

Deep learning for imaging genetics

UNIL FBM 2023 PhD Fellowship proposal outline

Translational Machine Learning Laboratory

Department of Radiology

<https://unil.ch/tml>

Imaging genetics is the study of the relationship between image-derived phenotypes and genetics. It has been applied to study the genetic bases of spatially-distributed spontaneous brain activity, heritability of cortical folding patterns, cardiovascular risk variants and ejection fraction, tumor mutations and malignancy from visual features, and more. It will become an increasingly important part of precision medicine.

From a machine learning standpoint, imaging genetics methods can be seen as multi-view methods: each patient (subject, sample) is represented by several *views* (modalities), such as a heart image, whole blood transcriptomics, and clinical data. Each view can be very high-dimensional (millions of voxels, millions of genetic variants, tens of thousands of gene expression levels).

Traditionally, such problems have been solved using multilinear methods including partial least squares (PLS), canonical correlation analysis (CCA), or reduced rank regression (RRR). These typically embody strong assumptions about the data such as linearity or Gaussianity. More recent versions include regularized, sparse, deep, and nonlinear variants, but typically fail to include modern and powerful deep learning concepts such as attention, self-supervised learning, or graph-based learning.

This project would build on existing methods and expertise in the lab to develop next-generation multi-view imaging genetics methods, with applications to a) cardiac imaging, cardiovascular/metabolic risk variants, and heart failure, b) brain imaging, spatial transcriptomics, and Dementia. In particular, one goal is to develop methods to explicitly leverage sample-sample similarities (in the image domain) and gene-gene similarities (gene networks) to act as regularizers for inference.

If you are applying to the UNIL FBM 2023 PhD fellowships, feel free to reach out to jonas.richiardi@chuv.ch for informal discussion.