A methodology for the design of quasi-optimal monitoring networks for lakes and reservoirs

Néstor Jiménez, F. Mauricio Toro, Jaime I. Vélez and Néstor Aguirre

ABSTRACT

A methodology for designing data colection networks in lakes and reservoirs is presented. The methodology is supported on numerical models, geostatistics and evolutionary strategies. The authors define four elementary steps for design, as follows: (i) modeling, to generate the data fields, (ii) sectoring, to make independent the regions inside the global domain, (iii) Kriging, to interpolate and get estimates from the available monitoring networks and (iv) optimization, to generate the set of locally optimal (accuracy vs costs) monitoring networks. The application case (Porce II reservoir in Colombia) is studied by splitting up the entire domain into five sub-domains (Dam, Transition, River, Stream A and Stream B). After splitting, outstanding features for each sub-domain strongly suggest further analysis. For instance, the Dam and River sub-domains have proven to be opposite (i.e. lentic vs lotic, respectively). As a result, the study case addresses the surface temperature of the Porce II reservoir and allows the recognition of structural patterns for surface temperatures.

Key words | genetic algorithms, geostatistics, hypothesis test, monitoring networks, numerical model

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INTRODUCTION

In order to help in localizing monitoring stations as objectively as possible, the authors have developed a methodology that uses computational tools for monitoring-network design (Jimenêz 2004).

In particular, the software program called MoNiToR (Monitoring-Network Tool and Risk Assessment) was developed for the analysis of the optimal location of the monitoring stations and the ELCOM model (ELCOM: Estuary and Lake COmputer Modeling), developed by the Centre of Water Research of the University of Western Australia, was used to generate (numerically) the hydrodynamics and temperature field for the application case presented here.

Recently, most of the applications in monitoring network design have been done for groundwater systems where human health is likely to be at stake (Carrera *et al.* 1983; Hudak & Loaiciga 1993; Sturck *et al.* 1997; Reed 1999, 2002). Most of the aforementioned applications locate measurement (monitoring) points by random search procedures, and those that are based on interpolation methods define the estimation variance as the main criterion to select the accepted set of stations (Journel & Huijbregts 1978). In Reed's work (Reed 2002) a methodology is applied to groundwater systems, where after using data for an interval of time from the temporal series of a pollutant, four criteria are analyzed in a multi-objective optimization procedure to design the most suitable network to detect the plume of the contaminant. In our case the underlying optimization algorithm used by Reed (the NSGA-II algorithm) is adjusted to free surface waters, so that a unique coding in the searching procedure is built on Kriging interpolation and four monitoring schemes are initally proposed (i.e. two for the surface and two for profiles). In this paper a first try is tested with surface networks using maximum temperatures obtained from a real case: the Porce II reservoir in the province of Antioquia in Colombia.

A METHODOLOGY FOR DESIGNING MONITORING NETWORKS FOR LAKES AND RESERVOIRS

Components of the methodology

The basic components of the proposed methodology are specified as follows (see Figure 1): (i) a numerical model is used due to the lack of field data; (ii) networks are generated randomly for which the Kriging criterion and amount of stations are assigned in order to conform the initial set of individuals for optimization; (iii) finally, optimization is possible through Genetic Algorithms in order to obtain the best set of solutions on a cost-effective basis. For the sake of improvement of the methodology there remains the feedback process; as optimized monitoring networks improve the quality of the recollected data, the model would generate better simulations based on minimum and reliable free-redundancy information (research is still needed on this).

Temperature modeling

Water temperature is one of the most robust parameters in lentic waters; for this reason it was considered for this first trial application (Palacio *et al.* 2002). The governing equations and temperature models used by ELCOM are summarized in its scientific manual (for more detail see URL: http://www2.cwr.uwa.edu.au/~ttfadmin/cwrsoft/doc/elcom_science) where equations for transport and surface thermodynamics (i.e. temperature transport and total heat flux) are represented for 3D modeling.

Ordinary Kriging interpolator (OK)

OK, when used as an evaluator to design monitoring networks, turns out to be an attractive method for its featuring minimum-estimation-error variance that ensures that those sites which, although not having been sampled, could be assigned a level of uncertainty (Carrera *et al.* 1983).

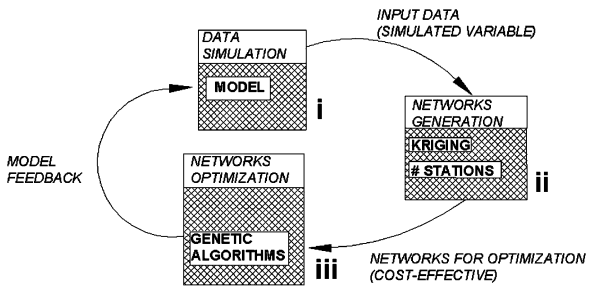


Figure 1 | Fundamental components of the methodology.

