

A hierarchical tensor framework for quantitative multiscale and multidirectional biomedical texture characterization

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Abstract. Histological images of skeletal muscle contain organization at several spatial scales and in several directions, from the edges of individual fibres to the arrangement of fibre bundles, yet texture analysis usually reports single-scale, orientation-averaged descriptors. This study formulates a hierarchical descriptor tensor indexed by descriptor channel, Gaussian scale, orientation and region of interest (ROI), derives its main analytical properties, and applies it to two published haematoxylin and eosin (H&E) cross-sections of normal skeletal muscle, one human and one from the fish *Pangasianodon hypophthalmus*. Ten channels (directional-derivative statistics, grey-level co-occurrence features and autocorrelation) were evaluated at four scales (1, 2, 4, 8 px) and four orientations, for one ROI (160 entries per image) and four ROIs (640 entries). The theory shows that the directional-energy block is a quadratic form of the regional structure matrix, so that four orientations determine the anisotropy index A and the texture axis exactly, and that pooling regions can only lower A . Against isotropic surrogates with the same radial spectrum, both images were anisotropic ($A = 0.208$ and 0.387 ; surrogate 95th percentile 0.008 and 0.011 ; $P \leq 0.005$). The texture axis agreed with the structure-tensor field, with the ordering of directional correlation lengths and, for the fish image, with the long-axis orientation of 207 segmented fibres (difference 1.4°). Four ROIs revealed regional heterogeneity that a single ROI attenuated (13% in the human image). Gradient channels were nearly collinear (Spearman $\rho \geq 0.98$), and co-occurrence contrast and correlation, linked by an exact variogram identity, decoupled on tissue. The results establish interpretable, internally consistent readings on real human and veterinary muscle histology; diagnostic value is not claimed.

Keywords: skeletal muscle histology, texture analysis, descriptor tensor, anisotropy, structure tensor, multiscale analysis, fish muscle, *Pangasianodon hypophthalmus*, quantitative histology.

Introduction. Skeletal muscle is one of the tissues in which histological architecture is most directly linked to function. In transverse sections stained with haematoxylin and eosin (H&E), fibres appear as polygonal profiles with peripheral nuclei, separated by endomysium and grouped into fascicles by perimysium; departures from this pattern (variation of fibre size and shape, widening of interstitial spaces, central nuclei, fibre splitting or disorganization) are the basic vocabulary of muscle pathology (Trovato et al., 2016; Nix & Moore, 2020). In fish, the same features are used to assess the quality of fillets, the effect of environmental and dietary conditions, and post-mortem changes such as freezing damage (Abdel-Latif et al., 2023; Strateva & Penchev, 2021), and the histology of small poeciliid fish is routinely used in toxicological testing (Țălu et al., 2012). These assessments are mostly qualitative or rely on segmentation of individual fibres, which is reliable only when fibres are well separated.

Texture analysis offers a complementary route that does not require segmentation: it describes how image intensity varies in space, through statistics of intensity differences, co-occurrences, filter responses or scaling behaviour (Ghalati et al., 2022; Di Cataldo & Ficarra, 2017; Haralick et al., 1973; Țălu, 2012b). Fractal, multifractal and lacunarity descriptors, which quantify scale-dependent complexity, have been applied to retinal and other biomedical images (Țălu & Giovanzana, 2011, 2012; Țălu, 2012a, 2013a, 2013b; Țălu et al., 2013; Ștefănuț et al., 2013), to biological and tissue surfaces

(Tălu, 2015; Tălu et al., 2015; Garczyk et al., 2017; Solaymani et al., 2019), to multimodal medical image fusion (Tălu, 2026b) and to aquaculture (Petrescu-Mag et al., 2026). Its use in biomedical images has been reviewed extensively (Ghalati et al., 2022; Di Cataldo & Ficarra, 2017; Gurcan et al., 2009), and standardization efforts have defined many radiomic features and filters precisely (Zwanenburg et al., 2020). Two difficulties remain. First, texture depends jointly on the scale at which it is observed, the direction in which it is probed and the region over which it is summarized (Depeursinge, 2017); a single number per descriptor hides this dependence. Second, descriptor values depend on the computational configuration (kernel, offset, quantization, region, boundary handling), which is often under-reported (Zwanenburg et al., 2020; Traverso et al., 2018). In muscle histology, where fibre outlines provide oriented edges at a scale set by the interfibre spaces and fibre bundles provide structure at a coarser scale, both difficulties are directly relevant.

The present study addresses them with a hierarchical descriptor tensor that keeps scale, orientation and region as separate indices of every measurement. The framework was first applied to the skeletal muscle of the guppy *Poecilia reticulata* in a companion paper (Tălu, 2026c); here the tensor is written in a form adapted to tissue analysis, its analytical properties that matter for interpretation are derived (Section 2), and it is applied to two published H&E images of normal skeletal muscle, one human (Trovato et al., 2016) and one from the fish *Pangasianodon hypophthalmus* (Abdel-Latif et al., 2023) (Sections 3–4).

Because real tissue has no known ground truth, the evaluation relies on three kinds of evidence: comparison with isotropic surrogate images, agreement with independent estimators of orientation and spatial correlation computed from the same image, and, where fibres can be segmented, agreement with a morphometric measurement. The aim is to establish whether the tensor yields interpretable and internally consistent readings on real muscle histology, as a step towards the multidimensional, measurement-based frameworks proposed for translational human and veterinary medicine (Tălu, 2026a), not to evaluate diagnostic performance.

Theoretical framework

Hierarchical descriptor tensor. Let $f(\mathbf{x})$, $\mathbf{x} \in \Omega \subset \mathbb{R}^2$, be the luminance of an H&E image, standardized to zero mean and unit variance. Structure at scale s is probed through the Gaussian scale-space $G_s = g_s * f$, where g_s is the isotropic Gaussian of standard deviation s (Lindeberg, 1998). Directional sensitivity is introduced by the unit vector $\mathbf{u}_\theta = (\cos\theta, \sin\theta)^\top$ (angle measured counter-clockwise from the image rows, with the y axis pointing upward) and the steerable directional derivatives (Freeman & Adelson, 1991)

$$\partial_\theta G_s = \mathbf{u}_\theta \cdot \nabla G_s, \quad \partial_\theta^2 G_s = \mathbf{u}_\theta^\top \nabla \nabla^\top G_s \mathbf{u}_\theta \quad (1)$$

For a set of regions $\Omega_1, \dots, \Omega_R \subseteq \Omega$, each channel m maps a local response to a regional summary $D_m(s, \theta, \Omega_r)$. Sampling K scales and L orientations, the measurements form the fourth-order array

$$\mathfrak{D} \in \mathbb{R}^{M \times K \times L \times R}, \quad \mathfrak{D}_{mklr} = D_m(s_k, \theta_l, \Omega_r) \quad (2)$$

The indices are kept separate on purpose: a value is meaningful only with its scale, orientation and region. In the reference configuration there are $M = 10$ channels (Table 1), $K = 4$ scales ($s = 1, 2, 4, 8$ px), $L = 4$ orientations ($\theta = 0, \pi/4, \pi/2, 3\pi/4$) and $R = 1$ or $R = 4$ regions, giving 160 or 640 entries per image (Figure 1). Filters are applied to the whole image with reflective boundaries and only the aggregation is restricted to Ω_r , so region borders do not create artificial edges.

From image to descriptor tensor: scale, orientation, region and stability

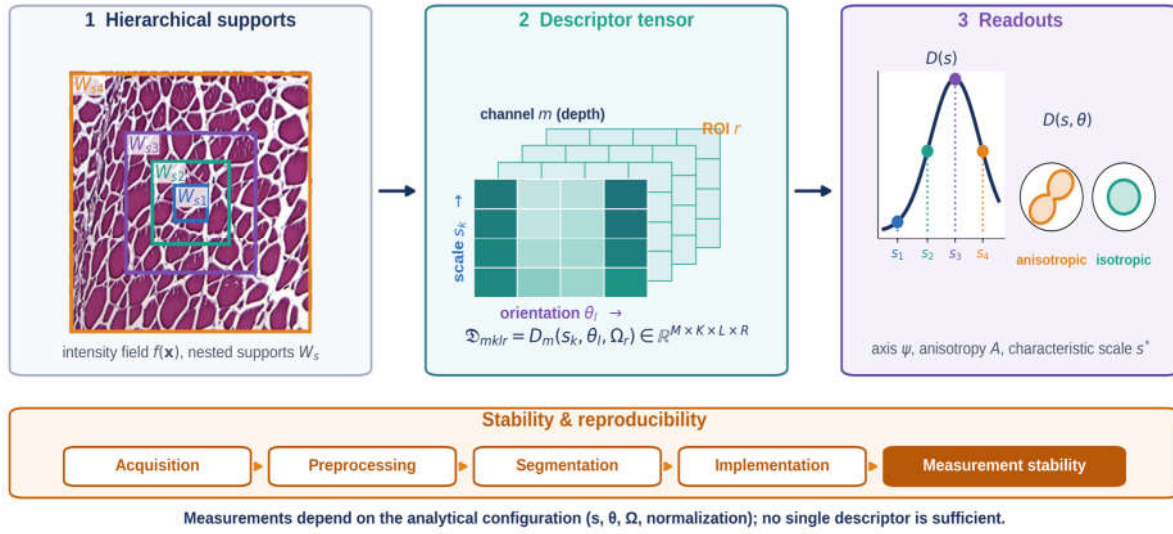


Figure 1. From image to descriptor tensor. (1) Nested spatial supports W_s of increasing scale on an H&E section of *P. hypophthalmus* muscle (image from (Abdel-Latif et al., 2023), CC BY 4.0). (2) The tensor $\mathfrak{D}_{mklr} = D_m(s_k, \theta_l, \Omega_r)$ with its four indices: channel, scale, orientation and ROI. (3) Readouts: the scale profile $D(s)$ with a characteristic scale s^* , and the directional profile $D(s, \theta)$ with anisotropy index A and texture axis ψ . Bottom: stability and reproducibility as an assessment layer applied to the measurement pipeline.

Table 1

Channels of the descriptor tensor.

All channels are evaluated for every $(s_k, \theta_l, \Omega_r)$; $\langle \cdot \rangle_r$ is the mean over Ω_r .

