# Alignments and Scores:

Below shows the input and outputs associated with the six run conditions requested in the homework assignment. I used two files (NWA.py and NWA62\_anchor.py) instead of three files, as the NWA62\_anchor.py file will call anchored or non-anchored depending on the input command.

### NWA.py

This file runs only the non-anchored Needleman-Wunsch algorithm.

This program will take two sets of inputs:

1. NWA.py Human\_HOX.fa Fly\_HOX.fa
2. NWA.py Human\_PAX.fa Fly\_PAX.fa

The associated outputs should be

1. Sequence 1:

RMKWKKEHKDEGPTAAAAPEGAVPSAAATAAADKADEEDDDEEEEDEEEMS-----S--SY----YVNA--LFSKY-TAG-TSL--------FQ--N---AEPTSCSF-----AP--N----------SQ---R-----S--GYG----A---G-----A----------GA-----FASTVPGL---------YNVNSPLYQSP--FAS-------GYGL------G----AD-AYG---N----L------PCA--SY------D-----QN--IPGLCSDLAKG-----A--CDKTDEGA---------LH-G---AAEAN---------FRIYPWMRS-SG--PDRKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQVKIWFQNRRMKWKKEHKDEGPTAAAAPEGAVPSAAATAAADKADEEDDDE-EEEDEEE

Sequence 2:

M--------------------------T---------------------MSTNNCESMTSYFTNSYMGADMHHGHYPGNGVTDLDAQQMHHYSQNPNQQGNMP-YPRFPPYDRMPYYNGQGMDQQQQQHQGYSRPDSPSSQVG-GVMPQAQTNGQLVSVAQQQQQTQQQQQAQTQQQQAQQAP-LQQQQHPQVTQQVTHPQQQQPVVYASCKLQAAVG-GLGMVQEGGSPPLVDQMGGHHMNAQMTLPHHMGHPQAQLGYTDVGVPDVTEVHQNHHNMGMYGQQQTGVPPVVAPPQAMMHPGAGQGPPQMHQGHPGQHTPPSQNPSSQSSGMPSPLYPWMRSQFGKCQERKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKENK----T-KGEP-G---S----------GGE-GDEITPPNSPQ

Alignment Score: -494

1. Sequence 1:

MQN--------------------------------------S--------------HSGVNQLGGVFVNGRPLPDSTRQKIVELAHSGARPCDISRILQVSNGCVSKILGRYYETGSIRPRAIGGSKPRVATPEVVSKIAQYKRECPSIFAWEIRDRLLSEGVCTNDNIPSVSSINRVLRNLASEK-QQ--------------------------------------------M------------GA----DG-----MYDKLRMLN-------G---------QTG-S---WGTR---P----G------------W----YPG----T--------------SV---------------P---------G-Q---P--T--------QDGCQQQE-G-G-GENTNSISSN-G--EDSDEAQMRLQLKRKLQRNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQVWFSNRRAKWRREEKLRNQRR----------------QASNT--P------------S-HIP----I---SS-S-FSTSVYQP-----I---PQPT-TP--VSSFTS----G--S-MLGR--TDTAL-----TNT---YS-------AL-P---P-----MPSF-TM-AN----NLPM-------QP-P------V-----PS----Q---T-SS-YSC-M-L-------------------P-----TS-PSVN-G----RS-Y---DTY--TPPHM-------------------QT--H---MNS--QP-MGTS--G-TTSTG----LISPGV------------S----VP-------VQV-PG-SEPDMS-QYWPRLQ\*

Sequence 2:

