Figure S1. Schematic representation of B-spline discretization method. In this figure, data are discretized to 4 bins (Lowest, Low, High, Highest) and the B-spline order is equal to 3. As shown, bins have overlap with each other. The dashed line represents a sample data point. The place that dashed line intersect with each bin, determines the weight of that bin. Note that sum of weights is always equal to one.
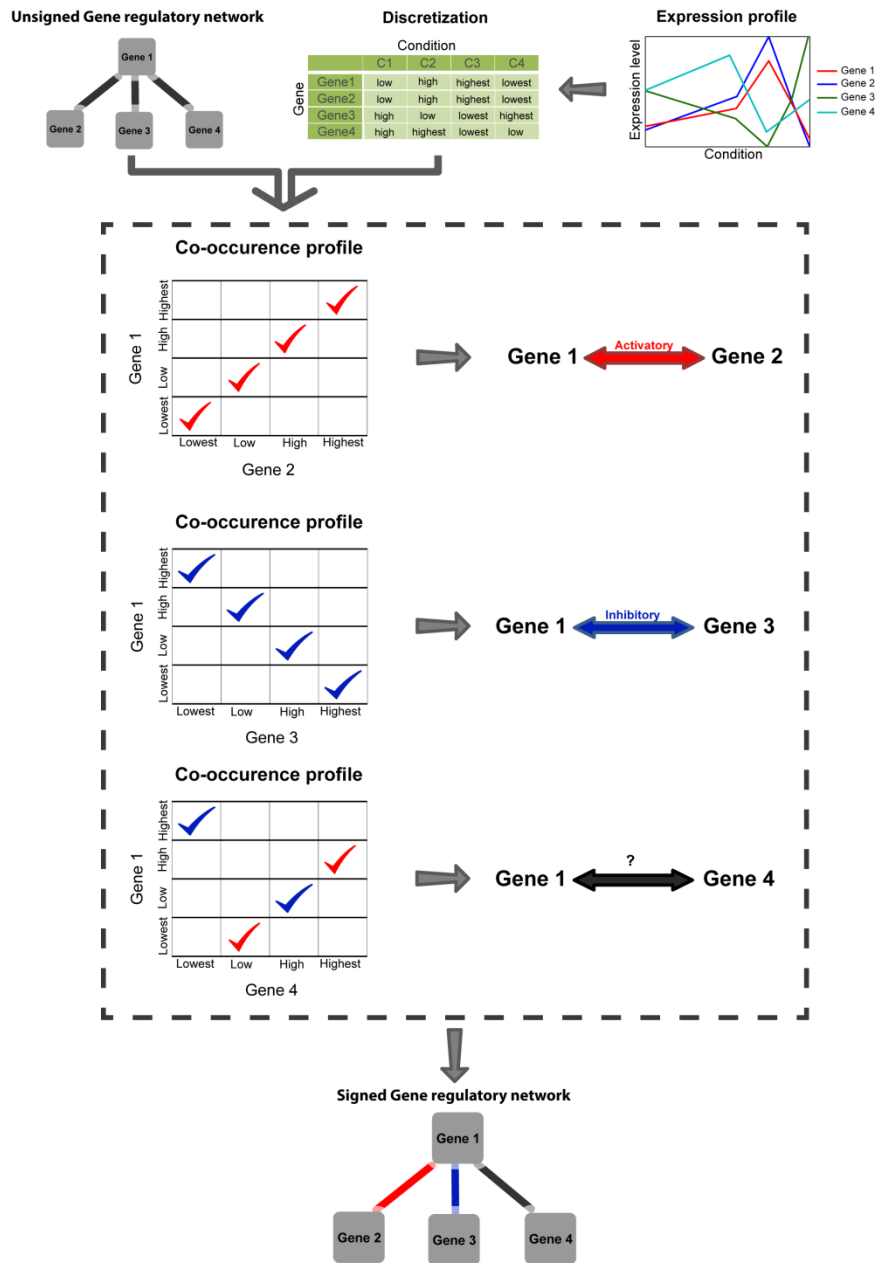
Figure S2. Schematic representation of SIREN algorithm. Given a GRN and corresponding transcriptome dataset, SIREN starts with discretization of continuous transcriptome data. Next, SIREN constructs a co-occurrence profile for each interacting genes in the GRN. Based on the patterns of co-occurrence, SIREN determines the type of interaction (Inhibitory or activatory).