# Bayesian calibration when old and new measurement methods are subject to sampling variation

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Molecular methods, such as quantitative real-time polymerase chain reaction (PCR), are replacing other types of assays for measuring the extent of biological contamination, for example fungal contamination in consignments of crop seeds and in soil. The molecular methods offer higher throughput than is available with traditional assays. Future use of any molecular method in such a context requires it to be calibrated against the traditional assay. If the old and new measurements are performed on separate samples from the consignments then they are both subject to sampling variation: they may also be subject to experimental errors. In order to take realistic account of the sources of variation affecting both methods, we consider a Bayesian solution to such calibration problems.

Aitchison and Dunsmore (1975) describe a Bayesian approach to calibration which leads to consideration of the prior distribution of the traditional measurement and the posterior predictive distribution of the new measurement for a future sample. Their approach assumes that measurements by the traditional method are precise: we consider a generalization that allows for sampling variation in both methods. Two illustrations are given in which the new method is quantitative PCR and the traditional methods involve counting spores of the fungus *Tilletia caries* taken from samples of wheat seed (Roberts, Theobald and McNeil 2007), and counting the number of seeds that are infected by the fungus *Microdochium nivale*.

## References

Aitchison, J. and Dunsmore, I.R. (1975), *Statistical Prediction Analysis*. Cambridge University Press.

Roberts, A.M.I., Theobald, C.M. and McNeil, M. (2007), Calibration of quantitative PCR assays, *Journal of Agricultural, Biological, and Environmental Statistics*, 12, 364-378