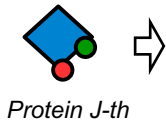
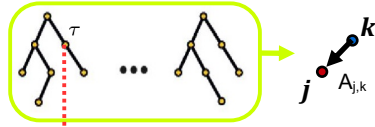


Response

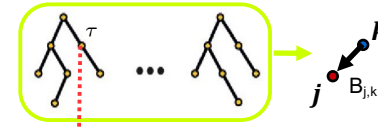
Global Proteomics



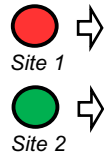
Model protein as function of other proteins



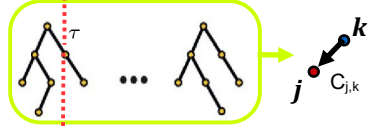
Model protein as function of other proteins



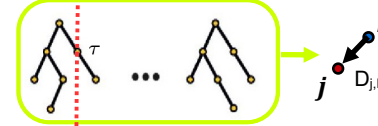
Tumor Phospho Proteomics



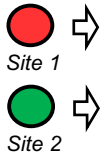
Model phospho site 1 as function of other tumor protein phospho sites



Model phospho site 2 as function of other tumor protein phospho sites



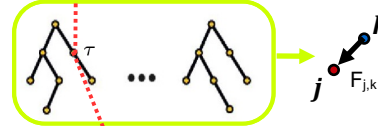
Normal Phospho Proteomics



Model phospho site 1 as function of other normal protein phospho sites



Model phospho site 2 as function of other normal protein phospho sites



Global Proteomics

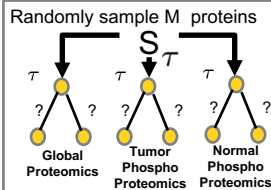
For each edge (j,k), take average to find final score $G_{j,k}$, i.e., $(A_{j,k} + B_{j,k})/2$

Final Weights

Phospho Sites

For each edge (j,k), take average to find final score $H_{j,k}$, i.e., $(C_{j,k} + D_{j,k})/2$ and $I_{j,k}$, i.e., $(E_{j,k} + F_{j,k})/2$

The three tree ensembles use the same protein for the splitting rules



For each k in S_τ

- For the Global proteomic tree, find the best splitting rule (minimize node impurity) based on protein k. **Impurity** = $U_1(k)$
- For Phospho trees, find the best splitting rule based on the phosphosites of protein k. Choose the phosphosites with the best splitting rule. **Impurity** = $U_2(k)$ and **Impurity** = $U_3(k)$

Split node based on protein $K=K^*$ which minimizes $U_1(K) + U_2(K) + U_3(K)$