

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

$$\begin{array}{ll} \text{Basis Step:} & \mathbf{A} \in S, \mathbf{C} \in S, \mathbf{U} \in S, \mathbf{G} \in S \\ \text{Recursive Step:} & \text{If } s \in S \text{ and } b \in B, \text{ then } sb \in S \end{array}$$

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

$$\begin{array}{ll} \text{Basis Step:} & \text{If } b \in B \text{ then} & rnalen : S & \rightarrow \mathbb{Z}^+ \\ & & rnalen(b) & = 1 \\ \text{Recursive Step:} & \text{If } s \in S \text{ and } b \in B, \text{ then} & rnalen(sb) & = 1 + rnalen(s) \end{array}$$

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

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