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3/13/16
CS 312 Section 1
Lab 4 Report-Gene Sequencing

Lab Code:

```
//////////////////////////////////////////////////////////////////////////////////////////////////
/////////////////////////////////////// Helper Functions /////////////////////////////////////////
//////////////////////////////////////////////////////////////////////////////////////////////////
    /**
    * This function fills the first row and column with the cost of insert/delete for each one
    * Time Complexity: O(n+m) where n is the length of the first sequence and m is the length
of the second sequence.
    *             This is because it iterates over all letters in each sequence once
    * Space Complexity: O(1) because it passes the values by reference meaning it does not
create a copy and
    *             it does not create any variables that depend on the size of the input.
    */
    void fillStartCells(ref int[,] values, ref directions[,] prev, int lengthA, int lengthB, bool
banded)
    {
      for (int column = 0; column < lengthB + 1; column++)
      {
        if (banded == true && (column > distance))
        {
          break;
        }
        values[0, column] = column * 5;
        prev[0, column] = directions.LEFT;
      }
      for (int row = 0; row < lengthA + 1; row++)
      {
        if (banded == true && (row > distance))
        {
          break;
        }
        values[row, 0] = row * 5;
        prev[row, 0] = directions.TOP;
      }

    }

    /**
```

```
        * This function creates the alignments for both sequences using the previous pointers array
        * Time Complexity: O(n) where n is the length of the larger sequence because it the best
alignment
        *               is as long as the length of the longest sequence
        * Space Complexity: O(n) where n is the length of the larger sequence as it creates a string
as long as it
        */
        void createAlignments(ref string[] alignment, ref directions[,] prev, ref GeneSequence
sequenceA, ref GeneSequence sequenceB,
                                              ref int lengthOfSequenceA, ref int lengthOfSequenceB)
        {
            int rowIterator = lengthOfSequenceA, columnIterator = lengthOfSequenceB;
            StringBuilder first = new StringBuilder(), second = new StringBuilder();
            while (rowIterator != 0 || columnIterator != 0)
            {

                if (prev[rowIterator, columnIterator] == directions.DIAGONAL) // match/sub
                {
                    first.Insert(0, sequenceA.Sequence[rowIterator - 1]);
                    second.Insert(0, sequenceB.Sequence[columnIterator - 1]);
                    rowIterator--;
                    columnIterator--;
                }
                else if (prev[rowIterator, columnIterator] == directions.LEFT) //insert
                {
                    first.Insert(0, '-');
                    second.Insert(0, sequenceB.Sequence[columnIterator - 1]);
                    columnIterator--;
                }
                else // delete
                {
                    first.Insert(0, sequenceA.Sequence[rowIterator - 1]);
                    second.Insert(0, '-');
                    rowIterator--;
                }
            }

            // Limiting the length of the string to 100 if it exceeds it
            alignment[0] = first.ToString().Substring(0, Math.Min(first.Length, 100));
            alignment[1] = second.ToString().Substring(0, Math.Min(second.Length, 100));
        }
```

```
////////////////////////////////////////////////////////////////////////////////////////////////
/////////////////////////////////// Unrestricted Algorithm ////////////////////////////////////
////////////////////////////////////////////////////////////////////////////////////////////////
        /**
        * This function performs the unrestricted algorithm on the two sequences using dynamic programming to come up with
        * the best alignment for both.
        * Time Complexity: O(nm) where n is the length of the first sequence and m is the length of the second sequence. This
        *               is because the algorithm iterates over all cells in the array of n x m
        * Space Complexity: O(nm) where n is the length of the first sequence and m is the length of the second sequence. This
        *               is because the algorithm creates an array of n x m
        */
        void unrestrictedAlgorithm (ref int score, ref string[] alignment, ref GeneSequence sequenceA, ref GeneSequence sequenceB)
        {
            // Limiting the lengths of the sequences to the max characters to align
            int lengthOfSequenceA = Math.Min(sequenceA.Sequence.Length, MaxCharactersToAlign);
            int lengthOfSequenceB = Math.Min(sequenceB.Sequence.Length, MaxCharactersToAlign);

            // Create two arrays to hold the intermediate values and the alignment details
            int[,] values = new int[lengthOfSequenceA + 1, lengthOfSequenceB + 1];
            directions[,] prev = new directions[lengthOfSequenceA + 1, lengthOfSequenceB + 1];

            // first fill first row and column with cost of inserts/deletes
            fillStartCells(ref values, ref prev, lengthOfSequenceA, lengthOfSequenceB, false);

            // Now iterate through the rest of the cells filling out the min value for each
            for (int row = 1; row < lengthOfSequenceA + 1; row++)
            {
                for (int column = 1; column < lengthOfSequenceB + 1; column++)
                {
                    // Compute values for each direction
                    int costOfTop_Delete = values[row - 1, column] + 5;
                    int costOfLeft_Insert = values[row, column - 1] + 5;
                    // Compute cost of moving from diagonal depending on whether the letters match
                    int costOfMovingFromDiagonal = (sequenceA.Sequence[row - 1] == sequenceB.Sequence[column - 1]) ? -3 : 1;
                    int costOfDiagonal = values[row - 1, column - 1] + costOfMovingFromDiagonal;
```

