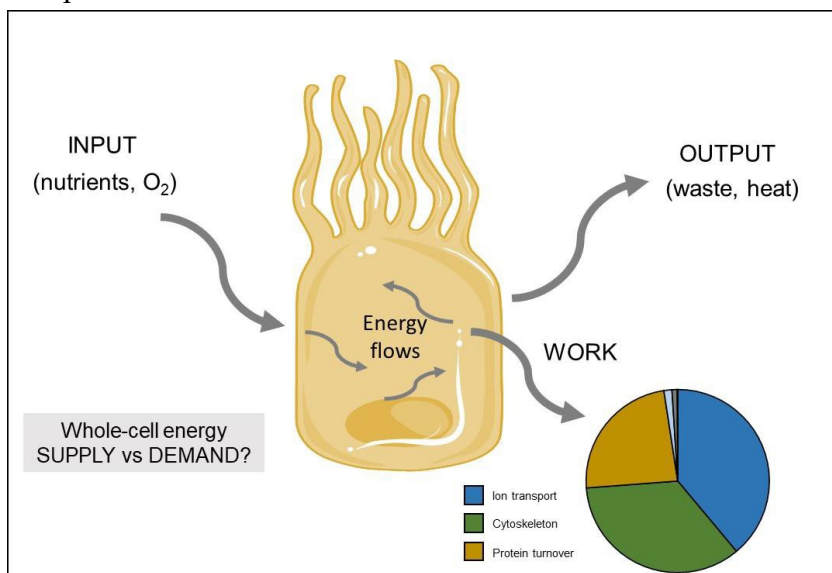


Project title: Computational energy supply and demand model of retinal pigment epithelium cells
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Background: Visual processing starts in the outer retina (OR), where photoreceptor (PR) cells sense photons that trigger electrical responses. Retinal pigment epithelial (RPE) cells are located external to the photoreceptor layer and have critical functions in supporting cell and tissue homeostasis and thus sustaining a healthy retina. The visual system is highly energy demanding. It is suggested that with progressive ageing or in the context of risk factors that promote age-related blinding diseases, RPE cells are increasingly unable to execute all tasks at an optimum level. Therefore, RPE cells may compromise their own vital functions and/or stop supporting the PR cells, which either way ultimately results in PR cell death and vision loss. It remains enigmatic how RPE cells integrate and prioritize different interlinked processes, and the associated energy demands of the whole (OR and choroid) system.

The PhD project will address the following questions:

- How is available energy distributed along energy-demanding (repair) processes?
- How does energy supply and demand change in the aging RPE?
- Can we identify targets for network-and energy-centric steering that are likely to shift energy priorities in the RPE towards restoration?



The approach is to develop an integrative computational network model of the RPE that focuses on key cellular energy supply and consumption processes.

The mechanistic models will be constrained by the incorporation of gene (and protein) expression levels based on bulk data and individuals from different age-groups. Additionally, we will model anatomical changes during aging and how this causes cell networks to

rewire. The generated models will be exploited to predict how alterations of networks and associated energy-requiring processes steer the systems towards favouring homeostasis and restoration processes.

Techniques: Computational methods to ODE-based model building and analysis (e.g. Matlab, Python); translate cell and tissue processes from publications into computer-readable language and rules; protein-protein-interaction network analyses (network representation using Cytoscape and Cell Designer); bioinformatics databases; statistical analysis of gene and protein expression data in single cells and bulk/ tissue samples (R programming language).