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**Analyzing Single Molecule Measurements With Bayesian Non-Parametric Methods** IOANNIS SGOURALIS, STEVE PRESSE, Arizona State University — Single molecule measurements are commonly modeled and analyzed by means of Bayesian statistics. Despite their popularity, the traditional Bayesian methods can lead to overfitting mainly because they require the number of different states the molecule attains to be pre-specified and fixed. In the talk, I will present methods that lift this requirement and thus that avoid overfitting. These methods utilize novel concepts from Bayesian non-parametric statistics and allow full posterior inference without assuming a pre-specified or fixed number of molecular states. This characteristic makes them ideal for the analysis of biophysical data, especially as alternatives to the existing methods which are based on model selection and information criteria.

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