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Horizontal highway segmentation optimisation using genetic algorithms

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This paper presents the use of genetic algorithms (GAs) for optimising different global positioning system-based procedures for horizontal roadway alignment extraction. Two algorithms are proposed – one uses design information to guide the GA, aiming to evaluate the segmentation procedures' precision, while the other uses curve-similarity measures. The linear matching model, the discrete Fréchet distance and the modified Hausdorff distance were tested for guiding the optimisation algorithm in cases when there is no design information available. This paper also presents an extension to a segmentation method available in the literature for increasing the optimisation performance. The proposed algorithms were evaluated on a synthetic data set with 2100 curves. In the experiments, both algorithms correctly identified all the curves, with the best segmentation precision achieved by the algorithm with design information, closely followed by the curve-similarity metrics. Compared with manual segmentation, all showed good results.

Notation

a	chromosome
b	set of values that represent a chromosome
C	curve on design project
C_r	segmented curve
D	δ_F: Fréchet distance
E_1	error for comparison rule 1
E_2	error for comparison rule 2
n	number of curves
P_c	curvature point of a curve
P_t	tangency point of a curve
R	radius error
V	metric space
$\boldsymbol{v}$	distance vector from a set of points to curve f
$\boldsymbol{v}_\mathrm{r}$	distance vector from a set of points to curve g
X	curvature point error
x	point in curve f
Y	tangency point error
y	point in curve g
Z	centre point error
α, β	arbitrary continuous nondecreasing function from [0,1] onto [a,b]

1. Introduction

Transportation studies frequently require geometric information on road infrastructure. Among such data, horizontal curves are of particular interest because they have been shown to be hazardous roadway components (Bogenreif *et al.*, 2012; Hummer *et al.*, 2010; IfT, 2012). Furthermore, information such as curve radius and length is also used for speed estimates (Castro *et al.*, 2011; Garcia *et al.*, 2013) and service-level models (Hashim and Abdel-Wahed, 2012; TRB, 2000).

An example of this information use is the selection of federal highway segments suitable for the installation of the new Brazilian model for the weight control of cargo vehicles (integrated and automated supervision stations, known as Piafs). The location of these Piafs must meet some geometric restrictions: they must be in a straight (tangent) of at least 700 m or in a curve of at least 1000 m radius and, up to 400 m from that point, there must be another point that is a straight of at least 110 m. There is an estimate to install 300 Piafs.

Usually, horizontal curve information is only available in design projects. However, since many roadways were designed and built decades ago, their design projects, when available, do not always provide support for automatic information extraction, making this a laborious task. In addition, data extracted from design projects can be inaccurate due to differences between the road design and the as-built status. Such differences could be caused by corrective actions or faulty project execution.

Traditionally, curve information could only be extracted in field visits, which makes the cost of creating and maintaining a nationwide or statewide curve database prohibitive. However, nowadays, using global positioning system (GPS), it is possible to obtain raw alignment data precisely with vehicles driving at highway speed. This information is then post-processed to extract roadway elements (Rasdorf *et al.*, 2012).

Several algorithms for horizontal alignment extraction can be found in the literature, such as those presented by Drakopoulos and Örnek (2000), Imran *et al.* (2006), Worrall and Nebot (2007) and Harpring (2010). Each algorithm uses a different segmentation approach, with different parameters, and achieves different results. The value of each parameter in each algorithm strongly affects the segmentation accuracy, and its optimal value should be tuned according to the input segment. This situation makes comparisons between different segmentation algorithms on large and heterogeneous data sets either inaccurate, by using default parameter values for all the data, or laborious, by manually adjusting each parameter for each input data to its optimal value. Moreover, optimal parameter values are usually established by comparing the achieved results to expected ones (ground truth), thus affecting the suitability for sets of unknown data.

Genetic algorithms (GAs) are stochastic search and optimisation mechanisms that mimic natural selection and biological reproduction processes, guided by a fitness function (Guo *et al.*, 2010). First introduced in the early 1970s, GAs have been successfully applied to a large number of situations, such as automated component design (Bolchini *et al.*, 2010), design optimisation (Guo *et al.*, 2010), robotics (Alvarado-Velazco and Ayala-Ramirez, 2012) and feature extraction (Cateni *et al.*, 2012).

