

Algorithmic Solution of Luminaries Placement - Reflections and Symmetry Issues

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Abstract—The paper deals with lighting road design. The demands on illuminance are defined in standard ČSN EN 13201 in case of Czech Republic. There are several parameters that a designer can change to get the optimal solution to fulfill the standard. The distance between pillars, their heights, the lamp overlap and tilt have to be defined. Such number of parameters make the optimization difficult. This paper solves the optimization via genetic algorithm. The fitness function that is convergent to good solutions is a vital point for this type of algorithms. The paper shows that solutions found by the genetic algorithm fulfill the demands and it also shows the way, how the fitness function can be created.

Keywords - genetic algorithm, lighting, design, illuminance

I. INTERIOR LIGHTENING DESIGN ISSUES

II. PHOTOMETRIC VALUE CALCULATION

III. ALGORITHM DESCRIPTION

A. Genetic Algorithm

The algorithm must determine positions and number of luminaries in dependency on target illuminance and uniformity. This is the multicriteria and multiparametric type of the problem. The genetic algorithm offer quite simple way how to solve it, therefore they were used in this case. The genetic algorithms are well known today so only specific settings are further described.

The best solution was saved (elitism) from every population in two specimens. The first one was unable to change its DNA via mutation, the second one had the same probability of mutation like other solutions. Other parent solutions were selected via tournament selection. It consisted of making random group of 4 solutions from the population and take the one with the best fitness. This type of selection had vital role for the algorithm. It avoided premature convergence of the best solution in comparison with the roulette selection. Similar effect was ensured also by recombination probability set less than 1. There was used just one point crossover during the tests. Overview of the all GA settings is shown in table I.

B. Fitness Function

The fitness function defines how good the solutions are. The target value of average illuminance and target value of

Table I. GENETIC ALGORITHM SETTINGS

First Population	Random logic vectors
Termination Cond.	Maximum number of generations
Number of Gen.	40
Population Size	50
Recombination Prop.	90%
Mutation Prop.	2%
Parent Selec.	Tournament 1 of 4
Mutation Mech.	Inverted bit
Survival Selec.	Elitism

uniformity are watched in the algorithm. In common case the average illuminance is given especially by number of the luminaires. The uniformity is given especially by placement of the luminaires on the other hand. The count of the luminaires is proportional to the investment cost to the lighting system. So the number of luminaires that exactly fulfill the target average value of illuminance is appropriate. The uniformity is always required as much as possible for defined number of luminaires. Therefore the fitness function was determined within discussed facts as follows:

$$f_{DNA}(E_{avg}, U_0) = g_1(E_{avg}) + g_2(U_0) \quad (1)$$

$$g_1(E_{avg}) = \begin{cases} e^{\frac{E_{avg} - E_{avgT}}{E_{avg}}} & , \langle 0, E_{avgT} \rangle \\ e^{\frac{E_{avgT} - E_{avg}}{E_{avg}}} & , (E_{avgT}, \infty) \end{cases} \quad (2a)$$

$$g_2(U_0) = \begin{cases} \frac{U_0}{2 \cdot U_{0T}} & , \langle 0, U_{0T} \rangle \\ 1 - \frac{e^{U_{0T} - U_0}}{2} & , (U_{0T}, \infty) \end{cases} \quad (3a)$$

$$g_2(U_0) = \begin{cases} \frac{U_0}{2 \cdot U_{0T}} & , \langle 0, U_{0T} \rangle \\ 1 - \frac{e^{U_{0T} - U_0}}{2} & , (U_{0T}, \infty) \end{cases} \quad (3b)$$

where:

E_{avg} is a calculated average value of illuminance,
 E_{avgT} is a target average value of illuminance,
 U_0 is a calculated uniformity,
 U_{0T} is a target uniformity.

The function $g_1(E_{avg})$ has peak value equal to 1 at target value of average illuminance. Because the illuminance cannot

be less than zero, the function reaches two limits:

$$\lim_{E_{avg} \rightarrow 0+} g_1(E_{avg}) = 0 \quad (4)$$

$$\lim_{E_{avg} \rightarrow \infty} g_1(E_{avg}) = e^{-1} \quad (5)$$

Both limits have different values and the limit in infinity is higher than that in the 0. This means that it is preferred the solution with the higher average illuminance for the same absolute difference from the target value.