Channel	Definition	Type
D1	$\langle \partial_\theta G_s \rangle_r$	Gradient amplitude
D2	$\langle (\partial_\theta G_s)^2 \rangle_r$ (Directional energy)	Gradient energy
D3	Kurtosis of $\partial_\theta G_s$ over Ω_r	Gradient distribution
D4	Shannon entropy of $\partial_\theta G_s$ (32 bins over ± 4 SD, bits)	Shape
D5	$\langle \partial_\theta^2 G_s \rangle_r$	Gradient distribution shape
D6–D9	GLCM contrast, homogeneity, energy, correlation of G_s (16 levels; symmetric offsets $\pm d$, $d = s$ along θ , rounded to integer pixels)	Second-derivative amplitude
D10	Normalized autocorrelation of G_s at lag $2s$ along $\pm \theta$	Co-occurrence (Haralick et al., 1973)
		Spatial correlation

Directional energy as a quadratic form. Define the regional second-moment (structure) matrix (Bigün & Granlund, 1987)

$$\mathbf{J}_{s,r} = \langle \nabla G_s \nabla G_s^\top \rangle_r = \begin{pmatrix} J_{xx} & J_{xy} \\ J_{xy} & J_{yy} \end{pmatrix} \quad (3)$$

Proposition 1. For every scale and region, $D_2(s, \theta, \Omega_r) = \mathbf{u}_\theta^\top \mathbf{J}_{s,r} \mathbf{u}_\theta$, that is

$$D_2(\theta) = 1/2 (\lambda_+ + \lambda_-) + 1/2 (\lambda_+ - \lambda_-) \cos 2(\theta - \varphi) \quad (4)$$

where $\lambda_+ \geq \lambda_-$ are the eigenvalues of $\mathbf{J}_{s,r}$ and φ the direction of its leading eigenvector. With the configured orientations, $J_{xx} = D_2(0)$, $J_{yy} = D_2(\pi/2)$ and $J_{xy} = 1/2 [D_2(\pi/4) - D_2(3\pi/4)]$.

Proof. $\partial_\theta G_s$ is linear in $\mathbf{u}_\theta$, so $(\partial_\theta G_s)^2 = \mathbf{u}_\theta^\top \nabla G_s \nabla G_s^\top \mathbf{u}_\theta$; averaging over Ω_r gives the quadratic form, and the spectral decomposition of $\mathbf{J}_{s,r}$ gives (4). Evaluating (4) at $0, \pi/2, \pi/4, 3\pi/4$ gives the three entries. ▀

Three consequences are used throughout. First, the anisotropy index and the texture axis

$$A = \frac{\max_{\theta} D_2 - \min_{\theta} D_2}{\max_{\theta} D_2 + \min_{\theta} D_2} = \frac{\lambda_+ - \lambda_-}{\lambda_+ + \lambda_-}, \quad \psi = \varphi + \frac{\pi}{2} \pmod{\pi} \quad (5)$$

are determined exactly by the four tensor entries, although the true axis need not coincide with a configured orientation. Reading A directly from the four sampled values gives a lower bound A_4 with $A/\sqrt{2} \leq A_4 \leq A$; for this reason A and ψ are computed from (5). Second, the four entries satisfy $D_2(0) + D_2(\pi/2) = D_2(\pi/4) + D_2(3\pi/4)$, which is a computational check. Third, with the doubled-angle field $z_s = (\partial_x G_s + i \partial_y G_s)^2$, $A = |\langle z_s \rangle_r| / |\langle |z_s| \rangle_r|$: the anisotropy index is the energy-weighted mean resultant length of the doubled gradient directions (Mardia & Jupp, 2000). In a transverse muscle section, gradients are perpendicular to fibre boundaries, so ψ is the dominant direction of the boundaries and interfibre spaces in the image plane, and A measures how consistently they share it.

The same quantities define a local field. Replacing the regional mean in (3) by a Gaussian-weighted local mean of width ρ gives the structure-tensor field $\mathbf{J}_{s,\rho}(\mathbf{x})$, whose local axis and coherence $\kappa = (\lambda_+ - \lambda_-)/(\lambda_+ + \lambda_-)$ describe how orientation varies across the section (Bigün & Granlund, 1987). The regional A and the mean local κ are not the same quantity: A is high only if local orientations agree across the region.

Regional aggregation: the pooling inequality. The ROI index of the tensor allows a section to be summarized either as one region or as several. For mean-type channels (D1, D2, D5 and the elements of $\mathbf{J}$), the summary of a union of equal-area regions is the mean of the regional summaries. The anisotropy index is not additive in this way.

Proposition 2 (pooling inequality). Let $\Omega = \bigcup_{r=1}^R \Omega_r$ be a partition into regions of equal area, with regional anisotropy A_r and regional energy $E_r = \text{tr} \mathbf{J}_{s,r}$. Then

$$A(\Omega) \leq \frac{\sum_r E_r A_r}{\sum_r E_r} \quad (6)$$

with equality if and only if all regions with $A_r > 0$ have the same texture axis.

Proof. With equal areas, $\langle z_s \rangle_\Omega = R^{-1} \sum_r \langle z_s \rangle_r$ and $\langle |z_s| \rangle_\Omega = R^{-1} \sum_r E_r$. Since $|\langle z_s \rangle_r| = A_r E_r$, the triangle inequality gives $A(\Omega) = |\langle z_s \rangle_\Omega| / \langle |z_s| \rangle_\Omega \leq \sum_r A_r E_r / \sum_r E_r$, with equality if and only if the complex numbers $\langle z_s \rangle_r$ have the same argument, i.e. the same ψ . ▀

Proposition 2 makes precise a point that is often stated qualitatively: aggregating a heterogeneous region attenuates directional organization, and the attenuation is a direct measure of the disagreement between regional axes. The ratio $A(\Omega) / \sum_r E_r A_r / \sum_r E_r$ is therefore a scale-specific index of directional coherence across the section.

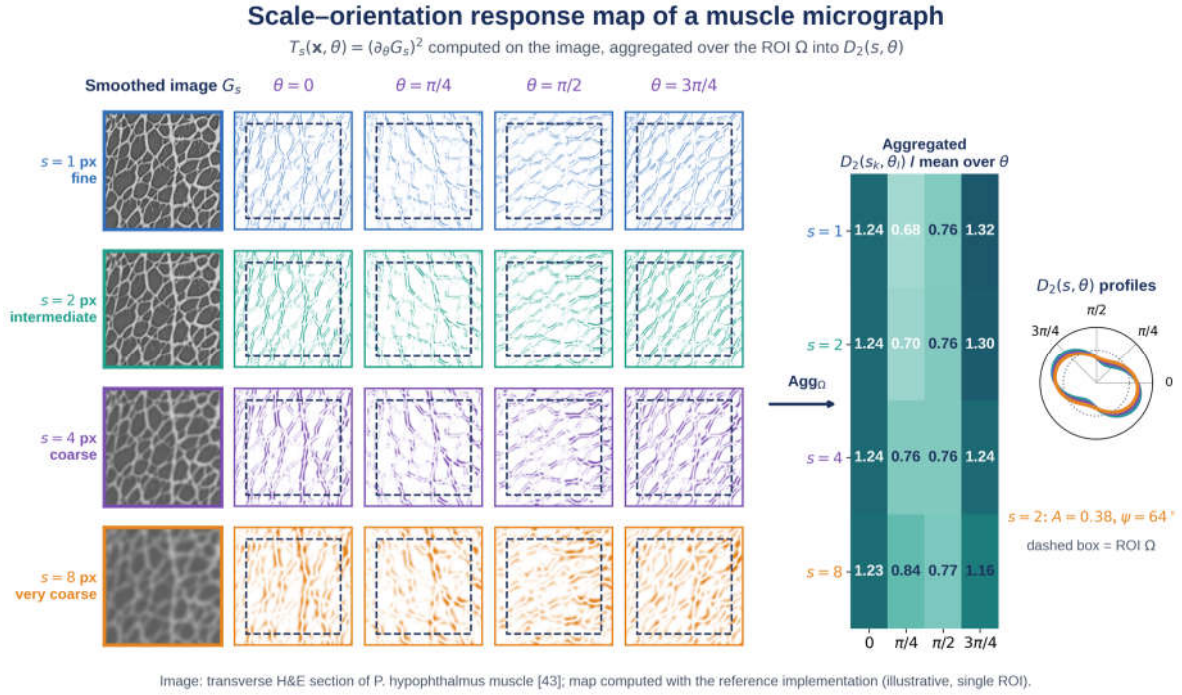


Figure 2. Scale–orientation response of a muscle micrograph. Left: smoothed image G_s and local energy maps $T_s(\mathbf{x}, \theta) = (\partial_\theta G_s)^2$ for $s = 1, 2, 4, 8$ px and $\theta = 0, \pi/4, \pi/2, 3\pi/4$; dashed box: ROI Ω . Right: aggregated block $D_2(s_k, \theta_i)$ divided by its mean over θ , and polar profiles $D_2(s, \theta)$ (at $s = 2$ px, $A = 0.38$, $\psi = 64^\circ$; values from the illustrative single-ROI configuration of this figure). Image: transverse H&E section of *P. hypophthalmus* muscle, reproduced from (Abdel-Latif et al., 2023) under the CC BY 4.0 licence.

Scale: variance loss and characteristic scale. Because the Gaussian scale-space satisfies the diffusion equation $\partial_t G = \Delta G$ with $t = s^2/2$, the variance $V(s) = \langle G_s^2 \rangle$ decreases with scale at a rate given by the total gradient energy. Under periodic or no-flux boundaries,

$$s^2 \text{tr} \mathbf{J}_s = -\frac{1}{2} \frac{dV}{d \ln s} \quad (7)$$

so the scale-normalized energy $s^2 \text{tr} \mathbf{J}_s$ (Lindeberg, 1998) is the rate at which image variance is lost per unit of log-scale (Figure 2). Its maximum s^* marks the scale at which the image loses most variance, i.e. the dominant width of its intensity transitions. For Gaussian random-field images, the characteristic scale corresponds to the correlation length; in tissues with sharp boundaries, however, this equivalence does not hold, and the scale is interpreted as a descriptor-specific indicator of the width of the dominant edges. A tissue whose variance is lost evenly over a range of scales shows a plateau rather than a peak.

