Revisiting the refraction of humans and ants through dijkstra's algorithm

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Abstract

In this paper we revisit the study on the refraction of humans and ants, using graph theory to construct models of connected flat graph of both systems. Subsequently, the Dijkstra algorithm is implemented through a MATLAB code, with which the corresponding data matrices are obtained. These matrices provide the optimal time trajectories for each of the graphing models, in their different configurations. In the case of the human system, the prediction turned out to be of the same order as predicted by the Fermat Principle in that cited literature reference. In the case of ants, the predictions are quite coherent according to the elaborated models of graph, although these do not obey the original experimental arrangements.

Keywords: Refraction of biological systems; Dijkstra Algorithm; Computer Systems; Algorithms

Abstract

En el presente artículo se revisita el estudio sobre la refracción de humanos y hormigas, utilizando la teoría de grafos para construir modelos de gráfica plana conexa de ambos sistemas. Posteriormente, se implementa el algoritmo de Dijkstra a través de un código de MATLAB, con el cual se obtienen las matrices de datos correspondientes. Dichas matrices proporcionan las trayectorias de tiempo óptimo para cada uno de los modelos de gráfica, en sus diferentes configuraciones. En el caso del sistema de humanos, la predicción resultó ser del mismo orden que la predicha por el Principio de Fermat en citada referencia de la literatura. Para el caso de las hormigas, las predicciones son bastantes coherentes de acuerdo a los modelos de gráfica elaborados, aunque estas no obedecen a los arreglos experimentales originales.

Palabras clave: Refracción de sistemas biológicos: Algoritmo de Dijkstra: Sistema de Cómputo; Algoritmo

I. INTRODUCCIÓN

Tas is well known throughout the scientific literature, the Fermat Principle in its formal structure refers to displacements by a particle from an initial to a final point, in the shortest possible time and regardless of whether the environment has constant or variable densities. Also, this formal structure does not refer to a specific type of particle (material, not material). Taking into account this last observation, it is considered the possibility of labeling a system of biological entities as "Living Material Particles" (LMP), as stated in [1], where an experimental arrangement is proposed to verify the Fermat Principle, Whose interface is made up of land and water and where the LMP are a group of humans. Another example of LMP that verifies the Principle of Fermat is showed in [2], where they predict theoretically and show experimentally, how a group of ants draw trajectories from an initial point to a final one,

crossing different types of rough interfaces. Both LMP examples verify such an optimal principle of nature, within the context of the formal structure. The application of this formal structure varies in complexity depending on the study system, for this reason, in the present contribution, it is emphasized the interest of revisiting the refraction of the systems studied with humans and ants, mentioned above, but with a different theoretical framework, which is known as Dijkstra's Algorithm [3], which also allows us to find the optimal path to be followed in order to arrive in the shortest time from point A to point B. The main feature of this framework is a graphical model of the system, whose constituents can be considered with relative ease.

Through the literature it is observed that this algorithm has played a relatively important role in the study of different types of systems (technological, biological, chemical, and physical, among others). For example, in [4] it is used to optimize navigation routes. In [5, 6], the algorithm is integrated with the genetic algorithm.

Likewise, [7, 8, 9, 10, 11, 12, 13, 14, 15] shows its utility within the biological context, so it can be said that one of its main roles is through biological networks and biochemical interactions, as well as used to find optimal paths of images of confocal microscopy of embryonic wounds. On the other hand, in the area of optics, there are a large number of applications, for example, within the context of optical networks, as shown by [16, 17, 18, 19, 20, 21, 22, 23, 24]. In [25], a navigation technique is presented on continuous surfaces, with the help of minimum cost paths and where vector networks are used. Likewise, in [26] the Dijkstra algorithm is applied in the context of spatial modeling, through the optimization of accumulated cost surfaces.

A case parallel to the refraction of light is known as refraction of biological species.

This phenomenon has been studied in recent years, as mentioned in the first two references of the present introduction and, reiterating, both studies are within the context of Fermat's formal principle. The contribution of the present work is to revisit this biophysical phenomenon, taking into account the theoretical framework of the standard Dijkstra algorithm, which will allow to consider it as an alternative framework for future research within the area of biophysics. In the second section, we describe the structure of the standard Dijkstra algorithm within the context of refraction of biological species (humans and ants). In the third section, we obtain the predictions of the optimal trajectory followed by both humans and ants. In the fourth section, the conclusion and final discussion of the research is presented.

