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:

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

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