Improving the Graphical Cadastre Based on Genetic Algorithm Principles

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SUMMARY

An unconventional approach for obtaining a legally supportive, 2D coordinate based cadastre is addressed. The proposed method considers natural selection or biological optimizations known as Genetic Algorithm (GA), which has been widely applied in solving complex computation problems in a variety of disciplines. This paper describes the implementation of GA in the cadastral domain employing its principle to achieve unique, accurate and homogeneous coordinates, with a standard deviation complying with Survey of Israel (SOI) requirements.

The existing method of land property registration in Israel is based on a definition of a land unit (parcel), identified by a unique number within a registered block, and graphically plotted based on field measurements linked to the national coordinate system. The products of the ground measurements are recorded in field books, following which the block borderlines, parcel turning points (vertices) and additional details are plotted on field sheets. As a result, the current cadastral system is of an analog nature and deals with surface properties only. Due to an increasing number of urban centers, urban and land development projects, and the urgent need for a more accurate cadastre in the digital era, the transition to an analytical cadastre is both crucial and inevitable. Some of the research addressing this issue includes RTK GPS technologies to reinstate parcel boundaries, advanced algorithms such as rubber-sheeting applied to cadastral maps, and most commonly, the Least Squares method for cadastral boundaries adjustment. All these methods are mainly analytical and straightforward. GA, on the other hand, offers a stochastic approach, which begins with a diverse range of possible solutions to a problem at hand and provides the optimal solution by mimicking the natural (biological) processes. Over a series of generations (iterations) the suggested algorithm quickly provides an encouraging and feasible solution, iteratively manipulating the initial population (randomly generated solutions). Each generation is evaluated by a fitness function, undergoing selection, mutation and recombination (crossover) to produce new and better solutions. The paper presents an implementation of GA principles in the cadastral domain. Based on a large number of simulations, and allowing for a clear resemblance between the GA solution and the conventional methods, in most cases the results of the GA are better – the coordinates are closer to their "true" value than those obtained from the common alternative, the LS technique.

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1. INTRODUCTION

Cadastre is a vital factor in proper management of land properties and the economy of a country. Thus an analytical, homogenous and accessible system, which contributes to faster property rights registration, is a top priority. The current cadastre in Israel, as in many other countries, is based on field surveys recorded over decades in field books and used to determine the boundaries of blocks and parcels. Cadastral measurement is a continuous process, due to changes in land ownership, joining and dividing parcels, and the constant necessity to redefine and update the ownership boundaries. Most information is currently kept on paper (field books, field sheets), not permitting computerized management (Kraus et al., 2007).

Over the past few years one of the main objectives on the SOI agenda has been the transition from the existing physical cadastre to a coordinate based cadastre with legal validity - by gathering and sampling graphic cadastral data (Steinberg, 2001; Doytsher and Gelbman, 1995). It is evident that such a transition involves numerous computations and data adjustment from different and varied sources and requires establishing accuracy definitions of the database (Fradkin and Doytsher, 2002). For the time being, it is estimated that renewal of the existing system will take approximately ten to fifteen years and will relate to financial, legal, engineering, social and even political matters (Amir M., 2006).

A digital homogeneous cadastral system will contain analytical data, i.e. unique coordinates of parcel turning points, and will enable reconstruction and reinstatement of boundaries, smart, efficient and computerized management of real estate, faster planning of development projects, minimizing border conflicts and keeping up with currently customary high work standards.

Digital cadastre is one of the concrete topics being discussed and researched in many countries throughout the globe, including Greece (Potsiou et al., 2001), the Netherlands (Jan Wakker et al., 2003), Japan and Israel (Fradkin and Doytsher, 1998), and proposing potential solutions.

Most customary solutions currently offered on the market, which attempt to transform graphic data into digital data with statutory characteristics, and/or manage the accuracy of the obtained data, are based mainly on the Least Square (LS) method which assumes the best fit to be the minimal sum of deviations squared (LS error) from the given data. Some methods attempt to solve the inconsistencies of the digitized and registered areas by applying constrained LS adjustment with regard to geometric and juridical constraints (Xiaohua et al., 2005), others include up-to-date technologies (RTK GPS) for boundaries reconstruction (Jarroush, 2002). Since most conventional methods used have their drawbacks, GA has great potential as a novel approach for improving the graphic cadastre.

