

AUTOTALKER: Variational Graph AUTOencoder for Interpretable Cell TALK Inference

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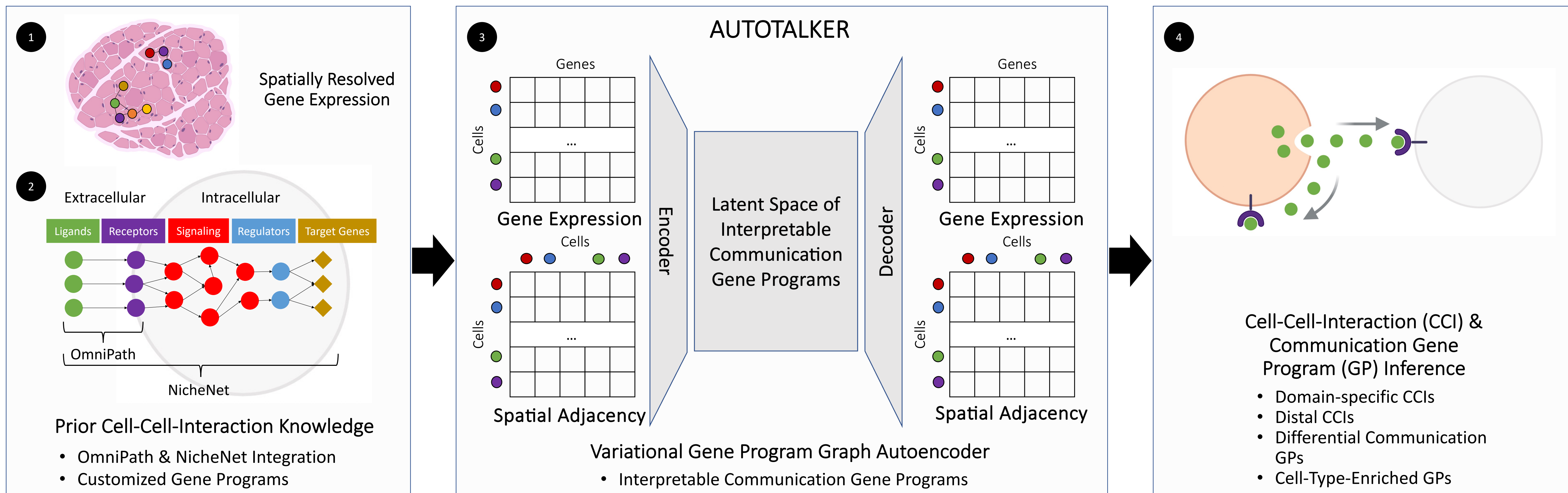
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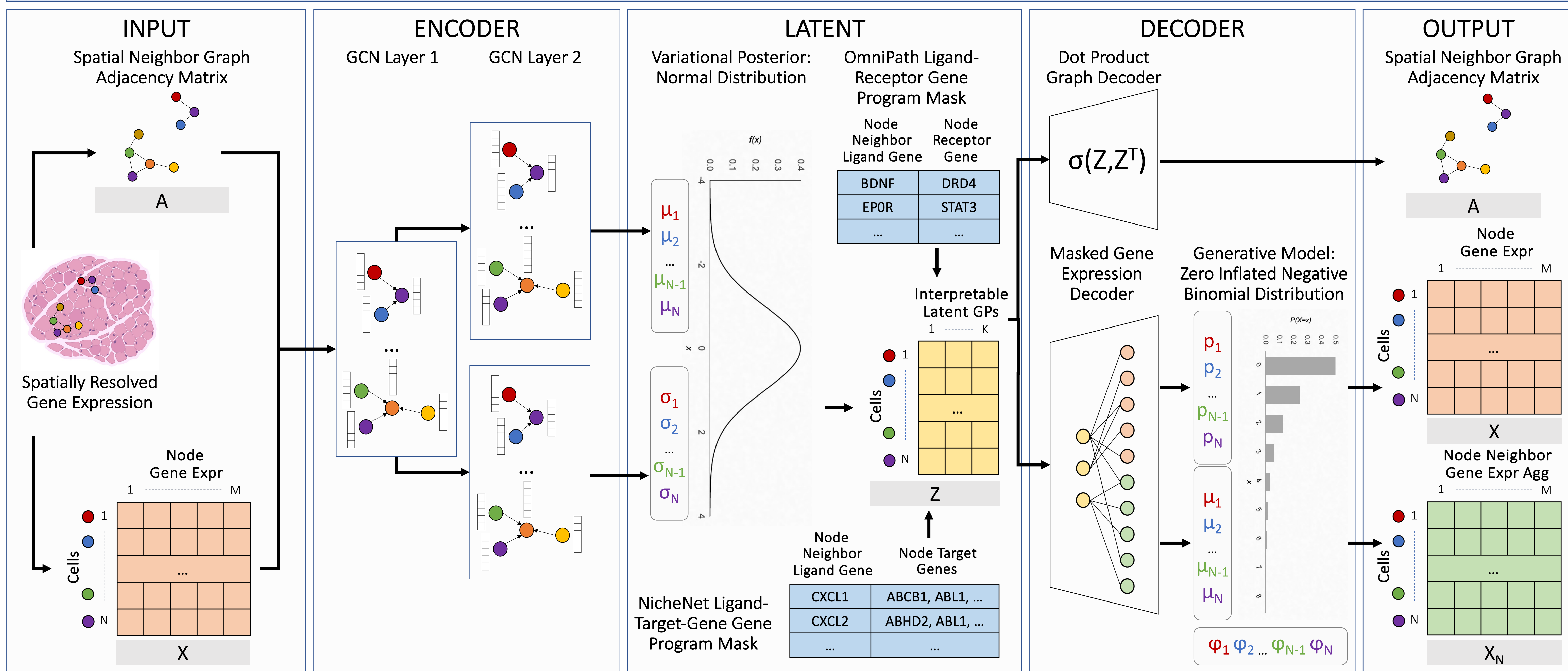


