

Multi-Objective NEAT: Genotypic Diversity and Task Performance in MRS

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ABSTRACT

This paper investigates the effect of replacing the speciation mechanism in NEAT (Neuro-evolution through Augmenting Topologies) with a multi-objective framework that evolves for task performance and genotypic diversity. The NEAT framework and the proposed framework each co-evolve the control policy (behaviour) and sensory configuration (morphology) of robotic teams in environments of varying difficulty. The task performance of best evolved networks is evaluated for each framework across each of the environments. Two experiments were conducted to fulfil this objective. The first experiment uses the NEAT framework to evolve the behaviour and morphology of robotic teams with the single objective of maximising task performance. The second experiment uses the proposed framework to evolve the behaviour and morphology of the robotic teams with the dual objective of task performance and genotypic diversity. The results show that the multi-objective framework did not perform better than the well-known NEAT algorithm in the context of multi-robotic systems. Despite this conclusion, the results are still promising as they indicate an avenue of future research.

1 INTRODUCTION

Multi-objective (MO) machine learning (ML) techniques are becoming ubiquitous in the context of evolutionary algorithms, especially those that aim to evolve the behaviour policy of autonomous agents. This is simply due to the multi-objective nature of the problems that these techniques are trying to solve. Previously, MO techniques aggregated their objectives into a single fitness function. The problem with this is that for any non-trivial multi-objective optimisation problem, no solution exists that simultaneously optimises each objective [10]. The resulting fitness score would, therefore, represent some arbitrary trade-off between objectives.

Recently, many Pareto-based learning approaches have been developed to solve this problem. MO pareto-based ML techniques ensure the convergence of solutions to a pareto optimal set or a set of trade off solutions. A set is considered pareto optimal if no objective function of an individual can be further optimised without degrading the optimal value achieved by an objective function of another individual. Since MO techniques optimise multiple objective functions, the principle of dominance is used to evaluate the optimality achieved by each individual. An individual A is said to dominate individual B if all objective function values in A are greater or equal to all objective function values in B with strict inequality at least once.

Historically, mathematical programming has been used to solve multi-objective problems. Despite the efficiency of these techniques, they are designed for problems involving convex solution spaces, in which global optima are guaranteed. When faced with a non-convex solution space, evolutionary algorithms (EAs) are often a suitable alternative. EAs contain mechanisms that allow them to efficiently explore solution spaces that contain diverse sets of local optima.

My research proposes a multi-objective evolutionary algorithm as an improvement upon the current state-of-the-art neuroevolutionary algorithm known as NEAT (Neuro-Evolution through Augmenting Topologies). NEAT implements a novel speciation mechanism that differs from every other neuroevolutionary algorithm of its time. The aim is to replace this mechanism with an adapted multi-objective framework that evolves for task performance and genotypic diversity. To implement this multi-objective replacement, I will be modifying an existing adaptation of NEAT known as NEAT-M-MODS.

My proposed method does not generalise the NEAT approach into a generic multi-objective NEAT method. It simply tries to quantify the effectiveness of the speciation mechanism by comparing it with a multi-objective replacement in

the context of multi-robotic systems. If this replacement proves to be better than NEAT, it may be worth developing a generic multi-objective NEAT method.

To compare NEAT with the proposed method, each method will be used to evolve the behaviour and morphology of a simulated team of robots tasked with completing a cooperative assignment.

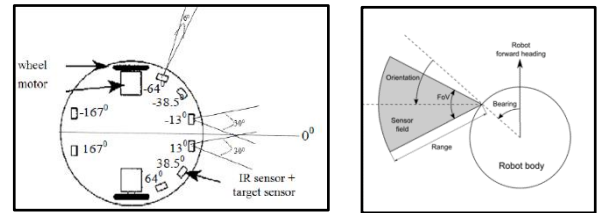


Figure 1: Left: A Khepera robot. The robot has a motor and a wheel as well as a series of sensors positioned around the circumference of the robot. The simulated robots used in this research are based on this robot. Right: The simulated robot model.

The robots performing this task will be homogenous as it has been shown that homogenous robots perform better at tasks that require agents to perform the same set of actions [11]. More specifically, all robots performing the cooperative assignment will have the same controller and sensory configuration. The cooperative assignment in question will be a well-defined benchmark task known as the *collective gathering task*. This task will involve a robotic team collecting resources and moving them into a designated gathering zone. This task will be evaluated for environments of varying difficulty. The difficulty of each environment will be determined by the size of the resources that are found in that environment. Higher levels of cooperation are needed to move larger resources than smaller resources.

