SIMILARITY METRICS FOR
GENETIC ADAPTATION OF SEGMENTATION PARAMETERS

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ABSTRACT:

The relation between the segmentation parameters values and the segmentation result is far from being obvious. Therefore, in order to produce the desired outcome a complex and time consuming trial and error process is usually required. Automatic methods based on Genetic Algorithms (GA) have been proposed that endeavor to adjust automatically the segmentation parameters to a given set of reference segments manually delineated by a human analyst. The method searches the parameter space for a set of values that optimizes a given fitness function, which should express numerically the similarity between the segmentation outcome and the reference segments. The fitness functions proposed for that purpose were designed so that they achieve their extreme value when a perfect match with the reference is produced. However, there is no theoretical foundation as well as no experimental study that confirms the adequacy of these adaptation methods when a perfect match is not possible. This corresponds to most practical applications, in which the best attainable outcome differs from the reference, and the obtained similarity value departs from the ideal one. This work addresses these issues and investigates the performance of the GA based adaptation methods for a number of different similarity metrics on different types of reference objects. Working on a Quickbird test image, the study compares the different metrics and examines their correlation degree. The work lastly assesses if these metrics lead the GA to the same solution and ultimately verify the assumptions underlying the GA adaptation method.

1. INTRODUCTION

Segmentation is a key step in object-based image analysis, mainly because attaining meaningful objects is indispensable for a good classification. However, finding the relation between the segmentation parameters values and the segmentation result is by no means an easy task. In fact, the search for suitable parameters usually requires a hard and time consuming trial and error process.

Automatic methods based on Genetic Algorithms (GA) have been successfully applied to tackle this issue (Pignalberi, (2003) and Zhang, (1996)). These methods aim to automatically adjust the segmentation parameters to a given set of reference segments delineated by a specialist, that represents what he/she considers a "good segmentation". The idea is to search the parameter space for a set of values that optimizes a given fitness function that numerically represents the similarity between segmentation and reference.

Nevertheless, there is no theoretical foundation that confirms the adequacy of these adaptation methods when the segmentation outcome differs from reference and the obtained similarity value departs from the ideal one. Different similarity metrics, for instance, may associate the same similarity value to different segmentations which probably would not be considered qualitatively equal by a human analyst. In fact, the relation between the evaluation given by these metrics and the human perception of a good segmentation is yet an open subject.

In Feitosa et. al (2006) a genetic method for the adaptation of segmentation parameters was proposed. In that work the formulation of the fitness function privileged applications in which the objects to be segmented were homogeneous. A later study (Feitosa, 2009) extended the previous work by proposing a new fitness function which considered the objects of interest to be non-homogeneous, though formed by an assembly of homogeneous parts. The software prototype that implemented the former approach was also extended.

This work evaluates these two and other six different metrics in two experiments: the first verifies if these metrics are correlated and the second validates if they lead the GA to the same set of parameter values.

The experiments were conducted on a *Quickbird* image of a urban area and used three different sets of reference objects. The software prototype formerly mentioned was extended with the metrics evaluated in this work and the segmentation procedure used is the one proposed in Baatz et. al (2000).

This paper is organized in the following way. The next section describes briefly some fundamentals about the segmentation procedure used in this work, the genetic adaptation method and correlation theory. A detailed description of the similarity metrics is then presented. The succeeding section reports the experimental results and the final section shows the conclusions and suggests future possible works.

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2. FUNDAMENTALS

This section presents a brief overview on techniques and concepts underlying this work.

2.1 Segmentation Procedure

The segmentation method used in this work is based on the region growing algorithm proposed in Baatz et. al (2000). It is a stepwise local optimization algorithm that minimizes the average heterogeneity of the image objects.

Objects start as single pixels and grow during the procedure merging to neighboring objects. In each processing step all the neighbors of an object are evaluated and the object is merged to the one which provides the smallest growth of heterogeneity, an arbitrary measure of heterogeneity, weighted by the object size, called *fusion factor*. But the fusion occurs only if this factor also satisfies another condition: it has to be smaller than the square of the so called *scale parameter*. The procedure stops when no more fusions can be done.

