Analyzing spatial transcriptomics and neuroimaging data in neurodegenerative diseases

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Stellingen behorend bij het proefschrift getiteld

ANALYZING SPATIAL TRANSCRIPTOMICS AND NEUROIMAGING DATA IN NEURODEGENERATIVE DISEASES

by

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1. Gene co-expression across brain regions is more relevant than co-expression across individuals (Chapter 3 and 6).
2. Cell-type deconvolution is important, but we still don't know how to do it (Chapter 2).
3. There is a puzzling disagreement on the effect of *SNCA* being deleterious or protective based on genetics and expression (Chapter 2).
4. Initiatives that chart molecular atlases from healthy individuals are more valuable than focusing on a specific disease (this thesis).
5. Gene expression is relative and only becomes valuable if you measure over multiple samples in multiple conditions.
6. Biology is not fixed as definitions change continuously, making validation difficult.
7. There are too many paradigms in biology and they can only be solved with data-driven approaches.
8. The cell is a system, so it does not make sense to analyze differential expression of single genes.
9. Expression is the essence of being present.
10. In the era of sequencing analysis, data analysis is still undervalued.