PROBLEM FORMULATION & MOTIVATION

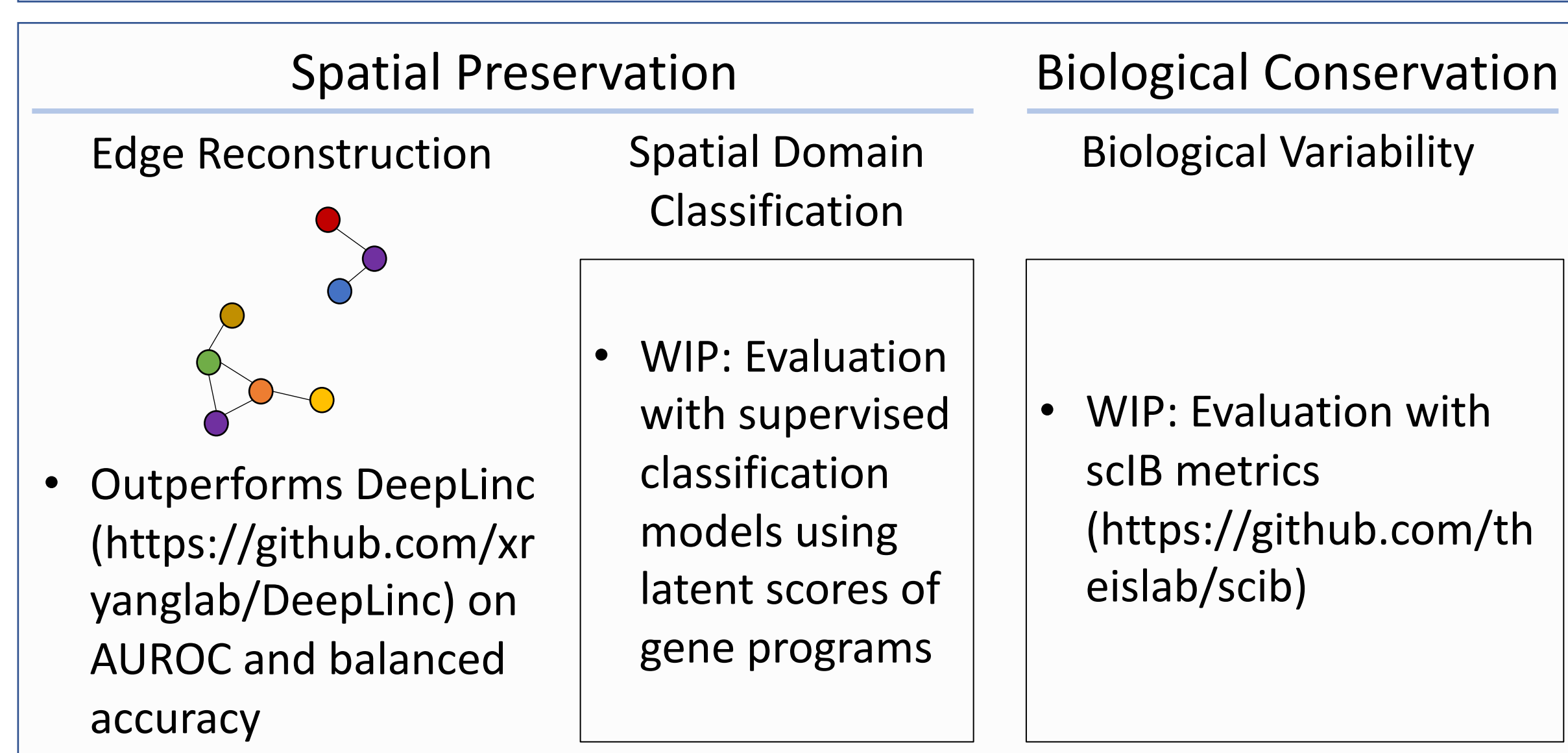
Can we use interpretable deep learning on spatial transcriptomics to infer distal and spatial-domain-specific cell communication dynamics in health and disease?



