PLOS Computational Biology Editorial Board

Sète, 25th March 2021

## Article Submission: Deep Learning and Trajectory Representation for the prediction of seabird diving behaviour

Dear Editor.

We are happy to present our draft of a research article so-called "Deep learning and trajectory representation for the prediction of seabird diving behaviour"

With technological advances in sensor technology, ecologists are able to collect larger amount of data than ever before. In particular, GPS are used to record high-resolution animal trajectories, and this makes more critical the need of new tools to analyze such trajectory data. This study provides insight on the use of deep learning tools for predicting animal behaviour from trajectory data.

Indeed, in this study we predict dives in seabird from GPS data using deep learning, and to this end we propose a novel deep learning model for trajectory data. It combines the computational efficiency of convolutional neural networks to distance-matrix-based representations of trajectory data. We report thus considerable increase in the ability of deep networks to infer behaviours, as well as their stability to different data inputs. The considered trajectory data representation enables deep networks to better capture spatial information than from longitude and latitude time-series considered in previous works.

We also wanted to notify that we have placed the "Material and Method" section after the introduction. Indeed, this work compares the performances of neural networks in response to different data input and representations. Thus, we believe that it is necessary for the reader to know precisely the data, and the different pre-processing approaches to better interpret the results. This trajectory-based segmentation case-study raises however very general question on representation of trajectory data for deep learning tasks. Our results at the interface of movement ecology and artificial intelligence could benefit to numerous biologists dealing with trajectory data. Thus, we think that our work fits the aim of PLOS Computational Biology.

Thank you for your consideration,

Yours sincerely,

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