磁共振成像

月刊
总第149期
2010年1月创刊

2024年第15卷第11期
2024年11月20日出版

刊名题写：时任第十一届全国人大常委会副委员长韩启德

主管单位 中华人民共和国国家卫生健康委员会

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出版单位 《磁共振成像》杂志社有限公司

发行范围 公开
发行单位 本刊发行部

国内发行 中国邮政集团有限公司北京市报刊发行局
邮发代号 2-855
国外总发行 中国国际图书贸易集团有限公司
国外发行代号 M 8958
印刷单位 北京科信印刷有限公司

电　话 010-67113815
E-mail editor@cjmri.cn
网　址 www.chinesemri.com
定　价 每册30元

国内统一连续出版物号
CN 11-5902/R
国际标准连续出版物号
ISSN 1674-8034

广告发布登记证号 京西市监广登字20170242号

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目　次

论　著

临床研究

基于种子点的功能连接对轻微型肝性脑病患者默认网络的研究
………牛芳，郑佳瑞，马文富，马万龙，金一萱，孙萌，丁向春，王晓东（1）
脑功能网络拓扑属性在评价tDCS改善缺血性脑卒中后认知障碍中的应用价值
………………………………………钟佳利，景小珊，梁莹，彭如臣，信瑞强（6）
基于T2WI放射组学模型评估帕金森病患者严重程度的研究
……………………………韦福利，刘丹，李鑫娅，曹婉君，彭永明，王芳（12）
早发性精神分裂症患者脑灰质结构改变:一项基于体素的形态学测量的元分析
……………………………王露，刘芮杉，廖娟，夏林枫，卓丽华，李宏伟（17）
多模态MRI对脑白质高信号伴抑郁状态患者脑微结构的研究
………周莹，张硕，谭中建，路一坤，高金阳，韩笑，马丽芳，崔方圆（24）
MOLLI T1 mapping定量技术在儿童脑发育评估中的应用可行性探讨
…………………………………………………杨雪，贾凤林，马鑫茂，李学胜，李珮，
张露，廖怡，宁刚，曲海波（32）
NODDI技术对颞叶癫痫认知障碍患者海马微结构的临床研究
………………………………杨文蕊，王旭聪，李健，宋邓妍，王卓，陈兵（39）
扩散峰度成像对遗尿症男童脑白质微结构改变的研究
……………………………杨子剑，马骏，杜小霞，林昕迪，陈群，王梦星（44）
集成机器学习模型联合磁共振视觉及DTI直方图预测成人弥漫性胶质瘤
IDH表型的研究 ……………………………………………韩鑫，李笑然，卢洁（51）
合成MRI联合酰胺质子转移成像在预测脑胶质瘤IDH1基因状态中的应用价值
…………孙萌，马文富，葛鑫，金一萱，牛芳，党佩，周嘉鑫，王晓东（60）
MRI时间依赖扩散诊断指标判断胶质母细胞瘤MGMT启动子甲基化
………………梁晓晶，张云，符永瑰，谢雁，魏倩倩，程流泉，王庆军（67）
基于压缩感知的心脏磁共振电影成像在左心室应变评估中可行性分析
……………………………王妮，吴琛，周运锋，谈忠孝，程亮，刘孟潇（75）
基于静息态脑活动及功能连接特征分类乳腺癌化疗相关认知障碍
………………………………………冯云，郭莉莉，鲍艺文，黄伟，柏根基（83）
表观扩散系数在预测肝泡状棘球蚴病发生远处转移的临床价值
…………………丹增耶昂，鲍海华，张雪倩，龙昌友，邢玉洁，田鹏启（90）

初探T1 mapping联合DWI识别早期肾间质纤维化的价值
………………孔欣悦，华晨辰，周乐汀，庄毅，刘晓斌，蔡婷，王凉（96）
磁共振结合临床指标对优化O-RADS MRI 4分肿块风险分层的价值
……………………………李彩红，李易，刘柳，周印，杨雅莹，毛芸（103）
mp-MRI影像组学术前预测子宫内膜癌微卫星不稳定性的应用研究
…………………………………………赵纪福，田燕，马密密，曹新山（110）