II. METHOD: STANDARD DIJKSTRA ALGORITHM AND REFRACTION OF LMP

Before describing the structure of the Dijkstra algorithm applied to the biological systems formed by humans and LMP ants, described in [1] and [2] respectively, it is important to describe the graphic models for them. Starting with the case of humans, Figure 1 shows the graph model for the human biological system, which will be refracted from ground to water (a more complete description of the experimental system is given in reference [1]). This figure shows the conformation of the nodes and edges through earth and water, where the distance between each node by earth is 1m.

You can easily notice the different possible paths that are drawn from starting point A to end point B, through the connected shaped graph. Also, in the left part of Figure 1 (parallel to the y-axis), sometimes are shown, which represent the weights associated with the edges of the multiple trajectories. Now, the experimental determination of the velocities of humans by earth and water in reference [1], y is what allows us to establish the magnitude of each of the weights between the edges.

As shown in Figure 1, the purpose of this group of humans is to move from the starting point A to the end point B through the optimal path, in the shortest time. It

shows the set of possible paths that humans can follow to accomplish this goal.
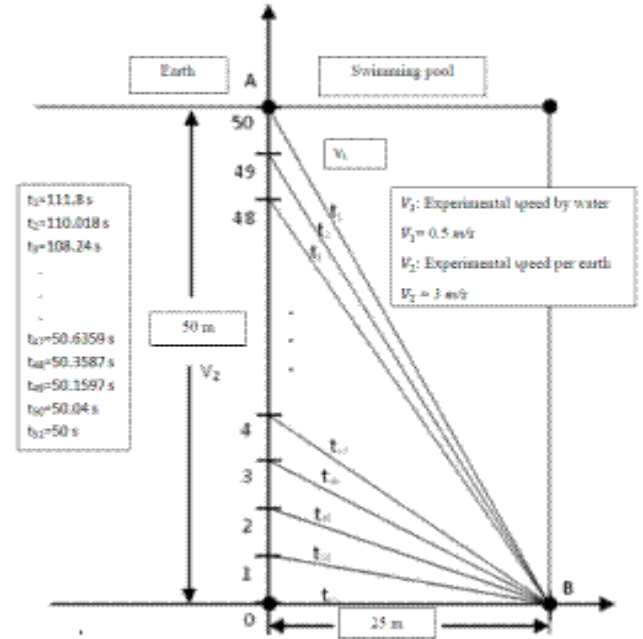

FIGURE 1. Related graph for the experimental arrangement of a human system described in [1], which will be refracted from earth to water.

For the case of the ant system, for simplicity, a graph model analogous to that of humans is used, even though the original experimental arrangement studied in [2] is not the same as that of humans. The implementation of the Dijkstra algorithm to the ant system is carried out taking into account three types of interface, as it is realized in [2]: polyethylene-soft felt, polyethylene-rough felt and soft felt-rough felt. Said configurations of related graphs are shown in Figures 2, 3 and 4, respectively.
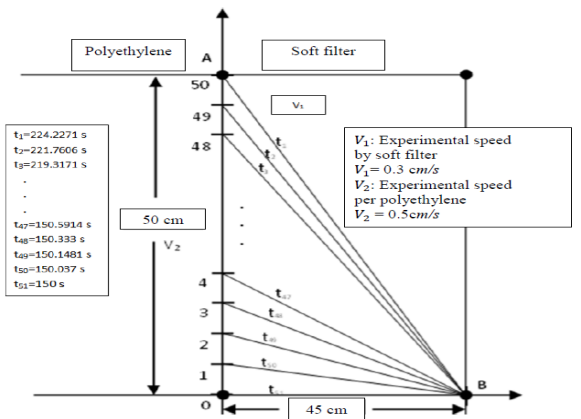

FIGURE 2. Related graph model for the experimental arrangement of an ant system described in [2], which will be refracted from polyethylene to soft felt.

