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<i>Position</i>	PhD Student
<i>Title</i>	Computational Discovery of Cis-Regulatory Sites in Eukaryotic Genomes by Collective Inference
<i>Presentation Preference</i>	Poster

Abstract

Background: Motif discovery in eukaryotic genomes is an abstraction process that describes regulatory DNA sequences as collections of cis-regulatory sites. The abstract representation enables researchers to decipher complex gene regulatory networks. In silico methods prioritize cis-regulatory sites and aim to increase the efficiency of arduous wet lab research. Computational discovery of cis-regulatory sites is however an ill-posed problem, resulting in many false positive detections.

Approach: We formulate the problem as a constraint-based inference problem (CBIP) [1] and infer a set of sites simultaneously (called cis-regulatory modules [2]) by adding consistency constraints in an attempt to make the problem well-posed. We describe how a collective of computational agents can serve as a framework to solve the combined CBIP. Each agent infers part of biological reality based on possibly different data sources. An appropriate coordination scheme ensures synergy [3].

Results: In a pilot study, we searched for heart-specific cis-regulatory modules. The results encourage us to investigate also alternative ways of designing the coordination scheme.

References

- [1] Chang L and Mackworth AK, '*Constraint-based inference: a bridge between constraint processing and probability inference*'. Proceedings of Principle and Practice of Constraint Programming - CP 2005, Springer-Verlag. (2005)
- [2] Gupta M and Liu JS, '*De novo cis-regulatory module elicitation for eukaryotic genomes*'. PNAS, 102.20, 7079-7084. (2005)
- [3] Rezek I, Roberts SJ, Rogers A, Dash RK and Jennings NR, '*Unifying learning in games and graphical models*'. Proceedings of 8th Int. Conference on Information Fusion, Philadelphia, USA. (2005)