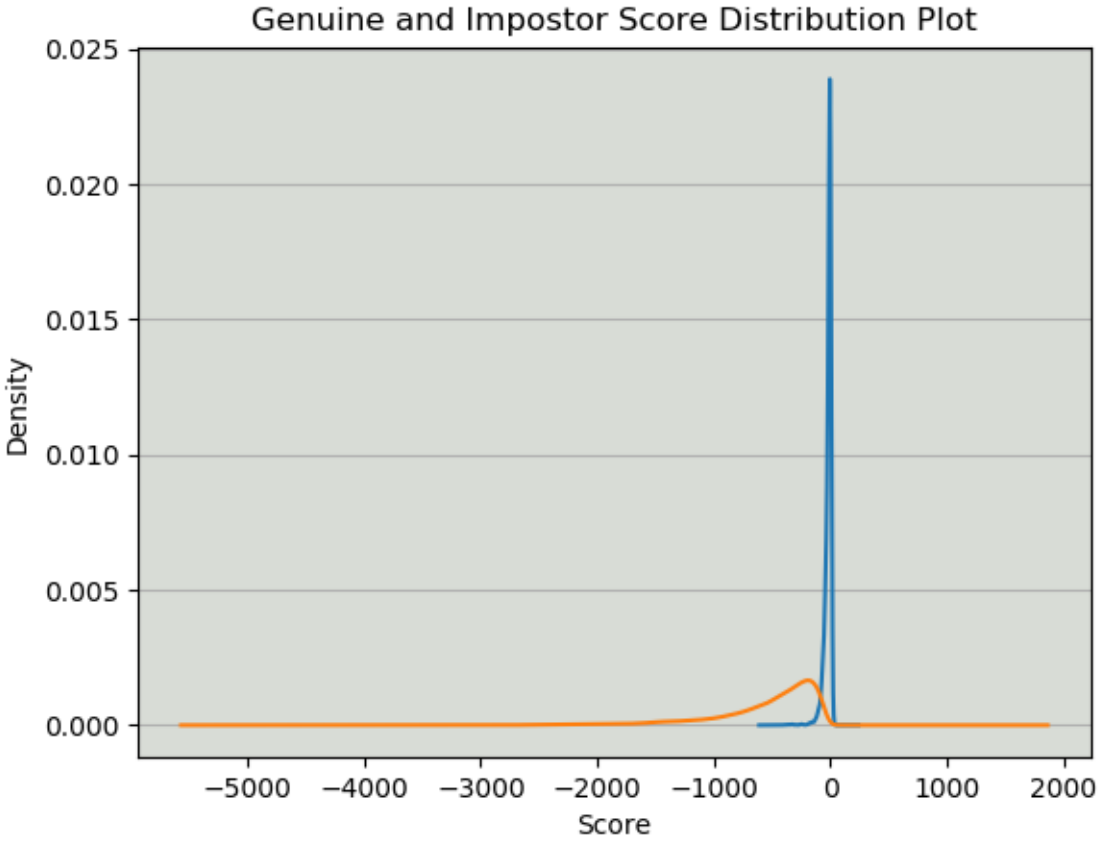
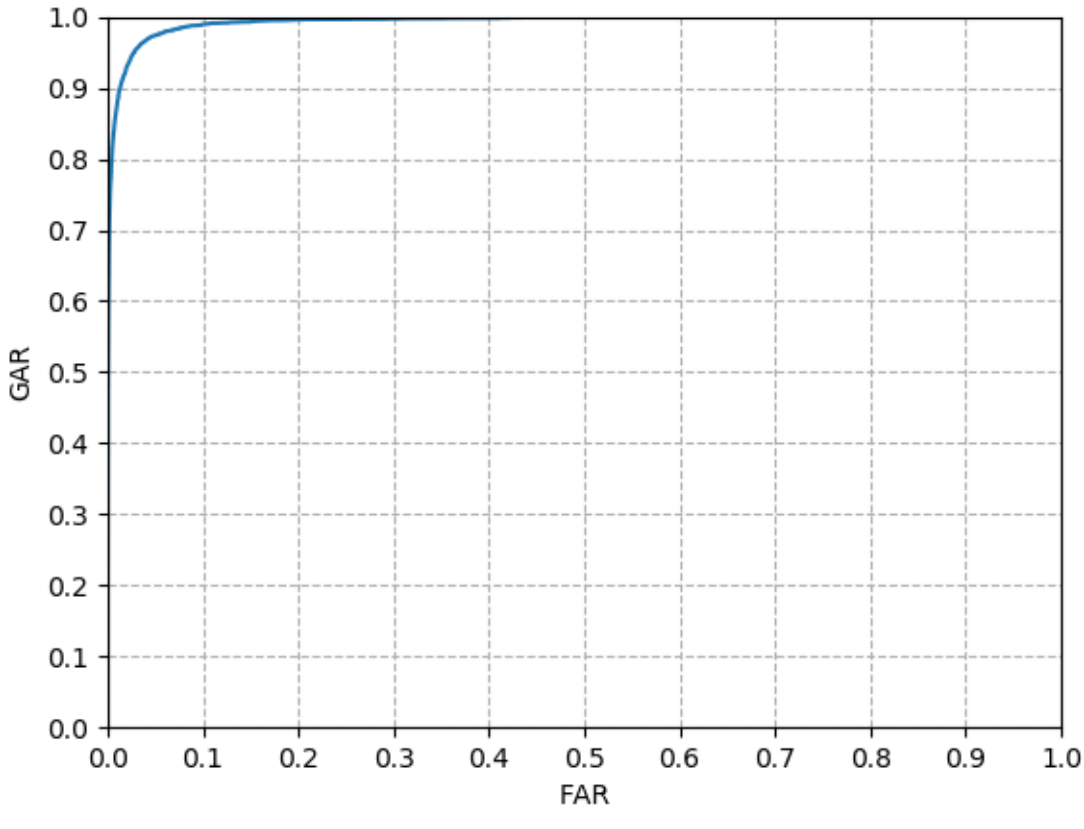
Giray Eryılmaz,

