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INTELLIGENT SYSTEM FOR DIAGNOSING VESTIBULAR SCHWANNOMA

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***Abstract*—** *This scientific work is devoted to the development of an intelligent system for the diagnosis of vestibular schwannoma. A new approach to the texture analysis of magnetic resonance images of vestibular schwannoma is proposed in order to determine the assessment of tumor growth. The use of this approach will prevent the risks of tumor progression and timely determine the need for surgical intervention. Several classes of texture descriptors were used in the study, including: first-order statistics (intensity histograms), gray level co-occurrence matrix, gray level run length matrix, gray level size zone matrix, gray level dependency matrix, as well as wavelet-transformed features. The complex use of these descriptors made it possible to formalize the internal microstructure of the tumor and implement an effective model for predicting its growth.*

Keywords—Vestibular schwannoma; diagnosis of schwannoma growth; MRI imaging; texture analysis; classification task.

I. INTRODUCTION

Schwannoma (neurinoma) is a benign tumor that comes from Schwann cells that form the myelin sheath of peripheral nerves. Most often in clinical practice, vestibular schwannoma is a tumor that arises from the vestibulocochlear nerve (VIII cranial nerve), extending from its vestibular part. This type of tumor can be approximately 8–10% of all intracranial tumors and up to 90% of tumors in the cerebellopontine angle.

Extent of illness. According to various epidemiological studies, the incidence of vestibular schwannoma is approximately 1–2 per 100,000 population. The frequency of diagnosis has increased over the past decade, which is associated with increased access to neuroimaging methods, including magnetic resonance imaging. Most often, schwannomas are diagnosed in the age group of 40–60 years, with a slight female predominance.

According to Scientific Reports, the United States is currently recording nearly 2,500 new cases of vestibular schwannoma, which accounts for approximately 8% of all intracranial neoplasms [1].

Linked to this is the urgent need for highly sophisticated automation of diagnostic processes, especially in the areas of artificial intelligence (AI). The use of these methods can effectively improve the diagnostic efficiency, reduce the impact of the human factor, and significantly shorten the hours required for the analysis of medical images.

II. METHODS

Detection of schwannoma is a complex, multi-step process, which includes a clinical examination, history taking, laboratory diagnostics (if necessary) and high-precision neuroimaging methods, such as computer tomography (CT) [2] and magnetic resonance imaging (MRI).

Current neuroimaging allows not only to detect the tumor, but also to assess the dynamics of growth, the level of damage to surrounding tissue, the presence of hydrocephalus and other complications [3]. However, due to the fact that the early stages of the disease may have mildly expressed symptoms or may be asymptomatic, early diagnosis of schwannoma requires the use of highly sensitive and automated instruments, powered by artificial intelligence.

A. The need for texture analysis

Significant progress has been made in automated segmentation of medical images using convolutional neural networks and transformers, and methods that focus more on the geometric and morphological characteristics of tumor, such as shape, size and localization. However, to fully understand the biological behavior of tumor tissue, particularly its growth potential, it is necessary to recognize microstructural tissue features that are not always visible in standard images.

In this context, texture analysis is of particular value – a method that allows one to clearly assess the internal heterogeneity of tissues by analyzing spatial variations in signal intensity in images. Textural signs, such as entropy, homogeneity, contrast and other statistical parameters, can reflect the histological features of the tumor, cell density, presence of necrosis, microvessel density/diameter.

The research shows that the use of texture analysis in combination with machine learning methods makes it possible to create predictive models that can assess the likelihood of growth of vestibular schwannoma. For example, the study by George–Jones et al. (2020) demonstrated that texture and morphological features extracted from MRI images can be useful in predicting significant increase in tumor after stereotactic radiosurgery. A model based on these characteristics achieved a sensitivity of 92% and a specificity of 65% in predicting a volume increase greater than 20% of the tumor volume [4].

In addition, a study published in the journal Otology & Neurotology [5] showed that the textural characteristics of vestibular schwannomas on MRI images can reflect the histological features of the tumor, such as the presence of mucin, lymphocytes and hemosiderin. It is important to note the potential of texture analysis in non-invasively measuring the biological behavior of tumor.

