5005-C1-11 **Lisa Marras*** (lisa@crs4.it), Loc. Pixinamanna, Tech Park of Sardinia, 09010 Pula, Cagliari, Italy, **Maria Persico** (m.persico@crs4.it), Loc. Pixinamanna - Tech Park of Sardinia, 09010 Pula, Cagliari, Italy, and **Enrico Capobianco** (ecapob@crs4.it), Loc. Pixinamanna - Tech Park of Sardinia, 09010 Pula, Cagliari, Italy. *Interactome Inference by Reducing Dimensionality Sparse Approximation and Decomposition of Protein-Protein Interaction Networks.* Preliminary report.

Important cellular functions information can be obtained from decomposing Protein-Protein Interaction Networks(PPIN) into constituent groups, that may be considered clusters. In most empirical studies, a given set of observations is processed through a huge number of pairwise interacting proteins (some physically observed, others computationally predicted). The differentiation between positive and negative cases allows computing the probability of interactions. Reasons inducing sparsity in PPIN are: 1. A small fraction of interacting pairs in the total set of potential protein pairs; 2. Many false positives; 3. Many missing values in biological datasets, with limited coverage; 4. Descriptive protein pairs features that are orders of magnitude less than the observed dimensionality. Overall, the degrees of freedom depend on a small number of variables, whose possible configurations are constrained by the available data sources. An integration step is needed to improve accuracy and confidence of cases. An approach aimed to shrink the interaction set to a unique putative interactome consists in building a gold standard reference set through connectivity scores (likelihood of interactions in the target interactome). (Received April 03, 2007)