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Patent Search

Invention Title	ANALYZING HUMAN PROTEIN ATLAS FOR SINGLE CELL CLASSIFICATION USING RCNN
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Abstract:

Cells, as the basic units of the human body's structure and function, have a significant impact on the body's ability to function normally. Cell inspection is an importar understanding human function in medical diagnosis. Cell examination would substantially improve the efficiency of pathological research and patient therapy if it we incorporated into medical diagnosis. Cell segmentation and identification technologies can also be utilized to evaluate and research cellular components quantitative molecular level. The dataset contains a total of 19 different labels (18 labels for. specific locations, and label 18 for negative and unspecific signal). The dataset is colle single imaging modality in a very standardized manner (confocal microscopy). The dataset, on the other hand, has 17 different cell types with vastly diverse morpholc which have an impact on the protein patterns of the various organelles. Target detection utilizing deep learning is used to detect cells in this study. The Region-based Convolutional Neural Network (R-CNN) algorithm is used to create a recognition network model, and the anchor box is tailored to fit the data set's properties. The ou cell detection are influenced by different design strategies. Detecting the cell picture using an object detection method based on our unique R-CNN framework can as cell detection speed and accuracy. When it comes to identifying flowing cells, the method has a lot of advantages.

Complete Specification

Title of the invention: -
Analyzing Human Protein Atlas for Single Cell Classification Using RCNN
Field of the invention: -
[0001] The subject of this disclosure is Artificial Intelligence (AI) and Deep Learning algorithms. The intervention is more specifically focused on a technique and syst evaluating the human protein atlas for single cell categorization using RCNN deep learning architecture.
Prior art to the invention: -
The Variant Classification method described in the patent document number "KR20200011444A" with the title "Deep Convolutional Neural Networks for Variant Classification" is a technique entails employing a backpropagation-based gradient update technique to gradually match the output of a convolutional neural networ classifier with the associated actual data marker when training a convolutional neural network-based classifier on training data. It's all about. Each group of parame the convolutional neural network-based classifier is parameterized by numerous convolution filters of the residual block, the convolution window size of the residu and the convolution size of the residual block. The size of the convolution window varies between groups of residual blocks, as does the convolution size. Positive a pathogenic training examples of translated sequence pairs created from positive and pathogenic variations are included in the training data.
[Non-patent 1] Ouyang, W., Winsnes, C.F., Hjelmare, M. et al. Analysis of the Human Protein Atlas Image Classification competition. Nat Methods 16, 1254-1261 (201 https://doi.org/10.1038/s41592-019-0658-6
[Non-patent 2] Fularczyk, N., Di Re, J., Stertz, I., et al. A Learning Based Framework for Disease Prediction from Images of Human-Derived Pluripotent Stem Cells of

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