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**Deep learning of biological models from data: applications to ODE models.** (English)

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Summary: Mathematical equations are often used to model biological processes. However, for many systems, determining analytically the underlying equations is highly challenging due to the complexity and unknown factors involved in the biological processes. In this work, we present a numerical procedure to discover dynamical physical laws behind biological data. The method utilizes deep learning methods based on neural networks, particularly residual networks. It is also based on recently developed mathematical tools of flow-map learning for dynamical systems. We demonstrate that with the proposed method, one can accurately construct numerical biological models for unknown governing equations behind measurement data. Moreover, the deep learning model can also incorporate unknown parameters in the biological process. A successfully trained deep neural network model can then be used as a predictive tool to produce system predictions of different settings and allows one to conduct detailed analysis of the underlying biological process. In this paper, we use three biological models – SEIR model, Morris-Lecar model and the Hodgkin-Huxley model – to show the capability of our proposed method.

**MSC:**

92B20 Neural networks for/in biological studies, artificial life and related topics

68T07 Artificial neural networks and deep learning

92D30 Epidemiology

92C20 Neural biology

**Keywords:**

deep neural network; residual network; mathematical biology; governing equation discovery

**Software:**

LSODE; TensorFlow; Adam; PDE-Net; VAMPnets; torchdiffeq; Keras; GitHub

**Full Text:** DOI

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