Summary of:

"Phenotypic variation of transcriptomic cell types in mouse motor cortex" by Scala et al.

A"

Aalto-yliopisto
Aalto-universitetet
Aalto University

The research is based on two previous articles

	Reference 1: Tasic et al., 2018	Reference 2: Yao et al., 2020	This article: Scala et al., 2020
Research question	How many different neurons are there in a brain?	How many different neurons are there in a single area of a brain?	If you add features other than RNA sequencing, would the cell type classifications remain the same?
Area of brain	VISp, ALM	MOp	MOp
Content of data	RNA sequencing	RNA sequencing	RNA sequencing, electrophysiological, morphometric
Conclusion	Identify a total of 133 cell types by single-cell RNA sequencing.	Discovers around 30 to 116 possible cell types using transcriptomic and epigenomic data.	Confirms broad cell families of primary marker genes and levels. However, suggests that Yao et al.'s cell types may not be discrete but continuous.

"Phenotypic variation of transcriptomic cell types in mouse motor cortex"
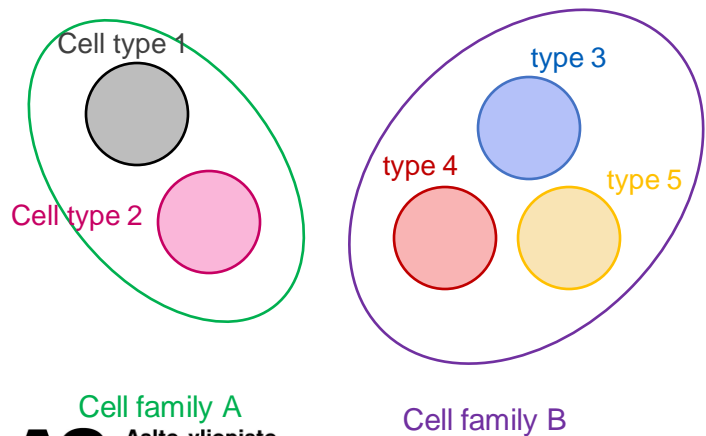
Analyses in the article

	Research Tasks	Details	Corresponding Figures
0.	Ground truth labeling	Give each neuron a broad cell family and a cell type from Yao et al.	Fig 1a
1.	Visualize t-SNE	Observe t-SNE representations of RNA sequence, electrophysiological, and morphometric features.	Fig 1c-e, 3a-c
2.	Perform RRR on ephys and RNAseq	Perform reduced rank regression to see how well electrophysiological features can be predicted from RNA sequencing.	Fig 2
3.	kNN of ephys and morph	Do kNN classification on morphometric and electrophysiological data and observe the confusion matrix.	Fig 3d, 5a
4.	Overlay ephys and morph on RNAseq	Overlay scatterplots and bubble charts of electrophysiological and morphometric data on the RNA sequence t-SNE representations.	Fig 4, 5c-d
5.	Ephys and morph variances	Observe the electrophysiological and morphometric variances of the transcriptomic cell types. K-means and Leiden clustering were used for comparison	Fig 5b

Conclusions

Scala et al. concludes that broad cell families are discrete groups but cell types within them might not be as clearly separated as RNA sequencing suggests.

Tasic et al. and Yao et al.
Though noting that the clusters are difficult to separate cleanly, attempts to identify discrete cell types

Scala et al.
The broad families are discrete groups but cell types show significant overlaps. Beyond cell families, the cell types may be a continuous spectrum

+ electrophysiological and morphometric features