

Course website: <https://cseweb.ucsd.edu/classes/fa20/cse20-a/>

Term	Examples: (add additional examples from class)
set unordered collection of elements <i>Equal means agree on membership of all elements</i>	$7 \in \{43, 7, 9\}$ $2 \notin \{43, 7, 9\}$
n-tuple ordered sequence of elements with n “slots” <i>Equal means corresponding components equal</i>	
string ordered finite sequence of elements each from specified set <i>Equal means same length and corresponding characters equal</i>	

$$\{-1, 1\} \quad \{0, 0\} \quad \{-1, 0, 1\} \quad \mathbb{Z} \quad \mathbb{N} = \{x \in \mathbb{Z} \mid x \geq 0\} \quad \emptyset \quad \mathbb{Z}^+ = \{x \in \mathbb{Z} \mid x > 0\}$$

Which of the sets above are defined using the roster method? Which are defined using set builder notation?

RNA is made up of strands of four different bases that match up in specific ways.

The bases are elements of the set $B = \{\mathbf{A}, \mathbf{C}, \mathbf{G}, \mathbf{U}\}$.

Definition The set of RNA strands S is defined (recursively) by:

Basis Step: $\mathbf{A} \in S, \mathbf{C} \in S, \mathbf{U} \in S, \mathbf{G} \in S$

Recursive Step: If $s \in S$ and $b \in B$, then $sb \in S$

where sb is string concatenation.

Examples:

Extra example: The set of binary strings, denoted $\{0, 1\}^*$ which we read as “zero one star”, is defined (recursively) by:

Basis Step: $\lambda \in \{0, 1\}^*$

Recursive Step: If $s \in \{0, 1\}^*$ then $s0 \in \{0, 1\}^*$ and $s1 \in \{0, 1\}^*$

where $s0$ and $s1$ are the results of string concatenation. The symbol λ , pronounced “lambda” is used to denote the empty string and has the property that $\lambda x = x\lambda = x$ for each string x .

Examples:

New! Recursive Definitions of Sets: The set S (pick a name) is defined by:

Basis Step: Specify finitely many elements of S

Recursive Step: Give a rule for creating a new element of S from known values existing in S , and potentially other values.

Definition (Rosen p. 123) Let A and B be sets. The **Cartesian product** of A and B , denoted $A \times B$, is the set of all ordered pairs (a, b) where $a \in A$ and $b \in B$

$$A \times B = \{(a, b) \mid a \in A \text{ and } b \in B\}$$

Definition: Let A and B be sets of strings over the same alphabet. The **set-wise concatenation** of A and B , denoted $A \circ B$, is the set of all results of string concatenation ab where $a \in A$ and $b \in B$

$$A \circ B = \{ab \mid a \in A \text{ and } b \in B\}$$

Set	Example elements in this set:
B	A C G U
	(A, C) (U, U)
$B \times \{-1, 0, 1\}$	
$\{-1, 0, 1\} \times B$	(0, 0, 0)
$\{A, C, G, U\} \circ \{A, C, G, U\}$	GGGG

Definition (Of a function, recursively) A function $rnalen$ that computes the length of RNA strands in S is defined by:

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

The domain of $rnalen$ is _____. The codomain of $rnalen$ is _____.

$$rnalen(ACU) = \underline{\hspace{10em}}$$

Extra example: A function $basecount$ that computes the number of a given base b appearing in a RNA strand s is defined recursively: *fill in codomain and sample function applications*

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

$$basecount(ACU, A) = \underline{\hspace{10em}}$$

$$basecount(ACU, G) = \underline{\hspace{10em}}$$