Essential Computing for Bioinformatics

Lecture 6

Files

MARC: Developing Bioinformatics Programs
July 2009

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Essential Computing for Bioinformatics

- The following material is the result of a curriculum development effort to provide a set of courses to support bioinformatics efforts involving students from the biological sciences, computer science, and mathematics departments. They have been developed as a part of the NIH funded project “Assisting Bioinformatics Efforts at Minority Schools” (2T36 GM008789). The people involved with the curriculum development effort include:

- Dr. Hugh B. Nicholas, Dr. Troy Wymore, Mr. Alexander Ropelewski and Dr. David Deerfield II, National Resource for Biomedical Supercomputing, Pittsburgh Supercomputing Center, Carnegie Mellon University.
- Dr. Ricardo González Méndez, University of Puerto Rico Medical Sciences Campus.
- Dr. Alade Tokuta, North Carolina Central University.
- Dr. Jaime Seguel and Dr. Bienvenido Vélez, University of Puerto Rico at Mayagüez.
- Dr. Satish Bhalla, Johnson C. Smith University.

- Most recent versions of these presentations can be found at http://marc.psc.edu/

Outline

- Text Files
- Reading from Text Files
- Writing to Text Files
- Examples

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What are Text Files?

- Persistent (non-volatile) storage of data
- Needed when:
  - data must outlive the execution of your program
  - data does not fit in memory (external algorithms)
  - data is supplied in batch form (non-interactive)
- Files are stored in your hard drive
- Files are maintained by your computer's Operating System (e.g. Linux, Windows, MacOS)

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Examples of Text Files

- Word documents
- Html documents retrieved from the web
- XML documents
- FASTA files
- GENBANK file
- Multiple Sequence Alignement Files (PFAM)

Text files contain a sequence of numbers that must be decoded using some standard in order to be converted to string form

Examples of encodings: ASCII, LATIN1, EBCDIC, Unicode

Check http://en.wikipedia.org/wiki/Character_encoding for more info

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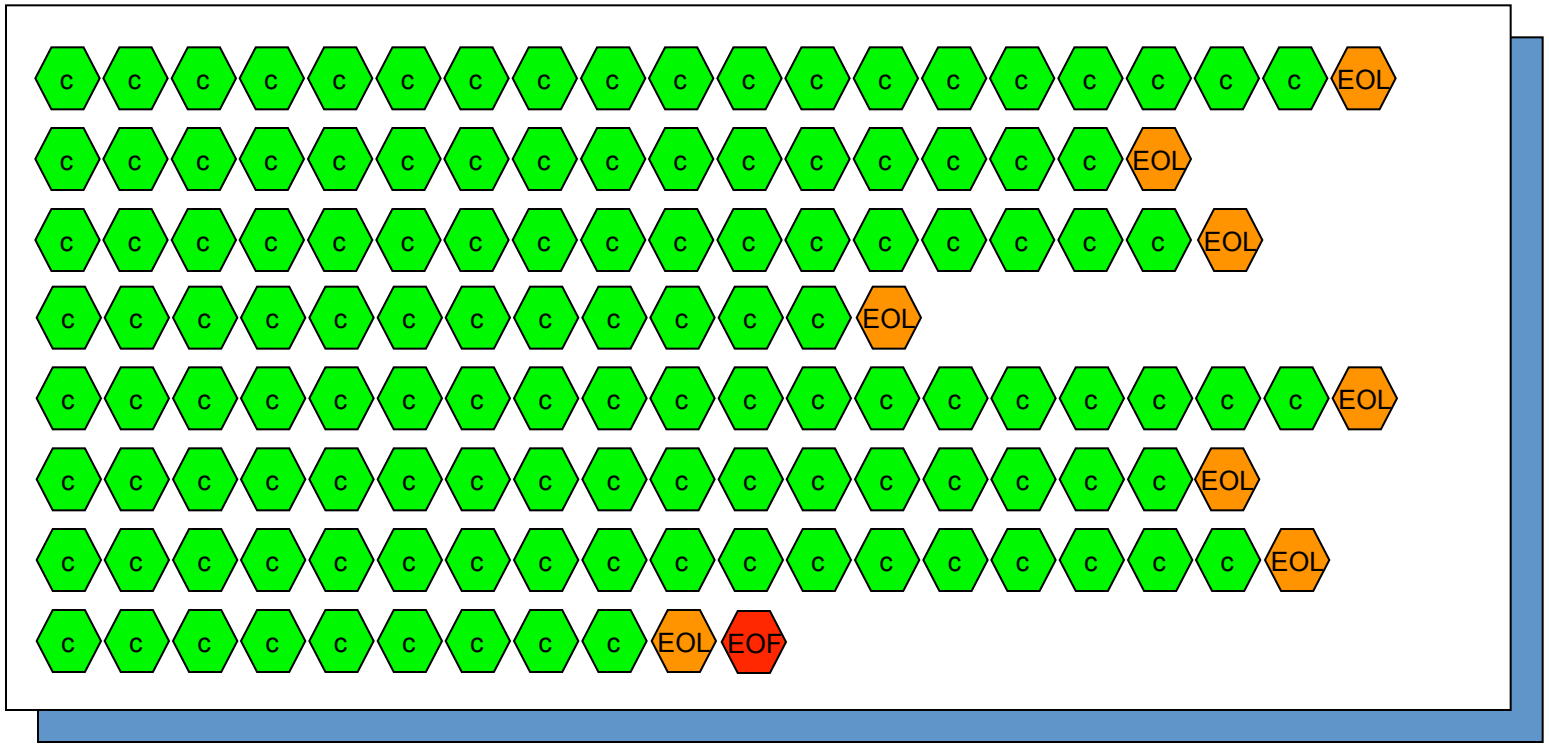
Top-level Anatomy of a Text File