Using OK, it is possible to estimate the value of any measurable parameter at those locations where there are not sampled data ($\hat{v}$: estimates) using a weighted linear combination of the available samples ($\omega \cdot v$, where ω are weights and v are available data) (Isaaks & Srivastava 1989):

$$\hat{v} = \sum_{j=1}^{n} \omega \cdot v. \tag{1}$$

In order to conquer an unbiased method for estimating, Kriging focuses its major efforts on making the difference between real values and estimates near zero (i.e. $m_R = 0$). This turns out to be quite complicated since there might not be enough information to obtain m_R(real mean). Assuming a stationary-random-function model as a conceptualization of the unknown values as the outcome of a random process, the expected value at any place is $E(V)$; where V is the variable to be estimated. If it is considered null error expectancy among the random variables to make the estimation unbiased the sum of the weights for estimation must be 1 (Isaaks & Srivastava 1989):

$$\sum_{i=1}^{n} \omega_i = 1. \tag{2}$$

Kriging distinguishes itself from other estimating methodologies in minimizing the variance of the estimation errors. The variance of the residuals contains covariances ($\tilde{C}_{ij}$) and statistic variance $\tilde{\sigma}^2$; the former builds on pairs of data and the latter is obtained from the entire set of available information, as follows:

$$\tilde{\sigma}_R^2 = \tilde{\sigma}^2 + \sum_{i=1}^{n}\sum_{j=1}^{n} \omega_i \omega_j \tilde{C}_{ij} - 2\sum_{i=1}^{n} \omega_i \tilde{C}_{i0}. \tag{3}$$

Before making the residual variance minimum the constraint imposed by the expression (2) has to be considered, which guarantees that there will exist a set of weights that yields 1 to avoid bias results after estimating. To solve a constrained minimization problem as an unconstrained one the technique of Lagrange multipliers is used, adding a new term to the set of equations (μ: Lagrange multipliers). As an outcome from all the features described above, Kriging is defined as the Best

Linear Unbiased Estimator (BLUE). The OK system, then, is defined by the following expression:

$$C \cdot \omega = D \tag{4}$$

$$\begin{Bmatrix} C_{11} & \cdots & C_{1n} & 1 \\ \vdots & \ddots & \vdots & \vdots \\ C_{n1} & \cdots & C_{nn} & 1 \\ 1 & \cdots & 1 & 0 \end{Bmatrix} \cdot \begin{Bmatrix} \omega_1 \\ \vdots \\ \omega_n \\ \mu \end{Bmatrix} = \begin{Bmatrix} C_{10} \\ \vdots \\ C_{n0} \\ 1 \end{Bmatrix}$$

where the dot product between a covariance matrix (C) and a vector of weights (W) yields a vector of covariance between those sites to estimate and those that are known (D). The solution of this system is the set of weights that will be assigned to the available data to compute estimates.

Evolutionary strategies: genetic algorithms

By providing the following definition and description of terms derived from Genetic Algorithms (GA) it is intended to make the reader familiar with the basics of the optimization procedure used by the proposed methodology.

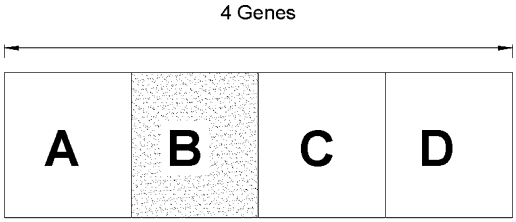
According to Mitchell (1996) Genetic Algorithms (GA) are stochastic techniques based on applications of analogies between nature and random-searching problems. Before choosing between evolutionary strategies and deterministic optimization procedures (DOP) there exist several conditions that should be taken into account by the designer when deciding on whether Evolution-based Multi-objective Optimization (EMO) is a better alternative when compared to DOP (Mitchell 1996). For example, false optimums (false maxima/minima) that might lead to premature convergence is a problem in which EMO performs very well. In addition to the latter, EMO is a good alternative when any of the following conditions are present: (i) knowledge of the searching field is minimal; (ii) objective functions are noisy; (iii) the designer is looking for solutions that are good enough for his/her own applications instead of getting an absolute maximum or minimum (Mitchell 1996). Many of the aforementioned set of conditions are present in monitoring designing; for instance, there might be a case where the designer does not intend to obtain the cheapest network but the one that supports a defined region that is very important for his/her particular aims.

Several terms from biology and computer science have been used in GA applications; the most important ones are: (i) a *chromosome* is defined as a structure that builds on *genes* to beget an individual, (ii) a set of *genes* constitutes a string of chromosome; (iii) a *generation* is the step in time through which evolutionary operators are executed; (iv) a *niche* is a group of individuals that share a limited resource; (v) a *population* contains a set of chromosomes among a universe of possibilities; (vi) basically, there are three *evolutionary operators* that are executed from generation to generation (i.e. *selection*, *crossover* and *mutation*). Through *selection* are identified the best individuals according to a selection probability. *Crossover* facilitates information sharing inside the population and *mutation* modifies the information of an individual by randomly introducing new information that was not available before.

One of the most promising technique from EMOs is the Nondominated Sorted Genetic Algorithms (NSGA). The advantage in using NSGA is the possibility to evaluate conflicts between multiple objectives. There are two basic concepts that NSGA apply from biology; namely: (i) the dominating action of individuals that constitutes the Pareto front and (ii) the niche as the limiting area that encircles the most representative solution (the king of the niche) (Deb *et al.* 2000).

