

## Presentation report: Multiple alignment

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### Alignments:

#### **Test sequences 1-3: (score of 782)**

ATGGATTATCTGCGGATCATGTTGAAGA-AGTACAAAATGTCCTCAATGCTATGCA-GAAAATCTTAG--AGTGTCCAATA-TGT  
CTGGAGTTGATCAAAGAGCCT-GTC-TCTACAAAGTGTGACC-A-CA-TATTTTGCAAATTTGTATGC-TGAAAC-T--TCTCAACC  
A-GAAGAAAGGGCCTTCACAATGTCC--TTTGTGTAAGAATGA

ATGGATTATCTGCGGATCGTGTGAAGA-AGTACAAAATGTTCTTAATGCTATGCA-GAAAATCTTAG--AGTGTCCAATA-TGT  
CTGGAGTTGATCAAAGAGCCT-GTT-TCTACAAAGTGTGATC-A-CA-TATTTTGCAAATTTGTATGC-TGAAAC-T--TCTCAACC  
A-GAGGAAGGGGCCTTCACAGTGTCC--TTTGTGTAAGAACGA

GCGAA---AT--GTA-A-CACGGTAGAGGTGAT-CGGGGTG-CGTTA-TAC-GTGCGTGGTGACCTCGGTCGGTGTT-GACGGTGC  
CTGGGGTTCCTCAGAGTGTGTTGGGGTCTGAAGGATG-GACTTGTCAGTGATT-GCCA-TTGGAGACGTGCAAAATGTGCTTT  
CAGCCATGCAGAA-GAAC-TTGG-AGTGTCCAGTCTGTTTAGATGTGA

#### **Test sequences 1-4: (score of 2337)**

ATGGATTATCTGCGGATCGTGTGAAGAAG-TAC--AA-AAT-GTTC-TTAATGCTATGCA-GAAAATCTTAG--AGTGTCCAATA-  
TGTCTGGAGTTGATCAAAGAGCCT-GTT-TCTACAAAGTGTGA--TCA-C--A-TATTTTGCAAATTTGTAT-G-C-TG-AAAC-T--T  
TCAACCA-GAGGAAGGGGCCT-T-CAC--AGT-GTCC--TTTGTGTAAGAACGA

ATGGATTATCTGCGGATCATGTTGAAGAAG-TAC--AA-AAT-GTCC-TCAATGCTATGCA-GAAAATCTTAG--AGTGTCCAATA-  
TGTCTGGAGTTGATCAAAGAGCCT-GTC-TCTACAAAGTGTGA--CCA-C--A-TATTTTGCAAATTTGTAT-G-C-TG-AAAC-T--T  
CTCAACCA-GAAGAAAGGGGCCT-T-CAC--AAT-GTCC--TTTGTGTAAGAATGA

GCGAAAT-GTA-AC--A-CG-GTAGAGGTGA-T-C--GG-GGT-GCG--TTA-TAC-GTGCGTGGTGACCTCGGTCGGTGTT-GACGG  
TGCCTGGGGTTCCTCAGAGTGTGTTGGGGTCTGAAGGATG-GAC-TTGTC--AGTGATT-GCCA-TTGGAGAC-G-TGCA-AAAT  
GTGCTTTCAGCCATGCAGAAGAA-C-T-T-GG---AGT-GTCCAGTCTGTTTAGATGTGA

GTACCTTGATTT-CGTATTCTGA-GAGGCTGCTGCTAGCGGTAGCCCCCTGGT-TTCCGTG-GCAA-CGGAAA--AGCGCGGGA  
-A-T-TACAGA-TAAATAAA-A-C-T-GCG-ACTGCGCGGCGTGAGCTCG-CTGA-GACTTCCTGGACGGGGGACAGGC-TGTGG  
GG-T--T-TC--TCA-GATAACTGGGCCCTGCGCTCAGGAGGCC--TTCAC-C-C-T-C-T

#### **Test sequences 1-5: (score of 3295)**

ATGGATTATCTGCGGATCATGTTGAAGA-AG-TAC--AA-AAT-GTCC-TCAATGCTATGCA-GAAAATCTTAG--AGTGTCCAATA-  
TGTCTGGAGTTGATCAAAGAGCCT-GTC-TCTACAAAGTGTGA-C-C-A-C--A-TATTTTGCAAATTTGTAT-G-C-TG-AAAC-T--T  
CTCAACCA-GAAGAAAGGGCCT-T-CAC--AAT-GTCC--TTTGTGTAAGAATGA

ATGGATTATCTGCGGATCGTGTGAAGA-AG-TAC--AA-AAT-GTTC-TTAATGCTATGCA-GAAAATCTTAG--AGTGTCCAATA-  
TGTCTGGAGTTGATCAAAGAGCCT-GTT-TCTACAAAGTGTGA-T-C-A-C--A-TATTTTGCAAATTTGTAT-G-C-TG-AAAC-T--T  
CTCAACCA-GAGGAAGGGGCCT-T-CAC--AGT-GTCC--TTTGTGTAAGAACGA

GCGAA---AT--GTA-A-CACGGTAGAGGTGA-T-C--GG-GGT-G-CG-TTA-TAC-GTGCGTGGTGACCTCGGTCGGTGTT-GACGG  
TGCCTGGGGTTCCTCAGAGTGTGTTGGGGTCTGAAGGATG-GA-C-TTGTC--AGTGATT-GCCA-TTGGAGAC-G-TGCA-AAAT  
GTGCTTTCAGCCATGCAGAA-GAAC-T-T-GG---AGT-GTCCAGTCTGTTTAGATGTGA

