Elucidation of an organism’s transcription regulatory network is of key importance in understanding normal and pathological cell function and differentiation. Built upon and significantly extending our previous *de novo* search algorithms, our Phylogenetic Gibbs Centroid Sampler algorithm locates DNA *cis*-regulatory elements, in mixed aligned and unaligned DNA sequence data, with good sensitivity and a low false positive rate.

The algorithm’s key improvements are the full incorporation of a phylogenetic model, to avoid the confounding effects of correlated sequence data, and its goal of seeking a centroid solution instead of a maximum posterior probability solution. By focusing on the centroid, the region of solution space containing the most posterior probability, rather than on the single solution that is most probable, we demonstrably enhance the sensitivity and predictive power of the algorithm. Furthermore, the calculation of a centroid solution does not require the integrating out of statistical “nuisance” variables, a task that has compromised the accuracy and speed of previous attempts to fully incorporate a phylogenetic model.

*The centroid approach is applicable beyond the immediate task; we expect that this facet of the poster presentation will be of use to computational biologists outside of the immediate cell-regulation field.*