

Possibilities of MRI Texture Analysis of Brain Images in Differential Diagnosis of Primary Extra-Axial Tumors

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Abstract. The possibility of using textural features for the differential diagnosis of primary extra-axial tumors on the basis of two-dimensional digital magnetic resonance (MR) images is being investigated. Histogram and correlation characteristics, as well as features based on run lengths, were considered as information features. The selection of effective features is based on the criterion of discriminant analysis. The applicability of the proposed approach to solving the problem of differential diagnosis between different types of extra-axial tumors is being studied experimentally on a set of 66 patients. The analysis of standard MRI data based on radiomics showed a better differential diagnosis result 33.3% superior to visual assessment. © 2023 Journal of Biomedical Photonics & Engineering.

Keywords: radiomics; texture analysis; diagnostics; feature selection; discriminant analysis; MRI.

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1 Introduction

Meningiomas and neurinomas are the most common intracranial primary tumors [1]. This is a heterogeneous group of tumors, including both benign and malignant tumors. The approach to treatment largely depends on the type of tumor, so the problem of differential diagnosis of primary extra-axial tumors (PExT) based on magnetic resonance imaging (MRI) images does not lose its relevance [2–4].

Currently, the interpretation of changes detected on medical images is based on visual analysis of a limited number of qualitative and quantitative criteria (localization, number, shape, size, structure, etc.). However, in addition to this small number of radiological features, the imaging data is rich in quantitative parameters (shape descriptors, histogram and texture characteristics) [5]. The analysis of these parameters modifies the task of interpreting diagnostic image data from subjective and qualitative to objective and quantitative. This approach is called radiomics [6]. Radiomics is a new high-tech approach to the analysis of imaging data. In neurooncology, radiomics allows not

only to carry out differential diagnostics, but also to determine the prognosis of the disease [5, 7]. The task of radiomics is the transformation of diagnostic images into biomarkers and the identification of imaging phenotypes through a comprehensive study by methods of histogram, texture, and morphometric analysis in combination with multidimensional clinical data [8, 9].

MRI with visual evaluation of tumor characteristics on routinely used sequences is the gold standard for diagnosing PExT [10]. The possibilities of differential diagnosis of PExT on the basis of their MRI patterns have been studied in detail, however, reliable differentiation of these neoplasms based on MR semiotics is often difficult [11–13]. The use of radiomics has demonstrated a high prognostic value for differential diagnosis between different types of PExT, including for determining the degree of their malignancy.

Extracting quantitative data from multimodal medical images using advances in data mining and machine learning allows you to identify the relationship between the digital properties of a medical image and clinical data for use in diagnostic decision support systems [14, 15]. Radiomic analysis includes several stages: acquisition

and pre-processing of images, segmentation, feature extraction, and construction of a statistical model for the relationship between clinical data and visualization parameters. These steps can be performed sequentially with manual selection of data for the final model. In the case of applying the methodology of artificial intelligence based on deep learning, the simulation occurs without preliminary separation of stages. The information content of radiomic features must be evaluated on a validation set and only then can it be used for diagnosis and prediction.

The radiomic analysis should include all tumor tissue without involving the surrounding structures and the possible edema zone. Therefore, the first and, in many respects, the determining step in the analysis of a diagnostic image is high-quality segmentation. Segmentation can be carried out both manually and by semi-automatic or automatic methods. With manual segmentation, the variability in the interpretation of the formation boundary by different specialists can be quite significant [16], while the final analysis parameters depend on how well the tumor was highlighted [17]. The use of semi-automatic segmentation reduces the variability in establishing the tumor's margin compared to manual methods [18].

After region of interest (ROI) segmentation, quantitative and qualitative data are extracted from the selected area. These include: shape features, histogram, texture parameters and high-order features describing the statistical features of the image obtained using Fourier transforms and wavelet analysis [9, 19–24]. The construction of a predictive model is most often performed on the basis of deep learning using neural networks. In addition, common information technologies in radiomics are logistic regression, various types of decision trees [19]. Since a large amount of data is needed to achieve the reliability of the obtained statistical models, research in the field of radiomics is often multicenter. However, MRI may differ in scanning parameters, the impact of which on the final results must be taken into account [25]. The impact of imaging protocols on retrievable radiomic features has been analyzed in a number of studies [26–29]. These works have shown that image filtering is able to level out technological features, and differences in data acquisition parameters and moderate differences in MRI slice thickness do not affect the results of texture analysis.

