

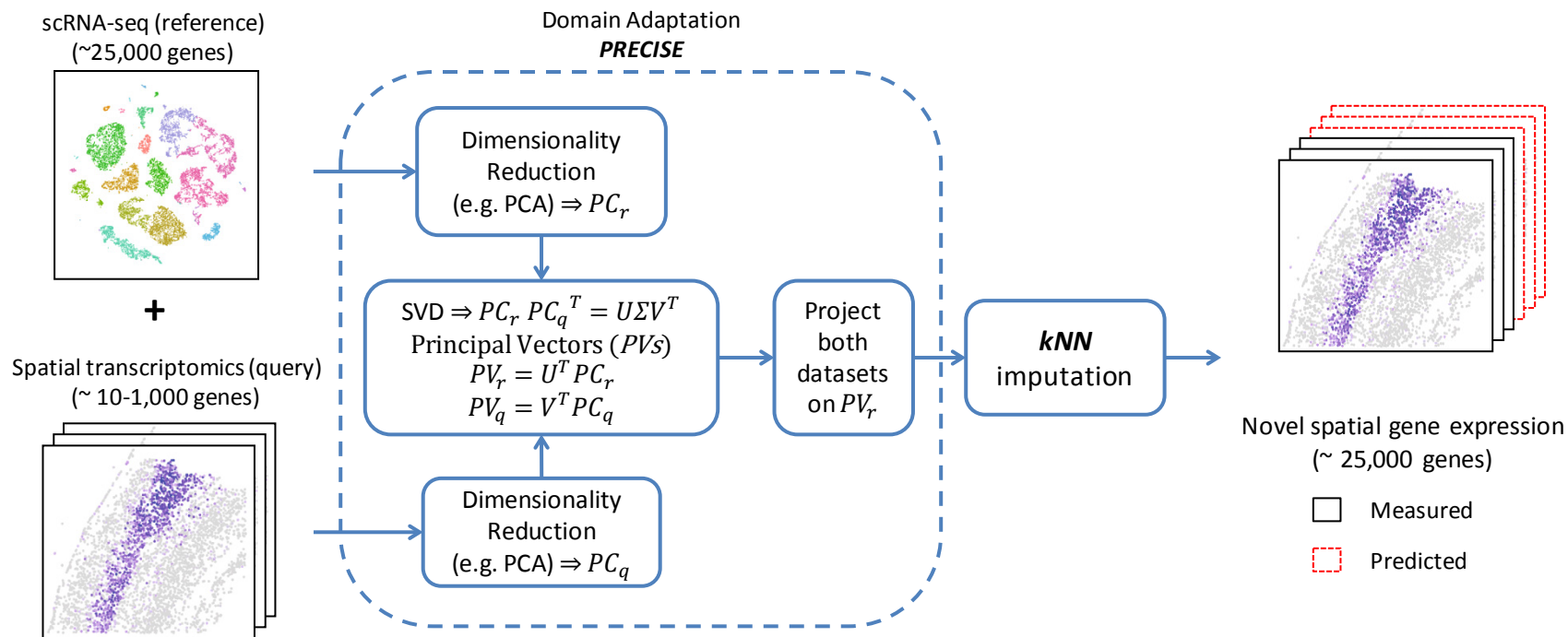
# SpaGE: Spatial Gene Enhancement using scRNA-seq

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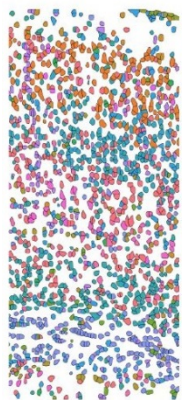
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<sup>3</sup>Computational Cancer Biology, The Netherlands Cancer Institute, the Netherlands



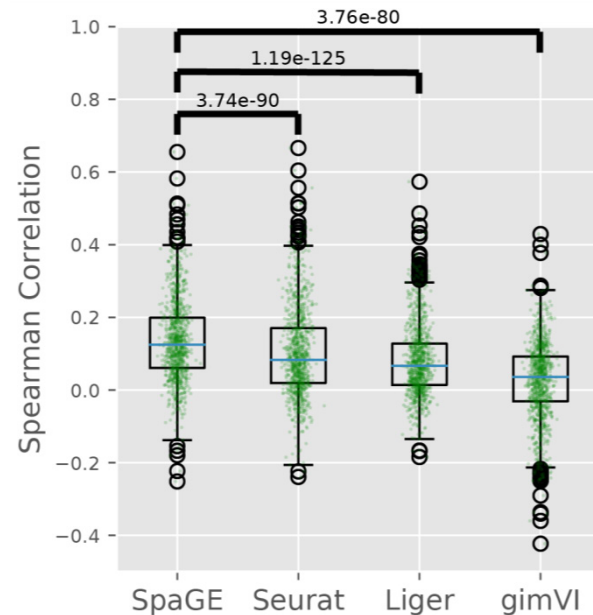
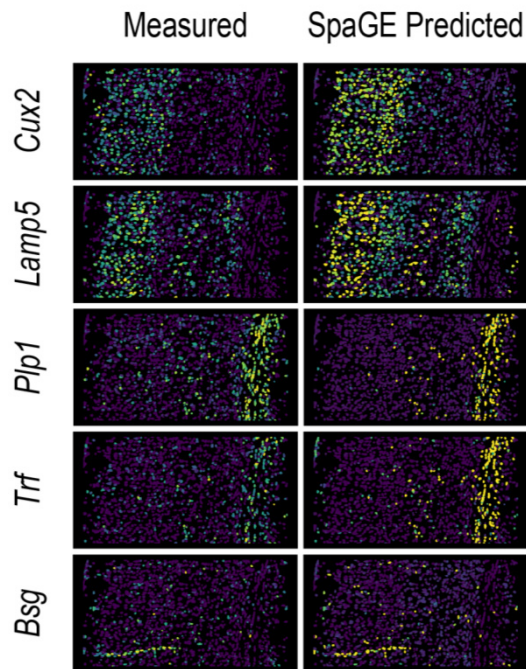
# SpaGE outperforms previous methods using mouse primary visual cortex



