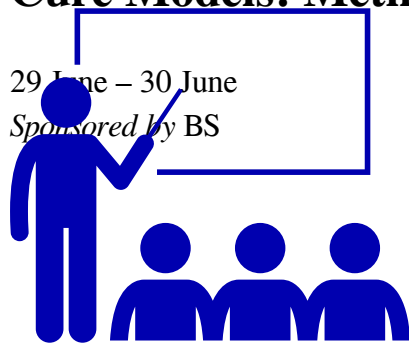


Cure Models: Methods, Applications, and Implementation



Instructors

Affiliated with Queen's University, Canada / AstraZeneca Oncology Biometrics, USA

Dr. Yingwei Peng

Yingwei Peng is a Professor of Biostatistics in the Departments of Public Health Sciences and Mathematics and Statistics at Queen's University and a senior Biostatistician at Queen's Cancer Research Institute. He has been an Associate Editor of the Canadian Journal of Statistics since 2010 and provided referee services to all mainstream statistical journals and Canadian federal funding agencies (NSERC and CIHR). He offered short courses on cure models, either by himself or with Jeremy Taylor (University of Michigan, USA), in Joint Statistical Meetings, ENAR Spring Meeting, and Université Catholique de Louvain, Belgium, in 2014. He is currently teaching online courses at Queen's University and has extensive experience in teaching with Zoom and Microsoft Teams software.

Dr. Binbing Yu

Binbing Yu is an Associate Director in AstraZeneca oncology biometric group. He has extensive experience in the applications of cure models in public health, clinical trials, and health economics and made notable contributions to the development and enhancement of cure modeling for the presentation and analysis of cancer survival data for the USA National Cancer Institute. He provides training and consultation and gives presentations regularly through Skype, Zoom, and Microsoft Teams software.

Course description

This course will provide a comprehensive introduction to cure models, including basics of the cure models as well as many recent developments related to the methodological issues and software implementations of cure models for right-censored time-to-event data subject to non-

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informative censoring. The course will feature real-world examples from clinical trials and population-based studies and a detailed introduction to R packages, SAS macros, and WinBUGS programs to fit some cure models. Applications of cure models in other disciplines will be discussed. This course will be useful for statistical researchers and graduate students, and practitioners in other disciplines to have a thorough review of modern cure model methodology and to seek appropriate cure models in applications.

Target audience

This course should appeal to a broad audience, including statisticians and graduate students in statistics/biostatistics as well as clinician-scientists, health researchers, health policymakers, and researchers in cancer research and the biopharmaceutical industry who have a good understanding of the basics of biostatistics. Graduate students in epidemiology, public health, and management who have strong training in biostatistics can also be benefited from this course.

Syllabus

This course will cover the following topics:

- Basics of parametric mixture and non-mixture cure models, the EM-based estimation methods, model assessment methods, some existing R packages, and SAS macros for parametric cure models, analysis of real-world data sets.
- Basics of the semiparametric and nonparametric mixture and non-mixture cure models, the estimation methods, and existing R packages and SAS macros illustrated with real-world data sets.
- Cure models for multivariate, recurrent-event, and competing-risks survival data based on both marginal and random-effects (frailty) approaches.
- Joint models of longitudinal and survival data with a cure fraction for clinical trial data analyses.
- Statistical testing for the existence and difference of cure rates and also the identifiability and sufficient follow-up issues in cure model estimation.
- New developments in Bayesian methods for cure models and general implementations of Bayesian analysis using BUGS program.
- Applications of cure models in the population-based cancer survival analysis.
- Statistical issues in the design and analysis of cancer clinical trials with a possible cure fraction and R programs of a suite of tools for applied researchers in clinical trials.

The instructors will provide course slides and software programs to the course participants. A recently published book on the topics by the authors is also available for purchase.

The course will be delivered via the GoToWebinar platform. Participants will have the opportunity to interact with the course instructors and practice data analysis using the software and data sets provided.

Required software

R, SAS, and WinBUGS programs may be used in the course. Some basic knowledge about the software program will be helpful.