



Berufungsvorträge “Computational Medicine“

Die Berufungsvorträge schließen folgende Punkte mit ein:

Didaktischer Vortrag (30 Minuten)
Wissenschaftlicher Vortrag (45 Minuten)
Fragen/Pause (30 Minuten)
Kommissionelles Hearing -
(Dekanatsbesprechungszimmer, 11. Stock)

Dienstag, 22. Oktober 2019, SR 15

**Spiros Denaxas
(University College London)**

13:00 Uhr: Didaktischer Vortrag

“Methods for translational research using electronic health records”

Electronic Health Records (EHR) are a rich source of information on human health and disease and offer substantially larger phenotypic depth and breadth compared to traditional research-driven studies and clinical trials. This talk will demonstrate the opportunities and challenges of using EHR for translational research and cover methods for creating and validating disease phenotypes using complex heterogeneous data.

13:30 Uhr: Wissenschaftlicher Vortrag

“Data-driven approaches for extracting actionable knowledge from electronic health records”

Electronic Health Records (EHR) are data generated and captured during routine clinical interactions and offer a wealth of information on disease and its progression. EHR however are noisy, complex and biased and require a significant amount of pre-processing in order to be transformed to research-ready datasets. The talk will cover data-driven supervised and unsupervised phenotyping methods and approaches for deriving clinically meaningful and actionable knowledge from EHR data and showcase the opportunities and challenges of such data for research and care.

Mittwoch, 23. Oktober 2019, HS 2

**Ruth Pfeiffer
(National Cancer Institute, Bethesda, Maryland)**

13:00 Uhr: Didaktischer Vortrag

“The survival function: The Kaplan-Meier nonparametric estimate”

In many medical studies, the main outcome of interest is the time from disease diagnosis to an event such as death. Such event times are often called “survival times”, but the ideas also apply to other types of events. If all patients could be followed indefinitely, all the survival times would be observed, and the empirical distribution function $\hat{F}(t)$ of survival times could be computed. Its complement, $\hat{S}(t)=1-\hat{F}(t)$ is called the estimated survival distribution. However, some patients may drop out of the study (are lost to follow-up) or the study ends before their survival times are observed. Their survival times are said to be “censored”; one only knows that the censored survival time of interest exceeded the censoring time. I will describe a non-parametric estimate of $S(t)$, called the Kaplan-Meier (KM) curve, which is widely used in medical and other scientific applications. I will show how to test the difference between two KM curves at a given time point.

13:30 Uhr: Wissenschaftlicher Vortrag

“Building, updating and validating risk models for clinical practice and public health”

Statistical models that predict disease incidence, disease recurrence, or mortality following disease onset have broad public health and clinical applications. I introduce various definitions of “risk”. Of great importance are models that predict absolute risk (also called ‘cumulative incidence’ or ‘crude risk’), the probability that an individual who is free of a given disease at an initial age, a , will develop that disease in the subsequent interval $(a, t]$. Absolute risk is reduced by mortality from competing risks. I discuss approaches to building risk models by combining data from various sources, and how one can update models when data on new risk factors become available. Before a risk prediction model can be recommended for clinical or public health applications, one needs to assess how good the predictions are. I will present some general criteria for model assessment and some criteria I developed to assess the usefulness of such a model to make screening decisions. Accommodating missing model predictors is an area of ongoing work that I will present. I also highlight some challenges to improving model performance. To illustrate many ideas, I use a risk model I developed to predict incidence of breast cancer in US women.