Effect of Asymmetry on Data Collection for Cranial Non-metric Traits Amanda Wissler School of Human Evolution and Social Change, Arizona State University

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Introduction

Biological distance analyses using cranial and dental non-metric traits have become an increasingly common approach for exploring kinship, migration and genetic relatedness. Despite its popularity, many aspects of the methodology are not standardized. Though seldom mentioned in the literature, trait asymmetry is not uncommon, and how to deal with it has been under-explored. If asymmetry is this common, recording data from only one side or antimere substitution to control for missing data may be inappropriate. This research investigates the effect of asymmetry on how different data analysis techniques influence the mean trait score.



Figure 1A. Gruneberg's (1952) threshold model of trait expresson. 1B. Ossenberg's (1981) expanded threshold model of trait expression.

Project Goals

To assess the impact asymmetry has on data collection and analysis procedures. Specifically, to explore the effects of different methods for handling missing data, and measuring effect different methods have on the mean trait score for each individual when combining data from the right and left sides.

Materials and Methods

Data on 8 cranial non-metric traits were collected from 42 individuals of the Hasanlu skeletal collection housed at the University of Pennsylvania Museum of Anthropology following Hauser and DeStefano (1989).

Cranial Non-Metric Traits

- Frontal Grooves (number and location)
- Hypoglossal Canal Bridging
- Infraorbital Foramen
- Mylohyoid Bridging (loca-
- tion and degree)
- Suprameatal Depression
- Supraorbital Foramen/ Notch
- Zygomaxillary Tubercle
- Squamomastoid Suture Per-
- sistence

Differences in mean trait scorewere assessed in among the following 5 methods

- 1) taking only the left side
- 2) taking the left side with antimere substitution when the left side is unobservable
- 3) taking the average of the right and left sides
- 4) taking the highest score with antimere substitution
- 5) taking the lowest score with anitmere substitution

Results

Percentage of Sample with Asymmetry

Figure 2 shows the percentage of the sample for each cranial non-metric trait with different right and left scores. Asymmetry was probably more likely to be found given that it was the aim of this study, so these numbers may be somewhat inflated due to observer error. Despite this potential bias, these results still suggest that asymmetry is relatively common. Almost every trait showed some asymmetry.



Figure 3. FGN-frontal grooves number, HGC-hypoglossal canal, IFF-infraorbital foramen, MHBD-mylohyoind bridge degree, SMD-suprameatal depression, SOF-supraorbital foramen, SQMS-squamomastoid suture

Difference in mean trait score among all 5 methods

Figure 4 shows the mean trait score among taking the average of the right and left sides, the highest scores and the lowest scores. Significant differences among the five methods were found (anova, F-value=3.526, p-value=0.007188, α=0.05). A post-hoc Tukey test indicates that the only significant difference is between taking the highest and lowest scores (p-value=0.002).

Antimere substitution increased the sample size by 9%. **Figure 3** shows the mean score for six traits using both methods; the results are almost identical. A paired T-test revealed no significant differences between each method (t=1.6055, p-value=0.1098, α =0.05), however the Hasanlu sample has very low trait expression overall.



toid suture, SMD-suprameatal depression, SMS-suprameatal spine, FS-foramen spinosum, SON-supraorbital notch, SOF-supraorbital foramen, FGD-frontal grooves degree, FGN-frontal grooves number, IFF-infraorbital foramen, HGC-hypoglossal canal, , MHBD-mylohyoind bridge degree, MHBL-mylohyoid bridge location

Left only vs. Left with antimere substitution



formation on individual variation. study. Hypoglossal Canal Bridging Zygomaxillary Tubercle

scores is warranted.

Thanks to Janet Monge at the University of Pennsylvania Museum of Anthropology for allowing me access to the Hasanlu skeletal collection. Thanks to Gary Schwartz and Chris Stojanowski for assisting in the development of this project. Finally, thanks again to Chris Stojanowski, Kathleen Paul and Sofía Pacheco-Forés for statistics help. Funding for this project was provided by the School of Human Evolution and Social Change at Arizona State University





Discussion

These results suggest that even in fairly uniform data and with a small sample size, how the data is processed can have significant effects. Using scores from only one side may bias the data or oversimplify the genetic-environmental interactions at play and eliminates potentially useful in-

In order to fully capture individual variation and account for different thresholds of trait expression, averaging the right and left sides may be recommended. Additional study needed to fully test the results of this







Supraorbital Foramen/Notch



Limitations

The results of this project were limited by the small sample size (n=42). Increasing the sample size would augment the singificance of the results. The Hasanlu skeletal sample also had very low trait expression overall. Additional study on a sample with a wider spectrum of non-metric trait

Acknowledgements

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