

Darwinian Rivers: Evolving Stream Topographies to Match Hyporheic Residence Time Distributions

Forrest Stonedahl
Computer Science and Mathematics
Centre College
Danville, Kentucky, USA
forrest.stonedahl@centre.edu

Susa H. Stonedahl
Engineering and Physics
St. Ambrose University
Davenport, Iowa, USA
StonedahlSusaH@sau.edu

ABSTRACT

We employed genetic algorithms to investigate the relationship between stream topographies and their associated hyporheic residence time distributions. A hyporheic residence time is the time it takes a water particle to enter the sediments below a stream, travel through the sediment, and re-enter the surface water of the stream. This subsurface journey affects stream chemistry and water quality, and increased knowledge of this process could be helpful in addressing the environmental problems caused by excess nutrients and waterborne pollutants in riverine ecosystems. We used a multi-scale two-dimensional model, lightly adapted from three previous models, to calculate residence time distributions from system characteristics. Our primary goal is the investigation of the “RTD inverse problem” – discovering stream topographies that would generate a specified target residence time distribution (RTD). We used genetic algorithms to evolve the shape of stream topographies (represented by Fourier series) to discover shapes that yield RTDs that closely match the target RTD. Our contributions are: a) the specification of the RTD inverse problem, b) evidence that genetic algorithms provide an effective method for approaching this problem, and c) the discovery of some unanticipated patterns among the evolved topographies. This early work seems promising and should encourage further applications of evolutionary computing in this area, with eventual application to stream restoration projects.

Categories and Subject Descriptors

G.1.6 [Numerical Analysis]: Global Optimization; I.6.6 [Simulation and Modeling]: Simulation Output Analysis

General Terms

Algorithms, Experimentation

Keywords

hyporheic exchange, genetic algorithms, stream topographies, rivers, geophysics, environmental science, Fourier series

1. INTRODUCTION

In rivers and streams water flows into and out of the subsurface (sediments) surrounding the channel in a process called hyporheic exchange [2, 31]. Studying hyporheic exchange is important because in the subsurface solutes are transformed and deposited, changing the make-up of the stream’s chemistry and affecting water quality [15, 17, 11]. The longer water stays in the subsurface, the more time microbial communities have to consume and transform the nutrients [28]. Excess unabsorbed nutrients often cause severe consequences for downstream riverine and oceanic ecosystems; a notable example is the “dead zone” that forms in the Gulf of Mexico from the overdose of nitrates emitted by the Mississippi River [10]. Hyporheic flow is frequently characterized by the subsurface flux (the rate at which water enters the subsurface) and hyporheic residence time distributions (RTDs). A hyporheic residence time is the amount of time a water particle spends in the subsurface before reentering the surface water. Both the subsurface flux and the hyporheic residence time distributions can be approximated as a function of the shape of the stream topography and select sediment and surface water flow properties [7, 26, 32].

Given a model for calculating subsurface velocity fields, residence time distributions may be estimated by measuring how long simulated particles take to move through the subsurface, as shown in Figure 1. Several previous studies have focused on calculating flux and hyporheic residence time distributions from the stream topography [7, 26, 4], which we will refer to as the *RTD forward calculation problem*. This is an important and challenging problem, but scientific models have been developed that can provide reasonable estimates (as we will discuss further in Section 2 below). However, in this work we investigated the *RTD inverse problem*, which is the problem of discovering what stream topographies would produce a specified residence time distribution. This inverse problem has not been well-studied; in fact, to the best of our knowledge this work is the first to explicitly pose and explore this question. To be fair, the RTD forward calculation problem has more immediate real-world application than the inverse problem, since topographical characteristics are more readily measurable by field practitioners than hyporheic residence time distributions (which may require costly and involved “solute tracer” experiments to measure). Nevertheless, we believe that investigation of the inverse problem is important because it could lead to a better understanding of the complex mapping between topography and residence time distributions. Despite the existence of predictive mathematical models for the RTD

