HiLL PUBLISHING

Journal of Applied Mathematics and Computation, 2023, 7(2), 317-323
https://www.hillpublisher.com/journals/JAMC/
ISSN Online: 2576-0653
ISSN Print: 2576-0645

Numerical Algorithm for Transportation Network

Jeffrey Liang

Shanghai Jiao Tong university (SJTU), Shanghai, China.

How to cite this paper: Jeffrey Liang. (2023) Numerical Algorithm for Transportation Network. *Journal of Applied Mathematics and Computation*, 7(2), 317-323.
DOI: 10.26855/jamc.2023.06.014

Received: June 3, 2023
Accepted: June 29, 2023
Published: July 30, 2023

***Corresponding author:** Jeffrey Liang, Shanghai Jiao Tong university (SJTU), Shanghai, China.

Abstract

We use the principle of minimum energy to get the differential equation we need. Construct a new algorithm with negative gradient flow to get the final result. Finally, through the method of cross-validation, we can compare the efficiency and complexity of each algorithm. For a long time, we have wondered whether the wings of drones could maintain strength while having little mass. Now we have found a possible solution. If we make the structure of an airplane wing like a dragonfly's wing, we can make the wing strong enough while keeping it light. Because the skeleton of the dragonfly's wings is very supervised, but the membrane is very light and thin, which allows the dragonfly to easily control its posture during flight. The global optimal solution and local optimal solution of optimization problems sometimes make us very contradictory. In order to find the global optimal solution, we have to consume too much time. But if we only spend a short time finding the local optimal solution, we cannot know what the global optimal solution looks like. In our article, we use the method of negative gradient flow, which will help us save time while being able to find the optimal solution.

Keywords

Algorithm, optimization, best structure

1. Introduction

Nowadays, more and more unmanned aerial vehicles are used in the logistics industry. Yet only large drones like the Global Hawk, are capable of carrying lots of heavy packages which common small-sized delivery drones can't. However, large drones need to be charged very often making them inefficient in practical use. We hope to solve these issues by reducing the weight of large drone wings by using an elastic transportation network based on energy optimization. This would help extend the work time of these drones and allow for maximum transportation amount. We first figured out the total elastic potential energy of the wings and the gravity potential energy. Then we minimized the total energy to find the best geometric value (radius of each pipeline within the wings). Next, simulated on MATLAB, wings were built according to the pipeline wing radius and the total energy result was updated continuously to constantly minimize the energy with a more ideal pipeline radius. We expect a final pipeline elastic structure similar to that of a dragonfly's wing with minimum total energy that will significantly help reduce the weight of large drone wings.

This project will help design significantly lighter wings of drones based on elastic transportation networks mainly through MATLAB simulations. Normal delivery drones can then be expanded in size and utilize these newly designed wings to transport more products while flying for long periods without constant recharging.

2. Model establishment

If the physarum polycephalum is placed in an environment with food surrounding it, it will "build" a network of biological pipelines to the food and obtain food through these pipelines to survive. The main purpose of our model is to explain the biological mechanism of how the slime mold constructs a biological pipeline network through a mathe-

matical model, which is an important method for studying natural phenomena [1].

For my model, I set the environment where the physarum polycephalum is located as a regular hexagon. The slime mold is initially located at the lower left corner of the regular hexagon, which is marked as point A. The food source is randomly distributed in the regular hexagon. In order to simplify the model, the regular hexagon is "discretized:" each side of the regular hexagon is divided into N equal parts, so that there are N+1 nodes on each side. Then for each node, connect it to the matching nodes on the sides adjacent to the node's opposite side (both left and right), so that the entire regular hexagon is divided into a network structure by three types of parallel lines (left to right diagonal, right to left diagonal, and horizontal) as the following graph shows(fig 1):

