Cross-References

- ▶ Biological Distance in Bioarchaeology and Human Osteology
- ▶ Evolutionary Anthropology: Issues, News, and Reviews
- ▶ Osteology: Definition
- ▶ Pathological Conditions and Anomalies in Archaeological Investigations
- ▶ Skeletal Biology: Definition

Further Reading

Agarwal, S.C. & B.A. Glencross. (ed.) 2011. *Social bioarchaeology*. Chichester: Wiley-Blackwell.

Buikstra, J.E. & L.A. Beck. (ed.) 2006. *Bioarchaeology: the contextual analysis of human remains*. Burlington: Academic Press.

Larsen, C.S. 1997. *Bioarchaeology: interpreting behavior from the human skeleton*. Cambridge: Cambridge University Press.

Larsen, C.S. & P.L. Walker. 2010. Bioarchaeology: health, lifestyle, and society in recent human evolution, in C.S. Larsen (ed.) *A companion to biological anthropology*: 379-94. Chichester: Wiley-Blackwell.

Biological Distance in Bioarchaeology and Human Osteology

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Introduction

Biological distance, or biodistance, is a measure of relatedness or divergence among groups separated by time and/or geography based on morphological variation (Buikstra et al. 1990). Biological distance studies, which are undertaken to reconstruct population history and to assess ancestry, dominated bioarchaeological research during the nineteenth and early twentieth centuries. The earliest attempts to comprehend human variation and measure relatedness among human groups, through the construction of typological racial classifications, fell short of their predicted goals. These early attempts were flawed due to limitations of the approach, which included the mistaken belief that humanity could be divided into a finite number of pure races, and the lack of adequate quantitative methods. Advances in evolutionary theory, including quantitative and population genetics, and improvements in computing and statistical procedures in the early twentieth century provided a much sounder basis for measuring and interpreting morphological variation within and between human groups.

Because of the demonstrated correlation between phenotypic and genotypic similarities, measures of biological distance in bioarchaeology are generally determined through the application of quantitative methods to metric and nonmetric variation recorded in skulls, teeth, and skeletons. Ancient DNA (aDNA) and other biochemical and geochemical traits are beginning to find their way into biodistance studies.

Studies of cranial form, most notably cranial measurements (or craniometrics) that quantify morphology, figured prominently in the early development of the discipline and continue to occupy a central role in modern biological distance studies. While morphological variation, especially quantitative variation, is subject to nongenetic or environmental influences, this category of variation is generally assumed to reflect genetic similarity resulting from neutral evolutionary forces (genetic drift, gene flow, and mutation). There is now an emerging consensus that craniometric data can be used as a proxy to genetic data, hence the popularity of this category of variation in biodistance studies.

The continuing interest in cranial form for reconstructing population history is supported by a number of factors including the precision and repeatability of measurements, the conservative nature of craniometric variation, the direct link with the past, and the demonstration of a genetic component for this category of biological variation. Likewise, the strong geographic patterning (e.g., Howells 1973), selective neutrality of phenotypic (craniometric) variation

(e.g., Relethford 2009), and the amenability of continuous variation to multivariate statistical analysis have ensured the continued use of this category of variation in biodistance analyses.

Teeth, especially dental nonmetric traits, have also figured prominently in assessing biological distance among ancient and modern populations. Standardization of dental scoring methods, high genetic component, and conservatism of this category of variation have made the dentition a popular choice for reconstructing population history.

Mathematically based methods, which are often based on quantitative and population genetic analyses, allow bioarchaeologists to address a broad array of research topics that include:

- Tracing biological relationships, temporally and spatially, for reconstructing past population history, origins, and movement of human groups
- Investigating microevolutionary processes (e.g., gene flow, genetic drift, selection) and the influence of geography and other isolating mechanisms on the observed patterns of biological relatedness
- Identification of postmartial residence patterns, familial and kin groupings, cemetery structure, social status, immigrants, and admixture
- Sorting of commingled skeletal and dental remains
- Assignment of an unknown individual (or skull) to a known reference group in repatriation claims and forensic cases

By identifying the population structure, biological distance studies provide an important context for addressing other topics in bioarchaeology such as paleopathology, paleodemography, health, and diet.

Definition

Biological distance, or biodistance, is the measure of biological relatedness (or divergence) between and within human groups, living and past, based on human skeletal and dental variation.

Key Issues

Although equally applicable to morphological/phenotypic variation, the discussion of the key issues in biological distance studies will focus on the use of cranial measurements, or craniometrics, unless otherwise noted.

Underlying Assumptions

While morphological variation, including craniometric variation, is subject to nongenetic or environmental influences, this category of variation is generally viewed as reflecting genetic similarity. It is assumed that groups that display more phenotypic similarity are the most closely related. Additionally, various studies have demonstrated a significant genetic component for many cranial measurements (e.g., Martínez-Abadías et al. 2009).

Geographic Patterning and Neutrality of Craniometric/Phenotypic Variation

Beginning with the pioneering work of W.W. Howells (1973), there is now near universal acceptance that human cranial variation is geographically structured making it highly attractive for reconstructing population history and for assessing ancestry.

While some aspects of cranial morphology (i.e., face and nose, Hubbe et al. 2009) are susceptible to climatic adaptation, numerous studies have demonstrated that phenotypic distance and global patterns of craniometric variation, on average, correlate with neutral genetic distance globally and are consistent with neutral traits under an isolation by distance model (Relethford 2004; Roseman 2004; Harvati & Weaver 2006; von Cramon-Taubadel 2009; Betti et al. 2010). Studies such as these reiterate that cranial form provides valuable information about past population history and for investigating microevolutionary processes (Smith 2011). Furthermore, that craniometric variation is geographically structured allows high levels of classification accuracy when crania from different parts of the world are compared (Relethford 2009).

Variables and Methods

Studies of biological distance, beginning in the 1970s, increasingly relied on the application of multivariate statistical procedures to craniometric data. Multivariate statistical procedures comprise a family of related mathematical procedures that allow the simultaneous analysis of many random but interrelated variables whose effects cannot be interpreted individually in a meaningful manner. These procedures are exceptionally well suited for investigating patterns of biological variation, measuring relatedness among groups, and making other inferences of the variables and groups selected. The primary multivariate statistical procedures applied to craniometric traits in biological distance studies include principal components analysis, stepwise discriminant function (canonical) analysis, and Mahalanobis' generalized distance statistic. Various clustering algorithms, such as the unweighted pair group method algorithm (UPGMA), facilitate interpretation of relatedness between groups through the construction of dendrograms (see Case Study 1). A more detailed discussion of the methods used for analyzing metric data is provided in Pietrusewsky (2008a). C.A.B. Smith's mean measure of divergence (MMD) remains one of the most popular distance statistics for analyzing dental and cranial nonmetric traits.

