***Advancing medical research with shape analysis of bioimaging data by Dr Nina Miolane***

The advances in bioimaging techniques have enabled us to access the 3D shapes of a variety of structures: organs, cells, proteins. Since biological shapes are related to physiological functions, statistical analyses in biomedical research are poised to incorporate more shape data. This leads to the question: how do we build fast reliable quantitative descriptions of shape variability from images?

This talk starts by introducing mathematical definitions of shapes and corresponding elements of "geometric statistics", with associated open-source implementation. We use this formalism to analyze the properties of the "template shape" algorithm - used for more than ten years in signal processing and imaging. This algorithm estimates the subspace of images that show the same shape, possibly rotated or translated. We show that the estimation has an asymptotic bias. We quantify the impact of this finding for neuroimaging studies, using the OASIS dataset of brain structural MRIs.

As an alternative, we introduce variational autoencoders (VAEs). VAEs are latent variable models that learn subspaces of images. We combine VAEs with generative adversarial networks (GANs) to estimate the shape subspace of a dataset of ribosome cryo-electron microscopy (cryo-EM) images from the Stanford Linear Accelerator Center. We show how geometry enables the disentanglement of latent variables governing images' orientations and appearances. This study opens the door to unsupervised fast orientation learning for (cryo-EM) biological shape estimation and analysis.