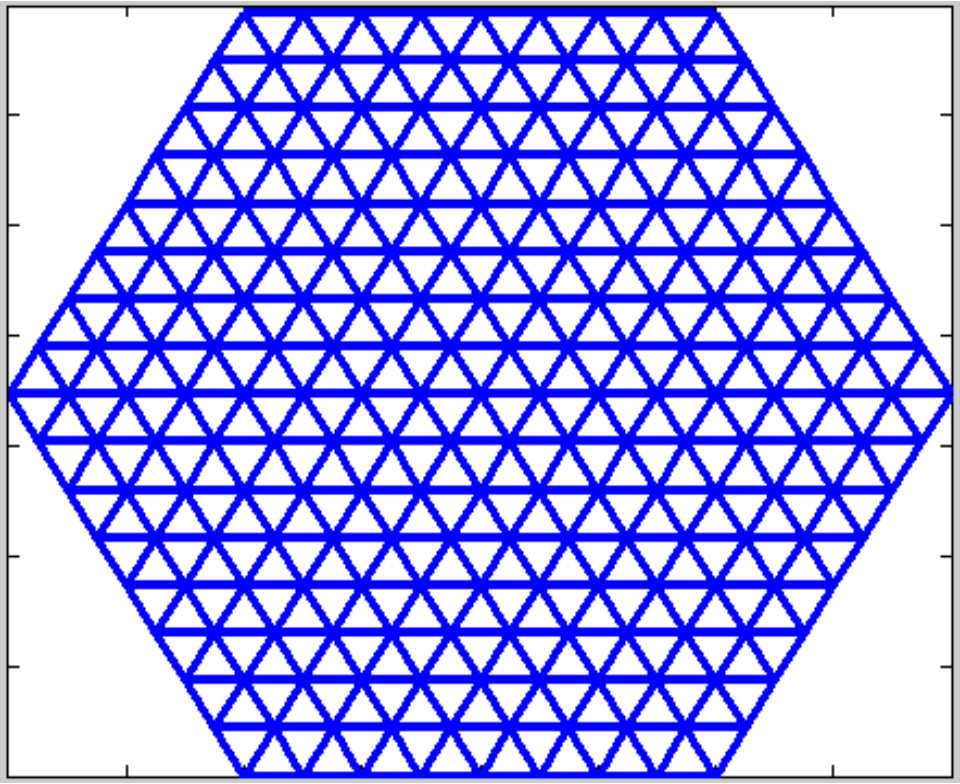

Fig. 1. The initial structure of the network.

The regular hexagon has N+1 nodes on each side and a total of $3N^2$ +3N+1 nodes. Assuming that the slime mold is initially in the lower left corner, that point in the lower left corner becomes the **source** of the network and the biological pipeline extends outward **from** that point. If there is a food source on a grid point, it is called a **sink** because the biological pipeline extends from the source **to** this point.

We number the nodes of this network from bottom to top, from left to right, from 1 to $3N^2$ +3N+1. As mentioned in the abstract of the paper, we compare the network to a circuit, and use C_{ij} to represent the conductance between node i and node j. Q_{ij} represents the flow between node i and node j, and p_i represents the pressure at node i. There is a flow between each node and its adjacent nodes. We call the algebraic value of the total outflow away from the node minus the total inflow to this node as the total flow of the node, denoted by Q_i. We stipulate that at each source, the total flow is a positive definite value; at each sink, the total flow is a negative definite value; at a node that is neither a source nor a sink, the total flow is 0. This is consistent with the definition of sink and source, the following are the equations.

$$Q_k = \sum_i Q_{ik} = \begin{cases} m & k \text{ is the source} \\ -1 & k \text{ is the sink.} \\ 0 & else \end{cases}$$

m is the number of sinks in the network. Since there is only one source in our model (node 1), the aforementioned statement ensures that the total flow in the system is 0: $\sum Q_i=0$.. The syntax (i,k) means that in our equations described above, nodes i and k are directly connected.

In the context of a circuit, we can assume that $Q_{ij} = C_{ij}(p_i - p_j)$, which also happens to be true for the model in our

paper. However, we do not take this as an obvious conclusion and will derive this formula in the following text.

The problem that the model focuses on is the amount of total energy that is consumed by the operation and construction of the network. This energy is the sum of two components. The first energy is consumed by friction in the pipeline, which is similar to a circuit's resistance, and is called "electric power": $\sum_{(i,j)} \frac{{Q_{ij}}^2}{C_{ij}}$. The sigma notation means to sum all connected nodes. This energy represents the energy consumed for the operation of the entire network. The second energy is the energy consumed to build a pipeline. The value of this energy is $C_{ij}{}^{\gamma}$ in our context and $\gamma = 0.5$, which we will prove in the following text.