LS is described as an analytical approach whereas GA is a very powerful stochastic method, founded on evolutionary ideas and Darwin's principles of selection and survival of the fittest, which operate on a population of solutions. This algorithm is very general, best suited for providing a high quality solution to a problem of which little is known. As such it is applicable in many fields, such as: computer science (Jia and Rajkumar, 2006), medicine (Dolled-Filhart et al., 2006), economics (Goyal, 2007), chemistry (Leardi, 2007), physics (Sanchis et al., 2004) and many others.

The generic framework of GA is composed of several basic elements:

- An initial *population* of *n* vectors is randomly generated with a group of *individuals* (*chromosomes*, any possible solution)
- The individuals in the population are evaluated by a *fitness* function with each assigned a *grade* based on given constraints or requests.
- A new population is then created by applying variation-inducing operators: *mutation* and *crossover* (recombination), repeating the following steps:
    1. **Selection -** two parent chromosomes are selected from a population according to their fitness (the higher the fitness, the higher the chance of being selected)
    2. **Crossover –** one or more *offspring* created. If no crossover was performed, each offspring is an exact copy of an initial *individual*.
    3. **Mutation -** the new offspring are changed randomly to ensure diversity.
    4. **Acceptance -** new offspring are placed in a new population for another run of the algorithm

The algorithm run is stopped once an end condition is satisfied (a suitable solution found) or a certain number of *generations* (iterations) have passed.

The analogy can be fitted to a cadastre: with a generation being coordinates of vectors representing turning points of parcels in a block. With each generation the vectors are altered according to the best solution proved – adjusted coordinates that optimally satisfy the given constraints.

As mentioned earlier, GA is applied in many areas, be they educational, commercial-marketing, the traveling salesman problem (Gupta et al., 2008), or scientific: information systems, robot vision (Leing et al., 2003). Once the problem is encoded correctly, the solution is simple and elegant.

Recent achievements accounted with GA include research in aeronautics sphere. Centralized operation of unmanned aerial vehicles (UAVs) motion planning for tracking in urban environments is approached using GA. A visual database of Tel-Aviv was used for the algorithm implementation, in which the tracing task was cast as optimization of the motion planning problem and the cost function was associated with the UAVs positions relative to visibility and restricted regions (Shaferman & Shima, 2008). Another example in this area: a good feasible solution is provided by GA in the case of integrated task assignment and path planning for a group of UAVs (Edison & Shima, 2008).

2. THE PROPOSED ALGORITHM MECHANISM

To implement a GA, the solutions to the addressed problem must first be encoded in a structure that can be stored in the computer. One may use binary strings (where each unit represents a different attribute of the solution), trees, lists, arrays or matrices. Any representation may be used for the individuals in the genetic algorithm as long as each individual depicts a complete solution to the given problem and the genetic operators (initialization, mutation, crossover) are defined.

In the present case the array representation is preferred. Each individual in the population represents a set of block coordinates stored in an array (vector) structure. Each vector contains all turning points within a given block; with some coordinates being mutual to several parcels (joint boundaries). An objective function is defined to minimize the differences between the legal (registered) coordinates and those provided by the solution under the conditions specified (best suited to the predefined criteria). During every evolution (iteration) parent vectors (two or more arrays) are selected to produce individuals of the next generation, by applying one or more variation operators, but single child crossover is suitable as well (a single vector undergoes mutation). Every individual may assumed to be a set of coordinates, representing acceptable observations received from different sources (GPS, Total Station measurements). The aim of the GA process is to attain suitable solution vectors, which take into consideration all observations made and meets the requirements of cadastral and geometric conditions.

