

INDISIM-YEAST:SACCHA, AN INDIVIDUAL-BASED MODEL TO TACKLE SACCHAROMYCES CEREVISIAE BATCH CULTURES

X. Portell¹, A. Gras¹, R. Carbó¹, **M. Ginovart**²

¹*Agri-Food Engineering and Biotechnology*, ²*Applied Mathematics III, Universitat Politècnica de Catalunya, Castelldefels, Spain*

INDISIM-YEAST is a generic individual-based model of the yeast biology already used within specific applications. From this, a model based on the fermentative metabolism of *Saccharomyces cerevisiae*, INDISIM-YEAST:*Saccha*, is being developed considering glucose and organic and inorganic nitrogen sources as growth substrates. In order to further a qualitative approach, the model needs to be properly parameterized and thoroughly analysed in order to gain knowledge of the modelled system. This contribution aims to perform a parameterization, giving a value or range of values to each individual microbial parameter, and a sensitivity analysis of the stated model. When the value of a model individual parameter cannot be inferred from the literature, then a broad range can be assigned to reflect the uncertainty of this value. Parameter ranges were reduced with a brute force exploration of the parameter space and the selection of the simulations best fitting the experimental data. Mean square deviation was used as goodness of fit measure. Available experimental data consisted of glucose depletion and total cell number curves. Sensitivity of model output was evaluated by conducting a global sensitivity analysis of the reduced parameter space. Considering available experimental data, three model outputs were selected: glucose depletion curve mean slope, maximum perpendicular distance between real and mean slope, and maximum cell number. The analysis performed helps to unravel the effect of the individual parameters on the system modelled, and suggests focusing on those parameters directly related to glucose uptake and metabolism rather than on those connected with reproduction.