

Analysis of the Protein Aggregation in the Neurodegenerative Diseases

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MODELLING AND ANALYSIS FOR MEDICAL AND BIOLOGICAL APPLICATIONS



1 Motivation

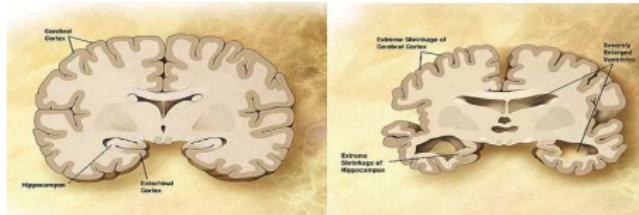
2 Experiments and Measurements

3 The Discrete Transcription

- Steady State - Equilibrium
- Parameter Estimation - Curve Fitting
- Hypothesis of a Stop Pathway

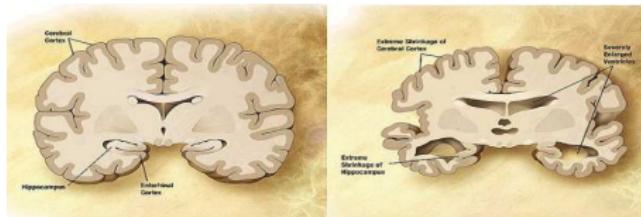
► What is the **neurodegenerative diseases** ?

↪ **Misfolding** of a monomeric protein, involving its aggregation into polymeric protein fibrils, **amyloïds**, forming a deposit and cavities **within neurons**.



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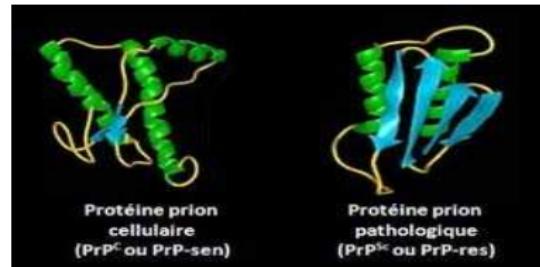


↪ More than 20 neurodegenerative diseases:

- Alzheimer ($A\beta$),
- Huntington (Poly Q),
- Parkinson,
- Prion Diseases (PrP),

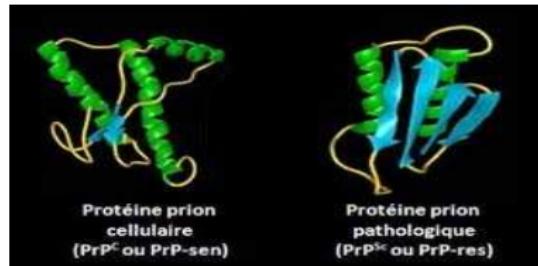
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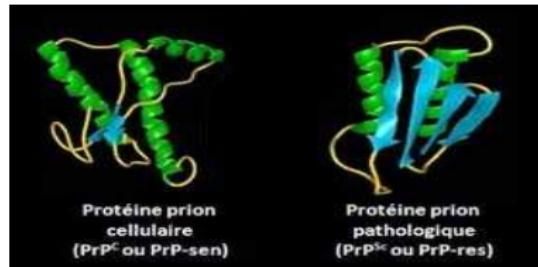


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Humans : Creutzfeldt-Jakob, Kuru, Fatal Familial Insomnia, ...

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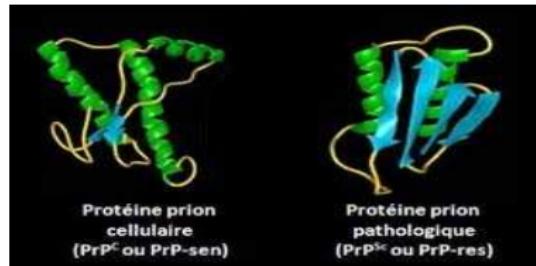
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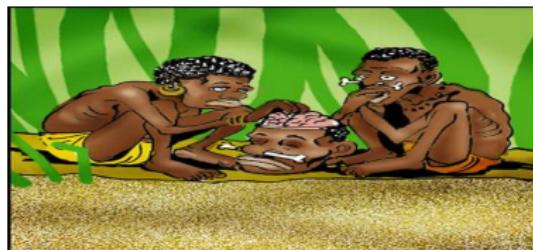