Obtaining a solution regarding analytical cadastre is a process which should be analyzed from two viewpoints: first, examining the solution’s convergence itself (whether a solution exists at all), and second, examining the solution’s quality (the accuracy of the final solution). The first analysis can be carried out on synthetic data as well as on “real” data, in both cases an answer whether a mathematical solution exists or not is obvious and very clear. Concerning the second part, synthetic data is preferred, considering the fact that a final validation of quality of the solution is needed, which can only be achieved when the target (the "true" solution) is known. The method at hand is expected to provide the initial, “true” values of simulation data. Consequently, the proposed GA method was applied on synthetic (simulation) datasets rather than on real cadastral information.

Performance of the GA was evaluated using synthetic data, since using "true" data analysis would not provide any indication of the solution's quality. The "artificial" block and its parcels were assumed to be legally valid, providing the necessary constraints and end conditions.

2.1 Definitions

The preliminary population (group of individuals, possible solution vectors) of *n* vectors is produced by randomly altering an "ideal" cadastral block (a registration block – a specified area within an administrative unit) containing parcels of different areas. To examine the GA process, a variety of conditions may be considered: planned road width, parcel borderlines, perpendicularity or parallelism, straight line requirement, etc. These constraints can be implemented separately, geminately or all may even be applied simultaneously, regardless of their number.

One of the most dominant and vital conditions is the registered area criteria. Area computed based on adjusted coordinates must be compatible with the legal area, within the surveying regulations. It was therefore appropriate at this stage of the research, to evaluate the data based on this condition.

After the population was generated, a primary test is performed to examine area criteria according to SOI regulations:

$$\min(\Delta A = 0.3\sqrt{A} + 0.005 \cdot A \ , \ \Delta A = 0.8\sqrt{A} + 0.002 \cdot A)$$

where

A – is the legal (registered) area of a given parcel

Once all of the vectors have qualified under the *ΔA* restriction, each is graded based on its fitness function. The guiding principle – the smaller the difference between the calculated and the "true" parcel areas, the higher the grade.

2.2 Cadastral conditions

The fitness function ascribes a value to each solution vector using the desirable MSE of parcels coordinates. The vector's (individual's) grade is then obtained by a weighted summation of parcel grades. Both the parcel grade and the vector grade are normalized to accept values from zero to hundred.

'0' – the difference exceeds the specified tolerance
'100' – the difference equals or less the specified tolerance

$$f(u) = \Sigma u_i \cdot p_i \qquad p_i = \frac{S_i}{\Sigma S_i}$$

$$u_i = \frac{\Delta A_i - \Delta S_i}{\Delta A_i - T_i} \cdot 100 \qquad (1)$$

$$T = \sqrt{\Sigma[(\frac{\partial S_i}{\partial Y_i})^2 + (\frac{\partial S_i}{\partial X_i})^2] \cdot m_{XY}^2}$$

Where

$f(u)$ - vector grade (block grade)

u_i - parcel grade

p_i - parcel weight

S_i - parcel's calculated area using Cartesian formula

ΔA_i - allowed area difference according to SOI

ΔS_i - actual area difference

T_i - parcel areal MSE

m_{XY} - coordinates MSE

2.3 Iterations

To create the successive generation of solutions the previous solution is divided into three groups: The first contains the best parents, to be combined to produce new offspring (undergo crossover); the second group contains inferior individuals, who are therefore to be mutated; and the last is composed of vectors with the lowest grades, vectors that are overcrossed and then mutated to complete the *n* vector population. Two successive generations' grades are then compared so as to proceed to the next iteration with the higher grades only.

