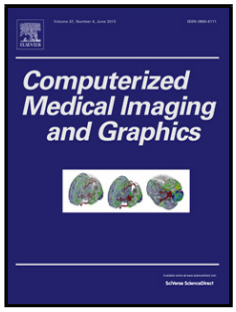
Accepted Manuscript



Title: Efficient Deep Learning Model for Mitosis Detection using Breast Histopathology Images

Author: Monjoy Saha Chandan Chakraborty Daniel Racoceanu

PII: S0895-6111(17)30122-2
DOI: https://doi.org/doi:10.1016/j.compmedimag.2017.12.001
Reference: CMIG 1534

To appear in: *Computerized Medical Imaging and Graphics*

Received date: 3-3-2017
Revised date: 28-6-2017
Accepted date: 7-12-2017

Please cite this article as: Monjoy Saha, Chandan Chakraborty, Daniel Racoceanu, Efficient Deep Learning Model for Mitosis Detection using Breast Histopathology Images, *<![CDATA[Computerized Medical Imaging and Graphics]]>* (2017), https://doi.org/10.1016/j.compmedimag.2017.12.001

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

ACCEPTED MANUSCRIPT

Efficient Deep Learning Model for Mitosis Detection using Breast Histopathology Images

Monjoy Saha[1], Chandan Chakraborty [+,1], Daniel Racoceanu[2,*]

Abstract

Mitosis detection is one of the critical factors of cancer prognosis, carrying significant diagnostic information required for breast cancer grading. It provides vital clues to estimate the aggressiveness and the proliferation rate of the tumour. The manual mitosis quantification from whole slide images is a very labor-intensive and challenging task. The aim of this study is to propose a supervised model to detect mitosis signature from breast histopathology WSI images. The model has been designed using deep learning architecture with handcrafted features. We used handcrafted features issued from previous medical challenges MITOS @ ICPR 2012, AMIDA-13 and projects (MICO ANR TecSan) expertise. The deep learning architecture mainly consists of five convolution layers, four max-pooling layers, four rectified linear units (ReLU), and two fully connected layers. ReLU has been used after each convolution layer as an activation function. Dropout layer has been included after first fully connected layer to avoid overfitting. Handcrafted features mainly consist of morphological, textural and intensity features. The proposed architecture has shown to have an improved 92% precision, 88% recall and 90% F-score. Prospectively, the proposed model will be very beneficial in routine exam, providing pathologists with efficient and - as we will prove - effective second opinion for breast cancer grading from whole slide images. Last but not the least, this model could lead junior and senior pathologists, as medical researchers, to a superior understanding and evaluation of breast cancer stage and genesis.

Keywords: Breast cancer, mitosis, deep neural network, handcrafted features, convolution, hematoxylin and eosin.

*Corresponding author
Email address: dracoceanu@pucp.edu.pe (Daniel Racoceanu)
[1]School of Medical Science and Technology, Indian Institute of Technology, Kharagpur, West Bengal, India. [+]Joint Corresponding author.
[2]University Pierre and Marie Curie (UPMC - Paris 6), Paris France and with the Pontifical Catholic University from Peru (PUCP).

Accepted Manuscript

دریافت فوری ← متن کامل مقاله

ISIArticles
مرجع مقالات تخصصی ایران

✓ امکان دانلود نسخه تمام متن مقالات انگلیسی
✓ امکان دانلود نسخه ترجمه شده مقالات
✓ پذیرش سفارش ترجمه تخصصی
✓ امکان جستجو در آرشیو جامعی از صدها موضوع و هزاران مقاله
✓ امکان دانلود رایگان ۲ صفحه اول هر مقاله
✓ امکان پرداخت اینترنتی با کلیه کارت های عضو شتاب
✓ دانلود فوری مقاله پس از پرداخت آنلاین
✓ پشتیبانی کامل خرید با بهره مندی از سیستم هوشمند رهگیری سفارشات