In addition to traditional landmark measurements (linear distances, areas, volume, angles), the use of Cartesian coordinates of cranial landmarks recorded in two or three dimensions using digitizing equipment is a recent alternative approach for quantifying size and shape. Geometric morphometric techniques, including Procrustes analysis, have become standard tools for analyzing coordinate data (Slice 2005).

Model-Free and Model-Bound Approaches

The earliest biological distance studies were largely model-free approaches that focused more on the overall similarities among groups than on the causes of the observed patterns of variation. Later studies applied a population genetic framework for analyzing quantitative traits (e.g., Relethford & Blangero 1990; Roseman 2004; Smith 2011). These model-bound approaches allowed the estimation of microevolutionary processes such as gene flow and genetic drift.

Selection of Samples and Variables

Because skeletal series represent only samples of past biological populations, which often span considerable periods of time and may be biased in their representation, extreme caution should be exercised when skeletal (cranial) samples are used in biological distance studies. Using relatively large samples that are free of systematic bias helps to alleviate some of the concerns. Likewise, the selection of traits that are less susceptible to environmental and cultural influences further ensures that the results of biological distance analysis more faithfully estimate genetic relatedness. Recent studies (e.g., von Cramon-Taubadel 2009; Smith 2011) suggest that some bones of the neurocranium such as the temporal bone because of its stronger correlation with neutral genetic data might be more reliable for reconstructing human population history than other regions of the cranium.

Current Debates

Origin and Dispersal of Modern Humans/New Hominin Species

Refinements in methods and techniques continue to influence work in biological distance studies. Some of the recent developments are associated with the debate over the origin and pattern of dispersal of anatomically modern humans (e.g., Smith 2011). The association of craniometric variation and geography has been viewed within the context of this larger debate. The question of whether long distance gene flow mediated by geographic distance (isolation by distance model) or population dispersal, such as with the spread of modern humans out of Africa 100,000–150,000 years ago, is responsible for

this observed correlation has been examined (e.g., Weaver et al. 2008).

Biological distance studies have also been used to evaluate claims for the designation of new hominin species, such as *Homo floresiensis*, in paleoanthropology.

Origins of Native Americans

Studies in biological distance contribute to reconstructions of population history at both the global and regional levels. Craniometric variation studies addressing the origin and dispersal of the first humans to reach the Americas are illustrative of regional analysis (e.g., Ross et al. 2003). Many other studies examining the population history of various regions and time periods, too numerous to cite in this entry, have appeared in the literature in recent years.

Transition from Hunting-Gathering to Agriculture

Another debate that biological distance studies have contributed to in recent years is the transition to farming in Europe and whether indigenous hunter-gatherers were replaced (demic diffusion model) by agriculturalists from the Near East or whether these indigenous groups adopted farming practices (cultural diffusion model) from their neighbors (e.g., von Cramon-Taubadel 2011). Studies that focus on the transition to farming in other regions of the world have also appeared.

Boas' Immigration Studies and Cranial Plasticity/Climate and Environmental Influences

Several recent investigations (e.g., Sparks & Jantz 2002) examined the statistical and biological significance of Franz Boas' immigration studies as they relate to cranial plasticity. Often, these studies are discussed within the broader context of the debate over genetic and environmental influences on craniometric variation and the degree to which skeletal and dental morphology are influenced by environmental and/or selection pressures (e.g., Harvati & Weaver 2006; Hubbe et al. 2009).

In the field of forensic anthropology, discussion continues over the existence of races and the use of computer software programs (e.g., FORDISC & CRANID) designed to assign unknown individuals to a reference group.

Individual Bones of the Skull and Biodistance Studies

Several recent studies have identified the possible influence of environmental factors that may affect craniofacial morphology. These, in turn, have led to specialized studies that examine the shape of individual bones of the cranium to identify which are more strongly correlated with neutral genetic expectation and thus better suited for use in reconstructing human population history and primate phylogeny (e.g., von Cramon-Taubadel 2009; Smith 2011).

Future Directions

Future work in studies of biological distance is anticipated to build on previous work in evolutionary quantitative genetics and contribute to a broad array of evolutionary questions in bioarchaeology and biological anthropology. Refinements in quantitative methods including Bayesian statistical modeling and new imaging technology will continue to shape future work in this field. The use of geometric morphometrics and Cartesian coordinates of cranial landmarks for analyzing size and shape will likely witness an increased presence in the field. While the use of digitizing equipment for recording 3D coordinate data is expected to become more common in future work, reliance on traditional landmark measurements made with calipers will persist as an attractive and convenient alternative.

The multivariate statistical procedures associated with traditional morphometric analyses, such as principal components analysis, discriminant (canonical) analysis, and Mahalanobis' distance, will continue to occupy an important role in future biodistance studies. The reliance on multivariate methods associated with biological distance studies, old and new, reinforces the need for students to be adequately trained in statistical and quantitative methods.

Biological Distance in Bioarchaeology and Human Osteology, Table 1 Fifty-six male cranial samples used in the example

