## Two decades of work on LCMs

*by Wes Johnson & Ian Gardner*

Polychronis asked us to write a few words for the newsletter.  First, we would like to say that we wholly support the concept of the newsletter as a forum for the discussion of diagnostic outcome models with unknown disease status structure. We have collaborated on such models for about 20 years with a number of our amazing students.  As associate editors of several journals over a number of years we have probably handled more papers involving diagnostic outcomes than any other single topic, which is a direct indication that there has been and continues to be voluminous activity in the development of statistical methodology in this area.  We hasten to mention that there are new prospects for handling test data from multiple biomarkers.  Wes just read a paper last night that was modeling over 50 biomarkers considered to be related to a particular disease status.  With the current emphasis on genomic data, there are certainly situations with thousands of biomarkers. Recently developed methods for modeling multiple correlated longitudinal/trajectory data are ripe for use in jointly modeling trajectories and disease outcomes. A few illustrations of our joint work with former students are Hanson et. al. (2000), Norris et. al. (2009) and Jafarzadeh et al. (2016). Another topic that continues to require considerable attention is the issue of identifiability in latent class models, see for example Johnson and Hanson (2005) and Jones et. al. (2010).   For many more references including code for a broad range of LCMs, we refer the reader to the Bayesian Epidemiologic Screening Techniques (BEST) website, which is located at: http://cadms.ucdavis.edu/diagnostictests/

*Wes Johnson is a Professor of Statistics at the University of California, Irvine. Ian Gardner is a Professor and holds a Canada Excellence Research Chair in Aquatic Epidemiology at the University of Prince Edward Island, Canada.*

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# LCMATE mailing list: Back to the future

*By Polychronis Kostoulas*

Traditionally, a mailing list was comprised of physical mailing addresses that allowed businesses and societies to get in touch with people who have declared interest in receiving communication from them. With the advent of internet, the mailing lists evolved to e-mailing lists, a tool dominant in the last decade, only to be superseded by social networks that came in to fill the continuously increasing networking lust of our society. Yet, from Facebook, the pioneer in social networking, to more research-specific networks like LinkedIn, I somehow feel that what seems to have become an obsolete tool may still server as the best way to assist someone looking for help on



*"Mailing lists seem to have become an obsolete tool but may still serve as the best way to assist someone looking for help on a specific subject"*

a specific subject. And this is what I hope that the LCMATE mailing list will do for those interested in the development and application of latent class models (LCMs) for the evaluation of diagnostic tests.

**Polychronis Kostoulas** *is an Assistant Professor of Veterinary Epidemiology at the University of Thessaly, Greece and the LCMATE Administrator.*

# LCM research at the Université de Montréal's Veterinary Medicine Faculty

*By Simon Dufour*

In our veterinary school, we have developed a small, but growing, research program that make use of the LCM methodology. Most of the work completed to date relates to estimation of disease prevalence and diagnostic tests accuracy in the absence of a gold standard, with a large part of that research program focusing on health of cattle (e.g. Dufour et al., 2017; Buczinski et al., 2015; Paradis et al., 2012). To bridge the gap between the complexity of these models and practical field considerations, this research program was developed as a collaboration between clinically- (e.g. Sébastien Buczinski, David Francoz) and epidemiologically oriented (e.g. Simon Dufour, Denis Haine) scientists. The collaboration of Nandini Dendukuri, a statistician at McGill University (our close neighbour) is also of tremendous help to the success of this research program.

*"...to bridge the gap between the complexity of these models and practical considerations, this program was developed as a collaboration between clinically and epidemiologically-oriented scientists."*



Université de Montréal's Veterinary Medicine Faculty

Another area of research that we are pursuing is the use of LCM methods to adjust estimates of association between exposure and disease, when disease is measured using a test with imperfect accuracy Condas et al., 2017a; 2017b; Dufour et al., 2012). On this matter, we are particularly interested in the challenges coming from longitudinal study designs, for which health status must be determined both at the beginning (for identifying individuals at risk of disease) and during the study (for identifying incident cases). In these studies, using an imperfect test can introduce both a selection and a misclassification bias. In our recent work on this matter, conducted in collaboration with Ian Dohoo and Henrik Stryhn (U of Prince Edward Island), and Daniel Scholl (U of South Dakota) we demonstrated the magnitude and direction of these biases for common udder health scenarios (Haine et al., 2017). In the near future, we would like to propose and validate a LCM that could be used for post hoc control of these biases in longitudinal studies.

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# Software note:  Just Another Gibbs Sampler (JAGS)

*By Matthew Denwood*

JAGS is a fully open-source, cross-platform alternative to WinBUGS and OpenBUGS that can be used to run the majority of BUGS models without requiring any modification to the model code. JAGS also supports the use of distributions and functions defined in external C++ modules, which have been used (i) by JAGS developers to expand the default set of distributions within JAGS and (ii) by other users to define and use distributions that are specific to their application. For more information and to download JAGS, go to: http://mcmc-jags.sourceforge.net



Just Another Gibbs Sampler...

The JAGS website also houses an active support forum, but questions about LCMs in JAGS are actively welcomed on the LCMATE mailing list! The seamless integration of JAGS models within R is at the heart of the JAGS project, and the

rjags package provides a direct, low-level interface between R and JAGS.  To supplement this, the runjags package automates some of the more common model-fitting and checking procedures, and helps less experienced users find their feet with BUGS models.  There are also useful utilities such as automatic chain parallelisation, code generation for generalised linear mixed models, and conversion of existing WinBUGS project files containing model, data and initial value specifications.  To read more about the runjags package take a look at the open-access publication in the Journal of Statistical Software: https://www.jstatsoft.org/article/view/v071i09

Experienced users of WinBUGS who are just looking for a fast introduction to JAGS might be more interested in the following document:

"…JAGS supports the use of distributions and functions defined in external C++ modules, which can be used by users to define and use distributions that are specific to their application."

http://runjags.sourceforge.net/quickjags.html
Happy sampling!

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