

Defective and redesigned highlight line sections are compared by using sample points too. For this purpose, points in geometric space are used, designated at identical lengths of arch (e.g. 1mm) along the line sections.

4.1 Structure of the Genetic Algorithm

Due to the continuous nature of the surface, the genetic algorithm applied is of real coding (RCGA). The search area and gene representation are individual, the operators applied are versions of those to be found in the literature [3], adjusted to this special task. They were applied by a software with VBA source code of own development, connected to Rhinoceros 4.0 NURBS modeler.

4.1.1 Search, and gene representation

The method searches for solutions by changing the position of affected control points. The size of the search space is the section of space defined by distance $t \cdot b$, normal to surface at affected control points. The value of t is to be determined by experience. The genes consist of control points, and the constant b assigned to them as an attribute of influence.

4.1.2 Generation of initial population

The algorithm was studied at a constant population of size 200. Initial variance is produced by the random modification of control point coordinates, which is identical for each coordinate direction:

$$\Delta P(x, y, z) = \pm \text{rnd} \cdot (t \cdot b)$$

4.1.3 Fitness function

The basis of fitness is the distance between the designed and the current highlight line. Partial functions valid by highlight line consist of the following:

$$f_{1j} = \sum_{i=1}^m (Q_i - A_i)^2, \quad f_{2j} = \sum_{i=1}^m a_i.$$

Where A_i is the current geometric point and Q_i is the geometric point on the designed line, m is the number of sample points. The second function examines whether the highlight line is close to the designed curve everywhere:

$$a_i = 0 \text{ if } d_i \leq \frac{1}{m} \sum_{i=1}^m |d_i - \bar{d}| + \bar{d} \quad a_i = d - \bar{d} \text{ otherwise.}$$

Where $d = Q_i - A_i$.

The fitness function valid for the examined part of surface:

$$F = \sum_{j=1}^l \frac{100}{1 + f_{1j} + f_{2j}}$$

Where l is the number of highlight lines.

4.1.4 Recombination

Recombination is performed on the coordinates x , y and z of control points. It is of the arithmetic type, BLX-alpha [3]. The use of the value $\alpha = 0.2$ yielded the best results. Similarly good results are yielded by single point 2D crossover [3] as well.

4.1.5 Mutation

As regards mutations, the best results were yielded by the non-uniform method [3], gradually decreasing the value of mutation with the progress of search. The mutation ratio applied is 0.12.

5. USABILITY TEST

The figures below show the proceeding of algorithm on an example of a car hood. On Fig. 3a, the initial state is shown. As the result of relatively high t value ($t=1.5$) in the beginning of search the average surface fitness is extremely low, as seen on Fig. 3b and Fig. 2.

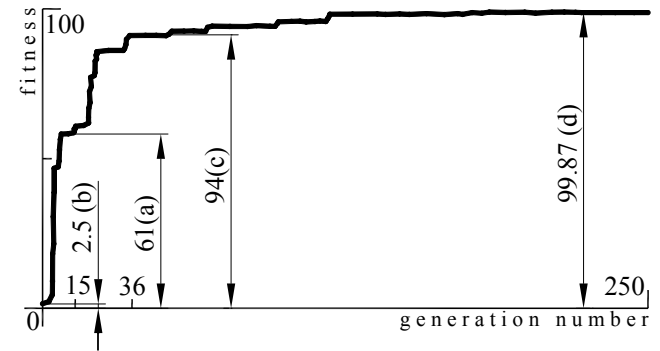


Figure 2. Runoff of the genetic search (Letters in brackets refer to Figure 3.).

The initial fitness was regained only after 15 generation, after which the fitness continued to increase rapidly, until it nearly stalled after 36 generation (Fig. 2). On Fig. 3d is shown the best surface reached after 220 generation.

The usability test performed was successful, the method was capable to find the surface corresponding to designed highlight lines.

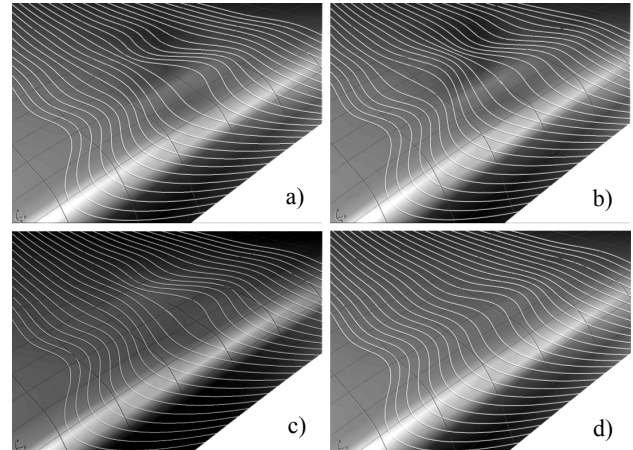


Figure 3. Highlight lines in different stages of search.

6. REFERENCES

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