Bones and Chromosomes:
The Ancient DNA Revolution in Archaeology
(Part 1)
SAA’s 84th Annual Meeting
April 10 - 14, 2019
Albuquerque, NM

Advance Registration Closes
March 12, 2019

Learn More at
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SPECIAL SECTION: BONES AND CHROMOSOMES: THE ANCIENT DNA REVOLUTION IN ARCHAEOLOGY (PART 1)

Introduction: Bones and Chromosomes: The Ancient DNA Revolution in Archaeology (Part 1)

The Office Odd Couple

Ancient DNA 101: An Introductory Guide in the Era of High-Throughput Sequencing

Ancient DNA’s Impact on Archaeology: What Has Been Learned and How to Build Strong Relationships

Show-and-Tell Genetics: Diagnosis and Treatment

How Can Archaeologists Make a Difference to Media and Public Perceptions of Ancient DNA?

Calendar

Report to the Board of Directors of the Society for American Archaeology Task Force on Revisions of the SAA Principles of Archaeological Ethics: Stage One

Erratum: Volume 18, Number 5, November 2018

On page 15 of the article “Process and Outcomes of the SAA ‘Professional Archaeologists, Avocational Archaeologists, and Responsible Artifact Collectors Relationships Task Force’ (2015–2018),” the Archaeological Institute of America was mistakenly listed as the American Institute of Archaeology. We apologize for the error.
The practice of archaeology has been affected by many technological advances over the past decades. Perhaps none have had bigger impacts (beyond perhaps the advent of radiocarbon dating) than the rise of ancient DNA (aDNA) research. The potential to address long-vexing challenges dealing with human ancestry and population movements around the globe has led to a wide array of new studies. However, this has also led to methodological and ethical challenges. Ancient DNA studies have now become pervasive to such a degree that I think it is worth a broad review of where we are today and what we should be considering as we go forward.

Guest editor Matthew Piscitelli has developed a collection of essays that we will publish in two consecutive special sections (January and March 2019) of The SAA Archaeological Record, titled “Bones and Chromosomes: The Ancient DNA Revolution in Archaeology.” Part I, this issue, provides discussions that introduce the topic and dissect a number of critical issues. Piscitelli offers an entertaining consideration of the challenges faced by archaeologists as they engage in collaborations with genetics specialists. Hofman and Warinner introduce the basics of aDNA studies from a practical field- and laboratory-oriented perspective. Sedig examines the sociality of aDNA research with emphases on communications and partnerships with different publics including indigenous groups. Terrell cautions archaeologists to be cognizant of some significant pitfalls awaiting novice archaeologists treading into the ancient DNA world, concluding with a series of recommendations. Finally, Hawks provides recommendations for working with the media and the general public regarding perceptions of aDNA research.

The January 2019 issue offers substantial additional content beyond ancient DNA considerations. We include columns from SAA President Susan Chandler and Executive Director Oona Schmidt, along with notes on the upcoming Annual Meeting from Matthew Schmader and E. Christian Wells. Finally, this issue also includes discussions of issues relevant to SAA policy (statement on sexual harassment), recommendations for best practice (no-collection projects and in-field analysis), and revisions to the SAA Principles of Archaeological Ethics. Our Volunteer Profile column will return in the March 2019 issue.
The SAA Board of Directors met in Washington, DC, in November, which gave us the opportunity to spend some time with SAA’s staff at headquarters. Although the Board works closely with our excellent staff, this was the first opportunity for many of them to meet face to face.

The Board appointed four new task forces. The Task Force for the Grant Program in Pre-Columbian Archaeology, which will be chaired by Deborah Nichols, will provide SAA with recommendations for awarding and administrating SAA’s newest grant opportunity, the H. and T. King Grant for Pre-Columbian Archaeology. The generous gift from the King family is intended to fund postdoctoral archaeological projects throughout Latin America.

The Task Force on Revisions of the SAA Principles of Archaeological Ethics: Stage Two, to be chaired by Sarah Miller, will implement the excellent plan of action outlined by the Stage One task force. It is charged with gathering and synthesizing feedback, comments, and ideas from the membership, standing committees, interest groups, and stakeholders regarding revisions to the ethics principles.

