PEC1.44 **Combined use of local and global sensitivity analyses for the investigation of an individual-based model of yeast populations**

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Microbial modelling deals with complex spatio-temporal systems, implying the building and use of increasingly complex models. This complexity often makes analytical or mathematical studies very difficult, when not impossible. New and recent modelling techniques are being applied to microbial systems nowadays, such as individual-based modelling (IbM). The only way to assess the mathematical properties of these models, including sensitivity, uncertainty, stability and error propagation, is the statistical study of well-designed computer experiments. A stochastic IbM of yeast populations growing in liquid bath cultures has already been designed and implemented in the simulator called INDISIM-YEAST. The mission of modelling the behaviour of a single yeast cell is one of the cores of this approach. Some interesting qualitative results have already been achieved with its use in the study of fermentation profiles, small inocula dynamics and the lag phase, among others. Nevertheless, in order to improve its predictive capabilities, a deeper understanding of how the variation of the output of the model can be apportioned, qualitatively or quantitatively, to different sources of variation, as well as how this model depends on the information input into it, must be further investigated. The current version of this simulator contains uncertain input factors that need to be parameterized and calibrated with several experimental sets of data. The aim, then, of this study is to show how insights into the individual cell parameters of INDISIM-YEAST can be obtained combining some of the known methods used for the assessment of local and global sensitivity. Among the various sensitivity analysis strategies that may be applied, this work deals mainly with the use of screening methods, as the main task to perform here is to identify the most influential factors for this virtual yeast culture. This screening exercise has allowed the establishment of significant input factors to this IbM on yeast population growth, and therefore, those that would require major attention in a calibration process. In addition, this type of information is also useful because the model suggests where efforts should be made to develop measuring parameters with greater accuracy than currently attainable in order to improve the predictive capability of this kind of modelling.