The purpose of work reported in this paper was to use GAs to automatically optimise parameters for horizontal segmentation mechanisms of polygons that represent road axes. The paper is organised as follows: the next section describes some of the horizontal segmentation mechanisms found in the literature; Section 3 provides a brief introduction to parameter optimisation using GAs; the developed optimisation algorithms are presented in Section 4; the test data set used in the experiments and the optimisation process results are described in Section 5. Finally, the paper ends by presenting conclusions and proposing future research topics.

2. Horizontal segmentation mechanisms

Most design projects represent highway axes as directed polygons composed of straight and curved segments. In design terminology, straight segments are called tangents and curved segments are divided into circular curves and transition curves. The information available on design projects consists of each segment description.

Segment extraction from a set of GPS points measured over a highway axis has already been subject to various studies. Mathematical models such as ψ–s curves (Joshi, 2006), clothoids (Song, 2006) and splines (Castro *et al.*, 2006) have been used for curve extraction. The inference of highway design features was also performed by least-square regressions (Lee *et al.*, 2001).

Besides mathematical models, procedural segmentation mechanisms have also been presented in the literature. Drakopoulos and Örnek (2000) proposed a two-step algorithm to automatically extract the curve length, direction and curvature degree (the algorithm only models circular curves) from data obtained by a vehicle equipped with a GPS and a compass. The first step is to identify the curvature (P_c) and tangency (P_t) points by analysing the difference between compass readings at consecutive points. When this difference is greater than the threshold, the point is marked as P_c. When the compass difference is below the threshold, the point is marked as P_t and a curve is defined. In the second step, curve segments with a degree of curvature below a predefined value are reclassified as tangents.

Another procedural segmentation mechanism was presented by Harpring (2010). In this method a circle is fitted to each three consecutive points. These points are then split into tangent and curve points using a predefined maximum radius. Circles with a radius greater than the maximum are considered part of tangents. The points below this value are then clustered according to the centre of the fitted circles (consecutive points with a distance between circle centres below a threshold are considered part of the same curve).

The algorithm to build digitalised maps from a cloud of GPS points presented by Worrall and Nebot (2007) also supports the identification of tangents and circular curves, including the extraction of curve radius and internal angle. This algorithm clusters the GPS data into a single polygon and then iteratively identifies tangents by using two thresholds, one for noise tolerance and another for tangent identification. Finally, on non-tangent points, it performs a non-linear least-squares fitting to obtain the curve radius and internal angle.

Imran *et al.* (2006) presented a mechanism supporting the extraction of tangent, circular curves and transition curves. This algorithm performs linear regressions to identify tangent segments, with a residue threshold for noise tolerance. It then performs a non-linear regression on the mid-section of each non-classified group to identify the circular curve. Points inside or close enough to the circle are identified as members of the circular curve and points outside the circle are considered members of the spiral part of a transition curve.

3. Overview of GAs

Computer science has adopted the principles of Darwin's theory of evolution to develop optimisation mechanisms known as GAs. A GA is a directed random-search technique to find solutions in multi-dimensional search spaces using the principles of natural selection and genetics. It requires no previous knowledge of the search space and supports the optimisation of non-differentiable or multi-modal functions (Angelova *et al.*, 2011).

Diverging from conventional search techniques such as the gradient search, GAs can handle a set of randomly created candidate solutions known as a population. Each element of the population is called a chromosome and each chromosome contains a genotype that stores the parameter values. The genotype can be represented as a binary vector or it can use high-order alphabets like integers or floating points. Algorithms that mimic natural selection, reproduction and mutation processes are then iteratively applied to the population. Algorithms help to find the fittest solutions of each generation by spreading its genetic traits to the next one. After several generations, the propagation of beneficial genetic traits produces better individuals, leading to an optimised population.

