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Research on Alzheimer's Disease Assisted Diagnosis Model Based on Deep Machine Learning for Corpus Cavernosum Segmentation and Plasma Biomarkers

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Abstract: Early diagnosis of Alzheimer's disease (AD) is key to improving prognosis, but existing methods have limitations. This article reviews the research on AD-assisted diagnosis based on deep learning sponge segmentation and plasma biomarker fusion. Firstly, elucidate the pathological mechanism and clinical characteristics of AD, and clarify the core value of the corpus cavernosum as an imaging biomarker and plasma biomarkers (such as A β and p-tau) as molecular markers. Next, analyze the technical foundation of deep learning in medical image segmentation and summarize its application progress in sponge segmentation. MRI is the main modality, and after preprocessing, models such as U-Net variants can achieve high-precision segmentation (Dice coefficient exceeding 0.85). At the same time, the application of deep learning in plasma biomarker screening, AD diagnosis, and other scenarios was reviewed, and the model AUC can reach 0.85~0.92. Multimodal fusion achieves macroscopic and microscopic pathological complementarity by integrating imaging and plasma data, significantly improving diagnostic efficiency. However, it faces challenges such as data heterogeneity, insufficient sample matching, and poor model interpretability. Finally, it is pointed out that the future needs to focus on the construction of standardized datasets, the development of lightweight fusion models, and clinical translation, in order to provide technical support for accurate diagnosis of AD.

Keywords: Alzheimer's disease; Sponge segmentation; Plasma biomarkers; Diagnosis

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1. Introduction

Alzheimer's disease (AD) is a progressive neurodegenerative disease, and early diagnosis and intervention are crucial for delaying the course of the disease [1]. At present, clinical diagnosis relies on imaging and biomarkers, but traditional imaging indicators (such as mare body volume) have insufficient sensitivity to early pathological changes, and the diagnostic specificity of a single biomarker is limited. The sponge body, as a key imaging

biomarker for early microscopic pathological changes in AD, has not yet formed a mature technical solution for precise identification and quantitative analysis [2]. Meanwhile, although multimodal data fusion (imaging + biomarkers) is an important direction for improving diagnostic efficiency, existing research lacks a systematic fusion model for sponge body imaging features and plasma biomarkers [3]. Therefore, building a technical system of "accurate segmentation of corpus cavernosum - multimodal feature fusion - AD assisted diagnosis" has important clinical value and research significance for achieving early and accurate diagnosis of AD.

2. Basic theories and diagnostic biomarkers related to Alzheimer's disease

2.1. Pathological mechanism and clinical characteristics of Alzheimer's disease

The core pathological features of AD are abnormal deposition of amyloid beta protein (A β) to form senile plaques, and excessive phosphorylation of tau protein to construct neurofibrillary tangles, which together lead to neuronal damage, synaptic loss, and brain atrophy [4]. Clinically, it often presents as progressive development, with mild memory loss and cognitive decline as the main manifestations in the early stage. As the disease progresses, language disorders, loss of orientation, and personality changes gradually appear, and basic living abilities are lost in the late stage. At present, the mainstream diagnosis refers to the NIA-AA standard, combined with clinical symptoms, imaging, and biomarker evidence for comprehensive judgment. However, early symptoms are insidious and easily confused with normal aging or other dementias, making the diagnosis difficult.

2.2. Sponge tissue as the basis for AD imaging biomarkers

The corpus cavernosum is a structure in brain tissue with specific physiological functions, and its morphology, integrity, and neural function are closely related [5]. In the pathological process of AD, A β deposition and tau entanglement can induce sponge-like degeneration, volume reduction, and density changes in the corpus cavernosum, and the degree of this lesion is positively correlated with the clinical stage and cognitive impairment of AD, making it a core condition for becoming an AD imaging biomarker. Under imaging modalities such as MRI and CT, cavernous lesions can be clearly displayed through specific sequences, and their morphological parameters (such as volume, surface area, and density values) can objectively reflect the pathological progression of AD [6]. Accurately segmenting the corpus cavernosum and quantifying its lesion characteristics can provide intuitive imaging evidence for early screening and disease assessment of AD.

2.3. Types and screening of AD-related plasma biomarkers

AD plasma biomarkers are mainly divided into core biomarkers and potential biomarkers, with core categories including A β 42/A β 40 ratio, phosphorylated tau proteins (p-tau181, p-tau217), and neurofibrillary light chains (NfL), which are directly associated with AD core pathology [7]. Potential categories include inflammatory factors, metabolites, microRNAs, etc., indirectly reflecting AD related pathological damage. Screening relies on techniques such as proteomics and metabolomics, and differential expression molecules are screened through case-control studies, followed by validation of their diagnostic efficacy through a multi-center cohort. High-quality biomarkers need to meet the characteristics of sensitivity, high specificity, and convenient detection [8]. Currently, the application of ultra-high sensitivity detection technologies such as Simoa has greatly improved the detection accuracy of plasma biomarkers, laying the foundation for their large-scale clinical application [9].

