

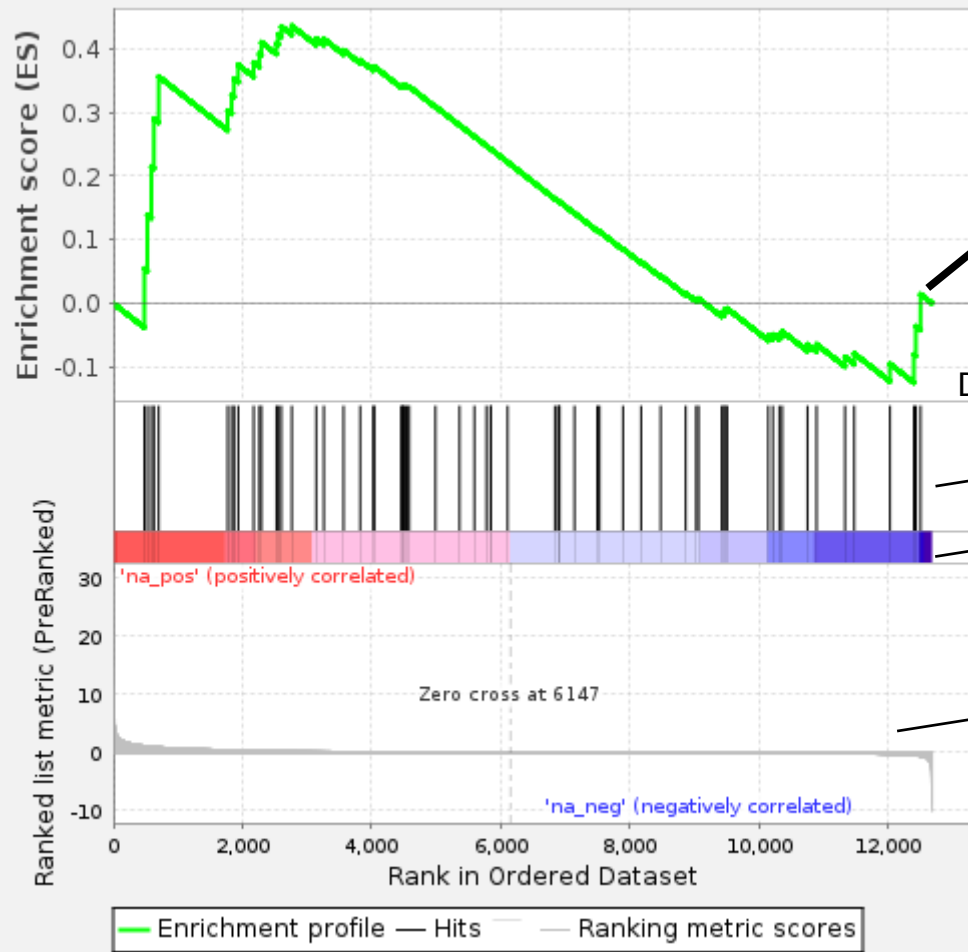
Gene Set Enrichment Analysis

Enrichment Score (Max)

Pathway/miR of interest

* The enrichment plot may sometimes have a different layout depending on the tool used

Enrichment plot: MIRNA:HSA-MIR-19A-5P

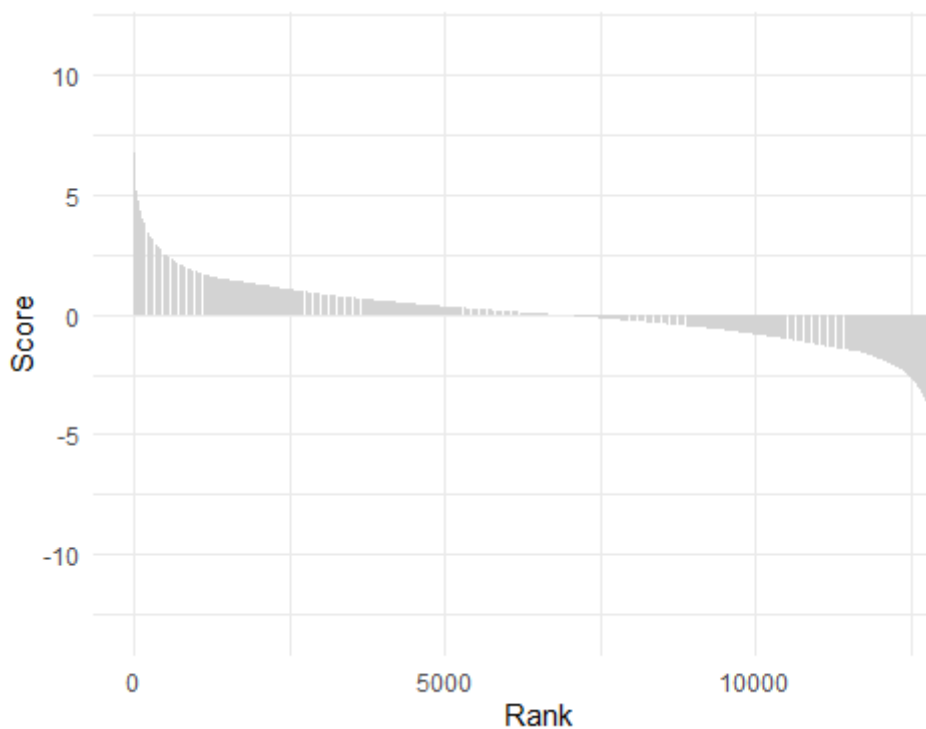


Enrichment profile

Distribution of genes in gene set
(in this case, miR targets)

Ranked gene list
(input from DEG analysis)

Distribution of scores contributing
to enrichment profile



GSEA ranks genes using a given metric (usually significance with direction of change between two conditions). The plot on the left shows the distribution of the scores assigned to each gene in order of their rank. Then, genes from a given pathway/process are searched for along the ranked list. Everytime there is a hit, the gene's score is added to the overall enrichment score. If the gene is not a hit, the enrichment score will step back toward 0. The most extreme enrichment score (maximum) is used as the overall enrichment score. This is repeated (usually 1000 times) using random gene ranks and an empirical p-value is generated to determine whether the pathway is enriched in the current ranking of genes (over random rankings). All enrichment scores and p-values are normalized/corrected.