Minimal Path Algorithms

O. Steinbock, Á. Tóth, and K. Showalter (*1*) suggest that the computational simulation of chemical waves gives rise to "a highly efficient algorithm for the determination of optimal paths." They state that "conventional path-finding methods typically rely on iterative searches, in which all possible pathways between a point of interest and a target point are successively determined."

Efficient algorithms for finding minimal paths between pairs of vertices of a graph are well known, and do not rely on searching all possible paths. The method presented, though different in its approach, appears to be essentially equivalent to these algorithms.

The Breadth First Search (BFS) algorithm (*2*, *3*) is applicable where the distances between adjacent vertices are all equal. The finish point F is labeled "0." All vertices adjacent to the "0" are labeled "1"; all unlabeled vertices adjacent to a "1" are labeled "2"; and so on until the whole graph is labeled. The minimal path (or paths) from any point to F may then be traced by moving through successively lower numbered vertices. A generalization of BFS to graphs with positive distances is Dijkstra's Algorithm (*2*, *3*).

Both algorithms may be interpreted as calculating the successive positions of a wave front propagating from point F. Dijkstra's Algorithm selects the vertices of the graph in the order in which they would be reached by a wave propagating at constant speed from F. As each vertex is included it is labeled with its minimal distance from F (equivalently, the time at which the wave reached it). The possibility of interpreting these algorithms in terms of a propagating wave strongly suggests that no advantage is to be gained by explicitly solving a wave equation. This conclusion is supported by an analysis of the time behavior of the algorithms. BFS runs in $O(n)$ time, where n is the number of vertices in the graph. For a general graph Dijkstra's Algorithm is $O(n^2)$ (*2*, *3*). However for large sparse graphs (to represent two-dimensional mazes) an efficient implementation should run in $O(n \log(n))$ time (*3*).

Each time step of the wave propagation algorithm will take machine time proportional to the number of grid points used, while the number of time steps required will be proportional to the length of the minimal path. For a general graph, the number of grid points would need to be $O(n^2)$, giving no better than $O(n^2)$ time behavior. Moreover, such a graph is not representable on a two-dimensional grid. For (sparse) graphs representing two-dimensional mazes, the number of grid points will be $O(n)$, and the minimal path length will grow at least as fast as $O(\sqrt{n})$, giving $O(n^{3/2})$ behavior.

Hence the proposed wave propagation algorithm does not improve on the established algorithms for finding minimal paths computationally.

D. Gareth Williams
Formal Software Construction Ltd.,
Cardiff Business Technology Centre,
Senghenydd Road
Cardiff CF2 4AY, Wales, United Kingdom

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Response: We thank D. G. Williams for pointing out that path-finding methods based on computing wave position as described in our report (*1*) are "essentially equivalent" to existing techniques such as the BFS algorithm. We wish to emphasize that path finding from reaction-diffusion waves, which was suggested by Babloyantz and his co-workers in 1991 (*2*), represents a mechanism by which physical and biological systems might optimize transit times and distances. Our study focused on determining optimal paths from chemical waves in the Belousov-Zhabotinsky reaction; however, other systems illustrate how the same process might play an important role in biological self-organization.

An example of path finding from reaction-diffusion waves is found in the slime mold *Dictyostelium discoideum*. The aggregation of individual *Dictyostelium* amoebas is organized by propagating reaction-diffusion waves of extracellular cyclic adenosine monophosphate (cAMP) (*3*). Of particular interest is the chemotactic cell motion that parallels the spatiotemporal dynamics of this chemoattractant. Experiments have shown that the velocity vectors of cell movement and wave propagation are always antiparallel (*4*). The pacemakers of the cAMP waves therefore coincide with the centers of cell aggregation. This relationship implies that the amoebas migrate according to optimal paths defined by the reaction-diffusion waves during the aggregation phase of the *Dictyostelium* life cycle. Because slime mold aggregation under natural conditions takes place in the three-dimensional "labyrinth" of forest soil, it seems likely that path-length optimization based on reaction-diffusion waves is relevant in the self-organization of this species.

O. Steinbock
K. Showalter
Department of Chemistry,
West Virginia University,
Morgantown, WV 26506–6045, USA

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