Spatial correlation: autocovariance, correlation length and co-occurrence. Let $C_s(\mathbf{h}) = \langle G_s(\mathbf{x}) G_s(\mathbf{x} + \mathbf{h}) \rangle$ be the autocovariance of the smoothed image and $\gamma_s(\mathbf{h}) = C_s(\mathbf{0}) - C_s(\mathbf{h})$ its semivariogram. Then

$$\mathbf{J}_s = -\nabla \nabla^T C_s(\mathbf{0}), \quad D_2(s, \theta) = \lim_{h \rightarrow 0} \frac{2\gamma_s(h\mathbf{u}_\theta)}{h^2} \quad (8)$$

so D_2 is the curvature of the autocovariance at the origin along θ : high directional energy corresponds to a rapid loss of correlation in that direction. At finite lags this motivates the directional correlation length $\xi(\theta)$, the lag at which the normalized autocorrelation falls to $1/e$ along θ ; ξ is expected to be shortest where D_2 is largest, but because it is measured at finite lag it weights coarser structure than D_2 at small s . The co-occurrence

channels have the same variogram structure. For the symmetric co-occurrence matrix of the quantized image Q at offset $\mathbf{d}$, the two marginals are equal, so contrast and correlation satisfy the identity

$$D_6 = 2\gamma_Q(\mathbf{d}), \quad D_9 = 1 - \frac{\gamma_Q(\mathbf{d})}{\sigma_Q^2}, \quad D_6 = 2\sigma_Q^2(1 - D_9) \quad (9)$$

where σ_Q^2 is the variance of Q over the pairs anchored in the region. D_6 and D_9 therefore carry the same information *only if* σ_Q^2 is constant across the entries compared; when σ_Q^2 varies with scale and region, as it does in tissue, their rank correlation weakens even though each entry obeys (9) exactly.

Reference for isotropy and uncertainty. A real image has no replicate realizations and no ground truth. Two constructions provide the missing references. (i) *Isotropic surrogates*: for each image, surrogate fields are generated from the radially averaged Fourier amplitude of the image with uniformly random phases (Theiler et al., 1992). They have no preferred direction but the same radial spectrum, hence the same finite-sample floor of A , which depends on ROI size and correlation scale; an observed A is compared with the 95th percentile of A over the surrogates. (ii) *Block bootstrap*: each ROI is divided into blocks that are resampled with replacement (Künsch, 1989), and percentile intervals of A and ψ are reported. Surrogates test departure from an isotropic spectrum; they are Gaussian and do not reproduce the non-Gaussian intensity distribution of stained tissue.

Material and Method

Test images. Figure 3 shows a transverse section of normal human skeletal muscle (Trovato et al., 2016) and Figure 4 a transverse section of normal dorsal muscle of *P. hypophthalmus* from a control group (Abdel-Latif et al., 2023). In both, fibres appear as polygonal profiles separated by endomysial connective tissue; in Figure 4 the interfibre spaces are wide and clear.

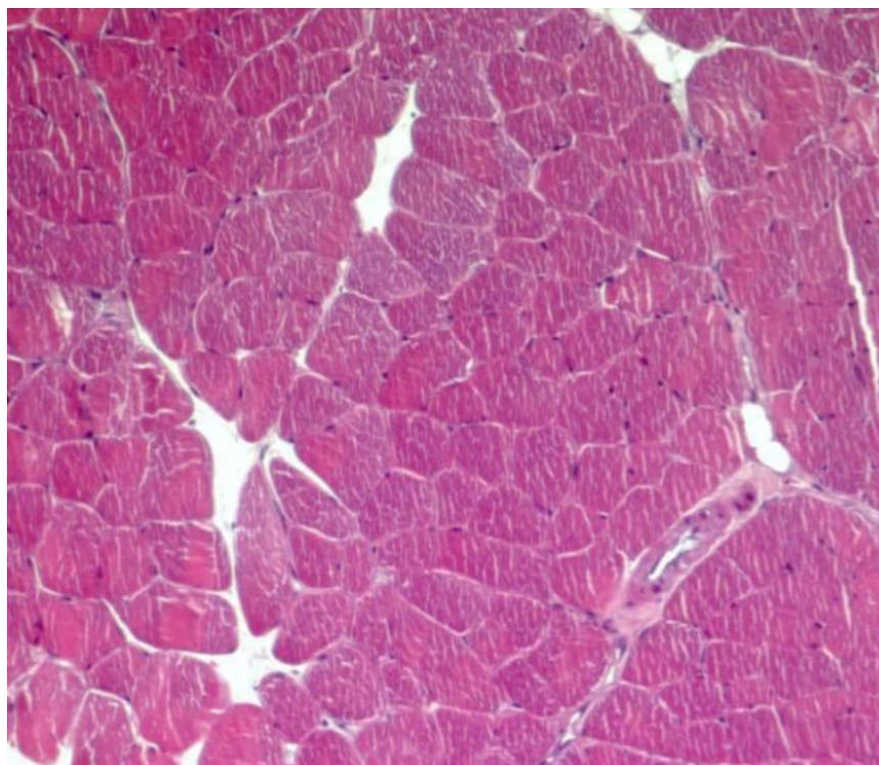


Figure 3. Representative hematoxylin and eosin (H&E)-stained cross-section of normal human skeletal muscle (10× magnification), showing muscle fibers of relatively uniform size arranged in bundles and surrounded by endomysium. Peripheral nuclei are stained dark purple, while the sarcoplasm is uniformly pink. Reproduced from Trovato et al. (2016).

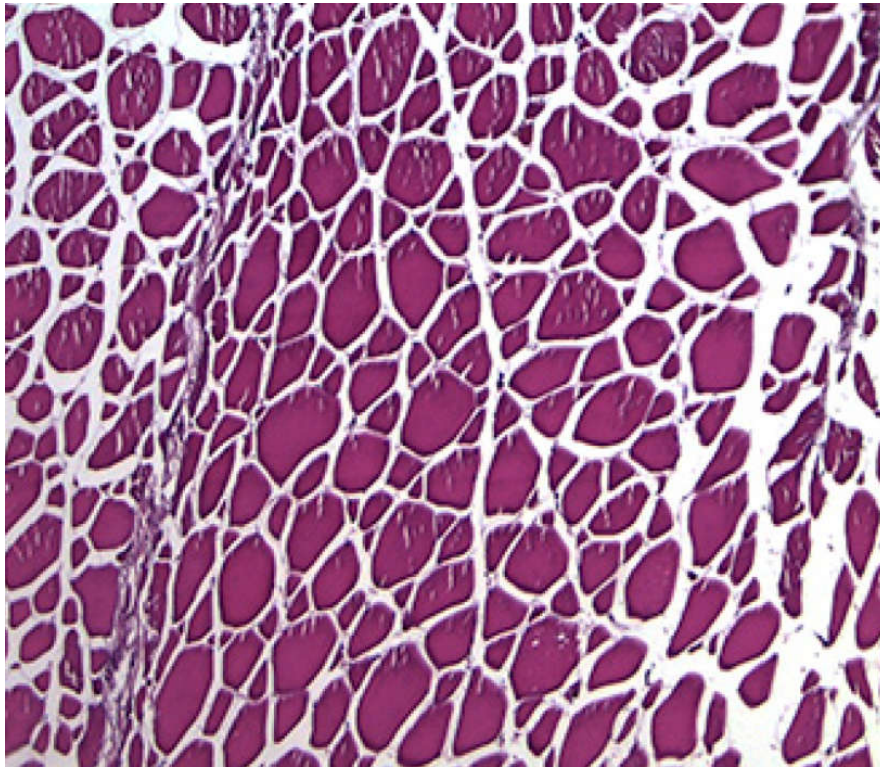


Figure 4. Representative photomicrograph of normal dorsal skeletal muscle tissue from *Pangasianodon hypophthalmus* (pangasius), stained with hematoxylin and eosin (H&E), showing normal muscle striation and histological architecture. Control group. Scale bar: 50 μ m. Reproduced from Abdel-Latif et al. (2023).

Image sources and permission to reproduce. Figure 3 is reproduced from Trovato et al. (Trovato et al., 2016), *Journal of Functional Morphology and Kinesiology* (MDPI), and Figure 4 from Abdel-Latif et al. (Abdel-Latif et al., 2023), *Fishes* (MDPI). Both articles are open access and distributed under the Creative Commons Attribution (CC BY 4.0) licence, which permits reuse, adaptation and redistribution in any medium provided that the original work is properly cited; no further permission is required. The images are reproduced unchanged except for resizing, and all derived panels (Figures 2 and 5–11) are new analyses produced by the author. The source publications are cited in each caption.

Analysis configuration. The images were analyzed as supplied (rasters of 861×741 px and 815×705 px). The raster of Figure 4 available for analysis does not contain the 50 μ m scale bar mentioned in its original caption, and the pixel size of neither image is known; all lengths are therefore expressed in pixels and cannot be converted to micrometres or compared between the two images in physical units. Because magnification, staining and image processing differ between the two sources, the comparison between the images is descriptive. Luminance was computed as $Y = 0.299 R + 0.587 G + 0.114 B$ and z-scored over the whole image (see the definition of the tensor). ROI = 1 is the central region left after removing a 48-px margin; ROI = 4 is its partition into four equal quadrants (1, upper left; 2, upper right; 3, lower left; 4, lower right). Derivative filters were applied to the whole image, with reflection at the borders, and aggregated over each ROI (Table 2, Figure 5).

The orientation and anisotropy of each ROI were obtained from the D_2 entries through the quadratic form of Proposition 1, $D_2(\theta) = 0.5(J_{xx} + J_{yy}) + 0.5(J_{xx} - J_{yy})\cos 2\theta + J_{xy} \sin 2\theta$, which the four configured orientations determine exactly. The anisotropy index is $A = (\max_{\theta} D_2 - \min_{\theta} D_2)/(\max_{\theta} D_2 + \min_{\theta} D_2)$ and the texture axis is the direction along which D_2 is minimal. In transverse sections this axis describes the

dominant orientation of the interfibre boundaries and spaces in the image plane, not the longitudinal direction of the myofibres. Because real images have no replicate realizations, two additions were needed. Uncertainty was estimated by a block bootstrap (the reference for isotropy described above) (Künsch, 1989): each ROI was divided into 8×8 blocks that were resampled with replacement 1000 times, and the 2.5th and 97.5th percentiles are reported as 95 % confidence intervals (CI). The reference for isotropy was an isotropic surrogate (the reference for isotropy described above) (Theiler et al., 1992): for each image, 200 surrogates were generated from the radially averaged Fourier amplitude of the image with random phases, z-scored and analyzed with the same ROI; the 95th percentile of A over the surrogates is the floor that an observed A should exceed (the smallest attainable P is $1/201 = 0.005$). This null removes preferred directions but keeps the radial spectrum, and therefore the finite-sample floor of A that depends on ROI size and correlation scale; it is Gaussian and does not reproduce the non-Gaussian intensity distribution of the tissue (Table 2).