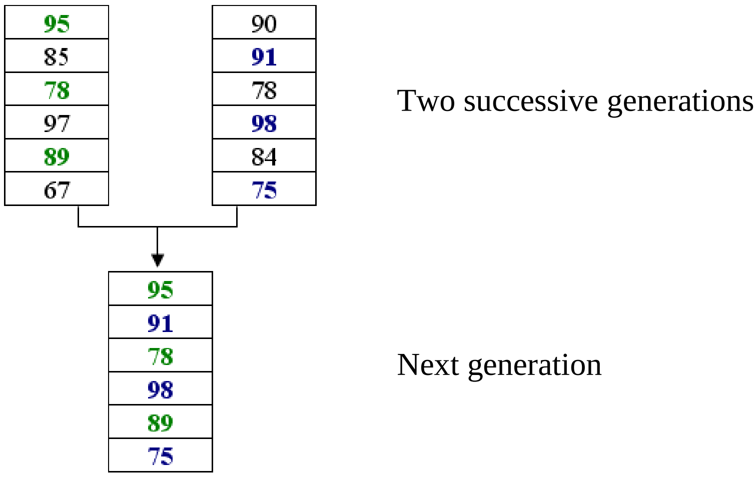

Figure 1. GA successive generations

Based on a large number of simulations runs, the best way of dividing the groups was found to be according to the following ranges:
(1) $90 \le f(u) \le 100$; **(2)** $75 \le f(u) < 90$; **(3)** $f(u) < 75$

The genetic process terminates when one of the vectors receives the highest grade possible (100) or a large specified number of generations has passed.

2.4 Alternative solution

In order to evaluate the solution's quality an alternative, iterative solution is provided: The Least Squares Method with constraints is applied, altering the coordinates of one parcel coordinates at a time. The process continues until the difference in the residuals vector (V) between two sequential iterations converges to zero.

$$AV + W = 0$$
$$V'V \to \min$$
$$W = \sum_{i=1}^{n} X_i (Y_{i+1} - Y_{i-1}) - 2S = 2S_{calculated} - 2S_{"ideal"}$$
$$AA'k + W = 0 \qquad k = \frac{-W}{AA'} \tag{2}$$
$$A = [\partial\delta_{X_i}, \partial\delta_{Y_i}]$$
$$\begin{cases} \delta_{X_i} = k(Y_{i+1} - Y_{i-1}) \\ \delta_{Y_i} = k(X_{i-1} - X_{i+1}) \end{cases}$$

3. SIMULATION RESULTS

In order to examine the proposed method's quality and accuracy, it has been tested on synthetic data, imitating a block and its included parcels. The main purpose of these simulations is to test the ability of the GA suggested algorithm to return to the initial theoretical state, in other words an ideal, errorless solution. To enable comparison an LS iterative adjustment was applied.

Table 1. Examples of solution parameters (meters)

Parameters	Example #1			Example #2			Example #3		
	Initial	GA	LS	Initial	GA	LS	Initial	GA	LS
$\min \Delta X$	-0.358	-0.258	-0.328	-0.390	-0.146	-0.406	-0.551	-0.229	-0.516
$\min \Delta Y$	-0.252	-0.138	-0.274	-0.351	-0.139	-0.266	-0.282	-0.176	-0.277
$\max \Delta X$	0.276	0.125	0.220	0.394	0.153	0.320	0.343	0.125	0.333
$\max \Delta Y$	0.327	0.183	0.416	0.449	1.145	0.480	0.332	0.174	0.342
$\Delta\bar{X}$	-0.029	-0.026	-0.029	-0.016	0.011	-0.016	0.017	-0.006	0.017
$\Delta\bar{Y}$	0.030	0.013	0.030	0.057	0.008	0.057	0.026	0.006	0.026
$\sigma_{\Delta X}$	0.148	0.088	0.134	0.175	0.083	0.163	0.187	0.088	0.161
$\sigma_{\Delta Y}$	0.165	0.086	0.165	0.199	0.078	0.178	0.158	0.085	0.155

Where

$\min/\max \Delta X, \Delta Y$ - minimal and maximal coordinate values differences

$\Delta\bar{X}, \Delta\bar{Y}$ - mean coordinate differences

$\sigma_{\Delta X}, \sigma_{\Delta Y}$ - standard deviation values

In Table 1 some characteristic examples of the two methods are given. The "initial" column correspond to the first generation values whereas the "GA" and "LS" columns correspond to the final results of the two methods. The examples in Table 1 were carried out with the following parameters: a standard deviation error of 0.35 meter; an expected 0.07 meter MSE of the coordinates; Maximum 30 generations (iterations). As can be observed from the table, the GA parameters are better than those of the LS: mean values and standard deviation values of the GA solution are lower than those of the LS.

