Classification of Medical Images in the Domain of Melanoid Skin Lesions

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Abstract. In the paper, computer-aided diagnosing and classification of melanoid skin lesions is dealt with. The main goal of our research was to elaborate and to promote via Internet a new skin lesions diagnosing computer program system. Its functionality and structure is here in short reported. In the current version of the system, five learning models are implemented to simultaneously supply five independent, partial results. Then, a special evaluation and voting algorithm is applied to select the correct class (concept) of the diagnosed skin lesion.

1. Genesis of the research

Available literature [1-3] shows, that above half of registered cases of cancer are different types of skin tumour. In the United States, recently about 800,000 of cases of BCC (Basal Cell Carcinoma) tumour, 200,000 of cases of SCC (*Squamous Cell Carcinoma*) tumour and about 48,000 of Melanoma Malignant were diagnosed. Global data shows that the most dangerous type of tumour is Melanoma Malignant. It caused most of fatal cases (7,700; 4,800 men and 2,900 women) in comparison to 1,900 fatal cases caused by other types of tumours. Additionally, it should be stressed that from different types of tumours, increase of melanoma malignant cases was fastest, and in the 1973-1994 years rise about 120%. Despite great scientific potential – especially in the US – involved into research on reasons of this tumour, just in the last time pra-genesis of melanoma was outlined. Scientists point at changes on the level of gene that codes protein Apaf-1. It makes possible to use an immune therapy, and more efficient and secure chemical therapy[1].

Recently, some decrease of the illness was observed, especially in Australia, Scotland and Ireland [4]. Some reasons of this phenomenon can be guessed: **(i)** dissemination of methods for early, non-invasive diagnosing of health risk degree, what creates possibility of self-diagnosing for society of Western Europe and United States; **(ii)** fast access to vast number of information sources about symptoms of melanoma malignant, access to the methods of calculating of parameters characterizing health risk degree (based on atypical pigment lesions on the skin, frequency of contacts with solar or ultraviolet radiation, colour of eyes or hair, etc.), or/and **(iii)** access to various methods of calculation chances to survive given number of years by a patient with diagnosed melanoma [1].

Results of European research in the field discussed have been usually focused on methodology of classification of tumour types, description of selected symptoms and description of pigment lesions, in a phase preceding incurable condition of illness or demanding surgical intervention [2, 3].

Our current research in the classification of medical images is aimed at the development and promotion via Internet a new skin lesions diagnosing computer program system, called by us the ***I**nternet **M**elanoma **D**iagnosing and **L**earning **S**ystem*, **IMDLS**. It is assumed, that present investigations should be devoted to profound extension the functionality of our lately

developed internet-based system for diagnosing of four categories of skin lesions: <*benign nevus*>, <*blue nevus*>, <*suspicious nevus*>, and <*melanoma malignant*> [5]. Until now, our system has supported three methods (learning models) of diagnosing: (*i*) ***classic ABCD rule*** (based on ***TDS*** parameter) [6, 7], (*ii*) ***optimized ABCD rule,*** (based on own ***New TDS*** parameter [8, 9]), and (*iii*) ***decision tree*** (based on ID3 algorithm) [10]. Recently, two another learning models have been implemented. The first model, called by us ***genetic dichotomization***, is based on a linear learning machine with genetic searching for the most important attributes [11]. The second model is based on application of a new classifier from the family of ***belief networks*** [12]. Hence, the system being investigated applies now five different learning models (classifiers) to identify partially skin lesions. From these five partial results, system suggests the final result, using a ***special evaluation and voting algorithm.***

