عنوان مقاله:

A Mathematical Probabilistic Modelling for the SingleMolecule Kinetics Problem

محل انتشار:

بیست و سومین کنگره بین المللی میکروب شناسی ایران (سال: 1401)

تعداد صفحات اصل مقاله: 1

نویسنده:

Reza Fallah Moghaddam - *Garmsar University, Garmsar, Iran*

خلاصه مقاله:

Background and Aim : In the past decades, advances in microscopy have made it possible tostudy the dynamics of individual biomolecules in vitro and to resolve intra-molecular kinetics thatwould otherwise be hidden in ensemble averages. Recently, single-molecule methods have beenused to image, localize, and track individually labeled macromolecules in the cytoplasm of livingcells, allowing the investigation of intermolecular kinetics under physiologically relevantconditions.Methods : Assume that a protein A bind to protein B. Also, the bound coplex AB can be convertedinto C. In this article, we try to derive time probability distributions for single-molecule kinetics.Assume that the probability of spices reacting in the time t is p. Also, consider that this probabilityis independent of any past history.Results : If in n consecutive intervals with the same amount as t, there is no reaction, theprobability of surviving is (۱-kt) ^n. Where, k represents the avarage frequency of te reaction.Notice that when n→∞, (۱-kt) ^n→e^(-kt).Conclusion : It is known that there exists connection between single-molecule techniques whenstudying kinetics in living cells and solutions to specific challenges associated with these methods.For Example recently, single molecule .kinetics of bacteriorhodopsin by HS-AFM is discussed byAlma P. Perrino

کلمات کلیدی:

Single-molecule kinetics, probability distributions, Modeling