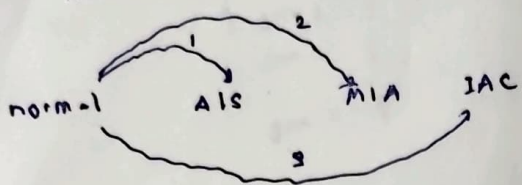① after drug-target filteration the gene x embedding matrix will be so small. (ie no of genes)

| AIS | MIA | IAC | normal |

| adcla | adaln | adrln | adaln |
| gene xcomb | gu ront | gen xon | gen xnb |

② find common genes & variable gene
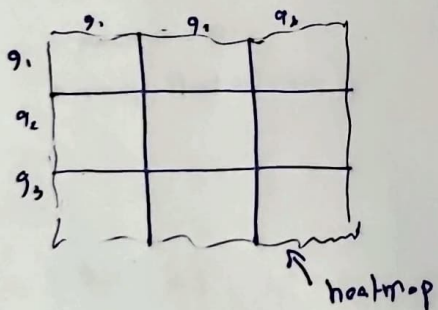

normal — AIS — MIA — IAC

assume comparison b/w (normal vs AIS)

common gens :
unique gens in AIS =

cons   construct similarity matrix for
common genes sort
normal and AIS embeddings

↑ heatmap

③ differential genes

assume b/w (normal , AIS)

differential-genes = unique genes in AIS

from common-genes what all we can append to differential-genes

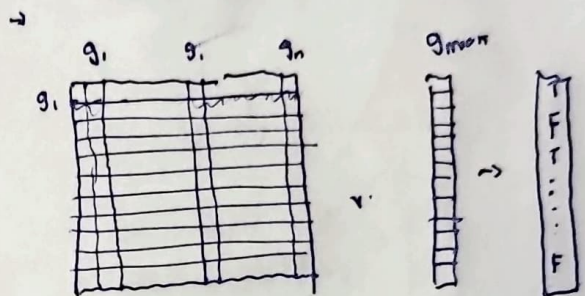④ plot the graph in each case.

⑤ from common-genes check all genes we can append to differential genes
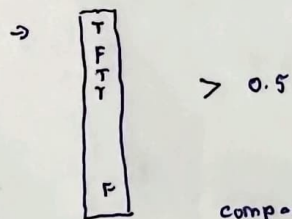
* initialization

similarity matrix (common)
b/w
(Normal, AIS)

threshold = 0.5

* for each gene in common

g_1 g_i g_n g_{mean}

check if $g_{1,}$ > g_{mean}
           column   mean is each
                      row

   > 0.5

compared against a threshold > 0.5
if yes added to differential-gene-list