How fit is the classic kinetic method of enzymatic analysis for the characterization of polymer hydrolysis?

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The classic method for the characterization of enzyme kinetics is based in the determination of the initial reaction rate for a given concentration of substrate, which is assumed nearly constant for the time course of each run. This strategy is often used since it is easy to implement and is easily automated. It is thus preferred over the estimation of kinetic parameters from the progress curve analysis, particularly given the computational difficulties aroused by the implicit nature of the Michaelis-Menten equation, although the later approach is considered more unbiased. In this work the two approaches were used to characterize the hydrolysis of inulin. Estimation of kinetic parameters from the Michaelis Menten equation was performed by graphical and non-linear regression methods. In the overall, non-linear methods provided more adequate fittings to experimental data as well as more adequate simulation of batch and continuous modes of operation for the intended biotransformation. $K_m$ of 34.0, 38.0 and 50.0 gL⁻¹ and $v_{max}$ of 0.039, 0.055 and 0.054 gL⁻¹min⁻¹ were obtained for trials performed at 40 °C, 50 °C and 60 °C, respectively.

Feasibility of yeasts and fungi monitoring during cheese maturation using fibre optic sensors

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UV-VIS spectroscopy is a powerful qualitative and quantitative technique. As in UV-VIS spectra there is no direct information on characteristic organic groups, vibrational spectroscopy (e.g. infrared) has been preferred for biological applications. In this exploratory study, we experiment the feasibility of using UV-VIS–SWNIR (200–1200 nm) fiber optics probes to obtain diffuse reflectance measurements of cheese (mixture of cow, goat and sheep) contaminated with the following fungi and yeasts: i) yeasts: Saccharomyces cerevisiae and Yarrowia lipolytica; and ii) fungi: Aspergillus aliaceus, Aspergillus ochraceus, Botrytis cinerea, Penicillium crustosum, Penicillium roqueforti, Penicillium commune. Results show that UV-VIS–SWNIR has great potential for identifying the selected microorganisms on the cheese surface. Scattering artefacts was significantly removed using a robust mean scattering algorithm, allowing also better discriminations between the scores obtained by SVD. Hierarchical clustering analysis of UV-VIS and VIS–SWNIR decomposed spectral scores lead to the conclusion that both fungi and yeasts are better identified in the UV region; and Botrytis cinerea, Yarrowia lipolytica, Penicillium roqueforti, Penicillium commune and Saccharomyces cerevisiae are successfully classified.