Series Name (abbrev.)[a]	No. of Crania	Location[b] and Number of Crania	Remarks
Polynesia			
1. Tonga-Samoa (TOG)	19	BER-3; AMS-2; DRE-1; PAR-1 BPB-4; AIM-2; AUK-5; SIM-1	Fourteen specimens are from Tonga and five are from Samoa. Included in the Tongan series are three skulls from Pongaimotu excavated by McKern in 1920; two from To-At-1 and To-At-2 excavated by Janet Davidson in 1965; and five from To-At-36 excavated by Dirk Spennemann in 1985/1986. The remaining specimens are from museums in Berlin, Paris and Sydney. Although the exact dates for a few specimens are not known, the majority are believed to be prehistoric
2. Easter Island (EAS)	50	BER-5; DRE-9; PAR-36	Most of the crania in Paris were collected by Pinart in 1887 at Vaihu and La Perouse Bay, Rapa Nui (Easter Island). The exact dates of these specimens are not known
3. Hawai‘i (HAW)	60	BPB-20; HON-20; SIM-20	An equal number of specimens have been randomly chosen from three different skeletal series: Mōkapu (O‘ahu), Honokahua (Maui), and Kaua‘i. All specimens are presumed to be prehistoric (pre-1778)
4. Marquesas (MRQ)	63	PAR-49; LEP-1; BLU-1; BPB-12	Crania are from four islands, Fatu Hiva, Tahuata, Nuku Hiva and Hiva Oa. The exact dates of these specimens are not known
5. New Zealand (NZ)	50	BRE-3; PAR-21; SAM-1; AIM-13; GOT-1; ZUR-5; DRE-6	A representative sample of New Zealand Maori crania from the North and South Islands of New Zealand. The exact dates of these specimens are not known
6. Chatham Islands (CHT)	45	DUN-8; OTM-2 WEL-4; CAN-10 AIM-3; DRE-5 AMS-2; DAS-3 GOT-4; PAR-4	Moriori crania from the Chatham Islands, New Zealand. The exact dates of these specimens are not known
7. Society Islands (SOC)	44	PAR-33; BPB-11	Crania are from the island of Tahiti, Society Islands. The exact dates of these specimens are not known
8. Tuamotu Archipelago (TUA)	18	PAR-18	The majority of the specimens are from Makatea in the Tuamotu Archipelago. The exact dates of these specimens are not known
Island Melanesia			
9. Fiji (FIJ)	42	BER-1; SAM-3 ; QMB-1; DRE-4 FRE-3; CHA-1; BPB-11; PAR-7 AMS-3; DUN-6; SIM-2	Crania are from all major islands including the Lau Group in the Fiji Islands. The exact dates of these specimens are not known
10. Vanuatu (VAN)	47	BAS-47	Most of the specimens were collected by Felix Speiser in 1912 from Malo, Pentecost and Espirtu Santo Islands, Vanuatu. The exact dates of these specimens are not known
11. Loyalty Islands (LOY)	50	BAS-43; PAR-7	Crania are from Mare, Lifou, and Ouvea Island Groups, Loyalty Islands The exact dates of these specimens are not known
12. New Caledonia (NCL)	50	BAS-34; PAR-16	Crania are from several coastal and inland locations on New Caledonia. The majority of these specimens were collected in the late nineteenth century. The exact dates of these specimens are not known

(*continued*)

Biological Distance in Bioarchaeology and Human Osteology, Table 1 (continued)

Series Name (abbrev.)[a]	No. of Crania	Location[b] and Number of Crania	Remarks
13. Santa Cruz Islands (SCR)	46	SAM-4; AMS-2; BAS-40	The crania in Basel were collected by Felix Speiser in 1912. The exact dates of these specimens are not known
14. Solomon Islands (SOL)	49	DRE-3; BER-1; NMV-1; QMB-3; AMS-16; DAS-10; BAS-14; GOT-1	Crania are from New Georgia (5), Guadacanal (9), San Cristobal Island (7), and other locations in the Solomon Islands. The exact dates of these specimens are not known
15. New Britain (NBR)	50	CHA-20; DRE-30	The specimens from New Britain in Dresden were collected by A. Baessler in 1900 and those in Berlin were collected by R. Parkinson in 1911. The specimens were collected from trading posts near Rabul in the Gazelle Peninsula and most likely represent Tolai crania. The exact dates of these specimens are not known
16. New Ireland (NIR)	53	AMS-4; BER-2; BLU-6; DRE-18; GOT-15; QMB-1; SAM-6; TUB-1	Most of the crania in Dresden were collected by Pöhl in 1887–1888 from the northern end of the island; the specimens in Göttingen were collected during the Südsee Expedition in 1908. The exact dates of these specimens are not known
17. Admiralty Islands (ADR)	50	DRE-20; GOT-9; CHA-6; TUB-15;	Specimens from Hermit, Kaniet and Manus Islands of the Admiralty Islands. The exact dates of these specimens are not known
New Guinea			
18. Sepik R. (SEP)	50	DRE-33; GOT-10; TUB-7	The specimens in Dresden were collected by Otto Schlaginhaufen in 1909 from various locations along the Sepik River, Papua New Guinea. The exact dates of these specimens are not known
19. Biak Island (BIK)	48	DRE-48	Most (45) of the specimens were collected by A.B. Meyer in 1873 on Biak Island (Mysore), Geelvink Bay, Irian Jaya. The exact dates of these specimens are not known
20. Purari Delta (PUR)	50	DRE-50	Decorated (engraved) skulls obtained by Gerard and Webster between 1900 and 1902 are from along the Purari River and Purari Delta regions, Papua New Guinea. The exact dates of these specimens are not known
Australia/Tasmania			
21. Murray R. (MRB)	50	AIA-39; DAM-11	Australian Aboriginal crania were collected by G.M. Black along the Murray River (Chowilla to Coobool) in New South Wales between 1929–1950. The exact dates of these specimens are not known
22. New South Wales (NSW)	62	AMS-21; DAS-41	Australian Aboriginal crania from the coastal locations in New South Wales. The exact dates of these specimens are not known
23. Queensland (QLD)	54	AMS-21; DAS-3; QMB-30	Australian Aboriginal crania from the southeastern and middle-eastern regions of Queensland. The exact dates of these specimens are not known
24. Northern Territory (NT)	50	AIA-4; AMS-3; MMS-1; NMV-38; QMB-1; SAM-3	Australian Aboriginal crania from Port Darwin (14) and Arnhemland (36) in the Northern Territory, Australia. The exact dates of these specimens are not known