2 Materials and Methods

2.1 Material and Used Features

The aim of the study is to compare the capabilities of visual semiotics and texture analysis of MRI for the differential diagnosis of PExT. The retrospective study included 66 patients with PExT, which were divided into two groups: training and validation. The training group included 39 patients (six men and 33 women) aged 33 to 62 years (median age 58 years). The validation group consisted of 27 patients (3 men and 24 women) aged 29

to 79 years (median age 59 years). Before surgical treatment, all patients underwent a standard MRI study using intravenous contrast (0.1 mmol/kg) on a tomograph with a magnetic field induction of 1.5 T. The scanning protocol included T2 weighted images (WI), T1 WI, FLAIR, and DWI (with subsequent ADC mapping). After contrasting, scanning was performed using a 3d sequence to obtain T1 WI (T1 CE). For each patient, about 20 images were obtained in various modes in which the tumor was observed.

The research included two directions.

1) Differential diagnosis of tumors based on visual evaluation of semiotics. Both qualitative (localization, shape, contour, structure, etc.) and quantitative (area and volume of the tumor, MR signal intensity) signs were evaluated.

2) Differential diagnosis of tumors based on textural parameters. Texture analysis was performed using the MaZda program [30, 31], which allows calculating the following groups of texture features: a) based on statistical characteristics, b) based on gradient parameters, c) based on the adjacency matrix, and d) based on run-length matrix. Before performing texture analysis, automatic segmentation of tumors was carried out using a convolutional neural network [32]. When performing texture analysis, the brightness of segmented images was normalized in the range $[\mu - 3\sigma, \mu + 3\sigma]$, where μ is the average value of the gray level, and σ is the standard deviation, Eq. (1):

$$Y_{i,j} = \frac{X_{i,j} - (\mu - 3\sigma)}{(\mu + 3\sigma) - (\mu - 3\sigma)}, \quad (1)$$

where $Y_{i,j}$ is normalized pixel brightness and $X_{i,j}$ is source pixel brightness.

Discriminant analysis was used as a method to perform statistical modeling based on the assessment of the cumulative contribution of various features to separate tumors.

2.2 Texture Features

As recent studies show, texture analysis has shown good results in identifying regions of interest in medical images, as well as in recognizing biomedical images and their further diagnostics [33–40]. Thus, in research [41] studied the problem of detecting pathologies in images of blood cells based on the analysis of textural features of various classes of initial images in different color subspaces; in research [42] the task of detecting lung or liver cancer; high accuracy of segmentation of fundus images showed in research [33, 43]. The results presented in research [44–47] indicate that the proposed technology of texture analysis is best suited for the analysis of X-ray images. The texture analysis used in research [40] showed that the proportion of correctly classified images ranged from 74% to 89%, depending on the selected area of interest. Most of the features used were based on run lengths feature. Below we present the

most common features used for informative feature selection (Eqs. (2–5)).

2.3 Histogram-Based Features

$$\text{– mean: } \mu = \sum_i^{N_g} ip(i); \quad (2)$$

where $p(i)$ is a normalized histogram vector (i.e. histogram whose entries are divided by the total number of pixels in ROI), $i = 0, 1, 2, \dots, N_g - 1$, N_g denotes the number of intensity levels;

$$\text{– variance } \sigma^2 = \sum_{i=1}^{N_g} (i - \mu)^2 p(i); \quad (3)$$

$$\text{– skewness } \mu_3 = \sigma^{-3} \sum_{i=1}^{N_g} (i - \mu)^3 p(i); \quad (4)$$

$$\text{– kurtosis } \mu_4 = \sigma^{-4} \sum_{i=1}^{N_g} (i - \mu)^4 p(i) - 3; \quad (5)$$

$$\text{– percentile-}n: i \text{ if } \sum_{k=0}^i p(k) \leq n,$$

where $n = 0.01, 0.1, 0.5, 0.9, 0.99$.