We do not limit the total energy for constructing these pipelines but include it in the total energy instead to get our unconstrained model, which must be minimized.

Minimize $f = \sum_{(i,j)} \frac{{Q_{ij}}^2}{C_{ij}} + \lambda \sum_{(i,j)} {C_{ij}}^{\gamma}$

$$Q_k = \sum_i Q_{ik} = \begin{cases} m & k \text{ is the source} \\ -1 & k \text{ is the sink.} \\ 0 & else \end{cases}$$

λ is a unit of energy to construct the network of a known value. The value of λ does not affect the structure of the terminal network [2].

We need to give an initial state of the slime mold biological pipeline. The most direct idea is that initially the slime mold starts from "nothing" and builds the pipeline from just one point, the source. But our subsequent research methods found that if the the initial value of C_{ij} is 0 in our model, the network never forms since our unconstrained model is already minimized when C_{ij} remains at 0. No energy is consumed because no pipelines exist. Therefore, setting the initial value like this has no meaning. Secondly, the initial values for C_{ij} does not affect the overall structural shape of the formed network and only affects the specific sizes of pipelines, such as the radius. For these two reasons, we take the initial value as the case where all C_{ij} between connected points in Figure 2 are equal. Let them all equal 1.

3. Determination of γ value

In the model established above, we mentioned that the value of γ is 0.5, which is derived in the following.

Assume that the pipe between any two nodes is cylindrical with length L and its cross section is a circle with radius R.

Use f to denote the shear force at the tube wall. The flow of the liquid in the tube can be regarded as laminar flow, that is, all liquid at the same distance r from the center axis of the tube have the same flow velocity V_r.

Set the viscosity coefficient between the liquid and the tube wall as μ and we get the following equation:

$$f = \mu \frac{\partial V_r}{\partial r} | r = R \cdot 2\pi R$$

Remember that the length of the pipe is L and the pressure difference between the two ends of the pipe is $\triangle p$. The liquid travels at a constant velocity under these two forces, so by balancing the pressure difference and shear force we get:

$$\pi R^2 \Delta p = \int_0^L f \, d\, x$$

$\Delta p = \frac{-4\mu L}{\pi R^4} Q$ * we consider $\frac{\Delta p}{Q}$ as the resistance $\left(\frac{1}{C_{ij}}\right)$ of the pipeline

Thus, resistance is proportional to $R^{-4,}$ and conductance (inverse of resistance) is proportional to R^4. The energy consumed to build a pipe is proportional to its volume, so, energy$\sim \pi R^2 L \sim R^2 \sim C^{\gamma}$ when $\gamma = 0.5$, since conductance is proportional to R^4.

4. Kirchhoff's law: $Q_{ij} = C_{ij}(p_i - p_j)$

The establishment of this formula mentioned above is called Kirchhoff's law in a circuit. In order to establish it in the biological network, here is the proof.

We assume that all C_{ij} has been determined at any given moment. Then, we need to find the Q_{ij} to minimize the total energy function denoted *f*. The following are our conditions:

$$Q_k = \sum_i Q_{ik} = \begin{cases} m & k\ is\ the\ source \\ -1 & k\ is\ the\ sink. \\ 0 & else \end{cases}$$

For the convenience of expression, the set composed of sources is denoted as S1, the set composed of sinks is referred to as S2, and the set composed of neither a source nor a sink is S3. By the Lagrange method of seeking conditional extremum, let the function F be:

$$F(Q_{ij}) = f + \sum_{k\in S_1} \lambda_k Q_k + \sum_{k\in S_2} \lambda_k Q_k + \sum_{k\in S_3} \lambda_k Q_k$$
$$= f + \sum_{k\in S_1} \lambda_k \sum_i Q_{ki} + \sum_{k\in S_2} \lambda_k \sum_i Q_{ki} + \sum_{k\in S_3} \lambda_k \sum_i Q_{ki}$$

