Capturing ENS cell and gene clusters in a Cat's Cradle

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Gastrointestinal physiology relies on the enteric nervous system (ENS), which coordinates diverse functions through integrated interactions with multiple cell lineages. The ENS encompasses all gut-intrinsic enteric neurons and enteric glial cells (EGCs) and is harboured in the tunica muscularis (TM) of the intestine surrounded by muscle, immune, endothelial and mesothelial cells, interstitial cells of Cajal and fibroblasts. Miscommunication between those cellular systems has adverse effects on intestinal health leading to pathology.We previously generated an atlas of all major cell types in the TM of the mouse intestine using single cell RNA-sequencing (scRNAseq) during homeostasis and disease using two previously published models of TM inflammation (namely helminth infection and EGC-specific abrogation of IFNγ signalling).

In a typical Seurat analysis of a scRNAseq dataset we analyse a gene expression matrix where the rows are genes and columns are cells. The Louvain algorithm then clusters cells into cell types and tools such as UMAP and tSNE allow us to visualise these cell clusters spread out in two dimensions. In a novel analysis, we transpose this expression matrix allowing us to cluster genes and visualise these gene clusters in two dimensions. These gene clusters reveal sets of genes cooperating to carry out particular functions during homeostasis and during inflammation. In addition, we are able to query the relationship between gene clusters and cell clusters and display this as a bipartite graph. This allows us to investigate which cell clusters up-regulate which gene clusters thereby revealing common functionality between distinct cell types.

Maybe we can also say something about inflammatory response genes that cluster together?

This whole abstract need a general summary paragraph. What is our final conclusion?

\* These people are all stars!