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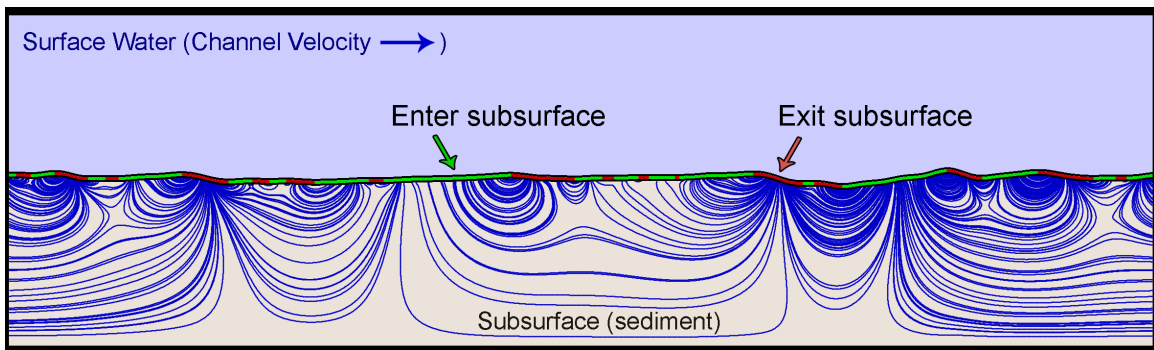


Figure 1: This figure shows the flume topography dataset used to generate the target RTD for our experiment, along with illustrative paths (dark blue) that particles take upon entering the subsurface (beige), based on the velocity field calculated by the forward model. The stream topography is shown in green (regions where water enters the subsurface) and red (regions where water leaves the subsurface). The surface water is shown (above) in light blue with the predominant channel velocity flowing from left to right.

forward calculation problem, this mapping is not well understood. The motivation for this work is not to find one specific topography for one specific empirical residence time distribution, but rather to discover patterns that could contribute to the scientific understanding of hyporheic exchange processes, which in turn would be beneficial for a number of real-world applications. The inverse RTD problem is particularly relevant to stream restoration projects, where one of the goals is to increase denitrification by extending the time that water spends in the hyporheic zone. Thus, we would like to know what features of the stream topography tend to yield desirable RTDs. An improved understanding of the mapping between topographies and RTDs could also lead to more accurate predictions of the impact of contaminant spills on riverine ecosystems.

The inverse problem would be trivial (and relatively uninteresting) if the mathematical models that have been developed for the RTD forward calculation problem were analytically invertible. However, because they are not, we employed genetic algorithms [12] (as well as uniform random search and a hill-climbing heuristic) to search through the space of possible topographies to find a set of topographies that closely matched a given residence time distribution (using a forward model to evaluate the goodness of fit compared with the target RTD.) Our work demonstrates that genetic algorithms are an effective and efficient technique, and that their use can reveal interesting patterns about the mapping between stream topography and hyporheic exchange.

2. RELATED WORK

A variety of models have been used to estimate hyporheic exchange. The transient storage model is able to characterize certain aspects of hyporheic exchange by fitting parameters to solute tracer data collected in field studies [11, 2, 16]. Computational fluid dynamics models can be used to calculate detailed flow fields, but only for systems of limited complexity or scale [4]. “Pumping models” are spatially explicit physically based models [7, 27, 3]. They treat the system as if water is being pumped into and through the surrounding sediments by gradients in pressure along the stream-sediment interface. Originally Elliott and Brooks [7] modeled hyporheic flow by approximating the pressure

distribution over small fluctuations in stream topography as a single two-dimensional sinusoidal curve. Wörman [32] extended this to three dimensions and allowed for a non-permeable bottom boundary to be incorporated into the velocity functions. Stonedahl et al. [26] further adapted the surface function equation to better account for the multiple scales and variations found in natural systems, but velocity calculations were done with numerical approximations rather than a closed form equation due to additional 3-D considerations. The velocity function used in this paper closely resembles that used in Stonedahl et al. [26], but since we are modeling a relatively simple system, we were able to use a closed form velocity equation by incorporating features of Elliott and Brooks [7] and Wörman et al. [32]. The closed form equation provides efficiency advantages that are crucial when searching a large parameter space.

Evolutionary algorithms have proven not only to be useful for a wide variety of challenging specific real-world problems, but more broadly we believe they will play an increasingly important role in contributing to how basic scientific research is performed. As a recent example, Schmidt and Lipson [24] applied genetic programming to automatically discover scientific laws from experimental data. Scientific research is full of hypotheses that require testing, and large combinatorial search spaces of possibilities. As such, genetic algorithms (or other evolutionary computation techniques) may assist researchers in understanding the complex adaptive systems that surround us [13].

There are several instances of prior work applying genetic algorithms in the general area of water resources research. For example, genetic algorithms have been used as a method to automatically calibrate a parameter intensive model of water quality to river and stream field data [18], and they have been used to optimize parameters controlling the performance of a hypothetical waste water treatment system in real time to reduce the pollution generated [19]. Genetic algorithms have also been used to optimize groundwater sampling rates and locations in order to quantify the trade-off between costs and accuracy [21, 22]. Fewer papers have combined evolutionary computing specifically with hyporheic exchange research, but there are examples, such as Rowinski et al. [23] who used genetic algorithms to fit five

solute breakthrough curves and quantify hyporheic exchange for a stream divided into five distinct reaches.