Equation 1 shows how the fusion factor f is calculated. It contains a spectral heterogeneity component h_{color} and a spatial heterogeneity component h_{shape}. The relative importance of each component is given by the color weight w_{color}.

$$f = w_{color} \cdot h_{color} + (1 - w_{color}) \cdot h_{shape} \qquad (1)$$

Equation 2 shows the formulation of the spectral component of the fusion factor. *Obj1* is the object selected for merging, *Obj2* is a neighbor object and *Obj3* is the result of the merging of *Obj1* and *Obj2*. In the equation, c is a spectral band index and w_c is an arbitrary band weight; n is the number of pixels of each object and σ_c is the standard deviation of the pixels' values of an object for band c.

$$h_{color} = \sum_c w_c (n_{Obj3} \cdot \sigma_c^{Obj3} (n_{Obj1} \cdot \sigma_c^{Obj1} - n_{Obj2} \cdot \sigma_c^{Obj2})) \qquad (2)$$

The formulation of the spatial component of the fusion factor is shown in Equation 3. It contains a compactness component h_{cmpct} and a smoothness component h_{smooth}. The relative importance of each component is given by the weight w_{cmpct}.

$$h_{shape} = w_{cmpct} \cdot h_{cmpct} + (1 - w_{cmpct}) \cdot h_{smooth} \qquad (3)$$

Equations 4 and 5 show how compactness and smoothness components are calculated. In the equations l represents the perimeter of the objects and b their bounding box.

$$h_{cmpct} = n_{Obj3} \cdot \frac{l_{Obj3}}{\sqrt{n_{Obj3}}} - (n_{Obj1} \cdot \frac{l_{Obj1}}{\sqrt{n_{Obj1}}} + n_{Obj2} \cdot \frac{l_{Obj2}}{\sqrt{n_{Obj2}}}) \qquad (4)$$

$$h_{smooth} = n_{Obj3} \cdot \frac{l_{Obj3}}{b_{Obj3}} - (n_{Obj1} \cdot \frac{l_{Obj1}}{b_{Obj1}} + n_{Obj2} \cdot \frac{l_{Obj2}}{b_{Obj2}}) \qquad (5)$$

The parameters used in merging decision are of major importance to this work as they represent an adjustable heterogeneity criteria. This criteria can be defined by setting the values of the external segmentation parameters: the spectral band weights (w_c), the color weight (w_{color}), the compactness weight (w_{cmpct}) and the scale parameter.

Considering all the possible scenarios for a segmentation to take place like different sensors, intrinsic characteristics of the investigated site and variable relevance for the same classes in different applications it is possible to conclude that finding a good set of parameters is far from being an easy task.

2.2 Genetic Algorithm

To obtain a good quality segmentation is necessary to find suitable parameters, however it is almost impossible to identify a relation between them.

The user can try a manual adjustment, nevertheless there are countless possible combinations, what usually leads to the utilization of an automatic search algorithm for that matter. The method used in this work was introduced in Feitosa et. al (2006) and is briefly described in this section.

Genetic Algorithms are stochastic algorithms for search and optimization based on the concepts of genetic inheritance and evolution. They are an heuristic to find the optimal solution for a given problem, leaded by a parallel search.

In this study, the desired solution is a set of parameters values that minimizes the evaluation function (objective function). This function represents how much a given solution fits to the reference set delineated by a specialist. The search is composed by a sort of genetic operators that act over the chromosomes which contain the segmentation parameters values codified in their *genes*.

In mathematical terms, given a set of reference segments R and a parameter vector P, the task of the GA consists in searching for the parameter vector P_{opt}, for which the value of F is minimum:

$$P_{opt} = arg_P (min[F(R, P)]) \qquad (6)$$

2.3 Correlation

In this work *rank correlation* was used to represent the relationship between variables, instead of the classical, so called Pearson correlation, which is only sensitive to linear relationships. The methods used in this work simply examine when there is a tendency for the two variables to increase or decrease together (*positive* correlation) or, alternatively, for one to decrease as the other increases and vice-versa (*negative* correlation); either kind of effect is known as *monotonicity* (Neave, 1988).

