

Robot Phylogenetics

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ABSTRACT

Bioinformatics techniques are introduced for the analysis of evolutionary search. These techniques are tested on buildable robots evolved in a virtual simulator for a locomotion task. By using bioinformatic visualizations properties of evolutionary search and relatedness between differing robot genotypes and phenotypes can be examined.

Categories and Subject Descriptors

I.2.9 [Computing Methodologies]: Artificial Intelligence—Robotics; I.6.6 [Computing Methodologies]: Simulation and Modeling—*Simulation Output Analysis*

General Terms

Design, Experimentation, Measurement

Keywords

Evolutionary Algorithms, Robotics, Evolution, Behavior, Phylogenetics, Evolutionary, Late Breaking Abstract

The study of evolutionary algorithms (EAs) is often complicated by local optima, fitness plateaus, and other degenerate behaviors. We introduce the use of bioinformatic visualizations to gain insights into search spaces and trajectories of EAs. Analysis techniques originally developed for the study of natural evolution are presented in the context of an artificial evolutionary substrate as robot phylogenetics.

Evolutionary robotics involves searching a space of genotypes that map onto robot phenotypes. Successful examples include searching through spaces of robotic truss structures [4] and L-systems [2]. Our robots, evolved in breve, a 3D multi-agent simulator [3] and shown in Figures 1a & 1b, are similar to [6]. Some structural and all control parameters are evolved. A genetic algorithm with two-point crossover, and mutation (single-point randomization and \pm unit shift) is used on genomes of 18 genes. A population of size 100 is evaluated for 100 generations with tournament selection.

Evolutionary computation has been used numerous times to solve bioinformatics problems [1]. However, bioinformatics techniques have not been used to solve evolutionary computation problems. We introduce the use multiple bioinformatics techniques to explore an EA. Heat maps of both the

historically-ranked, Figures 1c and 1d, and fitness-ranked individuals, Figures 1e and 1f, show the evolutionary trajectory and the similarity in fitness landscapes, respectively. A cluster heat map [7] of genotype/phenotype observations, Figures 1g and 1h, suggests separate basins within the space and a close coupling between fitness and limb length. Pearson's correlation metric [5] clusters individuals which tend to be closer by minor mutation and intra-cluster crossover. Comparison of fitness landscapes suggest that the wave compression gene is the primary difference between optimal radial and bilateral robot phenotypes. Finally, the long leg bias is made apparent by the fitness landscape.

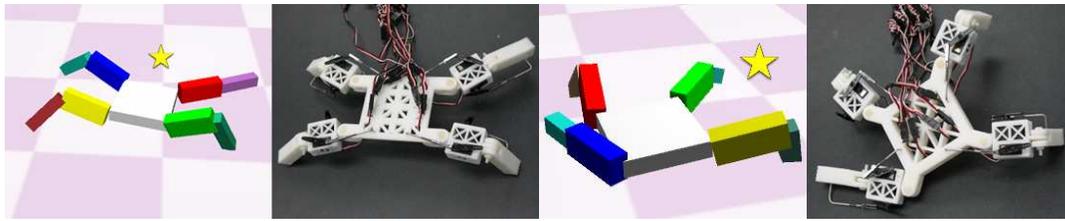
Bioinformatics techniques can elucidate analysis of evolutionary search. Clustering can provide insight into the roughness of a fitness landscape. Design of evolutionary systems can be clarified by using bioinformatics visualization of evolutionary trajectories, spaces, and fitness landscapes.

1. ACKNOWLEDGEMENTS

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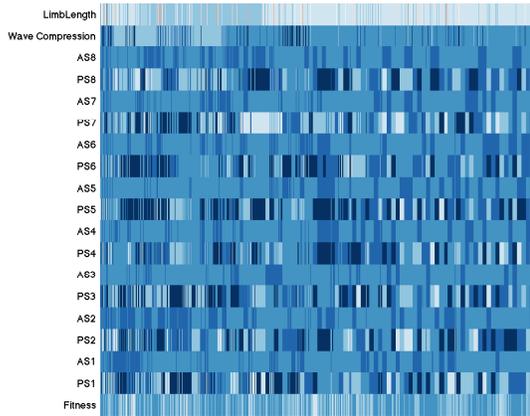
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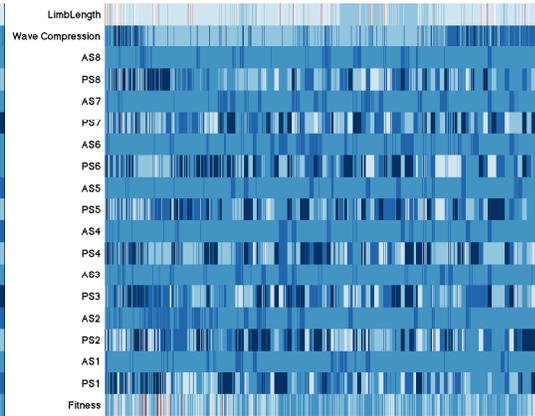


