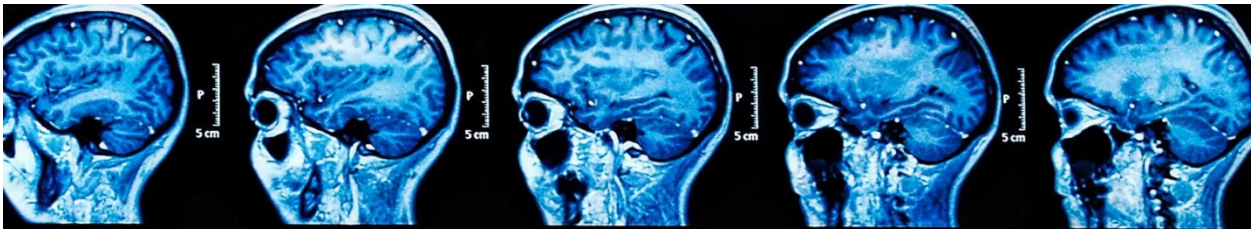
BMS-ANed Winter Meeting:

Biomedical Image Analysis

15 December 2017, Leiden



This year's Winter Meeting of the Dutch Biostatistics Society will focus on the statistical analysis of medical images. The advances in imaging and analysis of images have been plenty in the last decade and this meeting will focus on some of these breakthroughs. The general **afternoon** programme (13:00-17:00, **Havingazaal, Het Gorlaeus**, Leiden) features plenary talks by Joke Durnez (Stanford), Marie-Colette van Lieshout (CWI, Twente), Bieke Moerkerke (Ghent) and Christian Beckmann (Nijmegen) and is concluded with social drinks. In the **morning** (10:00-12:00, **Mathematical Institute**, Leiden), Joke Durnez (Stanford) will be teaching a short course for PhD students, postdocs and other people interested on the analysis of medical images.

The meeting is free for members of the VVS-OR and/or the Netherlands Region of the IBS. The meeting costs 10 euros for non-members. We want to point out that PhD students can sign up for free. Ordinary membership fee is merely 55 euros per year. If you sign up now for the year 2018, attending the winter meeting will be for free. Please register for the meeting **before 4 December** at:

http://www.bms-aned.nl/dnn/Archives/Archives2017/BMSANedfallmeeting2017.aspx.

Short Course (morning)

Title: Validating neuroimaging methods
Who: Dr Joke Durnez (Stanford University)
When: 10:00 – 12:00, 15 December 2017
Where: Room 412, Mathematical Institute, Neils Bohrweg 1
Costs: Free for IBS or VVS-OR members (10 euro otherwise), http://www.bms-aned.nl/dnn/

Course outline:

When analysing fMRI data, we assume that the statistical methods we use are thoroughly validated. However, Eklund (2016) recently showed how unrealistic assumptions on the data can render widespread statistical

inference procedures invalid, posing a threat to the entire scientific value of fMRI research. During this short workshop, I will show hands-on how we can validate statistical methods using simulations and real data.

With simulations, we can control the ground truth, which allows us to make claims about the statistical procedure with respect to its sensitivity and specificity. By varying properties of the data in a controlled way, we can get insight in how those properties affect the performance of a method.

However, all statistical methods make assumptions on the data, and many of those have been shown not to be valid in fMRI data. Only a few examples are stationarity, independence of measures and Gaussian noise. Therefore it is key to test and validate any statistical method using real data.

In this workshop, we will validate a simple statistical model by simulating fMRI data, as well as using data from the Human Connectome Project. After the workshop, attendees should be able to translate concepts of null models and methods performance to synthetic and real data.

