GeneFlow: mapping gene expression and imaging phenotypes

GeneFlow technology generates high-accuracy, high-resolution virtual tissue images from gene expression data, enabling new applications in minimally invasive diagnostics and virtual tissue reconstruction.

Researchers at Purdue University have developed a technology that enables the generation of high-resolution histopathology images directly from single-cell and multi-cell gene expression data. This technology addresses the inverse problem of mapping gene expression onto tissue morphology. Current approaches in the field typically focus on predicting gene expression from histological images (the forward problem), but GeneFlow solves the reverse task of visualizing how specific gene expression patterns manifest in tissue images. It outperforms existing diffusion-based models in both quantitative metrics and expert evaluation, offering significant improvements in the quality and accuracy of generated histology images. This technology can support applications in minimally invasive diagnostics, virtual tissue reconstruction, and disease mechanism understanding.

Technology Validation:

The technology demonstrated superior performance in generating realistic tissue morphology, outperforming diffusion models with up to 3-6x better FID scores. Expert evaluation revealed an 86% preference rate for GeneFlow-generated images, confirming its high accuracy and applicability in various biological contexts.

Advantages:

-Generates high-resolution histopathology images

-Outperforms existing methods

-Enables multiple staining modalities

Applications:

-Minimally invasive disease diagnosis

Technology ID

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Category

Biotechnology & Life Sciences/Biomarker Discovery & Diagnostics

Biotechnology & Life Sciences/Bioinformatics & Computational Biology

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Further information

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View online

-Virtual tissue reconstruction

-Study of gene-disease interactions

TRL: 3

Intellectual Property:

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Keywords: GeneFlow, high-resolution histopathology images, gene expression data, tissue morphology, inverse problem, virtual tissue reconstruction, minimally invasive diagnostics, disease mechanism understanding, diffusion models, gene-disease interactions

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