

A Bayesian change-point recursive model: an application on litter size and number of stillborn piglets
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The purpose of this study was to develop a change-point recursive model for the investigation of the relationships between litter size (LS) and number of stillborn piglets (NSB). This approach allows to estimate the change point in the analysis of a multiple segment modelling of non linear relationships between phenotypes, and to consider the continuity between the change points. Field data were provided by a Large White selection nucleus from a commercial breeding company. The data file contained LS and NSB of 4462 farrows. After the analysis, 2 change points were located ($T_{1LS} \sim 16$ and $T_{2LS} \sim 20$). Different structural (regression) coefficients between the change points were also obtained, since their interval highest posterior densities at 95% did not included zero and they were not overlapped. However, posterior distributions of correlations were similar across groups of LS (between change points), except for those between residuals. Posterior means of the heritabilities were low and similar to those obtained in a previous study using standard mixed models. The posterior means of the structural coefficients showed negative effect of LS on NSB. The NSB would increase by 0.13, 0.16 and 0.20 piglets for each additional born piglet, respectively. These results confirm the existence of a non linear relationship between LS and NSB and it would support the adequacy of a change-point recursive model. Nevertheless, a suitable model comparison with different number of change points would be convenient.

MolabIS: effective management of data in molecular farm animal biodiversity studies
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Recent advances of biodiversity studies in farm animals have rapidly increased the amount of processed and stored molecular genetics data. In different labs, the methodologies and procedures of data handling are also different. Besides, complex experiment workflows and heterogeneous data formats make the management of genetic data more challenging. To address these problems, we have developed an Web-based integrated information system (MolabIS) to effectively collect and manage farm animal genetic data. Our formalized data model meets the most common demands of various molecular genetics labs. The application allows samples and experimental results to be captured and tracked easily at each step in the workflow from sample collection to DNA sequencing and microsatellite genotyping. Lab data might be searched, updated and reported quickly at different levels. Under the Open Source GNU public licence, MolabIS will be released as a free application.

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