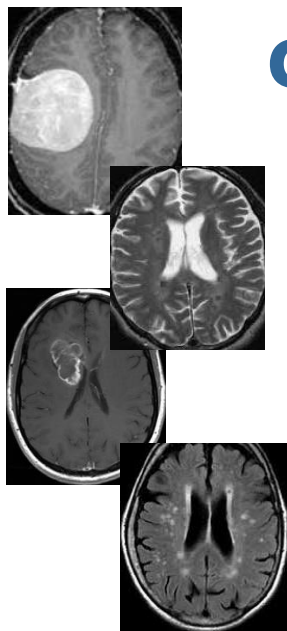


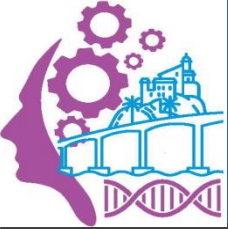


Utilização de características radiômicas para classificar gliomas de baixo grau com relação ao status da codeleção cromossômica 1p/19q



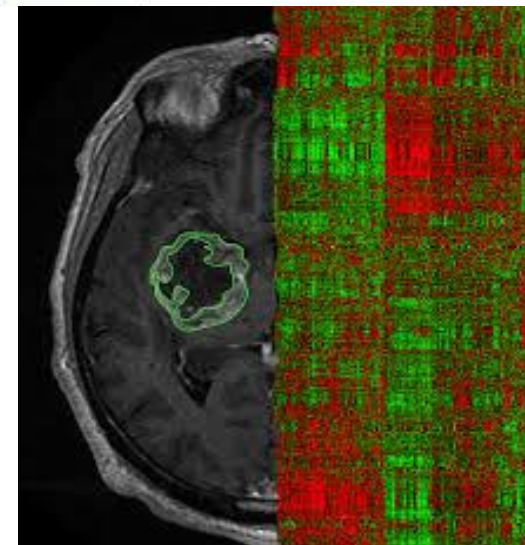
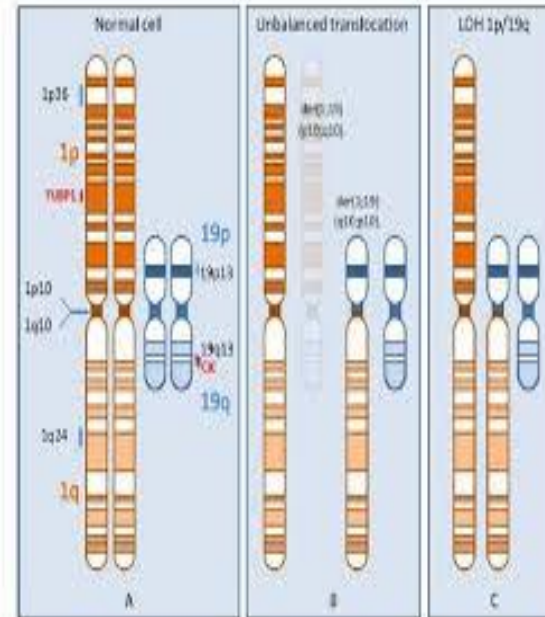
Tony Alexandre Medeiros da Silva
Guilherme de Souza e Cassia
João Luiz Azevedo de Carvalho

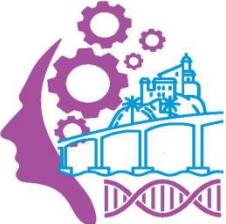




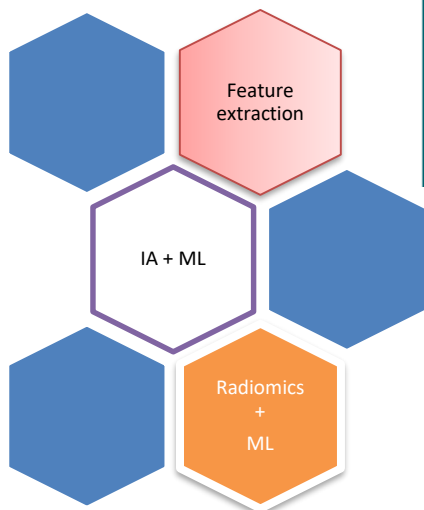
Contextualização

- ✓ Tumores cerebral
- ✓ Codeleção 1p/19q
- ✓ Radiômica





Trabalhos correlatos



Radiology

Radiomics: Images Are More than Pictures, They Are Data¹

Robert J. Gillies, PhD
Paul E. Kinahan, PhD
Hedvig Hricak, MD, PhD, Dr(hc)