3. METHODS

3.1 Model

Due to the periodic nature of stream morphology, previous work has found Fourier series to be a useful method for decomposing the topographic features of stream channels [32, 26]. Furthermore, because *any function* can be represented by a Fourier series, this representation for stream topography provides considerable freedom in the scope of topographies under consideration. Thus, Fourier series coefficients provide a natural representation scheme for stream topographies, both in the RTD forward calculation model that we used, as well as for the “genes” in the chromosomal representation for our genetic algorithm (described in section 3.2.2).

We characterized a stream topography as a series of 30 sine curves. (30 curves was chosen as a sufficient number to represent multiple scales of stream bedforms, without excessive computational cost for calculations.) Each sine curve is defined by an amplitude (A_i), and a phase shift (B_i). Specifically, our topography function is of the form:

$$T(x) = Sx + \sum_{i=1}^{30} A_i \sin \left(2\pi \left(\frac{i}{\lambda} x - B_i \right) \right) \quad (1)$$

In Equation 1, S represents the slope of the system, x the downstream distance, A_i the i th Fourier coefficient, λ the largest wavelength, and B_i the shift for the i th Fourier term.

We calculated residence time distributions for a given topography by tracking 1000 simulated particles through the system. (Using more simulated particles provides a smoother and more consistent RTD at the cost of increased calculation time; some preliminary experimentation suggested that 1000 particles provided a reasonable balance.) The particles are initially placed on the surface-subsurface interface, with the probability of being placed at a given point x weighted according to the positive (inward) flux at that point. The flux, $q(x)$, is calculated based on the topography and velocity functions, as described by the following equation.

$$q(x) = \left(\frac{dT}{dx} u(x, 0) - v(x, 0) \right) \sqrt{1 + \left(\frac{dT}{dx} \right)^2} \quad (2)$$

In Equation 2, $q(x)$ represents the speed at which water enters the subsurface at longitudinal distance, x , weighted by the slope of the topographic surface at x . T refers to the topography function given in Equation 1. The subsurface velocity in the horizontal direction, u , and in the vertical direction, v , are defined in Equations 3 and 4 respectively (displayed at the top of the following page).

The value h_m that appears in these equations can be calculated using Equation 5 below (from [7]):

$$h_m = \begin{cases} 0.28 \frac{(U_c)^2}{2 * g} \left(\frac{H/d}{.34} \right)^{\frac{3}{2}} & \text{if } H/d \geq 0.34 \\ 0.28 \frac{(U_c)^2}{2 * g} \left(\frac{H/d}{.34} \right)^{\frac{3}{8}} & \text{if } H/d < 0.34 \end{cases} \quad (5)$$

U_c is the mean channel (surface water) velocity, d is the mean depth of the system, g is the gravitational constant,

and H represents an estimated height of the topography as defined in Equation 6 (from [26]),

$$H = 2\sqrt{2}\sigma = 2\sqrt{\sum_{i=1}^{30} A_i^2} \quad (6)$$

where σ is the standard deviation of T , and A_i the i th Fourier coefficient. Equations 3 and 4 are an adapted combination of three similar models [7, 26, 32]. After a particle is placed, its movement through the velocity field (given by $u(x, y)$ and $v(x, y)$) is simulated using a constant distance step of 0.1 cm (chosen small enough to reasonably approximate particle paths). Once a particle reenters the surface water its travel time becomes a data point in the hyporheic residence time distribution. One way to visualize these distributions is by plotting the complementary cumulative distribution function for the residence time distribution. We will refer to this function simply as the cumulative residence time distribution function (CRTDF), which is plotted as the fraction of particles with residence times greater than a given time versus that time. The CRTDF starts at 1 (all particles have a positive residence time) and decreases at each residence time until it reaches 0 at the time when the last particle returns to the surface water. A variation on this function is the *flux-weighted* CRTDF, which scales the regular CRTDF by the average flux for the system. This additional information (about the total amount of water flowing in and out of the subsurface) allows for a better characterization of the system. The flux-weighted distribution associated with the original topography was used as our target distribution for the genetic algorithm’s search.

The RTD forward model for hyporheic exchange that we have described above was implemented using NetLogo [30], which is a multi-agent modeling language.