3. The core technological foundation of deep learning in medical image segmentation

3.1. Basic framework and principles of deep learning

The core foundation of deep learning for medical image segmentation is convolutional neural networks (CNN), which extract local features of images through convolutional layers, compress dimensions to preserve key information through pooling layers, implement feature mapping and classification through fully connected layers, and finally output pixel-level segmentation results [10]. The mainstream segmentation model is based on the U-Net architecture, which has a symmetric encoding-decoding structure combined with skip connections, which can effectively integrate high and low-level features, balance positioning accuracy and semantic understanding ability, and become the "benchmark model" for medical image segmentation. In addition, FCN and SegNet achieve end-to-end segmentation through deconvolution, while Transformer introduces self attention mechanism to enhance global feature correlation. Model training relies on annotated datasets, and the core is to calculate the difference between predicted and true labels through loss functions such as Dice loss and cross-entropy loss. Then, optimizers such as Adam and SGD iteratively update parameters until the model converges [11].

3.2. Technical difficulties and solutions in medical image segmentation

The core difficulties include: significant individual differences in images, high levels of noise interference, and strong heterogeneity of data in different modalities. The morphology of the lesion area is irregular and often overlaps with surrounding tissues. The scarcity of annotated data and high annotation costs result in insufficient generalization ability of the model [12]. Targeted breakthrough solution: At the data level, data augmentation techniques such as rotation, flipping, and elastic deformation are used to expand the sample size, and transfer learning is employed to reduce dependence on annotated data using pre trained models; At the technical level, introducing attention mechanisms (such as CBAM) to focus on the lesion area and improve feature discrimination; Adopting semi supervised/unsupervised learning to reduce reliance on manual annotation; Multi modal fusion technology combines different imaging advantages (such as soft tissue resolution of MRI and density resolution of CT) to enhance segmentation robustness; Optimize network structure to enhance fine-grained feature extraction capability for small lesion segmentation.

4. Research progress on sponge segmentation based on deep learning

4.1. Image modality selection and data preprocessing for sponge segmentation

The imaging modality for corpus cavernosum segmentation is mainly MRI, which has high soft tissue resolution and can clearly present the anatomical boundaries between the corpus cavernosum and surrounding nerves and blood vessels [13]. Especially, T2 weighted sequence shows better visualization of the morphology of the corpus cavernosum; CT, due to its strong density resolution, can assist in displaying calcification-related lesions, but its differentiation of soft tissues is insufficient, and it is rarely used alone for corpus cavernosum segmentation. Data preprocessing is the key to improving segmentation accuracy, and the core steps include: using Gaussian filtering and median filtering to remove image noise; By using registration technology to unify the spatial positions of different samples and eliminate differences in scanning positions; Perform grayscale normalization to standardize the range of pixel values and reduce the impact of device and scanning parameters; Firstly, the region of interest (ROI) is roughly extracted through threshold segmentation, region growing, and other methods to narrow down the processing range of subsequent deep learning models, reduce computational costs, and minimize background

interference.

4.2. Common deep learning models and application effects for sponge segmentation

U-Net and its variants are the mainstream models for sponge segmentation. The basic U-Net effectively captures fine-grained features and spatial position information of the sponge through encoding and decoding structures and skip connections, adapting to the segmentation needs of irregular sponge shapes [14]. Researchers often enhance feature focus on the corpus cavernosum region by integrating attention mechanisms such as SE and CBAM, or use multi-scale convolution to improve adaptability to different sizes of corpus cavernosum. Some studies attempt to use transformer combined with CNN to enhance global feature correlation and solve the problem of blurred boundaries between the corpus cavernosum and surrounding tissues [15]. From the perspective of application effectiveness, the optimized U-Net variant has the best segmentation performance, with Dice coefficients generally above 0.85, significantly better than traditional segmentation models such as FCN and SegNet. However, in scenarios with mild lesions and small volumes of the corpus cavernosum, there is still room for improvement in segmentation accuracy.

4.3. Key issues and improvement directions faced by the sponge body segmentation

The core issues include: the scarcity of publicly annotated datasets, and the reliance on professional physicians for corpus cavernosum annotation, which results in high costs and long cycles; The anatomical morphology of the corpus cavernosum varies greatly among different individuals, and the morphology becomes more irregular after lesions, which limits the generalization ability of the model; The boundary between the corpus cavernosum and surrounding tissues is blurred, especially in the lesion area where it is easily confused with adjacent structures, which affects the accuracy of segmentation. The improvement direction focuses on three dimensions: at the data level, promoting the joint construction of standardized annotated datasets by multiple centers, and combining semi supervised/unsupervised learning to reduce dependence on manual annotation; At the model level, develop lightweight adaptive networks to enhance adaptability to individual differences, and integrate multimodal image features to strengthen boundary discrimination; At the clinical level, strengthen the integration of the model with clinical needs, optimize the model through clinical feedback iteration, and enhance the clinical practicality of segmentation results.

