

SIA for Model 1 using the Taylor series approach

ODE system

$$\text{mRNA}'[t] = -k_1 - k_2 * \text{mRNA}[t]$$

$$\text{Protein}'[t] = k_3 * \text{mRNA}[t] - k_4 * \text{Protein}[t]$$

Initial conditions: mRNA[0]=2.5, Protein[0]=6.5

Both states are observed and all parameters are assumed to be unknown

First two derivatives for each state for when $t = 0$

$$\text{mRNA}'[0] = -k_1 - 2.5 k_2$$

$$\text{mRNA}''[0] = -(-k_1 - 2.5 k_2) k_2$$

$$\text{Protein}'[0] = 2.5 k_3 - 6.5 k_4$$

$$\text{Protein}''[0] = (-k_1 - 2.5 k_2) k_3 - (2.5 k_3 - 6.5 k_4) k_4$$

Recall that the derivatives are assumed to be known and have unique solutions which can be used to assess the SIA of models

Analysis of Taylor series coefficients

1. mRNA'[0] can be substituted into mRNA''[0] which leaves k_2 as the only unknown parameter and thus k_2 is identifiable
2. Since k_2 is identifiable, k_1 can be identified from mRNA'[0]
3. Use Protein'[0] to solve for k_3 : $k_3 \rightarrow 2.6 k_4 + 0.4 \text{Protein}'[0]$
4. Substitute new solution for k_3 into Protein''[0], which leaves k_4 as the only unknown parameter and thus k_4 is now identifiable
5. This means that k_3 can now be identified using step 3 and thus all the parameters have been identified and Model 1 is structurally identifiable