Extended abstract (250 characters at most):

Most previous methods based on Gibbs sampling aimed at detecting regulatory motifs in the promotor regions of co-regulated genes of one species, where motifs are detected by scoring their degree of overrepresentation. Although these Gibbs sampling based motif detection approaches have been successfully applied to also detect motifs in the orthologous space (in the promotor regions of orthologous genes) (1,2), they are in fact not suited to take into account the phylogenetic relatedness between the orthologs. Some of the more recent approaches overcome this problem by scoring the evolutionary relation of the detected motifs to a common ancestor. These phylogenetic footprinting algorithms can be classified into either comparative methods where motif evolution is ‘slower than’ background evolution (3), or the more advanced ab initio methods using an explicit motif evolution model (4).

In this study we adapted our previously developed motif detection tool MotifSampler in order to search for motifs in the coexpression and orthologous gene space simultaneously. NOrthoSampler - the adaptation of MotifSampler - uses a probabilistic approach, a Gibbs Sampling strategy, an explicit model for motif evolution, and it scores potential regulatory motifs with an integrated dual-space conservation score. NOrthoSampler does not need sequences to be prealigned which makes it attractive for datasets where such alignment is unreliable. The use of this algorithm will enable to study evolution of motifs over time, over species and over different genes within a species.

Reference List: