Optimal Channel Networks in Biology and Hydrology

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Abstract

A review on phase transitions in Optimal Channel Networks is presented. We then see how the theory of OCNs applies to biology by finding scaling relations between the metabolic rate and mass of living organisms. Finally, a similar scaling law is obtained for river morphology by drawing an analogy between variables used in the study of living organisms and varibles used in hydrology. Collapsed data for four different rivers is presented to support the validity of the scaling relationship found.

1 Introduction

We first go through some definitions used in theory of networks [1]. A network is a set of nodes that are connected by links as the two examples shown in Figure 1, where the nodes are represented by black dots and the links by black lines. In general there are different types of networks which depend on the atributes to both the nodes and links. The nodes can have different weights and the links can have different weights and preferred directions. Combinations of different kinds of nodes and links result in different kinds of networks. In this report we will deal with networks in which all nodes have the same weight and all the links have the same weight and no preferred directionality.

The conectivity k_s of a node s is the number of links connected to a node. For example, node s for the network in Figure 1(left) has a connectivity $k_s = 3$ since it has 3 links (links $\overline{st}$, $\overline{su}$ and $\overline{st}$) connected to it, whereas node s in the network on the right has a connectivity $k_s = 2$ since it is connected by 2 links (links $\overline{st}$ and $\overline{st}$). We will now define the clustering coefficient C or transitivity. The clustering coefficient is best understood by an example. If a node s is connected to a node t and the node t is connected to a node u, then the clustering coefficient C will be equal to one if node s is connected to node u. However, if s is connected to t, t is conncected to u and s and u are not connected, then the clustering coefficient C would be equal to zero. In general, the clustering coefficient C for the whole network is given indistinctly by equations 1 and 3.

$$C = \frac{3 \text{ x number of triangles in network}}{\text{number of connected triples of nodes}} \tag{1}$$

We can also define the clustering coefficient for the node s as:

$$C = \frac{3 \text{ x number of triangles connected to node } s}{\text{number of connected triples on node } s} \tag{2}$$

The clustering coefficient for a network of size N (N being the number of nodes) is the given by:

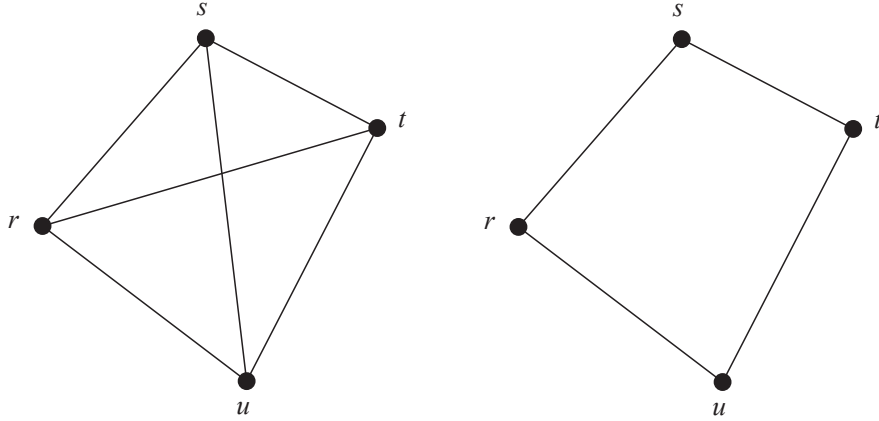$$C = \frac{1}{N} \sum_i C_i \tag{3}$$

Figure 1: Two networks with the same distribution of nodes but different link topology. The clustering coefficient for the network on the left is $C = 1$ as obtained from equation 1. Network left has four triangles ($\overline{rst}, \overline{rut}, \overline{stu}$ and $\overline{rsu}$) and each node has three connected triples (e.g. the three connected triples in node s are given by vertices $r\hat{s}t, r\hat{s}u$ and $u\hat{s}t$), which gives a clustering coefficient $C = 1$. A similar analysis can be performed for the network on the right which gives $C = 0$ since there are no triangles.