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            // value of cell would be the minimum cost out of the three directions
            int costOfMin = Math.Min(costOfTop_Delete, Math.Min(costOfLeft_Insert,
costOfDiagonal));
            values[row, column] = costOfMin;

            // Store the direction
            if (costOfMin == costOfDiagonal)
            {
               prev[row, column] = directions.DIAGONAL;
            }
            else if (costOfMin == costOfLeft_Insert)
            {
               prev[row, column] = directions.LEFT;
            }
            else
            {
               prev[row, column] = directions.TOP;
            }
          }
        }

        // score would be value of the last cell
        score = values[lengthOfSequenceA, lengthOfSequenceB];

        // Create the alignments
        createAlignments(ref alignment, ref prev, ref sequenceA, ref sequenceB, ref
lengthOfSequenceA, ref lengthOfSequenceB);

      }
////////////////////////////////////////////////////////////////////////////////////////////////
//////////////////////////////////////// Banded Algorithm ////////////////////////////////////////
////////////////////////////////////////////////////////////////////////////////////////////////
      /**
      * This function performs the banded algorithm on the two sequences using dynamic
programming to come up with
      * the best alignment for both. The band is set to whatever the distance is. Currently it is d =
3 which makes the
      * bandwidth equals 2d+1 = 7.
      * Time Complexity: O(n+m) where n is the length of the first sequence and m is the length
of the second sequence. This
      *              is because the algorithm iterates over a specific number of cells for each row
and column. As we don't
      *              care about constants, the time would depend on the length of sequence A and
B. Meaning each time
```

```
     *              the array size is increased by a row or a column, we have to compute those
bandwidth number of cells
     *              again, so it is O(n+m).
     * Space Complexity: O(nm) where n is the length of the first sequence and m is the length
of the second sequence. This
     *              is because the algorithm creates an array of n x m
     */
     void bandedAlgorithm(ref int score, ref string[] alignment, ref GeneSequence sequenceA,
ref GeneSequence sequenceB)
     {

        // Limiting the lengths of the sequences to the max characters to align
        int lengthOfSequenceA = Math.Min(sequenceA.Sequence.Length,
MaxCharactersToAlign);
        int lengthOfSequenceB = Math.Min(sequenceB.Sequence.Length,
MaxCharactersToAlign);

        // Create two arrays to hold the intermediate values and the alignment details
        int[,] values = new int[lengthOfSequenceA + 1, lengthOfSequenceB + 1];
        directions[,] prev = new directions[lengthOfSequenceA + 1, lengthOfSequenceB + 1];