The correlation coefficients (r) are conventionally defined between -1 and +1; -1 represents strong evidence of negative correlation (perfect disagreement), +1 represents strong evidence of positive correlation (perfect agreement) and values near 0 tend to occur when there is a little or no correlation between the two variables.

The distribution of the correlation is approximately normal with mean 0 when the sample size is large. The approximation is satisfactory for a sample size (n) greater than 50, which is the

case for this work. The methods described in this section are Spearman's (Spearman, 1904) and Kendall's rank correlation (Kendall, 1938).

2.3.1 Kendall Rank Correlation is defined by:

$$\tau = 1 - \frac{4 N_D}{n(n-1)} \qquad (7)$$

where $\qquad \tau$ = Kendall rank correlation coefficient
N_D = number of crossings in the graphical rank representation
n = sample size

In the graphical rank representation, the values of a pair of metrics being compared are represented in two separated axes. Lines connecting corresponding values are drawn and the number N_D of crossings in this lines is counted.

Considering the sample size of the experiments described in this work and assuming a normal distribution the critical value is approximately $\tau \geq 0.2852$.

2.3.2 Spearman Rank Correlation is defined by:

$$r_S = 1 - \frac{6 D^2}{n^3 - n} \qquad (8)$$

where $\qquad r_S$ = Spearman rank correlation coefficient
D^2 = sum of the squares of the differences between the two variables ranked values
n = sample size

Considering the sample size of the experiments described in this work and assuming a normal distribution the critical value is approximately $r_s \geq 0.4231$.

The calculated critical values point out above which thresholds a correlation value can be considered significant. Although a correlation value of 0.2852 indicates nothing more than a weak correlation between two similarity metrics, on the other hand it is high enough to guarantee that both metrics are monotonic.

3. SIMILARITY METRICS

Similarity metrics are used by the GA to determine how close it is to the optimal solution. In this work eight different metrics were selected for investigation. Figure 4.1 illustrates the entities used in the similarity metrics given by Equations 7-14.
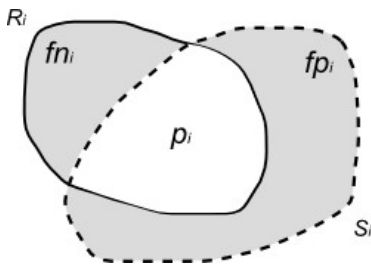

Figure 1. Entities used in the similarity metrics.

Let us assume that exist N reference segments delineated by a specialist. Let R_i (i=1,2,...,N) be the i-th reference object. And

let S_i be the i-th segment in the segmentation output that have the largest intersection with the respective reference (R_i). Let also VS_i (not shown in the figure) be the i-th segment in the segmentation output that have at least 50% of intersection with one reference. If no segment fulfills this condition VS_i will be empty.

Let us also define:

- fn_i as the number of pixels of R_i that do not belong to S_i so called false negatives;
- fp_i as the number of pixels of S_i that do not belong to R_i so called false positives;
- p_i as the number of pixels that belong to the intersection of S_i and R_i so called positives;
- B_i as the sum of all border pixels of R_i and S_i;
- b_i as the number of border pixels of VS_i that intercept the area of R_i;
- NS as the number of segments of S_i that do not belong to V_{S_i};
- #() as an area operator.

The similarity metrics examined in this work are described in the following.

3.1 Reference Bounded Segments Booster

Proposed in Feitosa (2006) this function corresponds to the division of the false negatives and false positives by the number of pixels (area) of the reference. $F1$=0 corresponds to a perfect fitting between segmentation and reference and $F1$>0 otherwise.

$$F_1 = \frac{1}{N} \sum_{i=1}^{N} \frac{(fn_i + fp_i)}{\#(R_i)} \qquad (9)$$

3.2 Larger Segments Booster

This function was proposed in Fredrich (2008). The fp_i and fn_i terms in Equation 9 favor solutions with a tight overlap with the reference segments, which most likely leads to solutions consisting of numerous small (in the limit of single-pixel) segments. The b_i term counterbalances this effect by granting a lower score to solutions with few, larger segments. Yields $F2$=0 for a perfect fitting.

