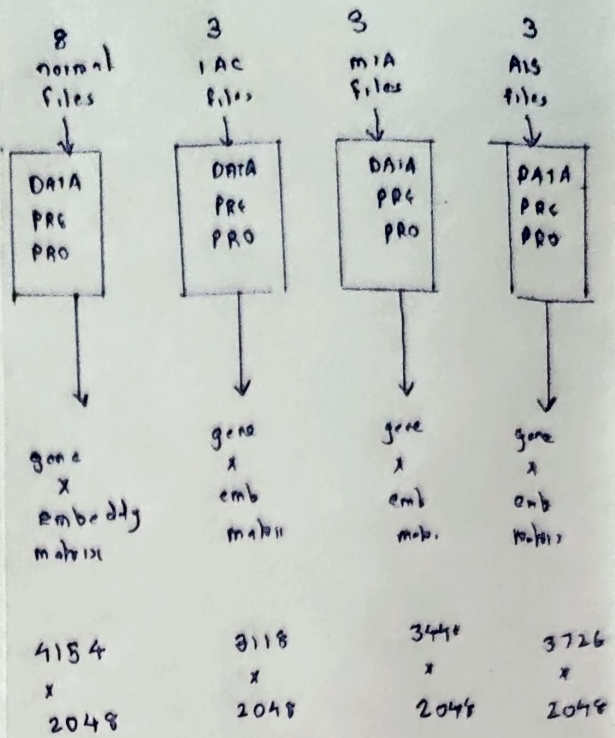
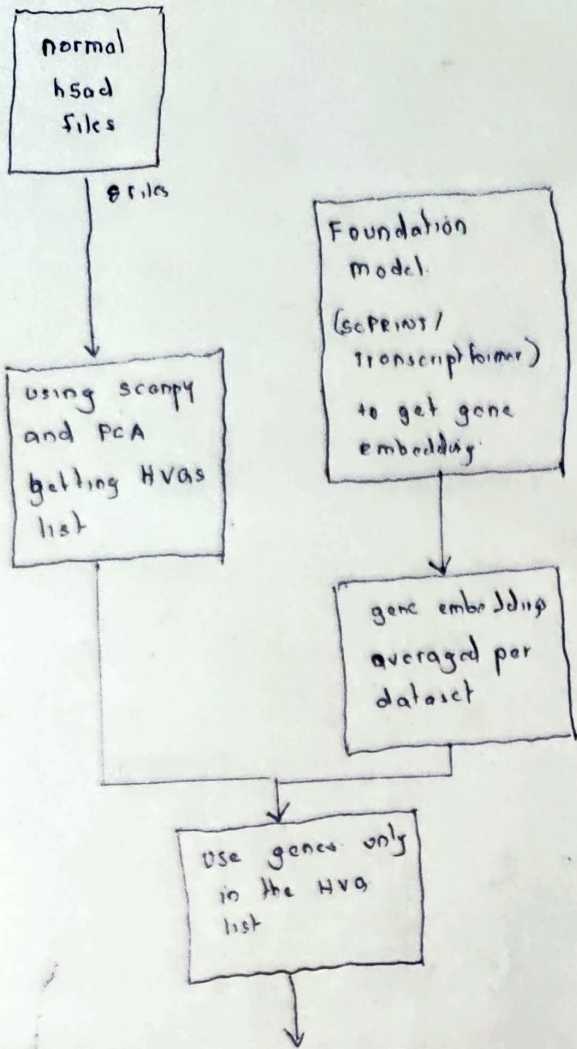


