B. **Data types: Environment Modifications Concentrations** Interactions Phosphorylation (MS, arrays) Protein-Protein (co-IP, MS) RNA (arrays, NextGen sequencing) Acetylation (MS) Protein-DNA (ChIP-chip/seg) Metabolites (MS) Methylation (MS) Cell Genetic Protein (MS) Ubiquitination/sumoylation (MS) sRNA-RNA Glycosylation (MS) Edge: Node: Type Type - regulatory interaction - gene, gene product or metabolite - functional interaction - single member or collection of entities - rate of influence/change (flux) e.g. set of genes and conditions in EGRIN Directed/Undirected Downstream genes - direction of regulatory interaction **Higher-order properties** - direction of a reaction - levels of a certain gene/gene product - undirected association Master regulator Middle manager Lower-tier - number of entities in the set Weight - importance of the gene/gene product - strength of the influence Motif: feed-forward loop - rate of the reaction - confidence in the association Cytosol **≻** Cu Cu (YvgX) AND-50 **→ Cu**, Zn, Ni, Co (ZntA) 702H/2581H (chaperone) VNG1845C 1179C Gene(s) (TRASH a. activate yvqX b. repress domain) (Cu efflux) c. activate or repress Bicluster Activates Gene Product Regulator Represses zntA Inhibit/Block (Cu, Zn, Ni, Co efflux) Logic gate Combines x and y