B. Classifiers Used

The study used five modern classification algorithms: Random Forest, Balanced Random Forest, RUSBoost, XGBoost, and LightGBM. All models were selected for their efficiency when working with high-dimensional tabular data, as well as the ability to work with unbalanced samples, which is typical for medical problems.

1) Random Forest

Random Forest is an ensemble machine learning algorithm based on the construction of a set of decision trees [6]. Each tree is trained on a random subsample of training examples using the bootstrapping method, as well as on a random subset of features. The final decision is made by voting among all trees. This approach allows to reduce the variance of the model and ensure high resistance to overfitting. The model is insensitive to feature scaling, is able to work with categorical and numerical variables, and is well suited for tasks where interpretability and assessment of the importance of features are important.

2) Balanced Random Forest

Balanced Random Forest [7] is a modification of the classical Random Forest that takes into account the problem of unbalanced classes. Each tree in the forest is trained on a subsample of data obtained by randomly undersampling examples from the more represented class to achieve a balanced proportion between classes. Thus, at each step of the simulation, the algorithm forms a new subsample that contains the same number of examples of the positive and negative classes, which allows to increase the sensitivity of the model to the less represented class without losing the overall generalization ability.

3) RUSBoost

RUSBoost is an ensemble algorithm that combines the Random Undersampling (RUS) method with adaptive boosting (AdaBoost) [8]. At each iteration of building the ensemble from the training sample, a random undersampling is performed from the majority of the class, after which a weak classifier is trained. Subsequent iterations adaptively change the weights of the examples based on the errors of the previous classifier. Thus, the model simultaneously achieves a reduction in the impact of class disparity and adaptation to complex examples. RUSBoost is effective in tasks with strong class skew, in particular in medical diagnostic tasks.

4) XGBoost (Extreme Gradient Boosting)

XGBoost is a highly efficient implementation of gradient boosting for decision trees, focused on speed and performance [9]. The algorithm builds a sequence of trees, where each subsequent tree learns from the errors of the previous ones. The objective function is minimized using the second order gradient, which allows faster convergence to the optimum. In addition, XGBoost includes regularization of the model complexity, which reduces the risk of overfitting. The model supports work with missing values, automatic feature selection and is one of the most effective methods for structured forecasting problems.

5) LightGBM

LightGBM is a gradient boosting system designed for fast processing of large datasets with high feature dimensions [10]. It uses tree construction in the "leaf-wise" direction, which allows you to significantly reduce losses compared

to "level-wise" strategies. In addition, LightGBM implements an efficient histogram method for feature binning, which reduces computational complexity. The model supports early stopping, automatic tree complexity control, and handling of unbalanced data via the `scale_pos_weight` parameter. Thanks to these features, LightGBM provides high accuracy and speed, especially in tasks with a large amount of descriptors.

III. Texture Analysis MRI Image

Texture analysis of MRI images is a powerful tool for the quantitative assessment of the heterogeneity of tumor tissue, which can represent the biological behavior of tumor tissue. It has the potential to grow. This approach makes it possible to identify microstructural features that are not always noticeable in the visual assessment of the image, and can be useful for predicting the clinical progression of illness.

1) The main signs that characterize the growth of tumor

A study by Itoyama et al. (2022) conducted a radiomics analysis of 64 patients with vestibular schwannoma, revealing that texture features such as low minimum signal and high inverse difference normalizing moment (IDMN) were significantly associated with rapid tumor growth. The model that increased texture and clinical factors achieved the highest diagnostic efficiency with an area under the curve (AUC) of 0.69, compared with models that were influenced by texture (AUC 0.67) or less clinical (AUC 0.63) factors [11].

Another study conducted by George–Jones et al. (2021), demonstrated that the textural characteristics of MRI images of vestibular schwannomas have a significant correlation with histological features of the tumor, such as the presence of mucin, lymphocytes and hemosiderin. It is important to note the potential of texture analysis in non-invasively measuring the biological behavior of tumor [5].