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Examples of Text Files: HTML

```
<html><head>
  <meta http-equiv="Content-Type" content="text/html; charset=utf-8"/>
  <meta name="robots" content="index, nofollow, noarchive"/>
  <title>NCBI Sequence Viewer v2.0</title>
<!--MUTABLE-->
<!--www.ncbi.nlm.nih.gov:80-->
<!--MUTABLE-->
  <link type="text/css" rel="stylesheet" href="http://www.ncbi.nlm.nih.gov/corehtml/ncbi_test.css"/>
  <link type="text/css" rel="stylesheet" href="../sviewer/viewer.css"/>
  <script type="text/javascript" src="../sviewer/viewer.js"> </script>

  <script type="text/javascript" src="http://www.ncbi.nlm.nih.gov/coreweb/javascript/popupmenu2/popupmenu2_6loader.js"> </script>
</head><body ><form name="frmQueryBox0" action="/sites/entrez" method="get" style="margin:0">
  <table width="100%" border="0" cellpadding="0" cellspacing="0">
    <tr>
      <td>
       <table width="100%" border="0" cellpadding="0" cellspacing="0">
         <tr>
          <td align="left" width="130">
            <a href="http://www.ncbi.nlm.nih.gov">

              <img src="http://www.ncbi.nlm.nih.gov/corehtml/left.GIF" width="130" height="45" border="0" alt="NCBI"/>
            </a>
          </td>
          <td align="left">
            <img src="/entrez/query/static/gifs/entrez_nuc.gif" alt="Nucleotide banner"/>
          </td>
          <td>
            <table class="medium1" border="0" bordercolor="#336699" cellpadding="2" cellspacing="0" align="right">
              <tr>
…
…
```


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Examples of Text Files: XML

```
<?xml version="1.0"?>
<!DOCTYPE Seq-entry PUBLIC "-//NCBI//NCBI Seqset/EN" "http://www.ncbi.nlm.nih.gov/dtd/NCBI_Seqset.dtd">
<Seq-entry>
 <Seq-entry_set>
  <Bioseq-set>
   <Bioseq-set_level>1</Bioseq-set_level>
   <Bioseq-set_class value="nuc-prot"/>
   <Bioseq-set_descr>
    <Seq-descr>
     <Seqdesc>
      <Seqdesc_source>
       <BioSource>
        <BioSource_genome value="genomic">1</BioSource_genome>
        <BioSource_org>
         <Org-ref>
          <Org-ref_taxname>Xanthomonas campestris pv. campestris</Org-ref_taxname>
          <Org-ref_db>
           <Dbtag>
            <Dbtag_db>taxon</Dbtag_db>
            <Dbtag_tag>
             <Object-id>
              <Object-id_id>340</Object-id_id>
             </Object-id>
            </Dbtag_tag>
           </Dbtag>
          </Org-ref_db>
          <Org-ref_orgname>
           <OrgName>
            <OrgName_name>
             <OrgName_name_binomial>
…
```


