Basic workflow

1. Ran PLS with 71 mRNA & 31 miRNA, calculated the association scores and stored them in a 71x31 matrix

2. Removed 1 column of the X variable (miRNA expressions) at a time, ran PLS & recorded the predicted values of Y (mRNA expressions)

3. Calculated the residuals by subtracting the predicted values from the observed ones

4. Bootstrapped by resampling from residuals and calculated new Y variables

5. Ran PLS with new Y variables and 31 miRNAs and calculated the new associated scores and repeated bootstrapping for 1000 times

6. Calculated the proportion of times a specific association score is less than the observed association scores amongst all the 1000 bootstrapped association scores, which were the estimated p-value. A small p-value implied strong miRNA-mRNA association/interaction

7. A Benjamini & Hochberg FDR correction to obtain an adjusted p-value. The mRNA which had strong association with a miRNA is deemed to be the target of that miRNA

Figure 1