Gradient-based parameters. For the gradient feature calculation the following neighborhood for image pixel $x(i, j)$ is defined:

A	B	C	D	E
F	G	H	I	J
K	L	$x(i, j)$	N	O
P	Q	R	S	T
U	V	W	Y	Z

Based on this neighborhood, the absolute gradient value ($|Grad(i, j)|$) is calculated for each pixel (Eqs. (6–7)):

– for 5×5 pixel neighborhood:

$$|Grad5(i, j)| = \sqrt{(W - C)^2 + (O - K)^2}; \quad (6)$$

– for 3×3 pixel neighborhood:

$$|Grad3(i, j)| = \sqrt{(R - H)^2 + (N - L)^2}. \quad (7)$$

For the $|Grad5(i, j)| = |Grad3(i, j)|$ matrix of M elements (which contains absolute gradient values for ROI pixels), the gradient features are defined as follows:

– mean absolute gradient Eq. (8):

$$GrMean = \frac{1}{M} \sum_{i, j \in ROI} |Grad(i, j)|; \quad (8)$$

– variance of absolute gradient Eq. (9):

$$GrVariance = \frac{1}{M} \sum_{i, j \in ROI} (|Grad(i, j)| - GrMean)^2. \quad (9)$$

2.4 Co-Occurrence Matrix-Derived Parameters

The second-order histogram is defined as the co-occurrence matrix $h_{da}(i, j)$. When divided by the total number of neighboring pixels $R(d, \alpha)$ in ROI, this matrix becomes the estimate of the joint probability, $p_{da}(i, j)$, of two pixels, a distance d apart along a given direction α having particular (co-occurring) values i and j . Formally, given the image $f(x, y)$ with a set of N_g discrete intensity levels, the matrix $h_{da}(i, j)$ is defined such that its (i, j) th entry is equal to the number of times that $f(x_1, y_1) = i$ and $f(x_2, y_2) = j$, where $(x_2, y_2) = (x_1, y_1) + (d \cos \alpha, d \sin \alpha)$.

This yields a square matrix of dimension equal to the number of intensity levels in the image, for each distance d and orientation α . In MaZda, the distances $d = 1, 2, 3, 4$ and 5 pixels with angles $\alpha = 0^\circ, 45^\circ, 90^\circ$, and 135° are considered. The co-occurrence matrix-derived parameters computed by MaZda are defined by the equations that follow, where μ_x, μ_y , and σ_x, σ_y denote the mean and standard deviations of the row and column sums of the co-occurrence matrix, respectively. Thus, the co-occurrence matrix-based parameters are computed up to 20 times, for $(d, 0); (0, d); (d, d); (d, -d)$.

Co-occurrence matrix-derived features:

– entropy Eq. (10):

$$Entropy = - \sum_{i=1}^{N_g} \sum_{j=1}^{N_g} p(i, j) \log(p(i, j)), \quad (10)$$

– difference entropy Eq. (11):

$$DifEntrp = - \sum_{i=0}^{N_g} p_{x-y}(i) \log(p_{x-y}(i)), \quad (11)$$

– correlation Eq. (12):

$$Correlat = \frac{\sum_{i=1}^{N_g} \sum_{j=1}^{N_g} ij p(i, j) - \mu_x \mu_y}{\sigma_x \sigma_y};$$

$$p_{x-y}(k) = \sum_{i=1}^{N_g} \sum_{j=1}^{N_g} p(i, j), |i - j| = k, k = 0, 1, \dots, N_g - 1, \quad (12)$$

– inverse difference moment or homogeneity Eq. (13):

$$InvDfMom = \sum_{i=1}^{N_g} \sum_{j=1}^{N_g} (p(i, j) / 1 + (i - j)^2). \quad (13)$$

2.5 Run Length Matrix-Based Parameters

Parameters based on run length matrix are calculated 4 times for each region of interest (for vertical, horizontal, 45-degree and 135-degree directions). $p(i, j)$ is the number of times a run of length j has grey level i . N_g is the number of grey levels and N_r is the number of runs.

