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FlowSP: AI-Powered Prediction of 3D Protein Distributions in Tissue

Stanford researchers have developed FlowSP, a generative AI model that predicts high-resolution 3D spatial maps of protein markers in tissue from limited imaging data. This technology enables researchers and clinicians to generate comprehensive protein information, including predictions of how tissues respond to genetic or therapeutic changes, without the time and cost of extensive experimental imaging.

Current prediction methods only work for 2D images and typically at low spatial resolution and limited number of protein markers. Researchers currently lack the tools to efficiently explore how proteins would change under different genetic or therapeutic conditions, forcing them to conduct costly trial-and-error experiments. Existing AI approaches using older generative models such as GANs cannot scale to capture the complexity of 3D protein distributions or predict how individual proteins respond to specific perturbations.

FlowSP uses a novel flow-based generative model, a type of AI architecture more powerful than previous approaches, trained on massive amounts of tissue imaging data to learn biologically meaningful patterns of how proteins co-express and distribute in 3D space. The model can accept multiple types of input conditions (tissue type, species, genetic knockouts, or therapeutic treatments as text descriptions, as well as partial imaging data), and then generates complete, high-resolution 3D protein maps at subcellular resolution. In a single model, it can predict over 100 different protein markers across multiple tissue types and species, and uniquely enables researchers to simulate "in silico perturbations" and forecast how protein distributions would change under genetic or drug interventions to prioritize targets for wet lab testing. The approach extends to other spatial omics modalities, including spatial transcriptomics.

Stage of Development: Prototype

Applications

- Drug discovery and screening through in silico simulation of drug effects on protein expression
- Genetic research via prediction of protein changes from gene knockouts or engineering
- Therapeutic development and optimization (e.g., predicting T cell therapy or vaccination responses)
- Predicts 3D drug distribution with and without perturbations in human solid tumors
- Scalable 3D spatial proteomics of intact, centimeter-scale tissue using fast, low-cost dye imaging
- Expands the marker panels and spatial dimensions, and improves spatial resolution of existing spatial omics instruments and datasets
- Clinical diagnostics, patient stratification, and precision medicine
- Biomarker discovery and validation for disease understanding

Advantages

- **First large-scale generative AI framework capable of *in silico* virtual tissue perturbation prediction**, enabling virtual experimentation to prioritize physical validation
- Handles both 2D and 3D tissue imaging and predicts 100+ protein markers with a single unified model
- Achieves subcellular, isotropic resolution and can predict detailed protein distribution pattern previously impossible with existing methods
- Reduces experimental costs and timelines by reducing and prioritizing expensive multiplexed imaging experiments
- More accurate and scalable than existing generative models (GANs and regression approaches) for complex spatial proteomics data

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