The core of a GA is the fitness function. This defines the overall quality of a solution and is used as an input for the selection mechanism, directing the search to better solutions. This function is traditionally expressed as a map function $f(a) \rightarrow b$ where a is a chromosome and b is the set of values that represent its quality as a solution.

4. Proposed optimisation algorithms

This paper presents two optimisation mechanisms. One is based on design information and aims to assess a segmentation algorithm precision. The other, based on curve-similarity measures, allows optimisation of unknown data. In order to fit the GA structure, optimisation algorithms were developed as fitness functions. This approach allows them to be used with different segmentation mechanisms and supports the use of different GA and genotype storage forms.

4.1 Optimisation with design information

The first developed optimisation algorithm uses design information to measure how close a segmentation mechanism could get to the real data. It is based on the number of correctly identified curves, alongside the radius, curvature and tangency points of each curve.

The use of different segmentation mechanisms or even small changes in the parameters of a single mechanism may produce different outputs. To measure the difference between segmentations, the first step is to match each curve (C) of the design plan with a curve (C_r) from the segmentation found by the algorithm.

This matching is performed by finding a curve (C_r) whose start and end points are close enough (with a certain threshold) to the start and end points of a design curve C. If more than one curve is found, the curve whose centre is closer to the design curve centre is chosen. Once the matching is done, the fitness of an individual is defined as a vector composed of the number of missing curves, the number of surplus curves and the distance between the curvature point, tangency point, centre point and radii for each design curve. An example of this fitness vector structure for a two-curve polygon is shown in Figure 1.

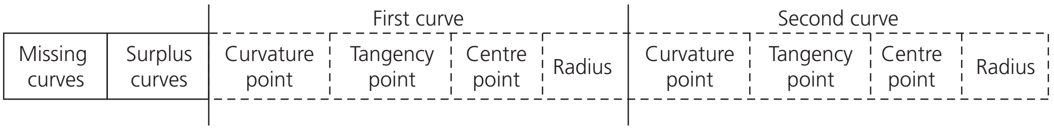
To compare the fitness vector of two chromosomes, four rules were defined. If a chromosome is considered better at any step, the mechanism stops and no further rule is evaluated. Considering a comparison between two chromosomes, the four rules are defined as follows.

Rule 1: the best chromosome is the one with the fewest missing curves.
Rule 2: the best chromosome is the one with the fewest surplus curves.
Rule 3: considering the curvature point error as X, the tangency point error as Y, the centre point error as Z and n as the number of curves, the best chromosome is the one with minimum total error (E_1) defined by

$$E_1 = \sum_{t=1}^{n} X_i + Y_i + Z_i \tag{1}$$

Rule 4: considering the radius error as R and n as the number of curves, the best chromosome is the one with the minimum total error (E_2) defined by

$$E_2 = \sum_{i=1}^{n} R_i \tag{2}$$



		First curve				Second curve			
Missing curves	Surplus curves	Curvature point	Tangency point	Centre point	Radius	Curvature point	Tangency point	Centre point	Radius

Figure 1. Example of fitness vector for a polygon with two curves

4.2 Optimisation with curve-similarity measures

The second optimisation algorithm uses curve-similarity measures to approximate the segmented alignment with its original one. Three curve-similarity metrics were evaluated – the linear matching model (LMM), discrete Fréchet distance (DFD) and the modified Hausdorff distance (MHD).

According to Shehu and Dika (2012) the LMM distance is the average distance between each pair of points. The DFD is a variation of the Fréchet distance for use with polygons, as proposed by Eiter and Mannila (1994). This metric searches all coupling possibilities between the polygon end points. Equation 3 presents such a distance, considering two curves f:[a, b] → V and g:[a_r, b_r] → V.

$$D = \delta(f, g) = \inf_{\alpha, \beta \in [0,1]} \max[f\,(\alpha(t)), g(\beta(t))] \tag{3}$$

The MHD, a metric based on the Hausdorff distance (Henrikson, 1999), was proposed by Dubuisson and Jain (1994). To apply this distance to two curves f:[a, b] → V and g:[a_r, b_r] → V, it is necessary to build a distance vector ($\boldsymbol{v}$) for f and a distance vector ($\boldsymbol{v}_r$) for g. Then, given a point $x \in f$, each position of $\boldsymbol{v}$ is defined as the minimum distance from x to the points belonging to g. In addition, given a point $y \in g$, each position of $\boldsymbol{v}_r$ is defined as the minimum distance from y to the points belonging to f. The MHD is the maximum value between the average of $\boldsymbol{v}$ and the average of $\boldsymbol{v}_r$.