In the past decade, the field of medical image analysis has grown exponentially, with an increased number of pattern recognition tools and an increase in data set sizes. These

ORIGINAL RESEARCH ■ SPECIAL REPORT

European Radiology
https://doi.org/10.1007/s00330-020-06737-5

NEURO



Machine learning and radiomic phenotyping of lower grade gliomas: improving survival prediction

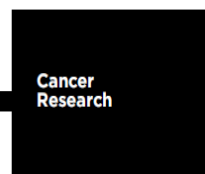
Yoon Seong Choi^{1,2} · Sung Soo Ahn¹ · Jong Hee Chang³ · Seok-Gu Kang³ · Eui Hyun Kim³ · Se Hoon Kim⁴ · Rajan Jain^{5,6} · Seung-Koo Lee¹

Received: 17 October 2019 / Revised: 4 February 2020 / Accepted: 10 February 2020
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Focus on Computer Resources

Computational Radiomics System to Decode the Radiographic Phenotype

Joost J.M. van Griethuysen^{1,2,3}, Andriy Fedorov⁴, Chintan Parmar¹, Ahmed Hosny¹, Nicole Aucoin⁴, Vivek Narayan¹, Regina G.H. Beets-Tan^{2,3}, Jean-Christophe Fillion-Robin⁵, Steve Pieper⁶, and Hugo J.W.L. Aerts^{1,4}



J Digit Imaging (2017) 30:469–476
DOI 10.1007/s10278-017-9984-3



Predicting Deletion of Chromosomal Arms 1p/19q in Low-Grade Gliomas from MR Images Using Machine Intelligence

Zeynettin Akkus¹ · Issa Ali¹ · Jiří Sedlář¹ · Jay P. Agrawal¹ · Ian F. Parney³ · Caterina Giannini² · Bradley J. Erickson¹

Automated MRI based pipeline for glioma segmentation and prediction of grade, IDH mutation and 1p19q co-deletion

Milan Decuyper and Stijn Bonte and Roel Van Hoken
Medical Image and Signal Processing (MEDISP), Ghent University, Ghent, Belgium

Karel Doblaere
Department of Radiology, Ghent University Hospital, Ghent, Belgium

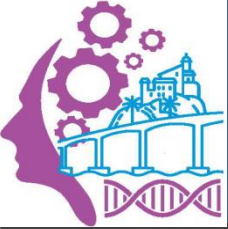
Abstract

In the WHO glioma classification guidelines grade, IDH mutation and 1p19q co-deletion play a central role as they are important markers for prognosis and optimal therapy planning. Therefore, we propose a fully automatic, MRI based, 3D pipeline for glioma segmentation and classification. The designed segmentation network was a 3D U-Net achieving an average whole tumor dice score of 90%. After segmentation, the 3D tumor ROI is extracted and fed into the multi-task classification network. The network was trained and evaluated on a large heterogeneous dataset of 628 patients, collected from The Cancer Imaging Archive and BraTS 2019 databases. Additionally, the network was validated on an independent dataset of 110 patients retrospectively acquired at the Ghent University Hospital (GUH). Classification AUC scores are 0.93, 0.94 and 0.82 on the T1A test data and 0.94, 0.86 and 0.87 on the GUH data for grade, IDH and 1p19q status respectively. **Keywords:** Glioma, IDH mutation, 1p19q co-deletion, deep learning, MRI

1. Introduction

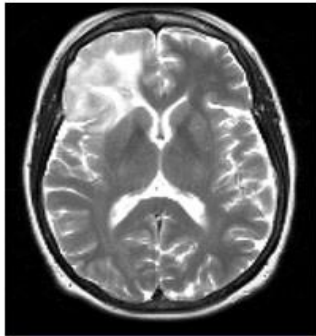
In the most recent WHO glioma classification guidelines three (genetic) markers, important for prognosis and optimal therapy planning, play a central role: WHO grade (glioblastoma, GBM versus lower-grade glioma, LGG), IDH mutation and 1p19q co-deletion (Louis et al., 2016; Yan et al., 2009; Walker et al., 2017). Biopsies to determine molecular information involve risks, are subject to sampling error and related to reduced OS compared to a wait-and-see approach (Jackson et al., 2001; Wijtenburg et al., 2017). Therefore, accurate non-invasive assessment of genetic mutations is desired. Most of the existing studies are not fully automatic, 2D, depend on expert opinion and are trained and evaluated on a small dataset (Yang et al., 2018; Choi et al., 2019; Akkus et al., 2017). In this study we propose a non-invasive fully automatic 3D pipeline to segment glioma and predict clinically relevant markers according to the most recent WHO guidelines. We collected a large dataset from multiple public databases and an independent dataset from our University Hospital (UH) to test generalization.