*where *i* and *k* are connected nodes

$$\frac{\partial F}{\partial Q_{ij}} = 0$$

When taking the partial derivative with respect to Q_{ij}, expanding sigma notation gives us only two terms that include Q_{ij} ($Q_{ij} = -Q_{ji}$) and the rest are all constants. We get: $\frac{2Q_{ij}}{C_{ij}} + \lambda_i - \lambda_j = 0, \forall(i,j)$

We manipulate the equation algebraically so that Q_{ij} is isolated on one side, and then substitute our conditions for Q_{ij} to get:

$$\sum_{(k,i)} -\frac{1}{2} C_{ki}(\lambda_k - \lambda_i) = \begin{cases} m & k\ is\ the\ source \\ -1 & k\ is\ the\ \text{sink} \\ 0 & else \end{cases}$$

*for a given k

We can solve the system of linear equations for λ_i; however, we solve the following system for p_i for convenience.

$$p_i = -\frac{1}{2}\lambda_i$$

Thus, we have $Q_{ij} = C_{ij}(p_i - p_j)$

$$\sum_{(k,i)} C_{ki}(p_k - p_i) = \begin{cases} m & k\ is\ the\ source \\ -1 & k\ is\ the\ \text{sink} \\ 0 & else \end{cases}$$

5. Principles, ideas, and methods

The equations mentioned above are solvable, where p_i is an unknown number and C_{ki} is a known coefficient. One of the main conclusions of this section is that although the equation has more than one solution, p_i-p_j is unique.

$$\sum_{(k,i)} C_{ki}(p_k - p_i) = \begin{cases} m & k\ is\ the\ source \\ -1 & k\ is\ the\ \text{sink} \\ 0 & else \end{cases}$$

It is not difficult to write the equations in the form of a matrix vector in the form of *A*P=I*, where *A* is a $(3N^2+3N+1)\times(3N^2+3N+1)$ matrix and

$$a_{kk} = \sum_i C_{ki}, a_{kl} = -C_{kl}(k \neq l)$$

P is a column vector with dimensions $(3N^2+3N+1)\times1$, and the element of the i-th row is p_i.

I is a column vector with dimensions $(3N^2+3N+1)\times1$, where element b_i equals 1 if node *i* is a source, equals -1 if *i* is a sink, and equals 0 if *i* is neither.

The following points can be seen from the element composition of A:

(1) A is a symmetric matrix, because $C_{ij} = C_{ji}$;

(2) The sum of all elements in each row of A is 0, so A is a singular matrix;

(3) A is a sparse matrix. In the k-th row, the only non-zero elements in this row are a_{ki} (k and i are connected nodes), which are negative values. The diagonal element a_{kk} is the absolute value of the sum of all negative values in the k-th row.

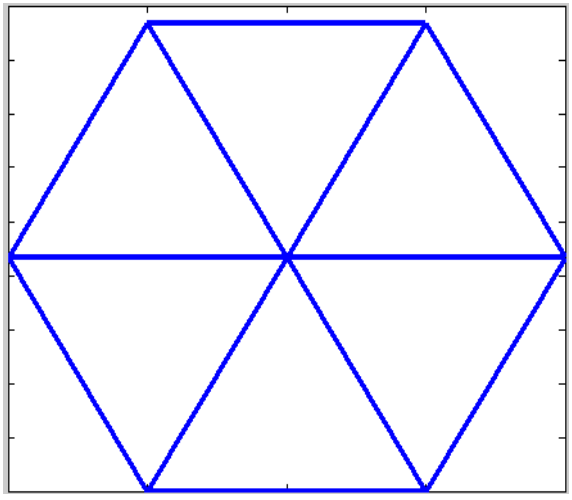

Fig. 2. Simple unit in the network.