In contrast to the previous optimisation algorithm, which maps a chromosome into a fitness vector that must be compared using a set of rules, this algorithm maps the chromosome into a floating point number, with smaller values representing better solutions.

To apply this metric on a solution, the segmentation results (i.e. the description of each segment) must be converted back into a polygon. To convert a tangent segment into a polygon, the number of points in the tangent and its start and end points are required. With this information it is possible to obtain the equation of the straight line that passes through its start and end points. Then, using this line equation, the number of points in the segment must be uniformly distributed over the line.

The conversion of a circular curve segment into a polygon requires the number of points, the curvature, tangency and centre points. This information differs from the information usually used in geometric design plans, where a curve is defined by its radius, curvature and tangency points. However, using this information, the non-linear equation system shown in Equation 4 returns two possible centre points. In Equation 4, r is the radius and S, E and C are the curvature, tangency and centre points, respectively. With the required information it is possible to distribute points uniformly over the curve using the equation of the circle.

$$\begin{cases} (S_x - C_x)^2 + (S_y + C_y)^2 = r^2 \\ (E_x - C_x)^2 + (E_y + C_y)^2 = r^2 \end{cases} \tag{4}$$

Once all segment descriptions are converted into polygons, they are merged into a single geometry whose total number of points is equal to the number of points in the original polygon. Those two polygons are then compared using one of the curve-similarity metrics.

5. Evaluation

Evaluation of a segmentation mechanism requires that results are compared to a known set of segments, either extracted from a geometric design plan (which may be inaccurate) or from field visits (which are expensive). To overcome this problem, a set of 200 synthetic polygons containing 2100 circular curves was created. The length and radius histograms of the curves in this data set are shown in Figure 2.

The generated data also included detailed segment description such as the start and end points of each tangent and curvature, tangency and centre points of each circular curve. Figure 3 shows an example of the generated output. The white and black dots on the curve represent the curvature and tangency points, respectively. The circle centres are marked, and the values next to these represent the curve radius (in m).

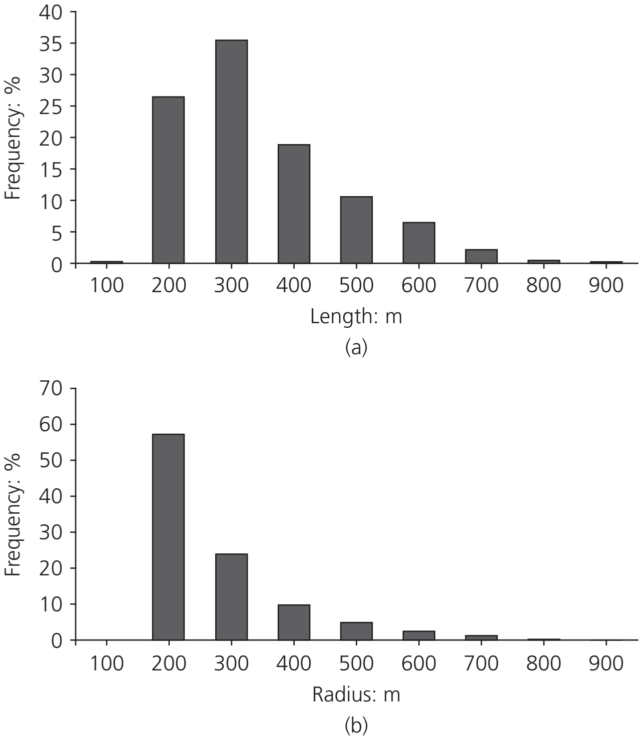


Figure 2. Histograms of synthetically generated polygons: (a) curve length histogram; (b) curve radius histogram

