# Identifying intercellular patterns in Vestibular schwannoma

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Cell–cell interactions orchestrate key processes in tumor development and immune regulation. In this study, we investigate the spatial architecture of vestibular schwannoma (VS) using a combination of spatial transcriptomics and advanced computational modeling. We applied the MISTy (Multiview Intercellular SpaTial modeling) framework to identify intercellular signaling patterns and to assess how local cellular environments influence gene expression profiles. To complement this, we employed Ficture, a segmentation-free approach, to define spatial domains based on transcriptional similarity rather than predefined cell types. This allowed us to detect functionally distinct regions within the tumor that may reflect structural or signaling compartments relevant to VS biology. By integrating these analyses, our approach provides a comprehensive view of the spatial signaling landscape in VS. This work highlights the power of combining segmentation-free methods with spatially informed intercellular modeling to uncover the organizational of the tumor microenvironment.