A Model Derivation

Each arrow in our network abstraction (presented in Figure **??**) corresponds to a coalescing or dissolving aggregation reaction. These reactions follow the law of mass action, allowing us to transform the list of chemical reactions into a system of differential equations that describe the concentration of each Amyloid-β species. The governing equations reflect the dynamics of aggregation, dissociation, and conversion of the various oligomers in the system. The parameters associated with these reactions are summarized in Table **??**.

The system of equations that governs the evolution of the concentrations of each Amyloid-β species is given by:

$$
\begin{aligned}
&\frac{dA_1}{dt} = nk_2^- A_n - nk_2^+ A_1^n + k_1^- A_1' - k_1^+ A_1 L,\\
&\frac{dA_1'}{dt} = nk_3^- A_n' - nk_3^+ A_1'^n + k_1^+ A_1 L - k_1^- A_1',\\
&\frac{dA_n}{dt} = k_2^+ A_1^n + \frac{m}{n} k_5^- A_m + k_4^- A_n' - k_2^- A_n\\
&-k_4^+ A_n L^n - \frac{m}{n} k_5^+ A_n^{\frac{m}{n}},\\
&\frac{dA_n'}{dt} = k_3^+ A_1'^n + k_4^+ A_n L^n + \frac{m}{n} k_6^- A_m' - k_3^- A_n'\\
&-\frac{m}{n} k_6^+ A_n' - k_4^- A_n^{\frac{m}{n}},\\
&\frac{dA_m}{dt} = k_5^+ A_n^{\frac{m}{n}} - k_5^- A_m,\\
&\frac{dA_m'}{dt} = k_6^+ A_n'^{\frac{m}{n}} - k_6^- A_m,
\end{aligned}
$$

The reaction constants are defined as:

$$
\begin{aligned}
&\alpha_1 = \frac{k_2^-}{k_1^-}; \alpha_2 = \frac{k_2^+ A_0^{n-1}}{k_1^-}; \alpha_3 = \frac{k_1^+ L}{k_1^-}; \alpha_4 = \frac{k_4^+ L}{k_1^-};\\
&\alpha_5 = \frac{k_5^-}{k_1^-}; \beta_1 = \frac{k_3^-}{k_1^-}; \beta_2 = \frac{k_3^+ A_0^{n-1}}{k_1^-}; \beta_3 = \frac{k_5^+ A_0^{\frac{m}{n}-1}}{k_1^-};\\
&\beta_4 = \frac{k_4^-}{k_1^-}; \beta_5 = \frac{k_6^-}{k_1^-}; \beta_6 = \frac{k_6^+ A_0^{\frac{m}{n}-1}}{k_1^-}
\end{aligned}
$$

This system is then non-dimensionalized. Using A_0 as the characteristic concentration of monomers and $\frac{1}{k_1^-}$ as the characteristic time, we define the dimensionless species as follows:

$$B_1 = \frac{A_1}{A_0}; B_n = \frac{A_n}{A_0}; B_m = \frac{A_m}{A_0}; \tag{1}$$

$$B_1^{'} = \frac{A_1^{'}}{A_0}; B_n^{'} = \frac{A_n^{'}}{A_0}; B_m^{'} = \frac{A_m^{'}}{A_0} \tag{2}$$

B Parameter Identifiability

Profile likelihood is a statistical method particularly useful for evaluating the confidence intervals of parameters in complex models. The likelihood function for a set of parameters θ (of interest) and ψ (nuisance parameters) based on observed data X is given by:

$$L(\theta, \psi; X)$$

The profile likelihood for θ is defined by maximizing the likelihood function over the nuisance parameters ψ for each fixed value of θ:

$$L_P(\theta; X) = \max_{\psi} L(\theta, \psi; X)$$

To estimate a confidence interval for θ, we use the profile likelihood ratio:

$$R(\theta) = \frac{L_P(\theta; X)}{L_P(\hat{\theta}; X)}$$

where $\hat{\theta}$ is the maximum likelihood estimate of θ, obtained by maximizing $L_P(\theta; X)$ over θ.

A 95% confidence interval for θ can then be approximated by finding the values of θ for which $R(\theta)$ exceeds a critical value, typically based on the chi-square distribution:

$$\{\theta : -2 \log R(\theta) \leq \chi^2_{1,0.05}\}$$

This method adjusts the likelihood function to account for the uncertainty in the nuisance parameters, providing a more accurate and robust estimation of the confidence interval for the parameter of interest.