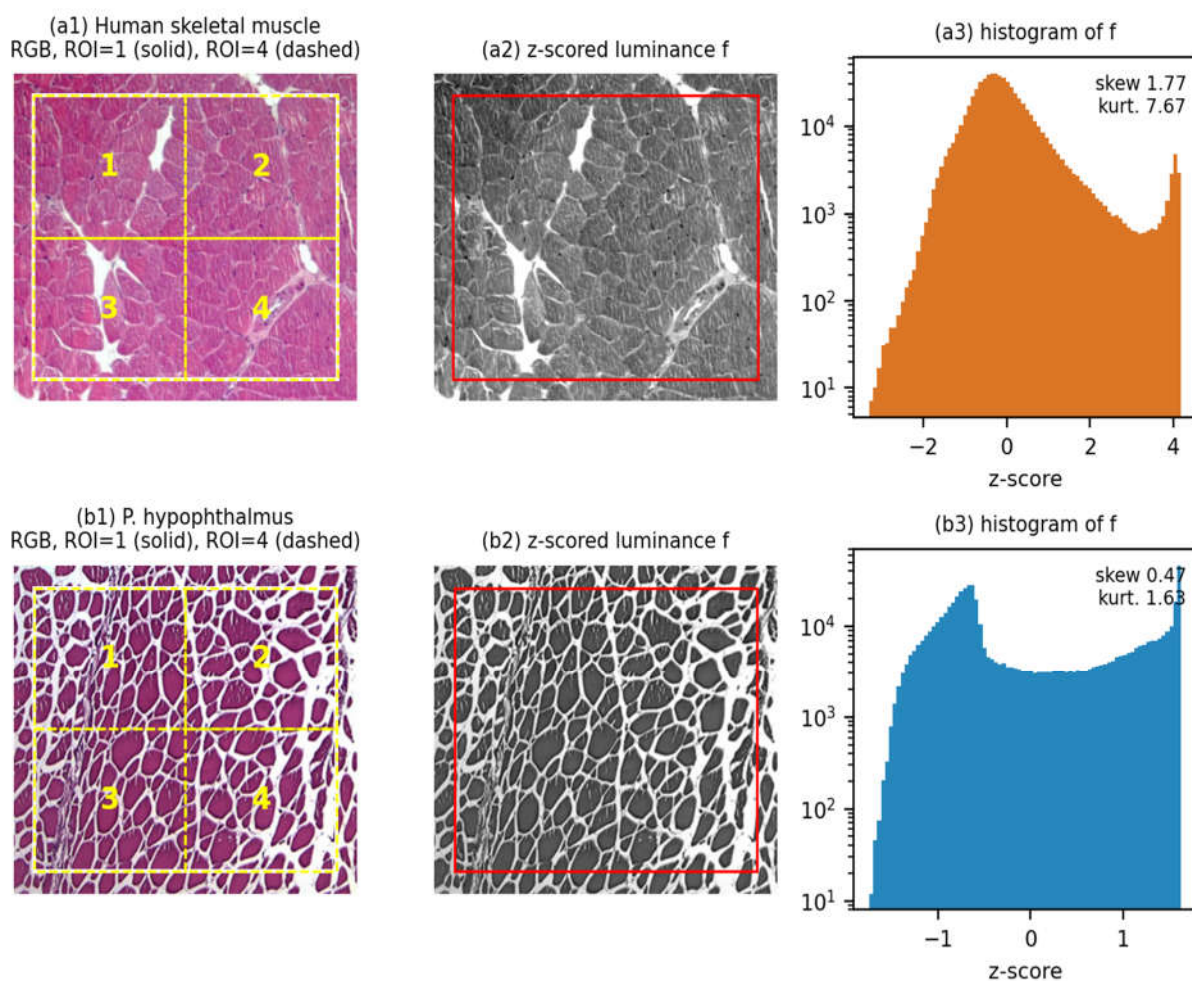


Figure 5. Test images and ROI layout. (a1,b1) RGB image with ROI = 1 (solid white rectangle) and the four ROIs of the R = 4 configuration (dashed, numbered). (a2,b2) Z-scored luminance f used for the tensor, with ROI = 1 (red). (a3,b3) Histogram of f (logarithmic ordinate) with skewness and kurtosis (Gaussian: 0 and 3). Row a: human skeletal muscle (Figure 3); row b: *P. hypophthalmus* (Figure 4).

Table 2

Test images and analysis geometry (W × H in px)		
Parameter	Human muscle (Figure 3) *	<i>P. hypophthalmus</i> * (Figure 4)
Source, specimen	(Trovato et al., 2016); t section, H&E, 10×	Ransverse (Abdel-Latif et al., 2023); transverse section of dorsal muscle, H&E, control group
Raster size	861 × 741	815 × 705
ROI = 1 (48-px margin removed)	765 × 645	719 × 609
ROI = 4, each quadrant	382–383 × 322–323	359–360 × 304–305
Tensor entries, R = 1 / R = 4	160 / 640	160 / 640
Luminance skewness / kurtosis	1.77 / 7.67	0.47 / 1.63
Pixel size	Not available	Not available

Results

Single-ROI tensor ($R = 1$): directional response and anisotropy. Figure 6 shows the $R = 1$ tensor in three complementary representations: polar profiles of $D_2(s, \theta)$ normalized by their mean over θ (panels a,b), a radar chart of the directional modulation of the ten channels (panel c), and the D_2 block of the tensor as bars (panels d,e) together with $A(s)$ against the isotropic floor (panel f). Table 3 gives the quantities at $s = 2$, providing a quantitative reference for interpreting the real-image results.

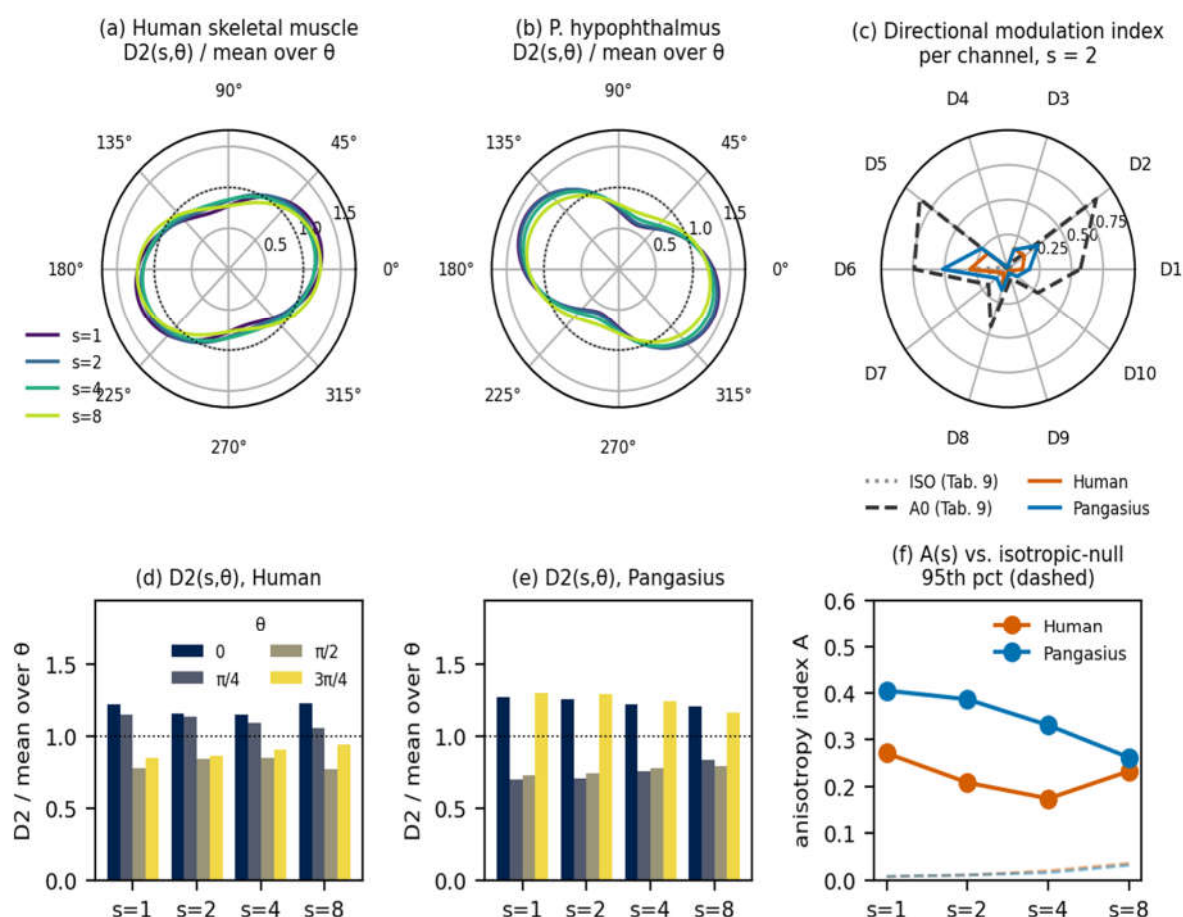


Figure 6. Single-ROI tensor. (a,b) Polar profiles $D_2(s, \theta) / \text{mean over } \theta$ for $s = 1, 2, 4$ and 8 (the profile is symmetric under $\theta \rightarrow \theta + \pi$); dotted circle: no directional preference; grey spokes: the four configured orientations. (c) Directional modulation index of the ten channels at $s = 2$ for the two images, with the isotropic field (ISO) and the anisotropic field at 0° (A0) as references. (d,e) $D_2(s_k, \theta_i)$ divided by its mean over θ . (f) Anisotropy index A against scale; dashed lines: 95th percentile of the isotropic surrogates.

Table 3

R = 1 tensor at s = 2: share of D₂ energy at the four configured orientations, anisotropy index A with 95 % bootstrap CI, 95th percentile of A for isotropic surrogates, and texture axis (°, from +x, y upward) with 95 % CI

Image	$\theta = 0$	$\theta = \pi/4$	$\theta = \pi/2$	$\theta = 3\pi/4$	A [95 % CI]	Null 95th pct	Axis [95 % CI]
Human muscle	0.290	0.284	0.210	0.216	0.208 [0.157, 0.264]	0.008	110.1 [99.8, 118.8]
<i>P. hypophthalmus</i>	0.314	0.177	0.186	0.323	0.387 [0.351, 0.424]	0.011	65.6 [62.8, 68.3]

Interpretation. In both images A exceeds the isotropic floor by more than an order of magnitude: 0.208 (95 % CI 0.157–0.264) against a surrogate 95th percentile of 0.008 for the human muscle, and 0.387 (0.351–0.424) against 0.011 for *P. hypophthalmus* ($P \leq 0.005$ in both).

