

Instruction	Description
<allocate>	Allocates extra memory for the organism to copy it's genome into. This genome can be used for either tissue accretion or propagule formation. Appears in source code as <h_alloc>.
<copy>	Duplicates the instruction pointed to by the read head into the position pointed to by the write head, then increments both heads. This duplication process is subject to mutations. Appears in source code as <h_copy>.
<search>	Identifies other positions in the genome based on complimentary patterns of nop instructions. Appears in source code as <h_search>.
<if_less>	Compares two values in memory. Executes the next instruction if the first value is less than the second; otherwise skips it.
<if_equal>	Compares two values in memory. Executes the next instruction if the first value equals the second; otherwise skips it.
<if_not_equal>	Compares two values in memory. Executes the next instruction if the first value does not equal the second; otherwise skips it.
<if_label>	Reads the series of nops that follow this instruction. If a complementary series of nops was just copied, executes the next instruction, otherwise skips it.
<jump_head>	Reads a value from memory and shifts the position being executed in the organism's genome by that amount.
<mov_head>	Moves heads (read, write, or execution) to the position of the flow head in the genome.
<pop>	Retrieves a number from the stack.
<push>	Stores a number on the current stack for later use.
<swap>	Swaps two values in the organism's memory.