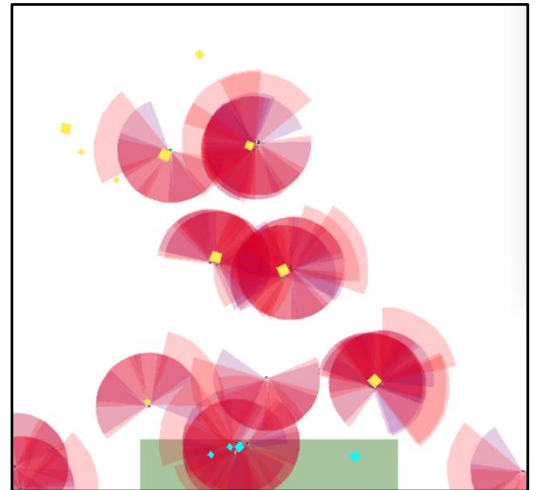


Figure 2: shows an environment in which a robotic team is moving resources into a designated gathering zone. Resources that have not yet been moved into the zone are yellow whilst the ones that have are blue. The gathering zone is represented by the green strip at the bottom of the environment. [4]

The hypothesis of my research is as follows:

H₀: *the task performance of best evolved networks using the proposed algorithm will be significantly higher than the task performance of best networks evolved using NEAT in the context of a multi-robotic system evolved to complete a collective gathering task.*

2 BACKGROUND

2.1 NSGA-II

The NSGAII (Non-Dominated Sorting Genetic Algorithm II) method improves upon the non-dominated sorting strategy formulated by NSGA and replaces its sharing approach to diversity preservation with its own diversity preservation mechanism. The proposed non-domination sorting strategy improves the efficiency with which a population is sorted into different non-domination levels. Elitism is also incorporated into this strategy to aid the convergent properties of the genetic algorithm. The strategy of using non-domination ranks and crowding distance, as used in NSGA-II [3], is used by many subsequent methods [1][4] including proposed method NEAT-M-MOGD.

2.1 NEAT

NEAT (Neuro-Evolution through Augmenting Topologies) [14] is a neuroevolutionary algorithm for evolving the weights and topology of ANNs. NEAT differs from your generic neuroevolutionary algorithm in several key areas as outlined below:

- (1) *Complexification*: the NEAT framework takes advantage of the structure of ANNs as a way of minimising dimensionality in the search space. Evolution starts with a population of genomes of simplest complexity (consisting of only an input layer and an output layer). Genes are then added to the genomes over subsequent generations thereby adding dimensionality in each generation. This allows the genomes to increase in complexity over time, only adding new dimensions when necessary. A genome refers to the set of genetic encodings that encode for a particular ANN phenotype.
- (2) *Historical Marking (innovation numbers)*: An ordered numbering system which maintains records of topological mutations throughout evolution. Tracking genes across each of the generations allow for a novel crossover method that is both effective and efficient.
- (3) *Speciation*: NEAT separates the genomes in a population into different niches to protect any structural innovation that may occur during the evolutionary process. Speciation protects structural innovation because any newly evolved genome will only compete with other genomes in its niche. NEAT assigns genomes into different species by using a compatibility function which measures how different a genome is from another genome.

2.3 NEAT-MODS

The NEAT-MODS (Neuro-Evolution through Augmenting Topologies – Multi-Objective Diversified Species) method modifies the NEAT algorithm to incorporate multi-objective evolution. NEAT-MODS has a specialised selection process that combines the novel speciation mechanism of NEAT with the non-domination sorting strategy of NSGA-II. The selection approach is outlined below:

- (1) *Selecting species for the next generation*.
NEAT-MODS adheres to the principle of elitism and, hence, the selection process uses a combined population which is comprised of the children of the current generation and their parents. The individuals in the combined population are sorted using a non-domination sorting and crowd-distance approach.