Both values are substantially lower than those observed for strongly anisotropic patterns, indicating a more moderate degree of directional organization in the tissue; so the tissue is directionally biased but not strongly oriented, as expected for polygonal fibre profiles in cross-section.

The images separate clearly: A of the pangasius section is 1.9 times that of the human section and the confidence intervals do not overlap. The estimated axes are 110.1° (99.8–118.8°) and 65.6° (62.8–68.3°).

Neither coincides with a configured orientation, and the largest D₂ shares are found at the configured orientations closest to the direction perpendicular to the axis ($\theta = 0$, 29.0 %, in the human image; $\theta = 3\pi/4$ and $\theta = 0$, 32.3 % and 31.4 %, in the pangasius image), as the quadratic form predicts.

Reading the modulation directly from the four sampled orientations would underestimate the anisotropy of the human image (0.159 against $A = 0.208$), which is why A and the axis are computed from the quadratic form.

The directional profile is nearly independent of scale (Figure 6a,b): between s = 1 and s = 8 the axis varies by 12.8° (97.3–110.1°) in the human image and by 5.3° (65.6–70.9°) in the pangasius image.

The isotropic floors (0.008–0.011) are substantially lower for the present images, highlighting the dependence of the anisotropy baseline on ROI size. Accordingly, the isotropic floor should always be reported together with the ROI dimensions.

Four-ROI tensor (R = 4): regional heterogeneity. The R = 4 tensor assigns one 10 × 4 × 4 block to each quadrant. Figure 7 and Table 4 report, for each ROI, the directional profile at s = 2, the anisotropy index with its bootstrap interval and surrogate floor, and the texture axis with its interval.

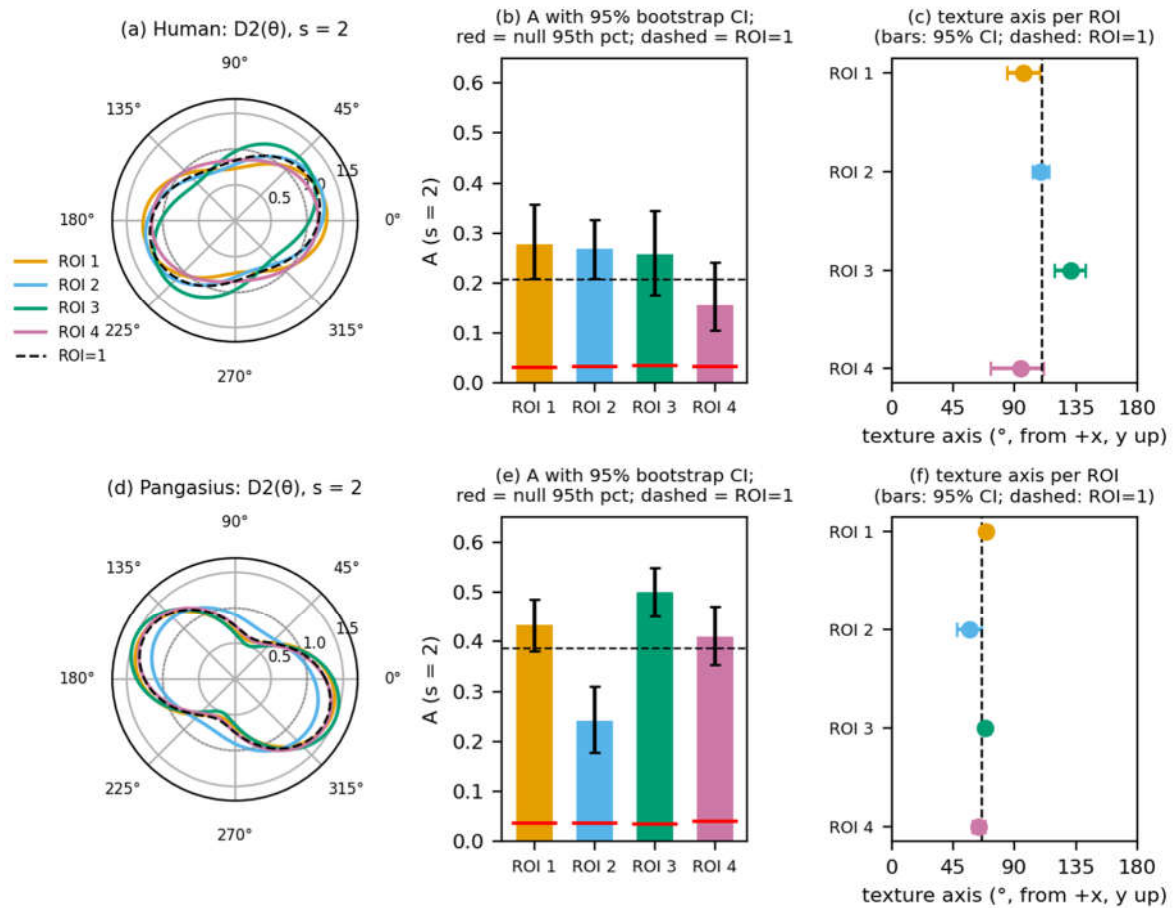


Figure 7. $R = 4$ tensor. (a,d) Polar profiles $D_2(\theta)/\text{mean over } \theta$ at $s = 2$ for the four ROIs (colours) and for ROI = 1 (dashed). (b,e) Anisotropy index A with 95 % bootstrap CI; red bars: 95th percentile of A for isotropic surrogates; dashed line: A of ROI = 1. (c,f) Texture axis of each ROI with 95 % CI; dashed line: axis of ROI = 1. Row a–c: human muscle; row d–f: *P. hypophthalmus*.

Table 4

$R = 4$ tensor at $s = 2$: D_2 shares, anisotropy index A with 95 % bootstrap CI, 95th percentile of A for isotropic surrogates, and texture axis (°) with 95 % CI. H1–H4: human muscle; P1–P4: *P. hypophthalmus*; ROI = 1 shown for reference

ROI	$\theta = 0$	$\theta = \pi/4$	$\theta = \pi/2$	$\theta = 3\pi/4$	A [95 % CI]	Null 95th pct	Axis [95 % CI]
H (ROI = 1)	0.290	0.284	0.210	0.216	0.208 [0.157, 0.264]	0.008	110.1 [99.8, 118.8]
H1	0.318	0.265	0.182	0.235	0.279 [0.210, 0.359]	0.031	96.3 [84.7, 108.3]
H2	0.303	0.291	0.197	0.209	0.269 [0.209, 0.327]	0.033	108.9 [103.5, 115.2]
H3	0.258	0.314	0.242	0.186	0.259 [0.177, 0.346]	0.034	131.3 [119.0, 142.2]
H4	0.288	0.256	0.212	0.244	0.156 [0.105, 0.242]	0.032	94.6 [72.7, 111.2]
P (ROI = 1)	0.314	0.177	0.186	0.323	0.387 [0.351, 0.424]	0.011	65.6 [62.8, 68.3]
P1	0.331	0.179	0.169	0.321	0.433 [0.381, 0.485]	0.038	69.3 [66.0, 72.6]
P2	0.274	0.195	0.226	0.305	0.241 [0.178, 0.310]	0.037	56.7 [47.9, 65.4]
P3	0.341	0.164	0.159	0.336	0.501 [0.451, 0.549]	0.036	68.2 [64.9, 71.7]
P4	0.313	0.169	0.187	0.331	0.410 [0.353, 0.471]	0.040	64.0 [59.1, 68.4]

Interpretation. All eight ROIs lie above their surrogate floor (smallest observed $A = 0.156$, largest floor = 0.040), but they are not equivalent. In the human image A ranges from 0.156 to 0.279 and the axes from 94.6° to 131.3° (circular SD 14.8°); the axis of H3 (131.3° , CI 119.0 – 142.2°) lies outside the interval of H2 (103.5 – 115.2°), so the image contains regions with different dominant orientations of the interfibre boundaries, and H4 is the least anisotropic ROI (0.156) with the widest axis interval. In the pangasius image the axes are tightly grouped (56.7 – 69.3° , circular SD 5.0°), whereas A varies from 0.241 (P2) to 0.501 (P3); the interval of P2 (0.178–0.310) does not overlap those of P1, P3 and P4. This is the situation described by Proposition 2: pooling the four ROIs into $R = 1$ gives $A = 0.208$ for the human image, below the mean of the four ROI values (0.241), because quadrants with different axes partly compensate, exactly as required by the pooling inequality of Proposition 2 (Eq. (6)); the loss is 13 % for the human image and 2 % for the pangasius image, where the axes agree. The $R = 1$ value is therefore a summary that is accurate when the ROI is directionally homogeneous and attenuated when it is not, and the $R = 4$ tensor makes the difference visible.

Channel-level behaviour on tissue. Table 5 gives, for the ten channels at $s = 2$ and $R = 1$, the mean over the four orientations and the directional modulation index. The modulation index is computed from the four configured orientations and is therefore a lower bound of the modulation along the true axis.

Reference fields. To interpret the tissue values, two synthetic Gaussian random fields of 256×256 px were analysed with the same implementation and the same parameters (z-scored images, central ROI after removal of a 48-px margin, $s = 2$, $R = 1$, four orientations). The isotropic field (ISO) has equal correlation scales in all directions ($\sigma = 2.2$ px). The anisotropic field (A0) was synthesized in the Fourier domain with correlation scales $\sigma_{\parallel} = 9$ px along the texture axis and $\sigma_{\perp} = 1.6$ px across it (aspect ratio 5.6), the axis being at 0° , so that its direction is exact on the pixel grid. Each field was generated in 20 independent realizations with fixed seeds, and the values in Table 5 are means over these realizations. ISO has no preferred direction, so any modulation it shows is produced by the pixel grid and the finite set of orientations; in particular, diagonal co-occurrence offsets rounded to integer pixels are not as long as horizontal and vertical ones, which gives the co-occurrence contrast D6 a modulation of 0.30 that is not texture anisotropy. A0 gives the modulation expected for a strongly oriented texture.