We give the simplest network (fig 2) and matrix A when each side has only one node in order to grasp the form of the matrix, as shown in the figure below:

$$\begin{pmatrix} C_{12}+C_{13}+C_{14} & -C_{12} & -C_{13} & -C_{14} & 0 & 0 & 0 \\ -C_{21} & C_{21}+C_{24}+C_{25} & 0 & -C_{24} & -C_{25} & 0 & 0 \\ -C_{31} & 0 & C_{31}+C_{34}+C_{36} & -C_{34} & 0 & -C_{36} & 0 \\ -C_{41} & -C_{42} & -C_{43} & C_{41}+C_{42}+C_{43}+C_{45}+C_{46}+C_{47} & -C_{45} & -C_{46} & -C_{47} \\ 0 & -C_{52} & 0 & -C_{54} & C_{52}+C_{54}+C_{57} & 0 & -C_{57} \\ 0 & 0 & -C_{63} & -C_{64} & 0 & C_{63}+C_{64}+C_{67} & -C_{67} \\ 0 & 0 & 0 & -C_{74} & -C_{75} & -C_{76} & C_{74}+C_{75}+C_{76} \end{pmatrix}$$

Because A is a singular matrix, the original equation either has no solution or the solution has at least 1 degree of freedom [3].

We can prove that A is a positive semi-definite matrix by linear algebra [4].

We know that r(A) = $3N^2+3N$ (number of rows – 1) [5]. According to the conclusion of linear algebra, p_i - p_j can be determined by the system of linear equations after determining one variable [6, 7].

6. Numerical Simulation

As Q_{ij} has been determined by the system, we can rewrite the energy function [8, 9].

Minimize $f = \sum_{(i,j)} \frac{Q_{ij}(C_{ij})^2}{C_{ij}} + \lambda \sum_{(i,j)} C_{ij}^{\gamma}$

$$\begin{aligned} \frac{\partial F_\lambda(C_{ij})}{\partial C_{ij}} &= -\frac{Q_{ij}(C_{ij})^2}{C_{ij}^2} + \sum_{(i,j)} \frac{2Q_{ij}(C_{ij})}{C_{ij}} \frac{\partial Q_{ij}}{\partial C_{ij}} + \lambda\gamma C_{ij}^{\gamma-1} \\ &= -(p_i - p_j)^2 + 2\sum_{(i,j)} (p_i - p_j) \frac{\partial Q_{ij}}{\partial C_{ij}} + \lambda\gamma C_{ij}^{\gamma-1} \\ &= -(p_i - p_j)^2 + \lambda\gamma C_{ij}^{\gamma-1} + 2\sum_i \sum_j p_i \frac{\partial Q_{ij}}{\partial C_{ij}} - 2\sum_i \sum_j p_j \frac{\partial Q_{ij}}{\partial C_{ij}} \\ &= -(p_i - p_j)^2 + \lambda\gamma C_{ij}^{\gamma-1} + 2\sum_i \sum_j p_i \frac{\partial Q_{ij}}{\partial C_{ij}} - 2\sum_i \sum_j p_i \frac{\partial Q_{ji}}{\partial C_{ji}} \\ &= -(p_i - p_j)^2 + \lambda\gamma C_{ij}^{\gamma-1} + 4\sum_i p_i \sum_j \frac{\partial Q_{ij}}{\partial C_{ij}} \end{aligned}$$

For all of the nodes i,$\sum_j Q_{ij}$is a constant, so $\sum_j \frac{\partial Q_{ij}}{\partial C_{ij}} = 0$. Thus, $\frac{\partial F_\lambda(C_{ij})}{\partial C_{ij}} = -(p_i - p_j)^2 + \lambda\gamma {C_{ij}}^{\gamma-1}$. In order to optimize the total energy function with respect to time, we set $\frac{dC_{ij}}{dt} = d_{ij} = \left(-(p_i - p_j)^2 + \lambda\gamma C_{ij}^{\gamma-1}\right)$

so that $\frac{dF}{dt} = \frac{\partial F}{\partial C_{ij}} \cdot \frac{dC_{ij}}{dt} = -\left(\frac{\partial F}{\partial C_{ij}}\right)^2 < 0$

We then use the Runge-Kutta method [10, 11] to minimize C_{ij}.

$$
\begin{aligned}
{d_1}^{(n)} &= h({C_{ij}}^{(n)}),\\
{d_2}^{(n)} &= h({C_{ij}}^{(n)} + 0.5u{d_1})\\
{d_3}^{(n)} &= h({C_{ij}}^{(n)} + 0.5u{d_2})\\
{d_4}^{(n)} &= h({C_{ij}}^{(n)} + u{d_3})\\
{C_{ij}}^{(n+1)} &= {C_{ij}}^{(n)} + \frac{1}{6}u({d_1}^{(n)} + 2{d_2}^{(n)} + 2{d_3}^{(n)} + {d_4}^{(n)})
\end{aligned}
$$

Thus, we have the terminal network.

