



Consistency over time of spatial patterns of fibre diameter and staple length variation over sheep fleeces



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ABSTRACT

Macro-patterns of wool variation over sheep fleeces are markedly diverse among individuals. Assessing the *consistency over time* (i.e. repeatability) of those patterns would be relevant for sampling, individual selection, and raw wool classing, but there are no canonical procedures available to estimate the repeatability of 2D traits. We devised an approach to evaluate consistency over time as a proxy for repeatability in a 2D domain and applied it to a dataset of fibre diameter (FD) and staple length (SL) measurements. Data were collected over a regular grid of 128 sampling points from 10 Corriedale ewes sampled before shearing in two consecutive years. We scaled down the dimensionality of the data set from 128D to 2D, projected the new synthetic data ($n = 20$, one per animal per year) on principal coordinate axes, extracted all relevant Euclidean distances between pairs of data points, and applied an *ad hoc* coefficient (C_{sp}) designed to assess consistency of spatial patterns over time in a scale from zero (random dispersion independent of individual animal origin) to one (perfect overlapping of data points from the same animals in different years). Point estimates of C_{sp} (\pm bootstrap-estimated SE) were 0.78 ± 0.06 and 0.64 ± 0.08 for FD and SL, respectively. Estimated 95% confidence intervals excluded zero for both traits, FD: [0.60, 0.84]; SL: [0.43, 0.75]. Contributions of individual animals to overall C_{sp} coefficients were independent between traits ($r = -0.11$, $P = 0.76$). Main conclusions were that considering the spatial variability of wool traits over fleeces may help avoiding biases of phenotyping, estimation of genetic and phenotypic parameters, and selection decisions, that spatial patterns of variation of FD and SL over sheep fleeces are similarly repeatable across years, and that FD and SL pattern expressions may be independently regulated.

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1. Introduction

The fibre coat of sheep is produced by a population of epithelial appendages replicated according to a periodic pattern, a highly conserved trait in amniotes (Chung and Homberger, 2003). Morphogenetic mechanisms, strikingly similar across taxa, have already determined the

micro-structure of the spatial pattern of wool follicles over the skin by the time animals are born (Rogers, 2006). From then on, variation of raw wool traits over fleeces will depend upon (epi)genetic and environmental factors interacting at the wool follicle level; spatial *macro-patterns* will eventually emerge and presumably stabilize as individuals mature.

Macro-pattern features, such as gradients of variation over fleeces and regionalization of trait values, have been documented for a number of raw wool traits in different fibre-producing species (e.g., Angora goats: Newman and Paterson, 1999; alpaca: McGregor et al., 2012; sheep: Fish

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et al., 2002). We recently reported that when densely sampled at the scale of wool staples, fibre diameter (FD) and staple length (SL) show bilaterally symmetric spatial patterns characterized by non-linear trends over fleeces and ample variation among individuals, a result with possible implications for wool sampling, selection, and wool classing (Rodríguez Iglesias et al., 2009a,b, 2013). We also showed that sample point estimates of the repeatability of raw wool traits vary considerably over fleeces and that attributes of the spatial variation, such as the inter-sample distance required to ensure spatial independence of repeated measures, are also repeatable (Rodríguez Iglesias et al., 2013). In this study, instead of looking at the variation of the repeatability of raw wool traits over fleeces, we focused on estimating the consistency over time of the spatial macro-patterns themselves.

In an animal breeding context, repeatabilities of one-dimensional variables have precise meaning and associated estimation methods (e.g. Becker, 1992). That is not the case for traits expressing themselves in a higher-dimensional space, like fleece patterns. In particular, we are not aware of any general method of assessing the repeatability in time of unspecific 2D or 3D patterns. In this study we attempt to circumvent this limitation by first reducing the dimensionality of the problem, and then applying an *ad hoc* estimator of spatial consistency over time as a proxy of the repeatability of spatial patterns of wool traits over fleeces.

2. Materials and methods

2.1. Source of data

Data came from a 2-year observational field trial aimed at characterizing the spatial distribution of FD and SL over the fleece of adult Corriedale sheep. Full details on animals, sampling, and pattern visualization methods are offered in Rodríguez Iglesias et al. (2013). Briefly, following a regular grid pattern over the fleece, we collected 128 wool staples from the same 10 adult Corriedale ewes in two consecutive years. After allowing for ~340 d of growth, we removed staples (~1.5 cm of basal diameter) from the 120 intersection points of a rectangular grid of 10 longitudinal by 12 transverse lines plus 2 more sampling points from the upper part of each leg and aligned with the grid. We then determined FD in μm using an Optical Fibre Diameter Analyser (OFDA2000, Baxter et al., 1992) and assessed SL to the nearest 0.5 cm with the help of a ruler; both measurements were expressed as deviations from over-the-fleece means before analyses. Thus, for each trait the dataset consisted of 10 temporally correlated pairs of sets of 128 spatially correlated samples.