2. Structure and operation of the system

Our diagnoses support system employs user interface in the form of a website (Fig. 1), to get the access to its three main working layers (Fig. 2). The first layer is dedicated to persons without medical background, and serves to self-diagnosing. This layer consist of two modules: the first one (*Module 1*) allows to determine – in a very simple and clear way – all symptoms required for correct classification of a given skin lesion. Thus, using this module, user can be easily acquainted with the knowledge required for correct assignment of all symptoms (asymmetry, border, 6 colours, 5 different structures), related to a given lesion. The second module (*Module 2*) plays a role of an advanced calculator for non-invasive diagnosing of melanoid lesions. Input to this module creates a vector, conveying logical values of 13 previously pointed out descriptive attributes. These values, inputted by the user, are processed to calculate the 14-th attribute, the **TDS** (in a fact, also the **New_TDS**).Then, five different algorithms described briefly in section 2, are applied for development of five partial learning models (say, five partial classifiers). The classification process based on these models is described in Section 3.

The second layer, dedicated to dermatology specialists, uses only *Module 2*. The third layer is planned for the next stage of our research. This layer will be based on automatic analysis and recognition of melanocytic images. The initial results, gained along this line, are subject of another paper presented at this conference [13].

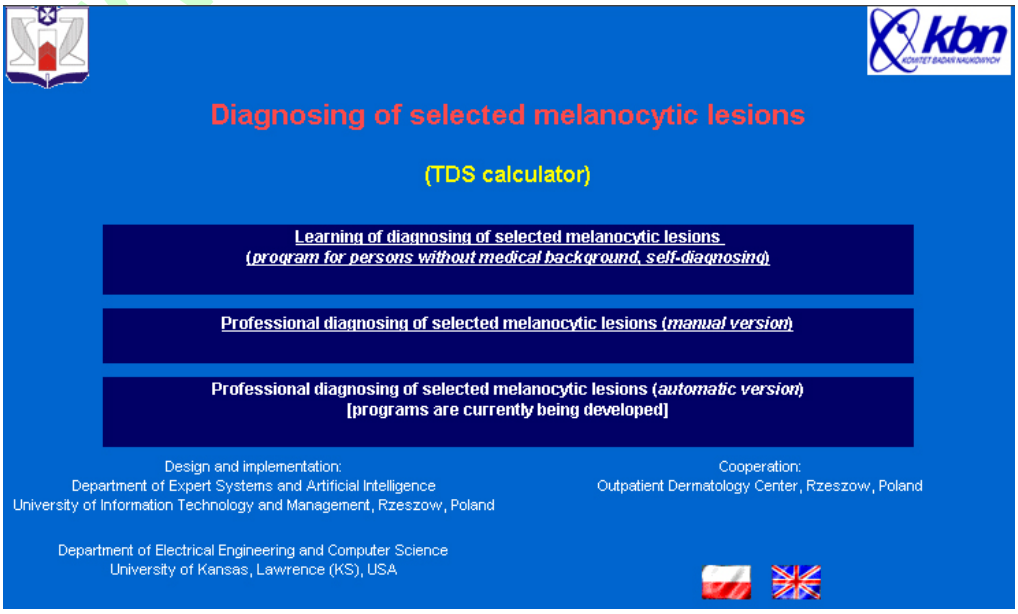

