Example lab

This is an example lab.

1 **Mathematics**

You can use inline mathematics: $a^2 + b^2 = c^2$ renders to $a^2 + b^2 = c^2$. Display math: \$\$... \$\$ but with empty lines above and below (otherwise it is rendered as inline math):

$$a^2 + b^2 + c^2$$

You can also align multiple equations. The syntax is important here since Math-Jax and Pandoc differ slightly. The \begin{align} ... \end{align} block need not have empty lines above and below. If not, the paragraph is uninterrupted in the PDF.

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\begin{align}
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N &= 5 + \text{dargmin}_{x \in \mathbb{R}} x^2
\end{align}
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$$x = \sum_{i=1}^{N} a_i^2 + b_i^2 + c_i^2$$
 (1)
$$N = 5 + \operatorname{argmin}_{x \in \mathbb{R}} x^2$$
 (2)

$$N = 5 + \operatorname{argmin}_{x \in \mathbb{R}} x^2 \tag{2}$$

2 **Question blocks**

The S matrix represents the sender: the first column contains the meanings (or situations) that the sender may want to express, the first row the signals that it can use to express these meanings. The numbers in the matrix represent the probabilities that the sender will use a certain signal to express a certain

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meaning. The matrix R describes the behaviour of the receiver in a similar way: the numbers in the matrix are the probabilities that the receiver will interpret a certain signal (first column) as having a certain meaning (first row).

QUESTION 1

What are the optimal *S* and *R*, for maximal communicative success in a population? How is ambiguity (i.e., one signal with multiple meanings) reflected in S and R matrices? And synonymity (two signals that have the same meaning).

By using a bit of a trick, we can study the evolution of such a communication system using the same protocol as in the first part of this assignment. The S and R matrices of an individual are uniquely defined by 18 numbers. Assume that we model this by saying that every individual is characterized by a genome of length 18, where each nucleotide codes for one value in S and R. Let's say A=3, G=2, C=1 and U=0. To construct the S and R matrices, we put the numbers corresponding to the nucleotides in two matrices and normalise the rows, such that the probabilities add up to 1.

QUESTION 2

What would a genome corresponding to the S and R matrix depicted above look like? Can you think of two strings that have a different genotype but the same phenotype?