$$F_2 = \frac{1}{N} \left[NS + \sum_{VS_i \neq \emptyset} \frac{fp_i + fn_i + b_i}{\#(R_i)} \right], \text{ se } NS < N$$

$$F_2 = \infty \text{ , otherwise} \qquad (10)$$

3.3 Janssen

This function (Janssen, 1995) corresponds to the square root of the ratio between the square of the positives and the areas product. $F3$=1 corresponds to a perfect fitting between segmentation and reference. $F3$=0 corresponds to the worst case when there is no match.

$$F_3 = \frac{1}{N} \sum_{i=1}^{N} \sqrt{\frac{(p_i)^2}{(\#(R_i) * \#(S_i))}} \qquad (11)$$

3.4 Spatial Overlap

This function (Gerig, 2001) corresponds to the division of the positives by the sum of false positives, false negatives and positives. Its behavior is similar to the previous function with *F4*=1 for a perfect fitting and *F4*=0 when there is no match.

$$F_4 = \frac{1}{N} \sum_{i=1}^{N} \frac{p_i}{(fn_i + fp_i + p_i)} \qquad (12)$$

3.5 Relative Absolute Area Difference

This function (Gerig, 2001) corresponds to the division of the area of the segmentation by the area of the reference. Yields *F5*=0 for a perfect fitting and *F5*>0 otherwise. It is important to point out that *F5*=0 can also be obtained for a non-perfect fitting, as long as the segmentation and reference have the same area.

$$F_5 = \frac{1}{N} \sum_{i=1}^{N} \left| \frac{\#(S_i)}{\#(R_i)} - 1 \right| * 100 \qquad (13)$$

3.6 Average Symmetric Absolute Perimeter Distance

For this function (Gerig, 2001) it is defined an operator $d(S_i, R_i)$ that computes the sum of the distances between each border pixel of the segment yielded by the segmentation procedure and the nearest border pixel of the respective reference and vice-versa. The average of these distances are then calculated. *F6*=0 for a perfect fitting.

$$F_6 = \frac{1}{N} \sum_{i=1}^{N} \frac{d(R_i, S_i) + d(S_i, R_i)}{B_i} \qquad (14)$$

3.7 Symmetric RMS Perimeter Distance

This function (Gerig, 2001) is similar to the previous function, but the square root of the average squared distances is calculated. *F7*=0 for a perfect fitting.

$$F_7 = \frac{1}{N} \sum_{i=1}^{N} \sqrt{\frac{\sum d(R_i, S_i)^2 + \sum d(S_i, R_i)^2}{B_i}} \quad (15)$$

3.8 Maximum Symmetric Absolute Perimeter Distance

This function (Gerig, 2001) is similar to the previous two functions, but only the maximum of all border pixels distances is taken instead of the average. *F8*=0 for a perfect fitting.

$$F_8 = \frac{1}{N} \sum_{i=1}^{N} max(d(R_i, S_i), d(S_i, R_i)) \qquad (16)$$

4. EXPERIMENTS

An area of 418x599 pixels of a *Quickbird* image with spatial resolution of 0.67m and 4 bands was used in the experiments. This region was chosen because of the wide variety of patterns observed. Three groups of reference objects were delineated for this image so called homogeneous, heterogeneous and mixed (homogeneous and heterogeneous) groups.

All the experiments were conducted on a software prototype called SPT (Segmentation Parameters Tuner) available for download at *www.lvc.ele.puc-rio.br*. This software implements an automatic method for segmentation parameters adaptation using GA.

Figure 2. *Quickbird* image.

4.1 First Experiment

In the first experiment the objective was to determine which metrics are equivalent as evaluation functions for the GA in our application. This was done by measuring the correlation coefficients between pairs of corresponding values delivered by the different metrics. The segmentation parameters values used in this experiment were:

color weight – 0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0
scale parameter – 5, 10, 15, 20, 25, 30, 35, 40, 45, 50
compactness weight – maintained in 0.5

From the combination of these values 121 parameter values sets were obtained. For each set, and for each reference group, the evaluations delivered by the metrics were calculated and the Kendall's and Spearman's rank correlation coefficients were obtained for each pair of values. The results are shown below.

