ProCoNA Blerb, April 26, 2012

ProCoNA (protein co-expression network analysis) is an R package aimed at constructing and analyzing peptide networks. These networks are constructed using data derived from mass spectroscopy experiments (primarily LC-MS). This package streamlines the process of building networks using modern S4 object methods to bundle relevant information for downstream analysis. The package is built around calls to WGCNA functions (weighted gene co-expression network analysis), which are fast and robust. ProCoNA adds a suite of statistical tests particularly suited to the unique challenges found in proteomics. These tests include permutation testing for module structure and within-protein topological overlap. Peptide co-expression networks bring novel approaches for biological interpretation, quality control, inference of protein abundance, potentially resolving degenerate peptide-protein mappings, and biomarker signature discovery.