Position identification of spotted hyena (Crocuta crocuta) tracks using different methods of data recording and features extraction

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CITED REFERENCES

Adams D.C., Otárola-Castillo E., Sherratt E. (2013). *Geomorph*: an R package for the collection and analysis of geometric morphometric shape data. Methods Ecol. Evol. 4(4), 393:399.

Agisoft LLC (2016). Agisoft PhotoScan User Manual: Professional Edition, Version 1.2. *User Manuals*. Available online at http://www.agisoft.com/downloads/user-manuals/, accessed 2 Feb 2017.

Andale, 2016. "Pillai's Trace". Available online at http://www.statisticshowto.com/pillais-trace/, accessed 8 Aug 2017.

Bertzky B., Corrigan C., Kemsey J., Kenney S., Ravilious C., Besançon C. et Burgess N.D., 2012. Protected Planet Report 2012: Tracking progress towards global targets for protected areas, Cambridge, UK, 1:60.

Bohm, T. and Höner, O.R. (2015). *Crocuta crocuta*. The IUCN Red List of Threatened Species 2015: e.T5674A45194782. Available online at http://dx.doi.org/10.2305/IUCN.UK.2015-2.RLTS.T5674A45194782.en, accessed 31 July 2017

Bookstein FL (1991). Morphometric tools for landmark data: geometry and biology. Cambridge University Press, Cambridge

Bookstein F.L. (1996). Biometrics, biomathematics and the morphometric synthesis. *In*: *Bulletin of Mathematical Biology*. Kluwer Academic Publishers, 313:365.

Bothma J du P, Le Riche EA (1984). Aspects of the ecology and the behaviour of the leopard Panthera pardus in the Kalahari Desert. Koedoe 27:259–279.

Caro T (2010). Conservation by proxy: indicator, umbrella, keystone, flagship, and other surrogate species. Island Press, Washington.

Charlton-Perkins W. and De la Harpe R. (1995). Hluhluwe-Umfolozi Park. Struik, Cape Town

CIA (2017). The World Factbook. Available online at https://www.cia.gov/library/publications/the-world-factbook/geos/sf.html, accessed 31 July 2017.

CloudCompare (2015). CloudCompare (version 2.6.1). Paris: EDF, R&D, Telecom, ParisTech. Available online at http://www.cloudcompare.org/, accessed 3 February 2017.

Cromsigt, J. P., Archibald, S., & Owen-Smith, N. (Eds.). (2017). Conserving Africa's mega-diversity in the Anthropocene: The Hluhluwe-iMfolozi Park story. Cambridge University Press.

Cucchi T., Baylac M., Evin A., Bignon-Lau O. et Vigne J.-D. (2015). Morphométrie géométrique et archéozoologie : Concepts, méthodes et applications. In: Balasse, M., Brugal, J.-P., Dauphin, Y.,

Geigl, E.-M., Oberlin, C., Reiche, I. éd. Messages d'os: Archéométrie du squelette animal et humain. 197:216.

EKZNW (2015). "Long Term Hyena Census Report", unpublished data.

Eloff F (1973). Ecology and behavior of the Kalahari lion. The world's cats 1:90–126.

Gargallo P, Prados E, Sturm P (2007). Minimizing the reprojection error in surface reconstruction from images. In: 11th IEEE International Conference on Computer Vision. Institute of Electrical and Electronics Engineers, p 1–8

Gittleman JL, Funk SM, Macdonald DW, Wayne RK (2001). Why "carnivore conservation"? In: Gittleman JL, Funk SM, Macdonald DW, Wayne RK (eds) Carnivore conservation. Cambridge University Press, Cambridge, pp 1–7.

Graf J.A., Somers M.J., Szykman Gunther M. and SLOTOW R (2009). Heterogeneity in the density of spotted hyaenas in Hluhluwe-iMfolozi Park, South Africa. Acta Theriologica 54: 333–343

Gu J, Alibhai SK, Jewell ZC, Ma J (2015). "Sex determination of Amur Tigers (Pantera tigris altaica) From Footprints in Snow". Wildlife Society Bulletin 38(3):495–502; 2014; DOI: 10.1002/wsb.432

Gunz P, Mitteroecker P (2013). "Semilandmarks: a method for quantifying curves and surfaces". Hystrix, the Italian Journal of Mammalogy 24:103–109

Gutteridge L, Liebenberg L (2013). Mammals of Southern Africa and their Tracks and Signs. Jacana Media, Sunnyside

Hayward MW, Boitani L, Burrows ND, et al. (2015). Ecologists need robust survey designs, sampling and analytical methods. Journal of Applied Ecology 52:286–290.

Heinemeyer KS, Ulizio TJ, Harrison RL (2008) Natural sign: tracks and scats. In: Long RA, MacKay P, Zielinski WJ, Ray JC (eds) Noninvasive survey methods for carnivores. Island Press, Washington, pp 45–74.

Holekamp, K. E., Smale, L., Berg, R. & Cooper, S. M. (1997). "Hunting rates and hunting success in the spotted hyena". J. Zool. 242, 1–15.

Holekamp K.E., Sakai S.T., Lundrigan B.L. (2007). "Social intelligence in the spotted hyena (Crocuta crocuta)". Phil. Trans. R. Soc. B (2007) 362, 523–538. doi:10.1098/rstb.2006.1993

Hluhluwe game Reserve (2017). Hluhluwe Game Reserve Info. Available online at http://www.gamereservehluhluwe.com/, accessed 20 July 2017.

Jewell, Z. C., Alibhai, S. K., Weise, F., Munro, S., Van Vuuren, M., Van Vuuren, R. (2016). "Spotting Cheetahs: Identifying Individuals by their Footprints". J. Vis. Exp. (111), e54034, doi:10.3791/54034.

Jewell, Z. C., Alibhai, S.K. & Evans, J. W. (2014). "Monitoring mountain lion using footprints: A robust new technique". Wild Felid Monitor: 7 (1) pp 26-27.

Karanth KU, Nichols JD, Seidenstricker J, *et al.* (2003). "Science deficiency in conservation practice: the monitoring of tiger populations in India". Animal Conservation 6:141–146.

Kruuk, H. 1972 The spotted hyena: a study of predation and social behaviour. Chicago, IL: University of Chicago Press.

Law, P.R., Jewell, Z.C. & Alibhai, S.K. (2013). "Using Shape and Size to Quantify Variation in Footprints for Individual Identification: Case Study with White Rhino (Ceratotherium simum)". Wildlife Society Bulletin 37(2):433–438; 2013; DOI: 10.1002/wsb.250

Liebenberg L (1990). A Field Guide to the Animal Tracks of Southern Africa. David Philip, Claremont

Liebenberg L (2006). Persistence hunting by modern hunter-gatherers. Current Anthropology 47:1017–1026.

Linder W (2009). Digital Photogrammetry, Third Edition. Springer, Berlin

MacKay P, Zielinski WJ, Long RA, Ray JC (2008). Non-invasive research and carnivore conservation. In: Long RA, MacKay P, Zielinski WJ, Ray JC (eds) Non-invasive survey methods for carnivores. Island Press, Washington, pp 1–7

Marchal A.F.J. (2017) Monitoring lions (*Panthera leo*) using digital 3D models of their tracks. PhD thesis. University of ULg and University of Pretoria.

Marchal A.F.J., Lejeune P. et de Bruyn P.J.N (2016) "Virtual plaster cast: digital 3D modelling of lion paws and tracks using close-range photogrammetry". J. Zool. doi:10.1111/jzo.12342

Marker, L., Dickman, A., Wilkinson, C., Schumann, B., and Fabiano, E (2017). "The Namibian cheetah: Status report". Cat News. 3, 4-13.

Mills M. G. L., Juritz J. M. and Zucchini W. (2001). "Estimating the size of spotted hyaena (Crocuta crocuta) populations through playback recordings allowing for nonresponse". Animal Conservation 4: 335–343.

Minitab Inc (2017). Minitab 17 Support. Available online at http://support.minitab.com/en-us/minitab/17/, accessed 2 July 2017.

Oxford University Press (2017). English Oxford Living Dictionaries. Available at https://en.oxforddictionaries.com/definition/morphology, accessed 12 Aug 2017.

Sayad Saed, 2017. An introduction to Data Mining. Available online at http://www.saedsayad.com, accessed on 5 July 2017.

Mitteroecker P. and Gunz P. (2009). "Advances in Geometric morphometrics". Evol. Biol. 36(2), 235:247.

Mucina L, Rutherford MC (2006). The vegetation of South Africa, Lesotho and Swaziland. South African National Biodiversity Institute, Pretoria

Mullin SK, Taylo PJ (2002). "The effects of parallax on geometric morphometric data". Comput Biol Med. 2002 Nov: 32(6):455-64.

Muñoz-Muñoz F., Perpiñán D. (2010). "Measurement error in morphometric studies: comparison between manual and computarized methods". Ann. Zool Fennici 47:46-56.

Mushegian, A. 2017. "What is biodiversity?"; Encyclopedia of Life. Available online at http://eol.org/info/464, accessed 31 July 2017.

Nicholls, H. "The truth about spotted hyenas". BBC Earth 28 Oct. 2014. Available online at http://www.bbc.com/earth/story/20141028-the-truth-about-spotted-hyenas, accessed 31 July 2017.

Pimm S.L. and Raven P (2000). Biodiversity: Extinction by numbers. Nature 403: 843:845.

Ogutu J. O. and Dublin H. T. (1998). "The response of lions and spotted hyaenas to sound playbacks as a technique for estimating population size". African Journal of Ecology 36: 83–95.

R Development Core Team (2011). R: A Language and Environment for Statistical Computing. Vienna, Austria: the R Foundation for Statistical Computing. ISBN: 3-900051-07-0. Available online at http://www.R-project.org, accessed 9 Aug 2017.

Ripple WJ, Estes JA, Beschta RL, et al. (2014). "Status and ecological effects of the world's largest carnivores". Science 343 :1241484.

Ritchie EG, Johnson CN (2009). "Predator interactions, mesopredator release and biodiversity conservation". Ecology Letters 12:982–998.

Schindelin J., Kusztos F., Schmid B., (2007). Virtual Insect Brain Lab. Segmentation Editor. Available online at https://132.187.25.13/home/?category=Download&page=SegmentationEditor, accessed 10 July 2017.

Schindelin J., Arganda-Carreras I. and Frise E. et al. (2012), "Fiji: an open-source platform for biological-image analysis", Nature methods 9(7): 676-682, PMID 22743772. Available online at http://www.nature.com/nmeth/journal/v9/n7/full/nmeth.2019.html?foxtrotcallback=true, accessed 2 Aug 2017.

Schipper J (2007). “Camera-trap avoidance by Kinkajous Potos flavus: rethinking the “non-invasive” paradigm”. Small Carnivore Conservation 36:38–41.

Sherratt E. (2015). Quick Guide to *Geomorph* v.2.1.6, 101.

Stander P (1998). “Spoor counts as indices of large carnivore populations: the relationship between spoor frequency, sampling effort and true density”. Journal of Applied Ecology 35:378–385.

The R Stats Package (2017). “Documentation for package ‘stats’ version 3.5.0”. Available online at https://stat.ethz.ch/R-manual/R-devel/library/stats/html/00Index.html, accessed 9 Aug 2017.

Trinkel M. and Kastberger G. (2005). “Competitive interactions between spotted hyenas and lions in Etosha National Park, Namibia”. African Journal of Ecology. DOI:10.1111/j.1365-2028.2005.00574.x

Venables W.N. and Ripley B.D. (2002). Modern Applied Statistics with S. Fourth Edition, Springer, New York.

Wegge P, Pokheral CP, Jnawali SR (2004). “Effects of trapping effort and trap shyness on estimates of tiger abundance from camera trap studies”. Animal Conservation 7:251–256.

