Networks and Co-evolution in the Interpretation of Epigenetic Regulation.

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My lab is interested in the computational developments in the interface of Network Biology and Co-evolution.

The description of biological systems in terms of networks offers the possibility of combining complex information to analyse the properties of individual components in relation to their interaction partners. In the other hand, Co-evolution based methods are potentially able to provide additional levels of functional interpretation of the network relations (1).

I will first present our recent work on the prediction of protein interactions sites (2) to introduce the basic concepts in co-evolution. In the second part of the talk, I will describe the use of co-evolution based approach to complement the information provided by a network of epigenetic components (i.e. chromatin binding proteins, DNA and Histone modifications) related by their co-localization at the genome level (3). Finally, I will show how the analysis of the network properties can help in the interpretation of complex relations between epigenetic components (4).

References
1) Emerging methods in protein co-evolution. de Juan et al., 2013 *Nat Rev Genet.*
2) Conservation of co-evolving protein interfaces bridges prokaryote-eukaryote remote homologies. Rodriguez-Rivas et al., 2016 *PNAS*
3) Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. de Juan et al., 2016 *Cell Reports*
4) Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. Pancaldi et al., 2016 *Genome biology*