        // first fill first row and column with cost of inserts/deletes
        fillStartCells(ref values, ref prev, lengthOfSequenceA, lengthOfSequenceB, true);

        int columnStart = 1;
        bool alignmentFound = false;
        int row = 1;
        int column = columnStart;
        // Now iterate through the rest of the cells filling out the min value for each
        for (row = 1; row < lengthOfSequenceA + 1; row++)
        {
           for (column = columnStart; column < lengthOfSequenceB + 1; column++)
           {
              if ((distance + row) < column)
              {
                 break;
              }
              // Compute values for each direction
              int costOfTop_Delete = values[row - 1, column] + 5;
              if ((distance + row) == column)
              {
                 costOfTop_Delete = int.MaxValue;
              }
              int costOfLeft_Insert = values[row, column - 1] + 5;
```

```
            if ((distance + column) == row)
            {
               costOfLeft_Insert = int.MaxValue;
            }
            // Compute cost of moving from diagonal depending on whether the letters match
            int costOfMovingFromDiagonal = (sequenceA.Sequence[row - 1] ==
sequenceB.Sequence[column - 1]) ? -3 : 1;
            int costOfDiagonal = values[row - 1, column - 1] + costOfMovingFromDiagonal;

            // value of cell would be the minimum cost out of the three directions
            int costOfMin = Math.Min(costOfDiagonal, Math.Min(costOfLeft_Insert,
costOfTop_Delete));
            values[row, column] = costOfMin;

            // Store the direction
            if (costOfMin == costOfDiagonal)
            {
               prev[row, column] = directions.DIAGONAL;
            }
            else if (costOfMin == costOfLeft_Insert)
            {
               prev[row, column] = directions.LEFT;
            }
            else
            {
               prev[row, column] = directions.TOP;
            }
            if (column == lengthOfSequenceB && row == lengthOfSequenceA)
               alignmentFound = true;
         }
         if (row > distance)
            columnStart++;
      }

      // score would be value of the last cell
      if (alignmentFound)
      {
         score = values[lengthOfSequenceA, lengthOfSequenceB];
         // Create the alignments
         createAlignments(ref alignment, ref prev, ref sequenceA, ref sequenceB,
                          ref lengthOfSequenceA, ref lengthOfSequenceB);

      }
      else {
```

```
            score = int.MaxValue;
            alignment[0] = "No Alignment Possible";
            alignment[1] = "No Alignment Possible";
        }
    }

////////////////////////////////////////////////////////////////////////////////////////////////
/////////////////////////////////////Main Entry Point//////////////////////////////////////////
////////////////////////////////////////////////////////////////////////////////////////////////
    /// <summary>
    /// this is the function you implement.
    /// </summary>
    /// <param name="sequenceA">the first sequence</param>
    /// <param name="sequenceB">the second sequence, may have length not equal to the
length of the first seq.</param>
    /// <param name="banded">true if alignment should be band limited.</param>
    /// <returns>the alignment score and the alignment (in a Result object) for sequenceA and
sequenceB.  The calling function places the result in the dispay appropriately.
    ///
    public ResultTable.Result Align_And_Extract(GeneSequence sequenceA, GeneSequence
sequenceB, bool banded)
    {
        ResultTable.Result result = new ResultTable.Result();
        int score;                                  // place your computed alignment score here
        string[] alignment = new string[2];                 // place your two computed
alignments here


        // ******these are placeholder assignments that you'll replace with your code  *******
        score = 0;
        alignment[0] = "";
        alignment[1] = "";
        // *********************************************************************

        if (!banded)
            unrestrictedAlgorithm(ref score, ref alignment, ref sequenceA, ref sequenceB);
        else
            bandedAlgorithm(ref score, ref alignment, ref sequenceA, ref sequenceB);