Wilson GJ and Delahay RJ (2001). “A review of methods to estimate the abundance of terrestrial carnivores using field signs and observation”. Wildlife Research 28:151–164.

WWF-India (2005). Reading pugmark: a pocket guide for forest guards. Tiger & Wildlife Programme. Available online at http://assets.wwfindia.org/downloads/reading_pugmarks.pdf, accessed 1 Aug 2017.

Zelditch ML, Swiderski DL, Sheets HD (2012). Geometric morphometrics for biologists: a primer, Second Edition. Academic Press, Amsterdam.

APPENDICES

Appendix A: Evolution of Spotted Hyena population in HiP

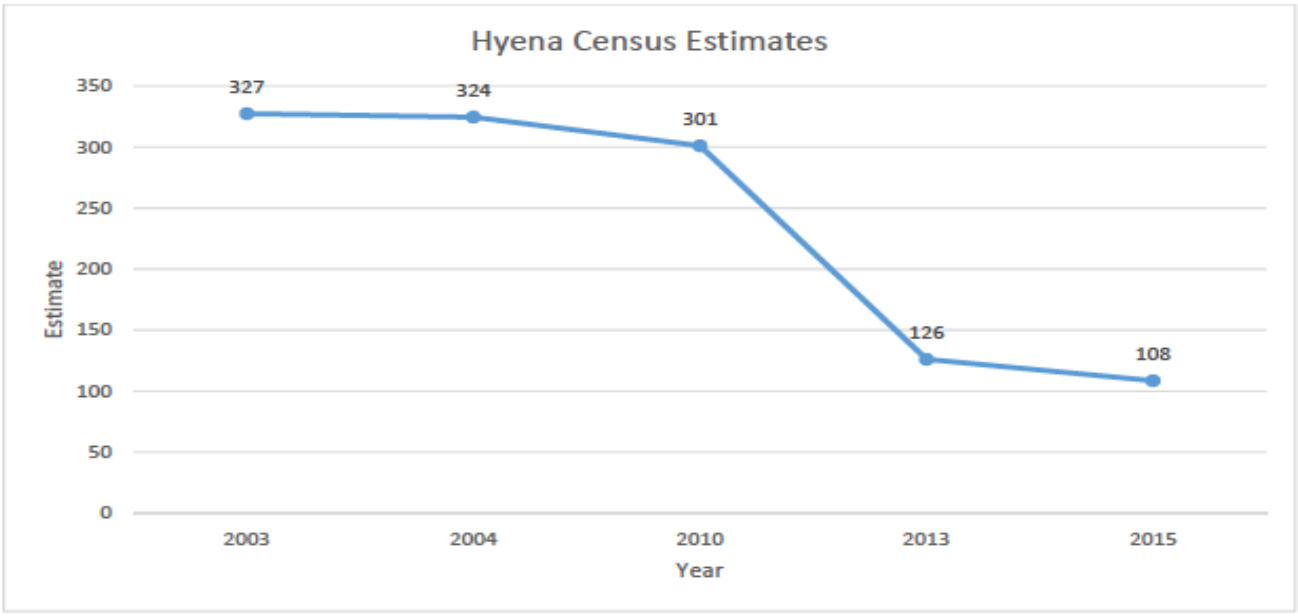

Figure 33 - *Census estimates of Spotted Hyena population in HiP from 2003 to 2015 (EKZNW, 2015).*

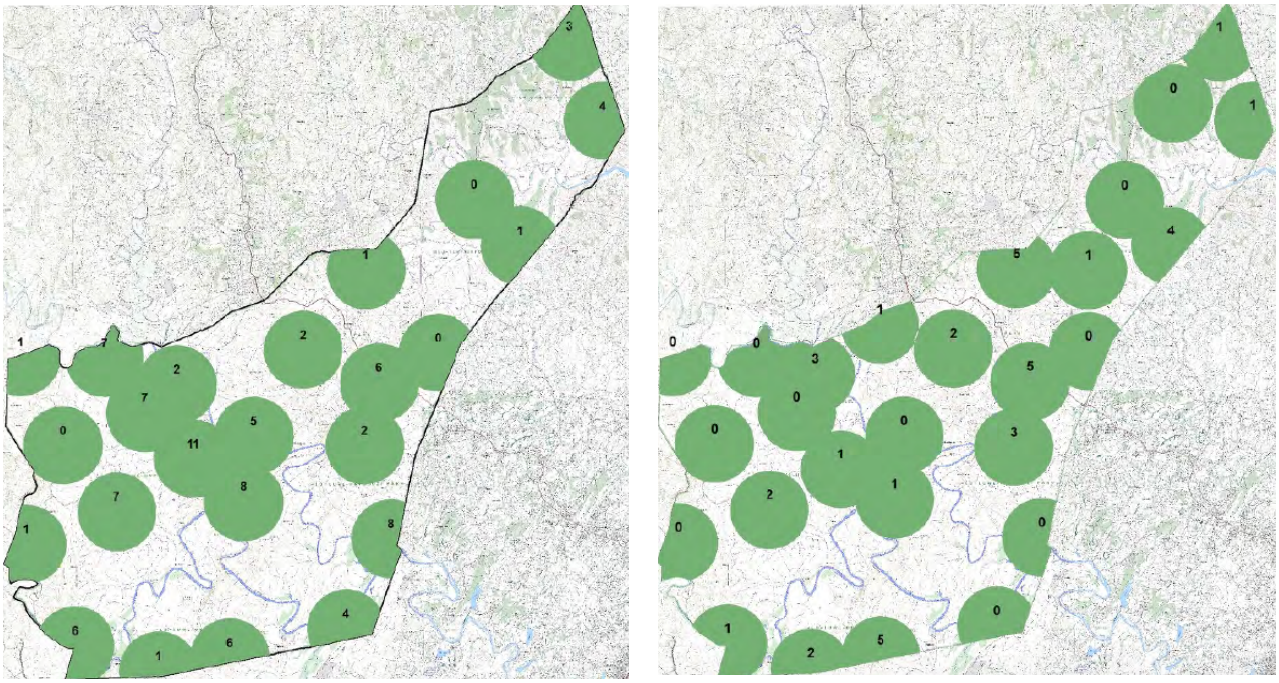

Figure 34 – *Location of the call-ins station for censoring spotted hyena population in HiP, and number of spotted hyenas having responded in 2010 (A) and 2015 (B) (EKZNW, 2015).*

Appendix B: Landmark displacements on 2D-entities

Fixed landmarks were initially digitized in *Geomorph* using the function digitize2d. The coordinates of the curve-sliders were exported from ImageJ, as suggested by Sherratt (2015), and joined to the coordinates of the fixed landmarks in a same *Geomorph* array. But after the Procrustes superimposition, displacements such as the one displayed by Figure 34 A, occurred for every pad. We assumed it was due to a modification of the scale of the image when it was imported in *Geomorph*. This scaling issue could not be solved at the time.

To get around this, fixed landmarks were digitized and exported from ImageJ (as for the curve-sliders), so that the same scale could be guaranteed for both types of landmarks. It worked for the main pads and toes 1 (Figure 34 B), but not for toes 2, 3 and 4, as displacements such as the one displayed by Figure 34 C kept occurring after the Procrustes superimposition. However, when the coordinates of the landmarks of the pads were grouped all together to represent the entire segmented track, no displacement occurred for any of the pad (Figure 34 D), although the same *.txt files containing the same coordinates were used both for the independent pads and for the entire track.

As this displacement issue could not be solved at the time, the scenarios involving the combination "2D –fixed+curve – independent pads" was not conducted and compared to the others.

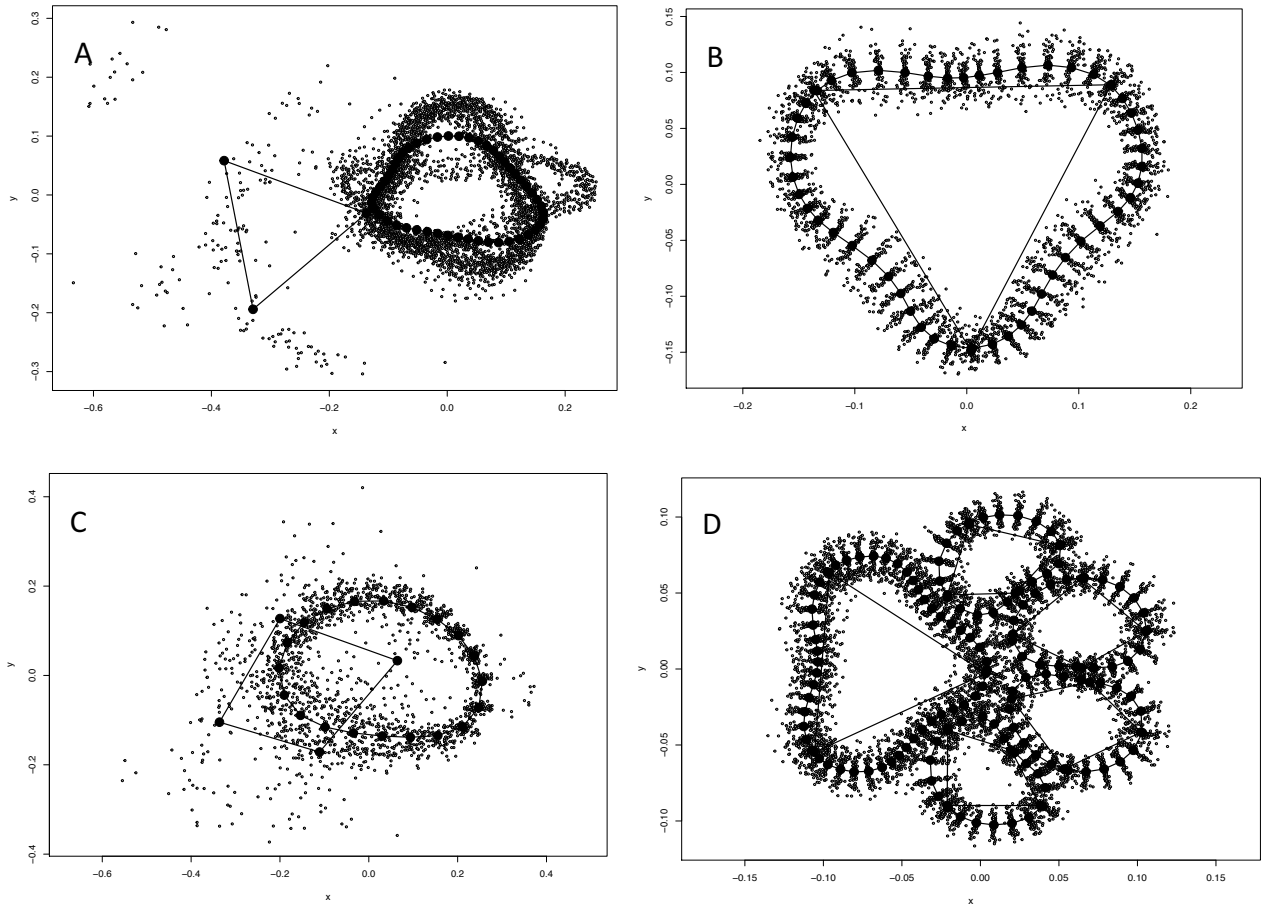

Figure 35 - *Displacements between mean configurations of fixed landmarks and curve-sliders in 2D. Each grey dot corresponds to the Procrustes coordinates of a landmark of a specimen; the black dots represent the landmarks of the mean shape. The straight lines connect the fixed landmarks of the mean shape to each other, while the curved lines surround the mean configuration characterized by the curve-sliders. Displacements between the two types of landmarks occurred when fixed landmarks were digitized in Geomorph (A), but not when they were positioned in ImageJ and exported as *.txt file. This was the case for main pads (B) and toes 1, but not for toes 2, 3 and 4, for which displacements kept occurring (C). However, when Procrustes superimposition was applied on the entire track, there was no displacement for any of the pads (D), although the coordinates of the landmarks originated from the same *.txt files both for the independent pads and for the entire track.*

