

## Inter-species comparison

**Title:** Comparing mice and human at the phenotypic level

**Type:** [ MA ]

**Category:** [ Data science ]

**Programming language:** [ R | python ]

**Language:** [ English ]

**Prior experience:** [ basic knowledge in programming, experience in R or Python, basic understanding in biology is a plus but not required ]

**Complexity/Risk:** [ medium ]

**Contact person:** Ludwig Lautenbacher and Mathias Wilhelm

**Brief background description:** Mouse models are the first stage of preclinical trials. Mice are infected with the examined disease type and then treated with the candidate drugs at different concentrations. Depending on the results, the drug candidate will then proceed to the next phase. Mice have many tissues in common with humans but these still differ in many ways, for example in size, and more importantly in the genome. Researchers have defined homologenes between the two species allowing inter-species comparisons.

**Brief description of the project:** In this project, you will compare protein expression values across species for the same tissue. The same will be done for other omics types e.g. transcriptomics. Later, the phenotypic results of the two organisms will be compared. For example, phenotypic studies can involve cell viability data that exist for both organisms; same tissues, or cell lines with the same origin (e.g. pancreas) treated with the same drug in a certain concentration range. The cell viability data can be compared across species and the results of this comparison can be further explored together with the tissue protein/transcript expression comparison that was done in the first step. The results have to be presented in a detailed and comprehensive way, both in table format but also in plots.

**Expected result:** How similar are phenotypic outcomes of mice and humans.