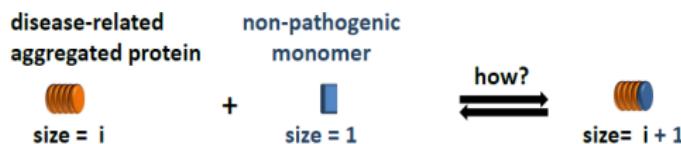
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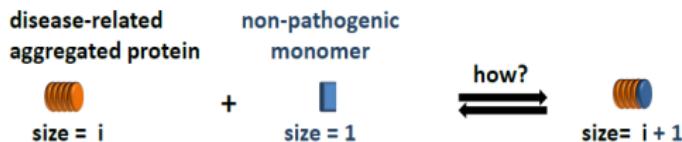
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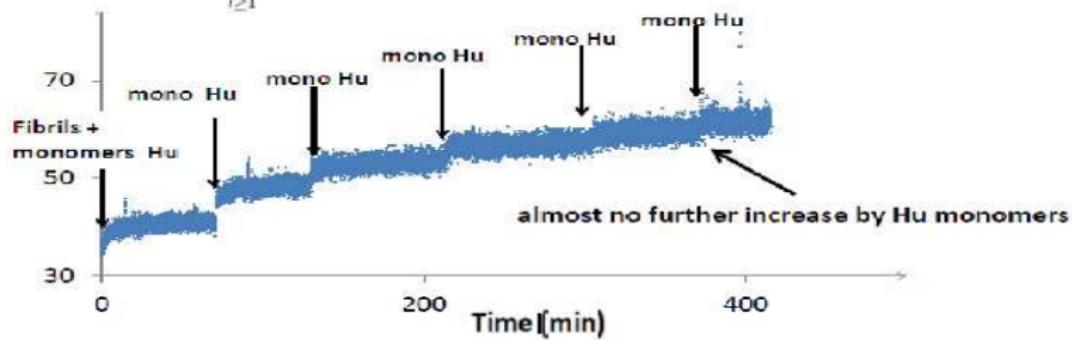
→ Transmittable.

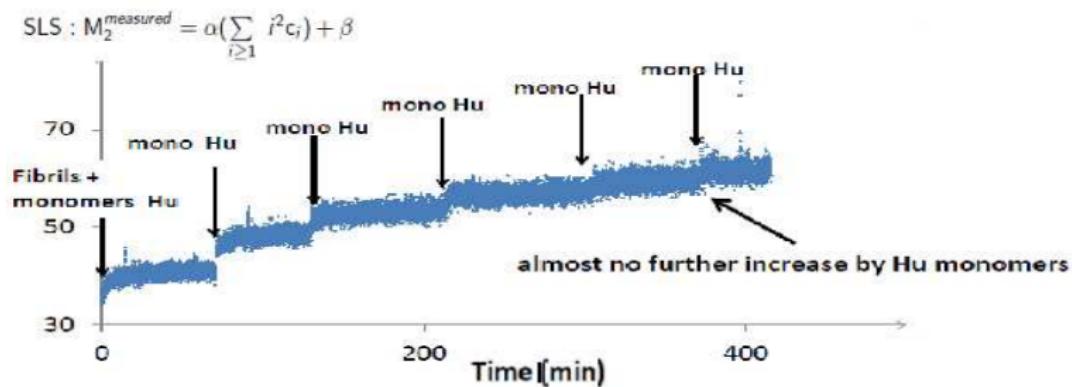
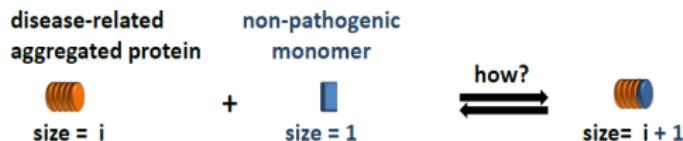






$$\text{SLS : } M_2^{\text{measured}} = \alpha \left(\sum_{i \geq 1} i^2 c_i \right) + \beta$$



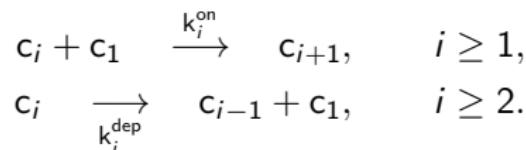


with c_i : the concentration in polymers of size i
 α and β experiment parameters.

