

Attention mechanism has demonstrated its power in Natural Language Processing, Statistical Learning, Speech and Computer Vision (Chaudhari *et al.*, 2019). It makes model tends to focus selectively on parts of the input which is help in performing the task effectively. Previous observation have shown that Cas9 preferentially binds sgRNAs containing purines but not pyrimidines (Wang *et al.*, 2014) and multiple thymine in the spacer impairing sgRNA activity (Wu *et al.*, 2014), that is to say some specific nucleotide and base position need more attention compared to others. The above is the premise of introducing attention mechanism. Strictly speaking, we are not the first to bring attention mechanisms into this field. The most similar approach to ours is the work based on transformer by Liu *et al.*. They use transformer, a components based on attention mechanism, instead of RNN to improve the ability of temporal feature extraction, hence, enhance the performance of their model (Liu *et al.*, 2019b; Vaswani *et al.*, 2017). In our work, the interpretability benefit from attention mechanism is more focused.

- Present a novel deep-learning-based model, which can extract potential feature representation of sgRNA sequence in both spatial and temporal domain parallelly. It doesn't belong to any of the above categories of existing approaches.
- Introduce attention mechanism into our model. As a result, It does not need post hoc explanations techniques based on input perturbation to explain itself. It is intrinsic interpretable at the nucleotide level in the temporal and spatial domains. The model we built could be approximated with a linear regression model, thus, it is transformed from a black box to an intrinsically interpretable model with the performance of deep learning based model. This seems to have something in common with the idea of two-layer additive models, built by Chen. He uses linear modeling with positive coefficients for feature, but inserts (interpretable) nonlinearities in several places to make the model more flexible and accurate (Chen, 2020).
- Through ablation analysis and testing a series of possible network structure, we find there are multiple components and strategy can improve the performance of our model and constructed AttCRISPR, which could outperform the current state-of-the-art tool on deepHF dataset

- ## 2 Approach

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5 Conclusion

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