2) Methods for processing MRI images for texture analysis

To carry out texture analysis of an MRI image, it is necessary to complete the following stages of image processing:

- front processing: includes normalization of signal intensity, image verification and artifact removal;
- segmentation: identifying a region of interest (ROI) that covers the tumor;
- feature extraction: calculation of statistical parameters such as entropy, homogeneity, contrast, correlation and others that characterize the texture of the image;
- analysis and modeling: the use of machine learning methods to generate forecasting models based on extracted texture marks.

Based on a review published in PubMed Central, texture analysis of MRI images of cerebral tumors, including vestibular schwannomas, can be an effective tool for assessing the characteristics of the tumor and predicting behavior [12].

Texture analysis of MRI images is promising for directly diagnosing and predicting the growth of vestibular schwannoma. It allows you to obtain additional information about the microstructural features of the tumor, which can help you achieve a more precise treatment strategy and reduce clinical results.

IV. Evaluating the Effectiveness of Classification Models

The evaluation of the performance of the classification models was based on a number of broad metrics that allow us to clearly assess the effectiveness of the algorithm and correctly assign objects to the target class (in this case - patients with progressive schwannoma) among others. For each model, a confusion matrix was created, including several key components:

- *TP (True Positive):* the number of correctly classified positive objects;
- *TN (True Negative):* the number of correctly classified negative objects;
- *FP (False Positive):* a number of negative objects, incorrectly assigned to the positive class;
- *FN (False Negative):* a number of positive objects classified as negative.

Based on these values, the following metrics were calculated:

1) Precision (accuracy of positive class classification)

This metric reflects the proportion of actively positive environments of all applications classified as positive:

$$\text{Precision} = \frac{\text{TP}}{(\text{TP} + \text{FP})}.$$

A high accuracy value indicates a low false positive rate.

2) Recall (sensitivity, recall)

Recall shows which part of the positive applications the model was able to correctly identify:

$$\text{Recall} = \frac{\text{TP}}{(\text{TP} + \text{FN})}.$$

This metric is critically important in medical tasks, where missing a positive case is unacceptable.

3) Accuracy (real accuracy of classification)

Accuracy means the proportion of correctly classified objects among all applications:

$$\text{Accuracy} = \frac{(\text{TP} + \text{TN})}{(\text{TP} + \text{TN} + \text{FP} + \text{FN})}.$$

Despite its popularity, this metric may not be informative in the minds of a strong imbalance of classes.

4) F1-score (harmonious average between Precision and Recall)

F1-score allows you to achieve a balance between Precision and Recall, which is especially important when it comes to compensation:

$$F1 = 2\frac{(\text{Precision} \cdot \text{Recall})}{(\text{Precision} + \text{Recall})}.$$

This metric is sensitive to both positive and negative decisions.

5) F2-score

F2-score is a modification of F1-score, which gives more Recall value. The F2 score is a modification of the F1 score that improves recall. It's extremely useful when recall is more important than precision:

$$F2 = \frac{5(\text{Precision} \cdot \text{Recall})}{(4\,\text{Precision} + \text{Recall})}.$$

This metric is useful for medical purposes such as screening and early detection of pathologies.

6) Gini Index

The Gini index is based on the differential value of the model and is directly related to the area under the ROC curve (AUC):

$$\text{Gini} = 2 \cdot \text{AUC} - 1.$$

The value of $\text{Gini} \in [0, 1]$, where 0 means the no discriminative power between classes, and 1 means perfect discrimination. The index is widely used in credit scoring tasks, as well as in biomedical information for assessing the strength of predictors.

V. Proposal Approach

The problem is formulated as a binary classification problem. Each patient should have two CT scans, separated by a time interval. According to the criterion for clinically significant growth, schwannomas that have increased in volume or area by more than 10% (the maximum threshold) during the control period are classified as class 1 (positive class). Lesions that remained stable or did not change significantly are assigned to class 0 (negative class).

Let us select a selection from *N* selections:

$$\mathcal{D} = \{(x_i, y_i)\}_{i=1}^{N},$$

where $x_i \in R^d$ is the vector of textural signs extracted from the image of schwannoma for the *i*th patient, and $y_i \in \{0,1\}$ is a significant change, which indicates the fact of a clinically significant increase in new creation between two time points.