DATA1

python analyze_similarity_matrix.py data1/data1_SM.txt data1/data1_Class_Labels.txt

ERR	=	3.65%	with threshold = -78.7435	
FRR	=	35.76%	at FAR point 0.1%	where t = -16.314
FRR	=	12.13%	at FAR point 1%	where t = -45.301
FRR	=	1.07%	at FAR point 10%	where t = -125.820

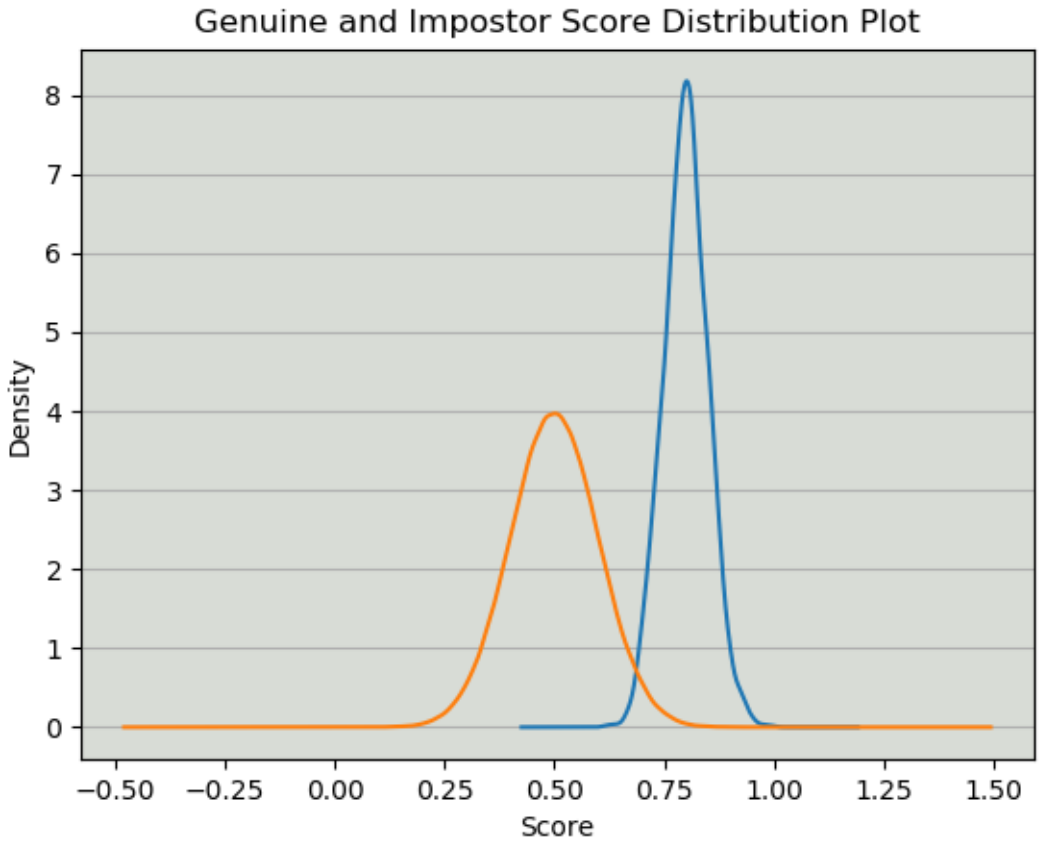