► Reactional scheme :



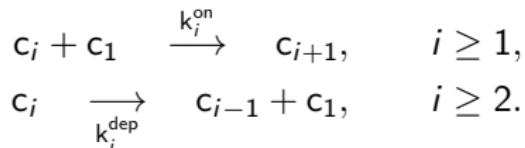
► Modelling :



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Mass Action Law

$$\left\{ \begin{array}{l} \frac{dc_i}{dt} = -k_i^{\text{on}}c_1c_i + k_{i-1}^{\text{on}}c_1c_{i-1} - k_i^{\text{dep}}c_i + k_{i+1}^{\text{dep}}c_{i+1} \quad i \geq 2, \\ \frac{dc_1}{dt} = -\sum_{i=2}^{\infty} (k_i^{\text{on}}c_1c_i - k_{i+1}^{\text{dep}}c_{i+1}) - 2(k_1^{\text{on}}c_1^2 - k_2^{\text{dep}}c_2). \end{array} \right.$$

↪ The Becker-Döring system (Becker-Döring, 1935, Burton, 1977)

Usually rewritten as:

$$\begin{cases} \frac{dc_i}{dt} = J_{i-1}(c) - J_i(c) & i \geq 2, \\ \frac{dc_1}{dt} = - \sum_{i=2}^{\infty} J_i(c) - 2J_1(c). \end{cases} \quad (1)$$

Growth rate : $J_i(c) = k_i^{\text{on}} c_1 c_i - k_{i+1}^{\text{dep}} c_{i+1}$ for $i \geq 1$.

- J. M. Ball and J. Carr and O. Penrose, Commun. Math. Phys., 1986.
- P. E. Jabin and B. Niethammer, J. Diff. Equa., 2003.
- J. A. Cañizo and B. Lods, J. Diff. Equa., 2013.

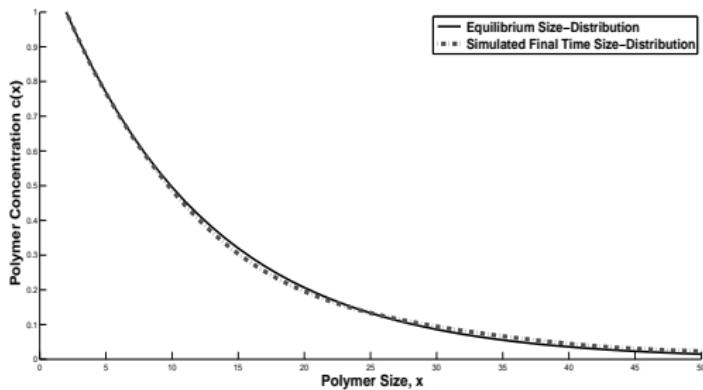
Let's consider :

$$k_i^{\text{on}} = k^{\text{on}} \mathbb{1}_{2 < i < \infty} \quad \text{and} \quad k_i^{\text{dep}} = k^{\text{dep}} \mathbb{1}_{2 < i < \infty},$$

Then:

$$\left\{ \begin{array}{l} \tilde{c}_i = P_1 \left(1 - \frac{\tilde{c}_1}{c_1^s} \right) \left(\frac{\tilde{c}_1}{c_1^s} \right)^{i-2} \\ \tilde{c}_1(\rho) = \frac{1}{2} (\rho - P_1 + c_1^s) - \sqrt{(\rho - P_1 - c_1^s)^2 + 4c_1^s P_1}, \end{array} \right. \quad \text{when } 2 \leq i \leq \infty,$$

$$c_1^s = \frac{k_{\text{on}}^{\text{dep}}}{k_{\text{off}}}, P_1 = \sum_2^\infty c_i(t=0).$$