25. Swanport, S.A. (SAS)	36	SAM-36	Australian Aboriginal crania representing the Tarildekald and Warki-Korowalde tribes in the lower Murray River basin. The specimens were collected by F. R. Zeitz in 1911 from an aboriginal cemetery located approximately 10 km southeast of the Murray Bridge in South Australia (Howells 1973:21). The exact dates of these specimens are not known
26. Western Australia (WA)	47	WAM-47	Australian Aboriginal crania from central (20), eastern (4), northern (14), and southern (9) regions of Western Australia. The exact dates of these specimens are not known
27. Tasmania (TAS)	26	THM-22; CHA-1; SAM-2; NMV-1	The crania represent Tasmanian Aborigines. The exact dates of these specimens are not known
Micronesia			
28. Guam (GUA)	46	BPB-42; PAR-4	Pre-Spanish Chamorro crania associated with *latte* structures collected in the 1920s by Hans Hornbostel along Tumon Beach, Tumon Bay, Guam. The majority of these specimens represent prehistoric (pre-1521) Chamorro
Island Southeast Asia			
29. Sumatra (SUM)	39	BER-1; BRE-1; DRE-5; LEP-4; PAR-3; ZUR-25	The specimens in Zürich are designated "Battak," specific locations within the island of Sumatra are not known. The exact dates of these specimens are not known
30. Java (JAV)	50	BER-1; BLU-8; CHA-9; DRE-1; LEP-24; PAR-7	Crania were collected from several different localities in Java. The exact dates of these specimens are not known
31. Borneo (BOR)	34	BER-2; BRE-2; DRE-6; FRE-4; LEP-8; PAR-12	A great many of the specimens are indicated as representing Dayak tribes, some have elaborate decorations. The exact dates of these specimens are not known
32. Sulawesi (SLW)	41	BAS-7; BER-10; DRE-4; FRE-7; LEP-5; PAR-8	An exact location is known for many of these specimens. The exact dates of these specimens are not known
33. Lesser Sunda Islands (LSN)	61	BAS-5; BER-15; BLU-2; CHA-1; DRE-24; LEP-1; PAR-6; ZUR-7	Crania from Bali (13), Flores (9), Sumba (1), Lomblem (2), Alor (2), Timor (11), Wetar (2), Leti (4), Barbar (1), Tanimbar (13), Kai (2) and Aru (1) Islands of the Lesser Sunda Islands. The exact dates of these specimens are not known.
34. Southern Moluccas Islands (SML)	65	FRE-48; DRE-17	Crania are from Seram (48) and Buru (17) Islands of the Southern Moluccas Islands. The exact dates of these specimens are not known
35. Sulu (SUL)	38	LEP-1; PAR-37	The specimens in Paris were collected by Montano-Rey c. 1900. The exact dates of these specimens are not known
36. Philippines (PHL)	28	BER-9; DRE-19	Most specimens are from Luzon Island. The exact dates of these specimens are not known
Mainland Southeast Asia			
37. Vietnam (VTN)	49	HCM-49	Near modern crania from Hanoi (Van Dien Cemetery) and Ho Chi Minh City
38. Bachuc Village, (BAC)	51	BAC-51	Victims of the 1978 Khmer Rouge massacre in Bachuc Village in western Angiang Province, Vietnam

(*continued*)

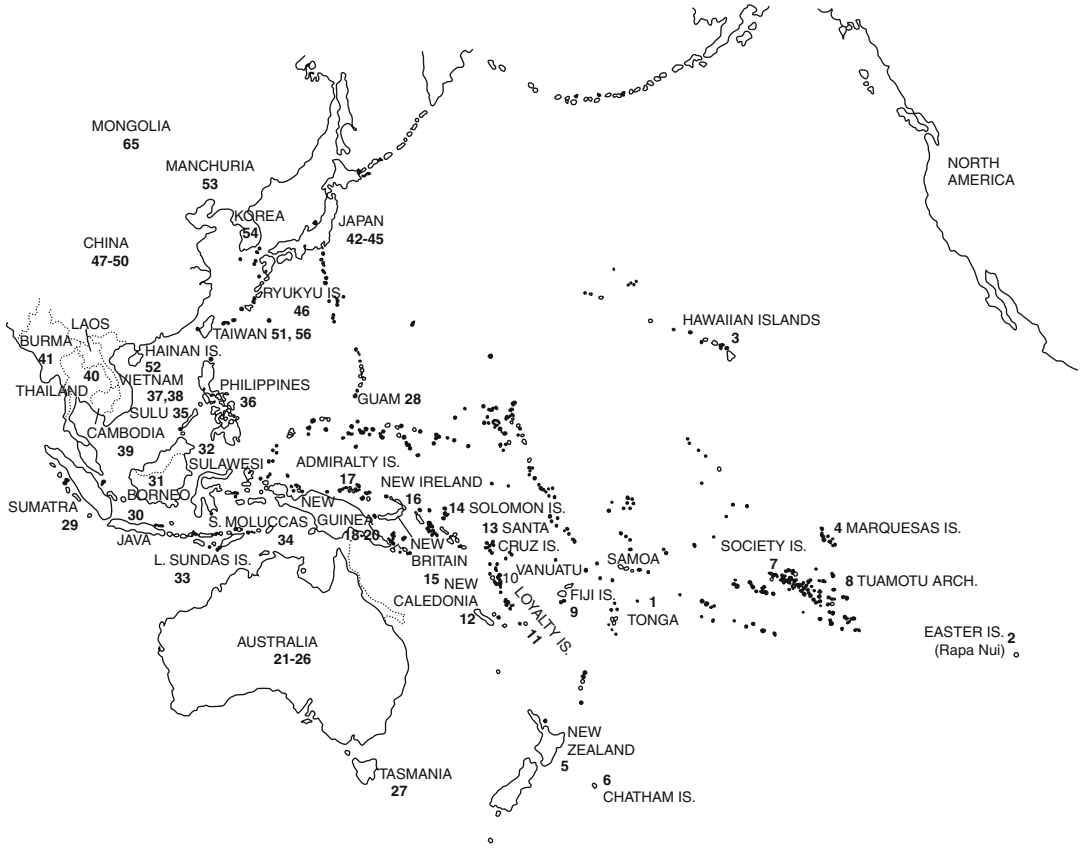
B

Biological Distance in Bioarchaeology and Human Osteology, Table 1 (continued)

