Analyzing the capacity of the colBiSBM to recover structure for missing data from other networks

`summarise()` has grouped output by 'prop_NAs'. You can override using the
`.groups` argument.

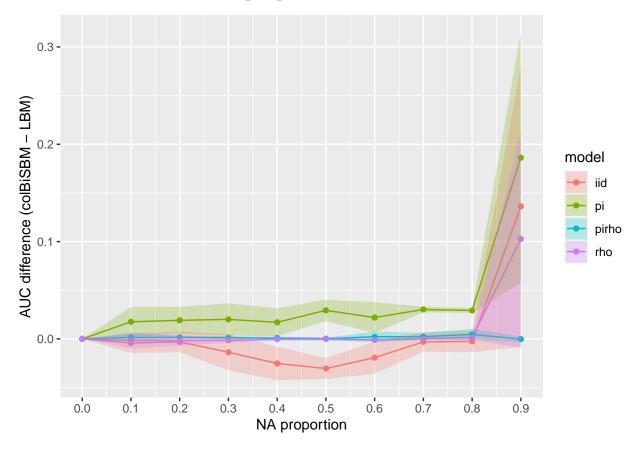
Simulation context

The idea is to benchmark the capacity of the models when NAs are in the data.

To do this, whe choose the below structure: ! PARAMETERS OF THE SIMULATION!

And set some randomly chosen interactions to NA. The below plots will show the different quality indicators in function of proportion of NAs in the first of the 3 networks.

AUC in function of the proportion of NAs



ARI in function of the proportion of NAs

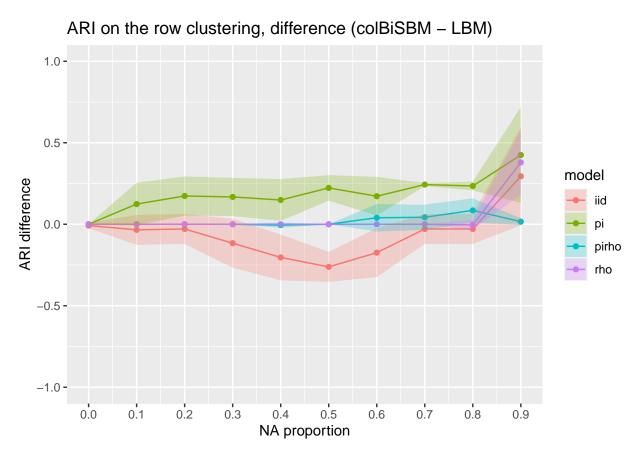


Figure 1: Difference of ARI for the row clusterings $\,$

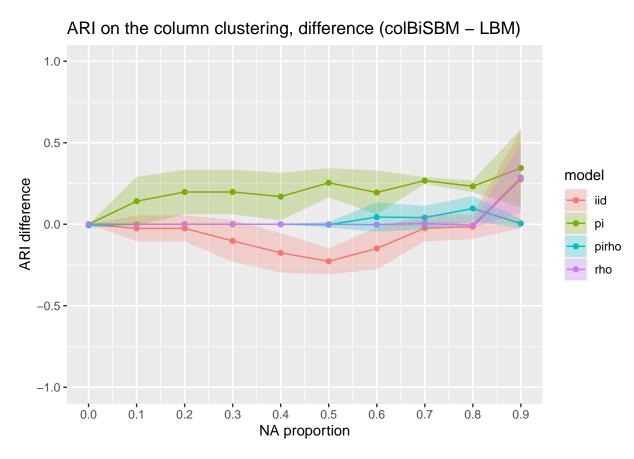


Figure 2: Difference of ARI for the columns clusterings