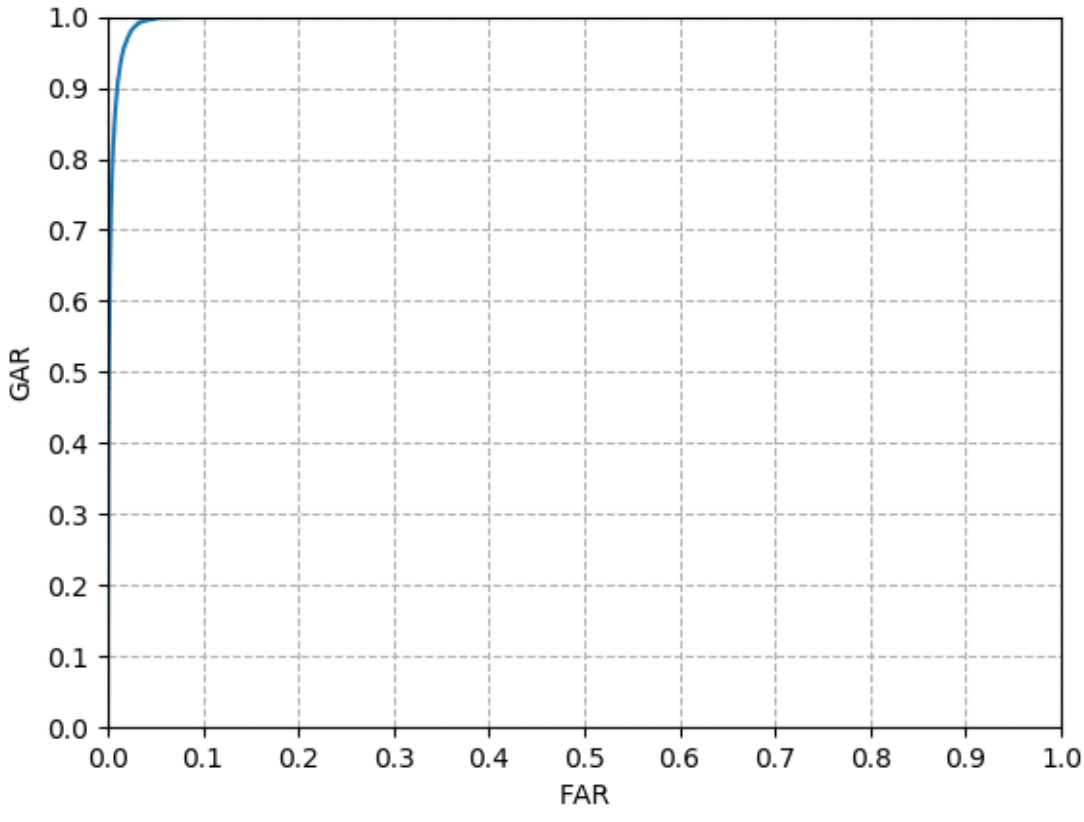


DATA2

python analyze_similarity_matrix.py data2/data2_SM.txt data2/data2_Class_Labels.txt

ERR = 2.32%			with threshold = 0.7001	
FRR	=	55.98%	at FAR point 0.1%	where t = 0.807
FRR	=	10.04%	at FAR point 1%	where t = 0.734
FRR	=	0.07%	at FAR point 10%	where t = 0.628