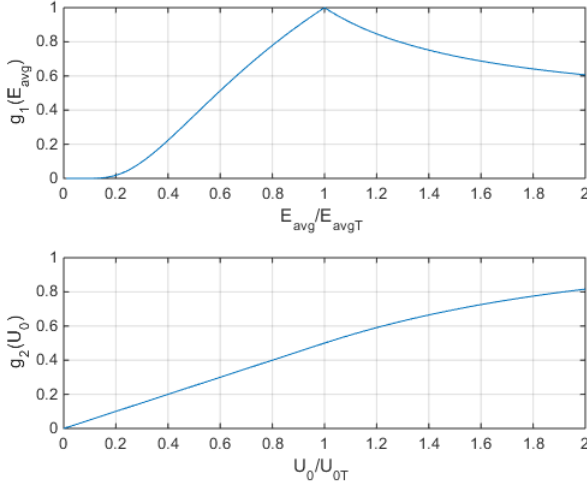


Figure 1. Graphs of parts $g_1(E_{avg})$ and $g_2(U_0)$ from the fitness function

The function $g_2(U_0)$ reach the value 0.5 at target value of uniformity. It has a bound at 0 for values less then target value. There is a limit for values in interval higher than target value:

$$\lim_{U_0 \rightarrow \infty} g_2(U_0) = 1 \quad (6)$$

So the function $g_2(U_0)$ has an horizontal asymptote equal to one. Function $g_2(U_0)$ is linear for values of uniformity less than the target value. The highest slope is obtained here. For higher values of uniformity is the slope smaller due to the saturation effect of the exponential function. Therefore the algorithm is forced to reach target value of uniformity because of big change in the fitness function. Higher values makes the fitness better too but there is smaller effect. Both functions $g_1(E_{avg})$ and $g_2(U_0)$ are shown in figure ?? for better understanding.

IV. PROPOSED DNA

A. Symmetric Solutions

One of the requirements to the output design was to get the symmetric solutions of luminaire placement. There seemed to be two approaches how this might be done. The First counts with introduction of the symmetry in the fitness function. On the basis of the fitness equation evaluation the algorithm can prefer symmetric solutions more than others. Unfortunately this approach was very difficult due to unknown function that could describe how good is the symmetry of the luminaire placement. Best experience came from using

least squares method. After adding the sum of squares of the differences towards the average value of illuminance, a lot of output results showed the symmetry towards axis or center. However some types of luminous intensity distribution curves were very sensitive to create a tight groups of luminaires in specific positions. This type of solutions were unable to realize in real conditions. At last the second approach dealing with introduction of the symmetry in the DNA was chosen. The symmetry towards the center and the symmetry towards the axis were further studied. The center symmetry was reached by proposing the luminaire positions only for one half of the room. The another half of positions were got by mirroring towards both axis. Similar for the axis symmetry was proposed the position only for one quarter of the room. Other quarters were got by mirroring. It is obvious that there must be even number of luminaires in case of center symmetry and number of luminaires divisible by four in case of axis symmetry. This approach works well but the designer must keep in mind that he never gets results for odd number of luminaires respectively for numbers of luminaires that are not divisible by four.

B. Grid of Allowed Positions

Some types of luminous intensity distribution curves were prone to place the luminaires to groups with almost the same coordinates as it was mentioned in the section IV-A. Very close distances are not allowed because of defined luminaire sizes. To fix this behavior of the algorithm, the luminaires are placed to the defined grid now. Positions out of the grid intersections are not allowed.

Grid of allowed positions also let the designer to define specific shape of area for the luminaire independently on the shape of the room. This might be useful for rooms with complex design on the ceiling or where the recessed luminaire are used. On the other hand the set of solutions is restricted always only on the grid.

C. DNA structure

The resulting DNA just defines logic vector of luminaire presence in the specific grid intersection. The length of the DNA depends on the number of grid intersections and on the type of the symmetry:

$$L_{DNA} = \frac{N_G}{2 \cdot sym} \quad (7)$$

where:

N_G is number of grid intersections,
 sym is the chosen symmetry that is equal to 1 for center symmetry and equal to 2 for axis symmetry.

Table II. STRUCTURE OF THE DNA

$\{0, 1\}$ for $[x_1, y_1]$	$\{0, 1\}$ for $[x_2, y_1]$...
$\{0, 1\}$ for $[x_1, y_2]$...	$\{0, 1\}$ for $[x_n, y_m]$

The proposed structure of DNA lets the algorithm determine needed number of luminaires. Therefore the designer just sets target value of illuminance, target value of uniformity, the luminous intensity distribution curve for chosen luminaires and the grid.

V. PROGRAM BEHAVIOR

dva typy symetrie. Pro středovou jsou výsledky více kreativní. Velká souvislost mezi délkou DNA a nastavenou mutací. Pro velkou mutaci program špatně konverguje. Optimalně je pro 200 0.01

VI. RESULTS IN PROGRAM BUILDING DESIGN

VII. CONCLUSION

Here comes conclusion.

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