Identifying, randomizing, canonically analyzing and formulating mixed models for designs for comparative experiments using R

Date: Monday, 2 December 2019
Time: 9am – 5pm
**Location:** University of Adelaide, Waite Campus, Plant Research Centre Auditorium
Cost: AU$200 (IBS Member), AU$250 (Non-member), AU$100 (Concession)
URL: https://ausbiometric2019.org/workshops/

Brien (2017) outlines a mixed-model-based paradigm for obtaining A-optimal designs for comparative experiments and deriving, from the allocation involved in the design, an initial mixed model for data from an experiment that employs the design. This course explores the use of R packages od and dae for implementing this paradigm: the od package can be used, if required, to generate designs that are A-optimal for a specified mixed model; the dae package can be used to randomize designs and to perform canonical analyses (eigenanalysis) of designs. The canonical analysis is useful in elucidating the properties of a design and in formulating and checking a mixed model for it.

The course covers those basic concepts in experimental design that are necessary for using the paradigm. Methods for describing the factor allocation in a design and their use in producing a canonical analysis of the design are discussed, along with interpreting the canonical analysis. The formulation of allocation-based mixed models from the canonical analysis is also exposited. That is, the trail from the recognition in the planning stages of important sources of variation through constructing the design to the mixed model for data from the experiment using the design is followed. Participants will rehearse the techniques in practical sessions, using the R packages dae and od.

Ref: Brien, C. (2017). *Aust. N. Z. J. Stat.*, **59**, 327.
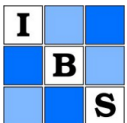
Chris Brien's (https://people.unisa.edu.au/Chris.Brien) career included positions at CSIRO Horticultural Research, Roseworthy Agricultural College and the University of South Australia (22 years). He retired in 2009 and is currently an Adjunct Associate Professor in Statistics with UniSA and more recently has been employed as a Senior Biostatistician at the Australian Plant Phenomics Facility, University of Adelaide. He has a substantial research record in the design and analysis of experiments, particularly multitiered experiments. He continues his work on multitiered experiments and is working in the area of high-throughput greenhouse experiments.

Sam Rogers has worked as a Biometrician in the Biometry Hub, University of Adelaide, since 2017. His work includes running professional development workshops for researchers using R, consulting on experimental design and analysis projects, and web and software development. His passions include statistical programming, writing elegant code, and helping people make use of their data.