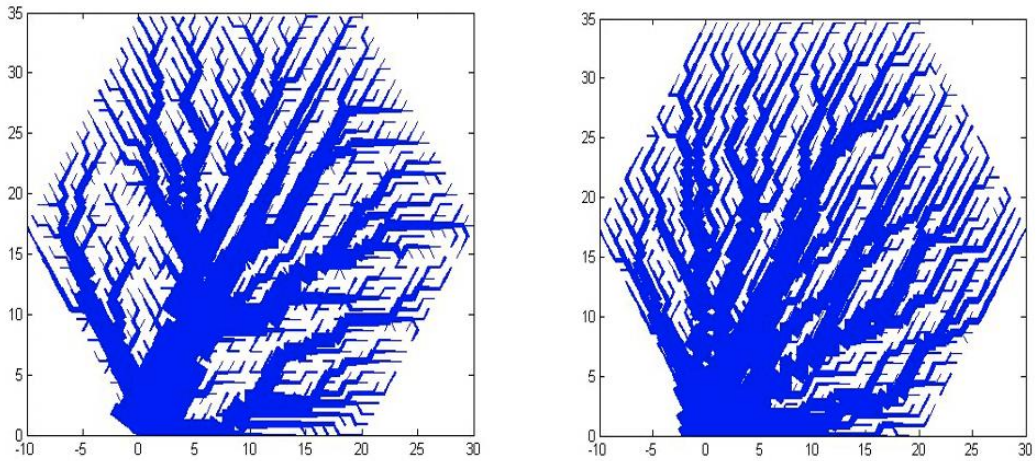

Fig. 3. The result of the network.

The figures above are depictions of the terminal network, where the source node is located at (0,0) in the grid. The right is the same network but given more time to develop and optimize than the left. In this paper, the method we used to search for the minimum energy point is called the negative gradient flow method [12]. Although this method takes longer to reach the terminal network, the network reaches a more minimized total energy consumption compared to other methods. The principle of natural selection tells us that in the process of evolution, organisms always tend to retain mechanisms that are more adapted to their environment. Thus, the advantage of lower energy consumption makes it more likely that slime molds follow the negative gradient flow method instead of other methods when constructing biological networks [11].

References

[1] Eleni Katifori, Gergely J. Szollosi and Marcelo O. Magnasco, “Damage and Fluctuations Induce Loops in Optimal Transport Networks”. Supplementary material, PRL 104, 048704.

[2] Steffen Bohn and Marcelo O. Magnasco. Structure, Scaling, and Phase Transition in the Optimal Transport Network, PRL 98, 088702.

[3] Gilbert Strang, Introduction to Linear Algebra Fifth Edition.

[4] AP physics for engineers and scientists. Sawyer.

[5] introduction to algorithms Clifford Stein.

[6] Partial differential equation. Asmar.

[7] Abualigah, L., Diabat, A. A comprehensive survey of the Grasshopper optimization algorithm: results, variants, and applications. *Neural Comput & Applic* 32, 15533–15556 (2020).

[8] Shehab, M., Abualigah, L., Al Hamad, H. *et al.* Moth–flame optimization algorithm: variants and applications. *Neural Comput & Applic* 32, 9859–9884 (2020).

[9] Abdel-mawgoud H, Kamel S, Ebeed M, Youssef AR. (2017). Optimal allocation of renewable dg sources in distribution networks considering load growth. In: 2017 nineteenth international middle east power systems conference (MEPCON). IEEE, pp 1236–1241.

[10] Abdelmadjid C, Mohamed SA, Boussad B. (2013). Cfd analysis of the volute geometry effect on the turbulent air flow through the turbocharger compressor. Energy Procedia 36:746–755.

[11] Abualigah LM, Khader AT, Hanandeh ES, Gandomi AH. (2017). A novel hybridization strategy for krill herd algorithm applied to clustering techniques. Appl Soft Comput 60:423–435.