In cases when a minimum is sought, Veldhuizen & Lamont (2000) mathematically define the concept of non-dominance as follows: a vector $\vec{u} = (u_1, \ldots, u_k)$ dominates a vector $\vec{v} = (v_1, \ldots, v_k)$ if and only if u is partially superior to v, i.e. $\forall i \in \{1, \ldots, k\}, \quad u_i \leq v_i \wedge \exists i \in \{1, \ldots, k\} : u_i < v_i$. The foregoing statement says that an individual from a population dominates another one if and only if the former performs better than the latter in one objective, at least; it must also accomplish that for the rest of the objectives, for which there is no thorough dominance, there must be equality with regard to the dominated individual.

Deb *et al.* (2000) have implemented the automatic speciation process to the original NSGA that initially demanded a set of parameters which turned out to be quite cumbersome while finding the king of the niche. This problem has been solved by the cuboid distance technique, through which it is possible to isolate unique solutions that guarantee a thorough covering over the searching field; as a result, a second version of NSGA was developed (NSGA-II).



Counting on (1/0)	1	0	1	1
X Coordinate (dist)	100	150	150	120
Y Coordinate (dist)	130	100	130	200
Datum (un)	0.1	0.3	0.1	0.5

Figure 2 | Individual coding. There exist three components that constitutes an individual: (i) station coordinates (coordinates are given in a 2D scheme); (ii) station data (the variable value is contained inside a computational cell) and (iii) the number of stations (by a binary system it yields the number of gauge stations).

Coding monitoring networks for GA

Before proceeding further through the basics of evolutionary strategies, it is necessary to be familiar with the analogy established between individuals inside an ecosystem and the monitoring networks specifically applied by the methodology for monitoring-networks design. The following is a brief description of the coding process for monitoring-networks design.

Individual coding

The monitoring network is to the set of solutions as the individual is to a population inside an ecosystem. The information that determines an individual (i.e. strings of chromosomes) is defined for monitoring networks as a number of monitoring stations with coordinates and data. For example, if the designer is allowed to choose networks that could contain a maximum of 4 gauge stations (i.e. 4 genes: the chromosome length), the foregoing implies that the number of stations could be up to 4 for each generated network (see Figure 2). The number of stations inside a network is defined by a binary system that either activates or deactivates a station to be included or not, respectively.

Evolutionary operators

Figure 3 represents the way a gauge station (gene) could be shared between pairs of chromosomes, depending on the probability of crossover. For this case, the point to point fashion has been chosen to share the information inside the population.

Figure 4 represents mutation, which makes possible the inclusion of monitoring stations that initially have not been considered. The practitioner should be aware that if the probability of mutation increases, the risk of losing important information (building blocks: BBs[1]) increases as well.

Objectives codification

There has been established two objectives to evaluate the set of candidates while optimizing, namely: (i) Mean Square Error, which is the parameter to evaluate the difference between real values (numerically modeled) and estimates (see expression (5)): this is only for the stations assigned to each monitoring network and (ii) the number of stations, by which costs are assessed exclusively based on the number of stations (i.e. the value is directly proportional to the quantity of the stations). There might be cases for which it is not possible to evaluate the Mean Square Error due to constraints on the interpolation method (Jimenêz 2004). In order to deal with these constraints expression (7), which is the penalization function, states that for those sites where estimation is not possible the maximum mean square error

[1] Reed (2002) defines BBs as "highly relevant subsets of the binary digits representing designs" and adds that they "are used by the GA to construct optimal solutions".

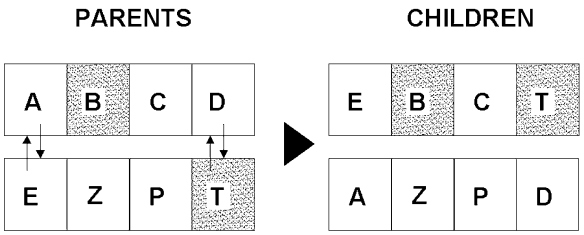


Figure 3 | Crossover. Point to point crossing. Both parents have exchanged information for their first and fourth gene.

must be assigned among the set of solutions during each generation:

$$f_{\text{Error}}(\tilde{x}_j) = \frac{\sum_{i=0}^{n}(Z_i - Z_i^*)^2}{n} \tag{5}$$

$$f_{\text{Costo}}(\tilde{x}_j) = \text{number of stations} \tag{6}$$

$$f_{\text{Penal}}(\tilde{x}_j)\{f_{\text{Error\_MAX}}(\tilde{x}_j)\} \text{ if and only if : } U(\tilde{x}_j) = 0. \tag{7}$$

The above set of expressions is gathered to make possible the minimization problem stated by the following equation:

$$\text{Min } F(\tilde{x}_j) = [f_1(\tilde{x}_j), \quad f_2(\tilde{x}_j), \quad f_3(\tilde{x}_j), \ldots, f_\beta(\tilde{x}_j)], \forall j \in \Omega. \tag{8}$$

STEP-BY-STEP PROCEDURE (TEST CASE: MAXIMUM SURFACE TEMPERATURE IN THE PORCE II RESERVOIR)

Numerical modeling

As mentioned above, the ELCOM model was used to simulate the hydrodynamics and water quality tracers such as water temperature. Water temperature was considered the steadiest parameter to use in a first trial of the methodology. That is, temperature is good enough to identify important phenomena that affect water-quality-related processes, such as eutrophication, and robust enough to make comprehensible its behavior during the simulation process (identifiable diurnal cycles).