The distance between two nodes (node i and node j) is traditionally given by the shortest path between these two nodes which accounts only for path length. For the optimal channel networks (OCNs) [2] the distance between two nodes will account not only for path length but also for traffic which will be represented by the connectivity. The distance between nodes i and j is defined as the path W that minimizes the sum of the connectivities k_w of all the w nodes such that $w \in W$.

$$d_{ij}(\alpha) = \min_W \sum_{w \ \in \ W: \ i \to j} k_w^\alpha \tag{4}$$

Including the connectivity k indicates the importance given to traffic. The exponent α reflects how much importance is actually given to traffic. Setting $\alpha < 1$ means that path length is more important than traffic whereas $\alpha > 1$ reflects the opposite. Note that $\alpha = 0$ implies that traffic does not play a role and we recover the traditional definition of distance between two nodes in a network.

2 Optimal Channel Networks

Let us consider N nodes distributed through a D-dimensional domain that we want to connect with ℓ links. The variable $r = \ell/N$ represents the ratio of number of links to number of nodes. The objective is to find the link configuration that minimizes the overall distance between the nodes while avoiding traffic. The distance and traffic are quantified by the cost function $H(\alpha)$ [2].

$$H_\alpha = \sum_{i<j} d_{ij}(\alpha) \tag{5}$$

The cost function H_α is given by $d_{ij}(\alpha)$ as defined in equation 4. Note that the exponent α defines whether H_α is concave up ($\alpha > 1$) or concave down ($\alpha < 1$).

We want to analyze the main features of the optimal topology as different variables are changed: N, r and α. The protocol to find the optimal configuration is as follows. The exponent α, the number of links ℓ and the number of nodes N are fixed. The system starts with a random configuration of the nodes and links. Then distribution of the nodes is fixed and the configuration of the links changed in order to minimize the H_α. This process is repeated until H_α has been minimized, which is the configuration of the OCN.

As α, N and r are changed, the resulting optimal topologies are quantified in two different ways. The first one is by using the degree distribution $P(k)$ (the fractions of nodes with connectivity k) for the resulting OCNs. The second is by plotting the mean clustering coefficient C_{opt} for different OCNs as a function of the ratio r. The mean clustering coefficient of the OCNs is normalized by the mean clustering C_{rand} of the random configuration.

When analyzing $P(k)$, we can divide the OCNs in two cases which depend on r being close to one or greater than one. First, the behavior for $r \sim 1$ is described. As seen in Figure 2(left), for $\alpha = 0.7$ and $r = 1.05$, the resulting OCNs for different N seem to be scale-invariant in $P(k)$. This scale invariance holds well for $r \sim 1$ and $\alpha < 1$, yet, as α increases, r has to be closer and closer to one to be able to obtain this scale invariance. For $\alpha > 1$, the scale invariance no longer seems to hold. An example of the behavior of $P(k)$ for $r > 1$ is seen in Figure 2(right) for $\alpha = 0.7$ and r equal to 1.05, 1.20 and 2.00. The scale invariant behavior no longer holds as a peak is formed around the average value of the connectivity k. The latter means that there are more nodes with the same connectivity.

We now move the mean clustering coefficient C_{opt} as a function of r. There are two different behaviors specified by $\alpha > 1$ and for $\alpha < 1$. In both cases, as seen in Figure 3, we can see a clear phase transition. For $\alpha > 1$, as r increases, the clustering coefficient C goes from a zero value to a nonzero value. An example is given in Figure 3(left) for $\alpha = 2$ with