(a) Virtual and real robot, bilateral.

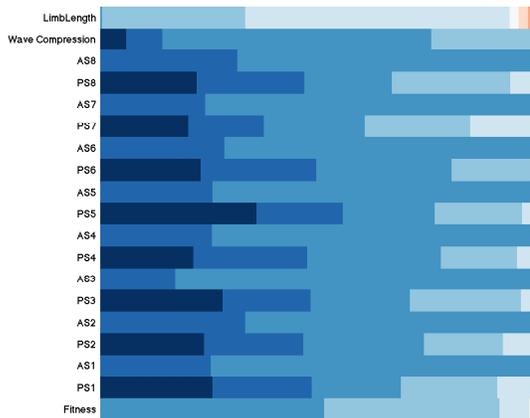
(b) Virtual and real robot, radial.



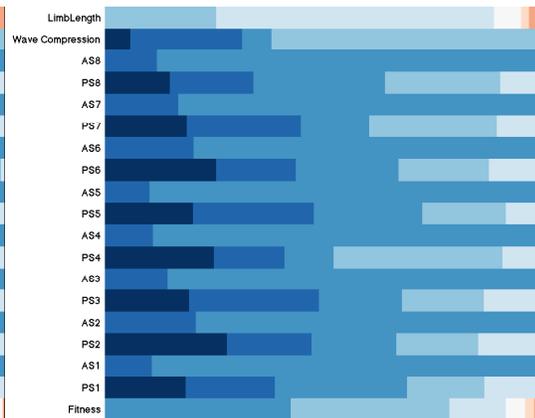
(c) Evolutionary trajectory, bilateral.



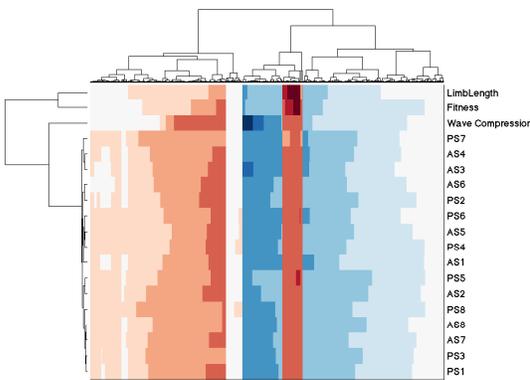
(d) Evolutionary trajectory, radial.



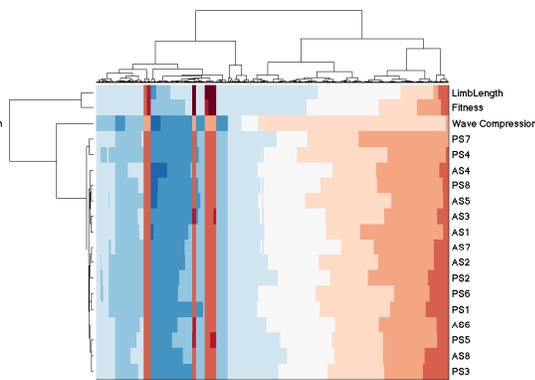
(e) Fitness landscape, bilateral.



(f) Fitness landscape, radial.



(g) Phylogenetics and clustering, bilateral.



(h) Phylogenetics and clustering, radial.

Figure 1: Bilateral and radial virtual robots next to respective posed real robots, (a) and (b). Heat map of evolutionary trajectories over 100 generations of populations consisting of 100 individuals, (c) and (d). Heat map of fitness-ranked explored genotypes, (e) and (f). Heat maps present 18-dimensional genome space as well as fitness score. Clustering of explored genotypes, (g) and (h). Colors indicate discretized value with dark red as the maximum and dark blue as the minimum. Rows are labeled with gene names, except the row containing fitness values.