Sorted Index	Individual Index (Internal)	Species	
#1	Individual #5	Species #1	→ Selected Species Species #1 Species #2 Species #3 ...
#2	Individual #2	Species #2	
#3	Individual #1	Species #1	
#4	Individual #4	Species #3	
...	
#2N	

Figure 3: visual representation of the selecting species phase of the NEAT-MODS method. [1]

The individuals are ranked according to their non-domination levels. The algorithm starts at the most highly ranked individual and selects the species to which that individual belongs. The algorithm continues down the list, selecting the relevant species corresponding to each of the individuals. For information on the constraints on the maximum number of allowed species, it is suggested that you view the NEAT-MODS paper [1].

- (2) *Selecting Individuals from the selected species*.

The individuals in each of the selected species are sorted according to ranking and distance measure following [1]. The highest ranked individuals are selected from each of the selected species.

	Species #1	Species #2	Species #3	Species #4
→ Individual #5	Individual #2	Individual #4	...	
→ Individual #1	...	Individual #7	...	
→ Individual #3		...		
...				

Figure 4: a visual representation of the selecting individuals phase of the NEAT-MODS method. [1]

The selection process iterates down the rows, starting at the top. As the algorithm continues down the list, it selects individuals from each species. In the case of an empty entry, the species will be skipped, and the next species will be evaluated for that row. This process continues until N individuals have been selected. Emphasis is placed on the selection process of NEAT-MODS as it is the process that is modified in the proposed method.

3 METHODS

3.1 NEAT-M

NEAT-M (Neuro-Evolution through Augmenting Topologies – Morphology) is a method developed by Hewland and Nitschke [12]. This method automates the behaviour-morphology design of robot teams that are tasked with performing a cooperative assignment. Methods that evolve the behaviour of robotic teams generally evolved teams with a fixed morphology. NEAT-M allows for the co-evolution of behaviour and morphology of robotic teams. The morphology of a robot is represented by its sensory configuration and is encompassed by the set of sensory input nodes of its controller. The parameters of each of these sensory input nodes include the *Sensor Type*, *Field of View*, *Range*, *Bearing*, and *Orientation*. A set of genetic operators are used to evolve a robot's sensory configuration, that which is defined by its set of sensory parameters. These genetic operators include the *Mutate Field of View* operator, *Mutate Range*, *Mutate Bearing*, and *Mutate Orientation* operator.

3.2 NEAT-M-MODS

The NEAT-M-MODS (Neuro-Evolution through Augmenting Topologies – Morphology – Multi-Objective Diversified Species) method [4] was created by Furman and Nagar and is the framework on which my proposed method extends. This method utilises the multi-objective optimisation technique employed by NEAT-MODS [1] and combines it with the controller morphology coevolution mechanism devised by NEAT-M [12]. This paper investigates the impact of imposing a cost on morphological complexity in the co-evolution of control policy (behaviour) and sensory configuration (morphology) for robot teams in different environments [4]. The code base that encompasses NEAT-M-MODS is the code base that was modified to test my experiments.

3.2 NEAT-M-MOGD

The proposed NEAT-M-MOGD (Neuro-Evolution through Augmenting Topologies – Morphology – Multi-Objective Genotypic Diversity) method introduced in this paper aims to modify the NEAT-M-MODS method to serve as a replacement of the state-of-the-art NEAT algorithm in the context of multi-robotic systems. This research intends to quantify the effectiveness of the speciation mechanism in its ability to improve task performance. The speciation mechanism in NEAT serves two purposes. The first is to protect structural innovation and the second is to maintain diversity of individuals in the population. (More information on how this mechanism does this can be found in the NEAT paper [14].) Both these purposes serve to increase task performance. Genotypic diversity increases task performance because diversified individuals are searching highly varied areas of the solution space and are, therefore, likely to converge on a desirable optimum quicker.

NEAT-M-MOGD uses a multi-objective learning algorithm in which the second objective is genotypic diversity (GD). This objective aims to maximise GD between every individual in a population. The diversity that results from the speciation mechanism is different from that of NEAT-M-MOGD because it is not part of an optimisation criteria. To elaborate, in NEAT-M-MOGD, genotypic diversity is selected for in the selection process; in NEAT, genotypic diversity is a result of the actual selection process. Selecting for GD aims to maximise the effects experienced by task performance due to genotypic diversity.

Diversity also differs between the two methods because speciation ensures diversified species and the proposed method ensures diversified individuals. Overall genotypic diversity is expected to be maximised in the second method.

