Francis X. McCormack Career Development Award - $180,000 for Three Years

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An Information Retrieval System for Multiomics Data Integration and LAM Biomarker Discovery

Lymphangioleiomyomatosis (LAM) is a rare lung disease occurring almost exclusively in women, causing tissue remodeling and progressive respiratory failure. Biomarkers are useful in LAM patient care and clinical studies: diagnostic markers can assist in non-invasive LAM diagnosis; prognostic markers enable prediction of an individual's likely course of the disease; and predictive biomarkers provide information on the likelihood of responses to specific treatments. Pivotal clinical trials and research demonstrated that serum VEGF-D is a clinically useful diagnostic, prognostic, and predictive biomarker of LAM. However, 30~40% of LAM patients have normal serum VEGF-D, highlighting an urgent unmet need for novel biomarkers, either used alone or in combination with VEGF-D, to improve LAM patient care. To address this, we collected a wealth of LAM multiomics and clinical data, which provides large-scale complementary information on RNA expression and chromatin states in individual lung cells in LAM and protein concentrations in blood samples of LAM. We reasoned that the integration of these data will enable robust and novel LAM biomarker discovery at single cell resolution. We will develop GLAMOR, a novel computational system that employs theories of search engines (e.g., Google), to map the complex data and rank molecular candidates for LAM biomarkers. We anticipate that GLAMOR will discover new biomarkers that can contribute to diagnostic, predictive and prognostic tools for LAM.

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