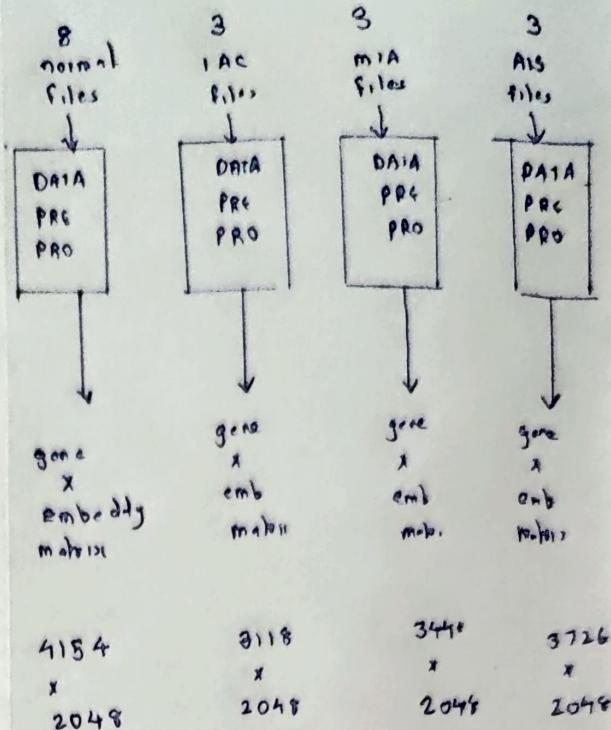
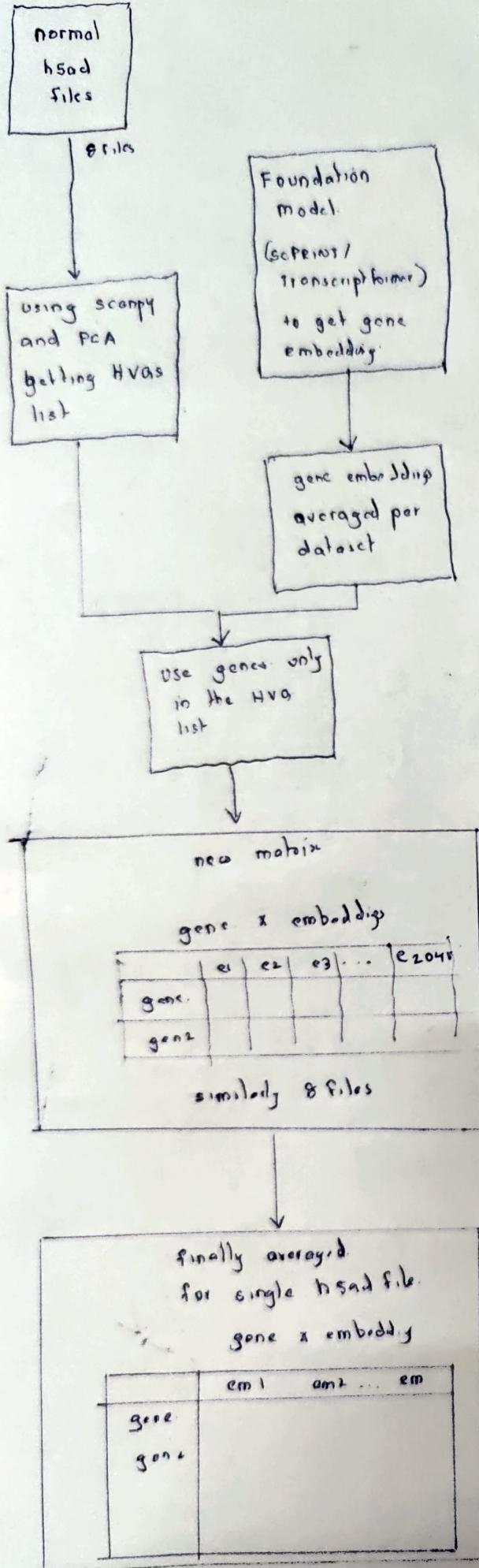


Steps

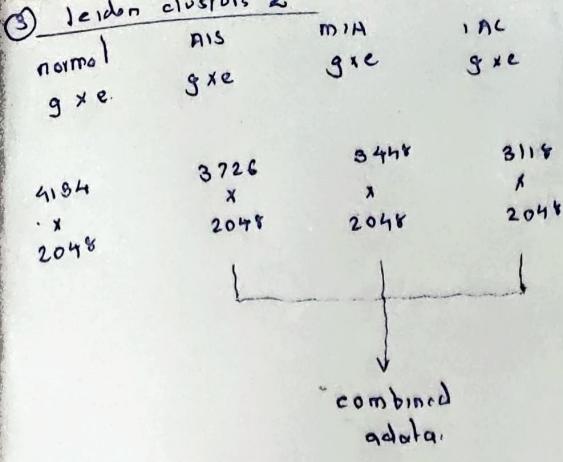
- ① DATA PREPROCESSING & HVG SELECTION
- ② LEIDEN CLUSTERS SET1
- ③ LEIDEN CLUSTERS SET2
- ④ DRUG TARGET GENES SELECTION
- ⑤ CREATING SIMILARITY GRAPH
- ⑥ GENE SET ENRICHMENT ANALYSIS

gene set enrichment analysis

① DATA PREPROCESSING AND HVAs

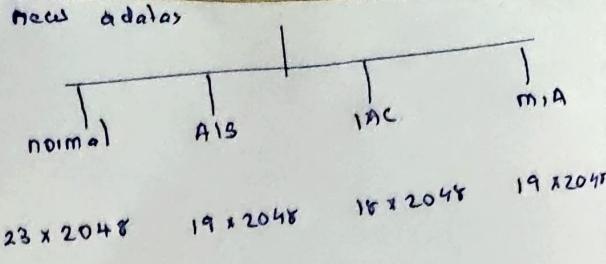


② Leiden clusters set 1.



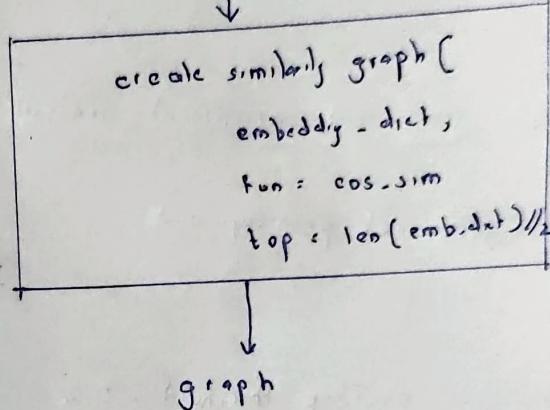
combined adata obs

cluster 2 here.

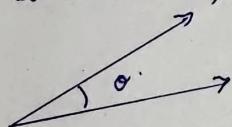


⑤ Create similarity graph

gene x embedding vector



cosine similarity

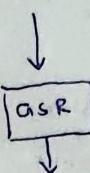


highest ranked gene pairs have highest cosine similarity.
means those two genes are close in that case

plot the graph here.

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

AIS



⑥ gene set enrichment analysis

gene set pathways used

= {

gene overlap threshold = 0.2

Results:

IAC



mA. was very bad at finding

pathways with high

overlap and not enough

overlaps in the

normal

not doing well

at all

normal