a critical value for $r_c \approx 2$. Systems with $\alpha < 1$ display a the opposite behavior as seen in the example for $\alpha = 0.35$ in Figure 3(right). In this case, the clustering coefficient C goes from a nonzero value to a zero value with $r_c \approx 1.2$. The two very different phase transitions for $\alpha > 1$ and $\alpha < 1$ can be explained by analyzing the exponent α in the definition of distance in a network (equation 4). When $\alpha > 1$, the connectivity k contributes more to the weighted distance d_{ij} than the path length. This means that the optimization process will rather reduce the connectivity of the nodes (i.e. minimize traffic) than reduce the path length. The opposite happens when $\alpha < 1$, which means that the system will try to minimize path length rather than connectivity (traffic).
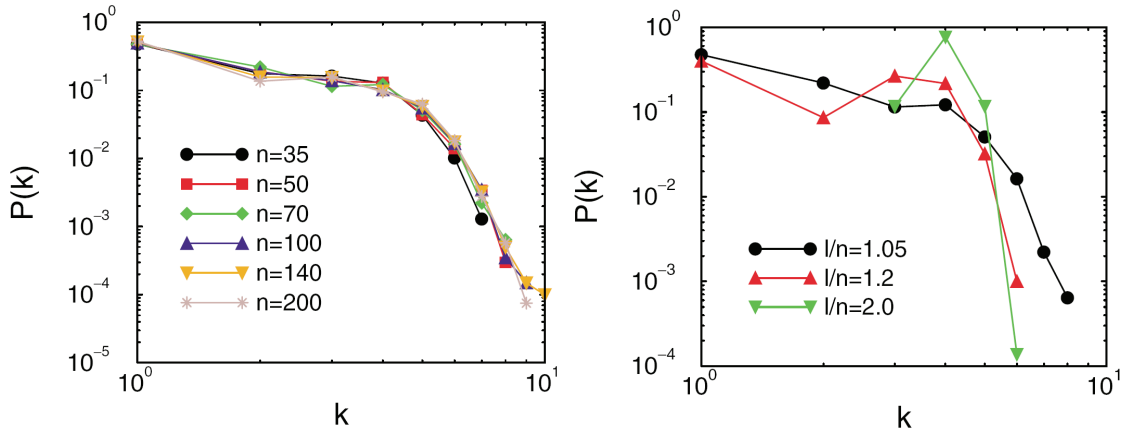

Figure 2: Plots of degree distribution P(k) averaged over two hundred realizations [2]. The figure on the left shows the results for systems of different size but same exponent $\alpha = 0.7$ and ratio $r = 1.05$. The figure on the right is for one system of size $N = 70$ with $\alpha = 0.7$ and different values of r.

