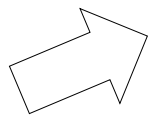
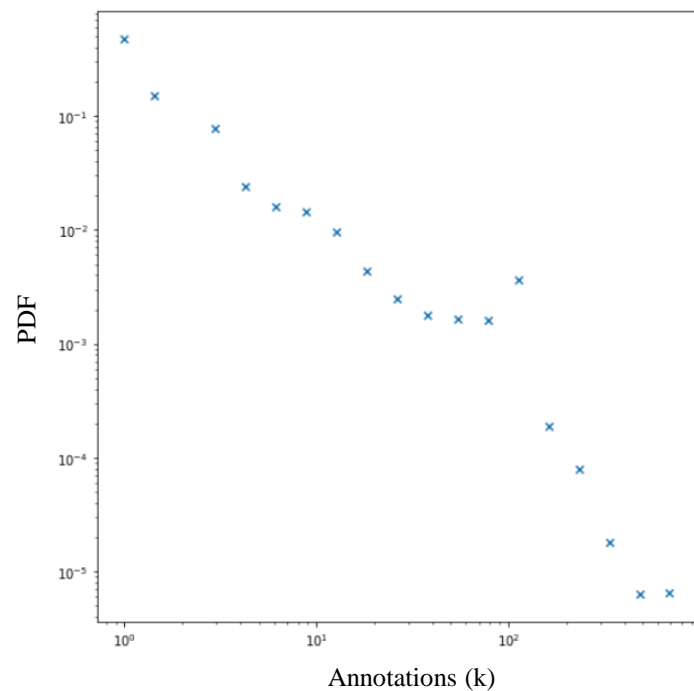
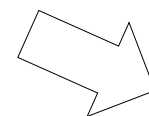
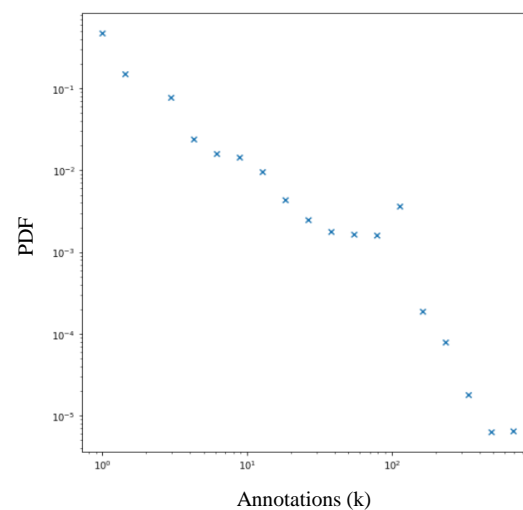
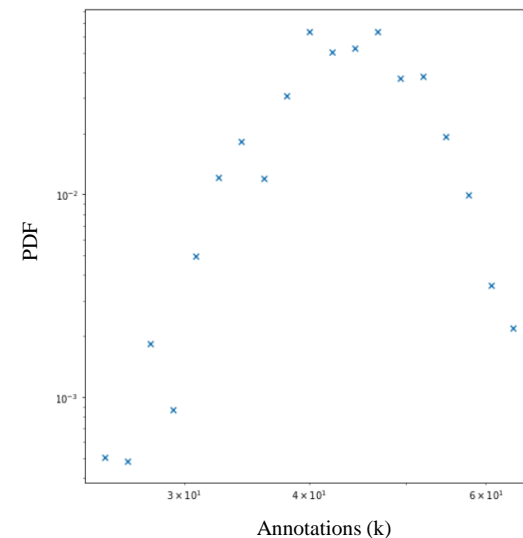
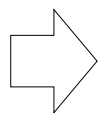
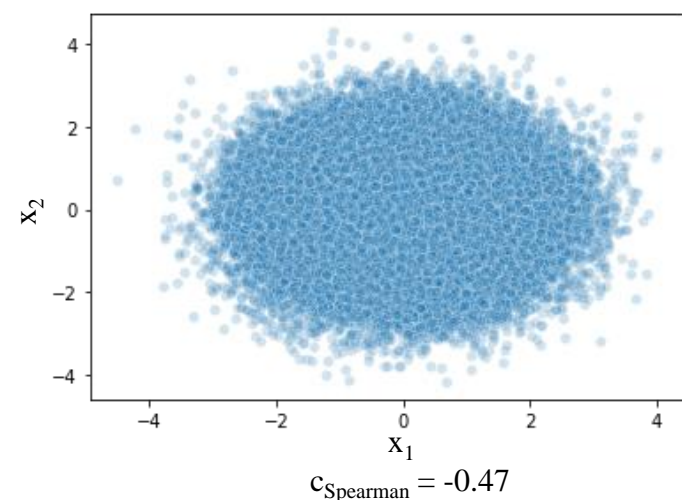
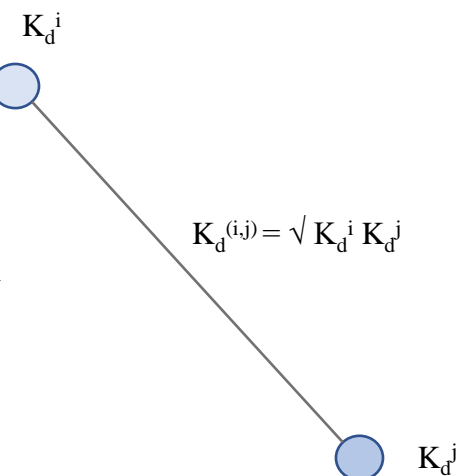
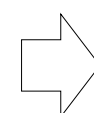
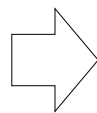
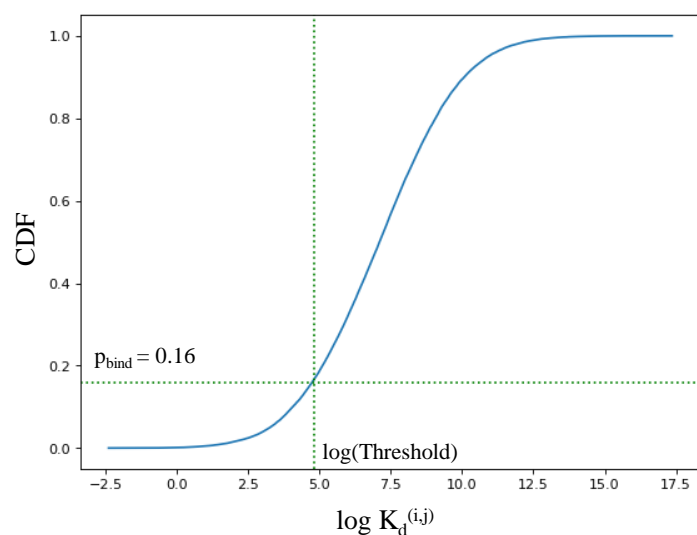


A*Benchmark BindingDB data*

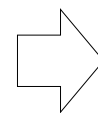
Protein degree sequence

 $\{d_1, d_2, \dots, d_N\}$ *Configuration Model*Power law degree
distribution with $N=1,507$ $\gamma_p=2.8$ $k_p^{\min}=1$ $k_p^{\max}=1,426$ *ER Graph*Poisson degree
distribution with $N=1,507$ $\langle k_p \rangle = 47$ **B***Gaussian Copulas* $c_{\text{Spearman}} = 0$  $k_i = \text{degree_seq_CDF}^{-1}(U1)$ $\log(\langle K_d \rangle^i) = \langle \log(K_d) \rangle + \sigma_{\log(K_d)} * \text{Gaussian_CDF}^{-1}(U2)$ *For each edge containing node i,* $K_d^i = \exp(\text{Gaussian}(\log(\langle K_d \rangle^i), \sigma_{\log(K_d)}^{k_i}))$ **C** $K_d^{(i,j)} < \text{Threshold}$

Positive Edge

 $K_d^{(i,j)} \geq \text{Threshold}$

Negative Edge

*Unipartite Version*