Table 5

Channel means over θ and directional modulation index at $s = 2$ ($R = 1$) for the two images, compared with the isotropic (ISO) and anisotropic 0° (A0) reference fields (ISO and A0: means over 20 realizations)

Channel	Human: mean over θ	Human: mod. index	Pangasius: mean over θ	Pangasius: mod. index	ISO	A0
D1	0.0773	0.11	0.0967	0.17	0.02	0.57
D2	0.0124	0.16	0.0214	0.29	0.03	0.86
D3	7.4	0.16	4.35	0.15	0.04	0.04
D4	3.89	0.01	3.75	0.01	0.00	0.00
D5	0.0313	0.19	0.0353	0.26	0.02	0.86
D6	0.361	0.30	1.98	0.52	0.30	0.74
D7	0.846	0.04	0.663	0.11	0.06	0.19
D8	0.119	0.13	0.054	0.16	0.15	0.44
D9	0.962	0.01	0.951	0.03	0.03	0.07
D10	0.891	0.02	0.775	0.09	0.04	0.29

Interpretation. The gradient-based channels D1, D2 and D5 are modulated (0.11–0.19 in the human and 0.17–0.29 in the pangasius image), well above the ISO values (0.02–0.03) and well below A0 (0.57–0.86), in line with the intermediate values of A . D4 is flat (0.01 in both images). The kurtosis D3 is 7.4 and 4.35, i.e. the directional derivatives

have heavy tails, as expected when strong edges (interfibre gaps, nuclei) are sparse; its modulation (0.16, 0.15) is larger than for the Gaussian reference fields (0.04), which is compatible with non-Gaussian edge statistics but was not tested further. The co-occurrence contrast D6 requires care: its modulation in the human image (0.30) equals the grid-induced value of ISO and cannot be read as tissue anisotropy, whereas the value in the pangasius image (0.52) exceeds it. The gradient channels are strongly redundant on tissue. Over the 128 entries of the $R = 4$ tensors of both images, the Spearman correlations (Spearman, 1904) are $\rho(D1,D2) = 0.99$, $\rho(D1,D5) = 0.99$ and $\rho(D2,D5) = 0.98$, whereas D4 is nearly independent of them ($\rho = -0.15$ and -0.23). The co-occurrence group is less compact: $\rho(D6,D7) = -0.98$ and $\rho(D6,D8) = -0.91$, but $\rho(D6,D9) = -0.59$. Each entry still obeys the exact identity $D6 = 2\sigma Q^2(1 - D9)$ of Eq. (9) (verified on all 32 $R = 1$ entries of the two images to a relative error below 10^{-14}); the weaker rank correlation arises because the variance σQ^2 of the quantized smoothed image changes with scale and region. Contrast and correlation therefore cannot be treated as equivalent on tissue, which supports retaining the full tensor and testing redundancy on the data of each application.

Scale dependence and characteristic scale. Table 6 gives D_2 , A and the axis at the four configured scales. The second question is whether the scale index carries a characteristic length, as for Gaussian fields (Eq. 7). For this purpose the scale-normalized energy $s^2 \cdot (J_{xx} + J_{yy})$, i.e. the variance-loss rate of Eq. (7), was evaluated at 15 log-spaced scales between 1 and 24 px (Figure 10a), and the position of its maximum was refined by a parabola in $\log s$.

Table 6

Scale dependence at $R = 1$: mean D_2 over θ , anisotropy index A (95th percentile of the isotropic surrogates in parentheses) and texture axis ($^\circ$)

Scale (px)	Human: D_2	Human: A (null)	Human: axis	Pangasius: D_2	Pangasius: A (null)	Pangasius: axis
$s = 1$	0.0302	0.271 (0.007)	107.2	0.0436	0.405 (0.008)	66.3
$s = 2$	0.0124	0.208 (0.010)	110.1	0.0214	0.387 (0.010)	65.6
$s = 4$	0.00342	0.174 (0.020)	105.7	0.00596	0.331 (0.015)	66.4
$s = 8$	0.000863	0.233 (0.036)	97.3	0.000973	0.262 (0.031)	70.9

Interpretation. A decreases with scale in the pangasius image (0.405 at $s = 1$ to 0.262 at $s = 8$), because a coarse operator averages over structures that are narrow in one direction; the human image is not monotonic (0.271, 0.208, 0.174, 0.233) and its axis turns by about 13° between $s = 1$ and $s = 8$. All values exceed the scale-specific floors (0.007–0.036), but anisotropy reported without its scale would again be incomplete. For the pangasius image the scale-normalized energy has a clear maximum at $s = 3.2$ px (ROI = 4: 2.6–3.9 px), with a half-maximum band of 1.3–9.7 px (2.95 octaves). The median width of the interfibre spaces in the segmentation of the morphometric check is 8.2 px (interquartile range 6.0–12.6 px), so s is of the order of half of the gap width and about one tenth of the median fibre diameter (34.1 px). For Gaussian fields s equalled the correlation scale; for tissue with sharp edges no such identity exists, and s should be read as a descriptor-specific indicator of the width of the dominant edges. The human image has no characteristic scale in this sense: the profile is a plateau between about 4 and 12 px, the half-maximum band covers the whole scale range examined, and the ROI-wise maxima are scattered (2.2–12.1 px). This is a finding rather than a failure, since the image combines fine intrafibre structure with fibre and bundle outlines at coarser scale, but it shows that a single value of s^* cannot summarize every tissue.

Complementary representations of orientation and spatial correlation. The structure-tensor field (derivative scale $s = 2$ px, Gaussian integration window of 10 px) maps the local texture axis and the coherence $\kappa = [(J_{xx} - J_{yy})^2 + 4J_{xy}^2]^{1/2} / (J_{xx} + J_{yy})$ of each position (Figure 8). The Fourier power spectrum and the two-dimensional autocorrelation function describe the same texture in the frequency and spatial-lag domains (Figure 9), and the correlation length $\xi(\theta)$, defined as the lag at which the autocorrelation falls to $1/e$ along direction θ , provides a second-order measure of directional elongation that is independent of the derivative estimator (Eqs. (8)-(9)). Table 7 summarizes the comparison with the tensor.

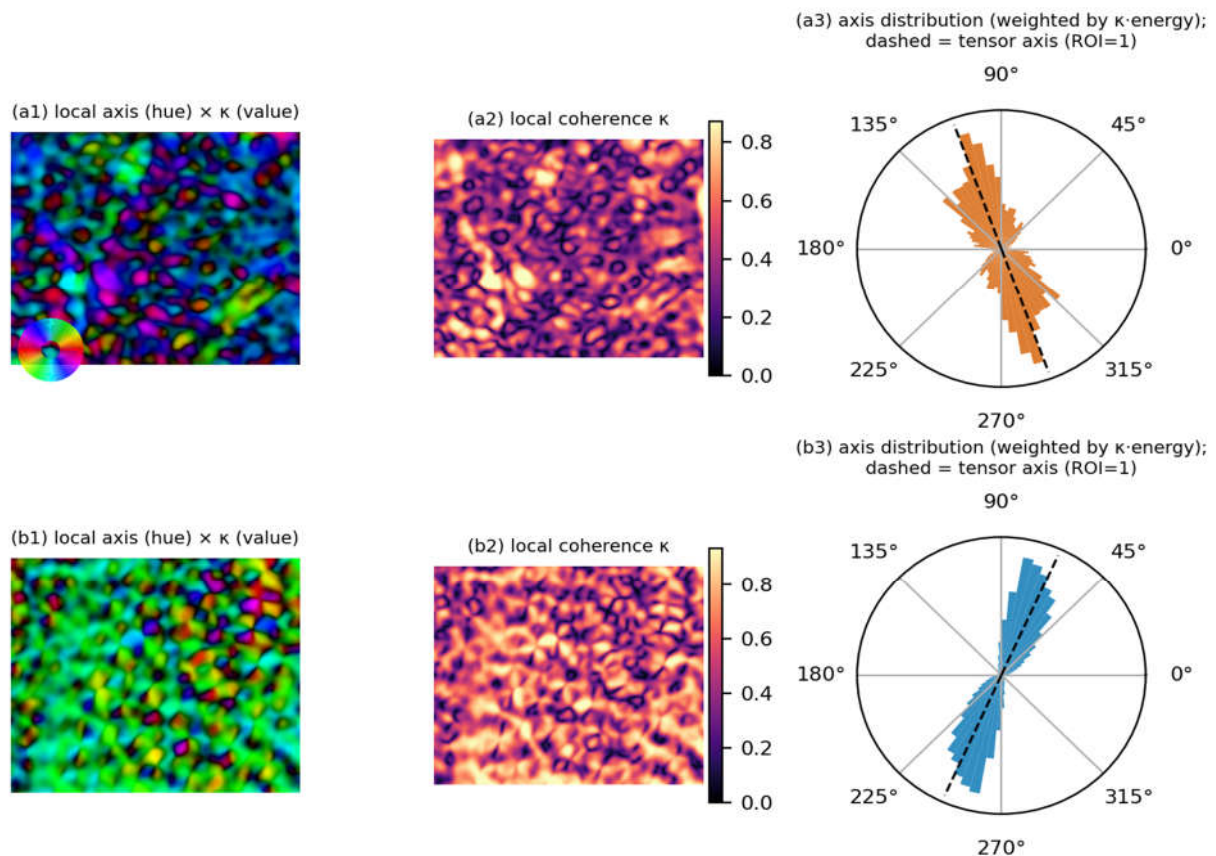


Figure 8. Structure-tensor representation of ROI = 1 ($s = 2$ px, integration window 10 px). (a1,b1) Local texture axis (hue; colour wheel in a1) modulated by coherence κ (brightness). (a2,b2) Coherence map. (a3,b3) Distribution of local axes weighted by κ and local energy; dashed line: texture axis from the tensor (Table 3). Row a: human muscle; row b: *P. hypophthalmus*.