Fig. 1. System's interface

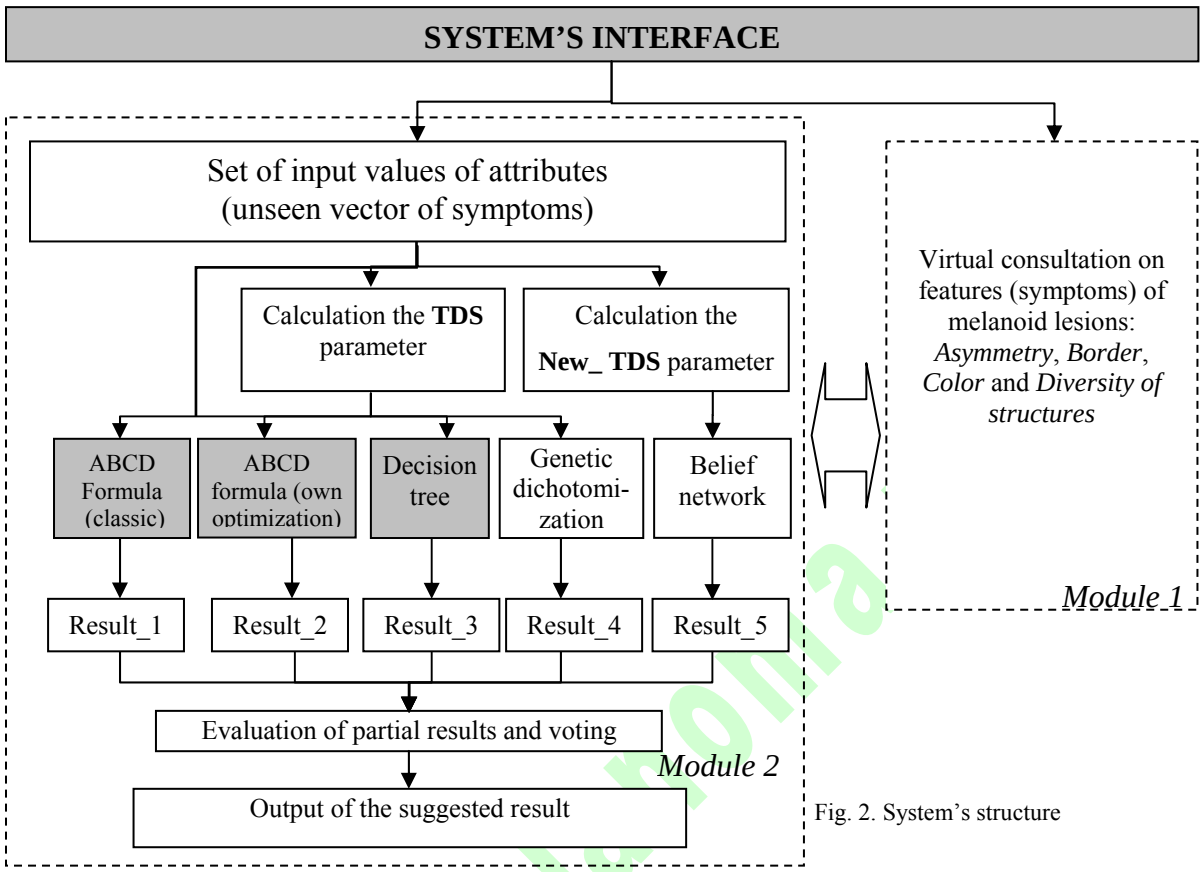

Fig. 2. System's structure

3. Recognition algorithms

3.1. Learning model based on a classic and optimized ABCD rule

Logical values of symptoms, inferred in the first or second layer, are processed using two different algorithms (1. Calculation of the **TDS** parameter, and 2. Calculation of the **New_TDS** parameter). It is worth to say, that both algorithms are based on a constructive induction [14], a very important methodology is machine learning. Then, the enlarged solution space (13+1 dimensions) is searched using the classic **ABCD** (see Equation 1),

$$\mathbf{TDS} = 1.3 * \mathbf{A}\text{symmetry} + 0.1 * \mathbf{B}\text{order} + 0.5 * \sum \mathbf{C}\text{olors} + 0.5 * \sum \mathbf{D}\text{iversity} \quad (1)$$

and simultaneously,
using the optimized formula, for calculation the **New_TDS** (see Equation 2)

$$\begin{aligned}\mathbf{New\_TDS} = {} & (0.8 * \text{Asymmetry}) + (0.11 * \text{Border}) + (0.5 * \text{C\_White}) + (0.8 * \text{C\_Blue}) \\ & + (0.5 * \text{C\_DarkBrown}) + (0.6 * \text{C\_LightBrown}) + (0.5 * \text{C\_Black}) + (0.5 * \text{C\_Red}) \\ & + (0.5 * \text{Pigment\_Networks}) + (0.5 * \text{Pigment\_Dots}) + (0.6 * \text{Pigment\_Globules}) \\ & + (0.6 * \text{Branched\_Streaks}) + (0.6 * \text{Structureless\_Areas})\end{aligned} \quad (2)$$

It was found, in numerous experiments, that the learning model based on the standard **TDS** parameter, classifies unseen objects with an error rate 9-11%, whereas learning model, based on optimized **New_TDS** parameter, classifies the same set of unseen objects with an error rate 5%.