MRNLPCLGTAGGSGLGGIAGKPSPTMEAVEASTASHPHSTSSYFATTYYHLTDDECHSGVNQLGGVFVGGRPLPDSTRQKIVELAHSGARPCDISRILQVSNGCVSKILGRYYETGSIRPRAIGGSKPRVATAEVVSKISQYKRECPSIFAWEIRDRLLQENVCTNDNIPSVSSINRVLRNLAAQKEQQSTGSGSSSTSAGNSISAKVSVSIGGNVSNVASGSRGTLSSSTDLMQTATPLNSSESGGASNSGEGSEQEAIYEKLRLLNTQHAAGPGPLEPARAAPLVGQSPNHLGTRSSHPQLVHGNHQALQQHQQQSWPPRHYSGSWYPTSLSEIPISSAPNIASVTAYASGPSLAHSLSPPNDIESLASIGHQRNCPVATEDIHLKKELDGHQSDETGSGEGENSNGGASNIGNTED-D--QARLILKRKLQRNRTSFTNDQIDSLEKEFERTHYPDVFARERLAGKIGLPEARIQVWFSNRRAKWRREEKLRNQRRTPNSTGASATSSSTSATASLTDSPNSLSACSSLLSGSAGGPSVSTINGLSSPSTLSTNVNAPTLGAGIDSSESPTPIPHIRPSCTSDNDNGRQSEDCRRVCSPCPLGVGGHQNTHHIQSNGHAQGHALVPAISPRLNFNSGSFGAMYSNMHHTALSMSDSYGAVTPIPSFNHSAVGPLAPPSPIPQQGDLTPSSLYPCHMTLRPPPMAPAHHHIVPGDGGRPAGVGLGSGQSANLGASCSGSGYEVLSAYALPPPPMASSSAADSSFSAASSASANVTPHHTIAQESCPSPCSSASHFGVAHSSGFSSDPISPAVSSYAHMSYNYASSANTMTPSSASGTSAHVAPGKQQFFASCFYSP--WV

Alignment Score: -850

### NWA62\_anchor.py

This file runs either the anchored or the non-anchored Needleman-Wunsch algorithm depending on the inputs. The first two inputs below should run the non-anchored algorithm.

This program will take four sets of inputs:

Non-anchored:

1. NWA62\_anchor.py Human\_HOX.fa Fly\_HOX.fa
2. NWA62\_anchor.py Human\_PAX.fa Fly\_PAX.fa

Anchored

1. NWA62\_anchor.py Human\_HOX.fa Fly\_HOX.fa Match\_HOX.txt
2. NWA62\_anchor.py Human\_PAX.fa Fly\_PAX.fa Match\_PAX.txt

The associated outputs should be

1. Your input arguments are: ['H:/My Drive/Fall 2021/CSCI 5481/Homework 1/files/NWA62\_anchor.py', 'NWA62\_anchor.py', 'Human\_HOX.fa', 'Fly\_HOX.fa']

Sequence 1:

--MS-----S--SYYVN----A-L-FSKYTA-G-TSL-------F-Q--NAE---P-TSC-SF--AP--N-------SQR-SGY------GA---G----A---G-----A-----F-----AST-------VP---GLY-NV--N-S-PLYQSP--FAS--------GYGL----GA----DAY-G---N----LP--C----A--SY-DQNIPGL--C--S--D--L-A--K-G-----ACDKT--DEGA------LH-G-AAE----A-N-------F-R-IYPWMRSS-G--PDRKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQVKIWFQNRRMKWKKEHKDEGPTAAAAPEGAVPSAAATAAADKADEEDDDEEEEDEEE

Sequence 2:

MTMSTNNCESMTSYFTNSYMGADMHHGHYPGNGVTDLDAQQMHHYSQNPNQQGNMPYPRFPPYDRMPYYNGQGMDQQQQQHQGYSRPDSPSSQVGGVMPQAQTNGQLVSVAQQQQQTQQQQQAQTQQQQAQQAPLQQQQHPQVTQQVTHPQQQQPVVYASCKLQAAVGGLGMVQEGGSPPLVDQMGGHHMNAQMTLPHHMGHPQAQLGYTDVGVPDVTEVHQNHHNMGMYGQQQTGVPPVVAPPQAMMHPGAGQGPPQMHQGHPGQHTPPSQNPSSQSSGMPSPLYPWMRSQFGKCQERKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKENKTKG-----EP-G---S-----GGE-GD-E---ITPPNSPQ