Appendix C: *Photoscan* parameters

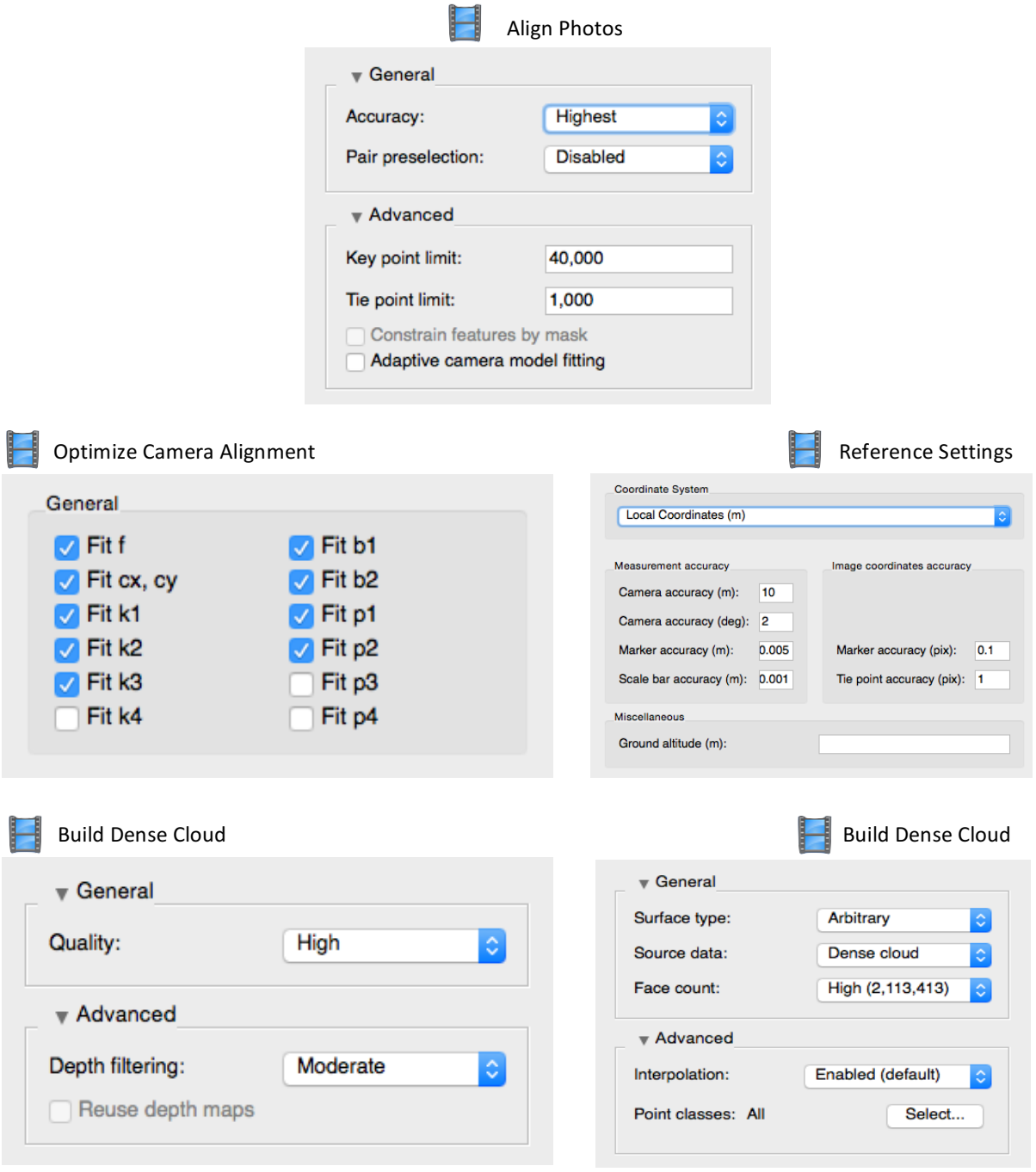

Figure 36 - *Parameters applied during the "Camera Alignment", "Build Dense Point", and "Build Mesh" steps of the 3D-modelling process in Photoscan.*

Appendix D: 2D and 3D arrays in *Geomorph*

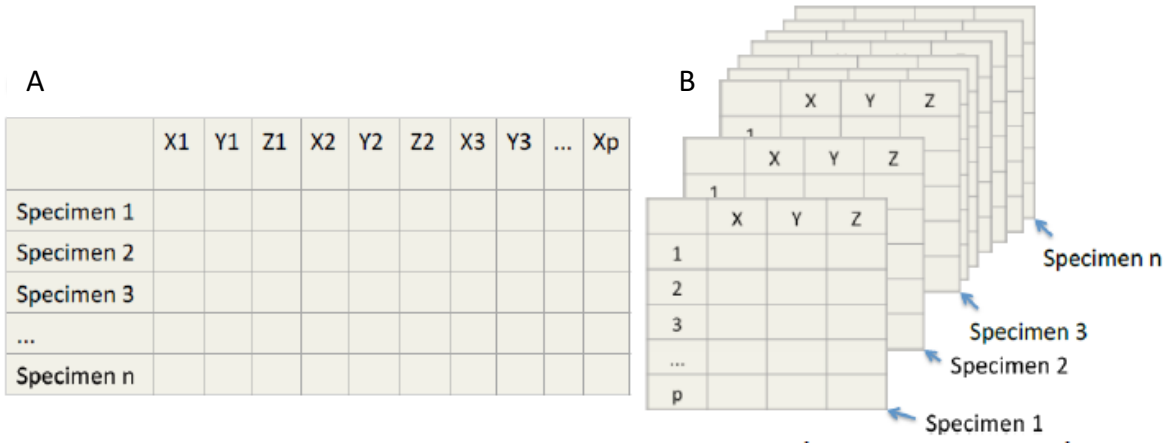

Figure 37 – *Schematic of 2D (A) and 3D (B) arrays, two formats used for data treatment in Geomorph, both for 2D and 3D landmarks. (Sherratt, 2015).*

Appendix E: Procrustes ANOVA

Table 6 - *Results of the Procrustes ANOVAs conducted on the different 2D objects (entire track, main pad (MP), or one of the four toes (T1 to T4)) which were characterized by fixed landmarks only (fixed) or by fixed landmarks and curve-sliders ("fixed+curve").*

Object	Fixed	Fixed + curve
Entire track	Df SS MS Rsq F Z Pr(>F) position 3 0.45024 0.150079 0.34647 13.43 9.0891 0.001 ** Residuals 76 0.84928 0.011175 Total 79 1.29952 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.20919 0.069729 0.35907 14.193 9.6005 0.001 ** Residuals 76 0.37339 0.004913 Total 79 0.58258 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
MP	Df SS MS Rsq F Z Pr(>F) position 3 0.31778 0.105926 0.33201 12.591 4.2529 0.001 ** Residuals 76 0.63935 0.008413 Total 79 0.95713 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.25626 0.085419 0.34408 13.289 6.2041 0.001 ** Residuals 76 0.48851 0.006428 Total 79 0.74477 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
T1	Df SS MS Rsq F Z Pr(>F) position 3 0.05143 0.0171429 0.089722 2.497 2.1728 0.005 ** Residuals 76 0.52177 0.0068654 Total 79 0.57320 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.05143 0.0171429 0.089722 2.497 2.1728 0.005 ** Residuals 76 0.52177 0.0068654 Total 79 0.57320 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
T2	Df SS MS Rsq F Z Pr(>F) position 3 0.11375 0.037918 0.15247 4.5576 3.5353 0.001 ** Residuals 76 0.63230 0.008320 Total 79 0.74605 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	NA
T3	Df SS MS Rsq F Z Pr(>F) position 3 0.11165 0.037218 0.17164 5.2491 3.6136 0.001 ** Residuals 76 0.53886 0.007090 Total 79 0.65051 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	NA
T4	Df SS MS Rsq F Z Pr(>F) position 3 0.05030 0.0167658 0.065652 1.78 1.4362 0.069 . Residuals 76 0.71583 0.0094188 Total 79 0.76612 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	NA

Table 7 - *Results of the Procrustes ANOVAs conducted on the different 2D objects (entire track, main pad (MP), or one of the four toes (T1 to T4)) which were characterized by fixed landmarks only (fixed), fixed landmarks and curve-sliders ("fixed+curve"), or fixed landmarks and curve- and surface-sliders ("fixed+curve+surface")*

Object	Fixed	Fixed + curve	Fixed + curve + surface
Entire track	Df SS MS Rsq F Z Pr(>F) position 3 0.68380 0.22793 0.41449 17.934 9.4914 0.001 ** Residuals 76 0.96593 0.01271 Total 79 1.64973 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.35809 0.119365 0.39187 16.325 10.404 0.001 ** Residuals 76 0.55570 0.007312 Total 79 0.91380 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.22478 0.074927 0.36451 14.531 10.995 0.001 ** Residuals 76 0.39189 0.005157 Total 79 0.61668 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
MP	Df SS MS Rsq F Z Pr(>F) position 3 0.86096 0.286988 0.61421 40.333 5.4301 0.001 ** Residuals 76 0.54078 0.007115 Total 79 1.40174 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.52453 0.17484 0.45402 21.066 7.4135 0.001 ** Residuals 76 0.63078 0.00830 Total 79 1.15531 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.32674 0.108914 0.37565 15.242 7.9913 0.001 ** Residuals 76 0.54305 0.007145 Total 79 0.86979 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
T1	Df SS MS Rsq F Z Pr(>F) position 3 0.04414 0.0147118 0.06249 1.6886 1.4545 0.067 . Residuals 76 0.66214 0.0087124 Total 79 0.70627 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.08405 0.028016 0.092726 2.5891 4.7649 0.001 ** Residuals 76 0.82238 0.010821 Total 79 0.90643 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.08097 0.0269907 0.097208 2.7278 5.5626 0.001 ** Residuals 76 0.75200 0.0098948 Total 79 0.83298 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
T2	Df SS MS Rsq F Z Pr(>F) position 3 0.02470 0.0082335 0.031294 0.8184 -0.29722 0.65 Residuals 76 0.76462 0.0100607 Total 79 0.78932	Df SS MS Rsq F Z Pr(>F) position 3 0.05603 0.018676 0.055318 1.4834 2.0895 0.021 * Residuals 76 0.95681 0.012590 Total 79 1.01283 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.04885 0.016283 0.049993 1.3331 1.5761 0.056 . Residuals 76 0.92826 0.012214 Total 79 0.97711 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
T3	Df SS MS Rsq F Z Pr(>F) position 3 0.06457 0.0215245 0.089936 2.5035 2.3535 0.006 ** Residuals 76 0.65342 0.0085976 Total 79 0.71799 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.05191 0.017303 0.06011 1.6202 2.4657 0.005 ** Residuals 76 0.81166 0.010680 Total 79 0.86357 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.05037 0.016791 0.054328 1.4554 1.8546 0.036 * Residuals 76 0.87685 0.011537 Total 79 0.92722 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
T4	Df SS MS Rsq F Z Pr(>F) position 3 0.05695 0.018984 0.057723 1.5519 1.2993 0.073 . Residuals 76 0.92971 0.012233 Total 79 0.98667 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.06696 0.022319 0.074045 2.0258 3.372 0.001 ** Residuals 76 0.83732 0.011017 Total 79 0.90427 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1	Df SS MS Rsq F Z Pr(>F) position 3 0.05523 0.018409 0.059664 1.6074 2.0732 0.032 * Residuals 76 0.87043 0.011453 Total 79 0.92566 --- Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Appendix F: Centroid size analyses