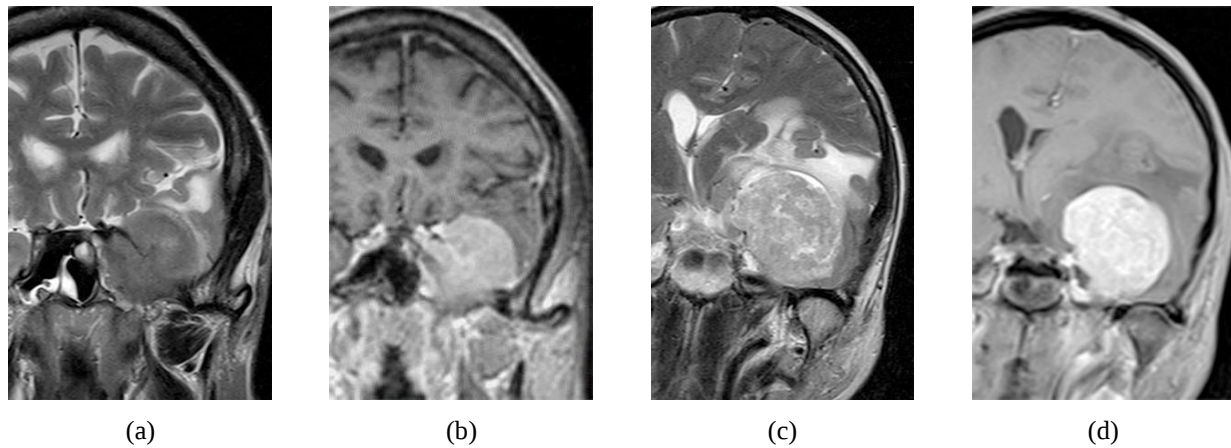


Fig. 1 Two meningiomas: malignant (a, b) and benign (c, d): T2 WI (a, c) and T1 CE (b, d). Differential diagnosis of these tumors, based on visual assessment of their signs, is difficult: both tumors are similar to each other, they have a rather heterogeneous structure and pronounced uniform contrasting. However, according to the results of histological examination, the first is malignant and the second is benign. Images dimensions: 200 px × 256 px.

Mazda definitions of run length matrix parameters are given below.

– short run emphasis inverse moments Eq. (14):

$$ShrtREmph = \frac{1}{n_r} \sum_{i=1}^{N_g} \sum_{j=1}^{N_r} \frac{p(i, j)}{j^2} = \frac{1}{n_r} \sum_{j=1}^{N_r} \frac{p_r(j)}{j^2}, \quad (14)$$

where $p_r(j) = \sum_{i=1}^{N_g} p(i, j)$, $n_r = \sum_{i=1}^{N_g} \sum_{j=1}^{N_r} p(i, j)$.

– grey level nonuniformity Eq. (15):

$$GLenNonUni = \frac{1}{n_r} \sum_{i=1}^{N_g} \left(\sum_{j=1}^{N_r} p(i, j) \right)^2. \quad (15)$$

3 Result and Discussion

According to the results of the reference test (histological examination of the surgical material): in the training group, benign meningiomas (M1) were diagnosed in 21 patients, malignant meningiomas (M2) in nine cases, the other nine formations were neurinomas (N).

The structure of detected tumors in the validation group: 15 of M1s, 6 of M2s, 6 of Ns. Classification of tumors based on semiotic features was difficult in some cases. Malignant tumors, in some cases, did not show typical MRI signs of malignancy (heterogeneity of structure, unevenness and lack of contrast) (Fig. 1) In some cases, with the localization of tumors in the region of the cerebellopontine angles, the differential diagnosis between benign tumors (benign meningiomas and neurinomas) was also difficult (Fig. 2).

Two statistical models were constructed based on the data of the training groups: using semiotic features (model 1) and based on textural parameters (model 2). The analysis of the diagnostic efficiency of the discriminant models consisted in calculating the operational characteristics of the tests: sensitivity, specificity based on the results of the validation of the models (Fig. 3). It can be noted that visual assessment of MRI data has a high sensitivity (73.3–100%) for benign

tumors, while the sensitivity for detecting malignant PET variants is only 50% (Fig. 3). Visual assessment of signs of tumors is not specific and subjective.

These results are consistent with world studies [48–50]. Visual assessment of MRI data has a high sensitivity (82.6–100%) for benign tumors (M1 and H), while the sensitivity for determining malignant variants of PET tends to zero (0–65.8%).