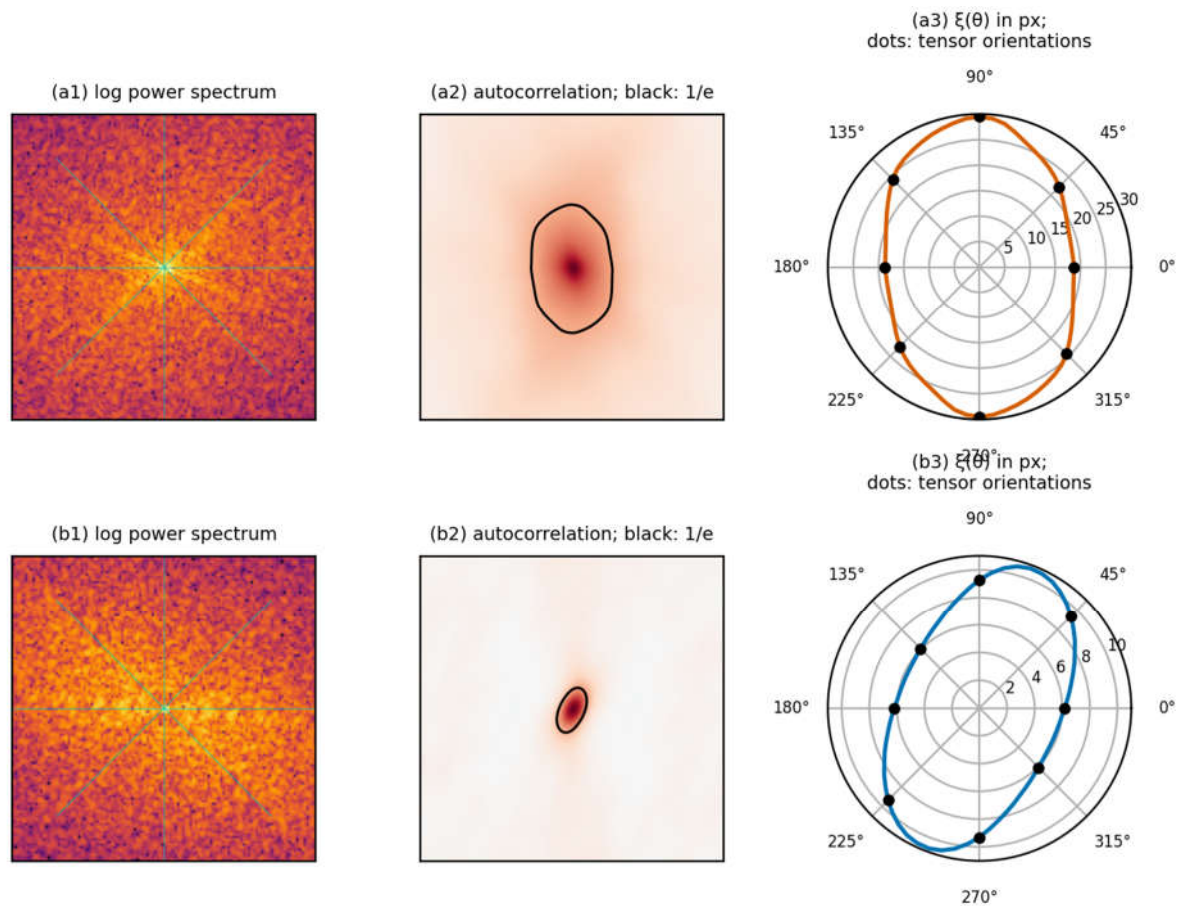


Figure 9. Spectral and spatial-correlation representation of ROI = 1. (a1,b1) Log power spectrum (Hann window); cyan lines mark the four configured orientations. (a2,b2) Two-dimensional autocorrelation function; black contour: 1/e level. (a3,b3) Correlation length $\xi(\theta)$ in px; dots mark the four configured orientations. Row a: human muscle; row b: *P. hypophthalmus*.

Table 7

Consistency of the tensor with independent representations of the same ROI = 1 ($R = 1$ unless stated)

Measure	Human muscle	<i>P. hypophthalmus</i>
$\xi(\theta)$, $\theta = 0, \pi/4, \pi/2, 3\pi/4$ (px)	18.7 / 22.3 / 29.5 / 24.3	6.2 / 9.4 / 9.3 / 6.0
$\xi_{\max}/\xi_{\min}$	1.58	1.55
Spearman ρ between $\xi(\theta)$ and D_2 share ($n = 4$)	-1.0	-1.0
Mean coherence κ (structure tensor)	0.41	0.56
Resultant length of local axes (weighted)	0.45	0.71
Weighted mean local axis ($^\circ$) / tensor axis ($^\circ$)	110.0 / 110.1	65.7 / 65.6
s^* (px): ROI = 1 (ROI = 4 range)	plateau; 8.0 (2.2–12.1)	3.2 (2.6–3.9)
Half-maximum band of $s^2 \cdot \text{tr } J$ (px)	1–24 (full range)	1.3–9.7
Mean A of four ROIs / pooled A ($R = 1$)	0.241 / 0.208	0.396 / 0.387
Circular SD of the four ROI axes ($^\circ$)	14.8	5.0

Interpretation. The structure-tensor field uses the same gradient energy as D_2 with a different spatial weighting, so its mean axis (110.0° and 65.7°) is expected to match the tensor axis; the agreement (110.1° and 65.6°) checks the implementation rather than the tissue. What the field adds is the spatial distribution: the local axes are much more dispersed in the human image (resultant length 0.45 against 0.71) and the mean coherence is lower (0.41 against 0.56), which is the local counterpart of the lower A. The autocorrelation provides an independent check on the orientation index. In both images the ranking of $\xi(\theta)$ over the four configured orientations is exactly the inverse of

the ranking of the D_2 shares ($\rho = -1$, with only $n = 4$ orientations, so the result is indicative): the energy is largest where the correlation length is shortest. The ratio $\xi_{\max}/\xi_{\min}$ is almost the same in the two images (1.58 and 1.55), although A differs by a factor of 1.9. The two measures are not interchangeable: ξ is determined at the $1/e$ level, at lags of 6–30 px, whereas A at $s = 2$ weights the fine edge structure, which is a further instance of the scale dependence of anisotropy discussed in the analysis of scale dependence. The correlation lengths of the human image (19–30 px) are about three times those of the pangasius image (6–9 px), consistent with the absence of a characteristic fine scale in the former.

Independent morphometric check (Figure 4). In Figure 4 fibres are separated by clear spaces and can be segmented automatically. Fibres were obtained by Otsu thresholding (Otsu, 1979) of the smoothed luminance, morphological opening and watershed splitting (Vincent & Soille, 1991) on the distance transform. Within ROI = 1, 207 fibres with area ≥ 150 px were retained; their median equivalent diameter is 34.1 px (interquartile range 25.6–47.1 px), the median aspect ratio (major/minor axis) is 1.86, 76 % of the fibres have an aspect ratio above 1.5, and fibres cover 63 % of the ROI.

The orientation of the long axis of the elongated fibres (weight 1 – minor/major, 158 fibres) was compared with the texture axis of the tensor (Figure 10, Table 8). The same segmentation was attempted for Figure 3 but over-segmented the fibres, because intrafibre cracks have the same luminance as the interfibre boundaries; no morphometric reference is therefore available for the human image.

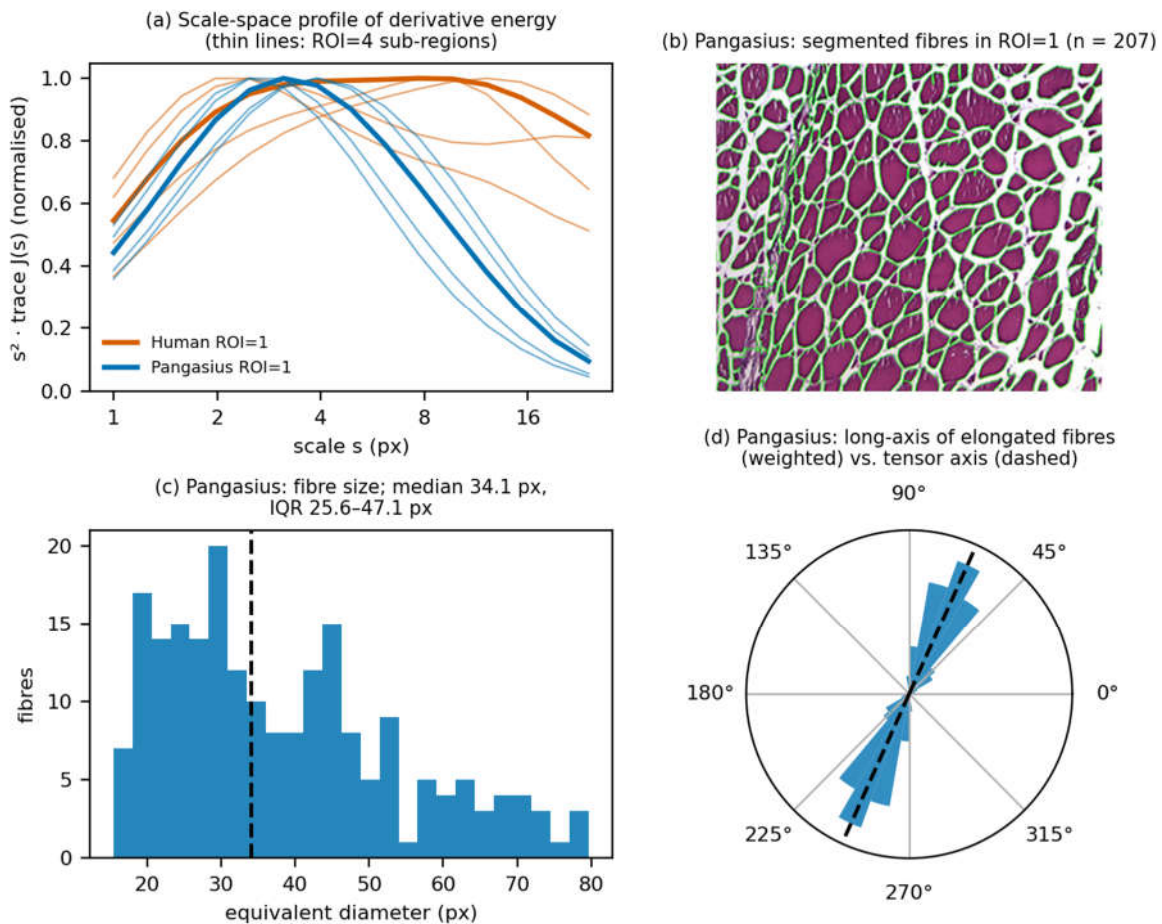


Figure 10. Scale-space and morphometry. (a) Scale-normalized derivative energy $s^2 \cdot (J_{xx} + J_{yy})$ against s for ROI = 1 (thick) and the four ROIs (thin), each normalized to its maximum. (b) Segmentation of the fibres of Figure 4 within ROI = 1 (green outlines). (c) Distribution of the equivalent diameter of the segmented fibres; dashed line: median. (d) Long-axis orientation of the elongated fibres (weighted); dashed line: texture axis of the tensor (ROI = 1).

