

神經可塑性的過程可用於具有治療、恢復和研究目的的神經網絡的認知重建。
 本報告試圖分析新創建的“三模態平台”（這是一個獨立的興趣）的可能性及其在任何複雜程度的人腦研究中的工作結果。
 在我們的案例中，我們談論的是急性腦血管意外（中風）和廣泛的情感障礙。
 該報告提供了神經網絡作為軟件元素的作用的語義比較，在人工智能詞彙方面，以及在創造性活動期間經歷自然和引入交互重建的大腦的真實可視化“區域”。
 神經網絡的畸變是精神和神經活動病理學的基礎，在抑鬱症和腦梗塞（中風）症狀的例子中得到了證明。

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Systems Theory, Algebraic Biology, Artificial Intelligence: Mathematical foundations and applications

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It remains challenge in bioinformatics to uncover underlying relationships between biological entities such as protein-protein interaction (PPI) or diseases similarity prediction tasks. Traditional methods use handcraft features to calculate the distance or similarity between different entities, which can be largely biased and may failed to capture the non-linear dependency.

However, the emergence of deep learning frameworks has allowed for the development of sophisticated models to predict complex biological relationships. We develop DeepTrio, a sequence-based model using mask multiple parallel convolutional neural network, for the task of PPI prediction. DeepTrio is significantly better than other state-of-the-art (SOTA) methods in terms of various metrics and can be extended to provide additional insights into the contribution of each input neuron to the prediction results. On the issue of disease similarity prediction, we present CoGO, a contrastive learning framework based on gene network and ontology structure, which incorporates the gene interaction network and gene ontology (GO) domain knowledge using graph deep learning models. We propose an inter-view graph neural network to encode the network structure information and a cross-view contrastive loss to mix up the representations learned from the gene network and GO graph. CoGO outperforms the SOTA on different evaluation metrics and extracts credible similar diseases which are significantly comparable with other disease similarity studies.

The above deep learning frameworks demonstrate the potential of deep learning in accurately predicting complex biological processes and provide insight into the development of future models. The use of deep learning frameworks has the potential to greatly advance our understanding of protein-protein interactions and disease relationships.

References

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系統論、代數生物學、人工智能：數學基礎與應用

陳明

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揭示生物實體之間的潛在關係（例如蛋白質-蛋白質相互作用（PPI）或疾病相似性預測任務）在生物信息學中仍然是一項挑戰。傳統方法使用手工特徵來計算不同實體之間的距離或相似度，這可能存在很大偏差，並且可能無法捕獲非線性依賴性。

然而，深度學習框架的出現允許開發複雜的模型來預測複雜的生物關係。我們開發了DeepTrio，一種使用掩碼多並行卷積神經網絡的基於序列的模型，用於 PPI 預測任務。DeepTrio 在各種指標方面明顯優於其他最先進（SOTA）方法，並且可以擴展以提供有關每個輸入神經元對預測結果的貢獻的更多見解。在疾病相似性預測問題上，我們提出了CoGO，一種基於基因網絡和本體結構的對比學習框架，它使用圖深度學習模型結合了基因相互作用網絡和基因本體（GO）領域知識。我們提出了一個視圖間圖神經網絡來編碼網絡結構信息和一個交叉視圖對比損失來混合從基因網絡和 GO 圖學習的表示。CoGO 在不同的評估指標上優於SOTA，並提取可信的相似疾病，這些疾病與其他疾病相似性研究具有顯著可比性。

上述深度學習框架展示了深度學習在準確預測複雜生物過程方面的潛力，並為未來模型的發展提供了洞察力。深度學習框架的使用有可能極大地促進我們對蛋白質-蛋白質相互作用和疾病關係的理解。

文學

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PneumoScreener: AI based tool for automatic detection of anomalies from Chest XR and CT images

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In many hospital systems, Chest imaging is required for all patients when being admitted to the hospital. During pandemic Chest imaging was essential diagnostics tool of COVID-19 disease and in the decision making on hospitalisation and the treatment options, at various stages of the disease. Fast and accurate diagnostics of the COVID-19 is possible with chest X-ray (CXR) and computed tomography (CT) scan images. Our project, PneumoScreener, used AI, in particular deep learning approaches, to build an automated system that can be used in processing CXR and CT scans for early, or advanced signs of the COVID-19 pneumonia, or any other related pathology. We selected ResNet50 [1], EfficientNet B0 [2], EfficientNetv2 B0 [2], VGG16 [2] and our custom