

GENERATED REPORT -- 2021-03-18 07:48:45.975937

DataBank source was found in:

BMAL Filepath:

/Users/chrismatthewcyril/Downloads/GeneBank/Needleman-Version5.0/venv/BMAL_CYC_FILES/BMA
L.fasta

CYCLE Filepath:

/Users/chrismatthewcyril/Downloads/GeneBank/Needleman-Version5.0/venv/BMAL_CYC_FILES/CYC
LE.fasta

This report can be found at:

/Users/chrismatthewcyril/Downloads/GeneBank/Needleman-Version5.0/venv/REPORT

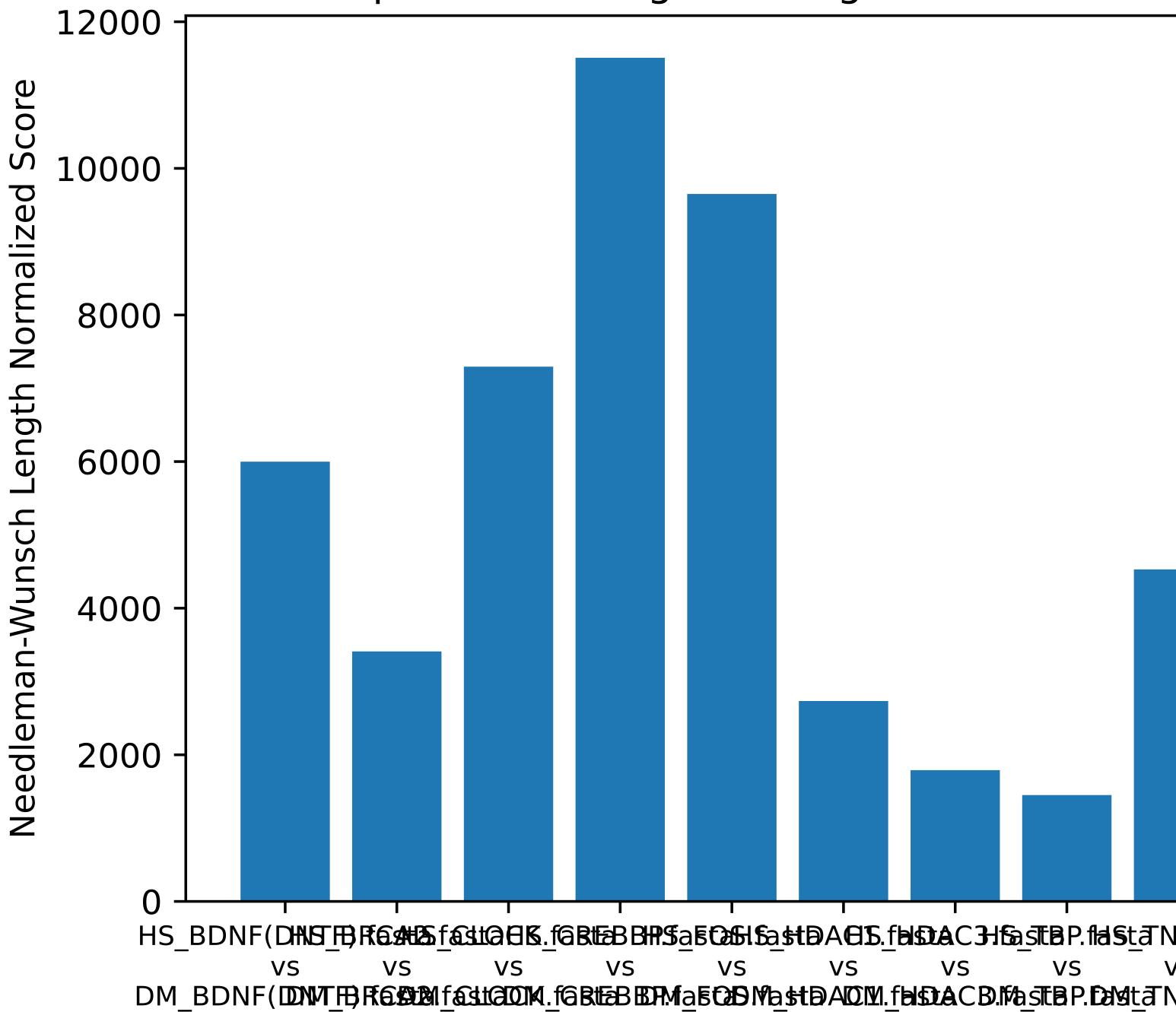
[GitHub Link To Code](#)

