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Prediction of therapeutic targets to halt inflammation-induced neurodegeneration.

Inflammation-induced neurodegeneration poses a clinical challenge in multiple sclerosis and aging. Despite intense research neuroprotective therapies are not available. Applying neuronal networks on “Omics”data holds the promise to identify novel therapies. We aim to establish a platform to find and prioritize genes that determine neurodegeneration. First, we will use generative neuronal networks of scSeq data with genetic perturbations, from different organs and neuronal perturbations to predict neuronal responses. Second, we will add gene-survival dependencies from cell lines to predict modulators of neuronal vulnerability. These genes will be iteratively deleted in neurons to measure viability which will feed further training. Thus, our platform will generalize transcriptomic changes between cell types, predict neuronal viability of genetic alterations, and prioritizes treatment targets.

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Keywords

Neurodegeneration
Multiple Sclerosis
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Autoren: Prof. FRIESE, Manuel (Institut für Neuroimmunologie und Multiple Sklerose (INIMS)); Dr. WOO, Marcel Seungsu (Institut für Neuroimmunologie und Multiple Sklerose (INIMS))