2.2. Visualization of spatial patterns

Using *ordinary kriging* for interpolation (Wackernagel, 2003) we mapped the spatial variation of each trait over the fleece for each individual in each year (Figs. 1 and 2). Kriging is an exact spatial interpolator routinely applied in many fields for mapping spatially referenced data collected in two or three dimensions. Maps are composed by producing massive interpolated predictions for unobserved locations using the original data while accounting for the spatial covariance between sampled points (as assessed by an experimental *variogram*) and their relative orientation. A moving neighbourhood of a minimum of 12 and a maximum of 24 samples was allowed to influence each point prediction. Maps consisted of 20,293 kriged points spread within a boundary shaped after a sheep pelt (Figs. 1 and 2). Predictions were generated using the VESPER software (Minasny et al., 2005) and plotted with S-Plus 2000 (MathSoft, 2000).

2.3. Assessment of pattern consistency over time

Apparently, there is no standard method for assessing the repeatability in time of unspecific spatial patterns. We reasoned that by reducing our 128D problem down to a 2D problem it would be possible to evaluate similarity in the same domain in which wool spatial patterns express themselves (i.e. wool follicles are arranged on a surface). For reducing dimensionality we applied a *metric multidimensional scaling* procedure (Johnson and Wichern, 2007). From a set of $n(n-1)/2$ measures of (dis)similarity between n items, multidimensional scaling generates a representation in few dimensions that attempts to match original (dis)similarities between items as closely as possible. For the sake of simplicity, we chose Euclidean distance as surrogate for similarity. When plotted on the 2D space determined by the first two *principal component* axes extracted from the original data, points corresponding to the 20 instances of spatial patterns for each trait (i.e. 10 animals by 2 years) would be expected to scatter according to whatever similarity was preserved through the scaling process.

If successive expressions of individual spatial patterns were consistently similar (i.e. repeatable in some sense), points corresponding to observations recorded on the same animal in consecutive years would be expected to lie closer to each other than to the rest of data points in the 2D domain. Those data pairs, in turn, would be closer to (or farther away from) other data pairs according to the (dis)similarity of patterns across animals. Following this logic, we formulated a measure of pattern consistency across years on the basis of calculating two sums of distances when n animals are evaluated twice:

$$\Sigma B = \sum_{i=1}^{n-1} \sum_{j=1}^2 \sum_{k=i+1}^n \sum_{l=1}^2 d_{ij,kl}; \quad l \neq j$$

where ΣB stands for sum of distances *between* animals, $d_{ij,kl}$ indicates Euclidean distance between animal i in year j and animal k in year l , provided measurements correspond to different years (i.e. when $l \neq j$), and

$$\Sigma W = \sum_{i=1}^n d_{1,i2}$$

where ΣW stands for sum of distances *within* animals.

A measure of *spatial pattern consistency* (C_{sp} , our surrogate for repeatability) was then synthesized on the basis of contrasting the average distance between repeated expressions of the spatial patterns of the same animals (i.e. *within* animals, $\Sigma W/n$) against the average distance between expressions of spatial patterns of different animals in different years (i.e. *between* animals, $\Sigma B/2C_2^n$) and expressing the difference relative to this latter term:

$$C_{sp} = \frac{\Sigma B/2C_2^n - \Sigma W/n}{\Sigma B/2C_2^n}$$

This C_{sp} coefficient will be equal to one when data points within animals across years superimpose exactly (i.e. when $\Sigma W=0$) and it will be equal to zero when the average distance *within* animals equals the average distance *between* animals (i.e., $\Sigma W/n = \Sigma B/2C_2^n$). Negative estimates are mathematically possible, i.e. when the average distance *within* animals turns out to be larger than the average distance *between* them, but biologically unreasonable. It would be hard to imagine any systematic biological process inducing less average similarity among instances of spatial patterns coming from the same rather than from different animals. In other words,

$$\text{if } 0 \leq \Sigma W/n \leq \Sigma B/2C_2^n \text{ then } 0 \leq C_{sp} \leq 1$$

for any biologically reasonable data set.

As it could be expected, C_{sp} will tend towards zero as the distribution of data points in the 2D domain approaches randomness in spite of the common origin (same animal) of individual points within data pairs. Although for very low n random samples may occasionally render small negative estimates of C_{sp} (simply due to sampling variation), estimates tend quickly towards zero as n increases (Rodríguez Iglesias et al., unpublished simulation results) thus ensuring a non-negative parameter space for any reasonable n .

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