"Polygenic risk prediction - a case report for schizophrenia"

Manuel Matthiesen from Department of Biomedicine in Aarhus

Abstract:

I'm an Associate Professor with the Department of Biomedicine, Aarhus University, and a member of the "Lundbeck Foundation Initiative for Integrative Psychiatric Research (iPSYCH)" and the "Center for Integrative Sequencing (iSEQ)". I'm a physician by training (medical genetics / psychiatry), and have a strong background in genetic epidemiology, biostatistics and molecular genetics. After attending medical school in Bonn, Germany, I work in parallel for two years as a postdoc and resident (medical genetics) at the Department of Human Genetics and the Institute for Medical Biometry, Informatics, and Epidemiology (both in Bonn, Germany). In 2011 I joined for my second postdoc position the Department of Biostatistics at Harvard School of Public Health and the Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School (both Boston, MA, USA). In 2013 I finally arrived in Denmark to work now in one of the most existing and largest projects psychiatric research has ever seen.

A major focus of my research work next to psychiatric genetics is the enhancement and development of biostatistical methods and tools for research into common multifactorial disorders. The impetus for this work stems from and is influenced by the interest in linking phenomics, molecular genetic- and biostatistical knowledge. Among others, this has led me to analyze polygenic, epigenetic and epistatic effects within different frameworks and more recently systems biology and network modeling approaches (during my time at the Channing). I am (IntegraMent) and was (MooDS) a co-PI on two large-scale national integrative research grants in Germany with responsibility for their respective biostatistic and bioinformatic focused subprojects.

My expertise in the analysis of large-scale molecular genetic studies is based on leading roles in GWAS in different phenotypes with a major focus on mental disorders. This led to identification of disease causing genetic variation in schizophrenia, OCD, major depression, alcohol dependency, and bipolar disorder. I am a member of several large international consortia that focus on neuropsychiatric research (Psychiatric Genomics Consortium, ENIGMA, iPSYCH) and work closely with some of the most innovative and productive groups in genetic and biostatistical research worldwide.

Time and place:

Monday March 2nd at 11am

J.B. Winsløws Vej 9b in room 4.39