

The 11th Conference of the IASC-ARS  
The Asian Regional Section  
of the International Association for Statistical Computing

# Book of Abstracts

See you  
in  
Kyoto!



Imadegawa Campus  
Doshisha University, Kyoto, JAPAN

21-24 Feb 2022

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IASC-ARS2022

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The Asian Regional Section of the International Association for Statistical Computing

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Imadegawa Campus, Doshisha University, Kyoto, Japan

<https://iasc-ars2022.org/>

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Data Science Everywhere:  
Innovations in Statistical Computing

# Preface

It is a great pleasure and honor to welcome you to the 11th regular conference of the Asian Regional Section (ARS) of the International Association for Statistical Computing (IASC).

The IASC-ARS has been established in 1993 to promote regional co-operation in pursuing the aims of the IASC. In particular, the IASC-ARS aims, in the Asia-Pacific context, to further the progress of the theory, methods, and practice of statistical computing and data science, and to foster interest and knowledge in effective and efficient statistical computing and data science.

The first regular conference of the IASC-ARS was held in Beijing in 1993, and since then, a total of 10 regular conferences have been held: Seoul (1995), Manila (1998), Busan (2002), Hong Kong (2005), Yokohama (2008), Taipei (2011), Seoul (2013), Singapore (2015) and Auckland (2017). And now, the 11th regular conference (IASC-ARS 2022) is held here in Kyoto with hybrid format. This IASC-ARS2022 was originally planned as the 12th conference, but because the 11th conference was cancelled twice due to severe local circumstances, this Kyoto conference was decided to be held as the 11th conference.

IASC-ARS2022 consists of Keynote Lecture, Invited Talk Session, Contributed Talk Session, and e-Poster Session. The theme is "Data Science Everywhere - Innovation in Statistical Computing", which is designed to discuss advanced statistical computing/computational statistics in a context where data science is becoming an essential part of any discipline. Presentations in the conference are thus cover a variety of topics in several areas and could be discussed with a very wide range of scientific audiences. To promote young statisticians, "Young Researcher/Student Award" will be given to some outstanding presentations from contributed talks and e-posters presented by young researchers/students.

IASC-ARS2022 is supported by the IASC, the Japanese Federation of Statistical Science Association and its six member societies, and the Institute of Statistical Mathematics (ISM). IASC-ARS2022 is also financially supported by the ISI Tokyo Congress Memorial Fund from the Japan Statistical Society, the grant from the ISM, Doshisha University, Kyoto city, NTT DATA Mathematical Systems Inc, and SAS Institute. We would express our gratitude to all persons and institutions who make IASC-ARS2022 possible: the colleagues from the Scientific Program Committee, the keynote and invited speakers, the

organizers of invited talk sessions and their speakers, the sponsors, Doshisha University, all staff of the conference, and all the people who contribute to the scientific program.

We believe that our IASC-ARS regular conference is a place not only for exchanging academic knowledges but also for deepening friendships with old and new friends. We would therefore hope you enjoy IASC-ARS2022 and look forward to an exciting conference.

Kyoto, February 2022

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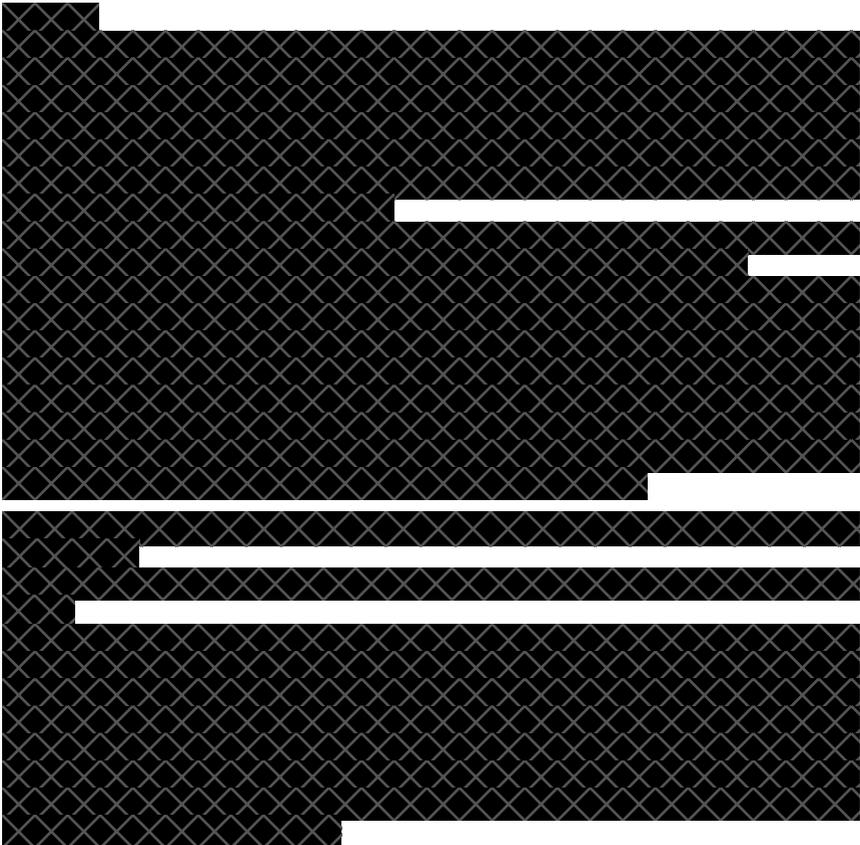
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### **Maximum likelihood estimation of hidden Markov models for continuous longitudinal data with missing responses and dropout**

Fulvia Pennoni (University of Milano-Bicocca, Italy), Francesco Bartolucci, Silvia Pandofi (University of Perugia, Italy)

We propose a Hidden Markov (HM) model for continuous longitudinal data with missing responses and dropout, thus extending the finite mixture model of multivariate Gaussian distributions. As known, the HM models assume the existence of an unobservable process, which follows a Markov chain with a discrete number of hidden states, affecting the distribution of the observed outcomes. We consider multivariate continuous responses that, for the same time occasion, are assumed to be correlated, according to a specific variance-covariance matrix, even conditionally on the latent states. For the analysis of such data, missing observations represent a relevant problem since dropout or non-monotone missing data patterns could occur. We propose an approach for inference with missing data by exploiting the steps of the Expectation-Maximization (EM) algorithm on the basis of suitable recursions. The resulting EM algorithm provides exact maximum likelihood estimates of model parameters under the missing-at-random (MAR)

assumption, where the missing patterns are independent of the missing responses given all the observed data. The resulting HM model accounts for different types of missing patterns: (i) partially missing outcomes at a given time occasion; (ii) completely missing outcomes at a given time occasion (intermittent pattern); (iii) dropout before the end of the period of observation (monotone pattern). The estimation algorithm is also employed when there are available covariates supposed to affect the distribution of the latent process and, in particular, the initial and the transition probabilities of the Markov chain. In this way, it is possible to identify latent or unobserved clusters of units with homogeneous behavior and understand the influence of the covariates on the dynamic allocation of the individuals between states over time.

The approach is illustrated by a Monte Carlo simulation study involving different scenarios. We also report an application based on the well-known primary biliary cholangitis dataset. These data are very sparse due to missing visits, and several dropouts occurred due to death. Continuous and binary covariates related to the patients are also available, allowing us to investigate how individual characteristics are associated with dropout risk. The application is particularly challenging and confirms the capability of the proposed method to deal with different types of missingness and to provide risk groups of patients derived by the model, which can be useful to make clinical decisions about therapy.