技术研究

基于深度学习的T2 Flair序列提升白质高信号图像质量的价值
……………………赵如盛，徐露露，李青，徐义程，张久楼，荣凡令（117）
三维高分辨压缩感知对比增强全身MRA技术的可行性研究
……李景阳，富青，刘小明，吴佳威，金腾，于群，雷子乔，孔祥闯（123）
5.0 T磁共振呼吸触发和单次屏气两种胰胆管成像序列价值比较
…………………胡翀，王朋，何野，李少朋，音大为，纵然，邓克学（130）
基于复合灵敏度编码的小视野扩散加权成像在宫颈癌中的临床价值
…………梅莞翠，汤倩，李铖铖，王赛，陈文，刘薇音，杨波，徐霖（136）

综 述

阿尔茨海默病患者血浆标志物及其与磁共振脑影像和认知功能关联的研究进展…………………………葛丹妮，陈夫涛，陈玖，张鑫，张冰（142）
神经退行性疾病认知灵活性改变的行为学及影像学研究进展
………………………………曹馨予，于瀛，胡博，颜林枫，崔光彬（148）
重度抑郁症患者脑网络有效连接的磁共振成像研究进展
…………………………………………孙进楠，伊伟，黄俊霖，任瑞（153）
阻塞性睡眠呼吸暂停患者脑结构及功能磁共振成像研究进展
……孙利强，李琳，胡婧，刘丽莹，崔凯歌，杨冀萍，贾娟，于佳琪（160）
伴中央颞区棘波儿童良性癫痫的MRI研究进展
…………………………………………………………陈译文，张志强（169）
功能磁共振成像技术诠释针刺治疗缺血性中风机制的进展
………………………………仲思潼，曹馨元，梁吉，孙忠人，尹洪娜（174）
磁共振成像技术在人脑胶质淋巴系统研究的现状与挑战
……………………杜晓岚，段曦瑞，李国臣，谭娜，周欣颜，廖承德（180）
无症状颈动脉狭窄的脑结构和功能MRI研究进展
………………………………………王俊君，宋林峰，田彬琳，江林（185）
基于深度学习的磁共振成像在冠心病诊疗中的应用进展
………………………………………………………………伍倩，郭辉（190）
T1、T2 mapping技术在急性心肌梗死中的应用进展
…………………………………………泥鲁莹，张前，曹赫，姜兴岳（198）
磁共振成像预测HER-2阳性乳腺癌新辅助治疗疗效的研究进展
……………………………………………………贺志远，王唯伟，孙占国（203）
合成MRI在乳腺癌的临床应用及进展
………………………………………………………………黄越，李锋（209）

封面文章

脑胶质瘤是最常见的原发恶性脑肿瘤，发病率约为每十万人5~6例，其中异柠檬酸脱氢酶（isocitrate dehydrogenase, IDH）野生型胶质母细胞瘤占比最高，预后较差，5年生存率仅7%。2021年版世界卫生组织中枢神经系统肿瘤分类将异柠檬酸脱氢酶状态作为成人弥漫性胶质瘤的重要分子诊断依据，IDH表型对于患者的预后风险分层和治疗反应评估至关重要，与IDH野生型胶质瘤相比，IDH突变型与总生存期和治疗反应的改善相关。精准的分子分型诊断能协助临床制订个体化治疗方案，延长患者生存期。目前对于胶质瘤异柠檬酸脱氢酶状态的判断有赖于手术病理组织DNA测序技术，但操作有创，仍需要精准的术前无创评估方法。

MRI作为胶质瘤患者术前评估的重要组成部分，包括了常规序列和功能序列，两种序列可以从不同方面提供胶质瘤特征信息。常规MRI特征与胶质瘤IDH状态相关，IDH野生型胶质母细胞瘤更易出现环形强化、坏死以及瘤周水肿等影像学特征。扩散张量成像（diffusion tensor imaging, DTI）不仅可以评估组织内水分子扩散受限情况，还可以评估水分子扩散各向异性程度，从而反映肿瘤组织微观病理特征，采用直方图特征分析方法可以对肿瘤异质性进行定量分析，从而进一步评估肿瘤的生物学特征。然而，如何整合常规MRI视觉特征与DTI定量参数特征共同预测IDH基因状态有待进一步探索。