The process followed by NEAT-M-MOGD is the same NEAT-M-MODS, except for the selection phase which is outlined below:

- NEAT-M-MOGD first combines the children of the current population with their parents to form a list of $2N$ individuals.
- The combined population is ranked and sorted using a non-domination sorting and crowd-distance approach. They are sorted into non-domination levels according to their task performance and genotypic diversity.
- The new population is selected to be the first N individuals of the combined list.

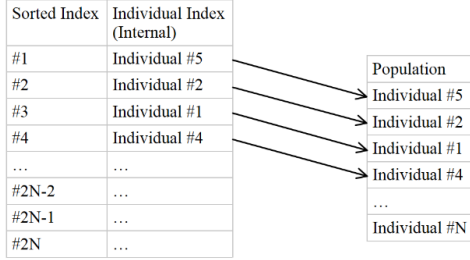


Figure 5: visual representation of the selection phase of NEAT-M-MOGD.

Note how the speciation mechanism used in NEAT-MODS is removed in the above selection process. Refer to NEAT-M-MODS for more information on the process of the algorithm [4].

4 EXPERIMENTAL SETUP

4.1 Simulated Robot Configuration

The evolved robotic teams are homogenous in nature with each robot having the exact same control policy and sensory configuration as the rest of the team. The morphology of the simulated robots is based on the Khepera-III robot which contains motors, wheels and sensors positioned around the circumference of the robot. The behaviour of a robot is governed by its ANN phenotype which represents the control policy of the robot. For specification details regarding the robots, refer to table 6 at the end of the paper.

4.2 Environment Configuration

The simulated environment is represented by a two-dimensional area comprised of a team of homogenous robots, a set of resources and a gathering zone. The robotic team is tasked with moving the resources into the gathering zone. The resources are depicted by square blocks that are randomly scattered throughout the environment at the start of a simulation. Blocks come in three different sizes, each size representing a different level of difficulty. The smaller blocks can be moved by a single robot, but larger blocks require more robots to move. The robots are also spawned at random locations with random orientations at the start of the simulation. The gathering zone is positioned at the same location throughout all simulations and all experiments.

	Number of blocks of size:		
	Small	Medium	Large
Experiment 1	10	5	0
Experiment 2	5	5	5
Experiment 3	0	5	10

Table 1: Simulated Task Environments. Environments are numbered from simplest to most difficult. Small, medium and large blocks require one, two and three robots respectively to be pushed. [4]

4.3 Fitness Functions

The first experiment uses the NEAT framework to evolve the simulated robots, thereby utilising only a single fitness function. Namely, that of task performance. The second experiment uses the multi-objective framework, NEAT-M-MOGD, which implements two fitness functions, one for each objective. The two fitness functions are task performance and genotypic diversity.

4.3.1 *Task Performance.* The first fitness measurement for a genome is calculated as the average task performance of that genome over five simulated task trials. Task performance F_1 is calculated as defined by Hewland and Nitschke [12].

$$F_1 = 100 \cdot \frac{v_c}{v_t} + 20 \cdot \left(1.0 - \frac{s_e}{s_t}\right)$$

v_c is the total value of resources in the gathering zone, v_t is the total value of all resources in the environment, s_e is the number of simulation timesteps elapsed and s_t is the number of trial evaluations per individual.

4.3.2 *Genotypic Diversity.* The Genotypic Diversity measurement of a genome is calculated as being the average distance between that genome and every other genome in the population. Distance is defined according to the formula laid out in NEAT. The distance δ between two network encodings is measured as a linear combination of the number of excess (E) and disjoint (D) genes, as well as the average weight differences of matching genes (\bar{W}) [14].

$$\delta = \frac{c_1 E}{G} + \frac{c_2 D}{G} + c_3 \cdot \bar{W}$$

The coefficients c_1 , c_2 , and c_3 adjust the importance of each of the three factors. The factor G refers to the number of genes in the larger genome. This normalises the measurement for large genome sizes. The fitness function for genotypic diversity F_2 is calculated as follows:

$$F_2 = \frac{\sum_{i=1}^N \delta_i}{N}$$

The factor N is the number of genomes in the population and δ_i is the distance between the genome in question and the i^{th} genome in the population.

5 RESULTS AND DISCUSSION

This section presents and analyses the results of the experiments. Statistical tests are used to validate or invalidate the outlined hypotheses and a general discussion will clarify why the relevant decisions were made. The NEAT-MOGD method was used to evolve MO (multi-objective) solutions and the NEAT-M method was used to evolve SO (single objective) solutions. The task performance of individuals evolved by the respective methods are compared in the forthcoming analysis.