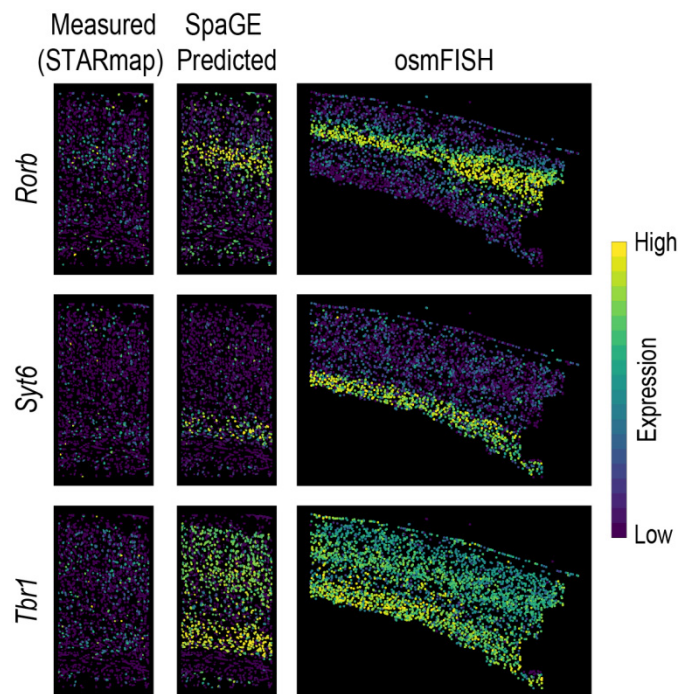
**STARmap**  
1,549 cells  
1,020 genes  
Wang et al. Science 2018



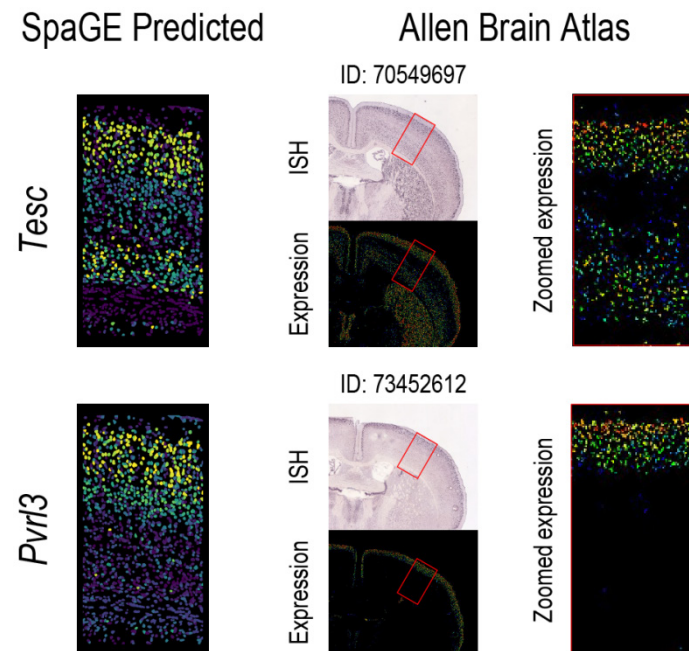
**scRNA-seq**  
14,249 cells  
34,617 transcripts  
Tasic et al. Nature 2018



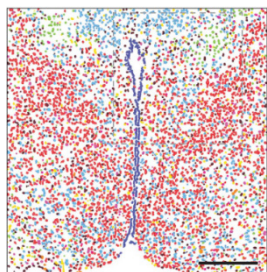
## Wrongly measured, correctly predicted



## Predicting unmeasured genes



# SpaGE scales to large spatial datasets



**MERFISH**  
64,373 cells  
155 genes  
Moffit et al. Science 2018

**scRNA-seq**  
31,299 cells  
18,646 transcripts  
Moffit et al. Science 2018