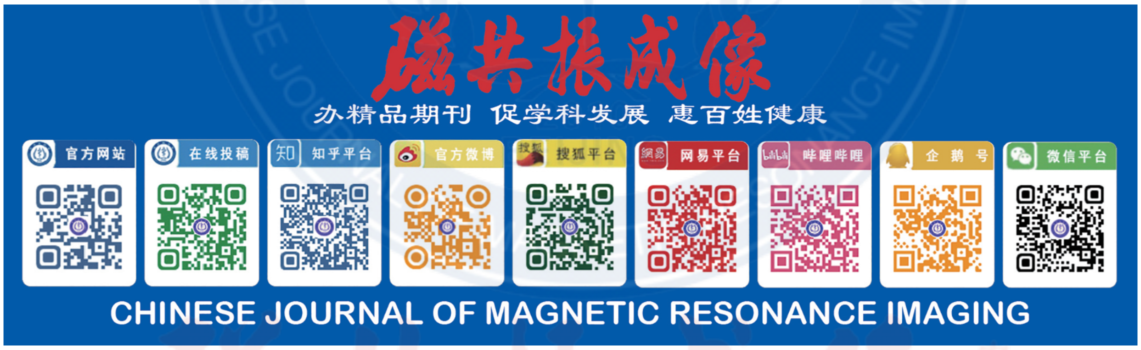
本研究分析了成人弥漫性胶质瘤患者术前常规MRI图像的视觉特征以及DTI定量参数特征，通过递归特征消除和Boruta算法进行特征筛选，首先采用高斯朴素贝叶斯模型分别建立常规MRI特征、常规DTI临床参数特征和DTI直方图特征的初级预测模型，并进一步基于堆叠泛化法集成各初级分类器与支持向量机，建立预测成人弥漫性胶质瘤IDH表型的集成式机器学习模型。结果显示模型具有良好的预测效能，能有效预测成人弥漫性胶质瘤的IDH表型，对于辅助临床制订个性化的治疗方案具有一定意义。详见内文第51页。

影像学预测肝切除术后肝衰竭的研究进展
……………………………………………………………张晓烨，贺业新（216）

子宫内膜异位症恶变为相关卵巢癌的MRI诊断现状及研究进展
……………………………………………………………刘思萌，赵德利（221）

磁共振核奥氏效应在精准医学中的潜力:从基础研究到临床应用
……………………………………………………赵楠楠，许东元，延根（227）

资讯 ……………………………………………………………………………（234）


磁共振成像
办精品期刊 促学科发展 惠百姓健康

CHINESE JOURNAL OF MAGNETIC RESONANCE IMAGING

磁共振成像 CHINESE JOURNAL OF MAGNETIC RESONANCE IMAGING
磁共振成像杂志社
www.chinesemri.com

CHINESE JOURNAL OF MAGNETIC RESONANCE IMAGING

ISSN 1674-8034, CN 11-5902/R, CODEN CCIHBW, Established in 2010 Monthly Vol. 15, No. 11, Nov 20, 2024

Responsible Institution
National Health Commission of the People's Republic of China

Sponsor
Chinese Hospital Association
Beijing Tiantan Hospital of Capital Medical University

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Publishing
Publishing House of Chinese Journal of Magnetic Resonance Imaging

General Distributor
Domestic: Beijing Newspaper and Periodical Distribution Bureau of China Post Group Co., Ltd.
Postal Code: 2-855
Overseas: China International Book Trade Group Co., Ltd., P.O. Box 399, Beijing, China
Code No.: M 8958

Mail Order
Third Floor, Building 4, No. 358,
Yudaihe East Street, Tongzhou District,
Beijing 101100, China

Tel & Fax 8610-67113815
E-mail editor@cjmri.cn
Website www.chinesemri.com
Price: USD 30.00

Contents

ORIGINAL RESEARCH

CLINICAL ARTICLES

1 A study of the seed-point functional connectivity network for the default mode network in patients with mild hepatic encephalopathy
NIU Fang, ZHENG Jiarui, MA Wenfu, MA Wanlong, JIN Yixuan, SUN Meng, DING Xiangchun, WANG Xiaodong

6 The application value of brain functional network topology properties in evaluating tDCS in improving cognitive impairment after ischemic stroke
ZHONG Jiali, JING Xiaoshan, LIANG Ying, PENG Ruchen, XIN Ruiqiang

12 Assessment of Parkinson's disease severity based on T2-weighted magnetic resonance imaging radiomic modeling
WEI Fuli, LIU Dan, LI Xinya, CAO Wanju, PENG Yongming, WANG Fang

17 Structural changes in gray matter of the brain in patients with early-onset schizophrenia: A meta-analysis of voxel-based morphometry
WANG Lu, LIU Ruishan, LIAO Juan, XIA Linfeng, ZHUO Lihua, LI Hongwei

24 Study on brain microstructure in patients with white matter hyperintensities and depressive symptoms based on multimodal MRI
ZHOU Ying, ZHANG Shuo, TAN Zhongjian, LU Yikun, GAO Jinyang, HAN Xiao, MA Lifang, CUI Fangyuan