        result.Update(score, alignment[0], alignment[1]);          // bundling your results into
the right object type
        return (result);
    }
}
```

Time and Space Complexity Analysis:

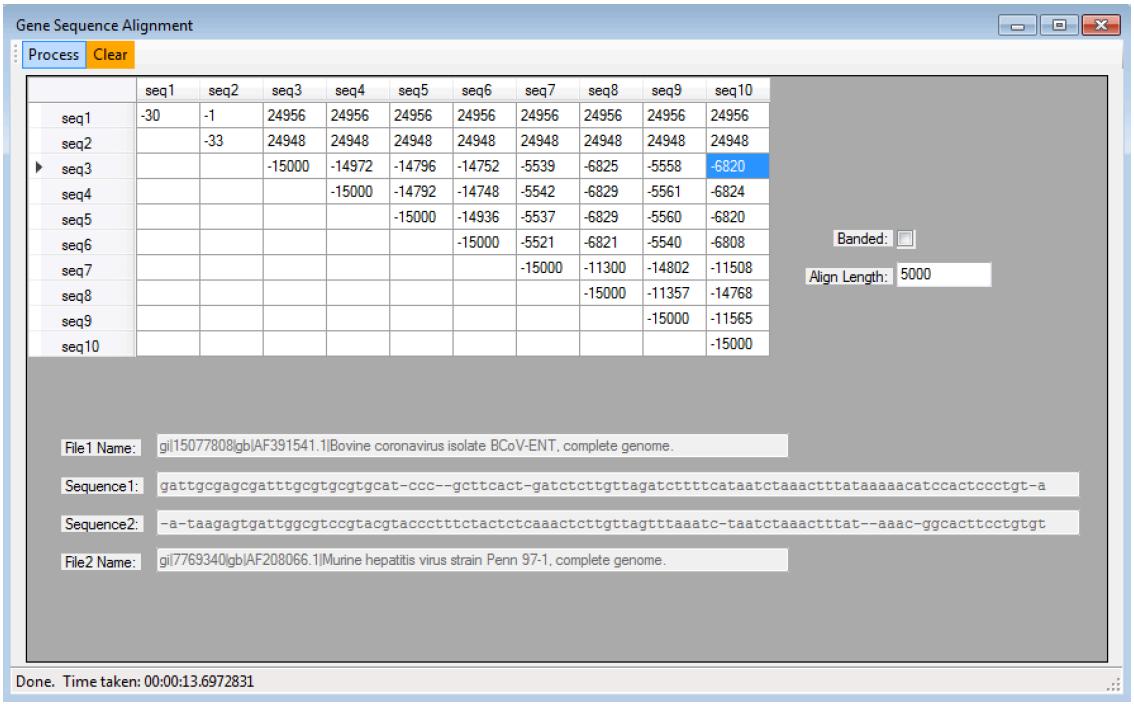
The analysis is presented as comment sections above each function in the lab code. Please refer to the comments above.

Alignment Extraction Algorithm:

The way this algorithm works is using dynamic programming by dividing the problem into sub problems and using those to compute our results. To go from one string to another, for each character there are three possibilities: inserting a character, deleting a character, and substitution. So for each character in the strings we compare the cost of inserting, deleting, and substitution and pick the minimum one as the way we go. Then to keep track of what we do for each letter, we keep another array that stores the choice we picked from each one. If we substitute, then we are moving diagonally in the list. If we insert, then we are moving across, and if we delete, then we are moving down. That way once we reach the last cell in the table, then we have