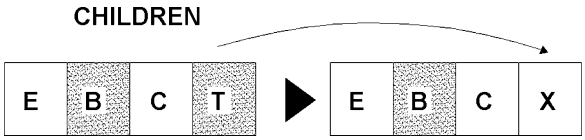


Figure 4 | Mutation. Transforming the chromosome by changing genes (stations).

The ELCOM-model calibration was possible through data provided by EPM (Empresas Públicas de Medellín) for a two-month-duration series (October–November, 2001). In Villegas' thesis (Villegas 2004) detailed calibration and validation processes were done by taking on the aforementioned set of data. The test case presented here is based on the results obtained from the modeling process that provided the following runs of MoNiToR with maximum surface water temperatures (see Figure 5).

Domain sectorization

Although the complexity of the spatial (and temporal) distributions of natural phenomena might risk the accuracy of the monitoring scheme, the chances are that by dividing the entire domain into sectors the monitoring scheme would adjust better to the studied variable; that is, there might be dominating patterns for the variable that impel the user to divide the domain into subdomains that eventually would increase the measuring accuracy of the monitoring network. In order to identify the limiting patterns it is recommended to use both qualitative and quantitative criteria (hydrodynamics, heterogeneity indices, variance indices, knowledge of the phenomena that might constrain the distribution of the variable, and other criteria defined by

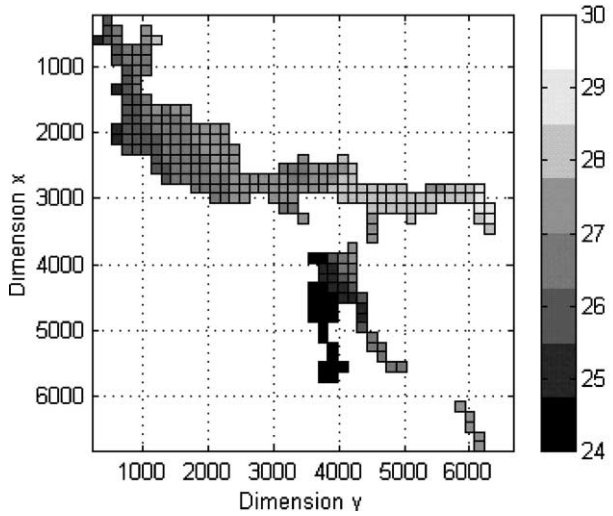


Figure 5 | Output from ELCOM postprocessor represented by gray-scaled small squares (maximum surface temperatures). Note that the shape of the reservoir is not fully represented by the small squares-computational cells; this is because of the lack of data reproduced by the model.

planners and designers of the network). The present application used temperature distributions and one-way ANOVA[2] indices to split the entire reservoir into subdomains. The qualitative factor used to design monitoring networks for individual subdomains was developed through direct observation of maximum-surface-temperatures maps (see Figure 5) complemented with one-way ANOVA techniques (Larson 1982). To set up the test for the ANOVA implementation it was defined that the null hypothesis (H_0) declares all means are equal, as the alternative hypothesis (H_1) states otherwise. It was assumed that 0.05 is the highest significant p value for this particular test to reject H_0.

According to the function value ($F = 107.8$) and the level of significance (p value $= 0$) derived from statistics of the hypothesis test, there is strong evidence that suggests that all the subdomains are different; there is no strong evidence to reject the null hypothesis (H_0 = all means are equal). In order to go further into the variance analysis an extra sectoring was done inside each subdomain (regions in Figure 6 were divide into halves), through which new sets of data were used to make comparisons inside each sector (see Table 1). According to the results obtained from the one-way ANOVA for each sector, it is concluded that the closest area to the dam site (i.e. Dam case) is the only case in which the values of the means are similar ($0.89 > 0.05$: there is no strong evidence to reject the null hypothesis – see the first row in Table 1). For the remaining cases differences for their means are evident as p values obtained though one-way ANOVA are close to zero (i.e. p values from 0.00E + 00 to 5.50E − 03: see Table 1). The foregoing turned out to be the featuring aspect to be considered for the sectoring procedure. For example, note that the region that embodies the river inflow is the least significant to reject H_0 among the remaining cases (p value = 5.50E − 03: the highest p value for the remaining four cases), while the area between the river and the dam site is the most significant to reject H_0 (p value = 0.00E + 00: the lowest p values for the remaining four cases), which states that

[2] One-way ANOVA has as its objective to find out whether data from several groups have a common mean. This is done by statistical evaluation through hypothesis tests (Larson 1982).

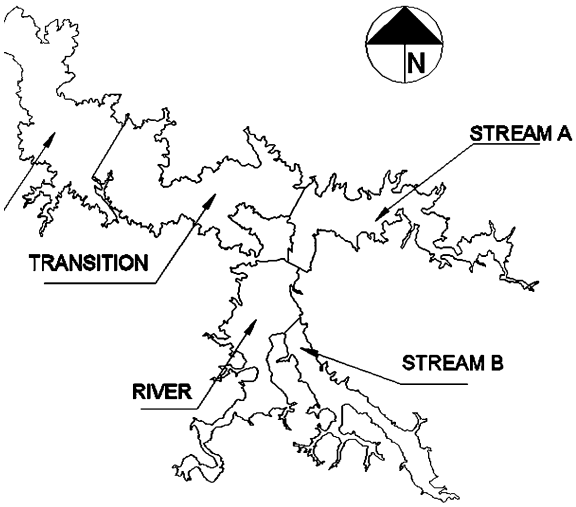


Figure 6 | Reservoir divided into five sectors. Small gray-scaled squares from Figure 5 are inside this domain.

there indeed exists a transitional area between a lotic environment (River) and a lentic one (Dam).