3.1 Geometric quality

An adjustment process may conclude with distorted areas of the original shape or with an overall shift of the entire area, even though the differences in the coordinates may be small and do not have any indication on the matter. To ensure area shape preservation and oversee shifting of coordinates, additional analyses were applied: for each parcel mean coordinate differences were computed, shifted coordinates were calculated, then union and intersection areas were calculated.

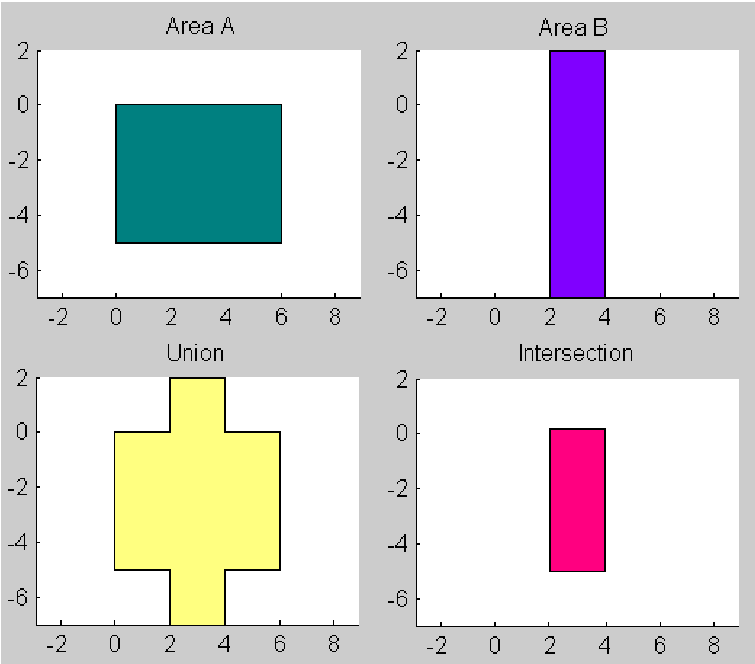

Figure 2. Union and intersection areas

$$\Delta\bar{X}_j = \frac{1}{n_j}\sum_{i=1}^{n_j}\Delta X_i \qquad \Delta\bar{Y}_j = \frac{1}{n_j}\sum_{i=1}^{n_j}\Delta Y_i$$

$$\tilde{X}_i = \hat{X}_i + \Delta\bar{X}_j \qquad \tilde{Y}_i = \hat{Y}_i + \Delta\bar{Y}_j \qquad (3)$$

$$S_u = \tilde{S} \cap S$$
$$S_i = \tilde{S} \cup S \tag{4}$$

Where

$\hat{X}, \hat{Y}$ - calculated coordinates, obtained from solution
$\tilde{X}, \tilde{Y}$ - shifted coordinates according to the parcel's mean coordinates differences
S, S_u, S_i - "ideal" area, union area, intersection area, respectively

3.2 Hypotheses tests dX, dY

In order to examine the quality of solutions and facilitate statistical decisions regarding the population (based on sample data – the experimental data), a series of statistical tests (confirmatory data analysis) have been carried out. In order to conduct such a test a general procedure must be followed, specifying population parameters such as: null (H_0) and the alternative (H_1) hypotheses are stated (the hypotheses complement one another, that is, if one is true the other one is false), a test statistic must be chosen (computed sample value). Based upon those values a decision is made to accept or reject the null hypothesis.

Common statistic tests include: for expected value analysis (σ is unknown) – the t (student) test is used, for standard deviation a χ^2 test is performed. To compare two samples an F test is performed (Hamilton, 1964).

The tests are carried out with significance level, the customary level being α of 5%, with which the following tests were carried out.
The null hypothesis H_0 is checked versus an alternative hypothesis H_1 for each solution (GA vs. LS).

