

*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:

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