**Towards Interpretable MultiTask Learning for Splice Site and Translation Initiation Site Prediction** (Espoir Kabanga, Arnout Van Messem, Wesley De Neve)

In the rapidly growing field of computational biology, researchers are continuously seeking innovative methods to address bioinformatics challenges. One such technique that is gaining attention is MultiTask Learning (MTL), which has demonstrated potential in resolving various problems. In this study, we investigate the effectiveness of MTL in handling two bioinformatics tasks: splice site prediction and translation initiation site prediction. For this purpose, we used the SpliceRover model as the foundation for our MTL approach. The SpliceRover model has previously proven successful in predicting splice sites. In our research, we expanded its application to the prediction of translation initiation sites. We applied two different pre-processing methods— one-hot encoding and 3-mer embeddings— and compared their results to determine the optimal approach. To evaluate the effectiveness of our MTL model, we focused on two metrics: F1-score and Matthews Correlation Coefficient (MCC). Our findings demonstrate that the MTL model outperforms the single-task model in both F1-score and MCC for translation initiation site prediction and shows slight improvement in acceptor splice site prediction. To further validate our quantitative results, we used two visualization techniques— Integrated Gradients and DeepLIFT— to analyze the effectiveness of our model. The outcomes indicate that our model effectively learned the relevant features for both tasks when compared to single benchmark models. In conclusion, our investigation offers valuable insights into the applicability of MTL in the field of computational biology. The results obtained suggest that MTL remains a promising technique for reducing label costs in bioinformatics analyses. As the field of computational biology continues to evolve, the ongoing exploration and implementation of MTL may pave the way for further advancements and discoveries in addressing future interesting bioinformatics challenges.