The model based on the signs of semiotics included the following signs: the average intensity of the MR signal, the minimum value of the measured diffusion coefficient, the volume of the tumor, the presence of necrosis zones, and changes in the underlying bone. The model built on the basis of textural features contains 20 parameters: gray level unevenness, features based on a matrix of series lengths that are significantly different for tumors of different histological types. These signs reflect the heterogeneity of the tumor structure.

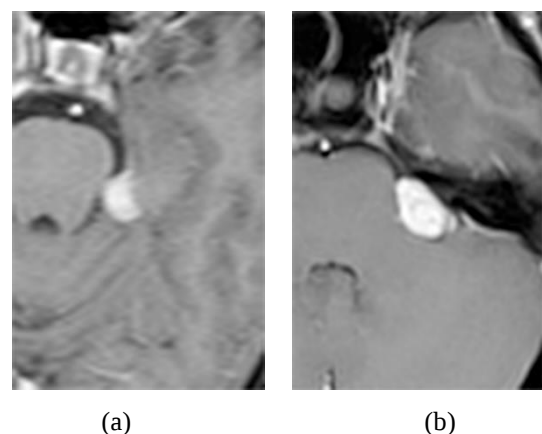


Fig. 2 T1 CE MRI images of meningioma (a) and neurinoma (b) of the cerebellopontine angles. Visual differentiation of neoplasms is difficult due to the similarity of signs: both tumors are widely adjacent to the meninges, their structure is homogeneous, contrasting is pronounced and homogeneous. Images dimensions: 100 px × 150 px.

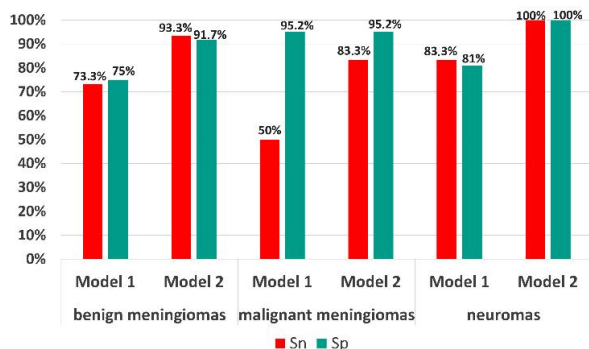
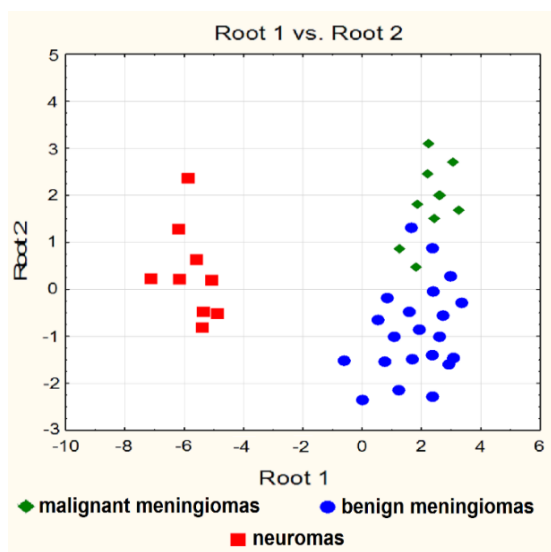
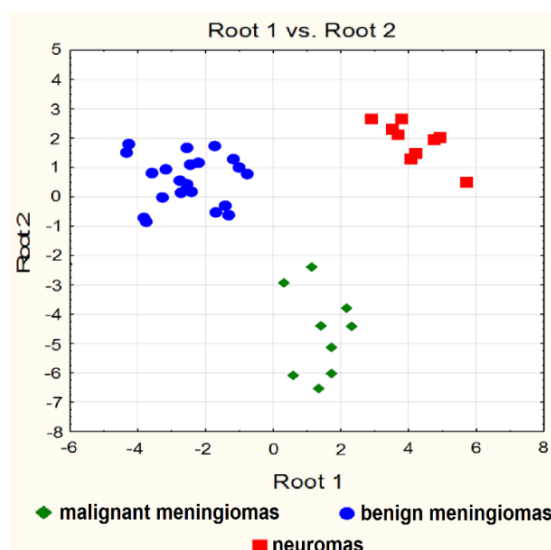


Fig. 3 Diagrams of sensitivity (Sn) and specificity (Sp) characteristics for various discriminant models based on the results of their validation.