Kendall Correlation							
	F1	F2	F3	F4	F5	F6	F7	F8
F1	1.00	0.33	0.72	0.70	0.85	0.85	0.83	0.77
F2	0.33	1.00	0.63	0.66	0.39	0.44	0.41	0.40
F3	0.72	0.63	1.00	0.96	0.71	0.78	0.74	0.70
F4	0.70	0.66	0.96	1.00	0.69	0.75	0.73	0.69
F5	0.85	0.39	0.71	0.69	1.00	0.82	0.80	0.75
F6	0.85	0.44	0.78	0.75	0.82	1.00	0.93	0.85
F7	0.83	0.41	0.74	0.73	0.80	0.93	1.00	0.89
F8	0.77	0.40	0.70	0.69	0.75	0.85	0.89	1.00

Spearman Correlation							
	F1	F2	F3	F4	F5	F6	F7	F8
F1	1.00	0.42	0.87	0.85	0.96	0.96	0.95	0.91
F2	0.42	1.00	0.81	0.83	0.49	0.57	0.55	0.54
F3	0.87	0.81	1.00	0.99	0.87	0.92	0.90	0.88
F4	0.85	0.83	0.99	1.00	0.86	0.91	0.89	0.87
F5	0.96	0.49	0.87	0.86	1.00	0.95	0.93	0.90
F6	0.96	0.57	0.92	0.91	0.95	1.00	0.99	0.96
F7	0.95	0.55	0.90	0.89	0.93	0.99	1.00	0.98
F8	0.91	0.54	0.88	0.87	0.90	0.96	0.98	1.00

Table 1. Correlation coefficients for the homogeneous reference group.

Kendall Correlation								
	F1	F2	F3	F4	F5	F6	F7	F8
F1	1.00	0.07	0.55	0.51	0.72	0.65	0.65	0.66
F2	0.07	1.00	0.57	0.62	0.33	0.33	0.32	0.23
F3	0.55	0.57	1.00	0.94	0.71	0.69	0.68	0.60
F4	0.51	0.62	0.94	1.00	0.68	0.66	0.65	0.57
F5	0.72	0.33	0.71	0.68	1.00	0.78	0.77	0.72
F6	0.65	0.33	0.69	0.66	0.78	1.00	0.94	0.78
F7	0.65	0.32	0.68	0.65	0.77	0.94	1.00	0.82
F8	0.66	0.23	0.60	0.57	0.72	0.78	0.82	1.00

Spearman Correlation								
	F1	F2	F3	F4	F5	F6	F7	F8
F1	1.00	-0.00	0.68	0.63	0.88	0.83	0.83	0.83
F2	-0.00	1.00	0.70	0.75	0.31	0.38	0.36	0.24
F3	0.68	0.70	1.00	0.99	0.85	0.86	0.85	0.77
F4	0.63	0.75	0.99	1.00	0.82	0.83	0.82	0.74
F5	0.88	0.31	0.85	0.82	1.00	0.93	0.92	0.88
F6	0.83	0.38	0.86	0.83	0.93	1.00	0.99	0.92
F7	0.83	0.36	0.85	0.82	0.92	0.99	1.00	0.94
F8	0.83	0.24	0.77	0.74	0.88	0.92	0.94	1.00

Table 2. Correlation coefficients for the mixed reference group.

Kendall Correlation								
	F1	F2	F3	F4	F5	F6	F7	F8
F1	1.00	-0.23	0.41	0.35	0.56	0.54	0.56	0.64
F2	-0.23	1.00	0.41	0.48	0.20	0.17	0.16	0.01
F3	0.41	0.41	1.00	0.92	0.67	0.65	0.64	0.53
F4	0.35	0.48	0.92	1.00	0.64	0.61	0.60	0.48
F5	0.56	0.20	0.67	0.64	1.00	0.76	0.76	0.66
F6	0.54	0.17	0.65	0.61	0.76	1.00	0.93	0.76
F7	0.56	0.16	0.64	0.60	0.76	0.93	1.00	0.80
F8	0.64	0.01	0.53	0.48	0.66	0.76	0.80	1.00

