

## **Inference and prediction in biological systems at the molecular, cellular, and cell-population levels**

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The traditional computational systems approach seeks to provide the emergent collective behavior from the properties of the constituent elements. This goal is severely challenged by the molecular and mechanistic complexity of typical biological systems, which often results in a nonexistent, deficient, or misleading characterization of the underlying molecular components and their interactions. I will discuss the state of the art of novel approaches that function in reverse, namely, that use the emergent behavior to infer precise properties of the molecular components and that are able to make accurate predictions about the system behavior even without a basic molecular description. I will illustrate the main points with key examples in gene regulation and signal transduction.