a) A network diagram showing interactions between various proteins, including Tnfα, IL-1α, LPS, TGFα, IGF1, RAS, PI3K, TRAF6, IL1α, MAP3K7, PI3K, P38, JNK12, MEK12, MAP3K1, AKT, MEK12, MKK4, MAP3K7, and others. The network includes pathways such as PI3K/AKT, MAPK, and others.

b) A graph illustrating the fraction of edges added randomly to the initial PKN. The graph compares the fraction of edges different in adjacency matrices of models trained to real PKN and trained models. The x-axis represents the fraction of edges added randomly to the initial PKN, and the y-axis shows the fraction of edges different in the adjacency matrices. The graph shows an increasing trend with error bars indicating variability.

c) Another graph depicting the fraction of edges between measured and treated species added to PKN that were removed during training. The x-axis represents the fraction of edges added randomly to the initial PKN, and the y-axis shows the fraction of edges between measured and treated species added. The graph shows a decreasing trend with error bars indicating variability.