A. Chromosome 1, Chromosome 2, ... Chromosome N

- Samples

- Altered copy number

- Frequently altered genes

B. Genes not altered in copy number

- Generate initial gene activity scores based on log ratio of copy number changes of altered genes & overlay scores on the network

- Propagate initial gene activity scores to assign activity scores to other genes

- Inferred gene activity scores using label propagation

C. Predefined pathways from Biocarta, Reactome, KEGG, or Subnetworks

- Collect member genes in pathways using prior knowledge

- Compute pathway activity scores

\[ M_{ik} = \frac{\sum_{j \in N_{M_i}} S_{jk}}{|N_{M_i}|} \]

where \( S_{jk} \) is the \( j \)th gene score in \( k \)th cancer and \( N_{M_i} \) is the set of member genes in pathway \( M_i \)

- Generate pathway activity scores across all types of cancers

- Cancers [\( L \times K \times N \)]

- Modules [\( 1 \times M \)]