GBSBC

Genetics, Bioinformatics, & Systems Biology Colloquium

presents

David Kelley, PhD

Principal Investigator

Calico Life Science

📅 **THURSDAY APRIL 6**
🕐 **12PM**
📍 **LEICHTAG AUDITORIUM**
📹 **ZOOM**

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scBasset: sequence-based modeling of single-cell ATAC-seq using convolutional neural networks

Single-cell ATAC-seq shows great promise for studying cellular heterogeneity in epigenetic landscapes, but there remain important challenges in the analysis of scATAC data due to the inherent high dimensionality and sparsity. I'll describe scBasset, a sequence-based convolutional neural network method to model scATAC data. We show that by leveraging the DNA sequence information underlying accessibility peaks and the expressiveness of a neural network model, scBasset achieves state-of-the-art performance across a variety of tasks on scATAC and single-cell multiome datasets, including cell clustering, profile denoising, data integration across assays and transcription factor activity inference.

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