

Netflix intro

What data should we encode about each Netflix account holder to help us make effective recommendations?

In machine learning, clustering can be used to group similar data for prediction and recommendation. For example, each Netflix user's viewing history can be represented as a n -tuple indicating their preferences about movies in the database, where n is the number of movies in the database. People with similar tastes in movies can then be clustered to provide recommendations of movies for one another. Mathematically, clustering is based on a notion of distance between pairs of n -tuples.

Set operations

To define a set we can use the roster method, set builder notation, a recursive definition, and also we can apply a set operation to other sets.

New! Cartesian product of sets and set-wise concatenation of sets of strings

Definition: 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 $b \in B$

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

Fill in the missing entries in the table:

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			

Defining functions

New! Defining functions A function is defined by its (1) domain, (2) codomain, and (3) rule assigning each element in the domain exactly one element in the codomain.

The domain and codomain are nonempty sets.

The rule can be depicted as a table, formula, or English description.

Example: The absolute value function

Domain

Codomain

Rule

In the table below, each row represents a user's ratings of movies: ✓ (check) indicates the person liked the movie, ✗ (x) that they didn't, and • (dot) that they didn't rate it one way or another (neutral rating or didn't watch).

Person	Fyre	Frozen II	Picard	Ratings written as a 3-tuple
P_1	✗	•	✓	$(-1, 0, 1)$
P_2	✓	✓	✗	$(1, 1, -1)$
P_3	✓	✓	✓	$(1, 1, 1)$
P_4	•	✗	✓	

Which of P_1 , P_2 , P_3 has movie preferences most similar to P_4 ?

One approach to answer this question: use **functions** to define distance between user preferences.

Define the following functions whose inputs are ordered pairs of 3-tuples each of whose components comes from the set $\{-1, 0, 1\}$

$$d_1((x_1, x_2, x_3), (y_1, y_2, y_3)) = \sum_{i=1}^3 ((|x_i - y_i| + 1) \text{ div } 2)$$

$$d_2((x_1, x_2, x_3), (y_1, y_2, y_3)) = \sqrt{\sum_{i=1}^3 (x_i - y_i)^2}$$

$d_1(P_4, P_1)$	$d_1(P_4, P_2)$	$d_1(P_4, P_3)$
$d_2(P_4, P_1)$	$d_2(P_4, P_2)$	$d_2(P_4, P_3)$

Extra example: A new movie is released, and P_1 and P_2 watch it before P_3 , and give it ratings; P_1 gives ✓ and P_2 gives ✗. Should this movie be recommended to P_3 ? Why or why not?

Extra example: Define the new functions that would be used to compare the 4-tuples of ratings encoding movie preferences now that there are four movies in the database.

Defining functions recursively

Definition (Of a function, recursively) A function $rnalen$ that computes the length of RNA strands in S is defined 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 domain of $rnalen$ is _____. The codomain of $rnalen$ is _____.

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

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*

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

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

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