I have a gene expression matrix dataset obtained from liver tissue, from this I am trying to use as reference for simulating gene-gene association networks. The goal now is to see if networks generated by a randomly selected set of pathways will have be statistically different from those of the simulated liver pathway genes.

[1] "NR1H2 & NR1H3 regulate gene expression to control bile acid homeostasis"

[2] "Recycling of bile acids and salts"

[3] "Synthesis of bile acids and bile salts"

[4] "Synthesis of bile acids and bile salts via 24-hydroxycholesterol"

[5] "Synthesis of bile acids and bile salts via 27-hydroxycholesterol"

[6] "Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol"

[7] "Transport of bile salts and organic acids, metal ions and amine compounds"