3.2 Experiment

3.2.1 Calculating fitness

We started with a two-dimensional measured flume topography that was presented in a previous hyporheic modeling study [26]. Besides the topography, we used the system’s hydraulic conductivity, porosity, mean velocity, and slope value (shown in Table 1). We increased the bed depth and sediment depth parameters each to 30 cm, so that our randomly generated topographies would never go above or below these boundaries (which would be illogical and/or characterize a topography that is outside the domain of reasonable input for the forward RTD model we are using). We used a Fourier transform to decompose the flume topography into 30 sine curves each with their own phase shift and amplitude. Then we calculated the flux-weighted CRTDF for this topography using the model described in Section 3.1.

The fitness function for each individual (which represents a stream topography) was calculated as the sum of the square of the differences between the flux-weighted CRTDF associated with the generated topography and that of the target topography. This function is shown in Equation 7.

$$fitness = \int_0^{t_{max}} E(t)^2 dt \quad (7)$$

Above, t_{max} is the maximum time considered (1.081×10^6 seconds, the time required for the target CRTDF to reach zero), t is time, and $E(t)$ is the difference between the evolved

$$u(x, y) = \frac{K}{\theta} \left(\left(\frac{S}{1 + S^2} \right) + \sum_{i=1}^{30} \left(\frac{h_m}{H/2} A_i \frac{2\pi i}{\lambda} \sin \left(\frac{2\pi i}{\lambda} x + 2\pi B_i \right) \right) \left(\left(e^{\frac{2\pi}{\lambda} i y} \right) + \left(e^{\frac{2\pi}{\lambda} i (-2B_o - y)} \right) \right) \right) \quad (3)$$

$$v(x, y) = -\frac{K}{\theta} \left(\left(\frac{S^2}{1 + S^2} \right) + \sum_{i=1}^{30} \left(\frac{h_m}{H/2} A_i \cos \left(\frac{2\pi i}{\lambda} x + 2\pi B_i \right) \right) \frac{2\pi i}{\lambda} i \left(\left(e^{\frac{2\pi}{\lambda} i y} \right) - \left(e^{\frac{2\pi}{\lambda} i (-2B_o - y)} \right) \right) \right) \quad (4)$$

Parameter	Description	Value	Units
K	Hydraulic Conductivity	0.15	cm/s
θ	Porosity	0.33	–
U_c	Average Stream Velocity	16.7	cm/s
S	Slope	−0.00022	–

Table 1: Description/values of model parameters taken from the flume dataset [26] used for the target topography in our experiments.

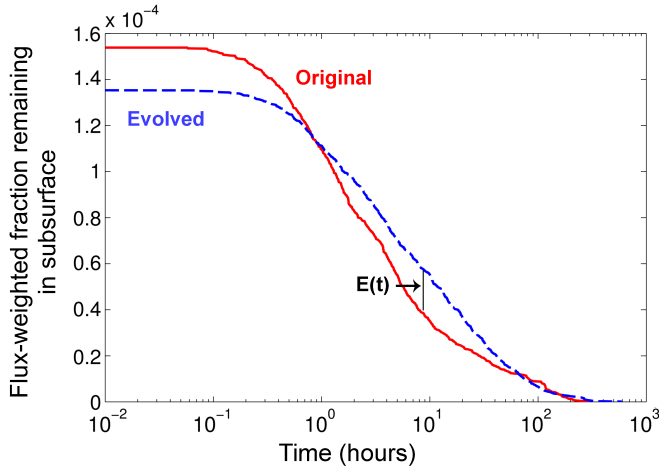


Figure 2: This figure shows two flux-weighted cumulative residence time distributions (CRTDFs). The original (target) CRTDF is shown in red. The blue dashed line shows the CRTDF for an evolved topography, whose fitness is calculated using the difference, $E(t)$, between the CRTDFs via Equation 7.

flux-weighted CRTDF and the original flux-weighted CRTDF at time t , as illustrated in Figure 2.

Since this is an *error* function, smaller values of the fitness function are desirable. Also, because our GA employed tournament-selection, only the rank-order of the individuals’ fitnesses mattered. As a result, optimizing the fitness function above is equivalent to minimizing the root mean-squared error (RMSE), or equivalent to minimizing the Euclidean distance (i.e. L^2 norm) between the vectors representing the target CRTDF and the individual’s CRTDF.