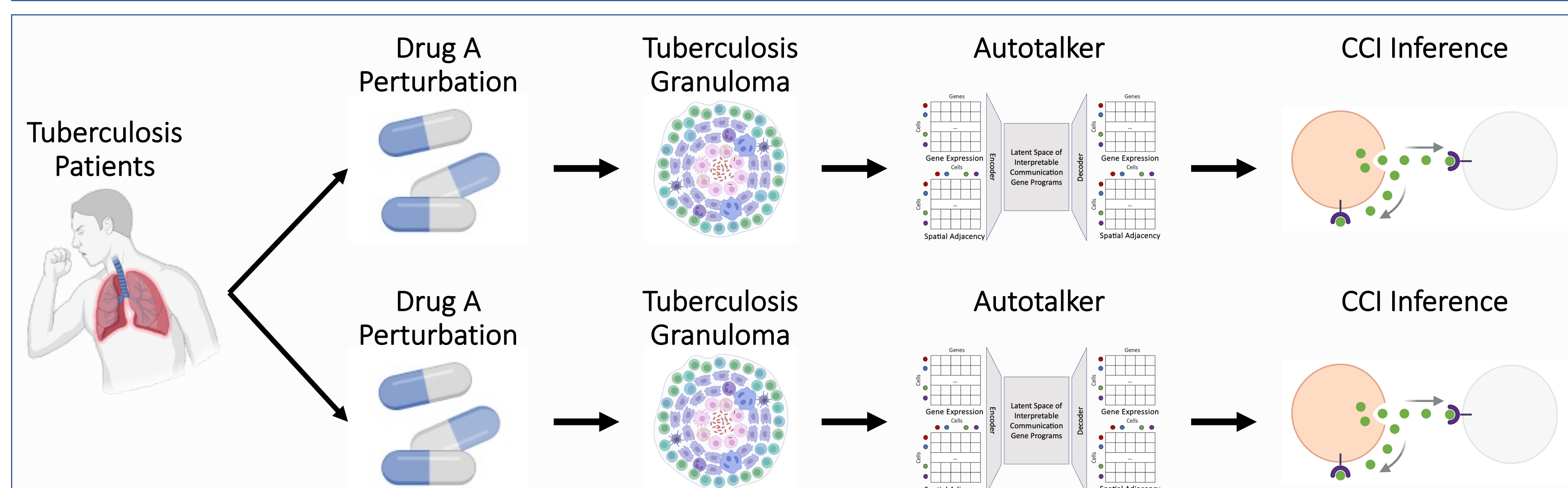
METHOD



BENCHMARKING (WIP)



USE CASE (WIP)



SUMMARY

AUTOTALKER...

- is a hierarchical Bayesian deep learning model to infer spatial domains/niches and cell-cell-interactions (CCIs) from spatially resolved gene expression data (it operates at cellular resolution)
- uses a variational graph autoencoder combined with dot product graph decoder and masked gene expression decoder modules to reconstruct the spatial neighbor graph and the gene expression of the cell itself and its neighbor cells (using attention aggregation)
- leverages prior CCI knowledge to constrain the latent space with communication gene programs
- will be available as a scalable Python package based on AnnData & PyTorch Geometric (QR code to the right)

RESOURCES

Presenter:

Repository: <https://github.com/Talavera-Lopez-Lab/autotalker>

Preprint:

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