

Abstract Submitted
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Discovering fine structure in big biological data¹ ALEXANDRE DAY, PANKAJ MEHTA, Boston University, AMIR EREZ, GRGOIRE ALTAN-BONNET, National Institute of Health — Modern experimental methods allow for an unprecedented high-dimensional single-cell resolution of complex tissues. We propose a novel and robust method to perform deep unsupervised learning to discover and analyze the structure of such data. Our approach harvest the power of neural networks to self-consistently identify and validate sub-structures in the data. We test our method on multi-dimensional protein distributions and show that while we are able to reproduce some experimental benchmarks, our approach is able to uncover previously unidentified structures in the data. We use our approach as a basis to modelling the population distribution of dynamical biological datasets.

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Alexandre Day
Boston Univ

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