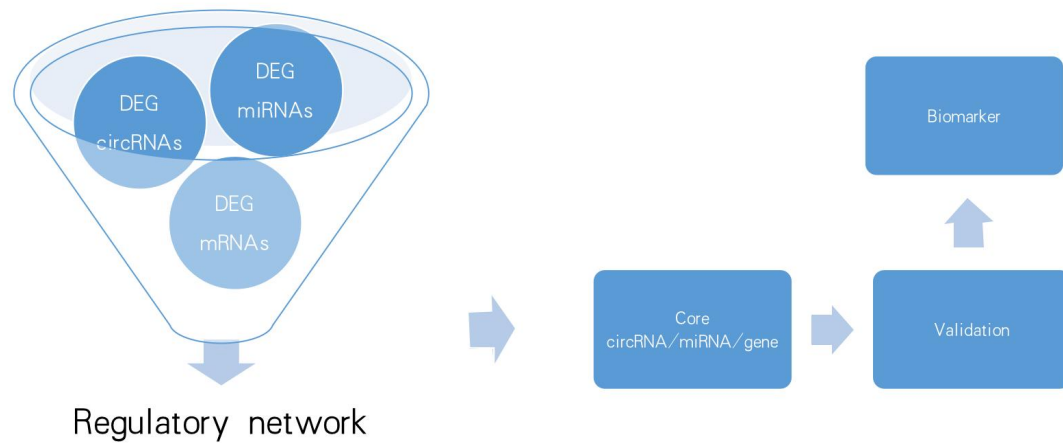




Three datasets, GSE122709, GSE133768, and GSE110993, from the GEO database, were enrolled in bioinformatics analysis. The targeting miRNAs and mRNAs were predicted via the circBase and miRWalk database. The circRNA-miRNA-mRNA network was created by Cytoscape software. The 'clusterProfiler' R package was utilized to conduct GO and KEGG analysis. We constructed the SH-SY5Y oxygen-glucose deprivation (OGD) model in vitro to simulate ischemic stroke. RT-qPCR and western-blot was utilized to detect the expression of corresponding genes. Cell Counting Kit-8 was utilized to detect cell viability. Flow cytometry was conducted for cell apoptosis analysis.