Table 8 - *Results of statistical analyses conducted on the Centroid sizes of the entire track and main pad of 2D-models of spotted hyena tracks. The 2D-models were characterized either by fixed landmarks only ("fixed") or by fixed landmarks and curve-sliders ("fixed+curve").*

2D – entire track – fixed	2D – entire track – fixed+curve	2D – MP – fixed

`> shapiro.test(data$Csize)`
 	
`Shapiro-Wilk normality test`
 	
`data: data$Csize`
`W = 0.98386, p-value = 0.4111`
 	
`> bartlett.test(data$Csize~as.factor(data$position))`
 	
`Bartlett test of homogeneity of variances`
 	
`data: data$Csize by as.factor(data$position)`
`Bartlett's K-squared = 2.8957, df = 3, p-value = 0.408`
 	
`> anova(analysis)`
`Analysis of Variance Table`
 	
`Response: data$Csize`
`Df Sum Sq Mean Sq F value Pr(>F)`
`as.factor(data$position) 3 682736 227579 43.808 < 2.2e-16 ***`
`Residuals 76 394810 5195`
`---`
`Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1`
 	
`> TukeyHSD(aov(analysis))`
`Tukey multiple comparisons of means`
`95% family-wise confidence level`
 	
`Fit: aov(formula = analysis)`
 	
`$`as.factor(data$position)``
`diff lwr upr p adj`
`FR-FL -11.37679 -71.24741 48.49384 0.9590199`
`HL-FL -204.19974 -264.07036 -144.32912 0.0000000`
`HR-FL -173.84528 -233.71590 -113.97465 0.0000000`
`HL-FR -192.82295 -252.69358 -132.95233 0.0000000`
`HR-FR -162.46849 -222.33911 -102.59787 0.0000000`
`HR-HL 30.35446 -29.51616 90.22509 0.5457995`
	`> shapiro.test(data$Csize)`
	
	`Shapiro-Wilk normality test`
	
	`data: data$Csize`
	`W = 0.98363, p-value = 0.3993`
	
	`> bartlett.test(data$Csize~as.factor(data$position))`
	
	`Bartlett test of homogeneity of variances`
	
	`data: data$Csize by as.factor(data$position)`
	`Bartlett's K-squared = 3.1512, df = 3, p-value = 0.3689`
	
	`> anova(analysis)`
	`Analysis of Variance Table`
	
	`Response: data$Csize`
	`Df Sum Sq Mean Sq F value Pr(>F)`
	`as.factor(data$position) 3 4451441 1483814 32.425 1.332e-13 ***`
	`Residuals 76 3477863 45761`
	`---`
	`Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1`
	
	`> TukeyHSD(aov(analysis))`
	`Tukey multiple comparisons of means`
	`95% family-wise confidence level`
	
	`Fit: aov(formula = analysis)`
	
	`$`as.factor(data$position)``
	`diff lwr upr p adj`
	`FR-FL -32.50588 -210.2012 145.1894 0.9631844`
	`HL-FL -520.03690 -697.7322 -342.3416 0.0000000`
	`HR-FL -449.62368 -627.3190 -271.9284 0.0000000`
	`HL-FR -487.53102 -665.2263 -309.8357 0.0000000`
	`HR-FR -417.11780 -594.8131 -239.4225 0.0000002`
	`HR-HL 70.41322 -107.2821 248.1085 0.7260468`
		`> shapiro.test(data$Csize)`
		
		`Shapiro-Wilk normality test`
		
		`data: data$Csize`
		`W = 0.97786, p-value = 0.1797`
		
		`> bartlett.test(data$Csize~as.factor(data$position))`
		
		`Bartlett test of homogeneity of variances`
		
		`data: data$Csize by as.factor(data$position)`
		`Bartlett's K-squared = 6.5611, df = 3, p-value = 0.08728`
		
		`> anova(analysis)`
		`Analysis of Variance Table`
		
		`Response: data$Csize`
		`Df Sum Sq Mean Sq F value Pr(>F)`
		`as.factor(data$position) 3 84998 28332.6 16.226 3.031e-08 ***`
		`Residuals 76 132703 1746.1`
		`---`
		`Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1`
		
		`> TukeyHSD(aov(analysis))`
		`Tukey multiple comparisons of means`
		`95% family-wise confidence level`
		
		`Fit: aov(formula = analysis)`
		
		`$`as.factor(data$position)``
		`diff lwr upr p adj`
		`FR-FL 14.36987 -20.34050 49.08024 0.6982131`
		`HL-FL -64.39719 -99.10756 -29.68681 0.0000343`
		`HR-FL -47.88793 -82.59830 -13.17756 0.0028775`
		`HL-FR -78.76706 -113.47743 -44.05669 0.0000004`
		`HR-FR -62.25780 -96.96817 -27.54743 0.0000634`
		`HR-HL 16.50926 -18.20111 51.21963 0.5976903`

Table 9 *- Results of statistical analyses conducted on the Centroid sizes of the main pad and toe 1 of 2D-models of spotted hyena tracks. The 2D-models were characterized either by fixed landmarks only ("fixed") or by fixed landmarks and curve-sliders ("fixed+curve").*

2D – MP – fixed+curve	2D – T1 – fixed	2D – T1 – fixed+curve

`> shapiro.test(data$Csize)`
 	
`Shapiro-Wilk normality test`
 	
`data: data$Csize`
`W = 0.98461, p-value = 0.4521`
 	
`> bartlett.test(data$Csize~as.factor(data$position))`
 	
`Bartlett test of homogeneity of variances`
 	
`data: data$Csize by as.factor(data$position)`
`Bartlett's K-squared = 3.8976, df = 3, p-value = 0.2727`
 	
`> anova(analysis)`
`Analysis of Variance Table`
 	
`Response: data$Csize`
`Df Sum Sq Mean Sq F value Pr(>F)`
`as.factor(data$position) 3 1053780 351260 16.45 2.481e-08 ***`
`Residuals 76 1622828 21353`
`---`
`Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1`
 	
`> TukeyHSD(aov(analysis))`
`Tukey multiple comparisons of means`
`95% family-wise confidence level`
 	
`Fit: aov(formula = analysis)`
 	
`$`as.factor(data$position)``
`diff lwr upr p adj`
`FR-FL 57.71981 -63.66265 179.10227 0.5978704`
`HL-FL -218.44727 -339.82973 -97.06481 0.0000598`
`HR-FL -170.47642 -291.85888 -49.09396 0.0023311`
`HL-FR -276.16708 -397.54954 -154.78462 0.0000004`
`HR-FR -228.19623 -349.57869 -106.81377 0.0000267`
`HR-HL 47.97085 -73.41161 169.35331 0.7276779`
	`> shapiro.test(data$Csize)`
	
	`Shapiro-Wilk normality test`
	
	`data: data$Csize`
	`W = 0.9694, p-value = 0.05197`
	
	`> bartlett.test(data$Csize~as.factor(data$position))`
	
	`Bartlett test of homogeneity of variances`
	
	`data: data$Csize by as.factor(data$position)`
	`Bartlett's K-squared = 3.822, df = 3, p-value = 0.2813`
	
	`> anova(analysis)`
	`Analysis of Variance Table`
	
	`Response: data$Csize`
	`Df Sum Sq Mean Sq F value Pr(>F)`
	`as.factor(data$position) 3 29676 9892.0 26.401 8.368e-12 ***`
	`Residuals 76 28476 374.7`
	`---`
	`Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1`
	
	`> TukeyHSD(aov(analysis))`
	`Tukey multiple comparisons of means`
	`95% family-wise confidence level`
	
	`Fit: aov(formula = analysis)`
	
	`$`as.factor(data$position)``
	`diff lwr upr p adj`
	`FR-FL -0.5046587 -16.58379 15.57448 0.9997973`
	`HL-FL -41.4556594 -57.53479 -25.37653 0.0000000`
	`HR-FL -35.6468803 -51.72601 -19.56775 0.0000008`
	`HL-FR -40.9510007 -57.03013 -24.87187 0.0000000`
	`HR-FR -35.1422217 -51.22136 -19.06309 0.0000011`
	`HR-HL 5.8087790 -10.27035 21.88791 0.7785301`
		`> shapiro.test(data$Csize)`
		
		`Shapiro-Wilk normality test`
		
		`data: data$Csize`
		`W = 0.97039, p-value = 0.06007`
		
		`> bartlett.test(data$Csize~as.factor(data$position))`
		
		`Bartlett test of homogeneity of variances`
		
		`data: data$Csize by as.factor(data$position)`
		`Bartlett's K-squared = 1.2797, df = 3, p-value = 0.734`
		
		`> anova(analysis)`
		`Analysis of Variance Table`
		
		`Response: data$Csize`
		`Df Sum Sq Mean Sq F value Pr(>F)`
		`as.factor(data$position) 3 187055 62352 32.553 1.225e-13 ***`
		`Residuals 76 145568 1915`
		`---`
		`Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1`
		
		`> TukeyHSD(aov(analysis))`
		`Tukey multiple comparisons of means`
		`95% family-wise confidence level`
		
		`Fit: aov(formula = analysis)`
		
		`$`as.factor(data$position)``
		`diff lwr upr p adj`
		`FR-FL -9.594784 -45.94882 26.75925 0.8993602`
		`HL-FL -108.643427 -144.99746 -72.28939 0.0000000`
		`HR-FL -92.546609 -128.90065 -56.19257 0.0000000`
		`HL-FR -99.048643 -135.40268 -62.69461 0.0000000`
		`HR-FR -82.951825 -119.30586 -46.59779 0.0000004`
		`HR-HL 16.096818 -20.25722 52.45086 0.6517867`

Table 10 - *Results of statistical analyses conducted on the Centroid sizes of toes 2, 3 and 4 of 2D-models of spotted hyena tracks. The 2D-models were characterized by fixed landmarks only ("fixed").*

2D – T2 – fixed	2D – T3 – fixed	2D – T4 – fixed

`> shapiro.test(data$Csize)`
 	
`Shapiro-Wilk normality test`
 	
`data: data$Csize`
`W = 0.98008, p-value = 0.2465`
 	
`> bartlett.test(data$Csize~as.factor(data$position))`
 	
`Bartlett test of homogeneity of variances`
 	
`data: data$Csize by as.factor(data$position)`
`Bartlett's K-squared = 5.0935, df = 3, p-value = 0.1651`
 	
`> anova(analysis)`
`Analysis of Variance Table`
 	
`Response: data$Csize`
`Df Sum Sq Mean Sq F value Pr(>F)`
`as.factor(data$position) 3 23883 7961.1 16.58 2.211e-08 ***`
`Residuals 76 36493 480.2`
`---`
`Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1`
 	
`> TukeyHSD(aov(analysis))`
`Tukey multiple comparisons of means`
`95% family-wise confidence level`
 	
`Fit: aov(formula = analysis)`
 	
`$`as.factor(data$position)``
`diff lwr upr p adj`
`FR-FL -1.524390 -19.72657 16.67779 0.9962105`
`HL-FL -38.211096 -56.41327 -20.00892 0.0000027`
`HR-FL -31.794257 -49.99643 -13.59208 0.0001006`
`HL-FR -36.686706 -54.88888 -18.48453 0.0000066`
`HR-FR -30.269867 -48.47204 -12.06769 0.0002253`
`HR-HL 6.416839 -11.78534 24.61902 0.7910112`
	`> shapiro.test(data$Csize)`
	
	`Shapiro-Wilk normality test`
	
	`data: data$Csize`
	`W = 0.964, p-value = 0.02372`
	
	`> bartlett.test(data$Csize~as.factor(data$position))`
	
	`Bartlett test of homogeneity of variances`
	
	`data: data$Csize by as.factor(data$position)`
	`Bartlett's K-squared = 1.282, df = 3, p-value = 0.7334`
	