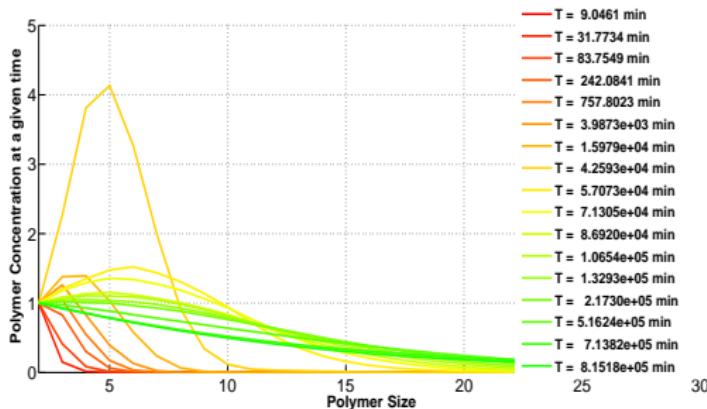
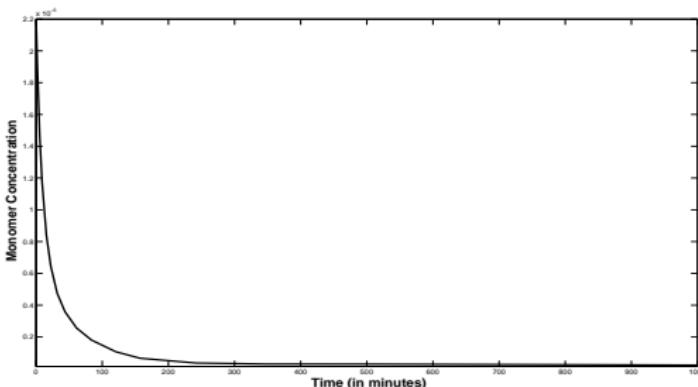
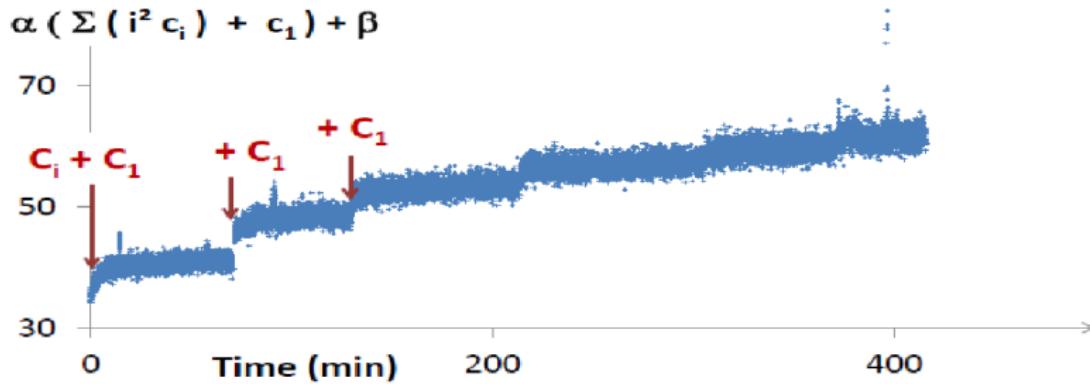
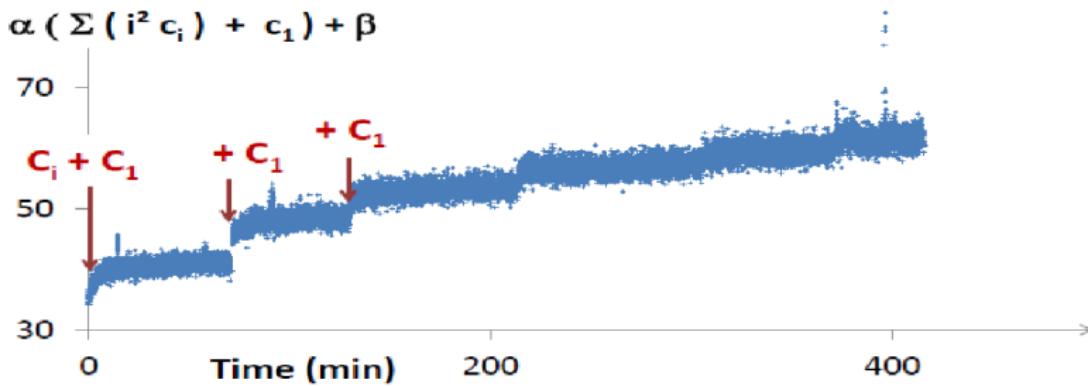


