Bone & Joint Research

Supplementary Material

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Methods

Shape analysis using the landmark-based geometric morphometric method

The geometric morphometric method (GMM) is based on landmarks that were defined as specific anatomical loci as well as Cartesian coordinates.[1] These landmarks have specific locations that are homologous between forms/individuals and can be marked on 2D images (such as an image from a CT scan) or 3D models. Commonly, general Procrustes analysis (GPA) is applied, whereby the landmark configuration is superimposed to examine and quantify differences between shapes.[1,2] Then, principal component analysis (PCA) is done to examine the shape variance. The process of superimposition includes scaling, translating, and rotating the landmark configurations, and will be briefly described: translation of all landmark configurations (i.e. for all individuals in the sample) so their centroid will be at the origin of the coordinate system, scaling of all configurations to have the same centroid size, and finally, rotating the landmark configuration, so the distances between homologous landmarks are minimized.[1] The distance between two corresponding landmarks is calculated as the square root of the sum of squared distances and defined as Procrustes distances, representing the differences between shapes.[2] The advantage of the GMM over traditional linear and angular measurements lies in its ability to preserve the geometry of the landmark configuration throughout the analysis. This ability permits representation of statistical results as actual shapes, independent of object size, position, and orientation, and allows for the assessment of developmental (and evolutionary) trajectories.[1] Moreover, the analyses are carried out on the complete configuration of the landmarks, not just on selected measures.[2]

An important aspect of studying growth and development is allometry, defined as a size-related change in shape or morphological traits. Although GPA includes scaling of the landmark configuration, it does not remove variation that might be related to size or change in size.[2] Size correction is typically done either by performing multivariate regression (typically on the log-transformed centroid size), or by projecting data points to a sub-space perpendicular to the first principal component (Burnaby's procedure).[2]

Table i. Calculation of lumbar lordosis and sacral slope angles (Figure 1 of the main text). All angles were extracted by calculating their arc tangent and inverting the angle from radians to degrees.

Angle description	Calculation
Angle between the upper epiphyseal plate of L1 and the horizontal plane (α)	$Tan\ \alpha = \frac{(y2 - y1)}{(x2 - x1)}$
Sacral slope, the angle between the endplate of S1 and the horizon	$Tan\ \beta = \frac{(y2 - y1)}{(x2 - x1)}$
Lordosis angle (γ) is the sum of L1 and S1 angles with the horizon	$\gamma = \alpha + \beta$

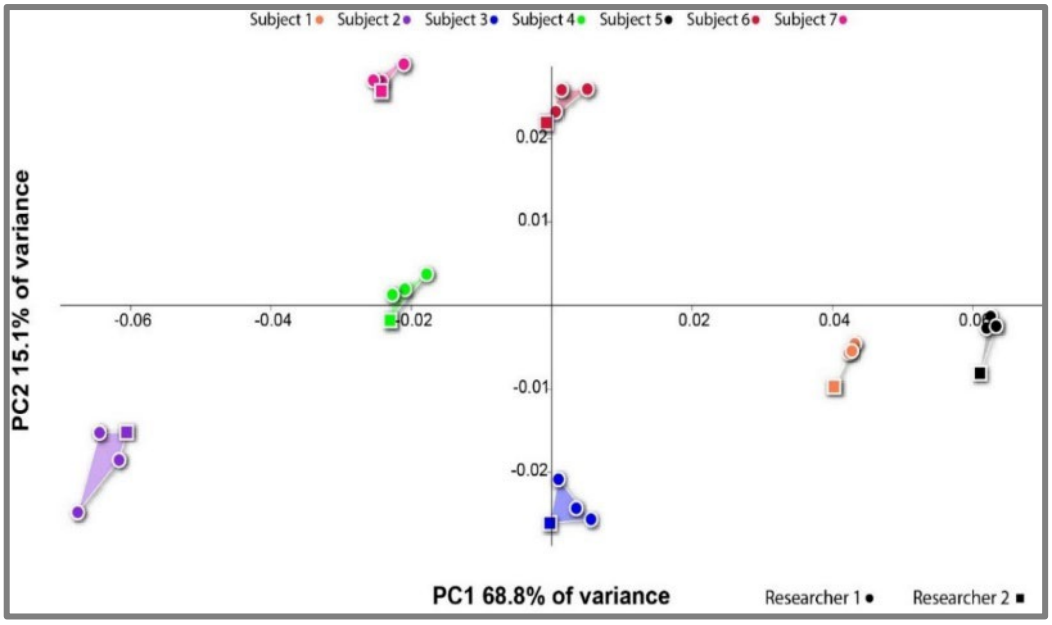

Fig a. Reliability of landmark placement and principal component (PC) analysis of shape variables of the lumbar spine. Note that the various landmarking sessions of each subject (represented by different colors) cluster together and are distinguished from others.

Table ii. Mean and SDs for lumbar lordosis and sacral slope, and intraclass correlation coefficient (ICC) results for intra- and interobserver variations.

Intraobserver variation	**Mean (SD)**		**ICC**
	1st session	**2nd session**	
Lumbar lordosis	39.81 (11.98)	36.94 (10.37)	0.936
Sacral slope	36.73 (10.01)	34.74 (8.301)	0.945
Interobserver variation	**1st researcher**	**2nd researcher**	
Lordosis angle	35.51 (13.758)	38.14 (16.109)	0.968
Sacral slope	32.73 (11.9)	34.45 (12.622)	0.968

References

1. **Mitteroecker P, Gunz P**. Advances in geometric morphometrics. *Evol Biol*. 2009;36(2):235–247.

2. **Klingenberg CP**. Size, shape, and form: concepts of allometry in geometric morphometrics. *Dev Genes Evol*. 2016;226(3):113–137.