

RegGen SIG 2013 - Abstract for poster presentation

**Authors:**

Marleen Claeys<sup>1</sup>, Kathleen Marchal<sup>1,2,3</sup>

<sup>1</sup> CMPG-bioi, Department of Microbial and Molecular Systems, KU Leuven, Belgium, <sup>2</sup> Department of Plant Biotechnology and BioInformatics, <sup>3</sup> VIB Department of Plant Systems Biology, UGhent, Belgium

**Title:**

Regulatory motif detection using different types of evolutionary conservation information.

**Abstract (250 words at most):**

Computational methods, which search *de novo* for conserved sites in a non-functional background, have been proven successful for the prediction of regulatory motifs. Conservation is typically quantified by overrepresentation (in the promotor regions of coregulated genes) and/or by evolutionary conservation in the promotor regions of orthologous genes.

We present 3 different adaptations of our well known overrepresentation based motif detection tool MotifSampler in order to search in both spaces of conservation simultaneously. Each adaptation quantifies evolutionary conservation in a different way : from 1) robust counting (MotifSampler-cPSP, allows the use of a position specific prior built by counting the occurrences of sites in orthologs), over 2) a comparative approach (NOrthoMotifSampler, assumes motif evolution is 'slower than' background evolution in orthologs), to 3) explicit evolution modeling (PhyloMotifSampler, uses a motif evolution model adapted from FelsensteinF81). MotifSampler-cPSP is most suitable for datasets with phylogenetically closely related orthologs whereas NOrthoMotifSampler is most sensitive in detecting sites that have mutated over time (in distantly related orthologs). PhyloMotifSampler finds motifs well in closely as well as distantly related orthologs yet with a lower site annotation accuracy and longer runtime. Neither of the newly developed tools requires prealignment of the orthologs which makes them attractive for datasets where such alignment is unreliable.