The R program, *Code get union diff expressed gene low IC20.r*, is designed to retrieve the differentially expressed genes for the drugs with low IC20.

The input data are the differentially expressed genes for all drugs, in which the differentially expressed genes are annotated with the names and p-values.

The loop extract the gene names of all the differentially expressed among drugs with low IC20. These drug names are pre-specified. Finally, only the unique gene names are merged.

The R program, *Code get syn ant scoring.r,* is designed to calculate the synergy and antagonism scores between differentially expressed genes from two drugs.

The input data are the differentially expressed genes from all the drugs, and the core gene set calculated from *Code get union diff expressed gene low IC20.r*.

The first loop calculate the synergy score for the drug pairs. The second loop calculate the antagonism score for all the drug pairs.