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Integration and disentanglement of single-cell and spatial transcriptomics in health and disease

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Stellingen behorende bij het proefschrift getiteld

Integration and disentanglement of single-cell and spatial transcriptomics in health and disease

1. Reference-based annotation should be the default approach in single-cell data analysis (this thesis).
2. Assuming that spatial proximity and gene co-expression in spatial transcriptomics equate to functional cell-cell communication ignores critical biological factors such as diffusible cytokines, the presence of proteases, and physical barriers like basement membranes (this thesis).
3. Biological systems are entangled, and attempting to fully separate their components may lead to oversimplified models that fail to capture critical emergent properties (this thesis).
4. When analysing precious biological samples, prioritising data acquisition over technical perfection yields greater scientific value (this thesis).
5. The emphasis on adapting general machine learning techniques to biological data hinders the development of biology-centric computational methods.
6. Iterative bioinformatic analyses often lead to chance findings rather than systematic scientific breakthroughs.
7. Industrial-academic PhD partnerships inherently conflict with the core mission of doctoral education and should be reevaluated.
8. Artificial intelligence will surpass human researchers in both generating and executing ideas for incremental scientific gains.
9. The concept of residential property as a form of private investment should be abolished, with housing treated exclusively as a public good.