CS106B
Spring 2013

Handout #10S
April 15, 2013

Section Solutions 2

Problem One: Xzibit Words

One possible implementation is shown here:

```
string mostXzibitWord(Lexicon& words) {
  /* Track the best string we've found so far and how many subwords it has. */
  string result;
  int numSubwords = 0;

  foreach (string word in words) {
    /* Store all the subwords we find.  To avoid double-counting
     * words, we'll hold this in a Lexicon.
     */
    Lexicon ourSubwords;

    /* Consider all possible start positions. */
    for (int start = 0; start < word.length(); start++) {
      /* Consider all possible end positions.  Note that we include
       * the string length itself, since that way we can consider
       * substrings that terminate at the end of the string.
      for (int stop = start; stop <= word.length(); stop++) {
        /* Note the C++ way of getting a substring. */
        string candidate = word.substr(start, stop – start);

        /* As an optimization, if this isn't a prefix of any legal
         * word, then there's no point in continuing to extend this
         * substring.
         */
        if (!words.containsPrefix(candidate))
          break;

        /* If this is a word, then record it as a subword. */
        if (words.contains(candidate))
          ourSubwords.add(candidate);
      }
    }

    /* Having found all subwords, see if this is better than our
     * best guess so far.
     */
    if (numSubwords < ourSubwords.size()) {
      result = word;
      numSubwords = ourSubwords.size();
    }
  }

  return result;
}
```

In case you're curious, the most Xzibit word is “foreshadowers,” with 34 subwords!

Problem Two: RNA Protein Codes

Here is one possible implementation:

```
Vector<string> findProteins(string rna, Map<string, string>& codons) {
  Vector<string> result;

  /* Track at which index we are in the string.  We'll be going one character
   * at a time through the string.
   */
  int index = 0;
  while (true) {
    /* Find the next start codon, stopping if none are left. */
    index = rna.find("AUG", index);
    if (index == string::npos) {
      return result;
    }

    /* Keep decoding codons until we hit a stop codon. */
    string protein;
    while (true) {
      /* Read the codon. */
      string codon = rna.substr(index, 3);
      index += 3;

      /* If it's a stop codon, we're done with this protein. */
      if (codons[codon] == "stop")
        break;

      /* Otherwise, add it to the result.  To get the commas right, we'll
       * only add commas if the string isn't empty.
       */
      if (!protein.empty()) protein += ", ";
      protein += codons[codon];
    }

    /* Add this protein to the result. */
    result += protein;
  }
}
```

A process similar to this one is actually going on *right now* in every single cell in your body. Isn't that amazing?