3.2.1 Expected value test

$$H_o : \mu_i \leq |\mu_0|\ m$$
$$H_1 : \mu_i > |\mu_0|\ m \tag{5}$$
$$reject\, H_0 \rightarrow t_o > t_\alpha^\nu \qquad t_0 = \left(\frac{\bar{X}_i - \mu_0}{s_i}\right)\sqrt{n}$$

3.2.2 Standard deviation test

$$H_0 : \sigma_i \le \sigma_0 \ m$$
$$H_1 : \sigma_i > \sigma_0 \ m \qquad (6)$$
$$reject\, H_0 \rightarrow \chi_0^2 > \chi_{\alpha,\nu}^2 \qquad \chi_0^2 = \frac{(n-1)s^2}{\sigma_0^2}$$

Where

μ_0 - 0.05 or 0.07 m, according to desirable accuracy, defined by the SOI
σ_0 - 0.10 m (Fradkin and Doytsher, 2002)

3.2.3 Standard deviation comparison test

$$H_0 : \sigma_{GA} = \sigma_{LS} \qquad F_0 = \frac{s_{GA}^2}{s_{LS}^2}$$
$$H_1 : \sigma_{GA} \ne \sigma_{LS} \qquad (7)$$
$$reject\, H_0 \rightarrow F_0 < F_{1-\frac{\alpha}{2},\nu_1,\nu_2} \quad or \quad F_0 > F_{\frac{\alpha}{2},\nu_1,\nu_2}$$

3.2.4 Expected value difference

$$\sigma_1 = \sigma_2 :$$
$$H_0 : \bar{X}_1 - \bar{X}_2 \ge \Delta_0$$
$$H_1 : \bar{X}_1 - \bar{X}_2 < \Delta_0 \qquad (8)$$
$$t_p = \frac{\bar{X}_1 - \bar{X}_2 - \Delta_0}{s_p\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} \qquad s_p = \sqrt{\frac{(n_1-1)s_1^2 + (n_2-1)s_2^2}{n_1+n_2-2}} \qquad \upsilon = n_1 + n_2 - 2$$
$$reject\, H_0 \rightarrow t_p < -t_{5\%,\nu}$$

$$\sigma_1 \ne \sigma_2 :$$
$$H_0 : \bar{X}_1 - \bar{X}_2 \ge \Delta_0$$
$$H_1 : \bar{X}_1 - \bar{X}_2 < \Delta_0 \qquad (9)$$
$$t_p = \frac{\bar{X}_1 - \bar{X}_2 - \Delta_0}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} \qquad \upsilon = \frac{(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2})^2}{\sqrt{\frac{(\frac{s_1^2}{n_1})^2}{n_1-1} + \frac{(\frac{s_2^2}{n_2})^2}{n_1-1}}}$$
$$reject\, H_0 \rightarrow t_p < -t_{5\%,\nu}$$

This test is performed in order to establish whether the GA solution is better than the LS
Δ_0 - 20% of coordinates' MSE

Table 2. Statistics test results example – dX, dY

Method	Calculated t_0		Tabular $t_{5\%,30}$	Test		Method	Calculated t_0		Tabular $t_{5\%,30}$	Test	
	dX	dY		dX	dY		dX	dY		dX	dY
GA	-6.067	-3.680	1.697	√	√	GA	-3.955	-4.467	1.697	√	√
LS	-3.680	-1.338	1.697	√	√	LS	-2.914	-0.415	1.697	√	√
Method	Calculated t_p		Tabular $t_{5\%,60}$	Test		Method	Calculated t_p		Tabular $t_{5\%,60}$	Test	
	dX	dY					dX	dY		dX	dY
GA vs. LS	1.676	1.680	1.671	√	√	GA vs. LS	1.681	1.683	1.671	√	√

where: t_0 - test statistic for mean calculated value
t_p - test statistic for expected value difference
√ - acceptance

The results of statistical tests as to coordinate differences (dX, dY) are given in Table 2. Two samples are given in the table - one on the left hand side and one on the right hand side of the table – where each sample (a sample means a single example of numerous algorithms' runs) is computed in the GA and LS methods. The upper part of the table contains calculated and tabular values for expected value (μ - mean value) test for each sample (for dX values as well as for dY), and the lower part displays the values for comparison test between the two methods. The outcomes of the tests (acceptance or rejection of the hypothesis – whether the results satisfy the expectations or not) are based on formulas (5) and (8 or 9). As can be observed from these examples, the tests show that the expected values of the two solutions are smaller than μ_0, but the GA solution is better than the LS solution.

