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Complex systems in BioEngineering: integrative approaches for Biotechnology

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Bioengineering has high potential for complex systems (CS) in modelling and simulation. Biological systems are composed of functional elements, with high variety of chemical and physical properties, presenting large diversity of structures at any scale. Composites and control structures that build-up from the different levels, form self-organised and regulated mechanisms, that provide adaptation and redundancy of systems supporting life. Therefore, CS modelling of cells, colonies and tissues is an important challenge in the post-genome era of Biotechnology. The authors' first CS technology was applied to macroscale simulations. The "legacy technology" provides bioengineering the fundamentals for scenario technologies to develop mesoscale to macroscale systems. Therefore, one of the main challenges for theoretical research in Biotechnology is to develop strategies that enable the description of systems at multi-scale levels, for biological, biochemical and physical components. Simulation tools are now being developed for process prototyping. These include both physics and cell dynamics (cycle and metabolism), cell to cell communications and colony dynamics (quorum sensing) inside bioreactors. Currently as a "work in progress", the authors present some of their strategies, as well as, theoretical and experimental CS challenges of modelling and simulating the flocculating yeast growth during fed-batch fermentations.

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Characterization and differentiation of aflatoxigenic species of *Aspergillus* section *Flavi* by MALDI-TOF MS

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Aspergillus is a large genus, with a complex taxonomy. The genus is easily identified by its characteristic conidiophore, but species identification and differentiation is complex, mainly because it is traditionally based on a range of morphological features. *Aspergillus* subgenus *Circumdati* section *Flavi*, also referred to as the *A. flavus* group, has attracted worldwide attention for its industrial use and toxigenic potential. Section *Flavi* is divided in two groups of species. One includes the aflatoxigenic species *A. flavus*, *A. parasiticus* and *A. nomius*, which cause serious problems in agricultural commodities, and the other one includes the non-aflatoxigenic species *A. oryzae*, *A. sojae* and *A. tamarii*, traditionally used for production of fermented foods. Species from *A. flavus* group are morphologically and genetically very similar, and are therefore difficult to differentiate by both cultural and molecular methods. Matrix Assisted Laser Desorption Ionization Time-of-Flight (MALDI-TOF) Mass Spectrometry has already shown high potentialities in discriminating very closely related taxa. This work intended to discriminate 30 strains, which were previously classified as *A. flavus* group by morphological methods, using MALDI-TOF MS. These results are compared with that previously obtained by conventional methods.

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