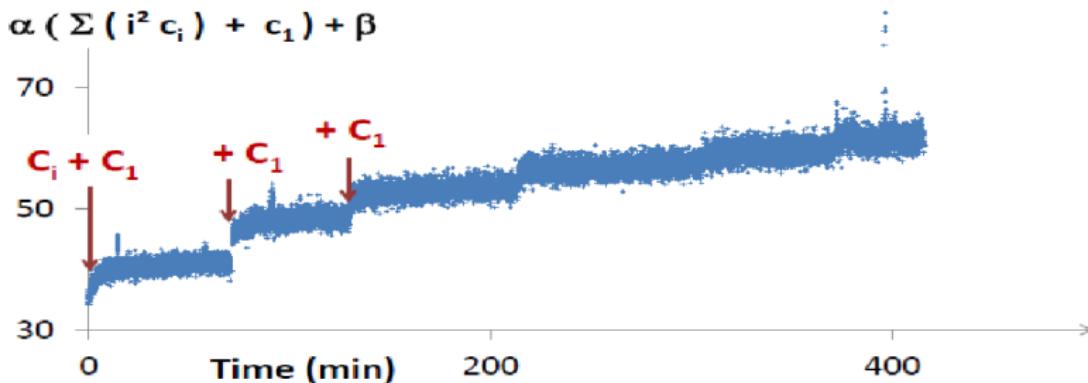
Figure: $\rho = c_1(t = 0) = 2.2 \cdot 10^{-5} \mu M$, $k^{\text{dep}}/k^{\text{on}} = 2.10^{-5} \mu M^{-1}$, $\tilde{c}_1 = 1.5 \cdot 10^{-7} \mu M$





which variation is written :

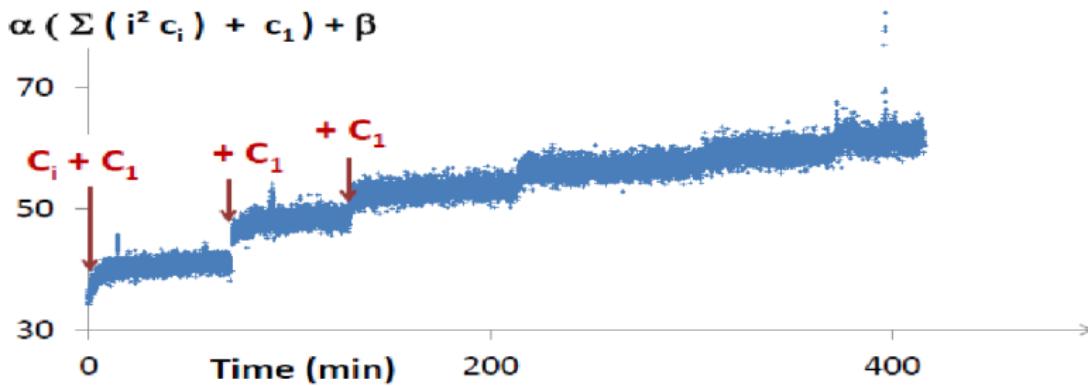
$$\frac{dM_2^{measured}}{dt} = \frac{d}{dt} \sum_{i \geq 2} i^2 c_i + \frac{dc_1}{dt},$$



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$$P := \sum_{i \geq 2} c_i(t) \text{ and } M := \sum_{i \geq 2} i c_i(t)$$

