**Predicting CAR-T Cell Therapy Response in Multiple Myeloma Through Single-Cell AI Modeling**

Multiple myeloma (MM) is the second most common blood cancer in humans and is defined by the uncontrolled growth of plasma cells within the bone marrow. Although the exact cause of MM remains unclear, the bone marrow microenvironment has been recognized as an important contributor to disease progression. Within this niche, malignant plasma cells interact with surrounding cells in ways that promote immune evasion and support tumor survival. These dynamic interactions result in notable heterogeneity among MM patients: the disease can vary widely from one individual to another in terms of cellular composition, disease progression, and treatment response. Recent advances in single-cell RNA sequencing enable high-resolution profiling of individual cells within the bone marrow, allowing simultaneous analysis of both tumor cells and the immune populations that influence disease progression and therapeutic outcome. In this study, multiple single-cell RNA-sequencing datasets from patients across different stages of MM were analyzed using Python in order to build a transformer-based artificial intelligence model, scGPT, that can characterize cellular heterogeneity across disease stages. The trained model is currently undergoing fine-tuning, where it will be applied to samples from patients who received CAR-T cell therapy to evaluate whether learned cellular patterns could distinguish treatment responders from non-responders. If successful, this model could serve as an important clinical tool that analyzes new patients' bone marrow and predicts how likely they are to respond to CAR-T cell therapy.