Having done the foregoing analysis (throughout the reservoir) six cases have been chosen to represent each subdomain, as follows: (i) Dam, which is the closest region to the dam. The hydrodynamics of this area resembles the lymnological characteristic of lentic waters more than the other subdomains. (ii) Transition. This is a transitional region between a lotic environment dominated by the mixing effects of the River and a Dam region whose hydrodynamics are common to create limnological features in lakes and reservoirs. (iii) the River case is above all an area where the Porce River inflow dominates over its limiting area. (iv) There remain the Stream A and Stream B cases that include the La Cancana and Guaduas Streams, respectively: the latter runs

Table 1 | ANOVA results for individual comparisons in each subdomain

	F	*p* value
Dam	0.02	8.90E − 01
Transition	241.3	0.00E + 00
River	8.27	5.50E − 03
Stream A	25.92	2.74E − 06
Stream B	75.3	5.32E − 11

Table 2 | Variogram and some statistics from Kriging-parameter fitting

	Range (m)	Sill	Nugget	Variance	Mean (°C)
Dam	1550	0.356	0.00	0.260	27.2
Transition	2580	0.274	0.00	0.183	28.0
River	1910	1.600	0.00	1.32	26.7
Stream A	1630	0.335	0.00	0.261	28.7
Stream B	1750	0.456	0.00	0.304	27.7

separately from the Porce River under different conditions regarding both the hydrodynamics and water quality features, while La Cancana contains the highest values for water temperatures compared to the rest of the reservoir. (v) Finally, the aforementioned set of cases is reevaluated as an entire domain to generate the Reservoir case (see Figure 6).

Kriging parameters

Mean square error and costs are the two criteria evaluated while obtaining the set of best solutions (see the following section). In order to compute the mean square error criterion a set of parameters for Kriging estimation must be fitted according to a cross-validation procedure. After setting the required parameters for Kriging the designer validates the estimates so that the parameters are adequate for the specific interpolation field. In summary, the following is the set of the most relevant parameters for ordinary Kriging: (i) the area of influence of a point over its neighbors is delimited by the Range; (ii) the average maximum variance between a set of points is defined as the Sill and (iii) the Nugget is considered as the discontinuity of the variogram at the beginning. For more detail see Isaaks & Srivastava (1989).

In Table 2 Transition turned out to be the most extending regarding the influence between samples; that is, within 2.580 m there is still some relationship between the data. On the other hand, the range for River is 1.910 m and the Sill is at 1.600 m, the highest of all, which matched with the distribution of maximum-surface temperatures over all its region. The foregoing means that over short distances there is high variability, mostly along the boundaries of the river inflow.

River and Stream A were the most relevant over-estimating cases. The former was due to the effects of higher temperatures over the lowest temperatures of the reservoir, while the latter is affected by the highest values of the variable over sites that are not that warm. Both cases had negative values (overestimation) for mean, median and quartiles (25% and 75%) (see Table 3), which confirms the aforementioned overestimation trends. However, not all of the cases are that easy to recognize as being prone to overestimation or underestimation; for example, Transition is one of those cases that, though being negatively skewed, does not strongly suggest an estimation trend. That is, because of its symmetry ($Q25\% = -3.17$, $Q75\% = 0.349$) and central tendency near zero (mean = 0.061, median = 0.195) doubts remain about this case. Note that for the rest of the cases (Dam, Stream B) their statistics provide evidence to consider these cases as underestimation-prone (positive error values); that is, means and medians were well above zero.

Table 3 | Error estimation statistics. Note that data number is equal to the number of computational cells reproduced by the numerical model

	Q25%	Q75%	Med.	Mean	Kurt.	Skew	St. dev.	Min.	Max.	Data
Dam	0.150	0.860	0.470	0.500	0.175	−0.108	0.526	−0.342	2.065	113
Transition	−0.317	0.349	0.195	0.061	0.371	−0.143	0.433	−1.059	0.989	121
River	−1.700	−0.568	−0.774	−1.240	0.526	−0.218	1.170	−4.063	0.254	64
Stream A	−0.954	−0.331	−0.557	−0.653	0.366	−0.190	0.493	−1.633	1.084	74
Stream B	−0.148	0.858	0.355	0.399	0.112	−0.089	0.569	−0.336	1.549	45

In the next section more references will be made to Tables 2 and 3 in designing the final monitoring networks.

Step 4: Optimization

The optimization process is pursued through two steps, as follows: (i) initially, costs and errors were taken together to find an adequate set of parameters (i.e. population size, chromosome length, and number of generations) while analyzing the balance criteria in order to strike patterns of conflicts between both criteria and (ii) based on the previous set of solutions (with two criteria) the designer is able to choose a number of gauge stations as a point of reference from which there may not be any improvement for the other criterion (estimation error). Consequently, there is a set of solutions that performs the best between networks with a unique number of gauge stations.

