
Data Assimilation for Systems and Mathematical Biology

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Abstract

Mathematical models are increasingly used as a tool to deal with the tremendous complexity of biological systems. Data Assimilation, defined as the process of combining models with experimental observations, is a key step in order to better align the model outputs with reality. Despite new and improved experimental techniques, it is usually impossible to directly observe all the states of a biological system. This renders Data Assimilation an inverse problem requiring sophisticated mathematical and statistical techniques and the systematic integration of prior knowledge or assumptions.

1 Introduction

2 The Data Assimilation problem

3 Outlook

$$\dot{\mathbf{x}} = \underbrace{\begin{pmatrix} k_t B_{max} - k_t x_1 - k_{on} x_1 x_2 + k_{off} x_3 + k_{ex} x_4 \\ -k_{on} x_1 x_2 + k_{off} x_3 + k_{ex} x_4 \\ k_{on} x_1 x_2 - k_{off} x_3 - k_e x_3 \\ k_e x_3 - k_{ex} x_4 - k_{di} x_4 - k_{de} x_4 \\ k_{di} x_4 \\ k_{de} x_4 \end{pmatrix}}_{\mathbf{f}(\mathbf{x})}$$
$$\mathbf{y} = \underbrace{\begin{pmatrix} \kappa_1 (x_2 + 2x_6) \\ \kappa_2 (x_3) \\ \kappa_3 (x_4 + x_5) \end{pmatrix}}_{\mathbf{h}(\mathbf{x})}$$

x_1 : EpoR

x_2 : Epo

x_3 : Epo-EpoR

x_4 : Epo-EpoR_{*i*}

x_5 : dEpo_{*i*}

x_6 : dEpo_{*e*}

y_1 : Epo + dEpo_{*i*}

y_2 : Epo-EpoR

y_3 : Epo-EpoR_{*i*} + dEpo_{*i*}

x_1	x_2	x_3	x_4	x_5	x_6
EpoR	Epo	Epo-EpoR	Epo-EpoR _{<i>i</i>}	dEpo _{<i>i</i>}	dEpo _{<i>e</i>}

y_1	y_2	y_3
Epo + dEpo _{<i>i</i>}	Epo-EpoR	Epo-EpoR _{<i>i</i>} + dEpo _{<i>i</i>}

To illustrate different aspects of DA we will use a model for the information processing at the erythropoietin (Epo) receptor (EpoR) as a running example [?]. The state $\mathbf{x} = (x_1, \dots, x_6)^T$ of this model is given by the concentrations of the Epo receptor (x_1) on the cell surface which can bind to Epo (x_2) and build the ligand-receptor complex (x_3). This complex is able to activate subsequent signaling cascades, e.g. the JAK-STAT signaling pathway. In addition the ligand-receptor complex can be internalized (x_4) and dissociate from Epo which then is degraded (x_5) and transported to the extracellular space (x_6).

$$\begin{aligned}
\dot{x}_1 &= k_t B_{max} - k_t x_1 - k_{on} x_1 x_2 + k_{off} x_3 + k_{ex} x_4 \\
\dot{x}_2 &= -k_{on} x_1 x_2 + k_{off} x_3 + k_{ex} x_4 \\
\dot{x}_3 &= k_{on} x_1 x_2 - k_{off} x_3 - k_e x_3 \\
\dot{x}_4 &= k_e x_3 - k_{ex} x_4 - k_{di} x_4 - k_{de} x_4 \\
\dot{x}_5 &= k_{di} x_4 \\
\dot{x}_6 &= k_{de} x_4 \\
y_2 &= \kappa_1 (x_2 + 2x_6) \\
y_1 &= \kappa_2 (x_3) \\
y_3 &= \kappa_3 (x_4 + x_5),
\end{aligned}$$

The complex regulation of this receptor is characterized by receptor mobilization, turnover and recycling. The rate constants correspond to (i) receptor turnover (k_t), (ii) ligand-receptor binding (k_{on}) or dissociation (k_{off}), (iii) ligand-induced endocytosis (k_e), (iv) recycling (k_{ex}) and (v) internal (k_{di}) or external (k_{de}) degradation of Epo. Only the the Epo concentration in medium (y_1), on surface (y_2) and in cells (y_3) can be measured up to some scaling parameters κ_j , $j \in \{1, 2, 3\}$.

$$\begin{aligned}
\dot{\mathbf{x}} &= \underbrace{\begin{pmatrix} k_t B_{max} - k_t x_1 - k_{on} x_1 x_2 + k_{off} x_3 + k_{ex} x_4 \\ -k_{on} x_1 x_2 + k_{off} x_3 + k_{ex} x_4 \\ k_{on} x_1 x_2 - k_{off} x_3 - k_e x_3 \\ k_e x_3 - k_{ex} x_4 - k_{di} x_4 - k_{de} x_4 \\ k_{di} x_4 \\ k_{de} x_4 \end{pmatrix}}_{\mathbf{f}(\mathbf{x}, \mathbf{u})} \begin{matrix} \text{EpoR} \\ \text{Epo} \\ \text{Epo-EpoR} \\ \text{Epo-EpoR}_i \\ \text{dEpo}_i \\ \text{dEpo}_e \end{matrix} \\
\mathbf{y} &= \underbrace{\begin{pmatrix} \kappa_1 (x_2 + 2x_6) \\ \kappa_2 (x_3) \\ \kappa_3 (x_4 + x_5) \end{pmatrix}}_{\mathbf{h}(\mathbf{x})} \begin{matrix} \text{Epo} + \text{dEpo}_i \\ \text{Epo-EpoR} \\ \text{Epo-EpoR}_i + \text{dEpo}_i \end{matrix}
\end{aligned}$$

A Appendix name