3 Optimal Channel Networks and Biology

OCNs can be used to study living organisms [3]. Suppose we have a D-dimensional living organism of mass M and characteristic linear dimension L. This living organism will need a given quantity of nutrients per unit time delivered to each part of its body. Each part of the the body that needs nutrients is represented by a node, all of which are uniformly distributed through the volume L^D. The total number of nodes N scales as the volume L^D. The amount of nutrients delivered to all sites per unit time is represented by the metabolic rate B. Assuming that all sites need a similar amount of nutrients we can infer that B scales as L^D since the nodes are uniformly distributed. These nutrients B need to be transported by an agent (e.g. blood) which we will label as C. The total amount of blood is obtained by adding at any given instant of time the amount of blood on each link (artery) throughout the whole organism. The question is how C is determined and also how C scales with L.
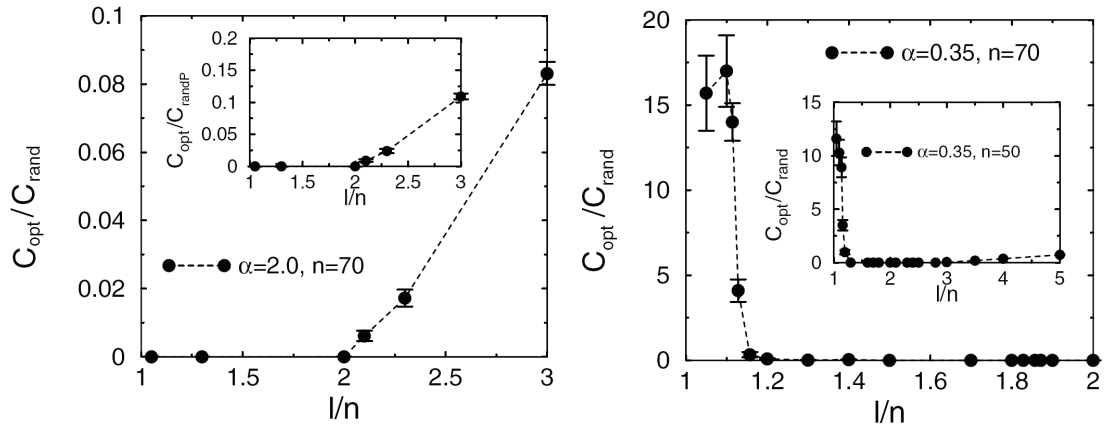
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Figure 3: Phase transitions in optimal channel networks [2]. The figure on the left shows a phase transition in the mean clustering coefficient C_{opt} as a function of r for $\alpha = 2$ while the figure on the right shows the phase transition in C_{opt} also as a function of r. The different behavior is a direct consequence of the effect that the exponent α has on the cost function that needs to be minimized.
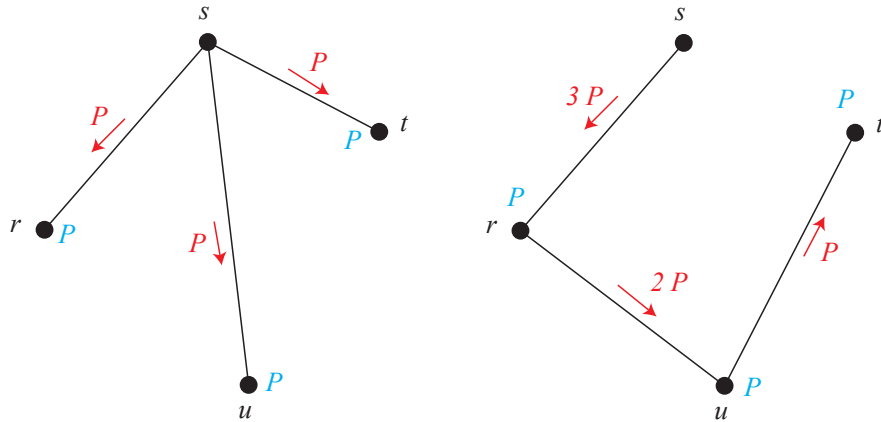

Figure 4: Two networks with the same node distribution but different link configurations. Eventhough the metabolic rate is the same for both of them, the amount of blood needed in each case is different.

OCN for living organisms are those in which the amount of blood C is minimized [3]. In order to answer how C scales with M we use Figure 4, which shows two networks with the same distribution of nodes but different link configuration. In each of the networks the node s represents the heart and the nodes r, u and t represent the parts of the body that need to be fed with nutrients. Let us assume that all the nodes need the same amount of nutrients per unit time. For example, if we say that the each of the nodes need P grams of nutrients every minute, then the metabolic rate B is defined as the total amount of nutrients consumed by the body per unit time. In our example, $B = 3 P \frac{\text{grams}}{\text{minute}}$ for both cases depicted in Figure 4. Eventhough the metabolic rate is the same for both networks, the amount of blood C needed to transport the nutrients is different for both cases. The network on the left needs, at every instant of time, to be carrying $3 P$ nutrients in the link $\overline{rs}$ to feed node r with P nutrients and then leave $2 P$ nutrients to feed nodes u and t. Under this rationale the amount of blood C needed by the network on the left ($C = P + P + P = 3 P$) is lower than the amount of blood needed by the network on the right ($C = 3 P + 2 P + P = 6 P$). Therefore, in the examples in Figure 4, the network on the left is more efficient than the network on the right.

In order to get the scaling for C we will state that C scales with L^D but we need an extra prefactor. This prefactor comes from the fact that the number hops needed for the nutrients to arrive to its destiny -as an average- scales at least with L and at most with L^D. We can then conclude that C scales at least with L^{D+1} and at most with L^{2D}. The most efficient network is that one for which we have the least amount of blood C which implies that $C \sim L^{D+1}$. Since $B \sim L^D$, we arrive to the conclusion that $C \sim B^{\frac{D+1}{D}}$ which tells us that the blood volume C increases faster than the metabolic rate B when the size of the system increases. As a final comment, some authors have found [3] that the amount of blood C scales with the mass M of the organism as $C \sim M$. The latter implies that the mass M scales with the charcteristic linear dimension as $M \sim L^{D+1}$ which is a pretty different way to relate mass and volume.