In Table 4 the summary for parameter calibration is shown sequentially from the Dam to the Stream B case. Those sets of parameters that performed clearly better in terms of minimum estimation errors obtained for each case in particular are highlighted in bold. For example, during the calibration of Dam it began with the minimum requirements (40 individuals for the initial population, 40 genes for chromosome length and 50 generations) from which 17.20 was found as the minimum estimation error among the resulting population of nondominated individuals. In order to get better results an increment for chromosome length (from 40 genes to 80 genes) is done; that is, assuming that the longer the string is the more the chances are to get relevant information from the variable. With the foregoing try more than 80% in estimation error was gained (3.26). Further searching was possible by increasing the number of individuals for the initial population (from 40 to 80 individuals), assuming that with a larger group of individuals the chances are greater to discover outstanding networks among a population and, as consequence, the evolution period (i.e. number of generations) must be longer (from 50 to 80 generations) in order to improve the quality of the individuals accordingly. The latter set of parameters performed poorly (15.09) due to a lack of generations that would have greatly enhanced the exchange of information toward the best solutions had it been for longer periods of evolution. In order to ameliorate the latter the number of generations was doubled systematically to 100, 200 and 400 generations, for which 5.34, 0.84 and 2.48 in estimation error were obtained, respectively. These results clearly state that for the Dam case 80 individuals, 80 genes as the chromosome length and 200 generations are evidently the most adequate set of parameters to get the best set of solutions.

Table 4 | NSGA parameters calibration

Dam			
Pop. size	**Chrom.**	**Generations**	**Min. error**
40	40	50	17.20
40	80	50	3.26
80	80	80	15.09
80	80	100	5.34
80	**80**	**200**	**0.84**
80	80	400	2.48
Transition			
80	**85**	**200**	**0.93**
80	85	400	0.97
River			
80	46	200	8.73
80	46	600	10.92
160	**46**	**800**	**2.19**
Stream A			
80	50	200	12.36
160	50	400	14.71
160	**50**	**800**	**3.36**
Stream B			
160	**30**	**800**	**3.70**
160	30	1200	3.79

For the remaining cases the set of parameters began in conditions similar to those of the Dam case when performing the best; that is, 80 individuals for the initial population, 80% of the longest chromosome string (maximum number of data) and 200 generations. The Stream B case is an exception to this rule; its set of parameters was established according to its relationship with the Stream A case. Both the Stream A and Stream B cases were quite complicated due to the scarcity of data and the high longitudinal variability with regard to the measured variable (maximum surface temperature), affecting the Kriging estimates.

As mentioned above, a second procedure is required to get the final network designs; that is, having set a number of stations from which there is no gain in estimation a second network-optimization phase is executed with a defined number of stations (see Figures 7–12). Through this coupled optimization procedure (i.e. multicriteria, unique criterion phases) it was possible to evaluate the performance of the first optimization phase (parameter calibration); for example, through the Dam case it was demonstrated that networks with five stations are of similar quality if compared to those networks of 10 stations (see Figure 7(a, b)). Likewise, for the Transitional case a network of 5 stations performs as well as one with 10 stations, mainly because of their getting information from regions of low and high temperatures, that is, the left and right sides of the domain, respectively (see Figure 5), which finally avoided biased estimations.

Figure 7 | Dam. Solutions of 5 and 10 gauge stations.

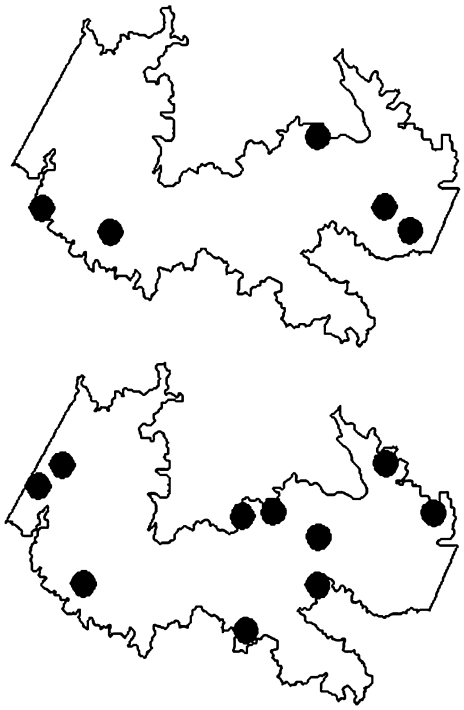


Figure 8 | Transition. Solutions of 5 and 10 gauge stations.

Not all of the cases approaching the final solutions were that easy; the River, Stream A and Stream B cases results were quite confusing since for neither one, while proceeding in the first phase nor during the second one, was there such strong evidence that a critical number of station existed. For example, the networks for Stream B showed that solutions with 7 and 10 stations (see Figure 11(a, b)) performed better compared to the results obtained from its first phase ($0.93 \ll 3.70$). This points out algorithm failures for the calibration phase. As for the River and Stream A cases (see Figures 9 and 10, respectively) there could have been a relationship in terms of estimation error values between both phases (i.e. calibration and final network design). However, both cases reached the highest estimation error values, which suggests a deeper analysis whether during the Kriging parameter step or on calibrating evolutionary parameters.

