

Direct model et inverse problem for prion protein oligomers

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Mots-clés : inverse problem, kalman filter, amyloid, protein oligomers.

Protein oligomer dynamics is a key step to understand amyloid formation, responsible for a wide range of diseases such as Alzheimer or prion, [2]. Our first goal has been to set a mathematical model to describe the primary aggregation reactions for protein oligomers. Our model is an ODE system in which the reaction rates appear as parameters.

We consider a combination of two types of measurements: on the one hand, size distributions (with size electron chromatograph) at several time points, and on the other hand the time evolution of the second moment of the oligomers, measured by Static Light Scattering.

We use a data assimilation method, specifically the Extended Kalman Filter [1], to solve an inverse problem estimating the initial oligomer distribution and identifying the kinetic parameters of our model. This approach leads us to the important conclusion that at least two different types of polymers are present.

Références

- [1] KALMAN R. E., *A New Approach to Linear Filtering and Prediction Problems*, Journal of Basic Engineering, 1960.
- [2] OW, SIAN-YANG AND DUNSTAN, DAVE E., *A brief overview of amyloids and Alzheimer's disease*, Protein Science, 2014.

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