

Predicting L-PART1 exon using deep learning

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Identifying and annotating Immunoglobulins (IG), T cell receptors (TR) genes of jawed vertebrate species effectively and precisely is still an arduous task, essentially due to the continuous avalanche of large genomic sequences produced by NGS technologies. In this study, to predict the L-PART1 exon (the first exon of IG and TR variable V-GENE), different Deep Neural Network-based models (DNN, CNN, RNN, CNN-RNN) were trained in a supervised manner, which automatically learn features from annotated IG and TR genes. Those models will then be used to predict the L-PART1 exon within newly given sequences. Correct detection of this component would dramatically increase the chances to find the subsequent components constituting the V-GENE of the IG and TR. Sequence data were extracted from IMGT/LIGM-DB, the IMGT® (Lefranc *et al.*, 2015) nucleotides database: around 2756 L-PART1 of 354 species tagged as positive samples, negative samples were generated with different noise strategies. The final training datasets were formed by shuffling a portion of positive and negative samples. The majority of the trained models showed promising results. However, further studies are needed to investigate the possibility of predicting and locating all the components within the V-GENE of IG and TR.

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