1057-92-130 **Steven N. Evans**, **Valerie Hower*** (`vhower@math.berkeley.edu`) and **Lior Pachter**. *Using sequence coverage statistics to determine protein binding sites in a genome.*

Inspired by the notion of persistence in topological data analysis, we introduce a tree depicting sequence coverage via fragment placement on a genome. We then describe statistically the trees that correspond to random fragment placement and use this theory to determine the binding sites for a given protein in a genome. Our method for calling statistically significant protein binding sites reduces to the study of certain tree-based statistics derived from the data. (Received January 18, 2010)