4   From Biology to Hydrology

We will go through some basic theory on river morphology before using OCNs to study hydrology [4] [5]. Rivers have a basin which can be divided in sub-basins. We can then describe the basin topology as a 2-D map where each node represents the region where tributaries are connected. For the case of rivers we define the term area -a- which is related to flux. The best way to understand the concept of area in river morphology is by imagining that a fixed amount of water is injected in every source. The flux at every node x is the area a_x. We can see that the area a_x of a point x is sum of the areas of all the points y which are upstream of x and are connected nearest neighbours of x. Adding the effect of rainfall R_x gives the equation for a_x.

$$a_x = \sum_{y \,\epsilon\, nn} a_y + R_x \tag{6}$$

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In an attempt to try to understand the analogy between biology and river morphology, we will first take a look at an equation that describes the evolution of rivers. Rivers can be described by studying the evolution of the elevation $z(\underline{x}, t)$ of the landscape points $\underline{x}$ at any time t.

$$\dot{z}\left(\underline{x}, t\right) = -\beta J\left(\underline{x}, t\right) \left|\vec{\nabla} z\left(\underline{x}, t\right)\right|^2 + \sigma \nabla^2 z\left(\underline{x}, t\right) + U \tag{7}$$

We first note that equation 7 does not depend explicitely on z so that it remains translationally-invariant. The first term represents erosion due to the flux $J\left(\underline{x}, t\right)$. The second term and third terms represent diffusion and tectonic uplifting respectively. It seems reasonable to think that diffusion may not play a major role in the evolution of z. This assumption leaves us with a simplified equation.

$$\dot{z}\left(\underline{x}, t\right) = -\beta J\left(\underline{x}, t\right) \left|\vec{\nabla} z\left(\underline{x}, t\right)\right|^2 + U \tag{8}$$

There is a cost function $E\left(s\right)$ that when minimized, describes the stationary solution for the river landscape.

$$E\left(s\right) = \sum_i J_i(s)^\gamma \tag{9}$$

Considering that both J and a represent flux, we can then set $J \propto a$ and obtain and describe the cost function as a function of the local areas a_i.

$$E \sim \sum_i a_i^\gamma \tag{10}$$

Now that we have the cost function that needs to be mnimized, we proceed to find a crude analogy between living organisms and river morphology. Every node x in the river can be compared to a node i in an organism. Each node in the organism needs an amount of nutrients proportional to the metabolic rate B (divided by the number of nodes) per unit time, which can be compared to the area a_x (flux) of the node x. For living organisms, the optimization consists on minimizing the amount of blood C that carries the nutrients to feed each node i. Similarly, we can see that the agents in charge of $feeding$ the area a_x are all the upstream nearest neighbors specified by $\sum_{y \, \epsilon \, nn} a_y$, which are related to the dissipation function E_s that is assumed rivers seek to minimize (see equation 10). We can now draw the correspondace $B \rightarrow a_x$ and $C \rightarrow \sum_{y \, \epsilon \, nn} a_y$. We have seen before that $C \sim B^\gamma$ where $\gamma = \frac{D+1}{D}$. Since we are working with a $2 - D$ case, then we expect $\gamma = 3/2$ which gives a scaling relationship for rivers.