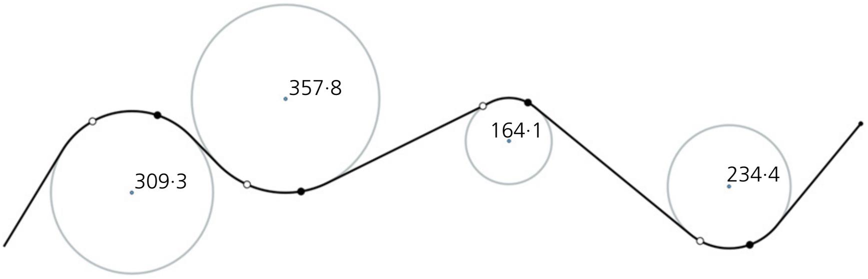


Figure 3. Example of synthetically generated polygon

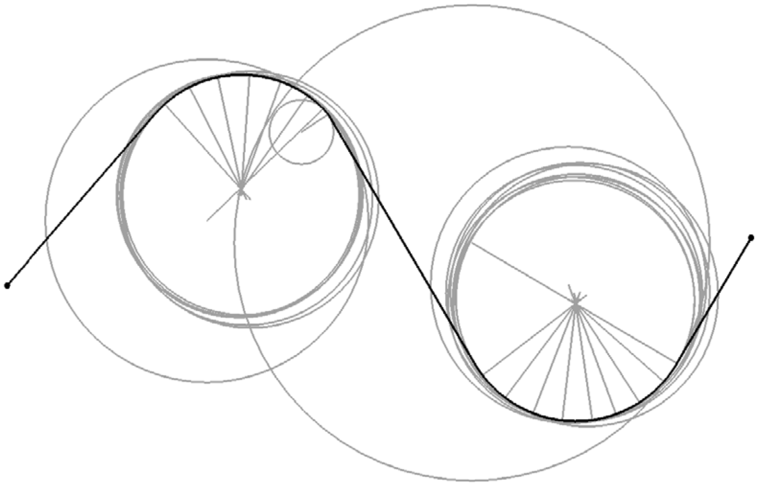


Figure 4. Faulty polygon segmentation as a result of the algorithm of Worrall and Nebot (2007)

Evaluation tests were performed using the algorithms proposed by Worrall and Nebot (2007) and Harpring (2010). The algorithms were first executed with a single manually adjusted parameter set for the whole data set and then calibrated using design information and the three curve-similarity metrics (LMM, DFD and MHD).

The parameters of the Worrall–Nebot algorithm are a coarse threshold, a fine threshold and a slope threshold, which must be optimised for each polygon. To use this segmentation mechanism with a GA, the chromosome genotype was encoded as 192-bit long by a grey-coded binary string (Mehta *et al.*, 1996). The code's first 64 bits represent the coarse threshold, the mid 64 bits represent the fine threshold and the last 64 bits represent the slope threshold.

The Harpring algorithm has a single parameter, the maximum distance between consecutive circle centres. The chromosome genotype was encoded as 64-bit long by a grey-coded binary string, representing the parameter value. The remaining GA parameters used were tournament selection (Mezura-Montes and Coello, 2005), two-point crossover (Koumousis and Katsaras, 2006), bit mutation (Beyer and Schwefel, 2002), a generation gap of 50%, a crossover probability of 70% and a mutation probability of 0·01% (the generation gap, crossover and mutation probabilities were configured according to the values presented by Srinivas and Patnaik (1994)).