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$$\frac{dP}{dt} = 0,$$

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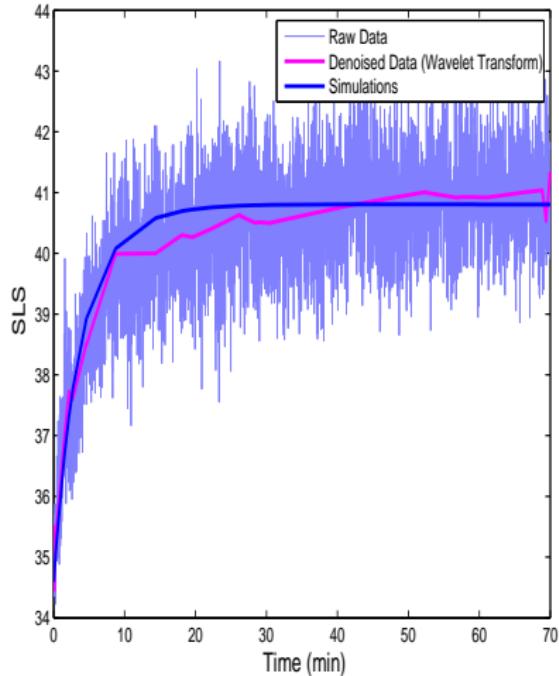
$$\Rightarrow \left. \begin{array}{l} P = P^{\text{in}} \\ M(t) = M^{\text{in}} - k^{\text{on}} (c_1^{\text{in}} - c_1^{\text{eq}}) e^{-k^{\text{on}} P^{\text{in}} t} P^{\text{in}} + (c_1^{\text{in}} - c_1^{\text{eq}}) \\ c_1(t) = (c_1^{\text{in}} - c_1^{\text{eq}}) e^{-k^{\text{on}} P^{\text{in}} t} + c_1^{\text{eq}} \end{array} \right.$$

$$\Rightarrow M_2^{measured} = M_2^{in} - \frac{2}{P^{in}}(M^{in} + c_1^{in} - c_1^{eq})(c_1^{in} - c_1^{eq})(e^{-k^{on}P^{in}t} - 1) \\ + \frac{(c_1^{eq} - c_1^{in})^2}{P^{in}}(e^{-2k^{on}P^{in}t} - 1) + 2k^{dep}P^{in}t,$$

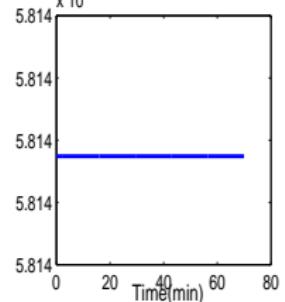
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\Rightarrow By the least squared method :

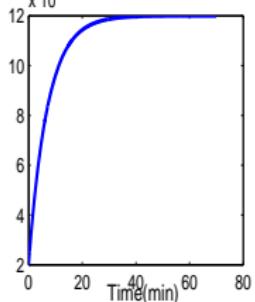
$$J(k^{on}, k^{dep}, \alpha, \beta) = \sum_{i=1}^n \left| \left(\alpha M_2^{measured} (t_i; k^{on}, k^{dep}) + \beta \right) - SLS(t_i) \right|^2$$



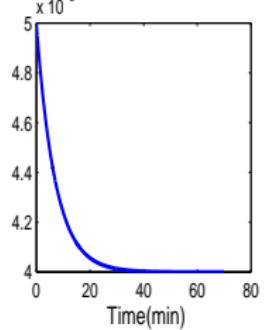
The total concentration of all fibrils



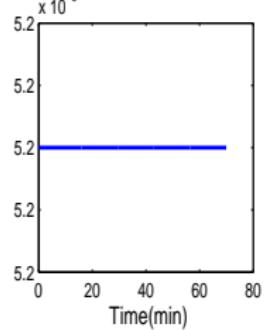
The total mass of all fibrils



The monomer concentration

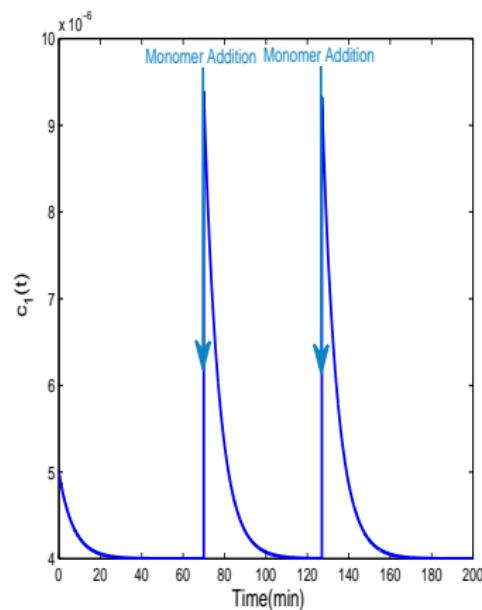
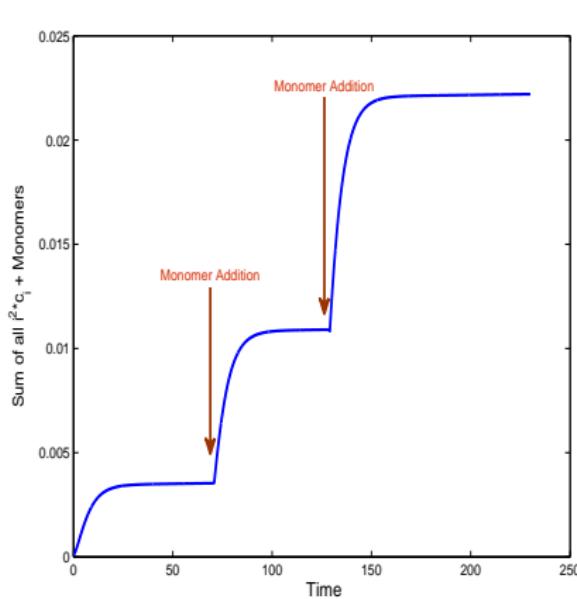