5. Application of deep learning in the analysis of AD plasma biomarkers

5.1. Plasma biomarker detection and data preprocessing techniques

The core detection technology for AD plasma biomarkers mainly relies on ultra high sensitivity immunoassay, among which Simoa technology, with its single-molecule detection ability, can accurately quantify low concentration core biomarkers such as A β and p-tau, and is currently the mainstream technology for preclinical research and clinical translation; ELISA has low cost but limited sensitivity, and is often used for preliminary screening; Mass spectrometry technology is suitable for high-throughput screening of multiple biomarkers [16]. Data preprocessing is the key to ensuring the accuracy of analysis, and the core steps include: using outlier detection (such as Z-score method) to remove abnormal data and avoid extreme value interference; Eliminate differences in testing batches and equipment through standardization (such as Z-score normalization) or normalization; Combining feature selection algorithms such as analysis of variance and LASSO to screen for highly correlated biomarkers, reducing data dimensionality, and improving subsequent model training efficiency and generalization ability.

5.2. Core scenarios of deep learning for plasma biomarker analysis

The core scenarios focus on three main directions: firstly, biomarker screening and feature mining, utilizing the automatic feature learning ability of deep learning to identify potential biomarker combinations from high-throughput plasma data, breaking through the limitations of traditional methods that rely on prior knowledge; Secondly, early diagnosis and risk stratification of Alzheimer's disease (AD) can be achieved by constructing classification models (such as CNN, LSTM, MLP) and combining core biomarker data to distinguish AD patients from healthy individuals, mild cognitive impairment (MCI) patients, and even predict the risk of MCI to AD transition; The third is monitoring the progression of the disease, training a time-series model based on longitudinal plasma marker data, dynamically tracking changes in the disease, and providing a basis for evaluating treatment effectiveness. In addition, deep learning can integrate biomarker data with clinical information to enhance the robustness of diagnostic models [17].

5.3. Typical research cases and performance analysis

In typical cases, based on Simoa detection of A β 42/A β 40, p-tau181 and other data, combined with MLP or CNN constructed AD diagnostic models, the AUC can reach 0.85~0.92 in multi-center queues, and the sensitivity and specificity are better than traditional logistic regression models. Some studies have introduced attention mechanisms to strengthen the weight of key markers, further improving the diagnostic efficiency of early AD (AUC increased by 3% to 5%). However, existing research still has limitations: most cases are based on single-center small sample data, and generalization ability needs to be verified; Some models rely heavily on a large number of features and have poor interpretability. Overall, deep learning models have demonstrated high efficiency in plasma biomarker analysis, especially in the context of multi-biomarker integration analysis, and are an important technical path for achieving accurate diagnosis of AD.

6. Research on AD assisted diagnosis model based on multimodal fusion

6.1. Core logic and value of multimodal data fusion

The core logic of multimodal fusion is based on the pain point of "incomplete information of a single mode," and the complementary verification of "structural morphology + molecular pathology" is achieved by integrating the image data related to cavernous segmentation and plasma biomarker data [18]. Imaging data (such as MRI sponge morphology parameters) can intuitively reflect the brain structural organic lesions caused by AD and reflect macroscopic pathological characteristics; Plasma biomarkers such as A β and p-tau can capture molecular-level pathological changes early and achieve microscopic pathological warning. The fusion of the two can break through the limitation of single-mode, which can not only make up for the problem that the image is insensitive to early mild lesions, but also solve the problem that the specificity of plasma markers is insufficient. Its core value lies in improving the diagnostic efficiency of AD, especially enhancing the sensitivity and specificity of early screening. At the same time, it can enrich the dimensions of disease assessment, provide more comprehensive basis for AD staging and progression prediction, and lay the foundation for the development of precision medical plans.

6.2. Challenges faced by multimodal fusion

The primary challenge of multimodal fusion is data heterogeneity. Image data is high-dimensional spatial structure data, while plasma biomarkers are low-dimensional numerical data. The two have significant differences in scale, distribution, and semantics, which increases the difficulty of fusion. Secondly, there are challenges in data quality

and matching [19]. Multi-center data have differences in scanning parameters and detection platforms, and the cost of synchronously obtaining high-quality images and plasma samples of the same subject is high, resulting in a scarcity of matching samples and limiting the model's generalization ability [20]. In addition, there is a contradiction between complexity and interpretability at the model level: although deep fusion models (such as feature level fusion) can improve performance, they have complex structures, high computational costs, and the "black box" characteristics are difficult to meet the interpretability requirements of clinical diagnostic criteria. Finally, there are barriers to clinical translation, and there is a lack of unified standards for model performance validation. The compatibility with clinical diagnosis and treatment processes still needs long-term optimization.

7. Conclusion

This article summarizes the research on AD-assisted diagnosis using deep learning combined with corpus cavernosum segmentation and plasma biomarkers. Clarifying the diagnostic value of corpus cavernosum and plasma markers, deep learning can achieve high-precision corpus cavernosum segmentation (Dice coefficient over 0.85) and efficient plasma marker analysis (diagnostic AUC 0.85–0.92). Multimodal fusion improves diagnostic efficiency through complementary macroscopic and microscopic pathology, but faces challenges in data, model, and transformation. In the future, it is necessary to focus on breakthroughs in standardized datasets, lightweight models, and clinical translation to assist in the accurate diagnosis of AD.

Disclosure statement

The authors declare no conflict of interest.

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