GTACCTTGATTT-CGTATTCTGA-GAGGC-TGCTGCTTAGCGGTAGCCCCCTTGGT-TTCCGTG-GCAA-CGGAAA--AGCGCGGG  
A-A-T-TACAGA-TAAATTA AAA-A-C-T-GCG-ACTGCGCGGCGTGAGCTC-G-CTGA-GACTTCCTGGACGGGGGACAGGC-TGT  
GGGG-T--T-TC--TCA-GATAACTGGGCCCTGCGCTCAGGAGGCC--TTCAC-C---C-TCT

ATGGATTATCTGCTGTTGCGTTGAAGA-AG-TAC--AA-AAT-GTCA-TTAATGCTATGCA-GAAAATCTTAG--AGTGTCCAATC-  
TGTCTGGAGTTGATCAAGGAACCT-GTC-TCCACAAAGTGTGA-C-C-A-C--A-TATTTTGACAGATTTTGCAT-G-C-TG-AAAC-T--  
TCTCAACCA-GAAGAAAGGGCCT-T-CAC--AGT-GTCC--TTTGTGTAAGAATGA

### ***Test sequences 1-6: (score of 5976)***

AT-G-GATTTATCTGCGGATCG-TGTTGAAGAAG-TAC--AA-AAT-GTTC-TTAATG-CT-AT-GCA-GAAAATCTTAG--A-GTGTC-C  
AAT-A-TGTCTGGAGTTGATCAAAGAGCC-T-GTT-TCTACAAAGTGTGA--TCA-C--A-TATTTTGCAAATTTGTAT-G-C-T-G-AA  
AC-T--TCTCAACCA-GAGGAAGGGGCCT-T-CAC--AGT-GTCC--TTTGTGTAAGAACGA

AT-G-GATTTATCTGCGGATCA-TGTTGAAGAAG-TAC--AA-AAT-GTCC-TCAATG-CT-AT-GCA-GAAAATCTTAG--A-GTGTC-C  
AAT-A-TGTCTGGAGTTGATCAAAGAGCC-T-GTC-TCTACAAAGTGTGA--CCA-C--A-TATTTTGCAAATTTGTAT-G-C-T-G-AA  
AC-T--TCTCAACCA-GAAGAAAGGGCCT-T-CAC--AAT-GTCC--TTTGTGTAAGAATGA

GC-G-AAAT-GTA-AC--A-CG--GTAGAGGTGA-T-C--GG-GGT-GCG--TTA-TA-C--GT-GCGTGGTGACCTCGGTCG-GTGTT--G  
AC-GGTGCCTGGGGTTCTCAGAGTGTT-TTGGGGTCTGAAGGATG-GAC-TTGTC--AGTGATT-GCCA-TTGGAGAC-G-TGC-  
A-AAATGTGCTTTCAGCCATGCAGAAGAA-C-T-T-GG---AGT-GTCCAGTCTGTTTAGATGTGA

GT-A-CCTTGATTT-CGTATTC-TGA-GAGGCTGCTGCTTAGCGGTAGCCCCCTTGGT-TT-CC-GTG-GCAA-CGGAAA--A-GCGC  
G-GGA--A-T-TACAGA-TAAATTA AAA-A-C--T-GCG-ACTGCGCGGCGTGAGCTCG-CTGA-GACTTCCTGGACGGGGGACAGG  
C-T-GTGGGG-T--T-TC--TCA-GATAACTGGGCCCTGCGCTCAGGAGGCC--TTCAC-C-C-T-C-T

AT-G-GATTTATCTGCTGTTGCG-CGTTGAAGAAG-TAC--AA-AAT-GTCA-TTAATG-CT-AT-GCA-GAAAATCTTAG--A-GTGTC-C  
AAT-C-TGTCTGGAGTTGATCAAGGAACC-T-GTC-TCCACAAAGTGTGA--CCA-C--A-TATTTTGACAGATTTTGCAT-G-C-T-G-AA  
AAC-T--TCTCAACCA-GAAGAAAGGGCCT-T-CAC--AGT-GTCC--TTTGTGTAAGAATGA

GTTCCGAAAGGCTAGCGC-TAGGCGCC-AAGCGG-C-C--GG-T-T--TCC-TTGGCGACGGAGAGCGCGGGAATTTTAG--ATAG  
ATTGTAATTG-CGGCTGC-GC-GGCCGCTGC-CCGT-GCA-GCCAGAGGATCCAG---CA-C--C-TCTCTGGGGCTTCTCCGT-C-C  
-TCG-GCGC-T--TGG-AAGTA-C-GGATCTTTTTTCT-CGG--AGA-AAAG--TTCAC-TG-GAACTG

### ***Full sequences 1-8: (score of ?)***

We reached the maximum recursion depth limit when we tried to run this. A solution could be either raise the recursion limit or to make the algorithms iterative instead, but as we spend a lot of time getting it to work recursively, we did not want to start over to get it to work iteratively.

### **Running time and space consumption:**

We have computed the scoring alignments following the code in the slides. Therefore we will think our method has a running time of  $O(k^2n^2)$ .

### **Reference:**

We couldn't get it to work. But in case someone is interested we have the alignments on our local computer, and can send them if necessary.