5.1 Data

Ten experiments were conducted for each environment. Five of these experiments evolved MO solutions and the other five evolved SO solutions. Simulator parameters can be found in table 6. The best networks from the MO solutions and the SO solutions were selected for comparison. A network is considered best if the task performance resulting from that network was the highest out of all the evolved networks for that method. A motivation for why only the best networks were compared is outlined below.

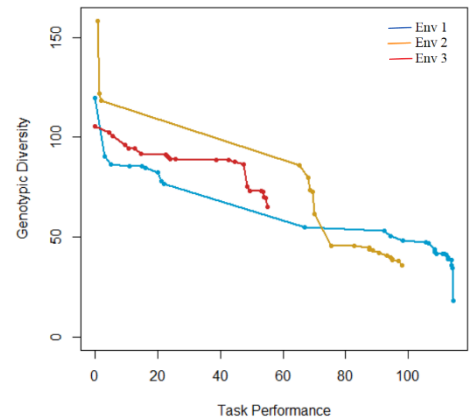


Figure 6: shows the pareto fronts of non-dominated individuals evolved by NEAT-M-MOGD for each of the environments. The experiments chosen for each environment were arbitrarily chosen. Note how no individual dominates any other individual in each of the three environments.

As can be observed in Figure 6, a pareto front of non-dominated individuals represents some trade-off between genotypic diversity and task performance. The genotypic diversity objective only has the intrinsic value of maintaining diversity whilst the population is evolving. The diversity measure of an

individual has no value once the evolutionary process is complete. Hence, the solution with the highest task performance in the non-dominated pareto front was chosen to be evaluated for each experiment. In figure 6, this is represented by the furthest right point for each of the environments. The sample sizes of the results were small enough to show in the tables below:

	MO (Simple)	SO (Simple)
Experiment	Max Score	Max Score
1.1	113.6364	114.1368
1.2	112.14	114.2532
1.3	112.1028	111.5864
1.4	114.3944	112.2544
1.5	112.8644	112.898
Average	113.0276	113.02576

Table 2: depicts the results of the MO and SO methods for the simplest environment. Five experiments were conducted for each method.

	MO (Medium)	SO (Medium)
Experiment	Max Score	Max Score
2.1	107.424	101.08907
2.2	106.0036	104.8292
2.3	82	97.557467
2.4	98.46853	107.0296
2.5	98.07933	103.4132
Average	98.395092	102.78371

Table 3: depicts the results of the MO and SO methods for the environment of medium difficulty. Five experiments were conducted for each method.

	MO (Difficult)	SO (Difficult)
Experiment	Max Score	Max Score
3.1	63.5	93.1176
3.2	74.5	51
3.3	55	56
3.4	56	60
3.5	75	65.0294
Average	64.8	65.0294

Table 4: depicts the results of the MO and SO methods for the most difficult environment. Five experiments were conducted for each method.

Disclaimer: a few of the MO experiments fell just short of the 250-generation mark. It can be observed that the remaining few generations of an evolutionary process have little to no effect on the overall task performance scores of best networks.

5.2 Hypotheses

The first statistical tests utilised in this analysis is non-parametric in nature. Due to the small sample size obtained for each environment, it cannot be inferred, with any reasonable level of significance, that the entire population for each environment follows a normal distribution. Hence, we use the Mann-Whitney-Wilcoxon Test to test whether the maximum task performance scores of MO and SO solutions were sampled from nonidentical populations. This test was conducted for each environment (represented by table 2, table 3 and table 4).

H₀: the population of maximum scores for the MO method is identical to the population of maximum scores for the SO method.

The results of the Mann-Whitney-Wilcoxon tests are summarised in the table below.

Environment	P-value
Simple Environment	1
Medium Environment	0.8413
Difficult Environment	0.9166

None of the p-values for any of the environments showed significance. Hence, we cannot reject the null hypothesis for any of the environments. Based on this statistical test, we can conclude that there is no significant difference in the max scores resulting from the MO method and the SO method for each of the environments.

The next test uses a randomised block design (RBD) to test the significance of the average test score achieved by the MO method with the average test score achieved by the SO method. This test allows us to have a sample size of 15 for the MO and SO methods as the observations of max score for each environment are combined for each method. The response for the RBD is the maximum task performance scores. The treatment is whether the MO or SO method was used. The blocks are the environments from which the max scores were obtained.

