Basel Biometrics Society Seminar
Basel, 4th February 2020

First announcement - BBS Seminar: Network meta-analysis: methods and applications

Date: Tuesday, February 4th, 2020, Time: 13:00 - 17:00
Venue: Roche Auditorium (to be determined), Basel

The BBS is pleased to host a half-day seminar on network meta-analysis methods and applications. The talks will present recent methodological advances and challenges as well as case studies from the pharmaceutical industry and academia. We welcome all quantitative scientists to this event, which will be a great opportunity to meet with colleagues and exchange ideas on this emerging and vibrant field.

The seminar is free of charge but registration is mandatory for organizational reasons. Please register via email to fred.sorenson@xcenda.com by Tuesday, January 21st, 2020, the latest.

Organizing committee: Máximo Carreras, Juliane Schäfer, Nicolas Städler.

Program:

13:00 - 13:10 Welcome and introduction

13:10 - 14:00 **Sylwia Bujkiewicz, University of Leicester**
Bivariate network meta-analysis for surrogate endpoint evaluation

14:00 - 14:50 **Gerta Rücker, University of Freiburg**
Component network meta-analysis compared to a matching method in a disconnected network: a case study

14:50 - 15:15 **Coffee break**

15:15 - 15:40 **Case study 1: Mark Pletscher, Roche**
Network meta-analysis of treatments for previously untreated metastatic PD-L1 positive triple-negative breast cancer

15:40 - 16:05 **Case study 2: Lilla Di Scala, Actelion**
An experience with indirect treatment comparisons using MAIC methods in a rare disease

16:05 - 16:30 **Case study 3: Marius Thomas, Novartis**
A network meta-analysis to compare treatment options for relapsing multiple sclerosis

16:30 - 17:00 **Panel discussion with all the speakers**

17:00 **Closure of the seminar**

We look forward to your participation!

Abstracts

Bivariate network meta-analysis for surrogate endpoint evaluation

Sylwia Bujkiewicz, University of Leicester

Surrogate endpoints are very important in health technology assessment (HTA) and regulatory decision-making in healthcare, in particular if they can be measured early compared to the long-term final clinical outcome and act as good predictors of clinical benefit. Bivariate meta-analysis methods can be used to evaluate candidate surrogate endpoints for their predictive value of treatment effect on the final outcome, by modelling the surrogate relationship between the treatment effects on the surrogate and final outcomes. However, such surrogacy patterns may vary depending on treatments' mechanism of action. This imposes a limitation on methods which do not differentiate between the treatments. To overcome this issue, we developed bivariate network meta-analysis (bvNMA) methods which combine data on treatment effects on the surrogate and final outcomes, from trials investigating multiple treatment contrasts (Bujkiewicz et al. 2019). The bvNMA methods estimate the effects on both outcomes for all treatment contrasts individually in a single analysis. At the same time, they allow us to model the trial-level surrogacy patterns within each treatment contrast and treatment-level surrogacy, thus enabling predictions of the treatment effect on the final outcome either for a new study in a new population or for a new treatment. Modelling assumptions about the between-studies heterogeneity and the network consistency, and their impact on predictions, will be discussed using an illustrative example in advanced colorectal cancer and in a simulation study. When the strength of the surrogate relationships varies across treatment contrasts, bvNMA has the advantage of identifying treatment comparisons for which surrogacy holds, thus leading to better predictions. Extensions to these methods will also be discussed.

Component network meta-analysis compared to a matching method in a disconnected network: a case study

Gerta Rücker, University of Freiburg

Network meta-analysis (NMA) is a method to combine evidence from randomized controlled trials that compare a number of different interventions for a given clinical condition. Usually, this requires a connected network. Otherwise, a possible approach is to add evidence from non-randomized trials, using propensity score or matching-adjusted indirect comparisons (MAIC) methods. However, nonrandomized comparisons may be associated with an unclear risk of bias. Schmitz et al. (2018) used single-arm observational studies for bridging the gap between two disconnected networks of treatments for multiple myeloma. We present a reanalysis of these data using component network meta-analysis (CNMA) models entirely based on RCTs, utilizing the fact that many of the treatments consisted of common treatment components occurring in both networks. We compare the results to those obtained by Schmitz et al. (2018). The CNMA models led to results similar to that obtained by Schmitz et al. (2018). We conclude that researchers encountering a disconnected network with treatments in different subnets having common components should consider a CNMA model. Such models, exclusively based on evidence from RCTs, are a promising alternative to matching approaches that need additional evidence from observational studies.