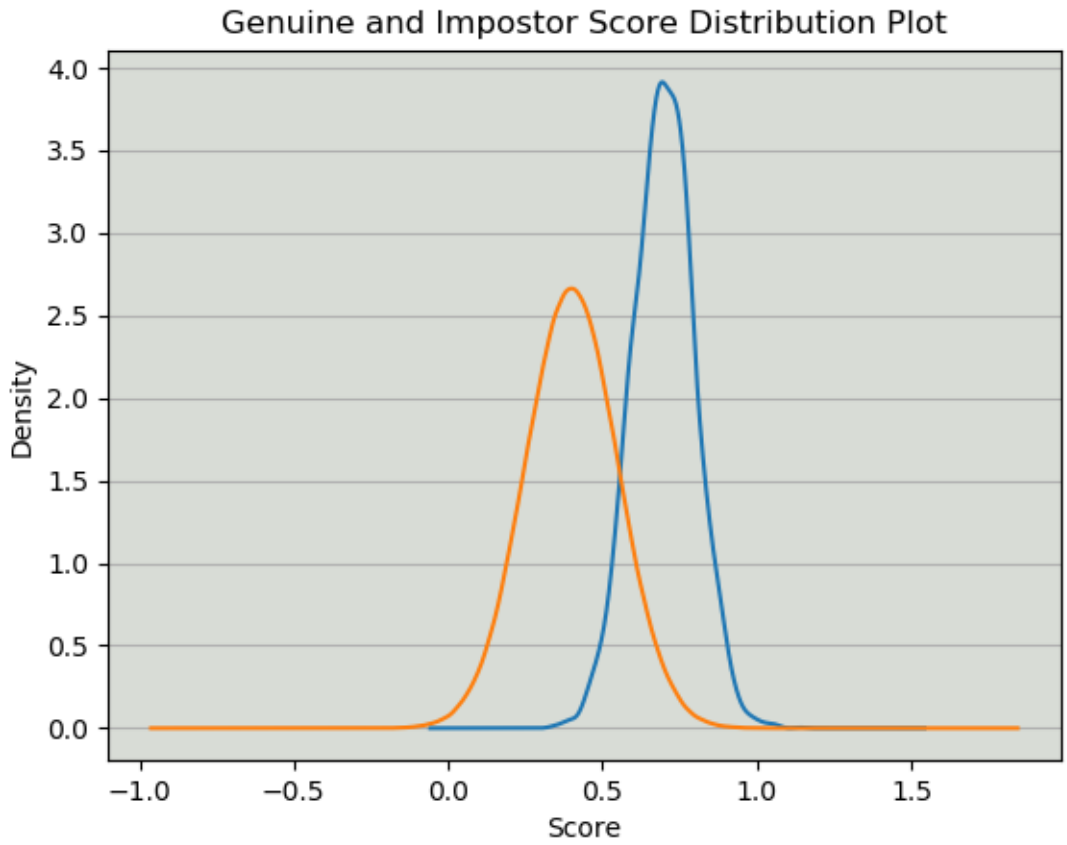


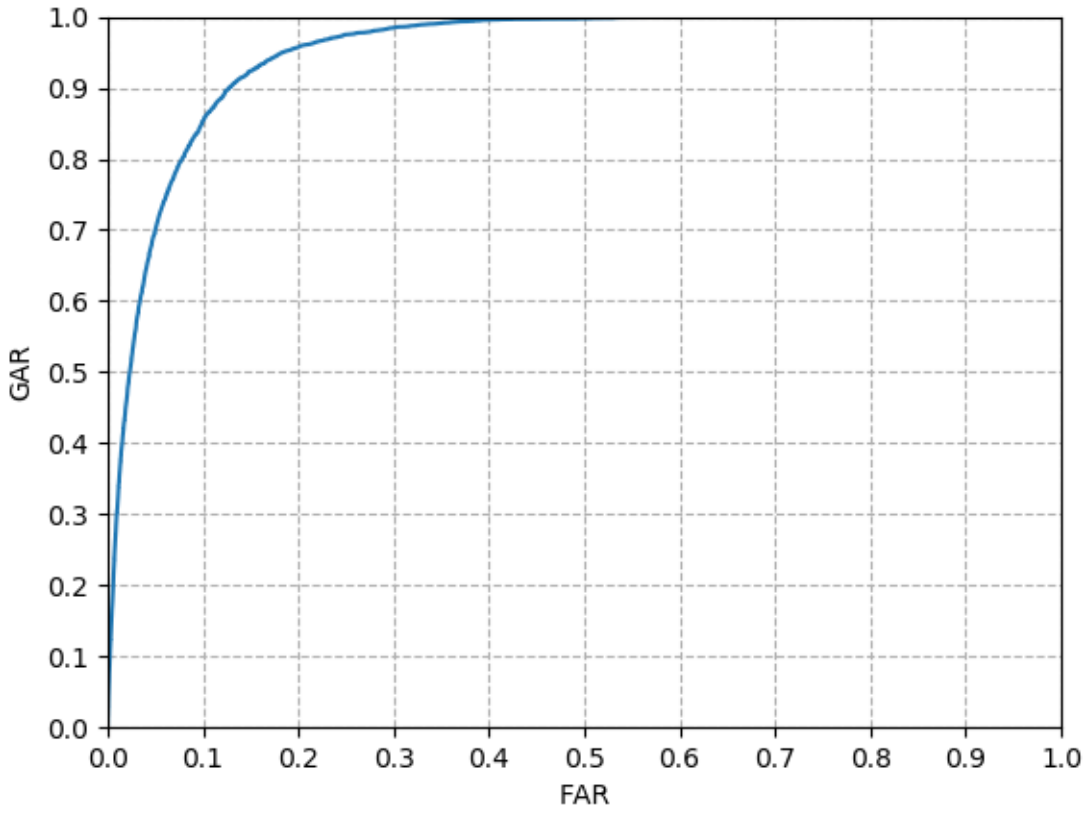


DATA3

python analyze_similarity_matrix.py data3/data3_SM.txt data3/data3_Class_Labels.txt

ERR	=	11.69%	with threshold = 0.5782	
FRR	=	94.76%	at FAR point 0.1%	where t = 0.861
FRR	=	69.20%	at FAR point 1%	where t = 0.748
FRR	=	14.64%	at FAR point 10%	where t = 0.592