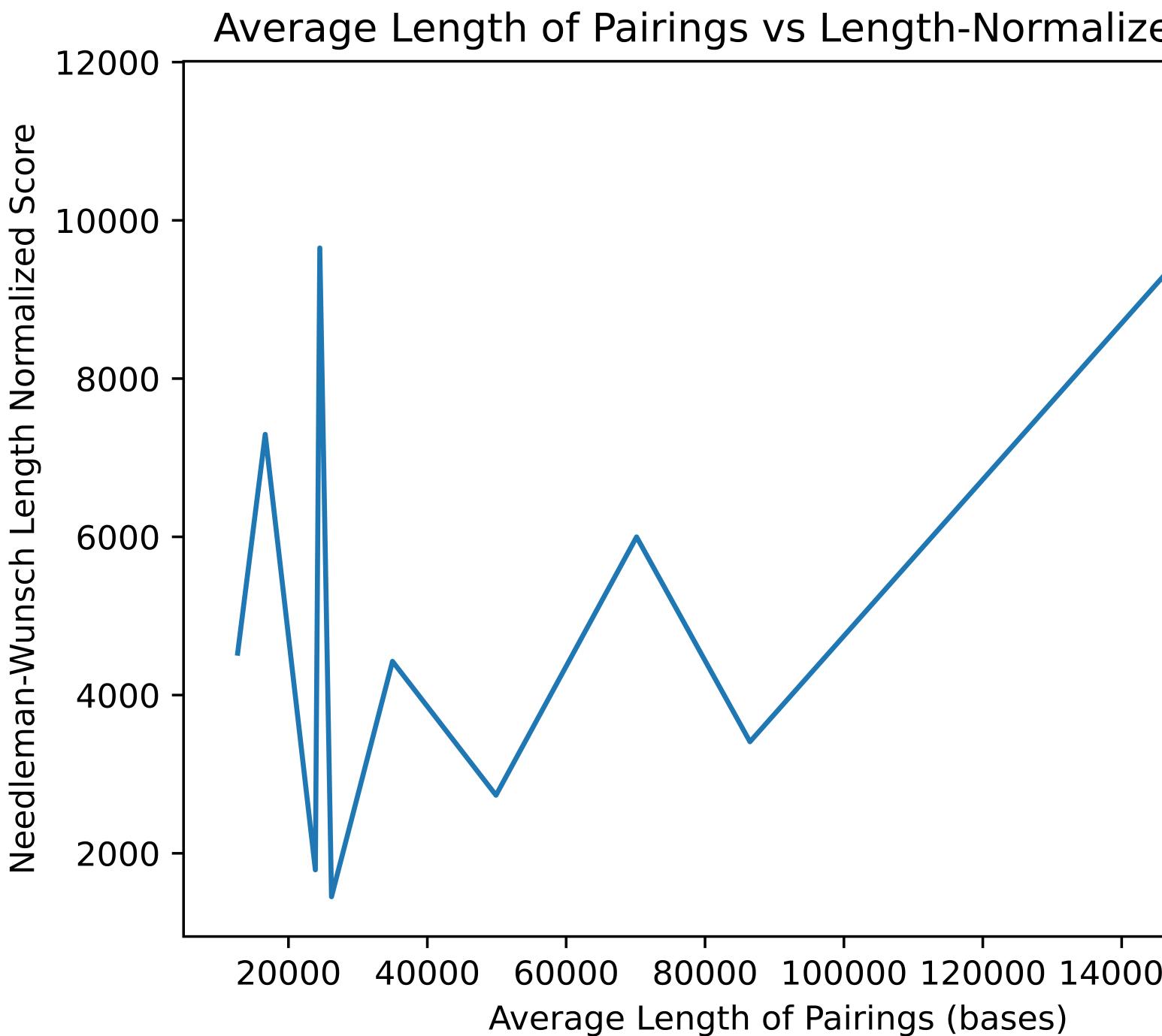
Calculated Gene Deviation Score: 0.2690033801934049

Number of Gene pairs: 10

Compared Files	Needleman-Wunsch Score
HS_BDNF(DNTF).fasta vs DM_BDNF(DNTF).fasta	5999.0
HS_BRCA2.fasta vs DM_BRCA2.fasta	3410.0
HS_CLOCK.fasta vs DM_CLOCK.fasta	7295.0
HS_CREBBP.fasta vs DM_CREBBP.fasta	11508.0
HS_FOS.fasta vs DM_FOS.fasta	9651.0
HS_HDAC1.fasta vs DM_HDAC1.fasta	2734.0
HS_HDAC3.fasta vs DM_HDAC3.fasta	1791.0
HS_TBP.fasta vs DM_TBP.fasta	1451.0
HS_TNF.fasta vs DM_TNF.fasta	4529.0
HS_TP53.fasta vs DM_TP53.fasta	4426.0

Comparison Pairings vs Length-Normalized Score





Thanks for an amazing quarter, Professor Schiffer and the TA's!

Best, as always,

Chris Matthew Cyril :)