FIGURE 3 A related graph for the experimental arrangement of an ant system described in [2], which will be refracted from polyethylene to rough felt.

```
function D = dijkstra(G, pairs)
  p = size(pairs, 1);% Number of pairs
  v = size(G, 1);% Number of vertices
  D = [];
  for i = 1:v
  for j = 1:v
  if G(i,j) <= eps;
  G(i,j) = inf;
  end
  end
  end
  for i = 1:p
  dist = inf(1, v);
  seen = ones(1, v);
  not_seen = v;
  dist(1, pairs(i,1)) = 0;
  while not_seen > 0
  [distance index] = min(dist .* seen);
  if distance == inf
  break;
  end
  if index == pairs(i,2)
  break;
  end
  seen(index) = inf;
  not_seen = not_seen - 1;
  for n = 1:v
  if seen(n) == 1
  alt = distance + G(index, n);
  if alt < dist(n)
  dist(n) = alt;
  end
  end
  end
  end
  D = [D; dist(pairs(i,2))];
  end
  end
```

These configurations show, as in the case of humans, the velocity information in each of the materials, which were used in [2]. With the velocities of the ants and the distances between each one of the nodes of the edges, the respective associated weights are obtained, these being of fundamental importance for the construction of each of the related graphs. Next, the implementation of the Dijkstra algorithm is shown through the structure of the present code in MATLAB, which allows to solve the different models of graph (introducing the information contained in each one of the configurations described above), finding the optimal

trajectory to move from the starting point A to the end point B in the shortest time. The following is the result of the calculations obtained by the MATLAB code, which will be described in the next section.
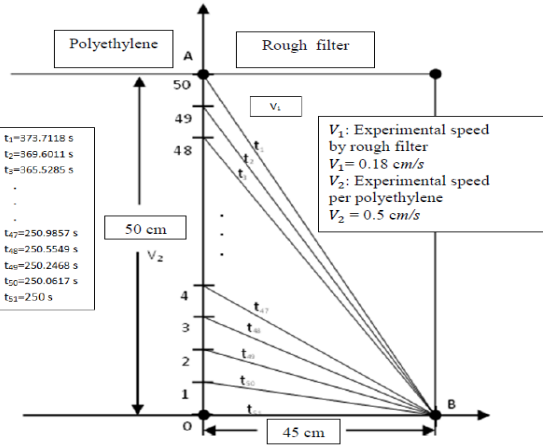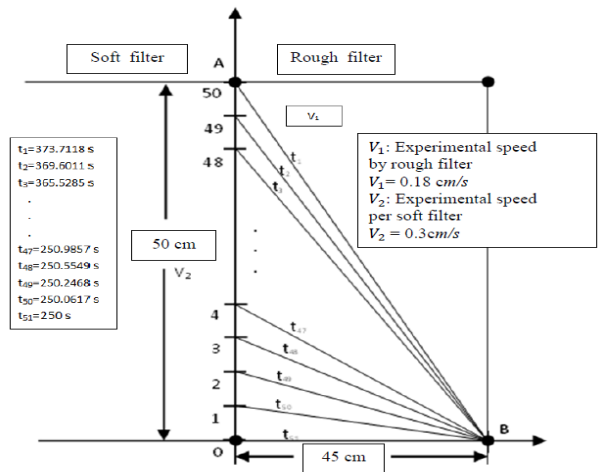

FIGURE 4. Related graph for the experimental arrangement of an ant system described in [2], which will be refracted from soft felt to rough felt.

III. CALCULATION RESULTS

It is showed the structure of the calculations made by the code implemented in MATLAB for each of the configurations of the models of the graph, for both humans and ants, respectively. Tables 1, 2, 3 and 4 describe all trajectory values for humans and ants.

TABLE I Information associated with the weights of the system configuration (eart-water), using the Dijkstra algorithm.

	0	0.33	0	.	.	.	111.8
	0.33	0	0.33	.	.	.	110.018
	0	0.33	0	.	.	.	108.24
A=	.			.			.
	.			.			.
	.			.			.
	0	0	0	.	.	.	50.04
	0	0	0	.	.	.	50
	111.8	110.018	108.24	.	.	.	0

TABLE II. Information associated with the weights of the ants system configuration (polyethylene-soft felt), using the Dijkstra algorithm.

Once the information contained in the previous matrices is processed, through the Dijkstra algorithm in the MATLAB code, the optimal time trajectories to be followed by human systems and ants are obtained. These trajectories are presented in Figures 5, 6, 7 and 8, respectively.

$$A = \begin{bmatrix} 0 & 2 & 0 & . & . & . & 224.2271 \\ 2 & 0 & 2 & . & . & . & 221.7606 \\ 0 & 2 & 0 & . & . & . & 219.3171 \\ & . & & & . & & . \\ & . & & & . & & . \\ & . & & & . & & . \\ 0 & 0 & 0 & . & . & . & 150.037 \\ 0 & 0 & 0 & . & . & . & 150 \\ 224.2271 & 221.7606 & 219.3171 & . & . & . & 0 \end{bmatrix}$$

