To do list:

1. Check if the random work is generated based on probabilities in net1 using pdb.set\_trace()
2. Check if the code in calculating the probabilities on paths is correct
3. Check why the drug is top ranked:

Does it have the highest number of paths?

What’s the probability of the path with the highest weights?

What's the weight distribution of length-2 and 3 paths?

If every path has similar weights then it must bias on the number of paths.

Check the path weights on known drugs. Understand why these drugs are on the bottom.

1. Check why the two networks have limited overlap in the ranking list:

Calculate the overlapping percentage of AD linked genes and drug linked genes,

the percentage of overlapped edges and nodes between two networks, and explain.

1. Try combining the result of two networks to see if the top ranked drugs shown promising candidates that have both highly path connections from the drug to AD in net2 and reverse expression relations in net1.
2. If the two networks do have no similarity and we cannot find any significant drugs by combining results of two networks. We should treat target related network result as the main result, and find supporting evidence of top ranked drugs in net2 from net1.

Check the path and genes for each drug in top20 drugs from target related network, for each drug, how many paths? How many genes involved? What is the function of the genes?

Find the supporting reverse differential expression relation of these genes in expression network.

For the drugs that can find reverse differential expression relations, increase the rank by a certain rule.