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Examples of Text Files: GENEBANK

```
LOCUS       NC_010688             5079002 bp    DNA     circular BCT 17-JUL-2008
DEFINITION  Xanthomonas campestris pv. campestris, complete genome.
ACCESSION   NC_010688
VERSION     NC_010688.1  GI:188989396
PROJECT     GenomeProject:29801
KEYWORDS    complete genome.
SOURCE      Xanthomonas campestris pv. campestris
  ORGANISM  Xanthomonas campestris pv. campestris
            Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
            Xanthomonadaceae; Xanthomonas.
REFERENCE   1
  AUTHORS   Vorholter,F.J., Schneiker,S., Goesmann,A., Krause,L., Bekel,T.,
            Kaiser,O., Linke,B., Patschkowski,T., Ruckert,C., Schmid,J.,
            Sidhu,V.K., Sieber,V., Tauch,A., Watt,S.A., Weisshaar,B.,
            Becker,A., Niehaus,K. and Puhler,A.
  TITLE     The genome of Xanthomonas campestris pv. campestris B100 and its
            use for the reconstruction of metabolic pathways involved in
            xanthan biosynthesis
  JOURNAL   J. Biotechnol. 134 (1-2), 33-45 (2008)
   PUBMED   18304669
REFERENCE   2  (bases 1 to 5079002)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAY-2008) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   3  (bases 1 to 5079002)
  AUTHORS   Linke,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-2007) Linke B., Center For Biotechnology,
            Bielefeld University, Universitaetsstrasse 25, 33501 Bielefeld,
            GERMANY
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
```


