# Modeling peroxisomal dysfunction in multiple sclerosis

#### Overview

This take-home challenge is designed to assess your ability to reason through complex biological questions using computational tools. Your task is to explore the role of peroxisomal dysfunction in multiple sclerosis (MS) by integrating transcriptomic and network data. Your aim is to connect transcriptomic alterations in MS with broader peroxisomal biology using systems-level, network-based reasoning.

## Objective

Build a computational workflow that integrates processed RNA-seq data and a protein–protein interaction (PPI) network to prioritize targets (broadly) associated with peroxisomal dysfunction in MS. We're especially interested in creative reasoning and modeling choices that go beyond the obvious. Show us how you think and code. Please approach the problem using all tooling and resources you would use in a real scenario.

#### Data sources

Please refer to the "Data availability" section of Schafflick, Xu, Hartlehnert, Cole *et al.*, see <u>here</u>, for GEO repository accession codes and Supplementary Dataset Tables.

### Deliverables

#### 1. Code

We'll work with Jupyter notebook and Python. Your code should be well-organized, readable, and reproducible. Please include comments or docstrings where appropriate, and ensure to reference sources where appropriate.

### 2. Report

Please submit a brief write-up (as Markdown or PDF) covering:

- Your overall approach and rationale
- Your strategy for integrating expression and network information
- How you prioritized novel candidate genes
- Limitations, assumptions, or areas for improvement

• Optional: visualizations of networks, scores, or top candidates

## 3. Outputs

- A table of ranked candidate genes with associated scores and interpretation
- Any plots or visualizations you used to support your conclusions

### Submission

## Please provide:

- Your code (in a folder or GitHub repo)
- Your report (PDF or Markdown)
- Any output files (e.g. results tables, visualizations)

Please don't over-polish: we're more interested in your reasoning and design choices than perfection.