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Type	Poster
Session	Systems Biology
Title	Emergent statistical laws in single-cell transcriptomic data
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Motivation

Large scale data on single-cell gene expression have the potential to unravel the specific transcriptional programs of different cell types. The structure of these expression data sets suggests a similarity with several other complex systems that can be similarly described through the statistics of their basic building blocks.

Methods

Transcriptomes of single cells are collections of messenger RNA abundances from a common set of genes just as books are collections of different words from a shared vocabulary or genomes of different species are specific compositions of genes belonging to different evolutionary families. Following this analogy, we identify several emergent statistical laws in single-cell transcriptomic data closely similar to regularities found in linguistics, ecology or genomics. A simple mathematical framework, inspired by statistical physics, can be used to analyze the relations between different laws and the possible mechanisms behind their ubiquity.

Results

Treatable statistical models can be useful tools in transcriptomics to disentangle general statistical effects present in most component systems from the consequences of the sampling process inherent to the experimental technique and the actual biological variability.

Info

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Figure

Availability	https://drive.google.com/file/d/1UWBvokzdKJ723mHJjHm1zwZFn3GeiR84/view?usp=sharing

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