TABLE III. Information associated with the weights of the configuration of the ants system (rough polyethylene-felt), which uses the Dijkstra algorithm

$$A = \begin{bmatrix} 0 & 2 & 0 & . & . & . & 373.7118 \\ 2 & 0 & 2 & . & . & . & 369.6011 \\ 0 & 2 & 0 & . & . & . & 365.5285 \\ & . & & & . & & . \\ & . & & & . & & . \\ & . & & & . & & . \\ 0 & 0 & 0 & . & . & . & 250.0617 \\ 0 & 0 & 0 & . & . & . & 250 \\ 373.7118 & 369.6011 & 365.5285 & . & . & . & 0 \end{bmatrix}$$

TABLE IV. Information associated with the weights of the system configuration ants (soft felt-rough felt), which uses the Dijkstra algorithm.

$$A = \begin{bmatrix} 0 & 3.33 & 0 & . & . & . & 373.7118 \\ 3.33 & 0 & 3.33 & . & . & . & 369.6011 \\ 0 & 3.33 & 0 & . & . & . & 365.5285 \\ & . & & & . & & . \\ & . & & & . & & . \\ & . & & & . & & . \\ 0 & 0 & 0 & . & . & . & 250.0617 \\ 0 & 0 & 0 & . & . & . & 250 \\ 373.7118 & 369.6011 & 365.5285 & . & . & . & 0 \end{bmatrix}$$

The results of the predictions of the Dijkstra algorithm are shown in Figures 5, 6, 7 and 8, where the optimal time trajectories are found, crossing by two different roughness material means. In the first case, which is that of humans, a refraction is predicted at ~ 4m, with an optimum time of 65.9692s. The second case corresponds to that of the group of ants, where they move in three different configurations: polyethylene-soft felt, polyethylene-rough felt and the soft felt-rough felt. In these configurations, the following predictions are obtained: the first configuration (polyethylene-soft felt) predicts that the ants will be refracted at ~ 34cm, with an optimum time of 220.0012s., the second configuration (rough polyethylene-felt), predicts an ant refraction at ~ 17cm, with an optimal time of 333.2447s, and the third configuration (rough felt-soft felt), predicts a refraction at ~ 34cm, with an optimal time of 366.6153s.
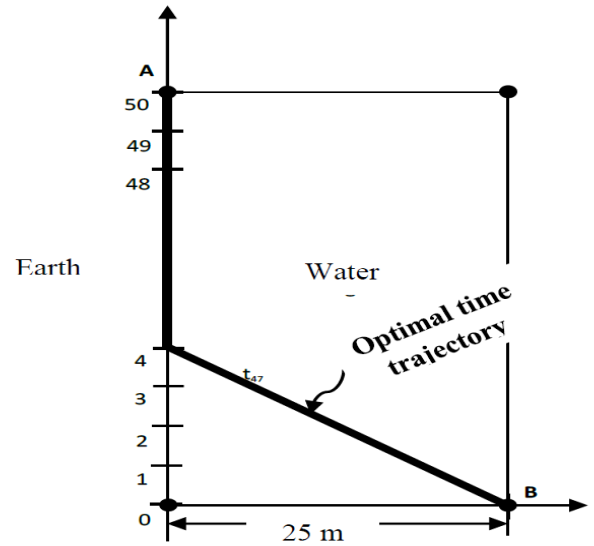

FIGURE 5. Optimal time trajectory (human system, eart-water interface), obtained by the Dijkstra algorithm
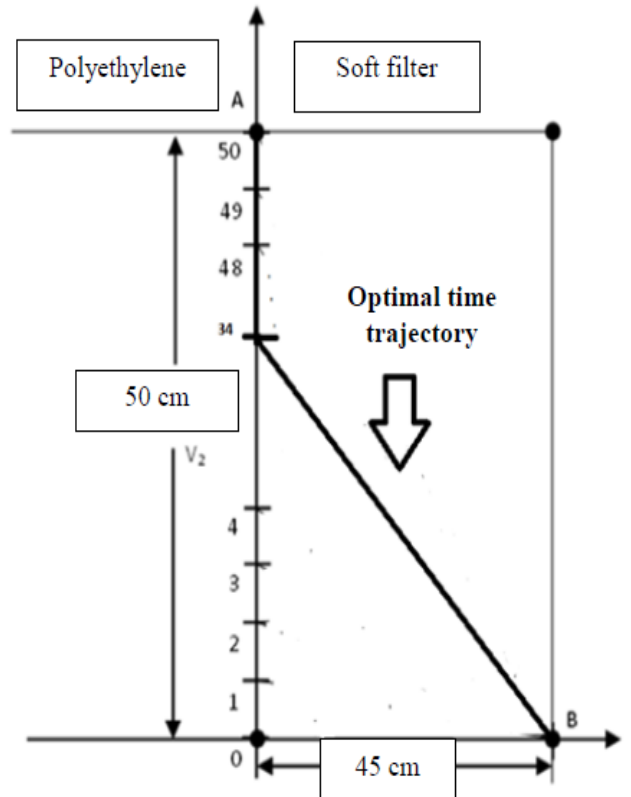