3.2.2 Chromosomal representation

For the RTD inverse problem, we must evolve stream topographies, which are represented by a set of Fourier coefficients. In our experiment, an individual (topography) is

made up of 60 real-coded¹ genes (an amplitude and a phase shift for each of the 30 wavelengths used in our Fourier representation of the surface). Despite schema-theory-based arguments for using binary (or other discrete small-alphabet) chromosomal encodings, real-coded genetic algorithms have proven quite effective for a variety of real-world problems, possibly due to their closer match with the problem representation [9]. For this experiment, the amplitude coefficient of each Fourier term is limited to range between 0.0 and 1.0 cm, and the phase shifts (measured as a fraction of their associated wavelength) also range from 0.0 to 1.0. Because the Fourier series representation defines a periodic function over the range of the largest wavelength λ , the phase shift (B_1) can be fixed at 0 without limiting the shape of the topographies that can be generated. By fixing $B_1 = 0$, we reduce the danger of the search discovering numerically different Fourier series which are actually equivalent to each other with respect to a periodic shift. (We are essentially reducing the dimensionality of the genotype search space by one dimension, without reducing the set of possible unique phenotypes.) Thus, our chromosome contains precisely 59 varying genes, each on the range from 0 to 1. The genes are placed in the following order on the chromosome, $A_1, B_2, A_2, B_3, A_3, \dots, B_{30}, A_{30}$. Our rationale for interleaving the A s and B s in this manner was that it would provide better linkage for the genetic algorithm’s crossover operator, since the amplitude and phase shift for a given wavelength would be adjacent to one another on the chromosome and thus be more likely to be inherited together during recombination.

3.2.3 Genetic operators

We define two genetic operators: mutation and crossover.

For mutation, each gene has an independent chance (based on the mutation-rate parameter, which is 3% in these experiments) of taking on a new floating-point value drawn from a Gaussian distribution that is centered on the gene’s current value, with a standard deviation of 10% of the range of valid gene values². If a mutation causes a gene to go outside its valid range (0.0 to 1.0), the gene is assigned the closest valid value.

The use of recombination/crossover operators in real-coded and continuous search spaces has a rather turbulent history.

¹We ran a second set of experiments using a slight variation, where the genes were each only allowed to take on 100 discrete numeric values, rather than range continuously. The results turned out very similar to those reported here (apart from worse performance by the hill climbing search algorithm), and did not warrant inclusion.

²These mutation parameters, along with several other GA parameters, were chosen based on the authors’ intuition and experience with previous problems; computational time forbidding performing sensitivity analysis or meta-optimization on these parameters.

Some influential real-coded methods, such as evolutionary strategies [20] (ES), eschew the use of crossover entirely, and rely on the forces of mutation and selection. In the genetic algorithms tradition, a variety of operators for combining numeric alleles (e.g., [6, 1]) have been proposed and their relative merits have been debated. For the sake of simplicity, we chose to apply crossover only in between whole genes in the chromosome representation: i.e. the value of each real-coded gene is inherited (intact) from either one parent or the other, without any averaging or other manipulation. Because we used a single splitting point and treated genes as atomic units, this crossover operator was almost identical to the standard one-point crossover operator for binary encodings, except with real-valued genes between 0.0 and 1.0, rather than binary digits.

3.2.4 Search algorithm setup

In our experiment, we tested the efficacy of three different search methods for finding solutions to the RTD inverse problem. These three methods were uniform random sampling (RS), a random-mutation hill climber (HC), and a real-valued generational genetic algorithm (GA). The uniform random sampling search technique is very simple; it consists of generating one random individual (set of Fourier coefficients representing a stream topography) after another, and recording the one with the best fitness function value. The random-mutation hill-climbing search heuristic is only slightly more sophisticated: it chooses a random initial starting position (representing an individual topography) from the search space, and then applies the Gaussian mutation operator (described above) to that individual to generate a new candidate position in the search space. If the fitness of the candidate position is superior, the hill-climber *moves* to that position, otherwise it remains at the same location. This process of attempted incremental improvement is repeated, with the now current location. Finally, the genetic algorithm (GA) is implemented as a simple generational GA [12], using the mutation and crossover operators described in the preceding section, and a population size of 100. The GA employed tournament selection (tournament size 3), a crossover rate of 70%, and a mutation-rate of 3% (matching that of the random-mutation HC). The parameters of all of the algorithms are summarized in Table 2. The genetic algorithm was run for 500 generations, and the other two search algorithms were run for the equivalent number of fitness evaluations (50000). We repeated each search 30 times for two reasons: 1) to provide statistically significant performance results, and 2) to obtain a set of multiple topographies to compare. All searches were performed using the tool *BehaviorSearch* [25], which is an add-on for the NetLogo modeling platform that provides facilities for evolutionary search of model parameters.