Table 8

P. hypophthalmus: texture axis of the tensor against the long-axis orientation of segmented fibres (°, from +x, y upward), by ROI

ROI	Fibres	Median diameter (px)	Median aspect ratio	Fibre axis	Tensor axis	$ \Delta $	A
P (ROI = 1)	207	34.1	1.86	64.2	65.6	1.4	0.387
P1	66	32.2	1.91	70.0	69.3	0.7	0.433
P2	49	34.1	1.62	51.2	56.7	5.5	0.241
P3	49	36.7	1.99	66.5	68.2	1.6	0.501
P4	43	37.0	1.92	60.5	64.0	3.5	0.410

Interpretation. The tensor axis agrees with the morphometric reference. For ROI = 1 the circular mean of the fibre long axes is 64.2° (95 % bootstrap CI $\pm 2.5^\circ$) and the tensor axis is 65.6° (62.8–68.3°), a difference of 1.4°; the two intervals overlap. By quadrant the differences are 0.7, 5.5, 1.6, 3.5° (mean 2.8°), and the ROI with the lowest A (P2, 0.241) is the one with the lowest median aspect ratio (1.62) and the weakest alignment of fibre axes, whereas the ROIs with A = 0.41–0.50 have median aspect ratios of 1.91–1.99. With only four ROIs this ordering is indicative, not a statistical test. The result demonstrates that, without any segmentation, the tensor recovers within about 3° the direction in which the interfibre boundaries and the fibres themselves are elongated. The reference is itself a segmentation with its own errors, and agreement was demonstrated for one image only.

Position relative to the synthetic references and distance between ROIs. Figure 11a places every A reported in this section on a common reference scale. In addition to the isotropic surrogate floor, it comprises three synthetic references of 256×256 px analysed with the same implementation and parameters ($s = 2$, central ROI after removal of a 48-px margin, 20 realizations with fixed seeds): the isotropic (ISO) and anisotropic (A0) Gaussian random fields described with Table 5, and sinusoidal stripes with axis at 0°, wavelength 10 px and additive Gaussian noise of SD 0.6 of the stripe amplitude, which represent a single, strongly oriented pattern. Their anisotropy indices are 0.032 ± 0.020 (ISO), 0.859 ± 0.013 (A0) and 0.958 ± 0.001 (stripes) (mean $\pm$ SD over realizations). All ROIs of both images lie between the isotropic and the anisotropic references, and none approaches the value of the stripes. Figure 11b shows the normalized Euclidean distance between the eight $R = 4$ tensors (each of the 160 entries standardized across the eight ROIs), ordered by average linkage.

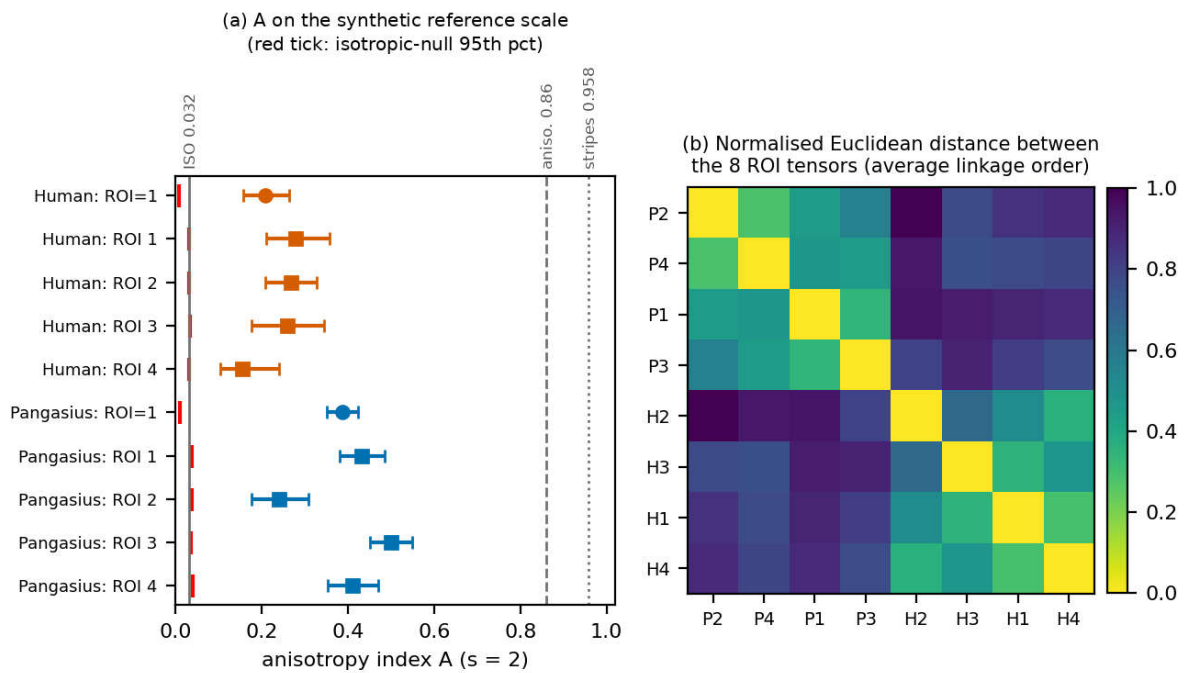


Figure 11. (a) Anisotropy index A at $s = 2$ with 95 % bootstrap CI for ROI = 1 (circles) and the four ROIs (squares), against the isotropic surrogate floor (red ticks) and the synthetic references analysed with the same implementation (isotropic field 0.032, anisotropic field 0.859, stripes 0.958; means over 20 realizations). (b) Normalized Euclidean distance between the eight $R = 4$ tensors (H1–H4: human muscle; P1–P4: *P. hypophthalmus*); rows and columns ordered by average-linkage clustering.

The mean distance between ROIs of the same image is 0.43 and between ROIs of different images 0.85 (ratio 1.97), and cutting the dendrogram into two clusters recovers the image of origin of all eight ROIs. This shows that the tensor responds to differences between the two textures; it does not show discrimination of tissue states, because the two images differ in species, magnification, staining and processing, and the quadrants of one image are adjacent and not independent observations.

Discussion. The two H&E sections support four statements within the limits stated below. First, on real muscle tissue the tensor entries are distinguishable from those of an isotropic texture with the same radial spectrum at every scale and in every ROI examined, and the anisotropy of the two sections differs in a way that the bootstrap intervals resolve ($A = 0.208$ versus 0.387 at $s = 2$ px). In transverse sections this anisotropy reflects the preferred direction of the fibre boundaries and interfibre spaces in the image plane, which in turn reflects the elongation of fibre profiles produced by a slightly oblique cut or by fibre packing; it is not a measure of the longitudinal fibre direction. Anisotropy indices of this kind complement scalar fractal and stereometric descriptors of biological surfaces and tissues (Tălu et al., 2015; Garczyk et al., 2017), which do not identify a preferred direction.

Second, the orientation index agrees with independent estimators: the mean axis of the structure-tensor field, the ordering of the directional correlation lengths and, for the *P. hypophthalmus* section, the long-axis orientation of 207 segmented fibres (difference 1.4° for the whole ROI and 0.7 – 5.5° by quadrant). Because the tensor needs no segmentation, it remains applicable where segmentation fails, as it did for the human section, whose intrafibre cracks have the same luminance as the interfibre boundaries.

Third, the four-ROI tensor reveals regional heterogeneity that the single-ROI summary attenuates. Proposition 2 explains this quantitatively: pooled anisotropy can never exceed the energy-weighted mean of the regional values, and the loss grows with the disagreement between regional axes. The loss was 13 % in the human section, whose quadrant axes span 94.6 – 131.3° , and 2 % in the fish section, whose axes span

56.7–69.3°. A single anisotropy value for a whole section is therefore an adequate summary only when the regional axes agree, and the $R = 4$ tensor shows when they do not.

Fourth, channel redundancy and artefacts must be checked on tissue. D1, D2 and D5 remain practically collinear, so one of them can represent the group; the grid-related modulation of GLCM contrast on diagonal offsets must be compared with the isotropic reference before it is read as tissue anisotropy; and contrast and correlation decouple on tissue because the variance of the quantized image changes with scale and region (Eq. (9)). Redundancy should therefore be tested on the data of each application rather than assumed; the same collinearity of D1, D2 and D5 was found in guppy muscle (Țălu, 2026c).

The scale behaviour differs between the two sections. The fish section has a characteristic scale ($s^* = 3.2$ px, about half of the median width of the interfibre spaces), whereas the human section shows a plateau between about 4 and 12 px. Within the variance-loss reading of Eq. (7), the fish section loses most variance at the width of its interfibre gaps, while the human section loses variance evenly across the scales of intrafibre structure, fibre outlines and bundle outlines. This is a finding about the images rather than a failure of the method, but it shows that a single characteristic scale cannot summarize every tissue. In guppy muscle, the same tensor gave characteristic scales of about 6 μm in control and 10 μm in *Tetrahymena*-affected tissue, together with a marked loss of anisotropy in the affected muscle (Țălu, 2026c); the method can therefore follow scale and orientation changes of muscle architecture in fish of different sizes and species.

Limitations. Only two published images were analysed, one per species, with unknown pixel size, compression and processing history, and different magnification and staining; absolute values are therefore not transferable, and the images cannot be compared in physical units. The isotropic surrogates are Gaussian, so their P-values (resolution 0.005) indicate departure from an isotropic spectrum, not biological significance. The block bootstrap treats blocks of one ROI as exchangeable, neglecting long-range correlation. The morphometric reference exists for one image only and is itself algorithm-dependent segmentation (Țălu, 2012c). Repeatability on tissue could not be estimated without repeated acquisitions, and single-scale co-occurrence or local-binary-pattern features (Ojala et al., 2002) were not compared. Next steps are calibrated muscle sections with several animals per group, field-to-field repeatability, and single-scale baselines.

Conclusions. A hierarchical descriptor tensor indexed by channel, scale, orientation and region was formulated for muscle histology texture analysis, and two properties were proved: the directional-energy block is a quadratic form of the regional structure matrix, so four orientations determine the anisotropy index and texture axis exactly, and pooling regions can only lower the anisotropy index, by an amount measuring the disagreement between regional axes. On two published H&E cross-sections of normal human and *P. hypophthalmus* skeletal muscle, the tensor gave anisotropy indices well above the isotropic floor ($A = 0.21$ and 0.39 , $R = 1$), texture axes consistent with independent estimators (within 1.4° of segmented fibre orientation in the fish section, where the characteristic scale matched interfibre spacing), and regional differences attenuated by the single-ROI summary. The tensor thus yields interpretable, internally consistent readings on real histology; diagnostic performance requires calibrated, replicated data and baseline comparisons.

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Conflicts of Interest. The author declares that there is no conflict of interest.

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