Predicting animal movement with deepSSF: a deep learning step selection framework

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Introduction

Predictions of animal movement are vital for understanding and managing wild populations. However, the fine-scale, complex decision-making of animals poses challenges for the accurate prediction of trajectories. Step selection functions (SSFs), a common tool for inferring relationships between animal movement and the environment, are increasingly used also to simulate animal trajectories for prediction. Although admitting a lot of flexibility, the SSF framework is limited to its reliance on pre-defined functional forms for fitting to data. SSFs that involve complex functional forms to model detailed processes can also be prohibitively difficult to fit and interpret, particularly when models include interactions such as multi-scale temporal dynamics.

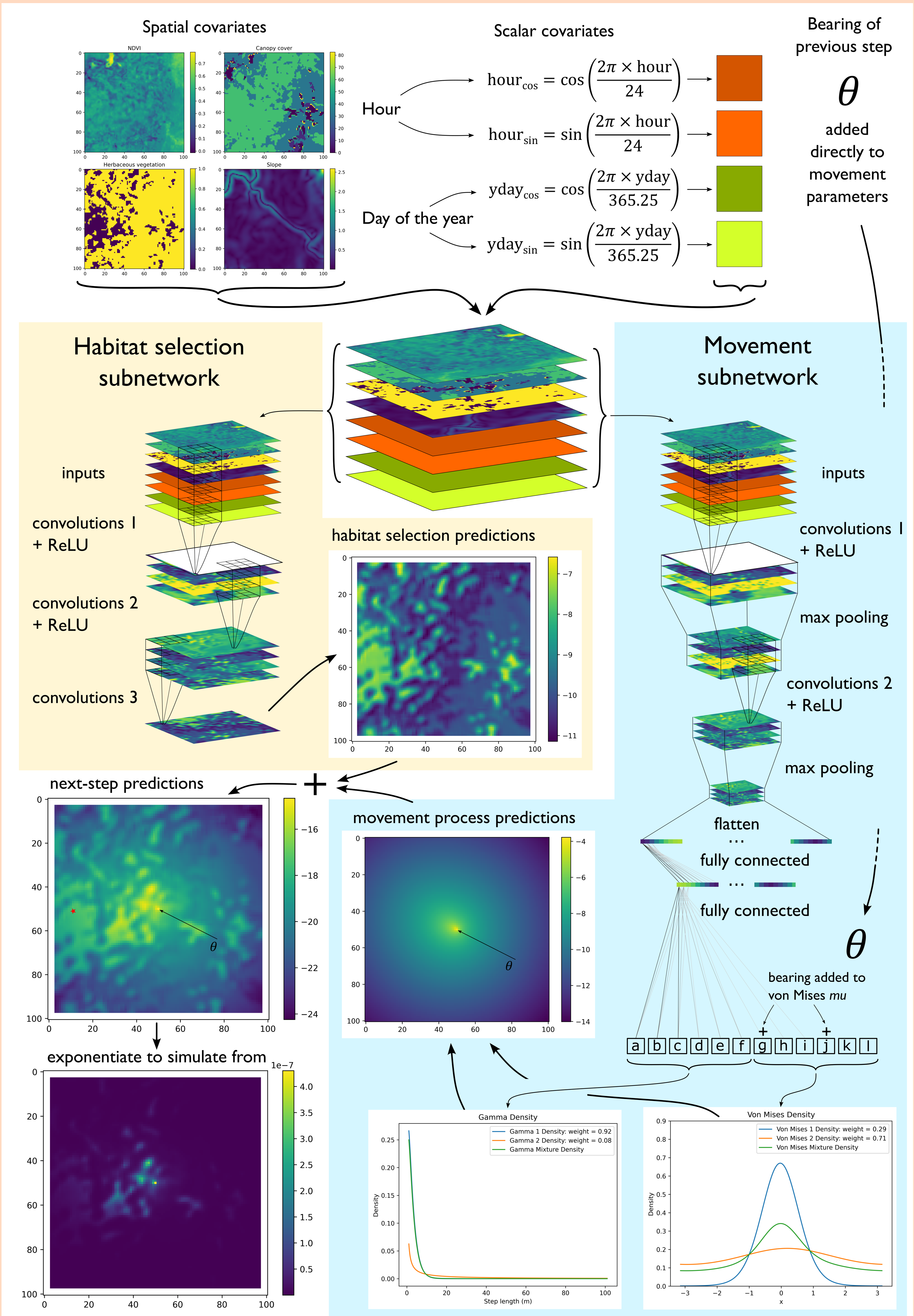
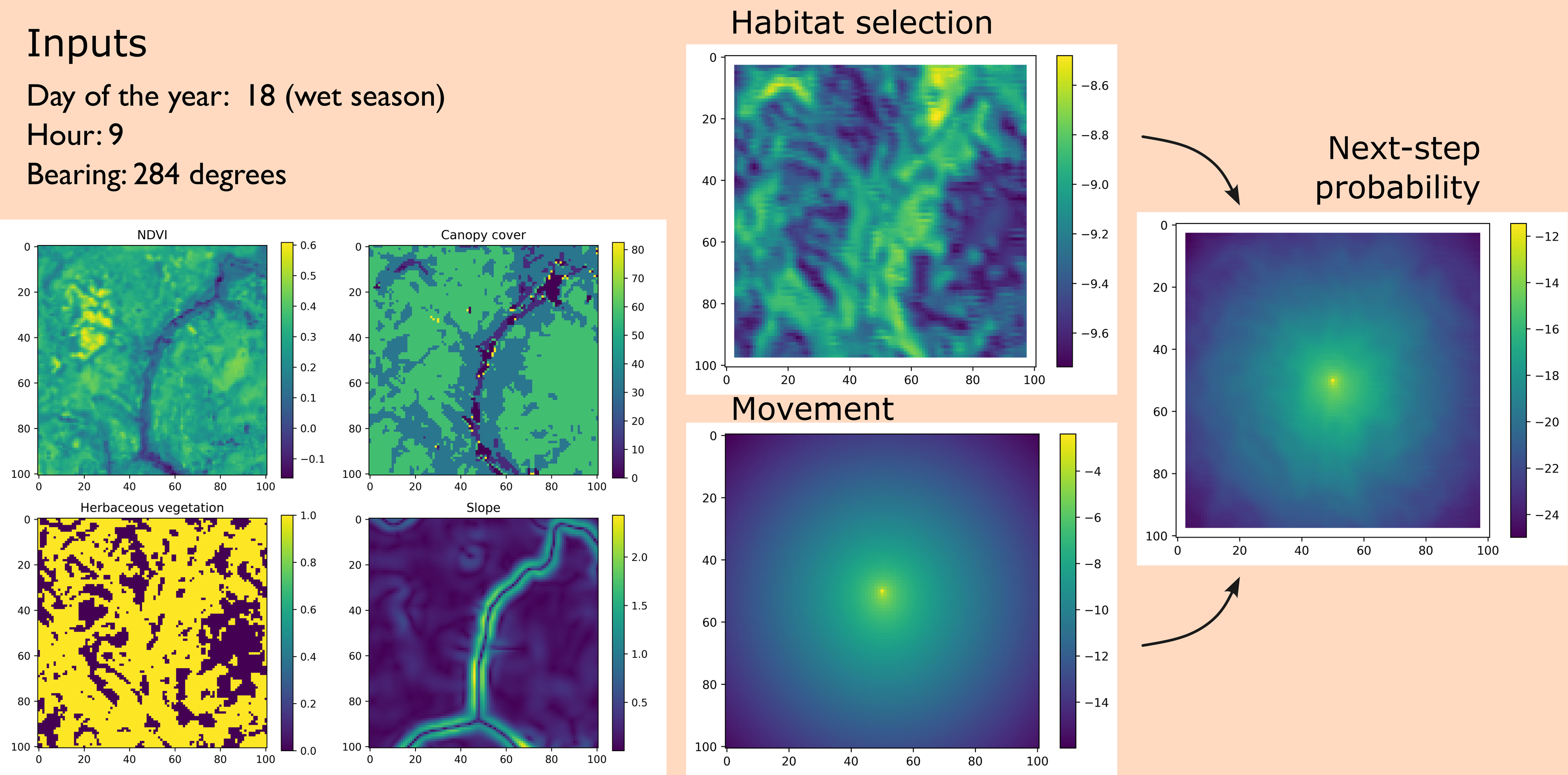


