



## Multivariate Methods Applied to Imaging Genetics Data Workshop

*Thursday, 27 October 2016*

**12:00-13:00**

*Coffee and Lunch*

### *Session I. Getting started!*

**13:00-13:15**

**Elisabeth Binder/  
Gunter Schumann**

*Welcome Address*

**13:15-13:45**

**Gunter Schumann:** Imaging genetics in population neuroscience: promises and challenges

**13:45-14:05**

**Andre Marquand:** From big data to precision medicine in psychiatry

**14:05-14:15**

+ Discussion

**14:15-14:35**

**Bertrand Thirion:** Machine learning for neuroimaging: current challenges and solutions

**14:35-14:45**

+ Discussion

**14:45-15:05**

**Bertram Müller-Myhsok:** Machine learning and genetics: newer methodological developments

**15:05-15:15**

+ Discussion

**15:15-15:45**

*Discussion: What are the best ways of applying machine learning methods in large cohort studies?*

**15:45-16:00**

*Coffee/Break*

### *Session II. Exploiting the image space*

**16:00-16:20**

**Nikolaos Koutsouleris:** NeuroMiner: A flexible MVPA tool to integrate multi-modal data using ensemble learning and stacked generalization

**16:20-16:30**

+ Discussion

**16:30-16:50**

**Robert Whelan:** A machine learning method for interrogation of multimodal neuroimaging data

**16:50-17:00**

+ Discussion

**17:00-17:20**

**Christian Wachinger:** BrainPrint: a new measure of brain morphology

**17:20-17:30**

+ Discussion

**17:30-18:15**

*Discussion: How can multivariate methods be applied to imaging-genetic data to meaningfully stratify different psychiatric groups? What are the main impediments to the use of these methods in a working clinical context?*

**~19:30**

*Leave for Dinner*

**Friday, 28 October 2016**

**Session III. A closer look at partial least squares**

9:30-9:50	<b>John Shawe Taylor:</b> Sparse partial least squares and canonical correlation analysis: promises and pitfalls
9:50-10:00	+ Discussion
10:00-10:20	<b>Andre Altmann:</b> Background on PLS and distributed PLS for meta analysis
10:20-10:30	+ Discussion
10:30-10:50	<b>João Matos Monteiro:</b> A multiple hold out framework for sparse partial least squares
10:50-11:00	+ Discussion
11:00-11:20	<b>Alex Ing:</b> Using sparse partial least squares with stability selection to discover biomarkers in psychiatry
11:20-11:30	+ Discussion
11:30-12:00	<i>Discussion: Can multivariate methods such as partial least squares and canonical correlation analysis be used to stratify data by biological subtype?</i>
12:00-12:30	<i>L u n c h</i>

**Session IV. Finding functional units**

12:30-12:50	<b>Philipp G. Sämann:</b> Sleep studied by different functional connectivity methods: conceptual points for functional connectomics
12:50-13:00	+ Discussion
13:00-13:20	<b>Juha Lahnakoski:</b> Independent components, networks and inter-subject similarity: from rest to naturalistic stimulation
13:20-13:30	+ Discussion
13:30-13:55	<b>Jean Liu:</b> Implementation of parallel independent component analysis to imaging genetics
13:55-14:05	+ Discussion
14:05-14:25	<i>Discussion: What are the best ways of discovering functional subtypes in imaging genetics?</i>
14:25-15:00	<i>C o f f e e / B r e a k</i>

**Session V. Enhancing classical association analysis**

15:00-15:20	<b>Elisabeth Binder:</b> Using multi-omics data sets to inform disease mechanisms for stress-related psychiatric disorders
15:20-15:30	+ Discussion
15:30-15:50	<b>Gökçen Eraslan:</b> DeepWAS: integrating regulatory information into GWAS using deep learning
15:50-16:00	+ Discussion
16:00-16:20	<b>Fabian Theiss:</b> Gene dynamics from snapshot single cell transcriptomics
16:20-16:30	+ Discussion
16:30-17:30	<i>Discussion: Can multivariate procedures be used to enhance common analysis approaches such as GWAS? Will this allow us to ask new questions?</i>