32 Application of MOLLI T1 mapping quantitative technology in the assessment of pediatric brain development
YANG Xue, JIA Fenglin, MA Xinmao, LI Xuesheng, LI Pei, ZHANG Lu, LIAO Yi, NING Gang, QU Haibo

39 Clinical study of hippocampal microstructure in patients with cognitive impairment of temporal lobe epilepsy by NODDI technique
YANG Wenrui, WANG Xucong, LI Jian, SONG Dengyan, WANG Zhuo, CHEN Bing

44 Research on the white matter microstructural changes in boys with enuresis using diffusion kurtosis imaging
YANG Zijian, MA Jun, DU Xiaoxia, LIN Xindi, CHEN Qun, WANG Mengxing

51 Prediction of adult-type diffuse gliomas IDH phenotype through an ensemble machine learning model with integrating of MRI visual and DTI histogram
HAN Xin, LI Xiaoran, LU Jie

60 The value of synthetic MRI combined with amide proton transfer imaging in projecting IDH1 gene state in gliomas
SUN Meng, MA Wenfu, GE Xin, JIN Yixuan, NIU Fang, DANG Pei, ZHOU Jiaxin, WANG Xiaodong

67 Feasibility of time-dependent diffusion MRI-based indicators for identifying MGMT promoter methylation in glioblastomas
LIANG Xiaojing, ZHANG Yun, FU Yonggui, XIE Yan, WEI Qianqian, CHENG Liuquan, WANG Qingjun

75 Feasibility of compressed sensing cine imaging for analysis of left ventricular strain in cardiac MRI
WANG Ni, WU Chen, ZHOU Yunfeng, TAN Zhongxiao, CHENG Liang, LIU Mengxiao
83 Classification of chemotherapy related cognitive impairment in breast cancer based on resting brain activity and functional connectivity features
FENG Yun, GUO Lili, BAO Yiwen, HUANG Wei, BAI Genji
90 Clinical value of apparent diffusion coefficient in predicting distant metastasis in hepatic alveolar echinococcosis
DANZENG Yeang, BAO Haihua, ZHANG Xueqian, LONG Changyou, XING Yujie, TIAN Pengqi
96 The value of T1 mapping combined with DWI in the early identification of renal interstitial fibrosis
KONG Xinyue, HUA Chenchen, ZHOU Leting, ZHUANG Yi, LIU Xiaobin, CAI Ting, WANG Liang
103 Value of MRI combining with clinical indicators in optimizing the risk stratification of O-RADS MRI Score 4
LI Caihong, LI Yi, LIU Liu, ZHOU Yin, YANG Yaying, MAO Yun
110 Application research of imaging genomics in preoperative prediction of microsatellite stability of endometrial cancer using mp-MRI
ZHAO Jifu, TIAN Yan, MA Mimi, CAO Xinshan

TECHNICAL ARTICLES

117 Value of T2 Flair sequence based on deep learning in improving image quality of white matter hyperintensities
ZHAO Rusheng, XU Lulu, LI Qing, XU Yicheng, ZHANG Jiulou, RONG Fanling
123 Feasibility study of 3D high-resolution compressed sensing contrast-enhanced whole-body MRA imaging technology
LI Jingyang, FU Qing, LIU Xiaoming, WU Jiawei, JIN Teng, YU Qun, LEI Ziqiao, KONG Xiangchuang
130 Comparison of respiratory-triggered and breath-holding sequences on 5.0 T magnetic resonance cholangiopancreatography
HU Chong, WANG Peng, HE Ye, LI Shaopeng, YIN Dawei, ZONG Ran, DENG Kexue
136 Clinical value of reduced field-of-view diffusion-weighted imaging based on composite sensitivity coding in cervical cancer
MEI Wancui, TANG Qian, LI Chengcheng, WANG Sai, CHEN Wen, LIU Weiyin, YANG Bo, XU Lin

REVIEWS

142 Research progress of plasma biomarkers and the association with MRI neuroimaging and cognitive function in patients with Alzheimer's disease
GE Danni, CHEN Futao, CHEN Jiu, ZHANG Xin, ZHANG Bing
148 Advances in behavior and imaging studies of cognitive flexibility changes in neurodegenerative disease
CAO Xinyu, YU Ying, HU Bo, YAN Linfeng, CUI Guangbin
153 Magnetic resonance imaging research progress of effective brain network connectivity in patients with major depressive disorder
SUN Jinnan, YI Wei, HUANG Junlin, REN Rui
160 The progress of brain structural and functional magnetic resonance imaging in patients with obstructive sleep apnea
SUN Liqiang, LI Lin, HU Jing, LIU Liying, CUI Kaige, YANG Jiping, JIA Juan, YU Jiaqi

