

Mathematical model for fragmentation of bacterial inclusion bodies

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ABSTRACT

Bacterial inclusion bodies are microscopic, ovoid-shaped aggregates of insoluble protein. Under protease exposure a digestion process is produced that reveals a variable fragmentation rate, not compatible with a surface-restricted erosion of body particles, or an uniform sensibility to the fragmentation agent. The modeling and fitting of experimental data is performed in two steps. (a) Due to poor estimation of protein amounts only first derivatives can be numerically evaluated, and a non-linear first-order fragmentation model is adopted. Although it is a very good approximation for intermediate points, the asymptotic behaviour of the solution is inconsistent with the fragmentation process. (b) The solution of previous kinetic modeling is used to compute higher-order derivatives in intermediate points and to adopt a higher-order lineal model for the overall interval with protein fragmentation. The resulting model consists in a superposition of Poisson processes associated with several populations of protein with different fragmentation resistance. Numerical estimation of model constants is also described and discussed. In particular, an iterative method of weighted least squares is used in order to obtain minimum variance parameters.

Keywords: *mathematical modelling, stochastic processes, finite mixture distributions, least squares estimation*

Mathematics Subject Classification: *92, 60, 62, 65*

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