Figure 12(a, b) illustrate solutions for networks with 10 and 20 stations, respectively, applied to an additional case through which it was possible make comparisons between solutions for individual sectors and those for a domain that contains all of them. It could be seen that if one compares

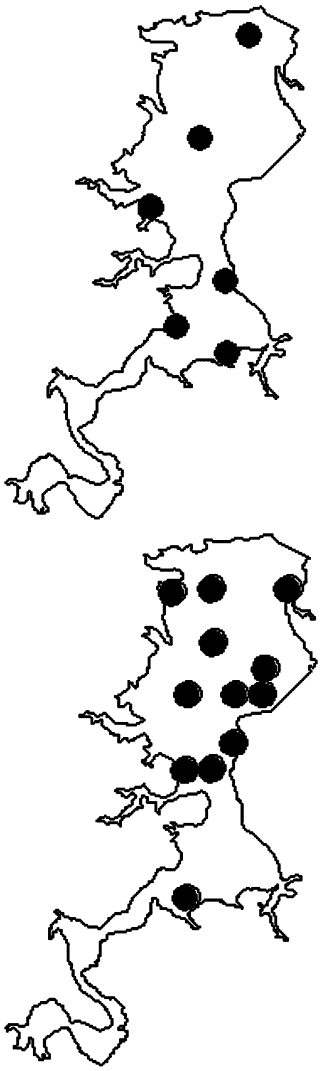


Figure 9 | River. Solutions of 6 and 12 gauge stations.

the network of 10 stations against that of 20 stations, it is evident that the latter is more accurate at getting information from the maximum surface temperatures. Upon comparing these results to the ones obtained from sectorized solutions, there exists an evident relationship between both approaches (i.e. complete and by sectors) as the solution for the entire reservoir corresponds to its distribution of stations; that is, more stations for the regions of cases River, Stream A and Stream B are necessary than those for Dam and Transition. That states that those regions where the structure of the maximum surface temperature is more complex a larger quantity of stations is required.

CONCLUDING REMARKS AND FUTURE RESEARCH

About the results

Three elements make this methodology unique among other proposals for monitoring schemes: (i) hydrodynamics-model application, (ii) interpolation by means of geostatistics and (iii) evolutionary strategies optimization. It is quite ambitious when trying to get enough information of natural processes through monitoring networks that are based on interpolation methods. As seen through the application cases, there were Kriging settings that do not fit accurately to what was represented through the hydrodynamics model. Therefore high estimation errors were registered. The authors suggest that the more complex the cases are (e.g. isotropic models) the deeper the analysis during Kriging parameter setting is required; that is, based on cross-validation tools (i.e. graphs of dispersion, histograms of frequency, statistics, outliers, etc.) the designer gets more reliable Kriging schemes. Not only does a well-fit set of parameters for Kriging estimates guarantee getting the best set of final solutions for monitoring designs; by a trial-and-error procedure the user has to discover the correlations between physical aspects of the phenomena and the effects of the evolutionary parameters over them. As was observed when designing for the Stream B case there remained doubts about how low could have been

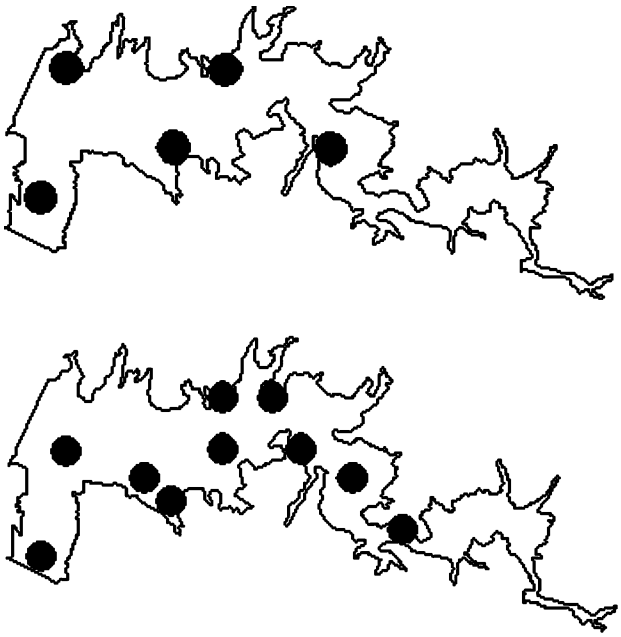


Figure 10 | Stream A. Solutions of 5 and 10 gauge stations.