In particular, label $y_i = 1$ assigned in cases where the relative increase in the volume (or area) of the schwannoma exceeds 10%:

$$\Delta V_i = \frac{V_i^{(t_2)} - V_i^{(t_1)}}{V_i^{(t_1)}} 100\%,$$

$$y_i = \begin{cases} 1, & \text{if} \quad \Delta V\_i \geq 10\%, \\ 0, & \text{else.} \end{cases}$$

The goal is to build a classification function:

$$f_\theta : R^d \to [0,1],$$

which approximates the probability that the neoplasm has a tendency to grow, i.e.:

$$f_\theta(x_i) \approx P(y_i = 1 x_i),$$

where θ are the model parameters that are tuned during the training process. Such a function should provide class prediction for new, previously unseen cases based only on the texture profile of the schwannoma in the initial image.

For each case (patient) from the original medical image (MRI or CT) of the schwannoma, the tumor is segmented. Then, quantitative descriptors characterizing its texture are extracted from the selected area.

VI. Description of the Descriptor Classes Used

In this study, several classes of descriptors were used that allow quantitatively describing both the intensity and textural characteristics of the region of interest (ROI) corresponding to the localization of schwannoma on the tomographic image. All descriptors were normalized by *Z*-normalization, i.e. by subtracting the mean value of the sample and

dividing by its standard deviation. This allows eliminating large-scale biases between different types of features and ensuring correct training of classification models.

The following classes of descriptors were used during model construction:

Intensity histograms (First-order statistics). This class describes the statistical characteristics of the brightness distribution within the ROI without taking into account the spatial context. The main metrics include mean, standard deviation, variance, skewness, kurtosis, median, minimum, maximum, entropy, and quantiles (e.g., 25th and 75th percentiles). Entropy is calculated $-\sum_i p_i \log_2(p_i)$, where p_i is the probability of intensity *i*. These features are basic indicators of the internal homogeneity of tissues.

GLCM (Gray-Level Co-occurrence Matrix). It takes into account the frequency of occurrence of pairs of pixels with given intensity values that are at a fixed distance from each other at a certain angle. Based on GLCM, the following descriptors are calculated: contrast (which measures local variations), homogeneity (reflects the smoothness of the image), energy (sum of squares of matrix elements), correlation (a measure of linear dependence between gray levels), and entropy. Contrast is defined as the $\text{sum}(i-j)^2 \cdot P(i,j)$, where $P(i,j)$ is the normalized value of the coincidence between levels *i* and *j*.

GLRLM (Gray-Level Run Length Matrix) – a matrix of gray level sequence lengths. It takes into account the number of consecutive voxels of the same value in a given direction. In particular, the metrics short-run emphasis (priority of short uniform areas), long-run emphasis (respectively, long ones), gray-level non-uniformity (non-uniformity of intensity levels), and others are calculated. For example, SRE is calculated as the sum $R(i, r) / r^2$, where $R(i, r)$ – the number of sequences of length *r* for intensity level *i*.

GLSZM (Gray-Level Size Zone Matrix) – matrix of gray level zone sizes. Unlike GLRLM, GLSZM is independent of direction and describes the number of pixels forming zones of equal intensity. Metrics used are small-zone emphasis, large-zone emphasis, zone size non-uniformity, etc. SZE is defined as the sum $Z(i, s) / s^2$, where $Z(i, s)$ – the number of zones of size *s* for intensity level *i*.

GLDM (Gray-Level Dependence Matrix) – gray level dependency matrix. It estimates how much a given voxel depends on its neighbors with similar intensity levels. Key features include dependence entropy and dependence non-uniformity. For example, DNUN is calculated as the sum of squares of the sum of dependencies at each gray level.

Wavelet-transformed texture features. For multi-level texture analysis, a wavelet transform (e.g., Daubechies or Haar) was used. Each image volume is transformed into a set of approximation and detail coefficients at several decomposition levels. For each subgroup of coefficients, the first statistics are calculated: mean, standard deviation, energy, etc. This allows us to detect patterns on both small and large spatial scales.

VII. Results

A sample of 427 pairs of images from 190 patients was used to train the models, of which 102 pairs showed a significant increase in the size of schwannoma (more than 10%). The data were taken from the work [13].