The total mass of all fibrils + Monomers



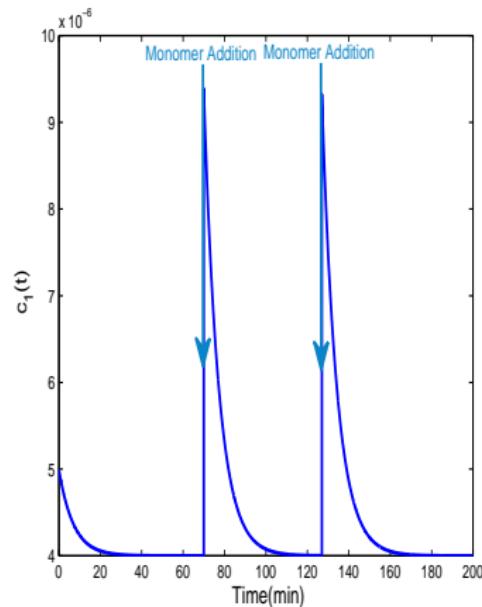
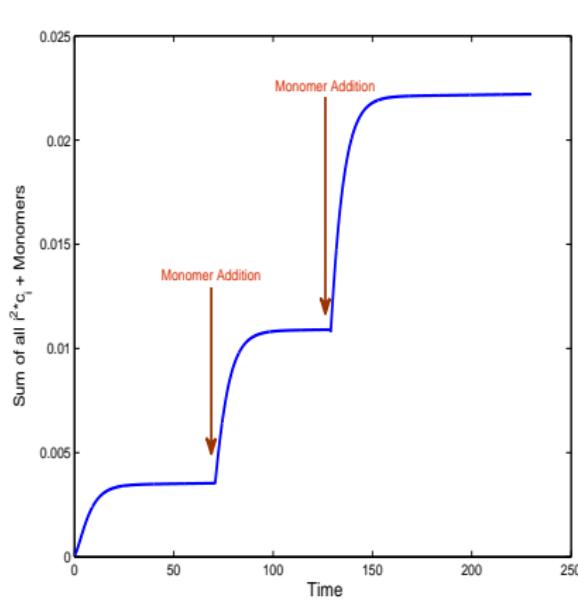
$$\Rightarrow k^{\text{on}} = 2.7 \cdot 10^8 \text{ mol.L}^{-1} \cdot \text{min}^{-1} \text{ and } k^{\text{dep}} = 950 \text{ min}^{-1}$$

► Further monomer addition :



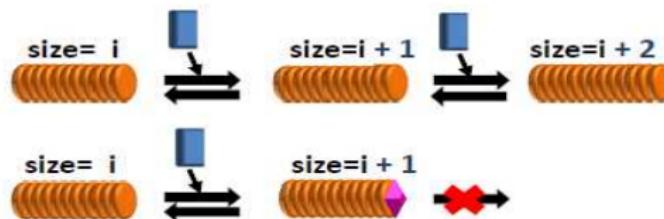
High monomer consumption \rightarrow High increase of i \rightarrow High gaps in $\sum i^2 c_i$.

► Further monomer addition :



High monomer consumption \rightarrow High increase of $i \rightarrow$ High gaps in $\sum i^2 c_i$.
 The polymerization is not slowing down.