	`> kruskal.test(x=data$Csize, g=data$position)`
	
	`Kruskal-Wallis rank sum test`
	
	`data: data$Csize and data$position`
	`Kruskal-Wallis chi-squared = 29.465, df = 3, p-value = 1.788e-06`
	
	`> TukeyHSD(aov(analysis))`
	`Tukey multiple comparisons of means`
	`95% family-wise confidence level`
	
	`Fit: aov(formula = analysis)`
	
	`$`as.factor(data$position)``
	`diff lwr upr p adj`
	`FR-FL 16.80907 -3.770900 37.389044 0.1482339`
	`HL-FL -30.49763 -51.077604 -9.917660 0.0011885`
	`HR-FL -15.96674 -36.546715 4.613229 0.1833381`
	`HL-FR -47.30670 -67.886676 -26.726732 0.0000003`
	`HR-FR -32.77581 -53.355787 -12.195843 0.0004359`
	`HR-HL 14.53089 -6.049083 35.110861 0.2563180`
		`> shapiro.test(data$Csize)`
		
		`Shapiro-Wilk normality test`
		
		`data: data$Csize`
		`W = 0.97915, p-value = 0.2161`
		
		`> bartlett.test(data$Csize~as.factor(data$position))`
		
		`Bartlett test of homogeneity of variances`
		
		`data: data$Csize by as.factor(data$position)`
		`Bartlett's K-squared = 6.9887, df = 3, p-value = 0.07226`
		
		`> anova(analysis)`
		`Analysis of Variance Table`
		
		`Response: data$Csize`
		`Df Sum Sq Mean Sq F value Pr(>F)`
		`as.factor(data$position) 3 33810 11270.1 26.312 8.925e-12 ***`
		`Residuals 76 32553 428.3`
		`---`
		`Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1`
		
		`> TukeyHSD(aov(analysis))`
		`Tukey multiple comparisons of means`
		`95% family-wise confidence level`
		
		`Fit: aov(formula = analysis)`
		
		`$`as.factor(data$position)``
		`diff lwr upr p adj`
		`FR-FL 9.914868 -7.276659 27.10640 0.4337085`
		`HL-FL -36.315617 -53.507145 -19.12409 0.0000024`
		`HR-FL -34.767210 -51.958738 -17.57568 0.0000062`
		`HL-FR -46.230485 -63.422013 -29.03896 0.0000000`
		`HR-FR -44.682078 -61.873606 -27.49055 0.0000000`
		`HR-HL 1.548407 -15.643121 18.73993 0.9953000`

Table 11 - *Results of statistical analyses conducted on the Centroid sizes of the entire track of 3D-models of spotted hyena tracks. The 3D-models were characterized either by fixed landmarks only ("fixed"), fixed landmarks and curve-sliders ("fixed+curve"), or fixed landmarks and curve- and surface-sliders ("fixed+curve+surf").*

3D – entire track – fixed	3D – entire track – fixed+curve	3D – entire track – fixed+curve+surf
> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95814, p-value = 0.01037 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 0.85103, df = 3, p-value = 0.8372 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.665, df = 3, p-value = 0.6447	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.9565, p-value = 0.008273 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 0.63072, df = 3, p-value = 0.8894 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.22, df = 3, p-value = 0.7482	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95683, p-value = 0.008654 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 0.59421, df = 3, p-value = 0.8978 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.3796, df = 3, p-value = 0.7103

Table 12 - *Results of statistical analyses conducted on the Centroid sizes of the main pad of 3D-models of spotted hyena tracks. The 3D-models were characterized either by fixed landmarks only ("fixed"), fixed landmarks and curve-sliders ("fixed+curve"), or fixed landmarks and curve- and surface-sliders ("fixed+curve+surf").*

3D – MP – fixed	3D – MP – fixed+curve	3D – MP – fixed+curve+surf
> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95831, p-value = 0.01062 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 0.60492, df = 3, p-value = 0.8953 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.3835, df = 3, p-value = 0.4967	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95724, p-value = 0.00916 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 0.56997, df = 3, p-value = 0.9033 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.2098, df = 3, p-value = 0.53	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95709, p-value = 0.00897 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 0.56803, df = 3, p-value = 0.9037 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.1944, df = 3, p-value = 0.533

Table 13 - *Results of statistical analyses conducted on the Centroid sizes of the toe 1 of 3D-models of spotted hyena tracks. The 3D-models were characterized either by fixed landmarks only ("fixed"), fixed landmarks and curve-sliders ("fixed+curve"), or fixed landmarks and curve- and surface-sliders ("fixed+curve+surf").*

3D – T1 – fixed	3D – T1 – fixed+curve	3D – T1 – fixed+curve+surf
> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95904, p-value = 0.01176 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.5037, df = 3, p-value = 0.6814 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.588, df = 3, p-value = 0.4596	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95902, p-value = 0.01173 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.8104, df = 3, p-value = 0.6127 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.6846, df = 3, p-value = 0.4428	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.96055, p-value = 0.01453 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.7071, df = 3, p-value = 0.6354 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.8413, df = 3, p-value = 0.4167

Table 14 - *Results of statistical analyses conducted on the Centroid sizes of the toe 2 of 3D-models of spotted hyena tracks. The 3D-models were characterized either by fixed landmarks only ("fixed"), fixed landmarks and curve-sliders ("fixed+curve"), or fixed landmarks and curve- and surface-sliders ("fixed+curve+surf").*

3D – T2 – fixed	3D – T2 – fixed+curve	3D – T2 – fixed+curve+surf
> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95729, p-value = 0.009215 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.367, df = 3, p-value = 0.7133 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.1191, df = 3, p-value = 0.5481	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95686, p-value = 0.008695 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.4398, df = 3, p-value = 0.6962 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.2956, df = 3, p-value = 0.5134	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95789, p-value = 0.01002 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.4653, df = 3, p-value = 0.6903 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.3933, df = 3, p-value = 0.4949

Table 15 - *Results of statistical analyses conducted on the Centroid sizes of the toe 3 of 3D-models of spotted hyena tracks. The 3D-models were characterized either by fixed landmarks only ("fixed"), fixed landmarks and curve-sliders ("fixed+curve"), or fixed landmarks and curve- and surface-sliders ("fixed+curve+surf").*

3D – T3 – fixed	3D – T3 – fixed+curve	3D – T3 – fixed+curve+surf
> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95557, p-value = 0.007276 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.0462, df = 3, p-value = 0.7901 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.8452, df = 3, p-value = 0.6052	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95582, p-value = 0.007528 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.224, df = 3, p-value = 0.7473 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.8137, df = 3, p-value = 0.612	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95684, p-value = 0.008666 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.3291, df = 3, p-value = 0.7222 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.7872, df = 3, p-value = 0.6177

Table 16 - *Results of statistical analyses conducted on the Centroid sizes of the toe 3 of 3D-models of spotted hyena tracks. The 3D-models were characterized either by fixed landmarks only ("fixed"), fixed landmarks and curve-sliders ("fixed+curve"), or fixed landmarks and curve- and surface-sliders ("fixed+curve+surf").*

3D – T3 – fixed	3D – T3 – fixed+curve	3D – T3 – fixed+curve+surf
> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95557, p-value = 0.007276 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.0462, df = 3, p-value = 0.7901 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.8452, df = 3, p-value = 0.6052	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95582, p-value = 0.007528 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.224, df = 3, p-value = 0.7473 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.8137, df = 3, p-value = 0.612	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.95684, p-value = 0.008666 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.3291, df = 3, p-value = 0.7222 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.7872, df = 3, p-value = 0.6177

Table 17 - *Results of statistical analyses conducted on the Centroid sizes of the toe 4 of 3D-models of spotted hyena tracks. The 3D-models were characterized either by fixed landmarks only ("fixed"), fixed landmarks and curve-sliders ("fixed+curve"), or fixed landmarks and curve- and surface-sliders ("fixed+curve+surf").*

3D – T4 – fixed	3D – T4 – fixed+curve	3D – T4 – fixed+curve+surf
> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.96179, p-value = 0.01732 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 0.97668, df = 3, p-value = 0.8069 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.0531, df = 3, p-value = 0.5614	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.96173, p-value = 0.01717 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.2586, df = 3, p-value = 0.739 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 1.9974, df = 3, p-value = 0.5729	> shapiro.test(data$Csize) Shapiro-Wilk normality test data: data$Csize W = 0.96151, p-value = 0.01664 > bartlett.test(data$Csize~as.factor(data$Position)) Bartlett test of homogeneity of variances data: data$Csize by as.factor(data$Position) Bartlett's K-squared = 1.284, df = 3, p-value = 0.7329 > kruskal.test(x=data$Csize, g=data$position) Kruskal-Wallis rank sum test data: data$Csize and data$position Kruskal-Wallis chi-squared = 2.1961, df = 3, p-value = 0.5327

Appendix G: PCA plots

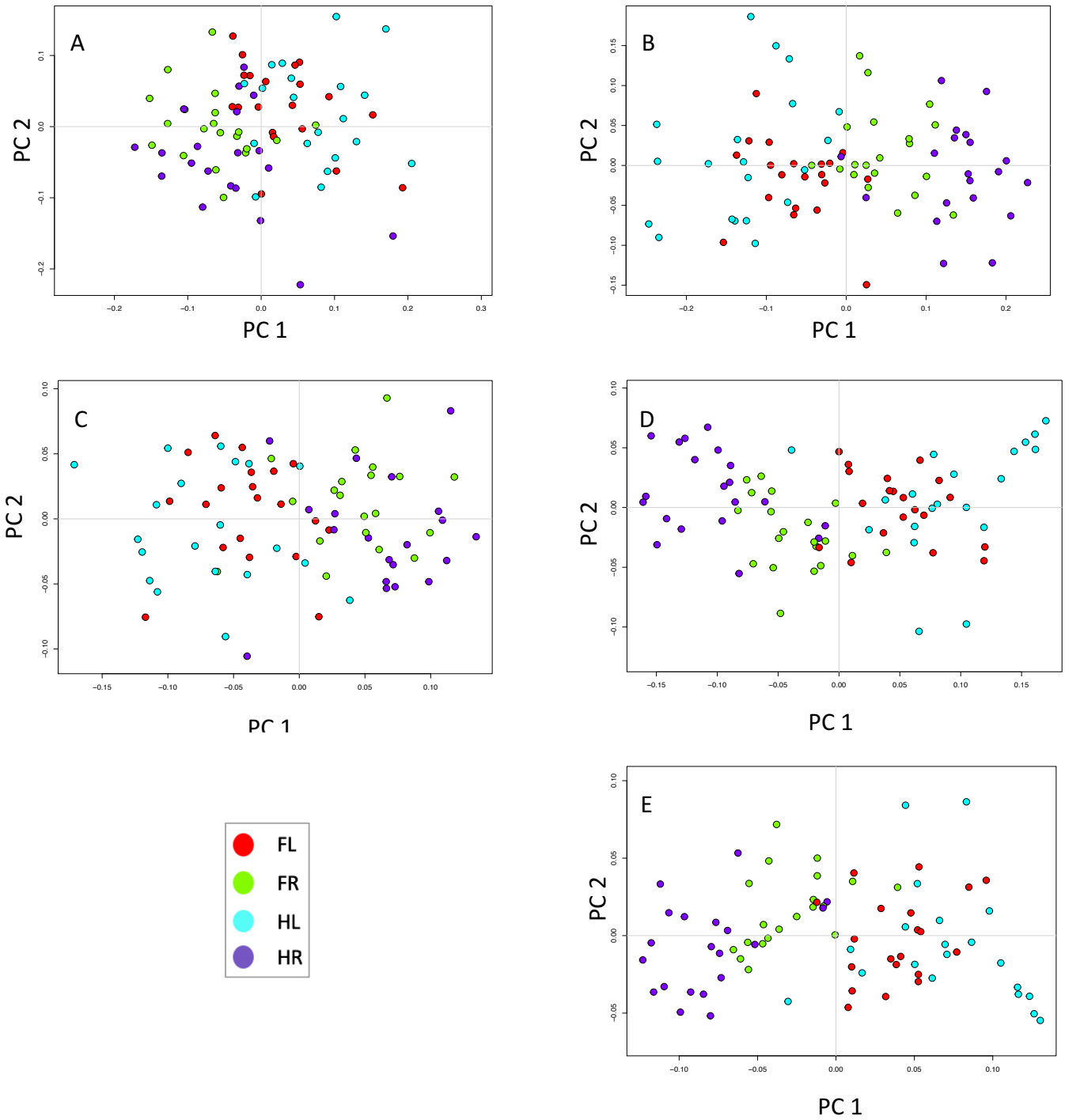

Figure 38 – *Principal Components Analyses conducted on main pads. Figures A and B display the PCA conducted on data that were extracted using fixed landmarks on 2D- and 3D-models respectively. Figures C and D display the PCA conducted on data that were extracted using fixed landmarks and curve-sliders on 2D- and 3D-models respectively. Figure E displays the PCA conducted on data that were extracted using fixed landmarks, curve- and surface-sliders on 3D-models. The colour code corresponds to the different track positions: red for Front Left ("FL"), green for Front Right ("FR"), blue for Hind Left ("HL"), and purple for Hind Right ("HR").*