FIGURE 6. Optimum time trajectory (ants system, polyethylene-soft interface), obtained by the Dijkstra algorithm.

FIGURE 7. Optimal time trajectory (ants system, polyethylene-rough felt interface), obtained by the Dijkstra algorithm

FIGURE 8. Optimum time trajectory (ants system, soft felt-rough felt interface) obtained by the Dijkstra algorithm.

IV. CONCLUSION

Taking into account that the phenomenon of biological refraction carried out by so-called LMPs (humans and ants, at least theoretically), which were first studied, using the Fermat principle of the minimum time, as mentioned at the beginning in references [1] and [2], it develops in conditions such that it satisfies certain physical and geometric constraints, in such a way that it allows the development of a connected flat graphical model of the biophysical systems in question.

From this inspection, the present work revisits the refraction using the Dijkstra algorithm, implemented in a MATLAB program. The results obtained are very close to those found by the Fermat principle, in the case of humans.

The case of the ants is different, because a similarly connected planar graph model was sketched similar to the human case, which does not satisfy the experimental arrangement proposed in [2]. For this reason, in the present work, the experimental verification of such predictions is pending, hoping it will be done in a future contribution.

On the other hand, to study the refraction of biophysical systems through the Dijkstra algorithm technique, results sometimes with certain advantages compared to the Fermat Principle method, as can be seen in the present work, that is, depending on type of system under study will be more feasible to measure the times and lengths, which are the elements necessary to elaborate the respective connected graph of the system. Likewise, the Dijkstra algorithm and the Fermat Principle are techniques that can complement in solving various current problems in the area of biophysics.
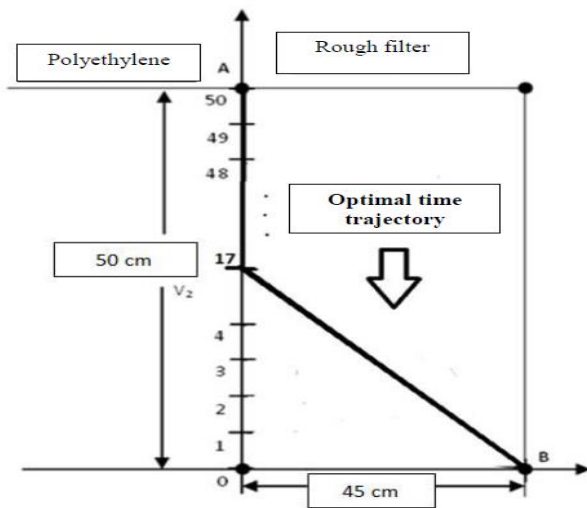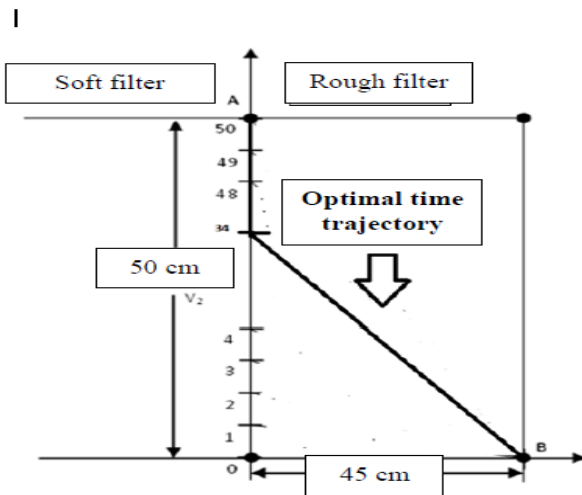
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