arXiv:2005.11965v1 [eess.IV] 25 May 2020



Pré-processamento

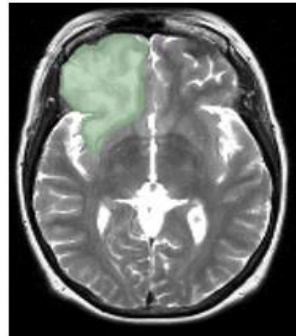
- ✓ Banco de imagens
- ✓ Região de interesse
- ✓ Extração de características



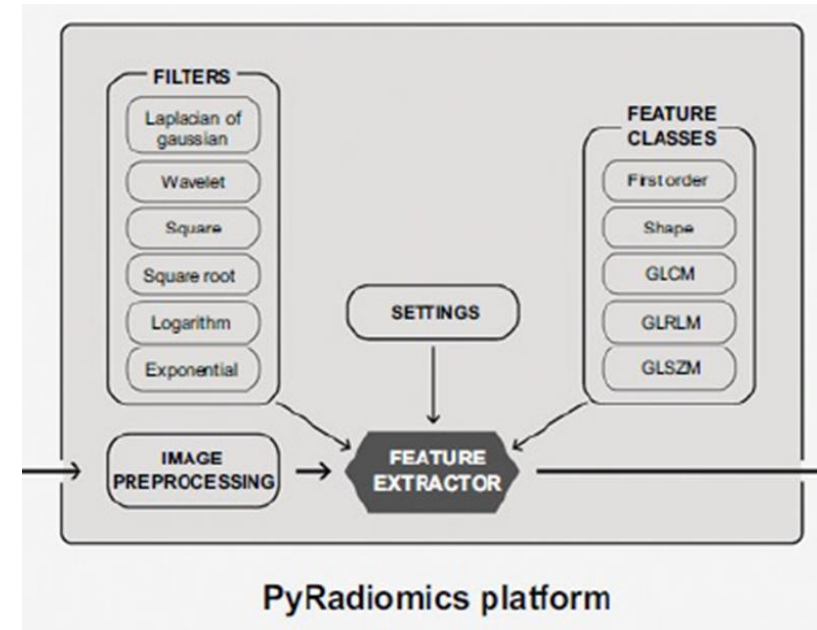
(a)

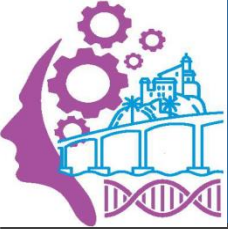


(b)



(c)



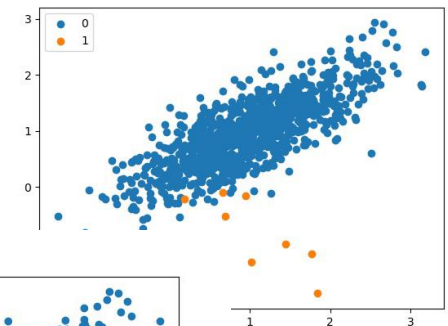
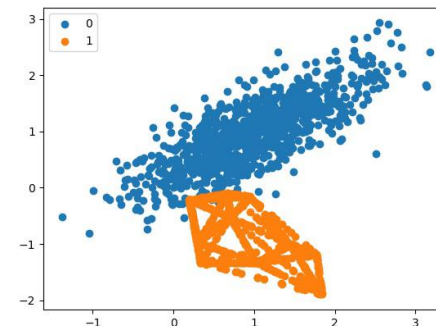
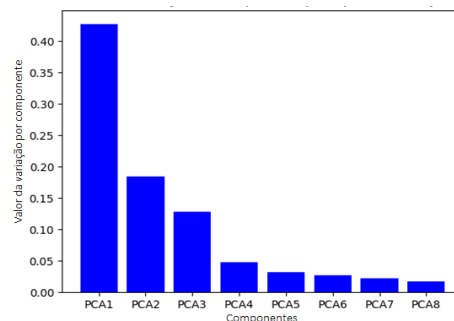