Series Name (abbrev.)[a]	No. of Crania	Location[b] and Number of Crania	Remarks
39. Cambodia & Laos (CML)	40	PAR-40	A combined sample of crania from various locations in Cambodia and Laos collected between 1877 and 1920. The exact dates of these specimens are not known.
40. Thailand (THI)	50	SIR-50	Most of the specimens represent dissecting room cases from Bangkok
41. Burma (BUR)	16	ZUR-16	The crania in Zürich are from a series (Cat. Nos. 93–125) of skulls collected in Mandalay, Myanmar (Burma), described in a catalogue dated c. 1900. The exact dates of these specimens are not known
East Asia: Japan			
42. Kanto (KAN)	50	CHB-50	A dissecting room population of modern Japanese from the Kanto District of eastern Honshu. The majority of the individuals were born during the Meiji period (1868–1911) and died well before 1940
43. Tohoku (TOH)	53	SEN-53	Dissecting room specimens of modern Japanese from the Tohoku District in northern Honshu Island
44. Kyushu (KYU)	51	KYU-51	Modern Japanese, which derive mostly from Fukuoka Prefecture in Kyushu Island. Other specimens are from Yamaguchi, Saga, Nagasaki and adjoining prefectures
45. Ainu (AIN)	50	SAP-18; TKM-5; TKO-27	Modern to near modern skeletons collected by Koganei in 1888–1889 from abandoned Ainu cemeteries in Hokkaido
46. Ryukyu Islands (RYU)	60	KYO-18; KAN-21; RYU-8; KYU-5; TKO-8	Eighteen near modern crania are from Tokunoshima Island of the Amami Islands located north of the Okinawa Group in the central Ryukyu Islands; 21 specimens are from two different locations on Kume Island, an island located west of Okinawa Island: Yattchi (17) and Hiyajo (4); 21 specimens are from five separate islands in the Sakishima Group of the southern Ryukyu Islands: Hateruma Island (2); Miyako (4); Iriomote Island (2); Ishigaki Island (1), and Yonaguni Island (12)
China and N.E. Asia			
47. Shanghai (SHA)	50	SHA-50	The specimens are mostly from post-Qing (post-1911) cemeteries in Shanghai
48. Nanjing (NAJ)	49	SHA-49	The series represents near modern crania exhumed from the modern city of Nanjing, Jiangsu Province, eastern China
49. Chengdu (CHD)	53	SHA-10; CHE-43	A majority of these specimens date to the Qing Dynasty (CE 1644–1911) and are from Chengdu, Sichuan Province in western China. Ten crania are from Leshan, Lizhong County, Sichuan Province
50. Hong Kong (HK)	50	HKU-50	Specimens represent individuals who died in Hong Kong between 1978 and 1979

51. Taiwan (TAI)	47	TPE-47	Modern Chinese living in Taiwan who trace their immediate origins to Fujian and Guangdong Provinces on the mainland of China
52. Hainan Island (HAI)	47	TPE-47	Near modern Chinese whose ancestors began migrating from the Canton region of China to Hainan Island around 200 BCE. This material was excavated by Takeo Kanaseki in Haikou City on Hainan Island
53. Manchuria (MAN)	50	TKO-50	Many of the specimens are from northeastern China or the region formerly referred to as "Manchuria," which today includes Heilongjiang and Jilin Provinces and adjacent northern Korea. A great many of these specimens are identified as soldiers, or cavalrymen, who died in battle in the late 19th century CE
54. Korea (KOR)	32	KYO-7; SEN-3, TKM-2; TKO-20	Specific locations in Korea are known for most of these near modern specimens
55. Mongolia (MOG)	50	SIM-50	The skulls are identified as coming from Ulaanbaatar (Urga), Mongolia and were purchased by A. Hrdlička in 1912
56. Atayal (ATY)	36	TPE-28; TKM-7; TKO-1	The Atayal are the second largest surviving Aboriginal tribe in Taiwan. The specimens are Atayal slain in the Wushe incident in 1930. The specimens were collected by Takeo Kanaseki in 1932

[a, b]AIM, Auckland Institute and Museum, Auckland, New Zealand; AIA, Australian Institute of Anatomy, Canberra, Australia; AMS, The Australian Museum, Sydney, Australia; AUK, University of Auckland, Auckland, New Zealand; BAC, Bachuc Village, Angiang Province, Vietnam; BAS, Naturhistorisches Museum, Basel, Switzerland; BER, Museum für Naturkunde, Berlin, Germany; BLU, Anatomisches Institut, Universität Göttingen, Göttingen, Germany; BPB, B. P. Bishop Museum, Honolulu, U.S.A.; BRE, Über-see Museum, Bremen, Germany; CAN, Canterbury Museum, Christchurch, New Zealand; CHA, Anatomisches Institut der Chairté, Humboldt Universität, Berlin, Germany; CHB, Chiba University School of Medicine, Chiba, Japan; CHE, Dept. of Anatomy, Chengdu College of Traditional Chinese Medicine, Chengdu, China; DAM, Dept. of Anatomy, University of Melbourne, Melbourne, Australia; DAS, Dept. of Anatomy, University of Sydney, Sydney, Australia; DUN, Dept. of Anatomy, University of Otago, Dunedin, New Zealand; DRE, Museum für Völkerkunde, Dresden, Germany; FRE, Institut für Humangenetik und Anthropologie, Universität Freiburg, Freiburg im Breisgau, Germany ; GOT, Institut für Anthropologie, Universität Göttingen, Göttingen, Germany; HCM, Faculty of Medicine, Ho Chi Minh City, Viet Nam; HON, Honokahua, Maui, Hawai'i, U.S.A.; HKU, University of Hong Kong, Hong Kong; KAN, Kanegusuku Storage Room, Board of Education Cultural Division, Kanegusuku, Okinawa, Japan; KYO, Physical Anthropology Laboratory, Faculty of Science, Kyoto University, Kyoto, Japan; KYU, Dept. of Anatomy, Faculty of Medicine, Kyushu University, Fukuoka, Japan; LEP, Anatomisches Institut, Karl Marx Universität, Leipzig, Germany; MMS, Macleay Museum, University of Sydney, Sydney, Australia; NMV, National Museum of Victoria, Melbourne, Australia; OTM, Otago Museum and Art Gallery, Otago, New Zealand; PAR, Musée de l'Homme, Paris, France; QMB, Queensland Museum, Brisbane, Australia; RYU, University of the Ryukyus, Naha, Okinawa Island, Japan; SAM, South Australian Museum, Adelaide, Australia; SAP, Dept. of Anatomy, Sapporo Medical College, Sapporo, Japan; SEN, Dept. of Anatomy, School of Medicine, Tohoku University, Sendai, Japan; SHA, Institute of Anthropology, College of Life Sciences, Fudan University, Shanghai, China; SIM, National Museum of Natural History, Smithsonian Institution, Washington, D.C., U.S.A.; SIR, Dept. of Anatomy, Siriraj Hospital, Bangkok, Thailand; THM, Tasmanian Museum and Art Gallery, Hobart, Australia; TKM, Medical Museum, University Museum, University of Tokyo, Tokyo, Japan; TKO, University Museum, University of Tokyo, Tokyo, Japan; TPE, Academia Sinica, Nankang, Taipei, Taiwan; TUB, Institut für Anthropologie u. Humangenetik, Universität Tübingen, Tübingen, Germany; WAM, Western Australian Museum, Perth, Australia; WEL, National Museum of New Zealand, Wellington, New Zealand; ZUR, Anthropologisches Institut, Universität Zürich, Zürich, Germany



Biological Distance in Bioarchaeology and Human Osteology, Fig. 1 Map showing the approximate locations of the 56 cranial samples used in the example (This figure, reproduced here courtesy of Etty Indriati, was originally published in Pietrusewsky (2008b))