3.2. Learning model in form of decision tree

Our recent experiments pointed out that the learning model, based on co called *certain* decisions tree (see Fig. 3), classifies unseen melanoid skin lesions with an error rate on the level of about 1.5%.

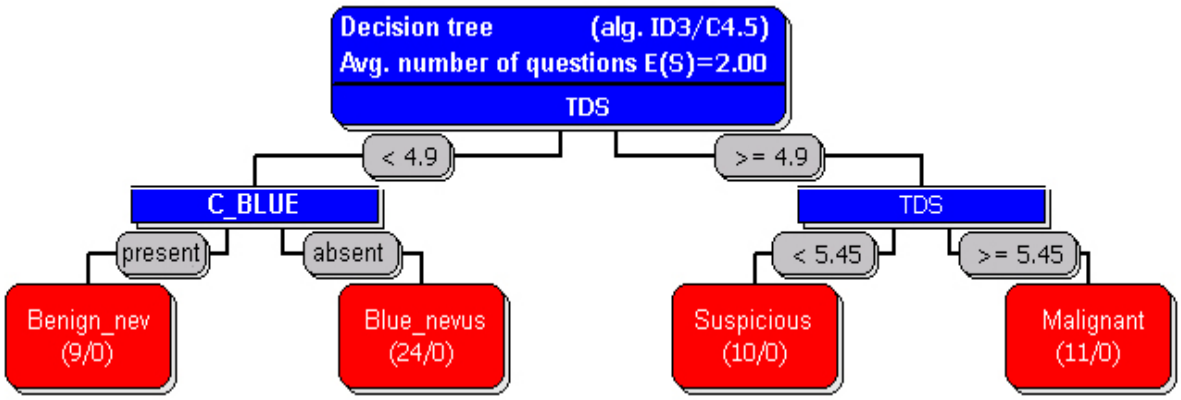

Fig. 3. Learning model in form of decision tree

3.3. Learning model based on the genetic dichotomization

This learning model contains **n(n-1)/2** number of vectors (where generally **n**- is the number of identified concepts, in our case **n**=4), trained outside the **IMDLS**, capable to classify correctly four classes of melanoid lesions. These vectors initially trained for searching dichotomous solution space, underwent to mutation and crossing, in order to extend their recognition capability and efficiency.

Table 1. Illustration of an example recognition process, realized by the genetic dichotomization model.

Vector:	**Capable to recognize:**	**Class assigned to example unseen case: (Melanoma malignant)**	**Final decision:**
#1	*Benign_nev* or *Blue_nevus*	*Benign_nev* or *Blue_nevus*	Melanoma malignant
#2	*Benign_nev* or *Malignant*	*Malignant*	
#3	*Benign_nev* or *Suspicious*	*Benign_nev* or Suspicious	
#4	*Blue_nevus* or *Malignant*	*Malignant*	
#5	*Blue_nevus* or *Suspicious*	*Blue_nevus* or *Suspicious*	
#6	*Malignant* or *Suspicious*	*Malignant*	

Recognition process of unseen cases is executed automatically (see Table 1): the **IMDLS** program assigns to unseen case a category, pointed out by the maximal number of vectors.

