

# Using registration methods for uncertainty visualization in high-dimensional biology

**Speaker : Susan Holmes**

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In statistical geometry as applied to multi domain data in biology (RNA-seq, 16s rRNA seq, sc-RNAseq), low dimensional projections provide ways to detect latent variables summarizing multivariate interactions. We show how we can use multivariate measures of correlation to create useful registration compromises onto which subjects can be projected together with uncertainty contours generated either by the bootstrap or by Bayesian posterior generation methods.

This is joint work with Lan Huong Nguyen, , Christof Seiler, Kris Sankaran, Julia Fukuyama, Sergio Bacallado and Boyu Ren