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Maximum entropy, Nonadditive entropies and Biology

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Gibbs once presciently noted that the elegance and simplicity of the principles of statistical physics were worthy of independent development outside of thermodynamics. Biophysical systems –from the single cell to the single protein level– provide an ideal framework in which to test and apply far-from-equilibrium generalizations of statistical physics. Here we discuss two theoretical topics at the intersection of statistical physics and biology. First, we will describe a recipe for deriving, from first principles, probabilistic equations of motion from limited biophysical single particle tracking data. That is, we will show that maximum entropy principles can be used to determine the most likely statistical weights of trajectories from an ensemble of allowed system trajectories. For instance, using this reasoning, we can show under what circumstances Markov processes and chemical master equations rigorously follow from the data. Second, we will explore the logical implications of using a principle other than maximum entropy to select models (e.g. a model could be a trajectory ensemble in conformational space of a biomolecule) from non-equilibrium biophysical data. In particular, we will show that nonadditive entropy maximization can lead to biophysical models with features that go beyond what is warranted by the data.