1. (8 points)
   Fewest Possible: \(2 \left\lceil \frac{M}{2} \right\rceil^3 \left\lceil \frac{L}{2} \right\rceil = 2048.\)
   Greatest Possible: \(M^4L = 202500.\)

2. (8 points)
   ```java
   boolean areSimilar(Node root1, Node root2) {
       if ((root1 == null) && (root2 == null))
           return true;
       else if ((root1 == null) && (root2 != null))
           return false;
       else if ((root1 != null) && (root2 == null))
           return false;
       else {
           boolean left = areSimilar(root1.left, root2.left);
           boolean right = areSimilar(root1.right, root2.right);
           return (left && right);
       }
   }
   ```
   If the two trees have \(m\) and \(n\) nodes, the running time is \(O(m + n)\).

3. (8 points)
   There are several solutions possible. One good choice is to interpret the DNA sequence as a number in base 4. Assuming \(f\) is a one-one function from \{A,C,G,T\} to \{0,1,2,3\}, the hash value of a sequence...
$S = s_0 s_1 \ldots s_n$ is given by:

$$h(S) = \left( \sum_{i=0}^{n} f(s_i)4^i \right) \mod \text{TableSize}$$

4. (8 points)
Load Factor = $100/256 = 0.391$.
Inserting an element takes $O(1)$ time since we can insert at the front of the list for any bin.
Finding an element takes $O(n)$ time if the element hashes to the occupied bin, otherwise it takes $O(1)$ time.

5. (6 points)

<table>
<thead>
<tr>
<th>Index</th>
<th>Data</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
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</tr>
<tr>
<td>1</td>
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<tr>
<td>2</td>
<td>673</td>
</tr>
<tr>
<td>3</td>
<td>409</td>
</tr>
<tr>
<td>4</td>
<td>804</td>
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<tr>
<td>8</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>239</td>
</tr>
</tbody>
</table>

6. (6 points)
Linear Probing: $h(x) = 0, 1, 2$ or 10.
Quadratic Probing: $h(x) = 1$ or 2.

7. (6 points)
Figure 1: Problem 7