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Examples of Text Files: FASTA

```
>gi|188989396|ref|NC_010688.1| Xanthomonas campestris pv. campestris, complete genome
ATGGATGCTTGGCCCCGCTGTCTGGAACGTCTCGAAGCTGAATTCCCGCCCGAAGATGTCCACACCTGGT
TGAAACCCCTGCAGGCCGAAGATCGCGGCGACAGCATCGTGCTGTACGCGCCGAACGCCTTCATTGTCGA
GCAGGTTCGCGAGCGATACCTGCCGCGCATCCGCGAGTTGCTGGCGTATTTCGCCGGCAATGGCGAGGTG
GCGCTGGCGGTCGGCTCCCGTCCGCGTGCGCCGGAGCCGCTGCCGGCACCGCAAGCCGTCGCCAGTGCGC
CGGCGGCCGCGCCGATCGTGCCCTTCGCCGGCAACCTGGATTCGCATTACACCTTTGCCAACTTCGTGGA
AGGCCGCAGCAACCAGCTCGGTCTGGCCGCGGCGATCCAGGCCGCACAGAAGCCTGGCGACCGGGCGCAC
AACCCGTTGCTGCTGTACGGCAGCACCGGGCTGGGCAAGACCCACCTGATGTTCGCGGCCGGCAACGCGC
TGCGCCAGGCCAATCCGGCCGCCAAGGTGATGTACCTGCGCTCGGAACAGTTCTTCAGCGCGATGATCCG
CGCGTTGCAGGACAAGGCAATGGACCAGTTCAAGCGCCAGTTCCAGCAGATCGATGCGCTGCTGATCGAC
GACATCCAGTTTTTTGCCGGCAAGGACCGCACGCAGGAGGAGTTTTTCCACACCTTCAACGCGCTGTTCG
ACGGCCGCCAGCAGATCATCCTGACCTGCGACCGCTATCCGCGCGAAGTCGAGGGCCTGGAGCCGCGGCT
GAAGTCGCGCCTGGCCTGGGGCCTGTCGGTGGCGATCGACCCGCCGGATTTCGAGACGCGTGCGGCAATC
GTGCTGGCCAAGGCGCGCGAGCGCGGCGCCGAGATTCCCGACGACGTGGCGTTTCTGATCGCCAAGAAGA
TGCGCTCGAACGTGCGCGACCTGGAAGGGGCGCTCAACACGTTGGTGGCCCGCGCCAACTTCACTGGCCG
TTCGATCACCGTGGAGTTTGCGCAGGAGACGCTGCGTGACCTGTTGCGTGCGCAGCAGCAGGCGATCGGC
ATTCCCAACATCCAGAAGACCGTGGCCGACTACTACGGCCTGCAGATGAAGGACCTGCTTTCCAAGCGCC
GCACCCGCTCATTGGCGCGCCCGCGCCAGGTGGCGATGGCGCTCGCCAAGGAGTTGACCGAGCACAGCCT
TCCCGAGATCGGCGATGCGTTTGCCGGCCGCGACCACACCACCGTGCTGCACGCCTGCCGGCAGATCCGC
ACGCTGATGGAGGCCGACGGCAAGCTGCGCGAGGACTGGGAAAAGCTGATTCGCAAGCTCAGCGAGTGAG
CGTTTGGCGCCCTTCTCGCCCGGCTTGGAAAAAAGCGTGGATGAGTTGGGGCCAAATGCGGGAGAATCTG
TGGATAAATGCGGCTGCAGCGTTGAGGCGGAAACTATCCACAGGTTTTCCCACCGCTCCAGGGGCACTAG
TCCATAGACTTTGAAGCTCAAAATGGTCTTTGGAAACAATACGTTAGTGTGGTTGTCCGCCGAAAACGGC
CCTACCATCACCACCAAGCTTTTGATTTATTCCACATCTTTAAAGCATAGGGGCACGGAACCACATGCGT
TTCACACTGCAGCGCGAAGCCTTCCTCAAGCCGTTGGCCCAGGTGGTCAATGTCGTCGAACGGCGTCAGA
CATTGCCGGTACTGGCGAACTTGCTGGTGCAGGTGAACAACGGCCAGCTGTCGCTGACGGGGACCGACCT
GGAAGTCGAAATGATCTCGCGCACCATGGTCGAGGACGCCCAGGACGGCGAAACCACGATCCCGGCGCGC
AAGCTGTTCGACATCCTGCGGGCCCTGCCTGACGGCAGCCGTGTCACCGTCTCGCAAACCGGAGACAAGG
TCACGGTGCAGGCCGGGCGCAGCCGCTTTACGCTCGCCACGCTACCGGCCAACGACTTCCCGTCGGTGGA
CGAAGTCGAGGCCACCGAGCGTGTGGCGGTGCCGGAAGCCGGGCTGAAGGAGCTGATGGAGCGCACGGCG
TTCGCCATGGCCCAGCAGGACGTGCGTTATTACCTCAACGGCCTGCTGTTCGACCTGCGCGATGGCCTGC
```


