1056-92-1506 **Valerie Hower*** (vhower@math.berkeley.edu) and **Lior Pachter** (lpachter@math.berkeley.edu). *A persistence tree-based method for calling peaks in ChIP-seq protein binding analysis.*

We present a new algorithm for analyzing ChIP-seq data. ChIP-seq is a relatively new assay for measuring the interactions of proteins with DNA. The binding sites for a given protein in a genome are "peaks" in the data, which is given by an integer-valued height function f defined on the genome. We present a method for identifying statistically significant peaks in ChIP-seq data that is inspired by the notion of persistence in topological data analysis. Our method reduces the peak calling problem to the study of certain tree-based statistics derived from the data. (Received September 22, 2009)