screenshots of INDISIM-YEAST in action from the website[1], showing the culture evolution from a single daughter cell (left) and the scars distributions along this growth (right).





[1] *https//aneto.upc.es/simulacio/hoja-portada.html*



Effect of genealogical age in culture evolution from single-cell inocula: time evolution of the number of viable yeast cells obtained with an initial cell of genealogical age: 0 for SimA, 3 for SimB, 7 for SimC and 10 for SimD.

CONCLUSIONS

The analysis of our results showed that classical continuous models are not useful to deal with small inocula because of the excessive influence of the discrete nature of the microbial division. These results also suggest that INDISIM builds a bridge between individual behaviours and collective observations.

REFERENCES

[1] Ginovart, M. et al., 2002. *J. Theor. Biol.* **214**, 305-319.
[2] Ginovart, M. and Cañadas, J.C., 2008. *J. Ind. Microbiol. Biotechnol.* **35**, 1359 - 1366.
[3] Prats, C. et al., 2006. *J. Theor. Biol.* **241**, 939-953.

ACKNOWLEDGEMENTS. We acknowledge the financial support of the Plan Nacional I+D+i of the Ministerio de Educación y Ciencia CGL2007-65142/BOS and the Universitat Politècnica de Catalunya.

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