

## **Hierarchical Generalised Linear Models (HGLM) relating bovine tuberculosis and milk production and quality in dairy cows**

Fiona Boland<sup>1</sup> and Gabrielle E. Kelly<sup>1</sup>

<sup>1</sup> UCD School of Mathematical Sciences, University College Dublin, Belfield, Dublin 4, Ireland

*Mycobacterium bovis* (*M. bovis*), the casual organism in bovine tuberculosis (TB) is an important infection of cattle in many countries, especially Ireland and the UK. Despite control measures the number of bovine TB infected cattle in Ireland has been approximately 24,000 animals per year for the three consecutive years 2004-2006. TB outbreak in a dairy herd causes monetary losses to the exchequer as the infected animals are slaughtered and farmers compensated but it also affects the farmer due to trade restrictions imposed on the whole herd. In recent years there has been intense research regarding the role of badgers (*Meles meles*) in bovine TB as they are seen as a reservoir of infection for cattle. For the first time in Ireland we examine the effects of bovine TB on milk production and quality. A random sample of Irish dairy herds restricted from trading with at least two or more TB infected animals between the 1st June 2004 and the 31st May 2005 is taken from veterinary records. Milk variables (fat, protein, milk yield) belonging to all lactations on an animal in the study are considered and TB and non-TB animals are compared on these variables. The TB data were obtained from the Department of Agriculture, Fisheries and Food (DAFF) and the milk production data comes from the Irish Cattle Breeding Foundation (ICBF). There is a defined hierarchical structure in the data, lactations are nested within animals and animals within herds. Since observations relating to lactations within an animal will be correlated and in addition the animals in the same herd will probably be correlated any model needs to incorporate these effects. HGLM's using the estimation methods of h-likelihood provide a useful class of models which do this. We consider such models incorporating both animal and herd level random effects as well as the fixed effects of TB/non-TB, parity, year and all their interactions. In addition HGLM's enable the variances of the random effects to be modelled. Likelihood criteria were used for both inclusion/exclusion of random and fixed effects to find the best model. Diagnostic plots were then examined and finally the implications of the results of the model and their implications for TB were interpreted. This practical example illustrates the novel use of HGLM's to model data with several random effects which occurs frequently in veterinary epidemiology.