Recall the definitions: The set of RNA strands S is defined (recursively) by:

Basis Step: $A \in S, C \in S, U \in S, G \in S$ Recursive Step: If $s \in S$ and $b \in B$, then $sb \in S$

where sb is string concatenation. The function rnalen that computes the length of RNA strands in S is defined recursively by:

Basis Step: If $b \in B$ then $rnalen: S \to \mathbb{Z}^+$ Recursive Step: If $s \in S$ and $b \in B$, then rnalen(sb) = 1 + rnalen(s)

The function basecount that computes the number of a given base b appearing in a RNA strand s is defined recursively by:

 $basecount: S \times B \rightarrow \mathbb{N}$ Basis Step: If $b_1 \in B, b_2 \in B$ $basecount(\ (b_1, b_2)\) = \begin{cases} 1 & \text{when } b_1 = b_2 \\ 0 & \text{when } b_1 \neq b_2 \end{cases}$ Recursive Step: If $s \in S, b_1 \in B, b_2 \in B$ $basecount(\ (sb_1, b_2)\) = \begin{cases} 1 + basecount(\ (s, b_2)\) & \text{when } b_1 = b_2 \\ basecount(\ (s, b_2)\) & \text{when } b_1 \neq b_2 \end{cases}$