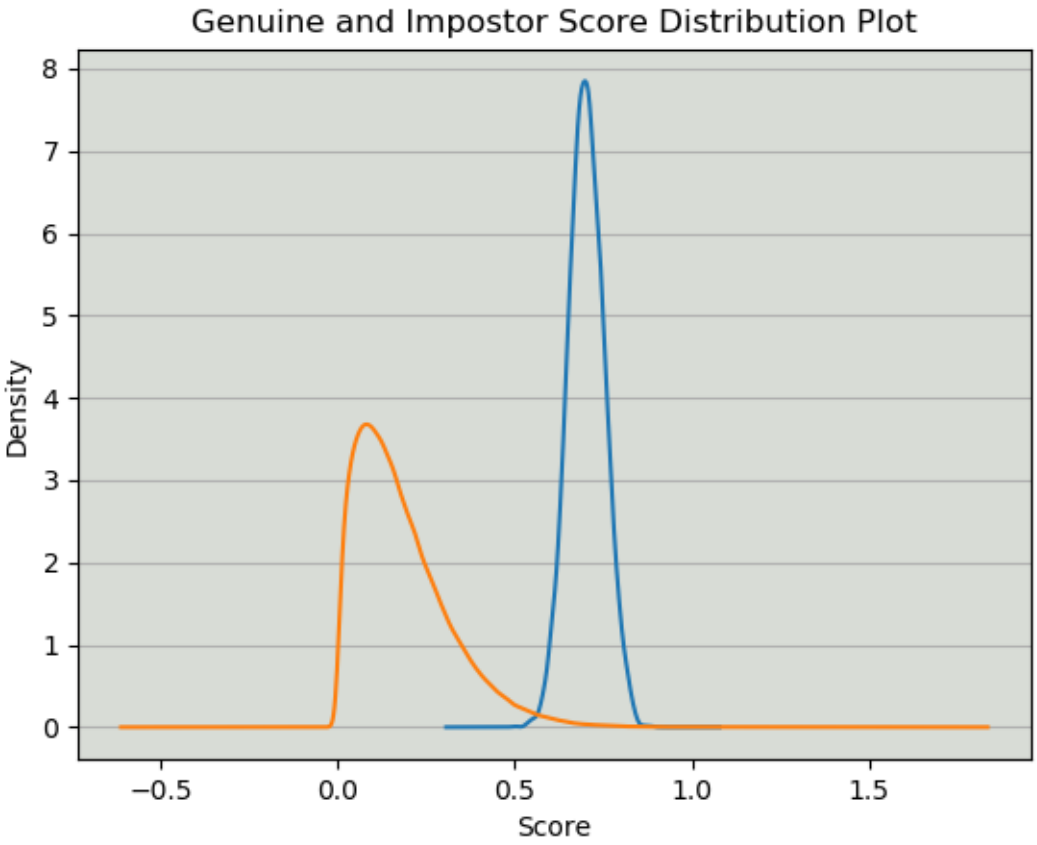


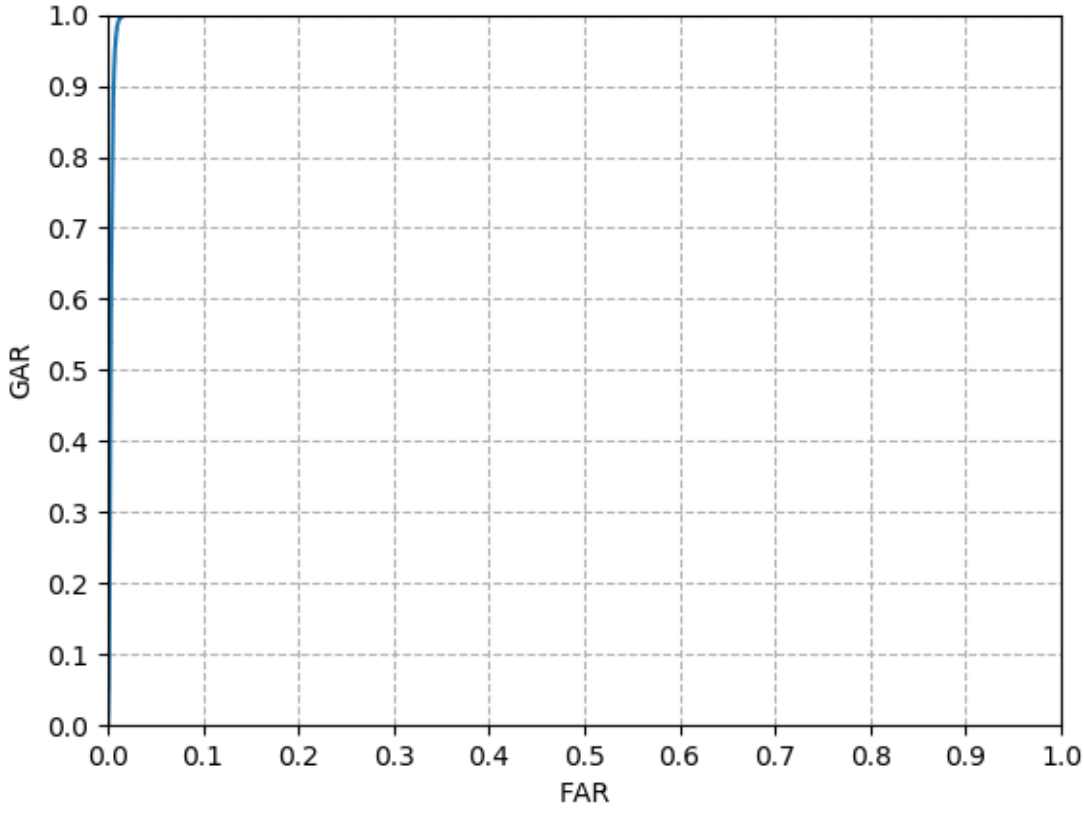


DATA4

python analyze_similarity_matrix.py data4/data4_SM.txt data4/data4_Class_Labels.txt

ERR	=	1.10%	with threshold = 0.5870	
FRR	=	97.13%	at FAR point 0.1%	where t = 0.797
FRR	=	1.56%	at FAR point 1%	where t = 0.595
FRR	=	0.00%	at FAR point 10%	where t = 0.363





4. Explain very briefly how you compute the EER?
ERR is the point where the False Match Rate equals False Non-Match Rate (FNMR = FMR). From the definition I search for the threshold of t that gives FNMR = FMR. I exploited the fact that FMR is monotonic increasing and FNMR is monotonic decreasing so FNMR – FMR is too monotonic decreasing, all are with respect to similarity scores.
I flattened and sorted similarity matrix, then I used a modified binary search that uses a key function (namely FNMR – FMR) on the array to find the insertion point of $t=0$. I simply used average of the similarity scores that gives the highest negative `FNMR – FMR` score and the one that gives lowest positive score. I reported the threshold t along with FNMR at t which has to be equal to ERR at that point.

For a more precise estimation one can interpolate FNMR – FMR scores to estimate underlying function and work on that instead of working on the array but I doubt that the improvement would be significant.