Single-Cell Transcriptomic Cell-type Annotation Using AI for the Study of Spinal Cord Injury

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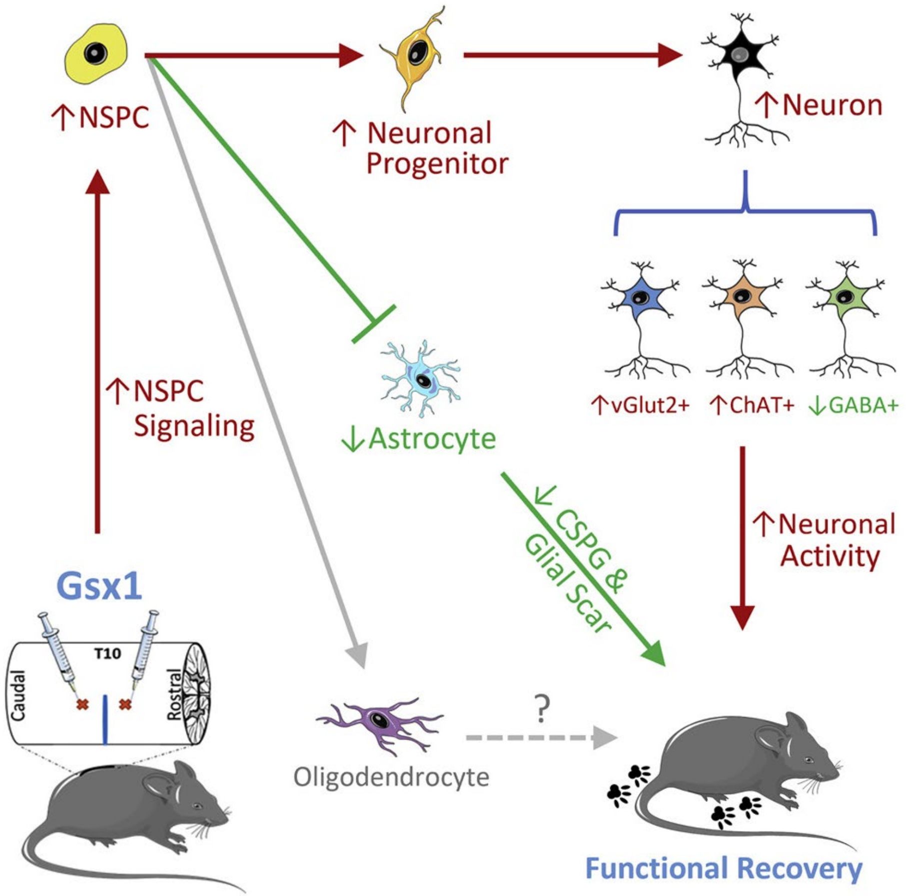
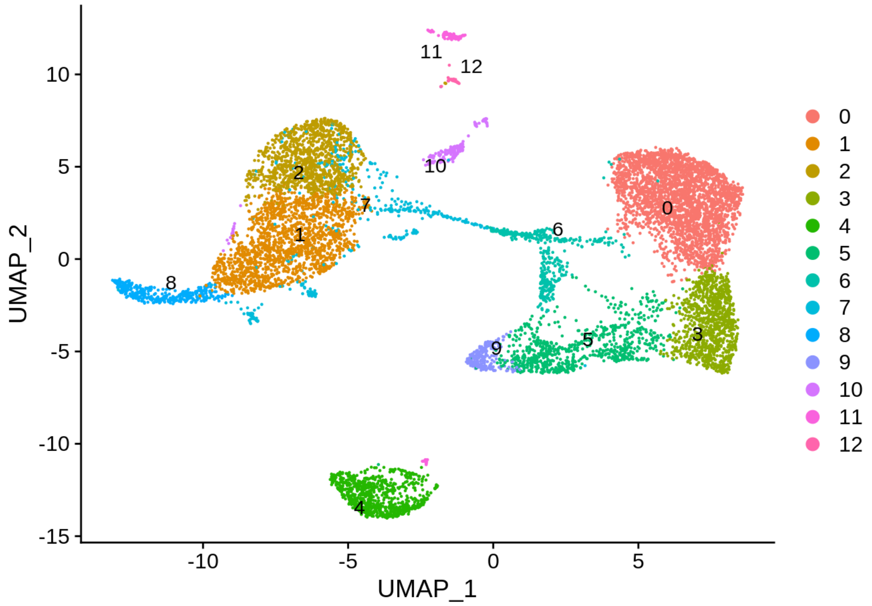
Gene therapy induces dynamic cellular changes in the injured spinal cord