Alignment Score: -251.0

1. Your input arguments are: ['H:/My Drive/Fall 2021/CSCI 5481/Homework 1/files/NWA62\_anchor.py', 'NWA62\_anchor.py', 'Human\_PAX.fa', 'Fly\_PAX.fa']

Sequence 1:

MQN--------------------------------------S--------------HSGVNQLGGVFVNGRPLPDSTRQKIVELAHSGARPCDISRILQVSNGCVSKILGRYYETGSIRPRAIGGSKPRVATPEVVSKIAQYKRECPSIFAWEIRDRLLSEGVCTNDNIPSVSSINRVLRNLASEK-QQ--------------------------------------------M------------GA----DG-----MYDKLRMLN-------G--Q-------TG-S---WGTR---P----G------------W----YPG----T--S---V---P----------G-------QPTQD-------G----C----Q------Q----Q--E-G-G-GENTNSISSN-GEDSDEAQMRLQLKRKLQRNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQVWFSNRRAKWRREEKLRNQRR-------QA-----S---N-T--P------SH-I------P----I---SS-S-FSTSVYQP-----I--PQ-PT-TP-V-SSFTS----G--S-----M-----L---GRTDT-AL-TNTYS---AL-P---P-M---P-SF---------T---M-----A-------N-N-L-PM-QP-PVPSQ---T-SS-YSC-M-L---P-T-S-----------PS-V--------N-G---R-S-YD--T-YT--PPHM------------------Q-T--H-M--NS--QPMGT-S--GTT-STGL----ISPGV-S---V------PVQ-V-P----G-S-E--PDMSQYWPR-L-Q--\*

Sequence 2:

MRNLPCLGTAGGSGLGGIAGKPSPTMEAVEASTASHPHSTSSYFATTYYHLTDDECHSGVNQLGGVFVGGRPLPDSTRQKIVELAHSGARPCDISRILQVSNGCVSKILGRYYETGSIRPRAIGGSKPRVATAEVVSKISQYKRECPSIFAWEIRDRLLQENVCTNDNIPSVSSINRVLRNLAAQKEQQSTGSGSSSTSAGNSISAKVSVSIGGNVSNVASGSRGTLSSSTDLMQTATPLNSSESGGASNSGEGSEQEAIYEKLRLLNTQHAAGPGPLEPARAAPLVGQSPNHLGTRSSHPQLVHGNHQALQQHQQQSWPPRHYSGSWYPTSLSEIPISSAPNIASVTAYASGPSLAHSLSPPNDIESLASIGHQRNCPVATEDIHLKKELDGHQSDETGSGEGENSNGGASNIGNTEDD-QARLILKRKLQRNRTSFTNDQIDSLEKEFERTHYPDVFARERLAGKIGLPEARIQVWFSNRRAKWRREEKLRNQRRTPNSTGASATSSSTSATASLTDSPNSLSACSSLLSGSAGGPSVSTINGLSSPSTLSTNVNAPTLGAGIDSSESPTPIPHIRPSCTSDNDNGRQSEDCRRVCSPCPLGVGGHQNTHHIQSNGHAQGHALVPAISPRLNFNSGSFGAMYSNMHHTALSMSDSYGAVTPIPSFNHSAVGPLAPPSPIPQQGDLTPSSLYPCHMTLRPPPMAPAHHHIVPGDGGRPAGVGLGSGQSANLGASCSGSGYEVLSAYALPPPPMASSSAADSSFSAASSASANVTPHHTIAQESCPSPCSSASHFGVAHSSGFSSDPISPAVSSYAHMSYNYASSANTMTPSSASGTSAHVAPGKQQFFASCFYSPWV

Alignment Score: -487.0

1. Your input arguments are: ['H:/My Drive/Fall 2021/CSCI 5481/Homework 1/files/NWA62\_anchor.py', 'NWA62\_anchor.py', 'Human\_HOX.fa', 'Fly\_HOX.fa', 'Match\_HOX.txt']