All models were trained on the same set of descriptors calculated from medical tomographic images, a total of 135 features were used. To ensure objective comparison, the same cross-validation and feature preprocessing procedures were used. The results are shown in Table I.

As we can see, the LGBM model performed best.

Accordingly, after training the model, the importance of the features for it was assessed, and therefore the informativeness of each of the descriptors. Accordingly, the following turned out to be the most informative:

1) wavelet_level_2_aad_mean

This descriptor represents the average value of the AAD (Approximation–Approximation–Detail) coefficients at the second level of three-dimensional wavelet decomposition. In 3D decomposition, the volume is divided into 8 subcomponents, each of which contains information about frequency changes along the corresponding axes. AAD means that the approximation was performed along the first and second axes, and the detailing was performed along the third. Thus, the descriptor reflects local variations in image intensity along the *Z* axis while preserving the global structure in *XY*. The value shows the average level of local complexity in the specified direction.

TABLE I. MODEL TRAINING RESULTS

Model	Precision	Recall	Accuracy	F1-score	F2-score	Gini
Balanced RF	0.5721	0.6842	0.6763	0.6238	0.6594	0.4279
LGBM	0.6284	0.7127	0.7291	0.6674	0.6951	0.5418
RUSBoost	0.5953	0.6498	0.7034	0.6221	0.6397	0.4912
Random Forest	0.5623	0.6294	0.6898	0.5947	0.6172	0.4691
XGBoost	0.6124	0.6843	0.7161	0.6473	0.6722	0.5176

2) wavelet_level_1_ddd_mean

This descriptor corresponds to the average value of the DDD (Detail–Detail–Detail) coefficients at the first level of wavelet decomposition. In this case, detailed information is preserved in all three spatial directions, which makes the descriptor particularly sensitive to high-frequency noise and fine inhomogeneities within the tissue. The value of such a descriptor allows us to assess the degree of textural complexity or chaoticity of the schwannoma structure in the volume.

3) wavelet_level_1_ada_mean

This descriptor denotes the average value of the ADA (Approximation–Detail–Approximation) coefficients at the first level of wavelet transformation. This orientation ensures the preservation of global features along the first and third axes (for example, *X* and *Z*), as well as detailed fixation of changes along the second (*Y*). It is sensitive to texture variations along the frontal plane, which allows us to detect changes in the structure during transverse scanning.

4) lbp_mean_bin_4

This descriptor refers to the local binary pattern (LBP) method, which encodes local texture patterns on each image slice. The method generates a histogram where each bin corresponds to a specific pattern of intensity transitions of pixels in the neighborhood. The value of lbp_mean_bin_4 is the average value of the fourth bin of the LBP histogram, calculated over all slices. It reflects the frequency of occurrence of one of the characteristic micropatterns associated with specific types of local heterogeneity.

5) wavelet_level_2_ddd_mean

The wavelet_level_2_ddd_mean descriptor is the average value of the detailed coefficients of the second level of wavelet decomposition obtained from filtering in all three directions. It is an extension of wavelet_level_1_ddd_mean, but characterizes larger-scale intensity fluctuations. This descriptor allows us to assess the presence of more global structural heterogeneities in tissue at lower spatial resolution.

The distribution of values of the 5 most popular descriptors is shown in Fig. 1.