Molecular Therapy, 2021
Neurotherapeutics, 2024

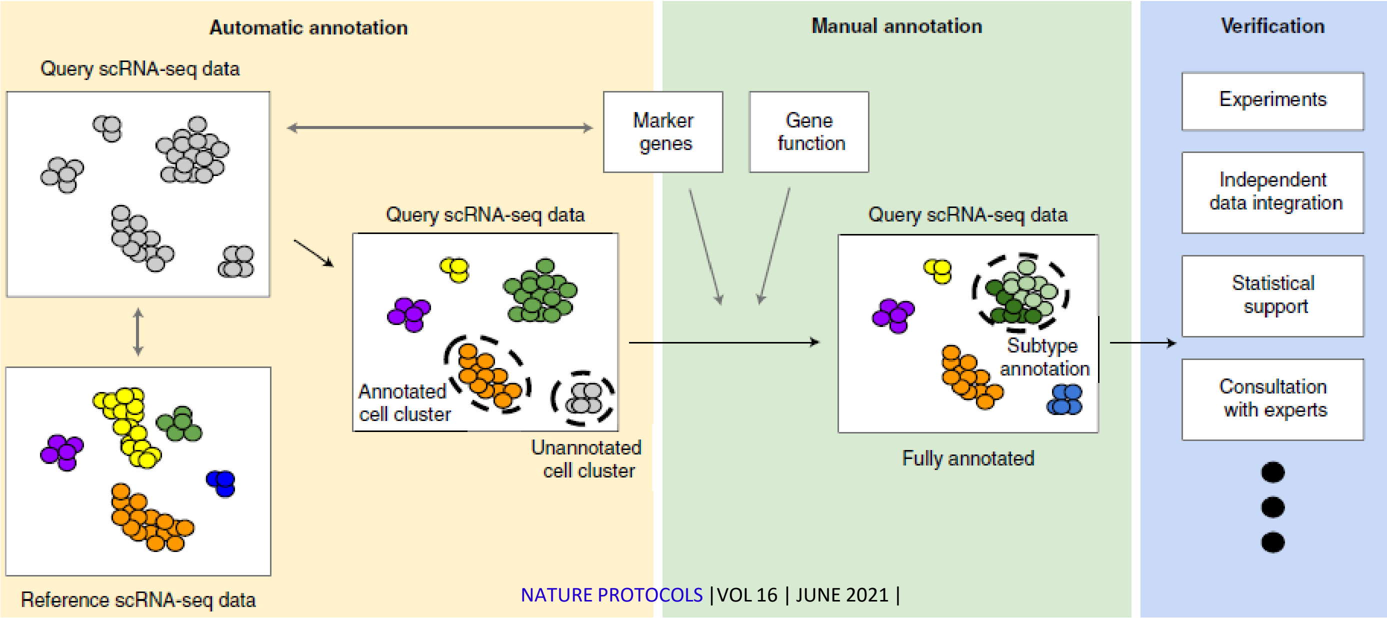
Single-cell transcriptomic analysis



- Extensive single-cell transcriptomic datasets
- Translating gene expression data into meaningful biological insights remains a significant hurdle.
- **Cell Type Annotation:** Accurately identifying cell types from gene expression profiles is challenging and often requires sophisticated methods and reference datasets.

AI-Driven Cell Type Annotation in SCI

Established Methods for Cell-type Annotation



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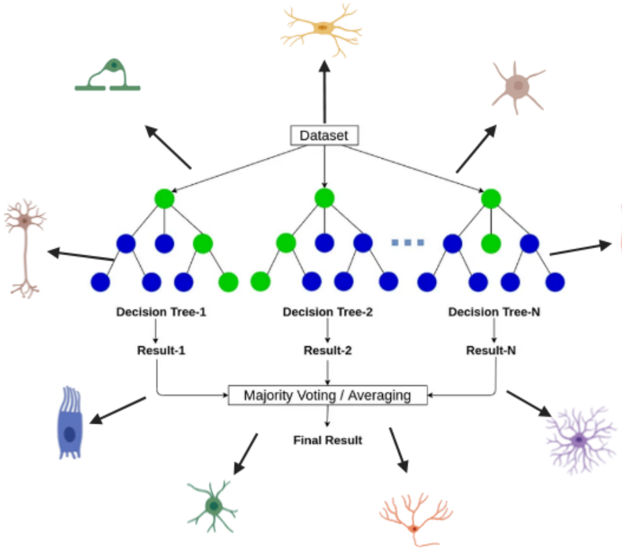
Major issues:

- Overreliance on Reference Datasets
- Limitations of Automated Tools
- Subjectivity in Manual Annotation, Marker Gene Dependency

Solution:

- Unsupervised and hybrid approaches: Combine marker-free clustering with expert knowledge

AI-Driven Cell-type Annotation



- Develop a random forest ML algorithm that combines multiple decision trees to improve cell-type classification.
- Enhance understanding of cellular responses and mechanisms underlying spinal cord injury.
- Inform strategies to improve patient outcomes.