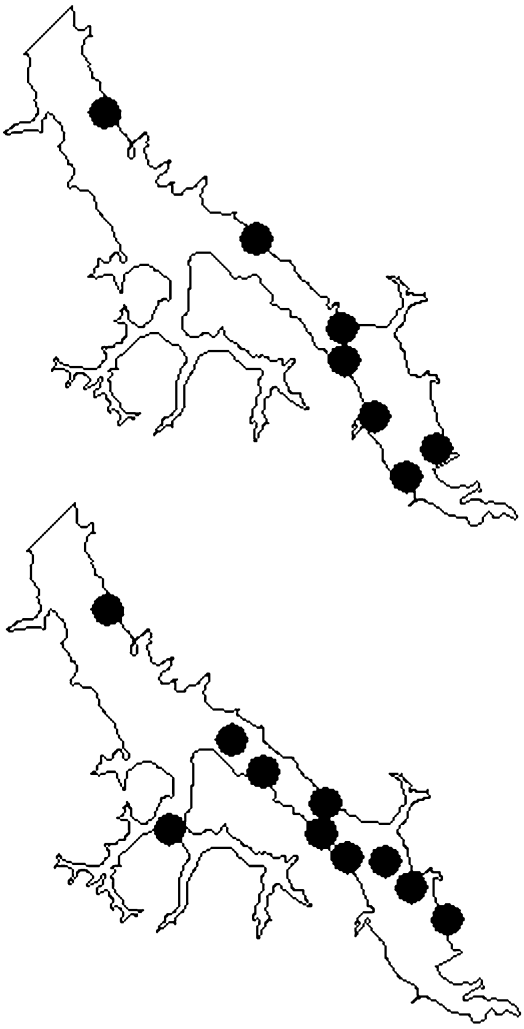


Figure 11 | Stream B. Solutions of 7 and 10 gauge stations.

the estimation error and how many stations are critical (the minimum number of stations to get reliable information) upon balancing both criteria (costs and error, see Table 4). This might have been because of the lack of generations, not enough individuals for the population or the chromosome strings were not long enough, that is, every parameter should be tested, producing several combinations until one gets comparable results in estimation errors with regard to the values obtained through the second phase (i.e. unique-criterion optimization, see Figure 11(a, b)).

Research

During this paper monitoring schemes for vertical data were not tackled. MoNiToR has its modules to compute RMS

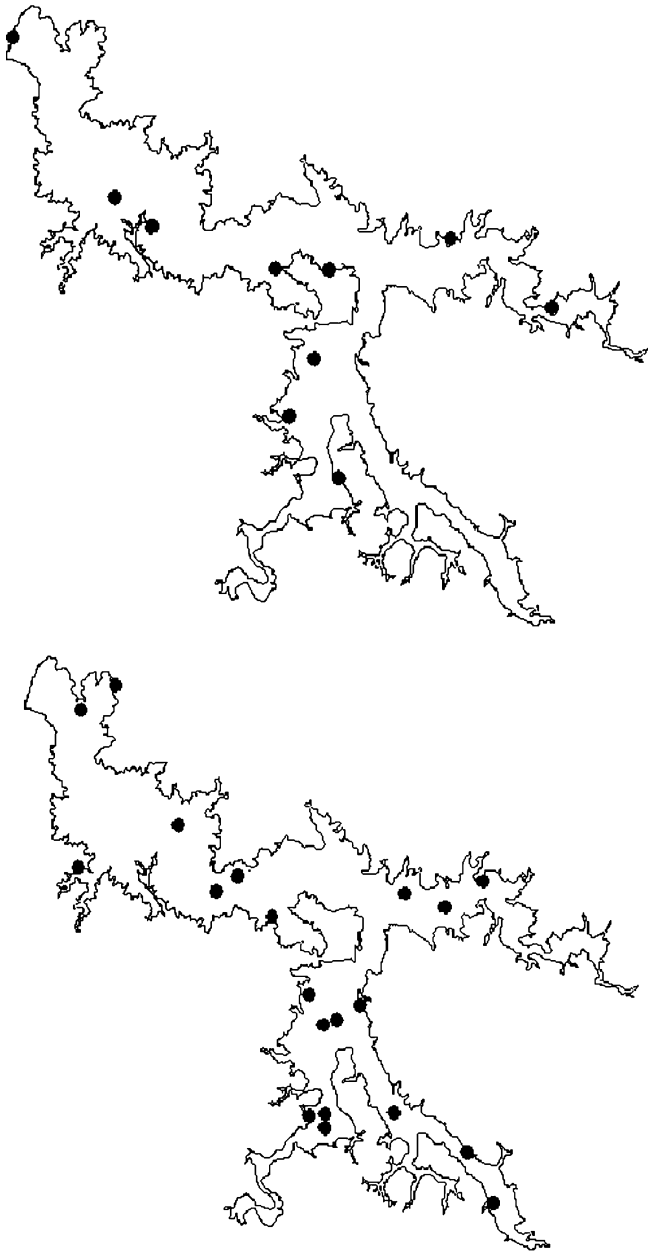


Figure 12 | Reservoir. Solutions of 10 and 20 gauge stations.

(Root Mean Squares) as a first approximation to design monitoring networks for profiles. Because Kriging estimation and cost are implemented only for 2D schemes, it is necessary to make a conversion from 3D data to 2D. One of the direct applications of monitoring networks for profiles is to be able to define how stratified the body of water is.

While sectorizing was used an statistical parameter to implement over the entire domain (i.e. ANOVA), it was a good first approach. Other criteria could have been implemented that would have been more related to the physics of the phenomena. For example, hydrodynamic parameters like *Pe* (Peclet number) could have been a better choice to select subdomains that, based on its rate of advection/dispersion, would have defined distinctive environments. Further research is required for this subject.

Improvements for MoNiToR are required; unexpectedly, the balance criteria were not that efficient for certain cases, mostly those where minimum data was available. The opposite occurred when there were more data. Furthermore, random generation for initial population, and coding for storing and crossing information, should be more related to the specific optimization problem.

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