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# Protein Interactions Analyzed With CoEvolution-Based Methods

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In this presentation I will describe the current status of the methods that inspired in co-evolution have been developed for the last 20 years for the prediction of protein interactions (inter protein) and protein contacts (intra protein). With particular emphasis in the ones developed by my group for the study of concerted evolution between interacting protein families (Juan et al., 2008), the detection of the residues potentially responsible of binding specificity (Rausell et al., 2010), and the potential implications of these and other developments for modeling protein complexes (Wass et al., 2011).

Together with the development of methods my group is interested the practical use of the computational methods for the analysis of the relation between proteins / protein networks and functional properties (see Baudot et al., 2009). In this context I will describe the practical possibilities and limitations of the current network/pathway based methods for the analysis of cancer genome projects (Vazquez et al., 2012).

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- Vazquez M, et al, *in preparation*.
- Wass MN, Fuentes G, Pons C, Pazos F, Valencia A (2011) Towards the prediction of protein interaction partners using physical docking. Mol Syst Biol. 7:469.