3.3 Hypotheses tests dS

3.3.1 Expected value test

$$H_o : \mu_i \le \mu_0\%$$
$$H_1 : \mu_i > \mu_0\% \qquad (10)$$
$$reject\, H_0 \rightarrow t_o > t_\alpha^\nu \qquad t_0 = (\frac{\bar{X}_i - \mu_0}{s_i})\sqrt{n}$$

3.3.2 Standard deviation test

$$H_o : \sigma_i \le \sigma_0 \%$$
$$H_1 : \sigma_i > \sigma_0 \% \qquad (11)$$
$$reject\, H_0 \rightarrow \chi_0^2 > \chi_{\alpha,\nu}^2 \qquad \chi_0^2 = \frac{(n-1)s^2}{\sigma_0^2}$$

Since the obtained coordinates are close to their "true" value, it is reasonable to expect that the difference between the area calculated from shifted coordinates and the original area is insignificant and homogeneously spread, therefore μ_0 is 1% and σ_0 is 0.5% (relatively small values).

3.3.3 Standard deviation comparison test

$$H_o : \sigma_{GA} = \sigma_{LS} \qquad F_0 = \frac{s_{GA}^2}{s_{LS}^2}$$
$$H_1 : \sigma_{GA} \ne \sigma_{LS} \qquad (12)$$
$$reject\, H_0 \rightarrow F_0 < F_{1-\frac{\alpha}{2},\nu_1,\nu_2} \quad or \quad F_0 > F_{\frac{\alpha}{2},\nu_1,\nu_2}$$

3.3.4 Expected value difference

The test was performed according to formulas (8), (9)
Δ_0 - 20% of μ_0

Table 3. Statistics tests result – dS

Method	Calculated t_0	Tabular $t_{5\%,12}$	Test	Method	Calculated t_0	Tabular $t_{5\%,12}$	Test
GA	-46.300	1.782	√	GA	-86.420	1.782	√
LS	-40.264	1.782	√	LS	-25.319	1.782	√
Method	Calculated t_p	Tabular $t_{5\%,24}$	Test	Method	Calculated t_p	Tabular $t_{5\%,24}$	Test
GA vs. LS	-0.354	1.714	√	GA vs. LS	0.468	1.714	√

where: t_0 - test statistic for mean value
t_p - test statistic for expected value difference
√ - acceptance

Few examples of the results of statistical tests as to area differences (dS) are given in Table 3. The table structure is similar to the structure of Table 2, the two approaches are evaluated separately and one versus the other. The upper part of the table contains calculated and tabular values for expected value (μ) test, and the lower part displays the values for comparison test between the two methods. The outcomes of the tests (acceptance or rejection of the hypothesis) are based on formulas (10) and (8 or 9). The examples show that the expected value in both cases is smaller than the specified value, but as can be observed from the table, the test indicates that the GA solution outcome has better results.

4. CONCLUSIONS AND FUTURE WORK

The current cadastre in Israel is physical, i.e., the mark on the ground in the field is what is acceptable in court and it determines the parcel's boundaries. Due to variety of surveying methods and different cadastral techniques that used throughout the years, mapping of a given area produces different and inconclusive results, which might lead to borderline conflicts and the need of litigation to obtain a legal decision. Therefore an analytical, accurate and conclusive cadastral system is a vital necessity.

The proposed method examines a new approach for achieving homogeneous coordinates by using an evolutionary algorithm, which imitates the natural process of evolving solutions. Applying the GA to synthetic data yields satisfactory results. Repeated simulation executions showed similar results (GA vs. LS) and in most cases the GA solutions were better than those of the LS method.

The simplicity of the algorithm enables considering additional cadastral and geometric conditions (restrictions), such as: road width, perpendicularity, parallelism, straight line requirement etc., all this without altering its fundamental mechanism.

Future aspects of this research consider implementing the algorithm on "real" data – present activities which include updated ground observations. Thus a control and equalization mechanism can be developed.

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