Spearman Correlation								
	F1	F2	F3	F4	F5	F6	F7	F8
F1	1.00	-0.43	0.53	0.44	0.71	0.71	0.73	0.80
F2	-0.43	1.00	0.52	0.61	0.15	0.19	0.17	-0.04
F3	0.53	0.52	1.00	0.98	0.83	0.84	0.83	0.71
F4	0.44	0.61	0.98	1.00	0.79	0.80	0.79	0.65
F5	0.71	0.15	0.83	0.79	1.00	0.92	0.92	0.83
F6	0.71	0.19	0.84	0.80	0.92	1.00	0.99	0.92
F7	0.73	0.17	0.83	0.79	0.92	0.99	1.00	0.94
F8	0.80	-0.04	0.71	0.65	0.83	0.92	0.94	1.00

Table 3. Correlation coefficients for the heterogeneous reference group.

In all tables the values that lied above the calculated critical value are highlighted with green and those which lied below this threshold are highlighted with red.

Most metrics are highly correlated. However, the F2 metric (Larger Segments Booster) proved not to be as correlated as the others presenting a correlation coefficient below the critical value most of the time. This characteristic can be imputed to the discontinuity present in this metric equation as seen in Section 3.

It was also possible to verify that the correlation coefficients were larger in the homogeneous reference group, after in the mixed group and at last in the heterogeneous group. This indicates the increasing difficulty of the GA, no matter which metric is used, to search for the optimal solution as the reference samples were getting more heterogeneous.

4.2 Second Experiment

In the second experiment the interest was on verifying if the metrics lead the GA to close, similar solutions. The GA was executed with 80 individuals, 50 generations and 3 experiments. The compactness weight was maintained in 0.5 and the band weights in 1.0. The evolution was executed for each reference group and evolved the scale and color weight parameters. The results are shown in Tables 4-6.

	Scale	Color
F1	34.01	0.11
F2	34.27	0.11
F3	34.46	0.11
F4	31.81	0.11
F5	24.61	0.07
F6	33.57	0.11
F7	34.82	0.11
F8	32.30	0.09

Table 4. Parameters values obtained with the homogeneous group.

	Scale	Color
F1	22.82	0.06
F2	30.18	0.07
F3	24.37	0.06
F4	30.36	0.08
F5	26.42	0.05
F6	24.43	0.06
F7	24.39	0.06
F8	30.93	0.08

Table 5. Parameters values obtained with the mixed group.

	Scale	Color
F1	24.41	0.06
F2	31.41	0.07
F3	24.36	0.06
F4	24.36	0.06
F5	24.02	0.05
F6	24.49	0.06
F7	24.52	0.06
F8	28.19	0.05

Table 6. Parameters values obtained with the heterogeneous group.

The experiment showed that the F1 metric (Reference Bounded Segments Booster) converged faster than the others when the sample was homogeneous or had a homogeneous part.

As expected the metrics evolved to very similar solutions. This is coherent with the results obtained in the first experiment.

5. CONCLUSIONS AND FUTURE WORKS

This work examined eight different similarity metrics in a GA based segmentation parameters adaptation method. In all steps this study verified the behavior of these metrics upon a set of reference segments with different characteristics, i.e., homogeneous, heterogeneous and mixed.

The first investigated aspect was the metrics correlation degree. For this experiment two correlation methods were used: Spearman's and Kendall's rank correlation coefficients. The experiment showed that for both methods almost all metrics were highly correlated, what suggests that they tend to rank the quality of different segmentation outcomes quite in the same way.

However, it is important to say that the F2 metric (Larger Segments Booster) is much less correlated than the others,

obtaining a correlation coefficient below the calculated critical value, what identifies an almost non-existent correlation.

The second experiment investigated if the metrics would lead the GA to the same optimal solution. For this verification, evolutions were carried out using each metric. The experiments had shown that the GA based method led to similar results for all metrics, although the F1 (Reference Bounded Segments Booster) metric presented better convergence behavior.

Another future investigation concerns to the comparison between the evaluation given by the metrics and the human perception of a good segmentation.

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