# Studies of Cellular Movement using Computational Cellular Ethology

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**Computational cellular ethology (CCE) is the evaluation of cellular behavior using a subsumption architecture of information-processing modules. This method has its roots in behavioral robotics, and allows the construction of a control structure for a cell by treating it as an autonomous agent. This approach is demonstrated with a CCE agent-based model of cellular foraging movement that recapitulates experimentally recognized bimodal correlated random walk behavior. This type of behavioral representation can provide insight into the process of cellular motility, both in terms of characterizing the roles of biochemical subsystems and identifying control structures involved in chemotaxis and tissue patterning.**

***Keywords* — Subsumption architecture, agent-based model, cellular motility, control systems, chemotaxis, systems biology.**

## I. Purpose

THE behavior of populations of cells determines the behavior of biological systems. One of the goals of systems biology is to link knowledge of intracellular processes with cellular behavior. We propose an analytical modeling approach, termed *computational cellular ethology (CCE),* that links cellular information processing to observed behaviors by decomposing complex cellular behavior into simpler behavioral modules. These modules are organized in a subsumption architecture control structure incorporating action selection with roots in behavioral robotics [1]. By identifying the information-processing procedures a cell needs to accomplish in order to generate a specified behavior, a CCE model provides a functional context for the extensive list of molecular components identified in the literature. CCE models are suited to instantiation in an agent-based model (ABM) and as an example of this method we present a CCE ABM of cellular foraging movement.

## II. Methods and Results

The default condition for cells, phylogenetically and morphologically, is movement. Cellular foraging behavior, i.e. movement in search of a target, is the most basic type of cellular motility, from which chemotaxis and migration arise. Cellular foraging been recognized to consist of a bimodal movement pattern, each phase of which have distinct characteristics [2].

### A. Methods

An ABM of cellular foraging was created in NetLogo [3] based on the bimodal characteristics described in [2]. There are two distinct movement modes: directional (DM) and re-orientation (RM). These two modes differ with respect to range of variance in heading-change per movement step (+/- 20° for DM, +/- 200° for RM), and distribution of time spent in each mode (exponential distribution for DM, uniform distribution for RM). Parameter values and control structure for action selection between modes were extrapolated from published observations [2].

### B. Results

The CCE ABM of cellular foraging movement reproduces the bimodal correlated random walk present in [2]. Overall movement displayed supra-diffusive behavior, consistent with the ballistic properties of the directional mode. The difference in total distance traversed in each mode was not statistically significant, though the degree of Cartesian displacement was greater in the directional mode versus re-orientation mode.

## III. Conclusion

Cells do not know math; however they do process information. The CCE method allows for the conversion of observed behavior into information processing rules. By treating cells as autonomous agents, CCE identifies the necessary and sufficient information processing steps to produce a complex behavior. These functional modules form a reference architecture into which biochemical subsystems can be placed. In circumstances where mechanisms are known, as in the differences between prokaryotic and eukaryotic movement, a CCE architecture can provide insight into default states and directionality of control structures. More complex behaviors, such as chemotaxis and tissue patterning, can be examined in terms of module and control modifications on the base architecture.

## References

[1] Brooks, RA. (1991) Intelligence without representation. Artificial Intelligence **47(1-3):** pp. 139-159

[2] Potdar, AA, Jeon, J, Weaver, AM, Quaranta, V and Cummings PT. (2010) Human Mammary Epithelial Cells Exhibit a Bimodal Correlated Random Walk Pattern. PLoS ONE **5(3):** e9636.

[3] Wilensky, U. (1999). NetLogo. http://ccl.northwestern.edu/netlogo. Center for Connected Learning and Computer-Based Modeling. Northwestern University, Evanston, IL

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