4. RESULTS AND DISCUSSION

4.1 Search Performance Results

Before examining the stream topographies that were discovered/evolved as a result of our experiment, it is worthwhile to observe and discuss the performance of the three different search methods in this problem domain. Unfortunately, there is some “noise” in the fitness evaluation, due to the random selection of the starting points for the 1000 particles. Thus, to measure search performance in an accurate

Method	Parameter	Value
RS	N/A (parameterless)	N/A
HC	<i>mutation-rate</i>	3%
GA	<i>mutation-rate</i>	3%
	<i>crossover-rate</i>	70%
	<i>population-size</i>	100
	<i>population-model</i>	generational
	<i>selection method</i>	tournament
	<i>tournament-size</i>	3

Table 2: Parameters for the 3 search methods we tested on our RTD inverse problem.

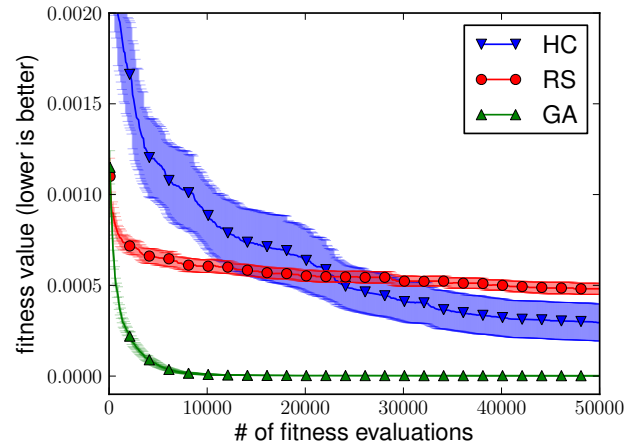


Figure 3: Average best-so-far curves for the three search algorithms tested: RS (uniform random sampling), HC (hill climbing), GA (genetic algorithm). Each performance curve represents the average of 30 searches with that method, with error bars showing 95% confidence intervals on the mean.

and unbiased manner, each time a new best-so-far individual was discovered, an additional 10 fitness evaluations were independently performed (extrinsic to the search process), and that average fitness value was recorded for performance evaluation purposes. The resulting performance curves (see Figure 3) demonstrate, for each search method, the average fitness measure (error function) for the best individual solution after any specified number of fitness evaluations. The key points to observe are:

1. The genetic algorithm significantly outperforms both the uniform random sampling method and the hill-climber, achieving a much lower error measure (by two orders of magnitude!) in much less time.
2. The genetic algorithm performs well consistently (as indicated by the small error bars).
3. The performance of the hill-climber is initially much

worse than uniform random sampling, since it progresses more slowly through the search space, but eventually surpasses it once the hill-climber has worked its way to a more promising area of the search space.

One explanation for the genetic algorithm’s strong performance stems from the building block hypothesis [8, 14], postulating that genetic algorithms work by combining small building blocks, which each contribute individually toward the individual’s fitness. Thus, the crossover operator may have combined various building blocks in order to make large strides early on in the evolutionary process, with the mutation operator serving the purpose of fine-tuning the solutions later on. Since the quality of the HC and RS results were comparatively poor, the remainder of the paper will focus on the results returned by the GA search.

4.2 Topography Results

Let us now turn our attention to the topographies that the genetic algorithm discovered, and interpret them in the context of the real-world domain (hyporheic exchange). The first question in our minds was whether the GA would rediscover the original topography that we had used to generate the target RTD. In theory, the original topography should yield a perfect match (with error 0) to the CRTDF that was generated from it. However, because we are approximating the RTD by placing 1000 particles randomly (in a flux-weighted manner) on the surface-subsurface boundary, the forward RTD model actually provides a (slightly) different RTD each time a simulation is run. Specifically, when the model was run with the original topography 100 times (each time estimating the RTD using 1000 particles), the average error (fitness) value was 6.5×10^{-6} , which is quite close to zero. (To help put this number in perspective, 100 *randomly* generated individuals yielded an average error value of 3.6×10^{-3} .) The first surprising feature of our results was that the genetic algorithm consistently (in all 30 searches) discovered a stream topography that provided a *better* match for the target CRTDF than the original topography itself did! The mean error value for the 30 GA results was 2.3×10^{-6} (around one third that of the original topography), and the largest error value among the 30 was 3.5×10^{-6} (close to half). This indicates that the genetic algorithm found other topographies which quite closely matched the target RTD, and was able to do so with less variation among the resulting distributions. In other words, the “evolved” topographies had similar hyporheic exchange profiles (both in terms of total flux and the distribution of residence times), but were less sensitive to the initial randomized placement of particles in the simulation. Furthermore, although all of the evolved topographies had similar fitness values, they represented disparate topographies. Figure 4 shows the 30 evolved topographies overlaid with the original topography.

