**Exploiting multiomics data in human disesese model alignment**

The use of **in vitro** and **in vivo** models is essential for studying biological systems, particularly for predicting their responses to external stimuli. These models play a critical role in evaluating both the toxicological and pharmacological effects of chemical compounds, contributing to the reduction of time, costs, and ethical concerns associated with experimental research. A key factor in their effective use is the ability to assess how closely these models replicate the tissue of interest and its specific phenotype.

This project aims to define and develop an integrated system that maps **in vivo** and **in vitro** models to corresponding tissues, providing a quantitative measure of model fidelity in terms of **molecular conformation**, leveraging **multi-omics** data.

The system will incorporate **machine learning (ML) algorithms** designed to:

* Position a given biological model within a reference space of pathological tissues using multi-omics profiles.
* Identify and quantify molecular divergences between models and target tissues.

The system will include ML-based functionalities to:

* Assist in the selection of the most relevant models from publicly available catalogs for a given tissue or phenotype.
* Predict which tissue types are best represented by a specific model, enabling reverse mapping from model to tissue.

This project will push the boundaries of current biological modeling approaches by delivering:

* A robust methodology to guide end users in selecting the most suitable models for studying specific phenotypes.
* Tools for the characterization, validation, and potential repositioning of existing biological models.

The primary deliverable will be a **systems biology platform** integrating a diverse set of multi-omics models. It will encompass publicly available data on biological models and tissues, while also supporting the integration and analysis of newly generated experimental data. This platform will serve as a comprehensive resource for researchers, facilitating informed decisions in model selection and biological hypothesis testing.

**Supervisor(s), Lab/Group details, other additional info.** (*please provide information about the group and available facilities*)
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