3.4. Learning model in form of belief network

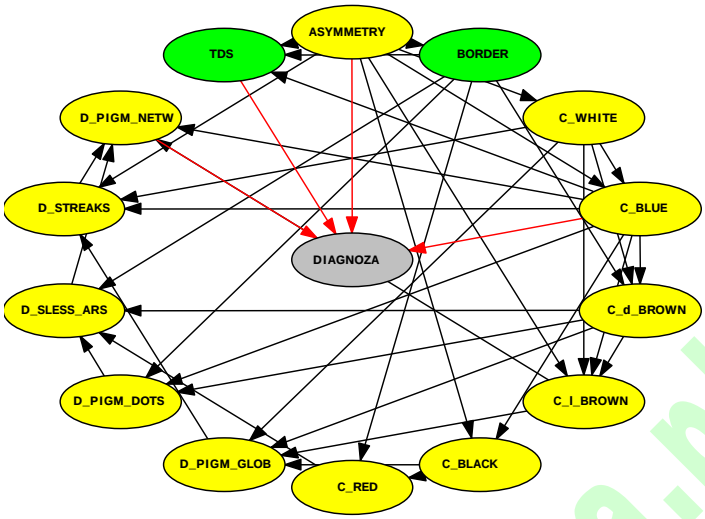

Fig. 5. Learning model in form of belief network

This learning model contains a belief network (see Fig. 5), trained – like the genetic dichotomization algorithm – outside the **IMDLS**. The belief network used showed an error rate equals roughly 4.5%. It was found, that from all 14 descriptive attributes (symptoms), the most important ones, having direct impact on the decision (diagnosis), were: classic **TDS** parameter (TDS on Fig. 5), asymmetry (ASYMMETRY), colour blue (C_BLUE), and a structure of the lesion, called pigment network (D_PIGM_NETW). Recognition process of unseen cases is executed automatically: the **IMDLS** program assigns to unseen case a category, which displays the highest value of marginal likelihood [12].

3.5. Evaluation and voting algorithm

The skin lesions diagnosing system supplies (five partial results) generated by the five learning models: classic **ABCD** rule, optimized **ABCD** rule, decision tree, genetic dichotomization and belief network. Each partial result has its own weight parameter, dependent on error rate characterized for the learning model used (see Table 2). These weight parameters are computed from one general formula:

$$W_x=(100\%-\textit{Error Rate of the Model})/100\% \qquad (3)$$

Table 2. Weight parameters for each learning model

No	Learning model	Weight parameter
1	**ABCD** formula (classic)	$W_1=(100\%-11\%)/100\%=0,89$
2	**ABCD** formula (own optimization)	$W_2=(100\%-5\%)/100\%=0,95$
3	Decision tree	$W_3=(100\%-1,5\%)/100\%=0,985$
4	Genetic dichotomy process	$W_4=(100\%-6\%)/100\%=0,94$
5	Belief network	$W_5=(100\%-4\%)/100\%=0,96$

The final result is prepared depending on sum of weight parameters for suggested diagnosis. It should be stressed, that all learning models developed in our group (i.e. models 2, 3, 4 and 5) seems to be more accurate than the model 1 (world-wide accepted model of Braun-Falco and Stolz [7], called here classical **TDS** model). Operation of the evaluation and voting algorithm is explained in Table 3.

Table 3. Calculating of the weight parameters

Diagnosis	Benign nevus	Blue nevus	Suspicious nevus	Melanoma malignant
ABCD formula (classic)	0,89	0	0	0
ABCD formula (own optimization)	0,95	0	0	0
Decision tree	0	0,986	0	0
Genetic dichotomy process	0,94	0	0	0
Belief network	0	0,96	0	0
Weight parameters	**2,78**	**1,946**	**0**	**0**

Here, Benign_nevus was identified three times, whereas Blue_nevus only twice. In addition, weight parameters (last row in Table 3) vote in ratio 2,78/1946 for Benign_nevus.