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Examples of Text Files: ClustalW

```
clustalw

0xOLI           RIILVTGASDGIGREAAMTYARY--GATVILLGRN----------------EEKLRQV--
1xMAN           KKVIVTGASKGIGREMAYHLAKM-GA-HVVVTARS----------------KETLQKV--
2xAST           KVILITGASRGIGLQLVKTVIEEDDECIVYGVART----------------EAGLQSL--
3xAST           KVILVTGVSRGIGKSIVDVLFSLDKDTVVYGVARS-------------------EAPL--
4xAST           KIAVVTGASGGIGYEVTKELARN--GYLVYACARR----------------LEPMAQL--
5xMAN           HVALVTGGNKGIGLAIVRDLCRL-FSGDVVLTARD----------------VTRGQAAV--
6xCSU           NTVLITGGSAGIGLELAKRLLEL--GNEVIICGRS----------------EARLAEAK--
7xEX            KTVIITGGARGLGAEAARQAVAA-GARVVLADVLD----------------E-EGAATA--
8xASP           KTVLLTGASRGLGVYIARALAKE--QATVVCVSRS----------------QSGLAQT--
9xCSU           KTALITGGGRGIGRATALALAKE--GVNIGLIGRT----------------SANVEKV--
10xOBR          KIALVTGAMGGLGTAICQALAKD-GCIVAANCLPN----------------FEPAAAWL--


0xOLI           ---ASHIN--EETG-RQPQWFILDLLTCTSENC-QQLAQRIAVNY----P-RLDGVLHNA
1xMAN           ---VSHCL---ELG-AASAHYIA-GT---MEDM-TFAEQFVAQAG--KLMGGLDMLILNH
2xAST           ---QREYG---------ADKFVYRVLD---ITDR-SRMEALVEEIR--QKHGKLDGIVANA
3xAST           ----KKLK--EKYG-DRFFYVVG--D---ITED-SVLKQLVNAAVK--GHGKIDSLVANA
4xAST           -----AIQ----FG-NDSIKPYK-LD---ISKP-EEIVTFSGFLRANLPDGKLDLLYNNA
5xMAN           ----QQLQ---AEG--LSPRFHQ-LD---IDDL-QSIRALRDFLR--KEYGGLDVLVNNA
6xCSU           ----QQLP---------N-IHTKQ-CD---VADR-SQREALYEWALK--EYPNLNVLVNNA
7xEX            -------R---ELG--DAARYQH-LD---VTIE-EDWQRVVAYAR--EEFGSVDGLVNNA
8xASP           ---CNAVK---AAG--GKAIAIP-FD---VRNT-SQLSALVQQAQ--DIVGPIDVLINNA
9xCSU           ---AEEVK---ALG--VKAAFAA-AD---VKDA-DQVNQAVAQVK--EQLGDIDILINNA
10xOBR          ----GQQE---ALG--FKFYVAE-GD---VSDF-ESCKAMVAKIEA--DLGPVDILVNNA


...
...
```


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Loading Fasta Sequences: Step 0

```
# ex. 1
#
# open a file for reading
# read a single line of the file and
# bind the line to variable 'line'
#

file = open(”test.txt","r") # Open the file
line = file.readline()      # Returns next line in a string
print line
file.close()                # Close the file
```

How can we scan the entire sequence of lines?

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Loading Fasta Sequences: Step 1

```
# ex. 3
#
# read all the lines of the file and store them in a list
# print the 3rd line
#

file = open(pathname,"r")
line = file.readlines()  # Reads all lines into a sequence
print line[2]
file.close()
```

Why is this NOT a great idea?

How can we do better?

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Loading Fasta Sequences: Step 2

```
# ex. 4
#
# read 1 line at a time
# print the line number and the line
#

def example4(pathname):
    file = open(pathname,"r")
    count = 0
    for line in file:
        print count,":",line
        count = count + 1
    file.close()
```

Now lets try to extract info from the Fasta file?

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A Fasta file with three sequences

```
>gi|188989396|ref|NC_010688.1| Xanthomonas campestris pv. campestris, complete genome
ATGGATGCTTGGCCCCGCTGTCTGGAACGTCTCGAAGCTGAATTCCCGCCCGAAGATGTCCACACCTGGT
TGAAACCCCTGCAGGCCGAAGATCGCGGCGACAGCATCGTGCTGTACGCGCCGAACGCCTTCATTGTCGA
GCAGGTTCGCGAGCGATACCTGCCGCGCATCCGCGAGTTGCTGGCGTATTTCGCCGGCAATGGCGAGGTG

>gi|194208364|ref|XM_001500342.2| PREDICTED: Equus caballus electron-transferring-flavoprotein …
GATACGTGACCCGGAAGCCTCTGCTGGCCATGGCGTCATGCGTGGCGCCGGCGCAGAGCGAGAGAGAGTC
GGGAGCGCTGTGAAGACAGAGCGGTCGGCTGATCAGAGACGAACTTCAGTGGAGGTGATGGCGCCCCCCG
CGGCCTAGAGGTCCAGAGCGTGCCGCGAGCTGCAGACAGTACGCCTCCCATTGTATCCGACGGAGACTCC
TCGTTGCAGGGAACATGTTGCTGCCGCTAGCCAAGCTGTCCTGTCCGGCATATCAGTGCTTTCATGCCTT
AAAAATTAAGAAAGATTATCTACCTCTGTGTGCTACAAGATGGTCTTCAACTTCTGTTGTACCTCGAATT

>gi|193087197|gb|CP001100.1| Chloroherpeton thalassium ATCC 35110, complete genome
ATGCTTATGAGCGAAGGACATGACCAGCCAGGCGCTCCTGTTTCTCATTTATCGGAACAGGCTTTAGCAC
AAATTGCGTGGAAAAAATGCCTCGATATCATTCGTGATGGCCTTCATAACCTGCAAAGCTTTAAGACTTG
GTTTGAGCCCATCGTGCCATTAAAACTTTCTGGCCAGGAATTGACCATTCAGGTGCCCAGCCAGTTTTTT
TATGAAATGATCGAGGAAAATTATTACTCGCTTTTAAAGCGCGCCTTGATGGAAGTGATGGGAACGGGAG
CCAAGCTGCGATATTCTGTTTTGGTTCAGGCGGCACAAGCTGAAACACCCGTCGTCGCTCGTATCCCCGA
GAAAAAAGGCAAGCACACTCCGGCGGCGCTTCCGAAAGTCATTTCTCATGCGAATGGCAAGCAGACAAAA
GAAGCTCAAGACTTATTTGCAAACAATGTACACCGCTTCGAAAGCTACCTAAATCCAAAATATCGCTTCG
```