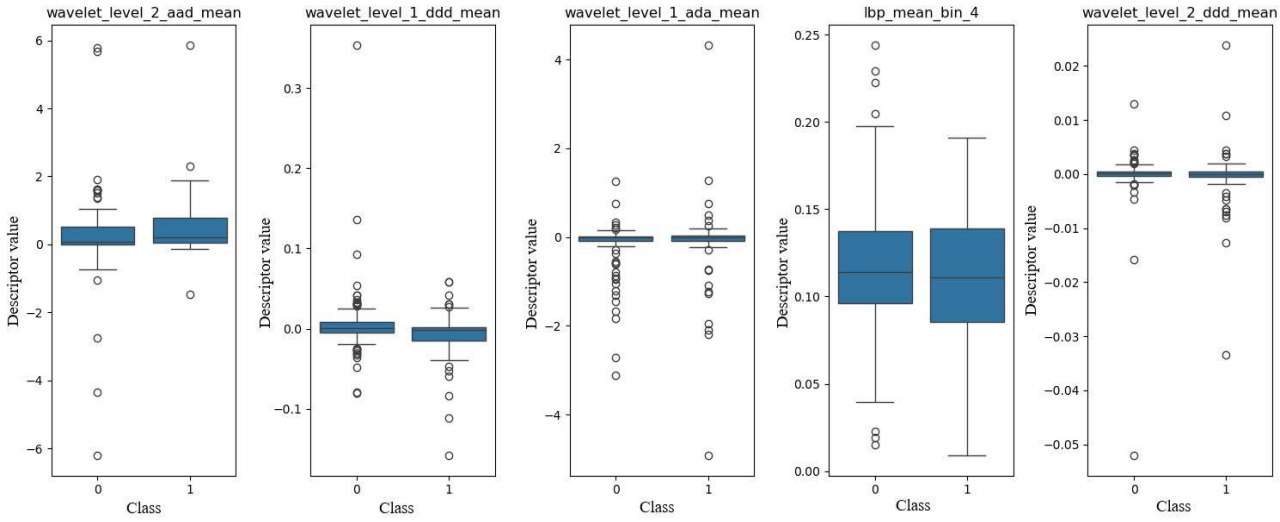

Fig. 1. Distribution of values of the 5 best descriptors

VIII. CONCLUSION

Diagnosis of vestibular schwannoma remains a complex clinical task that requires high accuracy, sensitivity, and interpretative objectivity. Given the increasing number of tumor diseases caused by both external factors (deterioration of the environment, lifestyle) and systemic health problems (lack of medical personnel, overload of institutions), there is an urgent need to implement new, intelligently guided diagnostic approaches.

The article reviewed modern methods for isolating tumor structures using MRI, where magnetic resonance imaging plays a particularly important role as an informative, highly sensitive method for visualizing schwannoma. Traditional MRI image processing is gradually giving way to automated algorithms based on artificial intelligence – in particular, convolutional neural networks and transformer architectures, which provide high accuracy in tumor segmentation and reduce the human factor.

In addition, the method of texture analysis has significant prospects, which allows building models for predicting tumor growth without significant computational costs, using conventional tabular classifiers. In this work, a classifier suitable for applied purposes (accuracy greater than 0.71) was trained and the best texture descriptors with significant potential for future use were selected.

However, it is important to understand that detecting the tumor itself is only the first step. For a deeper analysis of its growth potential, it is necessary to implement texture analysis – a method for quantitatively assessing tissue heterogeneity based on the spatial distribution of signal intensities. This approach allows not only to describe the morphological features of schwannoma, but also to build prognostic models of its growth. Studies show that the combination of texture and clinical features significantly increases the accuracy of predicting the biological behavior of the tumor.

Thus, the future of effective diagnosis of vestibular schwannoma lies in the integration of classical medical imaging methods with modern intelligent analysis systems. The combined use of MRI, deep neural networks, transformers and texture analysis opens the way to more accurate, faster and personalized medical diagnostics, which will significantly improve the quality of treatment of patients with brain tumors.

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В. М. Синєглазов, А. В. Шеруда, Шевченко М. В. Інтелектуальна система діагностики вестибулярної шванноми

Наукову роботу присвячено розробці інтелектуальної системи діагностики вестибулярної шванноми. Запропоновано новий підхід до аналізу текстури МРТ-зображень шванном як методу оцінки зростання пухлини. Використання цього підходу допоможе уникнути ризиків прогресування новоутворення та негайно усунути необхідність хірургічного втручання. В межах дослідження було об’єднано низку класів дескрипторів текстури, включаючи: статистику першого порядку (гістограми інтенсивності), матрицю співзустрічей рівнів сірого, матрицю довжин серій рівнів сірого, матрицю розмірів зон, матрицю залежностей рівнів сірого, а також ознаки, перетворені за допомогою вейвлет-перетворення. Комплексний аналіз цих дескрипторів дозволив формалізувати внутрішню мікроструктуру пухлини та реалізувати ефективну модель для прогнозування його зростання.

Ключові слова: вестибулярна шваннома; діагностування росту шваноми; МРТ-зображення; текстурний аналіз; задача класифікації.

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