(a)



(b)

Fig. 4 Feature distribution diagrams for models on training data (a) based on semiotic features, (b) based on histogram and texture parameters.

Differential diagnosis of meningiomas and neurinomas was carried out on the basis of histogram parameters. The informative features selected by discriminant analysis were characterized by the maximum contribution to the separation of tumors.

Diagrams (Fig. 4) clearly show the ability of discriminant models to separate tumors. The axes show the canonical roots of discriminant correlation analysis. There is an intersection of spaces for model 1 between benign and malignant meningiomas and a complete separation of tumors in model 2.

The superiority of the textural model of differential diagnosis is also confirmed by ROC analysis on validation. To build ROC curves, the data were converted in the format “true” (if the type of tumor identified by the model coincided with the results of the histological examination) “false” (if the simulation data differed from reality). The area under the curve for the texture model was 0.94, and for the model based on semiotics features it was 0.89 (Fig. 5).

For the practical use of the obtained statistical model for the classification of tumors based on textural features, it is necessary to use the discriminant classification function, which has the following form Eq. (15):

$$F = a_0 + \sum_{i=1}^{19} a_i x_i, \quad (15)$$

where x_i – features and a_i – coefficients, the values of which are presented in Table 1.

The discriminant function is calculated for each of the options (M1, M2, N). The tumor type is predicted based on which of the variants corresponds to the highest value of the discriminant function.

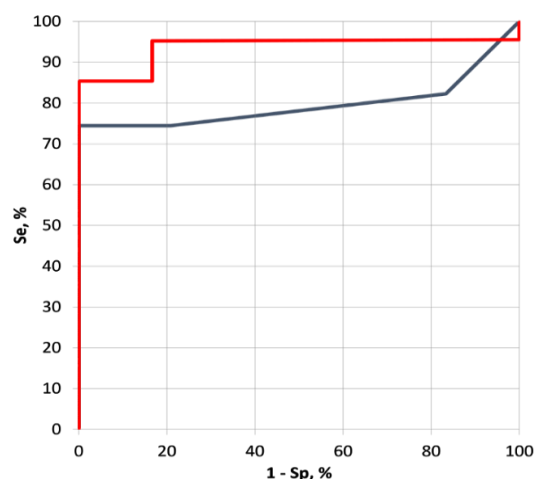


Fig. 5 ROC curves for two models of differential diagnosis on validation data: red – based on texture features, blue – based on MRI semiotics features. To build ROC curves, the data were converted in the format “true” (if the type of tumor identified by the model coincided with the results of the histological examination) “false” (if the simulation data differed from reality).