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Loading Fasta Sequences: Step 3

```
# ex. 5
#
# read 1 line at a time
# print only the fasta sequence header
#

def example5(pathname):
    file = open(pathname,"r")
    count = 0
    for line in file:
        if line[0] == '>':
            print count,":",line
            count = count + 1
    file.close()
```

Now lets try to extract info from the Fasta file?

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Loading Fasta Sequences: Step 4

```
# ex. 6
#
# read 1 line at a time
# identify the fasta sequence header and the sequence data
#

def example6(pathname):
    file = open(pathname,"r")
    for line in file:
        if line[0] == '>':
            print "header",line
        else:
            print "data",line
    file.close()
```

How about blank lines and trailing newlines?

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Loading Fasta Sequences: Step 5

```
# ex. 8
#
# read 1 line at a time
# identify the fasta sequence header and the sequence data
# account for blank lines and trailing space/newlines
# collect sequence data
def example8(pathname):
    file = open(pathname,"r")
    data = ""
    for line in file:
        # remove the trailing '\n' and trailing spaces
        line = line.rstrip('\n ')
        # if the line length is < 1, there nothing to do for this line
        # so move to the next line
        if len( line ) < 1:
            continue
        if line[0] == '>':
            print "data",data  #this data belongs to previous sequence
            data = ""
            print "header",line
        else:
            data = data + line
    file.close()
```


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Loading Fasta Sequences: Step 6

```
def readFastaFile(filename):
    file = open(filename,"r")
    sequence_data = []
    for line in file:
        # remove the trailing '\n' and trailing spaces
        line = line.rstrip('\n ')
        # if the line length is < 1, do nothing
        # so skip rest of iteration
        if len( line ) < 1:
            continue
        if line[0] == '>':
            sequence_data.append('')
        else:
            k = len(sequence_data) - 1
            sequence_data[k] = sequence_data[k] + line
    file.close()
    return(sequence_data)
```


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Summary of File Operations

Method	Action
Read([n])	Reads at most n bytes; if no n is specified, reads the entire file
Readline([n])	Reads a line of input, if n is specified reads at most n bytes
Readlines()	Reads all lines and returns the in a list
Xreadlines()	Reads all lines but handles them as a XRangeType
Write(s)	Writes string s
Writelines(l)	Writes all strings in list l as lines
Close()	Closes the file
Seek(offset[, mode])	Changes to a new file position=start + offset. Start is specified by the mode argument: mode=0 (default), start = start of the file, mode=1, start = current file position and mode=2, start = end of the file.