Sequence 1:

--MS-----S--SYYVN----A-L-FSKYTA-G-TSL-------F-Q--NAE---P-TSC-SF--AP--N-------SQR-SGY------GA---G----A---G-----A-----F-----AST-------VP---GLY-NV--N-S-PLYQSP--FAS--------GYGL----GA----DAY-G---N----LP--C----A--SY-DQNIPGL--C--S--D--L-A--K-G-----ACDKT--DEGA------LH-G-AAE----A-N-------F-R-I-PWMRSS-G--PDRKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQVKIWFQNRRMKWKKEHKDEGPTAAAAPEGAVPSAAATAAADKADEEDDDEEEEDEEE

Sequence 2:

MTMSTNNCESMTSYFTNSYMGADMHHGHYPGNGVTDLDAQQMHHYSQNPNQQGNMPYPRFPPYDRMPYYNGQGMDQQQQQHQGYSRPDSPSSQVGGVMPQAQTNGQLVSVAQQQQQTQQQQQAQTQQQQAQQAPLQQQQHPQVTQQVTHPQQQQPVVYASCKLQAAVGGLGMVQEGGSPPLVDQMGGHHMNAQMTLPHHMGHPQAQLGYTDVGVPDVTEVHQNHHNMGMYGQQQTGVPPVVAPPQAMMHPGAGQGPPQMHQGHPGQHTPPSQNPSSQSSGMPSPLYPWMRSQFGKCQERKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKENKTKG-----EP-G---S-----GGE-GD-E---ITPPNSPQ

Alignment Score: 278

1. Your input arguments are: ['H:/My Drive/Fall 2021/CSCI 5481/Homework 1/files/NWA62\_anchor.py', 'NWA62\_anchor.py', 'Human\_PAX.fa', 'Fly\_PAX.fa', 'Match\_PAX.txt']

Sequence 1:

MQN--------------------------------------S---------------SGVNQLGGVFVNGRPLPDSTRQKIVELAHSGARPCDISRILQVSNGCVSKILGRYYETGSIRPRAIGGSKPRVATPEVVSKIAQYKRECPSIFAWEIRDRLLSEGVCTNDNIPSVSSINRVLRNLASEKQQMGADGMYDKLRMLNG-QT-GSWGTRPGWYP-GT-SVPGQPTQDGCQQQE-G-G-GENTNSISSN-GEDSDEAQMRLQLKRKLQRNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQVWFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFST-SVYQPIPQPTTPVSSFTSGSMLGRTDTALTNTYSALPPMPSFTMANNLPMQPPVPSQTSSYSCMLPTSPSVNGRSYDTYTPP-HMQTHMNSQPMGTSGTTSTGLISPGVSVPVQVPGSEPDM-SQYW-PRLQ\*

Sequence 2:

MRNLPCLGTAGGSGLGGIAGKPSPTMEAVEASTASHPHSTSSYFATTYYHLTDDECHSGVNQLGGVFVGGRPLPDSTRQKIVELAHSGARPCDISRILQVSNGCVSKILGRYYETGSIRPRAIGGSKPRVATAEVVSKISQYKRECPSIFAWEIRDRLLQENVCTNDNIPSVSSINRVLRNLASVTAYASGPSLAHSLSPPNDIESLASIGHQRN-CPVATEDIHLKKELDGHQSDETGSGEGENSNGGASNIGNTEDD-QARLILKRKLQRNRTSFTNDQIDSLEKEFERTHYPDVFARERLAGKIGLPEARIQVWFSNRRAKWRREEKLRNQRRQSANLGASCS-GSGYEVLSAY-ALP-P-PPMAS--S-SAADSSFSAASSA-SA-NVTPHHTIA-----QESCPSPCSSAS-HFGVAHS-SGFSSDPISPAVSSYAHM-SYNYASSANTMTPSSASGTSAHV-APGKQQFFASCFYSPWV--

Alignment Score: 48