the minimum cost for aligning the two string sequences, and we have a back-trace stored in a second table that takes us back to the first cell. Now to come up with the alignment, we just follow that back-trace: for each cell, if it we moved diagonally, then we display the two letters, if we are inserting or deleting, then one of the letters will be a dash, and so on.

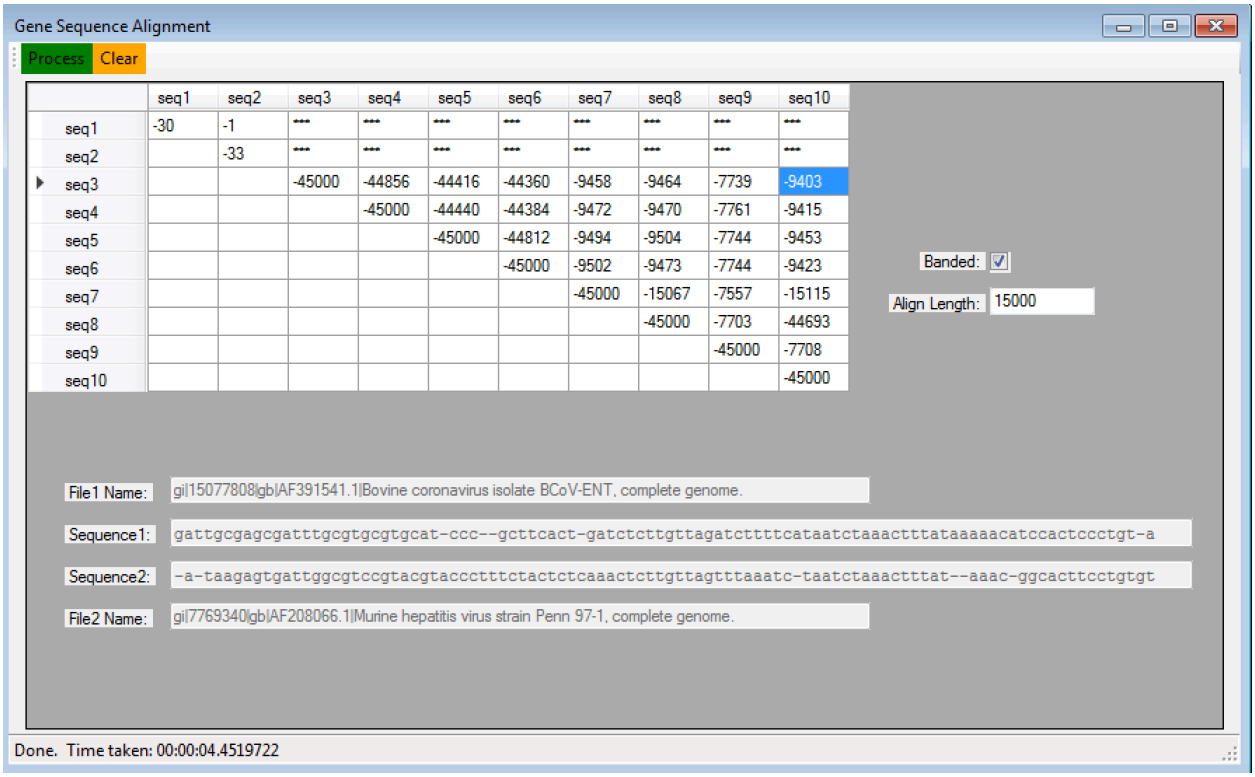
Results:

Unrestricted with K = 5000:

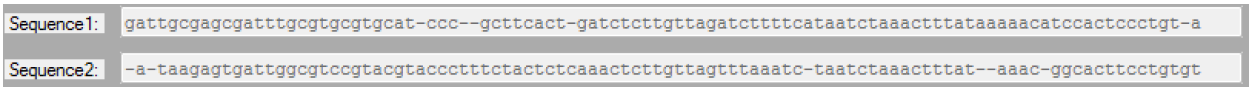


	seq1	seq2	seq3	seq4	seq5	seq6	seq7	seq8	seq9	seq10
seq1	-30	-1	24956	24956	24956	24956	24956	24956	24956	24956
seq2		-33	24948	24948	24948	24948	24948	24948	24948	24948
seq3			-15000	-14972	-14796	-14752	-5539	-6825	-5558	-6820
seq4				-15000	-14792	-14748	-5542	-6829	-5561	-6824
seq5					-15000	-14936	-5537	-6829	-5560	-6820
seq6						-15000	-5521	-6821	-5540	-6808
seq7							-15000	-11300	-14802	-11508
seq8								-15000	-11357	-14768
seq9									-15000	-11565
seq10										-15000

Banded with K = 15000:



As shows in the screenshot above, the extracted alignment for row 3, column 10 (unrestricted, K=5000) is:



(Banded, K=15000) is: