DEEPBleND - A CNN for subtype classification of nuclear dysmorphy

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Abstract

A vast array of pathologies is typified by the presence of nuclei with an abnormal morphology. Dysmorphic nuclear phenotypes feature dramatic size changes or folding, but also entail much subtler deviations such as nuclear protrusions called blebs. Due to their heterogeneous size, shape and intensity, dysmorphic nuclei are often not accurately detected in standard image analysis routines. To enable accurate detection of dysmorphic we have developed an automated segmentation algorithm called BleND[1–3], which is based on a two-pass thresholding combined with a dynamic programming algorithm to find the exact nuclear border. Shallow machine learning algorithms (i.e. random forest) were applied to the resulting morphological feature sets to classify normal and aberrant nuclei. To bypass the initial segmentation and further improve the accuracy, we have now trained a convolutional neural network, DEEPBleND to recognize distinct types of dysmorphic nuclei in various cell lines, including nuclei with subtle blebs, bean-shape or multiple lobes. We evaluated its performance on a set of laminopathy patient cells and glioblastoma cell lines and found that it was able to classify patient or cell types with high accuracy that outperformed the classical shallow scheme. Thus, we conclude that DEEPBleND enables a more accurate detection of distinct nuclear phenotypes and may be used to stratify patient cells according to their type of nuclear dysmorphy.

References

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