During the experiments, faulty behaviour was detected in the Worrall–Nebot algorithm. Due to the calibration, the algorithm split a single segment into multiple smaller ones, as shown in Figure 4. This behaviour is inconsistent with geometric design. There are no consecutive tangent segments in design projects, nor any consecutive curve segments with the same direction and a small radius variation. To overcome this problem, a merge procedure was applied to the results. Consecutive tangent segments were merged into a single tangent whose start point was the start point of the first tangent and the end point was the end point of the last tangent segment. Consecutive curve segments, with the same

Table 1. Optimisation results – valid and invalid identified curves

Algorithm	Metric	Curves: Valid	Curves: Invalid
Worrall and Nebot (2007) (original)			
	None	2100	281
	DP	2092	105
	LMM	1863	115
	DFD	1862	116
	MHD	1862	116
Worrall and Nebot (2007) (merged segments)			
	None	2096	3
	DP	2100	0
	LMM	2100	0
	DFD	2100	0
	MHD	2100	1
Harpring (2010)			
	None	1117	7
	DP	2082	3
	LMM	2047	7
	DFD	2052	7
	MHD	2052	7

Note: DP, design project.

direction, were merged into a single curve by fitting a new circle on the points of all consecutive curves.

The first analysis evaluated the number of valid and invalid curves identified by the algorithms. An identified curve was considered valid when it matched a project curve. Invalid curves were the non-matched ones, that is curves that did not exist in the original project (when the algorithm identified two or more curves within a single project curve, only the most similar curve was matched). The analysis results are shown in Table 1. To demonstrate the faulty behaviour of the Worrall–Nebot algorithm with the calibration, the table also includes the results achieved by the original method.

Once the curves were classified as valid or invalid, it was possible to evaluate the segmentation precision by comparing the valid curves with their equivalents on the design project (DP). This comparison analysed the average distance between the segmentation and project curvature, and the location of the tangency points. It also evaluated the average distance between the measured radii and their designed radii. The analysis results are shown in Table 2: as the Worrall–Nebot algorithm without merged segments performed significantly worse (as shown in Table 1), only the algorithms with merged segments were evaluated in this step.

6. Conclusion and future work

Two algorithms for parameter optimisation for horizontal segmentation mechanisms have been presented – one based on design information and another based on curve-similarity metrics. Tests were performed on a data set containing 2100 synthetic curves using two different horizontal segmentation mechanisms, one of which was extended for the tests.

In all the experiments, the optimisation allowed the segmentation algorithms to identify correctly more curves than with a single parameter set. It also led to a more precise identification of the curves' locations and radii. Comparing the calibrated segmentation algorithms, the algorithm proposed by Harpring (2010) significantly outperformed the original algorithm proposed by Worrall and Nebot (2007). However, when using the extension presented in this paper, the Worrall–Nebot algorithm outperformed Harpring's algorithm in every test.

Considering the number of identified curves, the best optimisation results were achieved using design information, regardless of the segmentation algorithm used. Among the distance-based optimisations, the DFD metric led to better segmentation with Harpring's algorithm and the extended

Table 2. Comparison of algorithm results and synthetic polygons using location and radius parameters

Algorithm	Metric	Location: m: Average	Location: m: Standard deviation	Radius: %: Average	Radius: %: Standard deviation
Worrall and Nebot (2007) (merged segments)					
	None	12·67	6·28	0·50	0·15
	DP	14·34	6·65	0·48	0·48
	LMM	13·36	23·83	0·73	0·28
	DFD	12·63	24·08	0·44	0·24
	MHD	12·66	23·72	0·45	0·25
Harpring (2010)					
	None	94·08	52·44	30·26	23·69
	DP	21·51	22·09	8·51	8·64
	LMM	31·62	18·36	10·69	14·41
	DFD	31·68	18·40	10·75	14·42
	MHD	31·60	18·41	10·71	14·41

Worrall–Nebot algorithm, closely followed by the MHD and LMM. The original Worrall–Nebot algorithm was best optimised using the LMM, with DFD and MHD identifying one less curve.

Regarding the precision of the segments' locations and radii (e.g. analysis of number of curves), the best optimisation results for both methods were achieved using design information. In contrast to the analysis of number of curves, the best results were achieved using a different metric for each algorithm. The difference between the metrics, however, was minimal.

This work could be extended by evaluating the behaviour of different curve-similarity measures in terms of the fitness functions. Future research possibilities also include evaluation of the proposed optimisation algorithms on segmentation mechanisms with transition curve support and the evaluation of optimised segmentation mechanisms on real data.

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