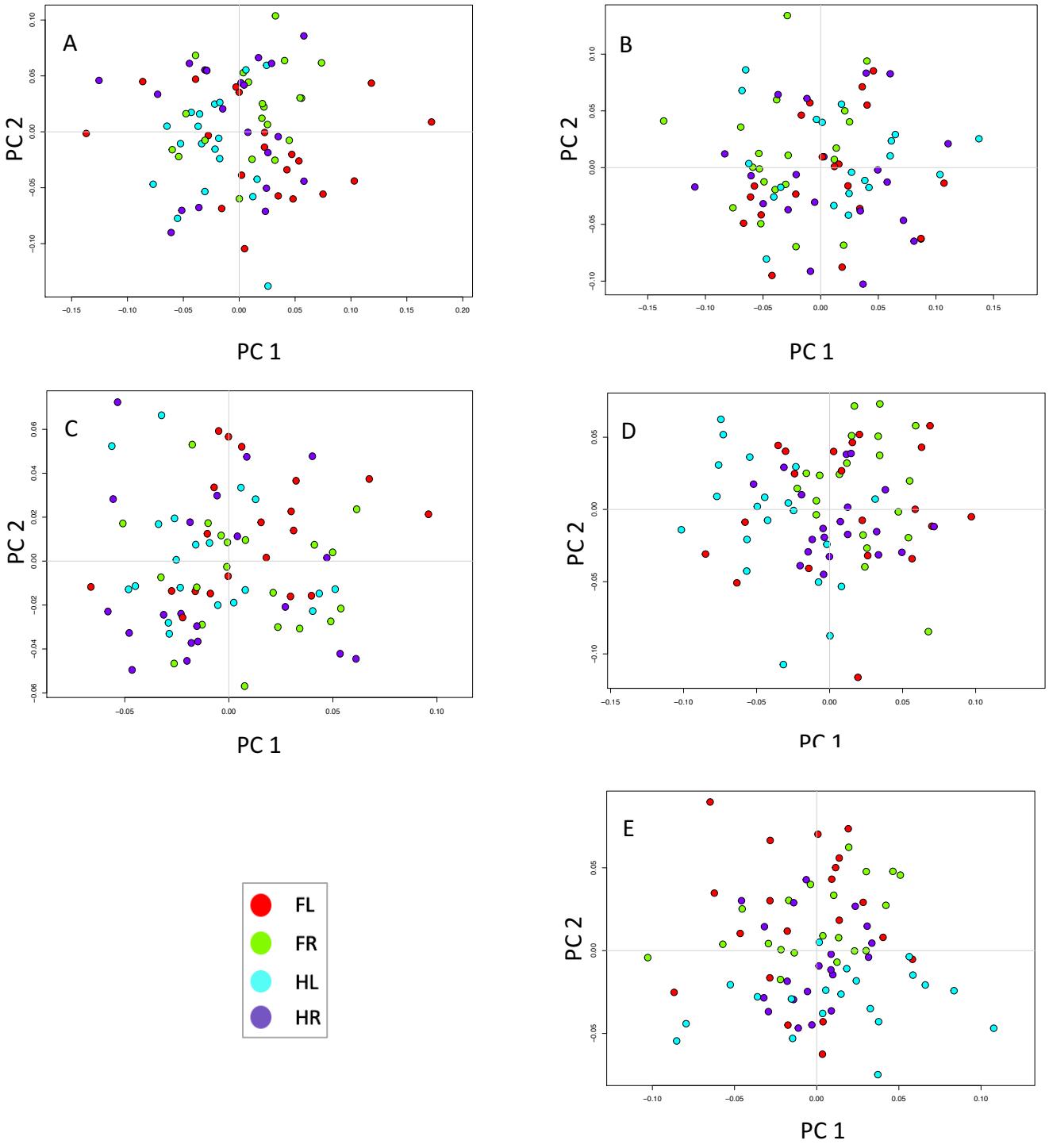

Figure 39 - *Principal Components Analyses conducted on toes 1. Figures A and B display the PCA conducted on data that were extracted using fixed landmarks on 2D- and 3D-models respectively. Figures C and D display the PCA conducted on data that were extracted using fixed landmarks and curve-sliders on 2D- and 3D-models respectively. Figure E displays the PCA conducted on data that were extracted using fixed landmarks, curve- and surface-sliders on 3D-models. The colour code corresponds to the different track positions: red for Front Left ("FL"), green for Front Right ("FR"), blue for Hind Left ("HL"), and purple for Hind Right ("HR").*.

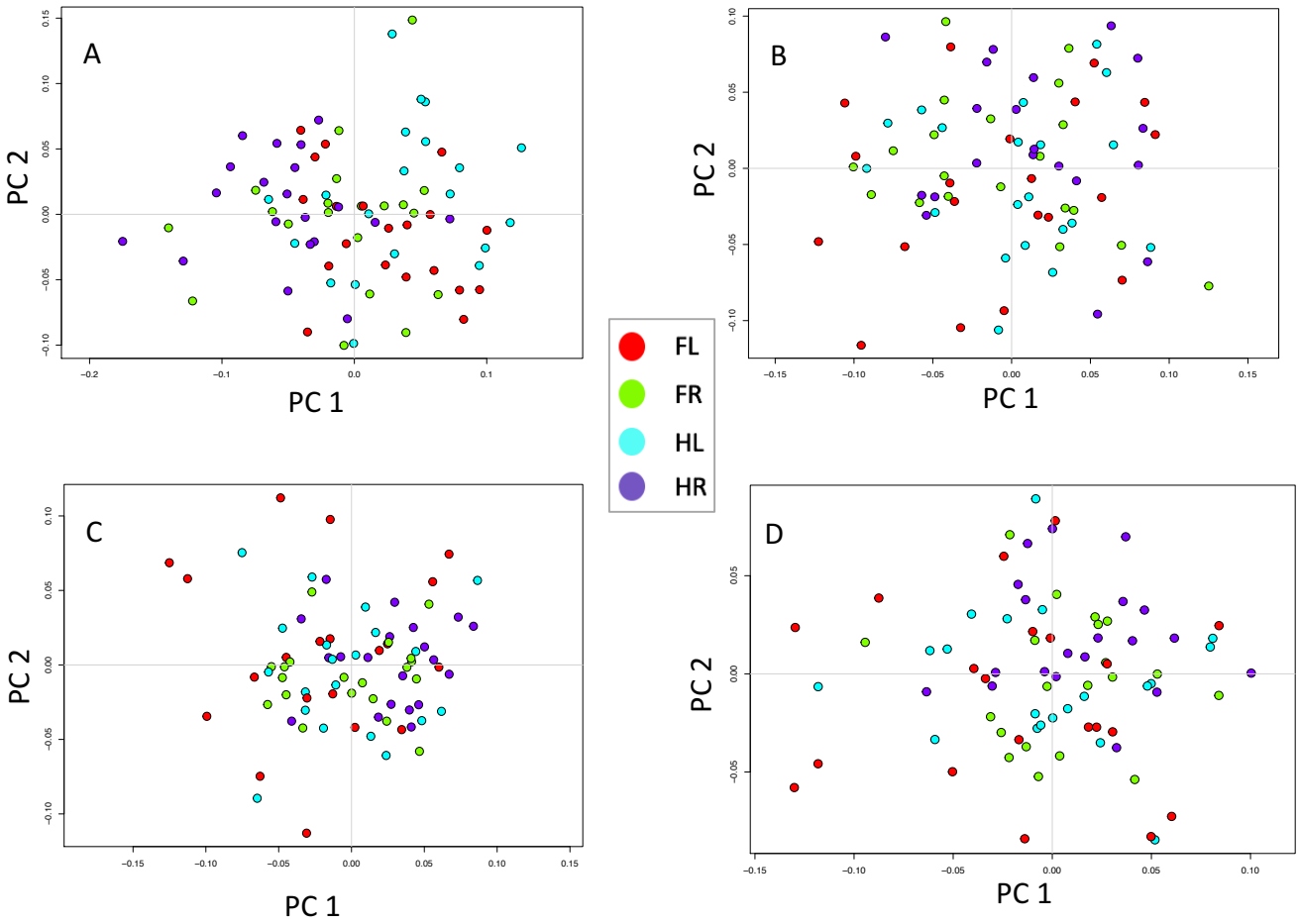

Figure 40 - *Principal Components Analyses conducted on toes 2. Figures A and B display the PCA conducted on data that were extracted using fixed landmarks on 2D- and 3D-models respectively. Figures C displays the PCA conducted on data that were extracted using fixed landmarks and curve-sliders on 3D-models. Figure D displays the PCA conducted on data that were extracted using fixed landmarks, curve- and surface-sliders on 3D-models. The colour code corresponds to the different track positions: red for Front Left ("FL"), green for Front Right ("FR"), blue for Hind Left ("HL"), and purple for Hind Right ("HR").*