Análise das características

✓ Padronização

✓ Redimensionamento

✓ Aumento sintético dos registros

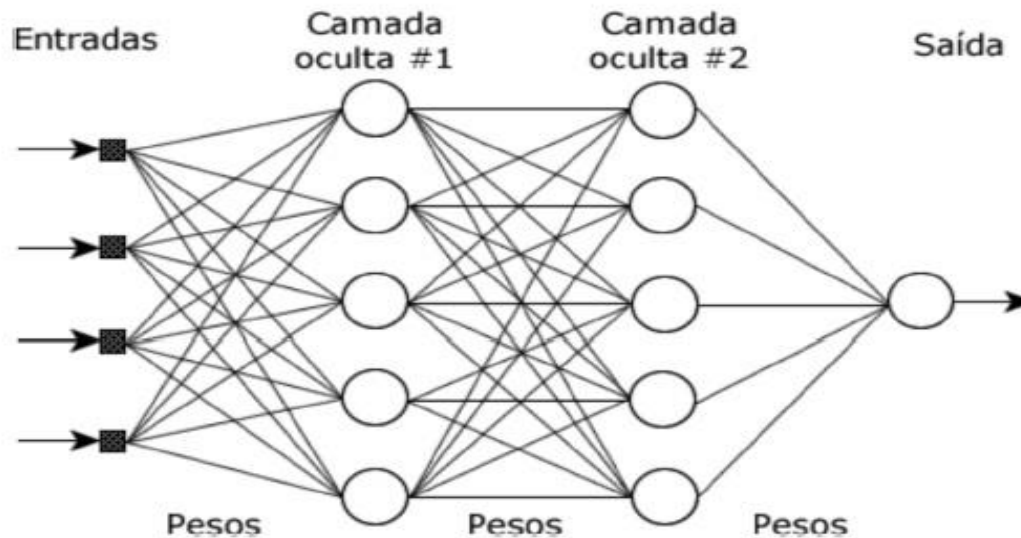


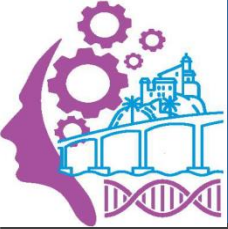


Implementação

✓ Classificação binária

✓ Rede neural perceptron multicamada (MLP)



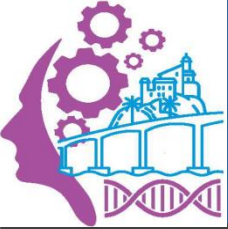


Configurações da rede MLP

MLP

- biblioteca Keras
- 1 camada entrada (8 neurônios)
- 2 camadas ocultas (5 neurônios)
- 1 camada saída (1 neurônio)
- 100 épocas
- 75% treinamento e 25% testes

Função	Descrição
ReLU	Função de ativação (camadas ocultas)
Sigmoid	Função de ativação (camada de saída)
Random_uniform	Inicialização de pesos
Adam	Ajuste dos pesos
Binary_crossentropy	Tratamento de cálculo do erro
Binary_accuracy	Avaliação da acurácia
Cross_val_score	Treinamento dos dados em subconjuntos
Epochs	Quantidade de treinamentos executados

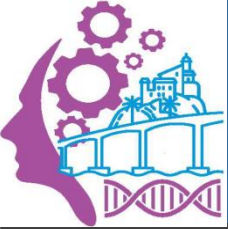


Resultados

✓ Métricas utilizadas: precisão, sensibilidade e especificidade.

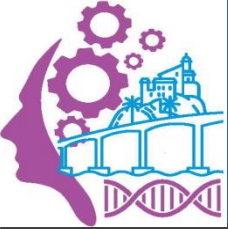
Algoritmo	Precisão	Especificidade	Sensibilidade
MLP	85,0	73,5	88,0
SVM	77,5	70,0	85,0
RF	75,0	75,0	75,0

casos de teste = 40	codeletado (real)	não-codeletado (real)
codeletado (predito)	22	4
não-codeletado (predito)	3	11



Conclusões

- ✓ Pyradiomics e características extraídas: adequadas para classificação da codeleção cromossômica 1p/19q
- ✓ Padronização, redimensionamento, aumento sintético: ganho de desempenho significativo nos três algoritmos
- ✓ MLP: percentuais de probabilidade de acerto satisfatórios na classificação da codeleção cromossômica 1p/19q
 - ✓ Precisão e sensibilidade maiores que RF e SVM
- ✓ Identificação de biomarcadores de imagem para genótipos tumorais da codeleção cromossômica 1p/19q:
 - ✓ Evolução mais lenta dos tumores cerebrais
 - ✓ Reduz necessidade de realização de biópsias cirúrgicas
 - ✓ Maior sobrevida



Agradecimentos

- ✓ Agradecemos a comissão organizadora do CBEB 2020.
- ✓ Agradecemos a toda a comissão avaliadora pelas sugestões, correções e críticas.

Contato 1º autor

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