The fact that the genetic algorithm returned results that were different from our original topography (and different from each other) is important. We are not attempting to use the genetic algorithm as a function optimizer in this case - rather we are using it to explore a large search space. If the genetic algorithm had always returned the exact same topography, we would have gained very little new or interesting information. For modeling applications where there is no stochastic component, it is possible that the GA results may be more consistent, which may not be desirable.

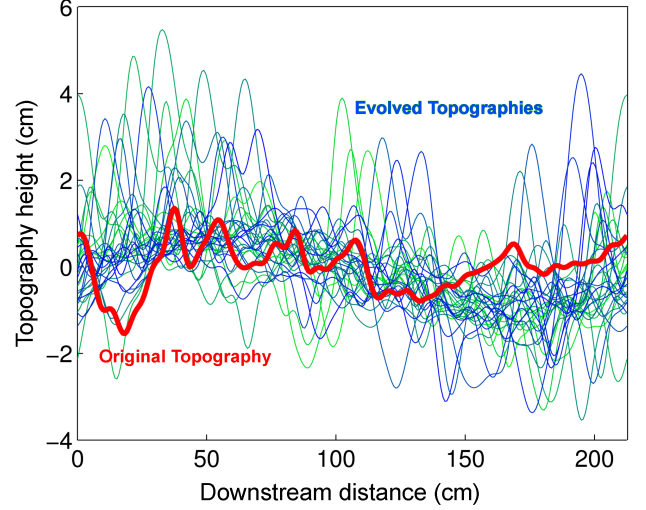


Figure 4: The original topography is shown in red (thick), while the 30 GA-evolved topographies are shown in shades of blue and green (thin). (Note that the axes are not 1:1.)

In such cases, practitioners may want to consider including additional factors to encourage diversity in the genetic algorithm (e.g., drawing inspiration from prior work on diversity maintenance [29]) or apply a multi-objective genetic algorithm [5] where one of the objectives is increased diversity. However, in the present case, the genetic algorithm provided us with a variety of results, and we can examine a range of topographies that yield the same (or an *very* similar) RTD. The rich variety among the topographies is also interesting because it reveals something about the mapping between topography and hyporheic residence-times: namely that the mapping is not a one-to-one correspondence, but rather a many-to-one correspondence. This result is not surprising, but we are unaware of any previous work that has explicitly demonstrated this.

Despite the variation among the topographies, there are some patterns/similarities among the results as well. Figure 5 shows the average Fourier amplitude coefficients of the 30 evolved topographies divided by their respective wavelengths, compared with those of the original topography. Dividing by the wavelength makes these amplitudes directly comparable to one another, and these ratios of amplitude to wavelength are also proportional to the coefficients in the Fourier series of the derivative of the topography ($\frac{dT}{dx}$), which has a large effect on both the flux and subsurface velocity functions. Thus, this plot may be interpreted as estimating the dominant scales of features affecting hyporheic exchange. There is a clear trend (not apparent in the original topography) suggesting that the scales of topography associated with medium-range wavelengths have the greatest influence on hyporheic exchange in this system.

We also plotted the coefficient of variation (CV) of the 30 Fourier amplitude coefficients, A_i , versus the corresponding wavenumbers, k (shown in Figure 6). The CV provides a normalized measure of the amplitude’s variability. Our

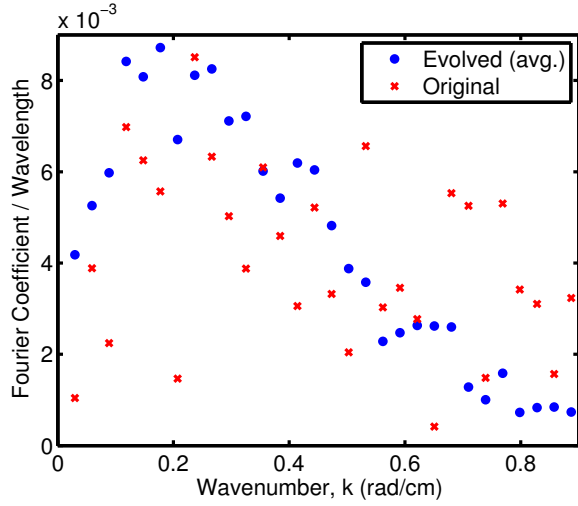


Figure 5: The average of the Fourier coefficients normalized by their corresponding wavelength are shown versus their wavenumber.

results show that as the wavenumber increases, so does the variability of the amplitudes for that wavenumber among the evolved topographies; evolved amplitudes for smaller wavenumbers (i.e. larger wavelengths) were relatively homogeneous. More variability is found among the smaller topographic features, possibly because wavelengths are closer together and thus individual Fourier terms may be more interchangeable and still have a similar impact on the RTD.

