

Section Solutions 1

Problem 1. Censorship

There are several strategies for implementing the character-removal problem. The implementations shown below go through the `text` string and then check to see whether the character in that position appears in the `remove` string. Another possible (but generally less efficient) approach would be to make several passes over the `text` string, moving one character from the `remove` string on each pass.

```
/*
 * Function: censorString1
 * Usage: s = censorString1(text, remove);
 * -----
 * This function takes two strings and returns the first string with
 * all the occurrences of letters in the second string removed.
 * It uses a for loop to iterate through the original string and
 * the find method to check whether that character is in the remove
 * string. This version builds a new string character by character.
 */

string censorString1(string text, string remove) {
    string result = "";
    for (int i = 0; i < text.length(); i++) {
        if (remove.find(text[i]) == string::npos) {
            result += text[i];
        }
    }
    return result;
}

/*
 * Function: censorString2
 * Usage: censorString2(text, remove);
 * -----
 * This function takes two strings and updates the first string
 * by removing all occurrences of letters in the second string.
 * Note that the implementation must decrement i after removing
 * the character to ensure that the following character is checked.
 */

void censorString2(string & text, string remove) {
    for (int i = 0; i < text.length(); i++) {
        if (remove.find(text[i]) != string::npos) {
            text.replace(i, 1, "");
            i--;
        }
    }
}
```

Problem 2. How Did We Do?

```
/*
 * Function: readStats
 * Usage: readStats(filename, min, max, mean);
 * -----
 * Reads a data file whose name is given in filename and computes the
 * minimum score, the maximum score, and the average score, storing
 * these values in the reference parameter variables min, max, and mean.
 */

void readStats(string filename, int & min, int & max, double & mean) {
    ifstream in;
    in.open(filename.c_str());
    if (in.fail()) error("Couldn't read " + filename);
    double total = 0;
    int count = 0;
    while (true) {
        int score;
        in >> score;
        if (in.fail()) break;
        if (score < 0 || score > 100) error("Score out of range");
        if (count == 0 || score < min) min = score;
        if (count == 0 || score > max) max = score;
        total += score;
        count++;
    }
    mean = (double) total / count;
    in.close();
}
```

Problem 3. Stacking Cannonballs

```
/*
 * Function: cannonball
 * Usage: n = cannonball(height);
 * -----
 * This function computes the number of cannonballs in a stack
 * that has been arranged to form a pyramid with one cannonball
 * at the top sitting on top of a square composed of four
 * cannonballs sitting on top of a square composed of nine
 * cannonballs, and so forth. The function cannonball computes
 * the total number based on the height of the stack.
 */

int cannonball(int height) {
    if (height == 0) {
        return 0;
    } else {
        return height * height + cannonball(height - 1);
    }
}
```

Problem 4: 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 “foreshadows,” with 34 subwords!

Problem 5: 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?