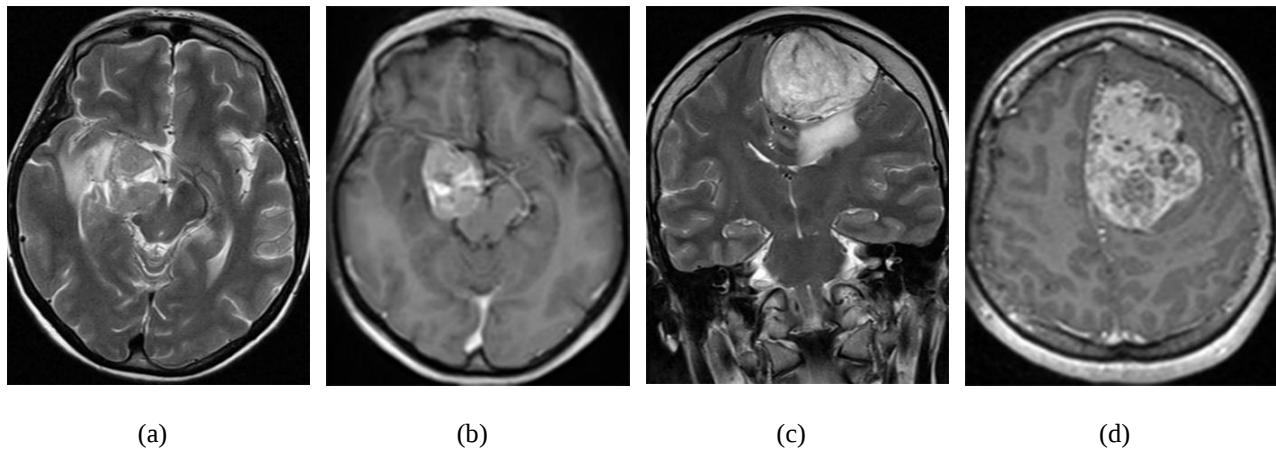


Fig. 6 Two meningiomas are shown: benign (a, b) and malignant (c, d): T2 WI (a, c) and T1 CE (b, d). The maximum value of the discriminant classification function for the first tumor indicated a benign meningioma, for the second formation it indicated a malignant meningioma. Images dimensions: 200 px × 256 px.

Table 1 Classification function coefficients of a discriminant model based on histogram and textural features for the differential diagnosis between benign meningiomas, malignant meningiomas and neurinomas.

i	Feature x_i			Coefficient a_i		
	Name	Scanning Protocol	MaZda feature	M1	M2	N
0	a_0			-153641	-146129	-166594
1	Sum of squares	T2	S(1, 0)SumOfSqs	-61786	-60247	-64529
2			S(5, -5)SumOfSqs	8518	8310	8946
3	Sum of variances		S(1, 0)SumVarnC	4144	4036	4332
4	Entropy sum		S(1, -1)SumEntrp	460974	449728	480528
5	Sum of averages		S(0, 5)SumAverg	-5187	-5085	-5444
6	Run length unevenness		135dr_RLNonUni	-3	-3	-3
7	Gray level unevenness		Vertl_GLevNonU	-5	-4	-5
8	Wavelet energy		WavEnLH_s-3	26	26	27
9	Entropy difference		S(2, -2)DifEntrp	5647	5304	5623
10	Inverse differential moment		S(5, 0)InvDfMom	-11028	-10480	-11018
11	Run length unevenness	T1	135dr_RLNonUni	-1	-1	-1
12	Wavelet energy	FLAIR	WavEnLL_s-2	1	1	1
13			WavEnHH_s-4	-23	-22	-24
14	Wavelet energy		WavEnLH_s-2	8	8	9
15	Sum of variances	ADC	S(0, 3)SumVarnC	2052	2004	2147
16	Run length unevenness		Horzl_RLNonUni	1	1	0
17	Histogram variance	T1 CE	Variance	8	7	8
18	Histogram skewness		Skewness	6117	5976	6373
19	Run length unevenness		135dr_RLNonUni	1	1	1

The results of the models are clearly demonstrated by the following clinical example (Fig. 6). In the world, 11 studies dealt with the differential diagnosis of

meningiomas, with 9 of them devoted to the differentiation between M1 and M2 (accuracy on average 88%) [51], and only one study devoted to the differential

diagnosis of meningiomas from neuromas (accuracy 96%) [52].

4 Conclusion

The possibilities of differential diagnosis of PExT by visual assessment of MRI images have been studied in detail, however, reliable differentiation of these neoplasms based on MR semiotics is often difficult. This is due to the insufficient information content of a number of signs, as well as the presence of the same or similar tomographic features in various types of tumors. Interest in studying the problem of PExT recognition based on the principles of radiomics is constantly growing, which is due to the desire to improve the diagnostic potential of MRI using the increase in computing power available to researchers, the improvement of the mathematical apparatus of machine learning and pattern recognition methods, among which the most promising is the texture analysis of tumors.

The results of the study showed that the analysis of standard MRI data based on radiomics shows a better

outcome in the differential diagnosis of PExT compared to visual assessment.

The proposed statistical model has high sensitivity and specificity for differential diagnosis between the three most common PExT: benign and malignant meningiomas and neurinomas. Modeling based on discriminant analysis demonstrated that textural features can be used for the differential diagnosis of PExT, and are highly informative, 33.3% superior to the model based on semiotics features. The use of quantitative indicators describing the structure of the tumor can improve the accuracy of differential diagnosis and is devoid of subjectivity.

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Disclosures

The authors declare no conflict of interest.

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