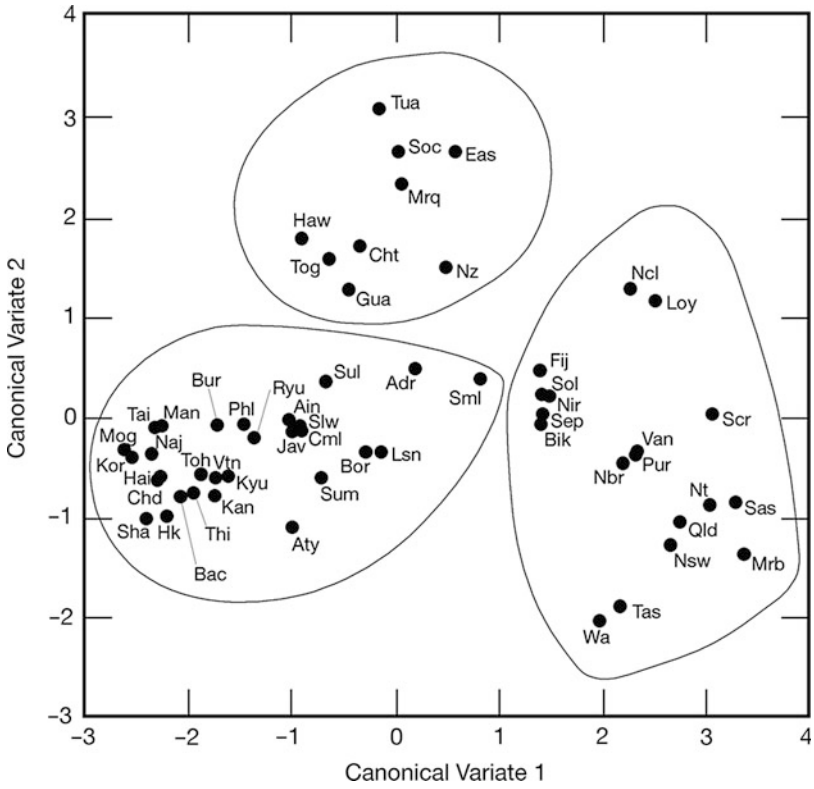
In addition to studies of skull form and teeth, the analysis of aDNA and other geochemical data will attract future research in biological distance. Combining data from multiple sources (e.g., Ricaut et al. 2010) will likewise provide new opportunities for reconstructing evolutionary and population history.

As never before, access to computers, imagining technology, user-friendly software for conducting biological distance studies, and sharing of data and quantitative methods will guide and encourage future studies.

Given the current repatriation claims and issues surrounding the accessibility of skeletal remains, the creation of data banks such as W.W. Howells' craniometric data bank, and the sharing of data worldwide will provide a wealth of information that is nonrenewal. Many of the skeletal series examined in biodistance studies just a few decades ago using traditional morphometrics (e.g., Polynesians and Australian Aboriginals) are no longer accessible to researchers.

Case Study 1: An Example of Biological Distance Analysis

In this example, two multivariate statistical procedures, stepwise discriminant function (canonical) analysis and Mahalanobis' distance, are applied to 27 landmark cranial measurements recorded in 56 modern and near modern male cranial samples for understanding the population history of the Asia-Pacific region (Table 1, Fig. 1) (Pietrusewsky 2008b). Discussion of these results is restricted to a canonical plot of group means and the dendrogram of Mahalanobis' distances, with detailed discussion provided in Pietrusewsky (2008a).



Biological Distance in Bioarchaeology and Human Osteology, Fig. 2 Plot of 56 group means on the first two canonical variates after applying stepwise discriminant function analysis to 27 cranial measurements. Abbreviations of the cranial samples are explained in Table 1 (This figure, reproduced here courtesy of Etty Indriati, was originally published in Pietrusewsky (2008b))

Stepwise Discriminant Function Analysis

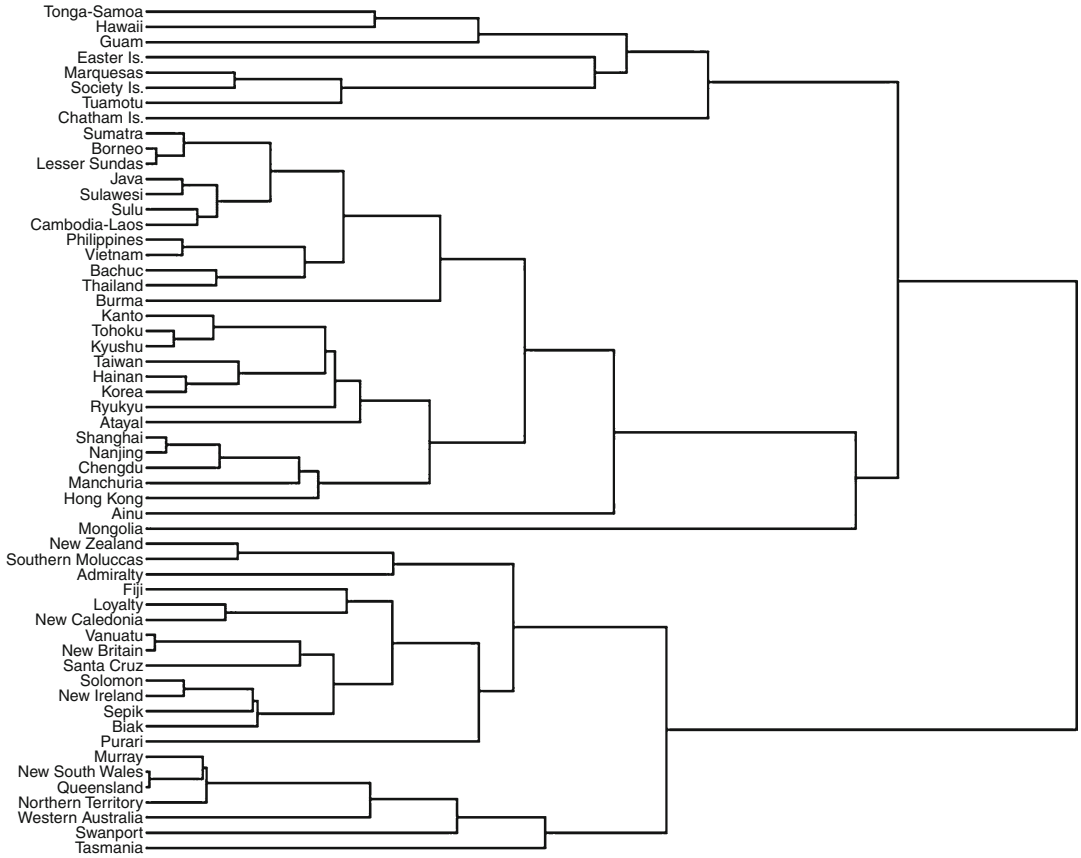
Three clusters emerge when the group means for the 56 group are plotted on the first two canonical variates (Fig. 2). One of these includes the cranial series from Australia, New Guinea, and geographical Melanesia. A second cluster includes the cranial series representing Polynesia and Guam. Cranial series from Mainland Southeast Asia and East Asia form a third major constellation. Of note, the cranial series from the Southern Moluccas, Admiralty Islands, and Lesser Sunda Islands occupy an intermediate position between the Polynesian and Australo-Melanesian cranial series.

