# Running MAGMA enrichment

1. Run the script ‘EnrichmentAnalysis/GenVizMAGMA\_Enrichment.R’ from steps 1 through 11. This will generate the module list required to perform the MAGMA enrichment.
2. Change the filename and execute step 7 of the file ‘EnrichmentAnalysis/ScriptGeneSetAnalysis’.

**Note:-** Step 2 requires a pre-processed file that is generated by Steps 1-6 of ‘EnrichmentAnalysis/ScriptGeneSetAnalysis’. These files are located in ‘IGAP\_files’. The file ‘IGAP\_geneAnalysis.genes’ is for IGAP-Stage 1 and ‘IGAP\_geneAnalysis2.genes’ is for Stages 1 & 2.

# Generating consensus modules

1. Install the github repository ‘mukhes3/AggregationMethods’
2. Run the file ‘ConsensusModulegen/RunningCC\_Pivot’

**Note:-** Depending on the R version in use, the installation instructions in the ‘AggregationMethods’ package may or may not work. In case it doesn’t work, simply download the package and install it manually.

# Running Shiny Apps

1. Run the file ‘RunShinyAppsViz\_Bar.R’