

Statistical Modelling of Spatial Transcriptomics for Gene Imputation and Cellular Communication

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Recent spatial transcriptomic (ST) technologies offer a lens for observing the spatial distribution of RNA transcripts in tissues, while multifaceted computational challenges hinder biological discovery. This talk will first introduce a method, TransImp [1], for addressing the imputation of unobserved genes by translating single-cell data to ST. Uniquely, this method proposed a regularization of spatial auto-correlation for achieving more reliable downstream analysis. Second, another statistical method SpatialDM [2] will be introduced that aims to rapidly detect cell-cell communications through spatially co-expressed ligands and receptors. By deriving an analytical null distribution, this method has the scalability to millions of spots and has been shown effective in human development and cancer contexts. Last, a few ongoing works regarding cell transition inference will also be mentioned.

References:

- [1] C. Qiao, and Y. Huang, Towards a reliable spatial analysis of missing features via spatially-regularized imputation. bioRxiv 524992, (2023).
- [2] Z. Li, T. Wang, P. Liu, and Y. Huang. SpatialDM: Rapid identification of spatially co-expressed ligand-receptor reveals cell-cell communication patterns. bioRxiv 504616. Nature Comm (in press).