4. Summary

In our research we followed the newest trend in diagnosing of skin lesions, namely, the turn to non-invasive identification methods. The **IMDLS** software, developed and extensively tested throughout our experiments, can be treated as a reliable and efficient tool that supports non-invasive classification of melanoid spots on the skin. Additionally, the **IMDLS** program displays some teaching functions, important for primary physicians. The **IMDLS** tool is now available on the website**:** http://www.wsiz.rzeszow.pl/ksesi.

References

[1] http://dermoncology.med.nyu.edu.

[2] Kreusch J., Rassner G.: *Standardisierte auflichtmikroskopische Unterscheidung melanozytischer und nicht-melanozytischer Pigmentmerkmale*, **Hautartzt 42**, 77-81(1991).

[3] Kenet R.O., Kang B.J.,Fitzpatrick T.B., Sober A.J., Barnhill R.L.: *Clinical diagnosis of pigmented lesions using digital epiluminescence microscopy*, **Arch. Dermatol. 129**, 157-158 (1993).

[4] Kirn T.F.: *Reasons Unclear for Worlwide Decline in Melanoma*, Skin & Allergy News 31 (5), 41-42 (2000).

[5] Grzymała-Busse J.W., Hippe Z.S., Knap M., Paja W.: *Infoscience Technology: An Impact Of Internet Accessible Melanoid Data On Health Issues*, Proceedings of the 19th International CODATA Conference, *The Information Society: New Horizons for Science*, 7-10 November 2004, Berlin, Germany.

[6] Braun-Falco O., Stolz W., Bilek P., Merkle T., Landthaler M.: *Das Dermatoskop. Eine Vereinfachung der Auflichtmikroskopie von pigmentierten Hautveranderungen*, **Hautartzt 40**, 131-136 (1990).

[7] Stolz W., Harms H., Aus H.M., Abmayr W., Braun-Falco O.: *Macroscopic diagnosis of melanocytic lesions using color and texture image analysis*, **J. Invest. Dermatol. 95**, 491-497 (1990).

[8] Alvarez A., Bajcar S., Brown F.M., Grzymała-Busse J.W., Hippe Z.S.: *Optimization of the ABCD Formula Used for Melanoma Diagnosis,* In: Kłopotek M.A., Wierzchoń S.T., K. Trojanowski (Eds.), Advances In Computing (Intelligent Information Systems and Web Mining), Physica-Verlag, Heidelberg 2003, pp. 233-240.

[9] Grzymala-Busse J.W., Bajcar S., Grzymala-Busse W.J., Hippe Z.S.: *Data Mining Analysis of the ABCD Formula Used for Diagnosis of Melanoma,* International Workshop on Concurrency Specification and Programming, Czarna (Poland) 25-27.09.2003.

[10] Grzymała-Busse J.W., Hippe Z.S., Knap M., Mroczek T.: A New Algorithm for Generation of Decision Trees TASK Quarterly 8 (2004, No 2) 243-247.

[11] Hippe Z.S., Wrzesien M., *Some Problems of Uncertainty of Data after the Transfer from Multi-category to Dichotomous Problem Space,* In: T. Burczyński, W. Cholewa, W. Moczulski (Eds.), Methods of Artificial Intelligence, Silesian University of Technology Edit. Office, Gliwice 2002, pp. 185-189.

[12] Hippe Z.S., Mroczek T.: *Melanoma classification and prediction using belief networks,* In: Kurzyński M., Puchała E., Woźniak M. (Eds.), Computer Recognition Systems KOSYR 2003, Univ. of Technology Edit. Office, Wrocław 2003, pp. 337-342.

[13] Kwasnicka H., Paradowski M.: *Spread Histogram – A Method for Calculating Spatial Relations Between Objects*, Proceedings of 4th International Conference on Computer Recognition Systems CORES'2005, Wrocław, Poland (in printing).

[14] Michalski R. S., Bratko I., Kubat M.: *Machine Learning and Data Mining, Methods and Applications*, J. Wiley & Sons, London 1998, pp. 79-80, 83, 104.