$$\sum_{y \, \epsilon \, nn} a_y \sim a_x^\gamma \tag{11}$$

We can see in Figure 5 how well the scaling relationship holds for four different rivers. In this figure, each of the plots has been arbitrarily displaced vertically in order to see the
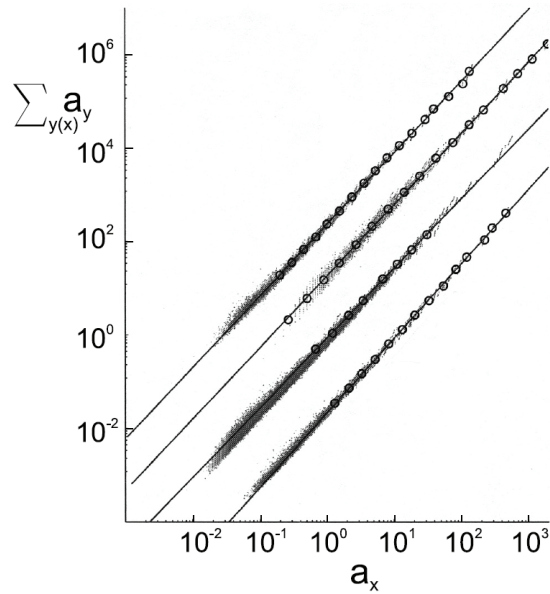
Figure 5: The power law relation in equation 11 is plotted for four different rivers. The data points have been shifted vertically in an arbitrary way to see the goodness of the fit for each case [5].
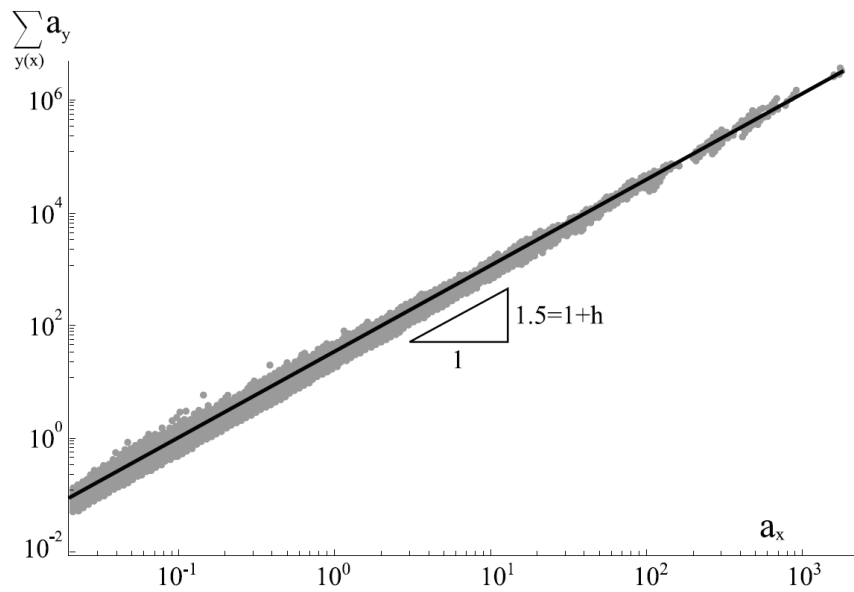

Figure 6: Ensemble average (data collapse) of the data [5] shown in Figure 5.

goodness of the fit. The ensemble average (data collapse) for all four rivers is shown in Figure 6.

5 Concluding Remarks

The theory of OCNs allows a very unique approach to study phenomena in biology and hydrology. In biology, there are different frameworks to obtain network topologies. There is work by West et. al. [6] specifically on plant vascular systems where the optimization process to obtain the final configuration is different from the one used by Banavar et. al. [3]. These two theories obtain power laws that relate important variables in living organisms (e.g. metabolic rate, number of leaves) with accuracy, however, the theory by Banavar et. al. is broader in the sense that it can be applied to any network irrespective of the entity studied (e.g. plant root systems, cardiovascular networks, rivers). It is a striking result that all these networks which are created by very different processes, can be studied with just one theory. Moreover, it helps connecting apparently disparate phenomena under the umbrella of criticality [7]. Regarding hydrology, the data collapse portrays a unique ansatz to study river morphology, which by means of a very simple model can describe phenomena in a very accurate way. River morphology has also been studied by Maritan et. al. [8] by obtaining critical exponents and using finite size scaling techniques on data for different sub-basins in one river.

Finally, the theory proposed by Banavar et. al. is a great achievement in the study of rivers. There is though a very old problem left in hydrology: river meanders, which occur in small slopes. There are several theories on why meanders occur and how they evolve [9] but the problem is not solved yet. It would interesting to see if criticality can help explaining this conundrum in hydrology.

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