About the cover

Glioma is the most common primary malignant brain tumor, with an incidence rate of about 5–6 cases per 100, 000 people. Among them, isocitrate dehydrogenase (IDH) wild-type glioblastoma accounts for the highest proportion, with a poor prognosis and a 5-year survival rate of only 7%. The 2021 edition of the World Health Organization Classification of Tumors of the Central Nervous System uses IDH status as an essential molecular diagnostic basis for adult-type diffuse gliomas. IDH genotypes are crucial for the risk stratification of patients' prognosis and the assessment of treatment response. Compared with IDH wildtype gliomas, IDH mutation gliomas are associated with improved overall survival and treatment response. Accurate molecular typing diagnosis can assist in formulating individualized treatment plans in the clinic and prolong patient survival. Currently, the assessment of IDH status in gliomas predominantly depends on DNA sequencing of surgically obtained pathological tissue. However, this approach is invasive. Moreover, there remains a need for precise, non-invasive preoperative evaluation methods.

MRI is an essential part of the preoperative evaluation of glioma patients and includes conventional sequences and functional sequences. The two sequences can provide information on glioma characteristics from different aspects. The characteristics of conventional MRI are related to the IDH status of glioma. IDH wild-type glioblastoma is more likely to have imaging characteristics such as ring enhancement, necrosis, and peritumoral edema. Diffusion tensor imaging (DTI) can not only assess restriction of water molecule diffusion in tissues but also the degree of anisotropy of water molecule diffusion, thereby reflecting the microscopic pathological characteristics of tumor tissue. Histogram feature analysis can be used to quantitatively analyze tumor heterogeneity quantitatively, thereby further assessing the biological characteristics of the tumor. However, how to integrate the visual features of conventional MRI with the quantitative parameters of DTI to jointly predict the IDH gene status remains to be further explored.

This study analyzed the visual characteristics of conventional preoperative MRI images and the quantitative DTI parameter characteristics of adult-type diffuse glioma patients. We performed feature selection using recursive feature elimination and the Boruta algorithm. We first established a primary prediction model for the conventional MRI features, conventional DTI clinical parameter features, and DTI histogram features using a Gaussian Naive Bayes model. We then ensembled each primary classifier with a support vector machine using the stacking method to create an ensemble machine learning model for predicting the IDH phenotype of adult-type diffuse gliomas. The results demonstrated the model's predictive solid efficacy and ability to accurately predict the IDH phenotype of adult-type diffuse gliomas, which is significant in assisting the clinical development of personalized treatment plans. Please see text page 51.

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169 MRI progress of benign childhood epilepsy with centrotemporal spikes
CHEN Yiwen, ZHANG Zhiqiang
174 Progress of functional magnetic resonance imaging technology in explaining the mechanism of acupuncture acupuncture treatment of ischemic stroke
ZHONG Sitong, CAO Xinyuan, LIANG Ji, SUN Zhongren, YIN Hongna
180 Current status and challenges of MRI technology in the study of the glymphatic system in the human brain
DU Xiaolan, DUAN Xirui, LI Guochen, TAN Na, ZHOU Xinyan, LIAO Chengde
185 Advances in structural and functional imaging in asymptomatic carotid artery stenosis
WANG Junjun, SONG Linfeng, TIAN Binlin, JIANG Lin
190 Application of deep learning-based magnetic resonance imaging in the diagnosis and treatment of coronary artery disease
WU Qian, GUO Hui
198 Research progress of T1 and T2 mapping techniques in acute myocardial infarction
NI Luying, ZHANG Qian, CAO He, JIANG Xingyue
203 Research progress of magnetic resonance imaging to predict the efficacy of neoadjuvant therapy for HER-2 positive breast cancer
HE Zhiyuan, WANG Weiwei, SUN Zhanguo
209 Clinical application and progress of synthetic MRI in breast cancer
HUANG Yue, LI Feng
216 Research process in imaging prediction of post-hepatectomy liver failure
ZHANG Xiaoye, HE Yexin
221 Current status and reseach progress of MRI diagnosis of endometriosis malignancy related to ovarian cancer
LIU Simeng, ZHAO Deli
227 Potential of the nuclear overhauser effect in precision medicine: From basic research to clinical applications
ZHAO Nannan, XU Dongyuan, YAN Gen

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