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## Kinetic analysis for the new enzymology

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Enzyme kinetics relies on a bulky corpus of knowledge which has been consolidated along with more than 100 years of biochemical research. The studies on sucrose hydrolysis by invertase made by Leonor Michaelis and Maud Menten led to the publication in 1913 of their homonymous equation, regarded as the fundamental equation of biochemistry. Since then, enzymologists have devised many different ways to measure and analyze kinetic data, and many different enzyme or inhibition mechanisms were identified.

The Michaelis-Menten equation and the relative “steady state” model however provide only an oversimplified description of the real enzyme behavior. The recent development of computer software for the global fitting of enzymatic reaction progress curves by numerical integration represents a fundamental breakthrough in the century-old field of enzymology. The resolution of kinetic mechanisms by computer simulation will foster a shift in the paradigm from the “steady state” to “transient state”, simplifying the study of complex mechanisms and pushing toward a next level understanding of enzyme catalysis.

Here a brief introduction will be given on this new method for the study of enzyme kinetic.

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