TCR specificity prediction technology has broad prospects in many fields such as cancer immunotherapy and autoimmune disease treatment. Compared with experimental methods, the computational methods that uses algorithms to achieve TCR-specific prediction has various advantages like high efficiency, economy, and repeatability. Inspired by previous work, we established a TCR generative specificity detection framework to efficiently screen out TCRs and corresponding antigens through TCR classifier and specificity classifier based on random forest. A series of comparisons and analyzes indicate that our model generally outperforms ordinary algorithms.

However, our model still has shortcomings and faces some challenges. First, scarcity and quality of data and high redundancy of the available data still exist (Montemurro et al., 2022b). On the one hand, relevant data collection work is required to obtain richer and high-quality available data. On the other hand, it is feasible to enhance the dataset using machine learning methods (GAN) or using data from multiple databases. Furthermore, the search time may be too long for some TCRs. If we have more time, we will optimize the algorithm for selecting target antigens in our model.

**Reference**

Montemurro, A., Jessen, L. E., & Nielsen, M. (2022b). NetTCR-2.1: Lessons and guidance on how to develop models for TCR specificity predictions. Frontiers in Immunology, 13. <https://doi.org/10.3389/fimmu.2022.1055151>