



Post-mortem modelling of pH and temperature in related lamb carcasses[☆]



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ABSTRACT

Exponential decay models have been used to model pH and temperature decline in lamb carcasses post mortem. Such models, once fitted to carcass data, can then be used to predict a carcass's pH at a temperature of 18 °C and its temperature when the pH equals 6. Unfortunately, these models frequently fail when fitted to limited pH/temperature data, because of either insufficient data or inappropriateness of the exponential decay model. To overcome these problems an alternative though similar modelling approach is proposed. This alternative approach replaces the exponential decay model with a more flexible spline modelling approach for the average trend and includes in the model, as random effects, individual deviations from average trend. Including the individual deviations from average trend as random effects in the model allows information on individual carcasses to be shared across carcasses.

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1. Introduction

The rate of post mortem pH and temperature decline can significantly impact on the resulting tenderness of meat (Hopkins et al., 2011). For optimal eating quality sheep meat destined for the domestic or overseas (air freight) markets should reach pH 6 when the carcass temperature is between 18 and 35 °C (Thompson et al., 2005). Research by the CRC for Sheep Industry Innovation has also shown that pH decline is an important covariate for the analysis of a number of meat quality traits (Warner et al., 2010). On this basis it is therefore essential to generate the best estimate of pH decline for each animal.

To jointly model pH and temperature in carcass muscle post mortem a number of models have been proposed. In a paper by Bruce, Scott, & Thompson (2001) an exponential decay model was proposed for modelling the decline for each trait separately with time. That is, $pH = A_{pH} + B_{pH} \exp(K_{pH} t)$ and $T = A_T + B_T \exp(K_T t)$ where t and T denote time and temperature respectively. The constants in each model, A , B and K , depend on the trait and hence the corresponding subscripts. In a later paper, Bruce (2004) suggested modelling pH directly as a function of temperature using the exponential decay model, that is $pH = \alpha + \beta \exp(\lambda T)$. As an application of this latter approach, that is modelling pH on temperature directly, Bruce (2004) fitted the model to 371 carcasses with a total of 1011

data points (i.e. less than 3 data points per carcass on average). Not surprisingly the model failed for 39 (10%) of the muscles, though it was concluded that the fitted models behaved well when they did converge.

It is not clear from the report of Bruce (2004) if there were any interrelationships across any or all of the 371 carcasses. Had some of the carcasses been related, for example by carcasses being subjected to the same chilling regime, then improvement in the model fitting could have been gained by jointly fitting a random effects exponential decay model to the related carcasses. In such cases the appropriate model to fit to the related carcasses, where pH_{ij} and T_{ij} denote the j th reading on the i th carcass for pH and temperature respectively, is;

$$pH_{ij} = \alpha_i + \beta_i \exp(\lambda_i T_{ij}) + \text{error}_{ij}. \quad (1)$$

The residuals in the above model will generally be assumed to be normally distributed with mean zero and variance σ^2 (i.e. $\text{error}_{ij} \sim N(0, \sigma^2)$). For the random effects model it is likewise, generally assumed that the parameters for the individual muscles ($\alpha_i, \beta_i, \lambda_i$), $i = 1, \dots, N$, are normally distributed. In particular, letting $\theta_i = (\alpha_i, \beta_i, \lambda_i)$, it is assumed that the θ_i are a random sample from a multivariate normal distribution having mean $\theta_0 = (\alpha_0, \beta_0, \lambda_0)$ and variance–covariance matrix Γ (i.e. $\theta_i \sim N_3(\theta_0, \Gamma)$).

In the special case when $\beta_i \lambda_i^2 \exp(\lambda_i T_{ij})$ is approximately zero for T_{ij} in its observable range, Model (1) can be approximated using a linear model. Modelling pH decline as a function of temperature in such cases using random effects modelling has been studied (van de Ven, Pearce, & Hopkins, 2011) in the context of determining the proportion of carcasses post mortem satisfying the pH decline criteria (i.e. pH equals 6 when 18 °C ≤ T ≤ 35 °C). van de Ven et al. (2011) clearly showed that

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estimation based on mixed effects modelling gave superior estimates to estimates based on fixed effects modelling. The more general case of the random effects exponential decay model, that is when the decline is not linear, has been studied in van de Ven, Pearce, and Hopkins (2012) and in such situations this modelling approach has also been shown to be superior to fixed effects modelling for this estimation problem.

One problem with modelling pH decline relative to temperature using Model (1) is that pH may not always monotonically decrease with temperature (Vetharaniam, Thomson, Devine, & Daly, 2010). In such cases, using Model (1) on the sampled data can result in failure, or worse, result in a totally inappropriate fit. Hence in this paper we propose an alternative modelling procedure to Model (1). In cases where the exponential decay model is appropriate our alternative model should perform as well as fit the exponential decay model, but will better accommodate those situations where there may be deviations from the exponential decay model, such as a non-monotone decline in pH with decreasing temperature. Having fitted the model to a sample of carcasses, the primary objective of this paper is to consider the problem of estimating, for each carcass, the pH when its temperature equals 18 °C and the temperature when its pH equals 6.

