# Challenges (and solutions?) in Xenium Spatial Transcriptomics Data Analysis.

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Our laboratory was recently equipped with the new Xenium instrument. Like other spatial transcriptomics platforms, Xenium can detect transcripts within a tissue sample. However, unlike many other methods, it is able to capture the exact position of transcripts, allowing to explore transcripts in subcellular spatial context. After our first Xenium run we encountered several challenges, such as an unexpectedly low transcript count. In this poster, we present the protocol we followed to analyze the data, how we tried to adapt to these challenges, and other key lessons we learned in the process. We are eager to discuss our experience with Xenium data, and hope to share practical insights and reusable code strategies that may benefit others working with spatial omics data in real-world research contexts.