BMS-ANed Winter Meeting (Afternoon)

Title: Biomedical Image Analysis
When: 13:00 – 17:00, 15 December 2017
Where: Havingazaal, Het Gorlaeus, Einsteinweg 55
Who: Dr Joke Durnez (Stanford University), Prof. Beatrijs Moerkerke (Ghent University), Prof. Christian Beckmann (Nijmegen University), Prof. Marie-Colette van Lieshout (CWI, Amsterdam)
Costs: Free for IBS or VVS-OR members (10 euro otherwise), http://www.bms-aned.nl/dnn/

13:00 – 13:15	**Opening** (announcement Van Houwelingen Award)
13:15 – 14:00	Marie-Colette van Lieshout (CWI, Twente)
14:00 – 14:45	Joke Durnez (Stanford)
14:45 – 15:15	**Break**
15:15 – 16:00	Beatrijs Moerkerke (Ghent)
16:00 – 16:45	Christian Beckmann (Nijmegen)
16:45 – 17:30	**Drinks**

Stochastic geometric models for image analysis – Marie-Colette van Lieshout (CWI, Amsterdam)

The new millennium has opened with what can only be described as a data explosion following advances in digital technology, a development that has led to a strong demand for tools for analysing digital data such as still images, video streams, audio signals, and text. In this talk, I shall focus on image and video data. As a field, statistical image analysis took off during the 1980s with the seminal work by Besag (1986) and Geman and Geman (1984) on the restoration of pictures degraded by noise. Much of the work in this period was focussed on `low level' tasks, that is, it aims to de-noise, sharpen, segment, or classify the image. With the

improvement in image quality, in the course of the 1990s, the emphasis has shifted towards the `high level' task of describing an image by its content, for example in terms of the objects it contains and the spatio-temporal relations between them. More recently, following theoretical advances in the field of random tessellations, the intermediate approach is popular that aims to maintain a global viewpoint without the need for a full scene modelling. In this talk, the listener will be introduced to thestochastic geometric models used in image analysis: from random fields to stochastic tessellations via Markov object processes.

Power and reproducibility in neuroimaging – Joke Durnez (Stanford)

There is increasing concern about statistical power in neuroimaging research. Over the past years, it has become clear that a large part of the literature is irreproducible and we need new tools and approaches to study the brain using neuroimaging. During this presentation, we will discuss how different parts of the scientific enterprise are not optimized for high-quality outputs.

One of the main culprits of the reproducibility crisis is low statistical power. During the second part of this presentation, I will present our recently developed interactive platform (www.neuropowertools.org) for sample size calculations and study design optimization. I will present a direct way to estimate power, and thus to optimize the sample size for neuroimaging experiments. Second, I will show recently developed tools to optimize the detection power within subjects. To this end, we use the genetic algorithm to optimize the experimental design, extended to allow complex experimental setups and a mix between blocked and event-related designs.

Meta-analyses of fMRI studies – Beatrijs Moerkerke (Ghent)

With the number of single neuroimaging studies flourishing, it is increasingly recognized that progress in understanding human brain function will not only require the acquisition of new data but a synthesis and integration of data across studies and labs (Yarkoni, Poldrack, Van Essen, Wager, 2010). Meta-analysis allows evaluating how findings within a domain replicate across studies. In this talk, I will talk about current practices in neuroimaging meta-analysis, highlight the difference between procedures and discuss remaining issues in dealing with meta-analytic data. I will specifically focus on publication bias. Meta-analyses of fMRI studies are prone to this bias when studies are excluded because they fail to show activation in specific regions. Further, some studies only report a limited number of local maxima that survive a statistical threshold resulting in an enormous loss of data. Coordinate-based techniques have been specifically developed to combine the available information of such studies in a meta-analysis. Potential publication bias then stems from two sources: exclusion of studies and missing information within studies due to censored reporting.

Big data for precision medicine: charting resting-state functional connectivity & connectopies

– Christian Beckmann (Nijmegen)

Large clinical and population cohort neuroimaging resources are increasingly coming online, forming a new field of imaging epidemiology. These offer a unified perspective that links brain connectional organization to behaviour and cognition. Currently, however, the full potential of these resources for understanding brain connectivity is not being realized. This is due to a lack of suitable analysis tools that explore relationships between and integrate across modalities, are sensitive to subtle changes in individual connectivity profiles and provide a means to move beyond simple case-control analysis towards understanding inter-individual differences in connectivity. In this talk I will outline novel approaches for charting the organisation of functional connectivity and introduce a ‘normative modelling’ strategy for utilising big cohort data for generating individualised predictions with application in clinical neuroimaging studies.