

Systems-level Integration of Neuroimaging and Genomic Maps in Health and Disease

Organizers:

Armin Raznahan

NIMH, Bethesda, United States

Edward Bullmore

University of Cambridge, Cambridge, United Kingdom

The scientific community gained open access to spatially comprehensive maps of brain gene expression approximately 5 years ago. Since then, the scope of publically available gene expression data has dramatically expanded to include different species and developmental periods. These data open up exciting new ways of using neuroimaging to understand brain organization, with major benefits for both basic and clinical science. These novel interdisciplinary opportunities come with new technical and theoretical challenges. We will delve into these issues by presenting multiple high-impact implementations of imaging-transcriptomics that (i) introduce key databases, (ii) address technical aspects of data QA, spatial alignment and statistical inference, (iii) link imaging-derived brain networks in development, phylogeny, and disease to underlying molecular substrates. Petra Vertes (Cambridge, UK) will present research linking regional differences in structural brain maturation in humans to patterns of cortical gene-expression in adulthood, which suggests that regions serving as key network hubs are enriched for expression genes involved in energetics and risk for psychosis. Fenna Krienen (Harvard, USA) will present research that compares cortical gene-expression across species and defines specialized gene sets likely to play a central role in patterning of the primate cortex. Alex Fornito (Monash, Australia) will present research integrating tract-tracing and gene-expression data in mice, to define connectional hubs with costly long-range wiring that bear the same enrichment for expression of energetic and neuronal communication genes seen in human brain network hubs. Armin Raznahan (Intramural NIMH, USA) will present studies in humans and mice that define molecular predictors of regional brain vulnerability by linking neuroanatomical effects of genetic risks to maps of brain gene expression.

Symposia Schedule:

14:45-15:00

Bridging the gap: What six “healthy” post-mortem brains can tell us about disease

Petra Vertes, University of Cambridge, Cambridge, United Kingdom

15:00-15:15

How does transcriptional variation relate to cortical specialization?

Fenna Krienen, Harvard Medical School/Broad Institute. Boston, MA/Cambridge, MA, United States

15:15-15:30

Genetic influences on large-scale brain network organization

Fornito Alex, Monash University, Melbourne, Australia

15:30-15:45

Linking genetic effects on brain anatomy in neurodevelopmental disorders to intrinsic patterns of cortical gene expression

Armin Raznahan, NIMH, Bethesda, United States

15:45-16:00

Questions and Answers