This design reduces variability within treatment conditions (i.e. reduces variability of task scores for a method due to different environments), which helps produce better estimates of treatment effects (i.e. effects of MO vs SO on max task performance). RBD also helps reduce potential confounding. We can formulate two hypotheses for this statistical test:

1. **H₀:** $\mu_{MO} = \mu_{SO}$
2. **H₀:** $\mu_1 = \mu_2 = \mu_3$ where μ_i is the mean max score for environment i .

The results of the RBD are as follows:

	Degrees of freedom	Sum of Squares	Mean Square Error	F-value	Pr (>F)
Method	1	17.8	17.8	0.2347	0.6321
Environment	2	12473.8	6236.9	82.4456	5.55E-12
Residuals	26	1966.9	75.6		

Table 5: RBD where the response is max task performance, the treatment is whether MO or SO was used and the blocks are the environment from which the max score was obtained.

We cannot reject the null hypothesis that $\mu_{MO} = \mu_{SO}$ but we can reject the null hypothesis that $\mu_1 = \mu_2 = \mu_3$ with a high-level of significance. We can, therefore, conclude that the average max score for the MO method is not significantly different from the average max score for the SO method. We can also conclude that the environment in which the individuals were evolved has a significant effect on task performance.

6 CONCLUSIONS

This study investigates whether a multi-objective NEAT that evolves for task performance and genotypic diversity results in best individuals that have a task performance greater than that of NEAT in the context of a multi-robotic system performing a collective gathering task. The results indicate that there is no significant difference between NEAT-M and NEAT-M-MOGD in their ability to evolve individuals for task performance. The result that NEAT-M-MOGD performed just as well as NEAT is still promising as it shows that speciation isn't the only option for maintaining genotypic diversity in a population. It also indicates possible avenues of future research.

7 FUTURE WORK

The most exciting result of this research is the possibility of future research. To improve upon NEAT-M-MOGD, an extra objective of quality genotypic diversity could be added to the model. Quality genotypic diversity could also be incorporated into the second fitness function F_2 as defined in the *Fitness Functions* section. There is a high possibility that an improvement of NEAT-M-MOGD in this regard will outperform NEAT in the context of the task evaluated in this research. If this proves to be the case, a generic multi-objective NEAT method could be developed.

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Neuro-Evolution Paramaters	
Generations per experiment	250
Trial evaluations per phenotype	5
Population size	150
ANN connection weight range	$[-1.0, 1.0]$
Sensor Mutation	0.08
Add Sensor Mutation	0.07
Sensor FOV / Range / Bearing / Orientation Perturb	Cauchy mutation (0, 5)
Connection weight mutation probability	0.335
Initial Connection Density	0.5
Initial Sensory Input Nodes / Output Nodes	5 / 2
Output Nodes	2
Crossover / Mutation	0.32 / 0.34
Simulation Parameters	
Timesteps per simulated trial evaluation	10000
Robot team size	20
Robot size (diameter) / Gripping distance	0.004 / 0.002 (Portion of environment size)
Maximum robot movement per timestep	0.013 (Portion of environment size moved per iteration)
Initial robot / block positions	Random (Outside gathering zone)
Environment width x height / Gathering zone size	1.0 x 1.0 / 0.5 x 0.2
Small / Medium / Large block size (Width / Height)	0.01 x 0.01 / 0.015 x 0.015 / 0.02 x 0.02
Ultrasonic sensor Range / FOV	(0.0, 1.0] / (0.0, π)
Infrared Proximity Range / FOV	(0.0, 0.4] / ($\pi/6, 5\pi/6$)
Colour Sensor Range / FOV	(0.0, 0.4] / ($\pi/6, 5\pi/6$)
Low Res Camera Range / FOV	(0.0, 0.8] / ($\pi/9, 8\pi/9$)
Bottom Proximity	Downward-facing
Sensor Bearing Range	$[-\pi, \pi]$ Radians
Sensor Orientation Range	$[-\pi/2, \pi/2]$ Radians

Table 6: Neuro-evolution and simulation parameters. This table was extracted directly from the NEAT-M-MODS paper [1] as all parameters remained the same for the NEAT-M-MOGD method.

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