Mahalanobis' Generalized Distance

Applying the UPGMA clustering algorithm to Mahalanobis' distances results in the dendrogram shown in Fig. 3. The primary division evident in this diagram places all the cranial series from Australia and Melanesia in one branch while the second includes the cranial series from Polynesia, Southeast Asia, and East Asia. Within these major divisions, there is internal differentiation that generally mirrors geography. It is also worth noting that New Zealand Maori (Polynesia), Southern Moluccas (Island Southeast Asia), and the Admiralty Islands (Melanesia) cranial series form a cluster that ultimately links with the Australian-Melanesian branch in this diagram.

Australia/Melanesia Versus Southeast/East Asia and Remote Oceania

The presence of two major divisions demonstrated in these results supports archaeological, linguistic, and genetic models that the indigenous inhabitants of Australia, Tasmania, and geographical Melanesia share a common origin that is unrelated to that for the modern inhabitants of Southeast Asia and East Asia. The sharp separation between Polynesian and Australian-Melanesians series further reinforces archaeological and linguistic models. These models hypothesize an earlier colonization of Australia,



Biological Distance in Bioarchaeology and Human Osteology, Fig. 3 Dendrogram (or diagram of relationship) that results from applying the UPGMA clustering algorithm to Mahalanobis' distances using 27 cranial measurements recorded in 56 male groups (This figure, reproduced here courtesy of Etty Indriati, was originally published as Fig. 4 in Pietrusewsky (2008b))

New Guinea, and neighboring regions of Near Oceania and a much later colonization that led to the peopling of previously uninhabited remote Oceania.

Southeast Asia and North/East Asia

These results further allow an examination of some of the current archaeological models advanced to explain the population history of East and Southeast Asia. The sharp contrast between East/North Asian and Southeast Asian cranial series does not support linguistic and archaeological models that argue that the indigenous inhabitants of Southeast Asia were replaced by immigrant groups of people of a more northern origin during Neolithic times.

Island Southeast Asia/Polynesian Homeland

Finally, these results also support an ancestral Polynesian homeland in East/Southeast Asia and not one within geographically adjacent Melanesia. The connection between New Zealand Maori (a Polynesian series) and the Southern Moluccas (Island Southeast Asia) cranial series supports a probable Island Southeast Asian origin of the Polynesians, an association also demonstrated in previous analyses of genetic data.

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Cross-References

- Ancestry Assessment
- Bioarchaeology, Human Osteology, and Forensic Anthropology: Definitions and Developments
- Demographic Transitions
- Dental Anthropology
- Forensic Anthropology: Definition
- Hokkaido Sequence and the Archaeology of the Ainu People
- Human Migration: Bioarchaeological Approaches
- Human Remains in Museums
- Hunter-Gatherer Subsistence Variation and Intensification
- Insular Southeast Asia at the Interface of Continent-Archipelago: Geography and Chronology
- Northern Asia: Origins and Development of Agriculture
- Skeletal Biology: Definition

References

Betti, L., F. Balloux, T. Hanihara & A. Manica. 2010. The relative role of drift and selection in shaping the human skull. *American Journal of Physical Anthropology* 141: 76-82.

Buikstra, J.E., S.R. Frankenberg & L.W. Konigsberg. 1990. Skeletal biological distance studies in American physical anthropology: recent trends. *American Journal of Physical Anthropology* 82: 1-7.

Harvati, K. & T.D. Weaver. 2006. Human cranial anatomy and the differential preservation of population history and climate signatures. *The Anatomical Record Part A* 288A: 1225-33.

Howells, W.W. 1973. *Cranial variation in man: a study by multivariate analysis of patterns of difference among recent human populations* (Papers of the Peabody Museum 67). Cambridge (MA): Peabody Museum, Harvard University.

Hubbe, M., T. Hanihara & K. Harvati. 2009. Climate signatures in the morphological differentiation of worldwide modern human populations. *The Anatomical Record* 292: 1720-33.

Martínez-Abadías, N., M. Esparza, T. Sjøvold, R. González-José, M. Santos & M. Hernández. 2009. Heritability of human cranial dimensions: comparing the evolvability of different cranial regions. *Journal of Anatomy* 214: 19-35.

Pietrusewsky, M. 2008a. Metric analysis of skeletal remains: methods and applications, in M.A. Katzenberg & S.R. Saunders (ed.) *Biological anthropology of the human skeleton*, 2nd edn: 487-532. New York: John Wiley & Sons Inc.

- 2008b. The modern inhabitants of Island Southeast Asia: a craniometric perspective, in E. Indriati (ed.) *Proceedings of the international seminar on Southeast Asian paleoanthropology: recent advances on Southeast Asian paleoanthropology and archaeology*: 185-201. Yogyakarta: Laboratory of Bioanthropology and Paleoanthropology, Faculty of Medicine, Gadjah Mada University.

Relethford, J.H. 2004. Global patterns of isolation by distance based on genetic and morphological data. *Human Biology* 76: 499-513.

- 2009. Race and global patterns of phenotypic variation. *American Journal of Physical Anthropology* 139: 16-22.

Relethford, J.H. & J. Blangero. 1990. Detection of differential gene flow from patterns of quantitative variation. *Human Biology* 62: 5-25.

Ricaut, F-X, V. Auriol, N. Von Cramon-Taubadel, C. Keyser, P. Murail, B. Ludes & E. Crubézy. 2010. Comparison between morphological and genetic data to estimate biological relationship: the case of the Egyin Gol Necropolis (Mongolia). *American Journal of Physical Anthropology* 143: 355-64.