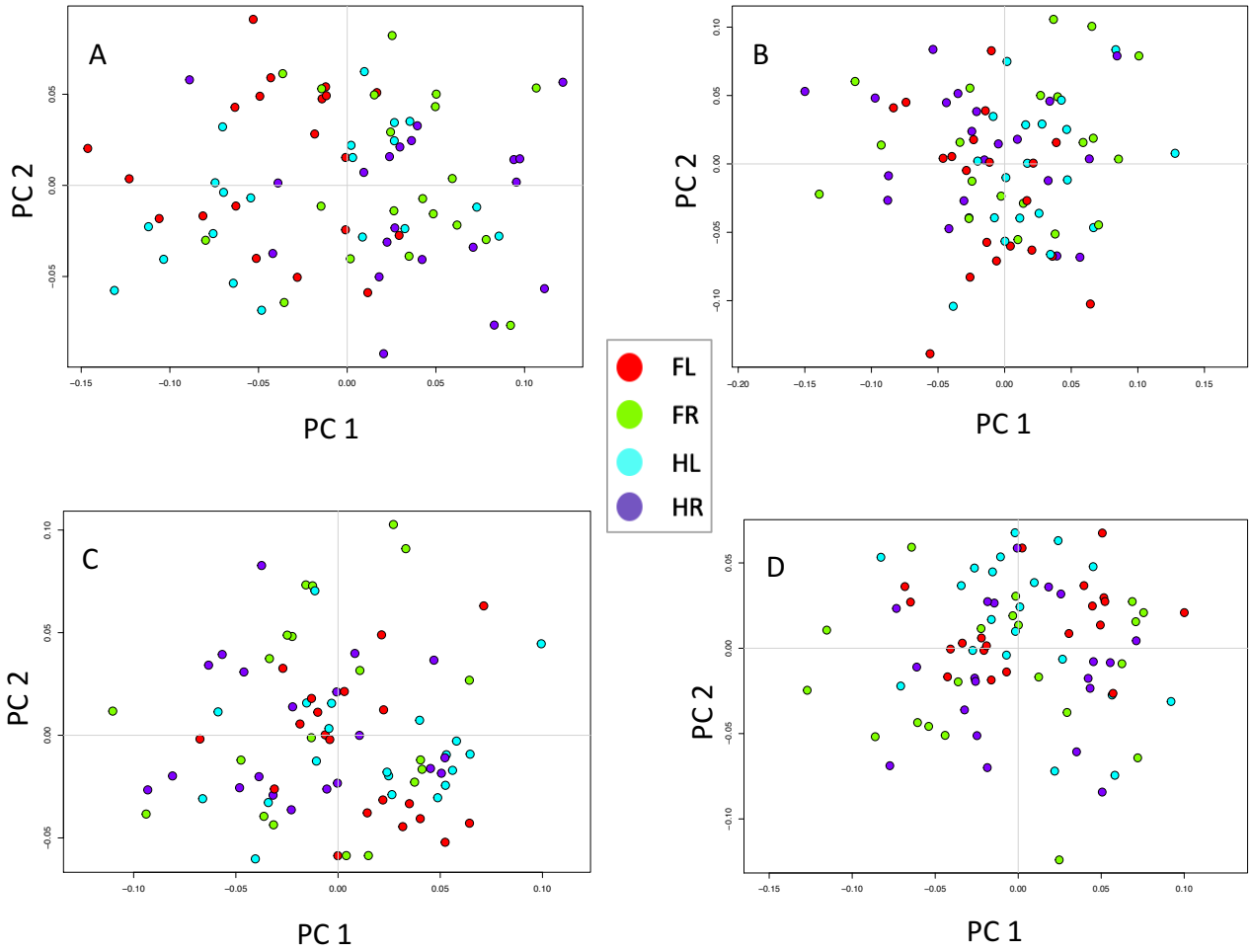

Figure 41 - *Principal Components Analyses conducted on toes 3. Figures A and B display the PCA conducted on data that were extracted using fixed landmarks on 2D- and 3D-models respectively. Figures C displays the PCA conducted on data that were extracted using fixed landmarks and curve-sliders on 3D-models. Figure D displays the PCA conducted on data that were extracted using fixed landmarks, curve- and surface-sliders on 3D-models. The colour code corresponds to the different track positions: red for Front Left ("FL"), green for Front Right ("FR"), blue for Hind Left ("HL"), and purple for Hind Right ("HR").*

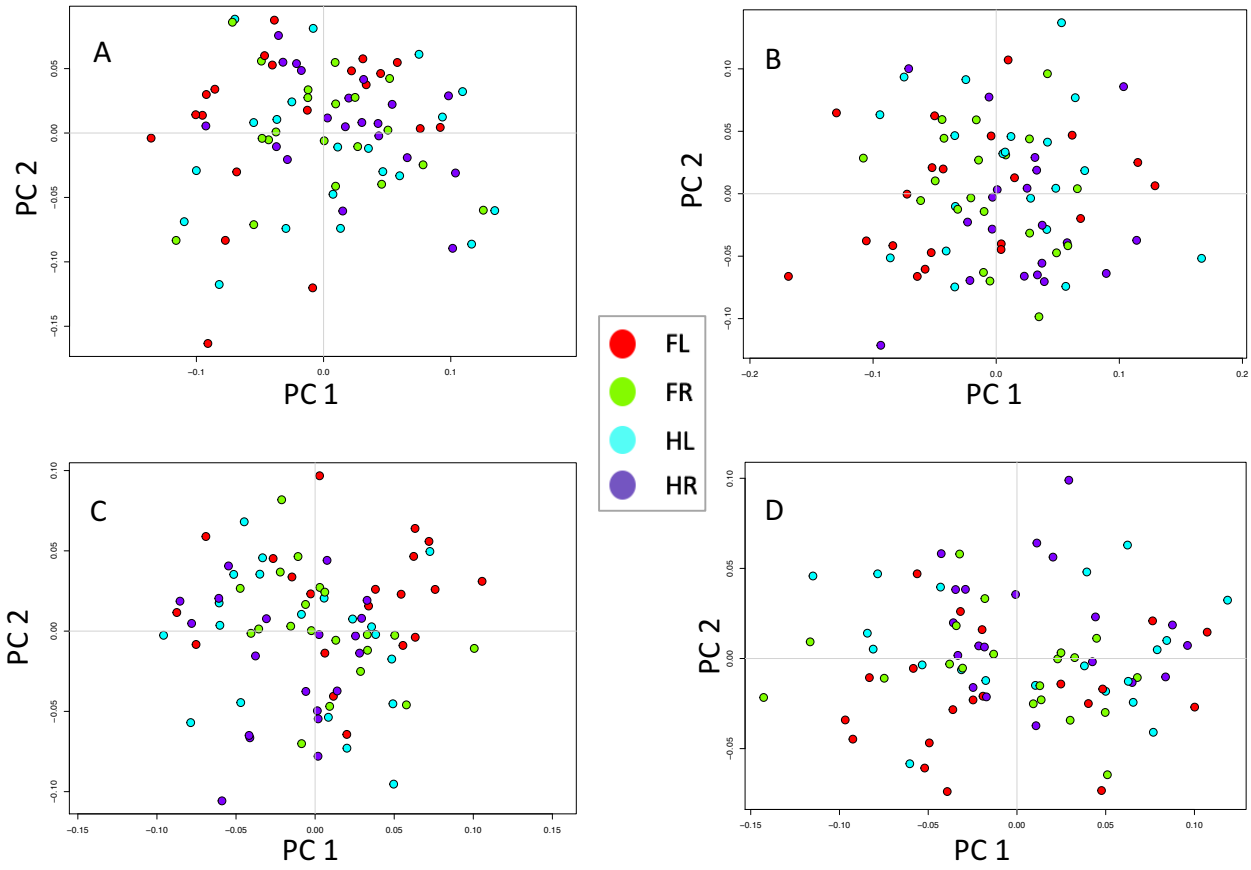

Figure 42 - *Principal Components Analyses conducted on toes 4. Figures A and B display the PCA conducted on data that were extracted using fixed landmarks on 2D- and 3D-models respectively. Figures C displays the PCA conducted on data that were extracted using fixed landmarks and curve-sliders on 3D-models. Figure D displays the PCA conducted on data that were extracted using fixed landmarks, curve- and surface-sliders on 3D-models. The colour code corresponds to the different track positions: red for Front Left ("FL"), green for Front Right ("FR"), blue for Hind Left ("HL"), and purple for Hind Right ("HR").*

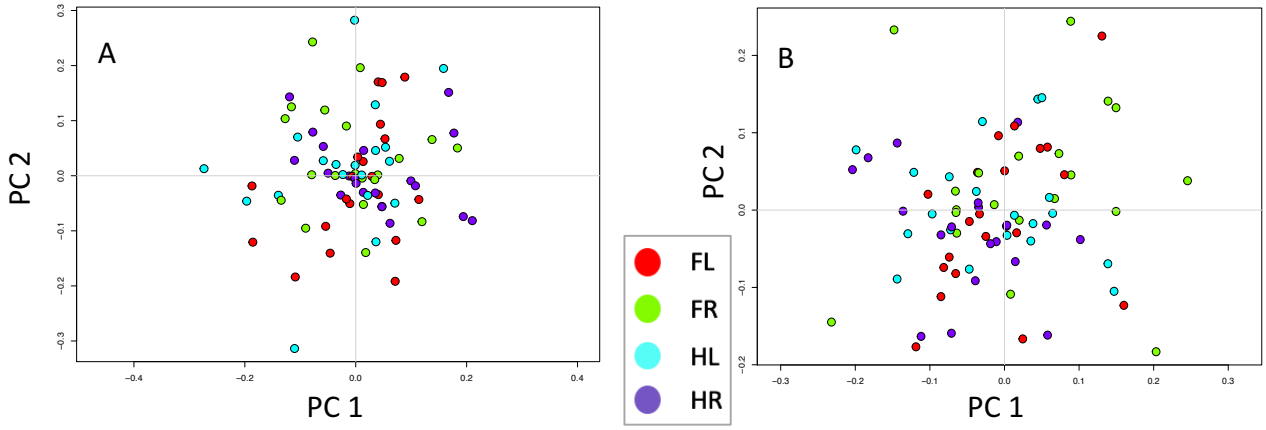

Figure 43 – *Principal Components Analysis conducted on entire tracks, on which traditional morphometrics (fixed landmarks) was applied to extract data from 2D (A) and 3D (B) entire tracks. red for Front Left ("FL"), green for Front Right ("FR"), blue for Hind Left ("HL"), and purple for Hind Right ("HR").*

