

This work focuses on simulation of anisotropy decay curves of a model system where protein  $P_1$  with one tryptophan interacts with regulating protein  $P_2$  without tryptophan to form a complex  $P_1P_2$  with simultaneous change of tryptophan fluorescence lifetime of the complex. Under these conditions, the heterogeneous solution of proteins  $P_1$  and  $P_1P_2$  exhibits non-exponential fluorescence anisotropy decay which is deduced also from equations presented in this work. Such curves analytically simulated with and without Poisson noise are the main results of this work. The heterogeneous curves were analyzed using computer programs developed earlier for homogeneous systems. As expected such analysis yields correct values of fluorescence lifetimes but does not recover anisotropy parameters used in simulations. Despite of high intensities of simulated data, anisotropy decay curves of homogeneous solutions are very noisy and can be used only on a relatively short time interval of their decay.