Roseman, C.C. 2004. Detecting interregionally diversifying natural selection on modern human cranial form by using matched molecular and morphometric data. *Proceedings of the National Academy of Sciences U.S.A.* 101: 12824-29.

Ross, A.H., D.H. Ubelaker & A.B. Falsetti. 2003. Craniometric variation in the Americas. *Human Biology* 74: 807-18.

Slice, D.E. 2005. *Modern morphometrics in physical anthropology*. New York: Kluwer Academic/Plenum Publishers.

Smith, H.F. 2011. The role of genetic drift in shaping modern human cranial evolution: a test using microevolutionary modeling. *International Journal of Evolutionary Biology*. doi:10.4061/2011/145262.

Sparks, C.S. & R.L. Jantz. 2002. A reassessment of human cranial plasticity: Boas revisited. *Proceedings of the National Academy of Sciences U.S.A.* 99: 14636-9.

Von Cramon-Taubadel, N. 2009. Congruence of individual cranial bone morphology and neutral molecular affinity patterns in modern humans. *American Journal of Physical Anthropology* 140: 205-15.

- 2011. Craniometric data support a mosaic model of demic and cultural Neolithic diffusion to outlying regions of Europe. *Proceedings of the Royal Society B*. doi:10.1098/rspb.2010.2678.

Weaver, T.D., C.C. Roseman & C.B. Stringer. 2008. Close correspondence between quantitative- and molecular-genetic divergence times for Neanderthals and modern humans. *Proceedings of the National Academy of Sciences U.S.A.* 105: 4645-49.

Further Reading

Bernal, V., S.I. Perez, P.N. Gonzalez, M.L. Sardi & H.M. Pucciarelli. 2010. Spatial patterns and evolutionary processes in southern South America: a study of dental morphometric variation. *American Journal of Physical Anthropology* 142: 95-104.

Carson, E.A. 2006. Maximum likelihood estimation of human craniometric heritabilities. *American Journal of Physical Anthropology* 131: 169-80.

De Azevedo, S., A. Nocera, C. Paschetta, L. Castillo, M. González & R. González-José. 2011. Evaluating microevolutionary models for the early settlement of the New World: the importance of recurrent gene flow with Asia. American *Journal of Physical Anthropology* 146: 116-29.

González-José R., C. García-Moro, S. Dahinten & M. Hernández. 2002. Origin of Fueguian-Patagonians: an approach to population history and structure using R matrix and matrix permutation methods. *American Journal of Human Biology* 14: 308-20.

González-José R., S. Van Der Molen, E. González - Pérez & M. Hernández. 2004. Patterns of phenotypic covariation and correlation in modern humans as viewed from morphological integration. *American Journal of Physical Anthropology* 123: 69-77.

González-José R., M.C. Bortolini, F.R. Santos & S.L. Bonatto. 2008. The peopling of America: craniofacial shape variation on a continental scale and its interpretation from an interdisciplinary view. *American Journal of Physical Anthropology* 137: 175-87.

Irish, J.D. 2010. The mean measure of divergence: its utility in model-free and model-bound analyses relative to the Mahalanobis D2 distance for nonmetric traits. *American Journal of Human Biology* 22: 378-95.

Konigsberg, L.W. 2006. A post-Neumann history of biological and genetic distance studies in bioarchaeology, in J.E. Buikstra & L.A. Beck (ed.) *Bioarchaeology. The contextual analysis of human remains*: 263-79. Oxford: Elsevier Press, Inc.

Manica, A., B. Amos, F. Balloux & T. Hanihara. 2007. The effect of ancient population bottlenecks on human phenotypic variation. *Nature* 448: 346-48.

Mckeown, A.H. & R.L. Jantz. 2005. Comparison of coordinate and craniometric data for biological distance studies, in D.E. Slice (ed.) *Modern morphometrics in physical anthropology*: 215-30. New York: Kluwer Academic/Plenum Publishers.

Powell, J.F. & A.W. Neves. 1999. Craniofacial morphology of the first Americans: pattern and process in the peopling of the New World. *Yearbook of Physical Anthropology* 42: 153-88.

Pucciarelli, H.M., R. González-José, W.A. Neves, M.L. Sardi & F.R. Rozzi. 2008. East–west cranial differentiation in pre-Columbian populations from Central and North America. *Journal of Human Evolution* 54: 296-308.

Relethford, J.H. 2001. Global analysis of regional differences in craniometric diversity and population substructure. *Human Biology* 73: 629-36.

- 2002. Apportionment of global human genetic diversity based on craniometrics and skin color. *American Journal of Physical Anthropology* 118: 393-98.
- 2004. Boas and beyond: migration and craniometric variation. *American Journal of Human Biology* 16: 379-86.
- 2010. Population-specific deviations of global human craniometric variation from a neutral model. *American Journal of Physical Anthropology* 142: 105-11.

Relethford, J.H. & H.C. Harpending. 1994. Craniometric variation, genetic theory, and modern human origins. *American Journal of Physical Anthropology* 95: 249-70.

Relethford, J.H., M.H. Crawford & J. Blangero. 1997. Genetic drift and gene flow in post-famine Ireland. *Human Biology* 69: 443-65.

Roseman, C.C. & T.D. Weaver. 2004. Multivariate apportionment of global human craniometric diversity. *American Journal of Physical Anthropology* 125: 257-63.

Ross, A.H. & E.H. Kimmerle. 2009. Contribution of quantitative methods in forensic anthropology: a new era, in S. Blau & D.H. Ubelaker (ed.) *Handbook of forensic anthropology and archaeology*: 479-89. Walnut Creek (CA): Left Coast Press Inc.

Schillaci, M.A. & C.M. Stojanowski. 2003. Postmartial residence and biological variation at Pueblo Bonito. *American Journal of Physical Anthropology* 120: 1-15.

Smith, H.F. 2009. Which cranial regions reflect molecular distances reliably in humans? Evidence from three-dimensional morphology. *American Journal of Human Biology* 21: 36-47.

Strauss, A. & M. Hubbe. 2010. Craniometric similarities within and between human populations in comparison with neutral genetic data. *Human Biology* 82: 315-30.

Von Cramon-Taubadel, N. 2009. Insights from a quantitative genetic approach to human morphological evolution. *Evolutionary Anthropology* 18: 237-40.

Biometry in Zooarchaeology

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Introduction

The measurement of bones is a routine aspect of zooarchaeological analysis. Requiring minimal