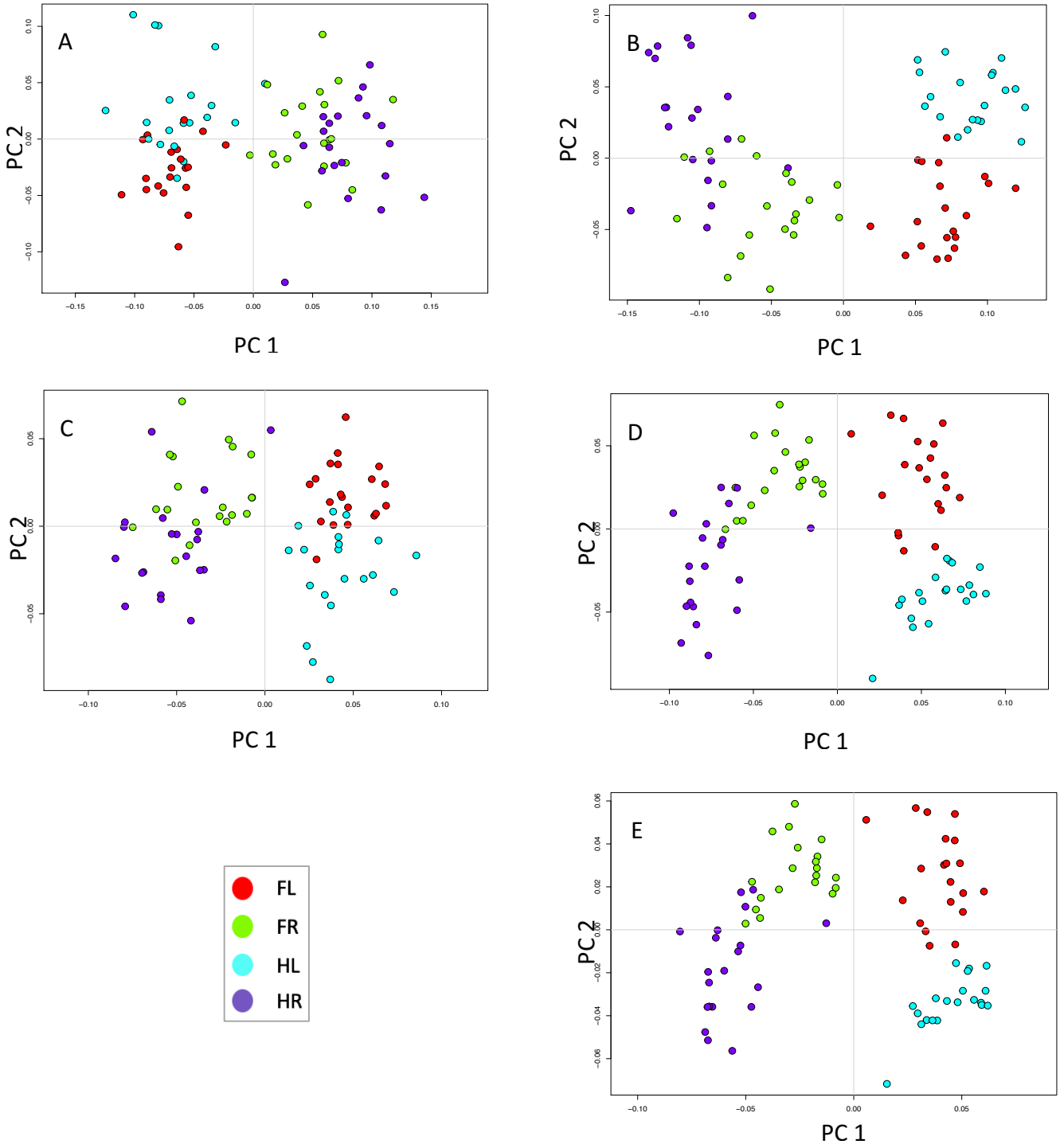

Figure 44 - *Principal Components Analyses conducted on entire tracks. Figures A and B display the PCA conducted on data that were extracted using fixed landmarks on 2D- and 3D-models respectively. Figures C and D display the PCA conducted on data that were extracted using fixed landmarks and curve-sliders on 2D- and 3D-models respectively. Figure E displays the PCA conducted on data that were extracted using fixed landmarks, curve- and surface-sliders on 3D-models. The colour code corresponds to the different track positions: red for Front Left ("FL"), green for Front Right ("FR"), blue for Hind Left ("HL"), and purple for Hind Right ("HR").*

Appendix H: accuracies of prediction

Table 18 – *Accuracy of prediction (in %) of the algorithms resulting from the LDA conducted on the scenarios that involved geometric morphometric analyses on 2D-models. The objects ("pads" or "track") were characterized either by fixed landmarks only ("fixed") or fixed landmarks and curve-sliders ("fixed+curve"). The variables taken into account by the algorithms were the centroid size only ("Csize"), the shape components only ("shape"), or both at the same time ("Shape&Size").*

Type of model		Two-dimension					
Feature extraction		Geometric Morphometrics					
Type of landmarks		fixed				fixed + curve	
Type of object		pad		track		track	
Type of variable		Csize: 56.25		Csize: 50.00		Csize: 26.25	
		Shape	Shape&Size	Shape	Shape&Size	Shape	Shape&Size
Number of PC used by the algorithm	1	21.25	51.25	58.75	91.25	72.50	88.75
	2	47.50	58.75	70.00	93.75	88.75	95.00
	3	53.75	67.50	80.00	95.00	92.50	95.00
	4	48.75	73.75	80.00	96.25	92.50	93.75
	5	50.00	76.25	81.25	95.00	91.25	95.00
	6	50.00	76.25	76.25	95.00	95.00	95.00
	7	51.25	73.75	87.50	97.50	95.00	95.00
	8	41.25	70.00	83.75	97.50	95.00	95.00
	9	48.75	68.75	85.00	96.25	95.00	95.00
	10	48.75	70.00	85.00	95.00	96.25	98.75
	11	43.75	68.75	86.25	95.00	95.00	98.75
	12	43.75	73.75	87.50	96.25	95.00	98.75
	13	48.75	68.75	85.00	96.25	95.00	97.50
	14	46.25	71.25	83.75	97.50	95.00	95.00
	15	48.75	68.75	86.25	98.75	95.00	96.25
	16	46.25	67.50	85.00	96.25	93.75	97.50
	17	43.75	66.25	83.75	96.25	93.75	96.25
	18	41.25	67.50	87.50	96.25	95.00	95.00
	19	45.00	68.75	83.75	96.25	93.75	93.75
	20	43.75	68.75	82.50	95.00	93.75	95.00
	21	47.50	67.50	80.00	92.50	93.75	93.75
	22	46.25	76.25	80.00	92.50	95.00	92.50
	23	47.50	75.00	77.50	93.75	96.25	93.75
	24	46.25	71.25	76.25	93.75	96.25	93.75
	25	46.25	75.00	78.75	92.50	95.00	90.00
	26	41.25	77.50	80.00	91.25	95.00	92.50
	27	41.25	76.25	80.00	92.50	93.75	91.25
	28	41.25	80.00	77.50	91.25	95.00	92.50
	29	38.75	77.50	77.50	93.75	95.00	92.50
	30	38.75	76.25	81.25	93.75	92.50	91.25

Table 19 - *Accuracy of prediction (in %) of the algorithms resulting from the LDA conducted on the scenarios that involved geometric morphometric analyses on 3D-models. The objects ("pads" or "track") were characterized by fixed landmarks only ("fixed"), fixed landmarks and curve-sliders ("fixed+curve"), or fixed landmarks and curve- and surface-sliders ("fixed+curve+surface", presented in Table 20). The variables taken into account by the algorithms were the centroid size only ("Csize"), the shape components only ("shape"), or both at the same time ("Shape&Size").*

Type of model		Three-dimension							
Feature extraction		Geometric morphometrics							
Type of landmarks		fixed				fixed + curve			
Type of object		pad		track		pad		track	
Type of variable		Csize = 38.75		Csize = 26.25		Csize = 41.25		Csize = 26.25	
		Shape	Shape&Size	Shape	Shape&Size	Shape	Shape&Size	Shape	Shape&Size
Number of PC used by the algorithm	1	27.50	31.25	77.50	72.50	35.00	28.75	72.50	70.00
	2	43.75	32.50	90.00	90.00	50.00	41.25	88.75	90.00
	3	35.00	42.50	90.00	90.00	55.00	51.25	92.50	92.50
	4	47.50	33.75	90.00	90.00	65.00	52.50	92.50	92.50
	5	52.50	45.00	93.75	92.50	65.00	60.00	91.25	88.75
	6	48.75	50.00	92.50	92.50	66.25	57.50	95.00	93.75
	7	47.50	46.25	95.00	92.50	67.50	66.25	95.00	93.75
	8	53.75	47.50	93.75	93.75	63.75	63.75	95.00	95.00
	9	53.75	55.00	95.00	93.75	66.25	60.00	95.00	93.75
	10	53.75	51.25	96.25	96.25	68.75	62.50	96.25	96.25
	11	53.75	51.25	97.50	97.50	70.00	65.00	95.00	95.00
	12	50.00	48.75	96.25	95.00	71.25	66.25	95.00	95.00
	13	55.00	50.00	95.00	95.00	65.00	66.25	95.00	95.00
	14	53.75	55.00	95.00	95.00	67.50	70.00	95.00	95.00
	15	53.75	56.25	95.00	95.00	70.00	71.25	95.00	95.00
	16	55.00	51.25	95.00	95.00	68.75	67.50	93.75	93.75
	17	55.00	55.00	93.75	93.75	72.50	68.75	93.75	93.75
	18	62.50	55.00	92.50	92.50	70.00	65.00	95.00	95.00
	19	60.00	61.25	92.50	92.50	72.50	70.00	93.75	93.75
	20	60.00	60.00	92.50	92.50	68.75	70.00	93.75	93.75
	21	57.50	61.25	91.25	91.25	66.25	67.50	93.75	93.75
	22	53.75	61.25	92.50	92.50	70.00	66.25	95.00	95.00
	23	60.00	58.75	91.25	91.25	72.50	68.75	96.25	96.25
	24	62.50	61.25	91.25	91.25	75.00	72.50	96.25	96.25
	25	65.00	62.50	90.00	90.00	73.75	70.00	95.00	95.00
	26	63.75	61.25	92.50	91.25	72.50	72.50	95.00	93.75
	27	63.75	61.25	91.25	91.25	72.50	71.25	93.75	93.75
	28	61.25	60.00	95.00	95.00	72.50	70.00	95.00	93.75
	29	61.25	58.75	93.75	93.75	73.75	75.00	95.00	93.75
	30	0.00	58.75	93.75	92.50	73.75	73.75	92.50	93.75

Table 20 - *Accuracy of prediction (in %) of the algorithms resulting from the LDA conducted on the scenarios that involved traditional morphometrics analyses on 2D and 3D models ("fixed" landmarks only, positioned either on "pads" or "tracks") and geometric morphometrics on 3D models (fixed landmarks and curve- and surface-sliders ("fixed+curve+surface"), positioned either on "pads" or "tracks"). In traditional morphometrics, the variables considered by the algorithms were the distances between each landmark. In geometric morphometrics, the variables considered by the algorithms were the centroid size only ("Csize"), the shape components only ("shape"), or both at the same time ("Shape&Size").*

Type of model		Two-dimension		Three-dimension		Three-dimension			
Feature extraction		Traditional morphometrics				Geometric morphometrics			
Type of landmarks		fixed				fixed + curve + surface			
Type of object		pad		track		pad		track	
Type of variable		Distance	Distance	Distance	Distance	Csize = 45.00		Csize = 26.25	
						Shape	Shape&Size	Shape	Shape&Size
Number of PC used by the algorithm	1	51.25	51.25	30.00	27.50	25.00	26.25	67.50	67.50
	2	51.25	91.25	43.75	58.75	23.75	26.25	90.00	90.00
	3	58.75	92.50	45.00	77.50	32.50	30.00	92.50	92.50
	4	53.75	92.50	46.25	80.00	37.50	35.00	91.25	91.25
	5	80.00	92.50	57.50	82.50	47.50	38.75	95.00	93.75
	6	80.00	96.25	57.50	78.75	50.00	46.25	93.75	92.50
	7	78.75	96.25	53.75	78.75	56.25	51.25	93.75	92.50
	8	77.50	97.50	52.50	83.75	56.25	58.75	96.25	96.25
	9	73.75	96.25	53.75	87.50	56.25	60.00	95.00	95.00
	10	76.25	95.00	52.50	87.50	56.25	56.25	93.75	93.75
	11	77.50	95.00	53.75	86.25	53.75	61.25	95.00	93.75
	12	80.00	95.00	52.50	85.00	50.00	57.50	95.00	95.00
	13	77.50	96.25	52.50	86.25	57.50	56.25	95.00	95.00
	14	77.50	95.00	51.25	87.50	57.50	60.00	95.00	95.00
	15	73.75	95.00	53.75	86.25	60.00	56.25	95.00	95.00
	16	78.75	96.25	50.00	85.00	57.50	56.25	95.00	95.00
	17	80.00	95.00	46.25	88.75	55.00	57.50	95.00	95.00
	18	78.75	95.00	43.75	88.75	53.75	52.50	95.00	95.00
	19	81.25	95.00	45.00	90.00	60.00	57.50	96.25	96.25
	20	82.50	95.00	46.25	90.00	62.50	62.50	96.25	96.25
	21	78.75	93.75	43.75	87.50	62.50	66.25	96.25	96.25
	22	82.50	95.00	47.50	88.75	61.25	65.00	96.25	96.25
	23	77.50	95.00	41.25	91.25	72.50	63.75	96.25	96.25
	24	77.50	95.00	45.00	91.25	72.50	66.25	96.25	96.25
	25	78.75	93.75	46.25	91.25	75.00	71.25	96.25	96.25
	26	77.50	93.75	42.50	91.25	71.25	70.00	96.25	96.25
	27	77.50	93.75	42.50	91.25	73.75	68.75	95.00	95.00
	28	0.00	93.75	0.00	88.75	71.25	71.25	93.75	95.00
	29	0.00	92.50	0.00	90.00	70.00	71.25	95.00	96.25
	30	0.00	95.00	0.00	88.75	75.00	73.75	93.75	93.75