2. Material and methods

The model proposed in this paper for modelling pH against temperature across a sample of related muscles is composed of two separate parts which are subsequently combined to form one model. First, the model includes an overall (average) trend in pH with temperature decline across the carcasses. This overall trend is modelled as a natural cubic spline (Green & Silverman, 1994). Deviations in pH with temperature for individual carcasses about this overall trend are then modelled as linear in temperature with random deviations about the linear trend for each carcass. Such a model, where pH_{ij} and T_{ij} denote the j th reading on the i th carcass for pH and temperature respectively, can be written as;

$$pH_{ij} = \text{spline}(T_{ij}) + a_i + b_i T_{ij} + \text{error}_{ij}. \quad (2)$$

For the spline component of the model some constraints need to be imposed and these are discussed below. Before discussing these it is noted that spline modelling has an extensive history in the scientific literature, which is replete with examples, including Meyer (2005), Misztal (2006) and Verbyla, Cullis, Kenward, & Welham (1999). When fitting Model (2) we use a natural cubic spline with a fixed number of knot points (k say) at the $q \times 100/(k-1)$ percentiles of the observed temperature values across all related carcasses ($q = 0, 1, \dots, (k-1)$). In addition, we assume that the regression parameters associate with the individual carcasses (a_i, b_i), denoted by \mathbf{v}_i , are randomly sampled from a bi-variate normal distribution with mean 0 and variance-covariance \mathbf{T} (i.e. $\mathbf{v}_i \sim N_2(\mathbf{0}, \mathbf{T})$). The error _{ij} is assumed to be independently sampled from a normal distribution with mean zero and variance σ^2 (i.e. error _{ij} $\sim N(0, \sigma^2)$). There are a number of software packages available to fit Model (2) to pH decline data, including ASReml (Gilmour, Gogel, Cullis, & Thompson, 2009) and R (R Development Core Team, 2010) using the *lmer* function in the package lme4 (Bates, Maechler, & Bolker, 2011). It is the latter software package, freely available, that is used to generate results in this paper.

Two separate examinations of the above modelling approach were undertaken. First, a real life data set, comprising 51 carcasses, illustrating non-monotonicity in pH decline was considered. The observed data is plotted in Fig. 1a. Three separate modelling approaches were used to model the pH decline across the 51 carcasses. First, where possible, separate fixed effects exponential decay models (Bruce, 2004) were fitted to each carcass. Next, a random effects exponential decay model (van de Ven et al., 2012) was fitted jointly to the 51 carcasses. Thirdly, the modelling approach proposed in this paper, Model

(2), was applied to this data. For this example the spline was fitted with four knots at temperatures 3.1, 16.2, 24.9 and 39.9 °C.

The second examination of the proposed modelling procedure was a limited simulation study. The simulation study was undertaken to assess the appropriateness of Model (2) as a model for predicting each carcass's pH when its temperature equalled 18 °C and temperature when its pH equalled 6. The study is based on twelve parameter settings, each associated with one of the twelve actual observed data sets. These twelve data sets were randomly chosen from a large set of such data sets (van de Ven et al., 2011). For each of the twelve observed data sets a random effects exponential decay model, Model (1), was fitted. This gave, for each of the twelve data sets, estimates of the parameters θ_0 , Γ and σ^2 . These parameters, θ_0 , Γ and σ^2 , for each parameter settings are given in Table 1, but with the components of Γ given as standard deviations and correlations, rather than variances and co-variances.

For each of the twelve parameter settings given in Table 1, results were simulated for four pH/temperature readings on each of twenty carcasses. First, parameter vectors θ_i ($i = 1, \dots, 20$) were independently simulated from a multivariate normal distribution having the corresponding θ_0 and Γ for the given parameter setting. Next, the temperatures at which the four readings for each carcass were measured were simulated from symmetric triangle distributions on the intervals (30.75, 36.00), (25.50, 30.75), (20.25, 25.50) and (15.00, 20.25) °C respectively. Hence the average temperatures at the four sequential readings were 33.4, 28.1, 22.9 and 17.6 °C respectively. At each observed temperature, the pH for a carcass at that temperature T was simulated from a normal distribution having mean $\alpha_i + \beta_i \exp(\lambda_i T)$ and variance σ^2 , where $(\alpha_i, \beta_i, \lambda_i)$ were the components of the simulated θ_i and σ^2 as given for the particular parameter setting.

Having simulated four pH/temperature data readings for 20 carcasses, the model given by Model (2), i.e. a natural cubic spline for average trend with random linear deviations for carcasses, was fitted to the simulated data. The spline model in each simulation was fitted with four knots, with the four knots at the 0, 33.3, 66.7 and 100 percentiles for the simulated temperatures. The model was fitted using the *lmer* function in the R package lme4 (Bates et al., 2011), in conjunction with the *ns* function in R for forming the base matrix for the natural cubic spline. Having fitted the model, the *predict* function associated with spline models was used to predict the pH for a given temperature for each carcass. This in turn allowed each carcass's pH at a temperature of 18 °C (*pH@Temp18*) and its temperature when the pH is equal to 6 (*Temp@pH6*) to be estimated. These estimates were compared with the true values determined from the simulated parameters associated with the random effects exponential decay model. This simulation procedure was repeated 1000 times for each of the twelve parameter settings given in Table 1.

3. Results

The real life data set considered, plotted in Fig. 1a, shows that pH tends to decrease as temperature decreases to 15 °C but then increases, at least for some of the carcasses, as temperature declines from 15 °C to 5 °C. If exponential decay models are fitted to each carcass separately (i.e. fitted as fixed effects models) the model fails for 12 of the 51 carcasses. The fitted fixed effects exponential decay models, for the 39 carcasses where the model converged, are given as solid lines in Fig. 1b. Fitting a random effects exponential decay model to the data for the 51 carcasses gives the fitted models as represented by the solid lines in Fig. 1c. Here it can be seen that by its nature the exponential decay models are unable to capture the increase in pH for some of the carcasses as temperature declines from 15 °C to 5 °C. Finally, fitting Model (2) with a spline having four knots at temperatures 3.1, 16.2, 24.9 and 39.9 °C to the data, gives the fitted models represented by the solid lines in Fig. 1d.

In the remainder of this section the results of the limited simulation study undertaken are summarised.

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