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This software is for generating wiring solutions for the Ana Bbot from JoHuCo (herein referred to as the “Braitenbot”), which is a battery-powered vehicle inspired by the writings of Valentino Braitenberg. The output writing solutions are the product of a novel genotype-phenotype map that implements notions of gene-interaction.

Within this code, the Braitenbot itself is represented by the “Organism” class and contains the necessary variables and parameters for creating a wiring solution for the intended robot.

The included code uses the jsonpickle Python library for encoding the resulting Organism object and storing it in a file.

Instantiating an organism object using the Organism class requires 7 input variables, and is capable of handling an additional three optional ones. They are listed below :

Generation: an integer relating to the generation the Organism belongs to; used for creating a filename with which to save the Organism to a file.

generational\_index: an integer relating to the Organism’s index within the Generation; used for creating a filename with which to save the Organism to a file.

genome\_size: the size of the Organism’s genome. i.e. the number of Base objects contained in the genome attribute.

num\_crossover\_points: The number of crossover points to distribute over the genome

unrestricted\_crossover\_point\_distribution: A Boolean value that when true specifies that crossover points can occur anywhere in the Organism’s genome. When false it specifies that crossover points can only occur between coding regions (i.e. threads)

thread\_length: The desired length of the coding regions (i.e. threads) to divide the genome into

mutation\_rate: an integer representing the probability (in terms of 1/mutation\_rate) of either the binary char or crossover values becoming inverted (1🡪0 or 0🡪1) as a result of random mutation

The following input variables are optional, but important for providing generational data for more accurate indexing, supplying a specific genome, or generating an organism in an “alternate mode” that does not include gene interaction. The

parent1=None,

parent2=None,

genome=None,

alt\_mode=False):