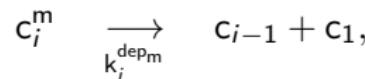
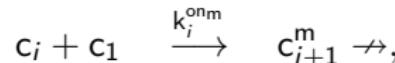
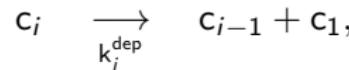
A “**deficient**” fibril would be created by the polymerization of a “**classical**” fibril with a polymerization rate k^{on_m} .



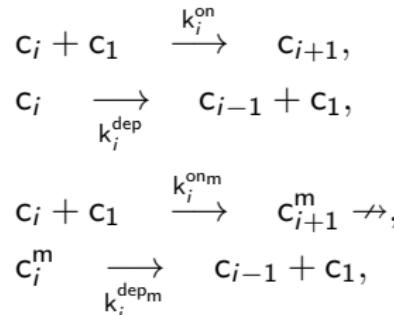
So that :

$$M_2^{measured} = \alpha \left(\sum_{i=1}^{\infty} i^2 c_i + \sum_{i=1}^{\infty} i_m^2 c_i^m \right) + \beta.$$

↪ The reactions scheme :

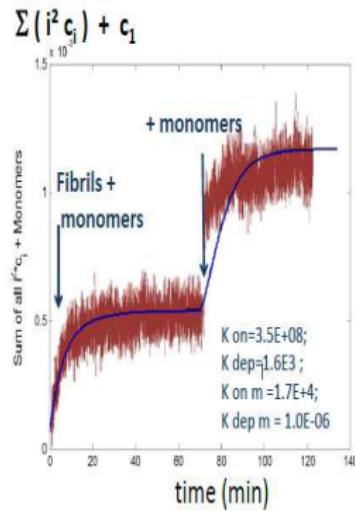
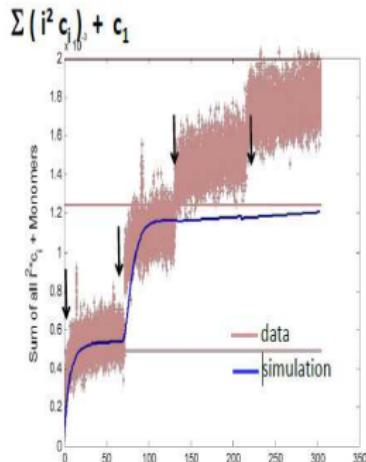


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 \begin{aligned}
 \frac{dc_i}{dt} &= -k_i^{\text{on}}c_1c_i + k_{i-1}^{\text{on}}c_1c_{i-1} - k_i^{\text{onm}}c_1c_i - k_i^{\text{dep}}c_i \\
 &\quad + k_{i+1}^{\text{dep}}c_{i+1} + k_{i+1}^{\text{dep}_m}c_{i+1}^m, \quad i \geq 2 \\
 \frac{dc_i^m}{dt} &= k_{i-1}^{\text{onm}}c_1c_{i-1} - k_i^{\text{dep}_m}c_i^m, \quad i \geq 3 \\
 \frac{dc_1}{dt} &= -\sum_{i=2}^{\infty} k_i^{\text{on}}c_1c_i - \sum_{i=2}^{\infty} k_i^{\text{onm}}c_1c_i + \sum_{i=2}^{\infty} k_i^{\text{dep}}c_i + \sum_{i=3}^{\infty} k_i^{\text{dep}_m}c_i^m \\
 &\quad - 2(k_1^{\text{on}}c_1^2 - k_2^{\text{dep}}c_2)
 \end{aligned}
 \right.$$

Fitting the 2nd plateau.Fitting till the 4th plateau.

On contrast to the basic model,
the defective fibril model => a correct 2nd plateau height

But slopes of the 2nd and next additions : not satisfactory.

- The discrete model is able to fit the first steps of the experiments, converging to a size-distribution that fits the size-distribution of fibrils experimentally formed.
 - Giving an idea about the order of the kinetics parameters.
- Further work :
- Trying a successive inactivation pathway.
 - Varying the kinetics parameters (Continuous model).
 - Use the new data with more known parameters (α, β, c^{in}).
 - Scheme considering a two-ends polymerization.