Steps

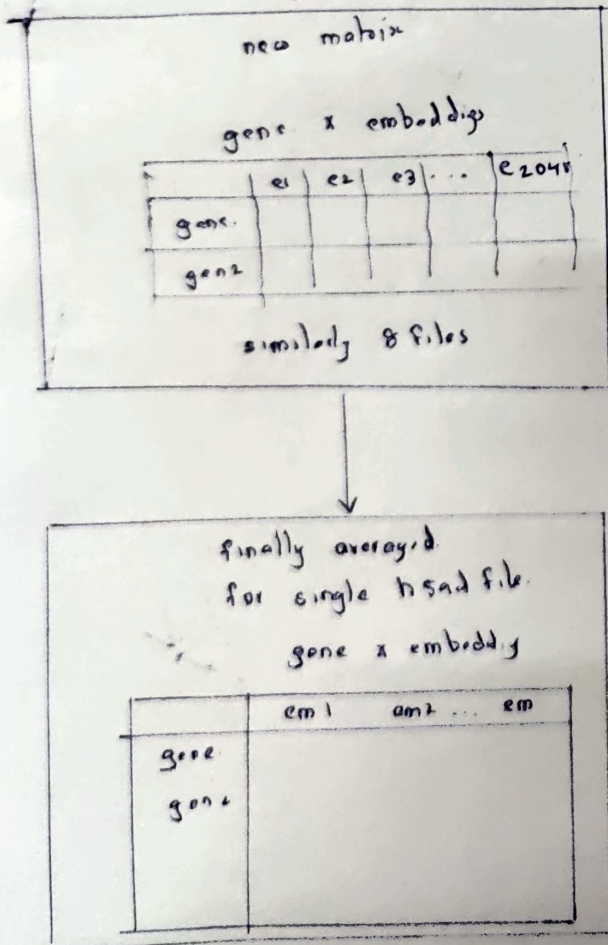
- ① DATA PREPROCESSING & HVG SELECTION
- ② LEIDEN CLUSTERS SET1
- ③ LEIDEN CLUSTERS SET2
- ④ DRUG TARGET GENES SELECTION
- ⑤ CREATING SIMILARITY GRAPH
- ⑥ GENE SET ENRICHMENT ANALYSIS

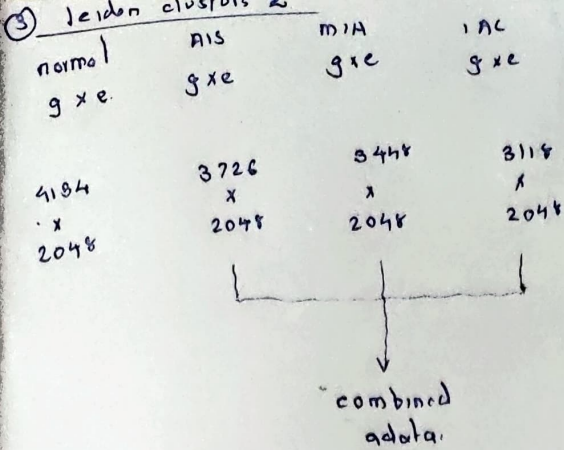
gene set enrichment analysis

① DATA PREPROCESSING AND HVAS



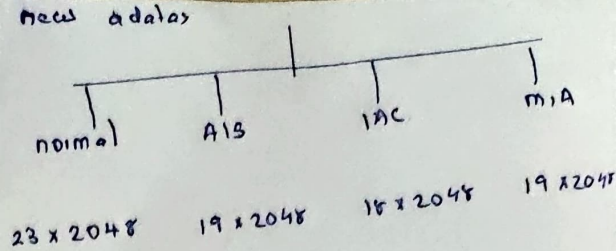
② Leiden clusters set 1



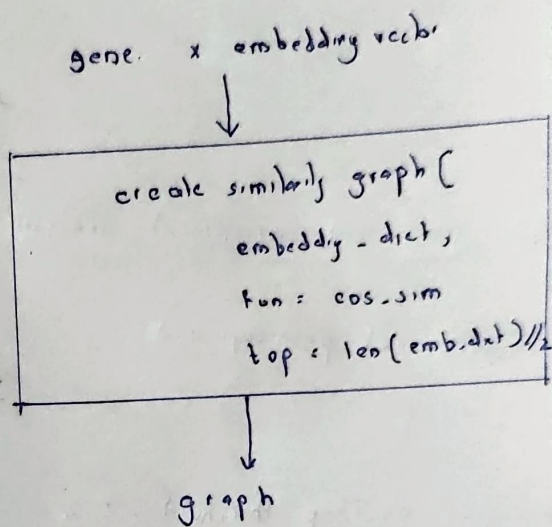


combined data. obs

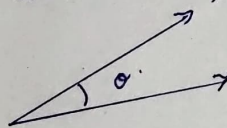
cluster 2 here.



⑤ create similarity graph.



cosine similarity



angle θ close to 0
cos sim close to 1

highest ranked gene pairs have
highest cosine similarity.
means these two genes are close
in that case

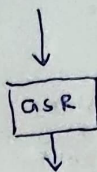
plot the graph's here.

④ DAUG TARGET GENE FILTERATION

pass list here.

Embeddings labels	no of missing genes
normal	9 missing
IAC	14
AIS	13
MIA	13

AIS



③ gene set enrichment analysis

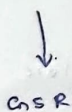
gene set pathways used

= {

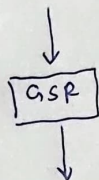
gene overlap threshold = 0.2

Results:

MIA



IAC



normal