5. CONCLUSIONS AND FUTURE WORK

We do not claim, in this work, to have “solved” the RTD inverse problem in any broad sense. We have merely investigated a single instance of the problem, using the RTD associated with one specific 2-D flume dataset. Nevertheless, we believe that this work has broken new ground with the following contributions:

- **Contribution 1:** We have posed the “RTD inverse problem” as a possible avenue for scientific study, to gain more insight into the complex mapping between stream topographies and the characteristics of flow through the subsurface.
- **Contribution 2:** We have identified an efficient method (genetic algorithms) for approaching instances of the RTD inverse problem.
- **Contribution 3:** We have identified several patterns in the search results that were unexpected, and which warrant further study.

Although contribution 1 (posing a problem) may seem relatively minor, it is striking how often in the course of history seemingly small shifts in perspective have led to breakthroughs in scientific understanding. Contribution 1 may actually be connected to contribution 2, since it is possible that others would have previously considered this problem, but lacked the computational/algorithmic tools to solve it. Contribution 2 is also important for the following reason. In addition to showing that genetic algorithms *were*

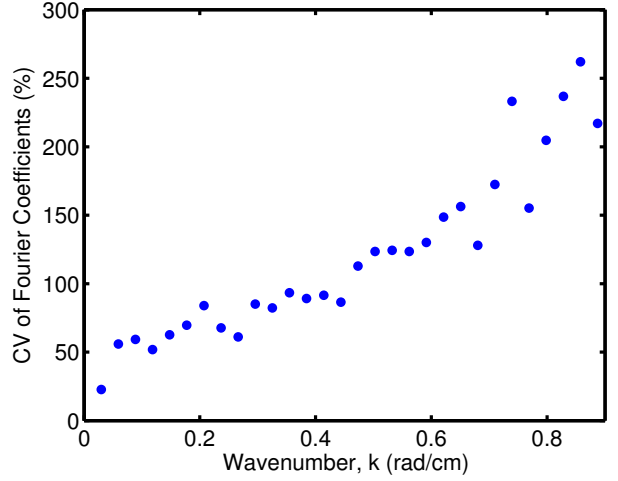


Figure 6: The CV (coefficient of variation) of the 30 Fourier coefficients corresponding to each wavenumber are shown versus that wavenumber.

effective for solving this problem, we also showed that uniform random sampling and random-mutation hill climbing (at least with the chosen mutation-rate) were not effective. This additional information is highly relevant for those pursuing research in this area in the future, who might otherwise adopt a naive sampling-based approach. However, additional experimentation is required to compare the relative merits of genetic algorithms versus other evolutionary methods (e.g., evolutionary strategies, differential evolution) or other metaheuristic search methods (e.g., simulated annealing, particle swarm optimization). The patterns/trends mentioned in contribution 3 were discussed briefly in Section 4.2 above, but the full implications of these patterns are not yet clear. This provides a natural segue into the topic of future work. In a narrow sense, specific future work includes further investigation of why the Fourier coefficients for mid-range wavelengths turn out to be more influential in the hyporheic exchange process for the case of our target RTD. More broadly, we would also like to explore what happens when evolving topographies to match a variety of target RTDs (possibly generated from additional empirically-measured topographies, or chosen to emphasize patterns characteristic of different river systems and flow conditions). An expanded array of experiments would also permit more robust inference about the correlations between the shape of the RTD and the magnitude of certain Fourier coefficients/wavelengths. Furthermore, our experiments thus far have centered on the simpler case of two dimensional hyporheic exchange, neglecting lateral stream effects and large-scale topographic features (such as meanders). Recent work has developed fully three dimensional models of hyporheic exchange [26, 32], and it would be interesting to extend work on the RTD inverse problem to these systems. Another important methodological issue surrounds the variability of simulation results: what does it mean for one topography to have a greater variance of possible RTDs that it produces, and is this dependent or independent of the shape of the RTD itself? An exciting aspect of this work is

that the preceding domain questions, which are both very interesting, would not have arisen if the evolutionary search process had not spurred them.

More broadly, we are enthusiastic about the potential for genetic and evolutionary computation to aid scientific research in hyporheic exchange. Hyporheic exchange modeling is a challenging field, brimming with unsolved problems and rough order-of-magnitude approximations. It is also an increasingly relevant field of study, as the appropriate use, management, and preservation of our natural water resources will become a crucial issue during the 21st century. The mathematical and computer models that are being created to characterize and/or simulate these systems are necessarily highly complex, and it is our hope that the use of evolutionary computation and other metaheuristic search techniques will help researchers develop new insights about these models.

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