Figure 1: Overview of the deepSSF model used to predict animal movement. There are two subnetworks: a habitat selection and a movement process subnetwork. Both receive the same inputs, which are spatial layers such as environmental covariates, scalar covariates such as the hour and the day of the year (yday), and the bearing of the previous step. The periodic components (i.e. hour and yday) are decomposed into sine and cosine components before being converted into spatial layers with constant values so they can be processed by the convolution layers. The ...

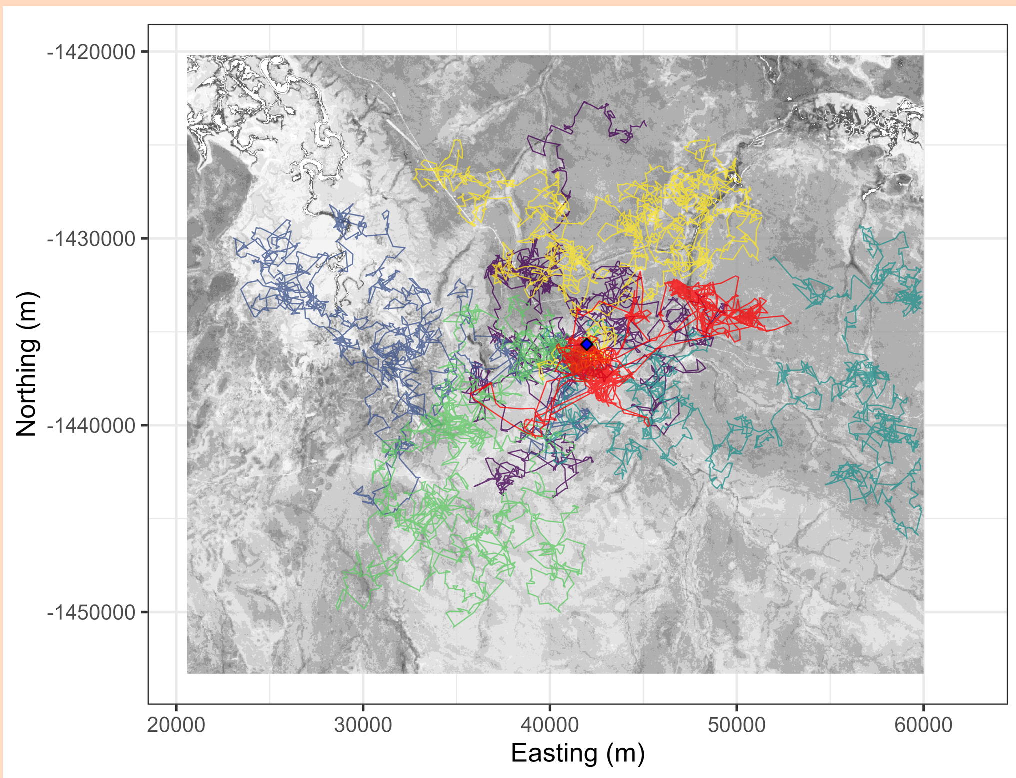
Approach and Methods

Here, we present **deepSSF**, an approach to fit and predict from animal movement data using deep learning. Whilst not specific to any particular model architecture, we denote the **deepSSF** approach as building and training a neural network architecture that receives multiple environmental layers and scalar values as inputs, and puts out a single layer representing the next-step probability. To demonstrate a **deepSSF** model, we built a model in PyTorch that has distinct but interacting habitat selection and movement subnetworks, which allows for explicit representation of both processes and for interpretable intermediate outputs. We apply our model to GPS data of invasive water buffalo (*Bubalus bubalis*) in Northern Australia's tropical savannas.



Main Results and Conclusions

The **deepSSF** model was able to learn features that are present in the habitat covariate layers, such as linear features (rivers, forest edges), and the composition or size of certain habitat areas, without having to specify them pre-emptively within the SSF framework. It was also able to capture the complex interactions between the habitat covariates as well as temporal dynamics across time of day and year. In the context of our buffalo data, we found habitat selection behaviour that varied drastically across the hours of the day, which aligns with previous research, and the model was able to accurately capture the observed movement dynamics. We were also able to generate landscape-scale habitat selection predictions from the trained convolution filters.



Scan for animations, additional details and results

Figure 2: Trajectories simulated from the deepSSF model. The red trajectory is the observed buffalo GPS data, and each of the other colours represents a simulated trajectory. The background is Normalised Difference Vegetation Index (NDVI), with higher values as darker colours, which roughly represents more productive vegetation.

.... habitat selection subnetwork uses convolution layers with parameters set to ensure that the output has the same spatial extent as the input, resulting in spatial, non-linear transformations of the input covariates, where all inputs can interact. The movement process subnetwork uses convolution layers with max pooling to extract features from the input covariates that are salient to movement, and fully-connected layers to process the convolution outputs whilst reducing the dimensionality. The predicted output of the movement subnetwork can be any number of parameters than govern a movement distribution, so we used finite mixtures of two Gamma distributions for the step lengths and two von Mises distributions for the turning angles. This results in a total of 12 predicted parameters - a shape, scale and weight for each Gamma distribution and a mean, kappa (concentration) and weight for each von Mises distribution. To ensure that the turning angles are relative to the previous step, the bearing of the previous step is added directly to the predicted mean parameters of von Mises distributions. The parameters are then converted to a two-dimensional movement probability surface which is added to the habitat selection predictions on the log-scale, resulting in a next-step probability surface. To generate trajectories, the next-step probability surface is exponentiated and a step is sampled according to the probability values. To highlight the directional persistence, the arrow and *theta* in the movement and next-step predictions denotes the bearing of the previous step, and the red star to the left of the next-step predictions is the location of the observed next step for those inputs.