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Importing ClustalW Files

```
clustalw

0xOLI           RIILVTGASDGIGREAAMTYARY--GATVILLGRN----------------EEKLRQV--
1xMAN           KKVIVTGASKGIGREMAYHLAKM-GA-HVVVTARS----------------KETLQKV--
2xAST           KVILITGASRGIGLQLVKTVIEEDDECIVYGVART----------------EAGLQSL--
3xAST           KVILVTGVSRGIGKSIVDVLFSLDKDTVVYGVARS--------------------EAPL--
4xAST           KIAVVTGASGGIGYEVTKELARN--GYLVYACARR----------------LEPMAQL--
5xMAN           HVALVTGGNKGIGLAIVRDLCRL-FSGDVVLTARD----------------VTRGQAAV--
6xCSU           NTVLITGGSAGIGLELAKRLLEL--GNEVIICGRS----------------EARLAEAK--
7xEX            KTVIITGGARGLGAEAARQAVAA-GARVVLADVLD----------------E-EGAATA--
8xASP           KTVLLTGASRGLGVYIARALAKE--QATVVCVSRS----------------QSGLAQT--
9xCSU           KTALITGGGRGIGRATALALAKE--GVNIGLIGRT----------------SANVEKV--
10xOBR          KIALVTGAMGGLGTAICQALAKD-GCIVAANCLPN----------------FEPAAAWL--


0xOLI           ---ASHIN--EETG-RQPQWFILDLLTCTSENC-QQLAQRIAVNY----P-RLDGVLHNA
1xMAN           ---VSHCL---ELG-AASAHYIA-GT---MEDM-TFAEQFVAQAG--KLMGGLDMLILNH
2xAST           ---QREYG---------ADKFVYRVLD---ITDR-SRMEALVEEIR--QKHGKLDGIVANA
3xAST           ----KKLK--EKYG-DRFFYVVG--D---ITED-SVLKQLVNAAVK--GHGKIDSLVANA
4xAST           -----AIQ----FG-NDSIKPYK-LD---ISKP-EEIVTFSGFLRANLPDGKLDLLYNNA
5xMAN           ----QQLQ---AEG--LSPRFHQ-LD---IDDL-QSIRALRDFLR--KEYGGLDVLVNNA
6xCSU           ----QQLP---------N-IHTKQ-CD---VADR-SQREALYEWALK--EYPNLNVLVNNA
7xEX            -------R---ELG--DAARYQH-LD---VTIE-EDWQRVVAYAR--EEFGSVDGLVNNA
8xASP           ---CNAVK---AAG--GKAIAIP-FD---VRNT-SQLSALVQQAQ--DIVGPIDVLINNA
9xCSU           ---AEEVK---ALG--VKAAFAA-AD---VKDA-DQVNQAVAQVK--EQLGDIDILINNA
10xOBR          ----GQQE---ALG--FKFYVAE-GD---VSDF-ESCKAMVAKIEA--DLGPVDILVNNA


...
...
```

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Reading from ClustalW Files

```
def loadClustalwAlignment(pathname):
    sequences = []
    id2SequenceMap = dict()  # Keep id -> seq dictionary to collect data
    f=open(pathname, 'r')
    f.readline()
    for line in f:
        line = line.replace('\n','')
        if (len(line)>1):
            sequenceID = extractID(line)
            if (sequenceID in id2SequenceMap):
                prevSequence = id2SequenceMap[sequenceID]
            else:
                prevSequence = ' '
            id2SequenceMap[sequenceID]= prevSequence + extractSequence(line)
    f.close()
    sequences = []
        for key in id2SequenceMap.keys():
        sequences = sequences + [key + ":"+id2SequenceMap[key]]
    return sequences
```


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Reading from ClustalW Files

```
def extractSequence(fileLine):
    sequence = fileLine[find(fileLine,' '):].replace(' ','')
    return sequence.replace('\r','').replace('\n','')



def extractID(fileLine):
    id = fileLine[:find(fileLine,' ')].replace(' ','')
    return id
```


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Writing to Text Files

```
def translateFastaFile(infilename, outfilename):
    infile = open(filename,"r")
    outfile = open(filename, "w")
    sequence_data = []
    for line in infile:
        # remove the trailing '\n' and trailing spaces
        line = line.rstrip('\n ')
        # if the line length is < 1, do nothing
        # so skip rest of iteration
        if len( line ) < 1:
            continue
        if line[0] == '>':
            outfile.write(line+'\n')
            writeSequenceToFastaFile(outfile,
                translateDNASequence(sequence_data))
            sequence_data.append('') #Reset for next sequence
        else:
            k = len(sequence_data) - 1
            sequence_data[k] = sequence_data[k] + line
    file.close()
    return(sequence_data)
```


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Homework

- Modify the translateFastaFile function to be able to do any translation specified as an argument function
- Use the above function to translata FASTA files to find complements and reverse complements of sequences

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