The Intersectionality Task Force will propose draft questions for inclusion in the 2020 Members’ Need Assessment Survey; will propose workshops and online seminars on the topic of intersectionality; and will work with the Ethics Task Force ensure their concerns about inclusion and diversity are reflected in the revised ethics principles. Kristen Barnett will chair the task force.

The Task Force of Sharing Public Outcomes of CRM, chaired by Joshua Wells, is charged with providing draft guidelines with regard to the conditions under which site data (including site location) could be shared for legitimate research purposes.

The Board gave approval to the Committee on Museums, Collections, and Curation (CMCC) to publish their “Guidelines for Preparing Legacy Archaeological Collections for Curation,” by Michelle K. Knoll and Bruce B. Huckell. This document resulted from the SAA Board’s 2017 request that the CMCC consider drafting guidelines for archaeologists who are responsible for, or are aware of, collections that should have been curated but, for whatever reason, are still languishing. It is our hope that these excellent and thorough guidelines will help archaeologists navigate what can seem to be an overwhelming process so that legacy collections will be curated and not abandoned.

The Board approved a new SAA Anti-Harassment Policy, intended to ensure that our meetings are safe spaces where all members can participate without feeling threatened or intimidated and where ideas can be exchanged in a respectful, inclusive atmosphere. The new policy is discussed in detail in this issue on page 6.

SAA also welcomed the Falls of Ohio Archaeological Society as the newest member of SAA’s Council of Allied Societies, formerly known as the Council of Affiliated Societies.

Minutes of the Board meeting are available in the Members’ section of the website.

SAA on the Web
SAA’s new website is finally live: check out the newly designed saa.org! I wish to extend my appreciation to SAA’s staff for the countless hours of work they have invested in the effort to create a more useful website and to task force members for the guidance they provided during the redesign.

SAA now has a YouTube channel that showcases the interviews of SAA members Paul Minnis and Jeff Dean conducted by the History of Archaeology Interest Group as part of their Archiving the Archaeologists Project. You can also find archived online seminars and a “What’s in Your Lab” feature conducted by SAA’s manager of Education and Outreach, Beth Pruitt. Take a look and subscribe so that you don’t miss out on upcoming interviews of our colleagues and other content: https://www.youtube.com/channel/UCj54dtuh9q8zAICBaHina6eQ/featured
European Archaeological Association (EAA) Conference

Several SAA members and I attended the EAA Conference in Barcelona in early September. I was invited to attend a working group luncheon for presidents of various archaeological associations on the topic, “What new skills do archaeologists need in the changing world?” The wide-ranging discussion focused on identifying new areas where diversification is taking place and the kind of new capacities archaeological associations should be seeking to build. The group pondered how archaeologists could acquire needed skills if they are not being taught in universities, and I talked about the role of professional organizations such as SAA in providing continuing education for our members. I also attended an interesting EAA session on “The self-organization of archaeologists in Europe: Roles and needs, responsibility and legitimacy.” With the EAA President, Felipe Criado-Boado, I gave a presentation in the symposium on synthesis of archaeological data that stated our joint goal of providing forums for archaeologists from Europe and the Americas to collaborate and for archaeologists working in academic settings to collaborate with their counterparts working on “developer-funded investigations,” as they say in Europe.

84th Annual Meeting in Albuquerque

I look forward to seeing you in Albuquerque in April 2019 for what promises to be an outstanding Annual Meeting as SAA returns to New Mexico for the first time in over 50 years. As evident in the Preliminary Program mailed to you a few weeks ago and available on www.saa.org, the Albuquerque meeting features a broad range of sessions, workshops, excursions, and networking opportunities (including the Student Welcome Reception hosted by SAA Board of Directors and Cambridge University Press).

The meeting begins on Wednesday evening, April 10, with my President’s Forum, “Learning from the Past, Looking Towards the Future: Archaeological Ethics and the SAA.” This forum will provide an opportunity for the Society’s members to engage in a discourse on which ethical concerns the membership wishes to consider in the process of evaluating and revising SAA’s ethical principles to reflect today’s standards and norms. I hope you will come to listen and to provide your input.

Posters After Hours will be back on Thursday night for a second year. You won’t want to miss this social event featuring 200 posters. I also encourage you to attend SAA’s annual business meeting on Friday evening.

I would also like to draw your attention to the Presidential-Sponsored forum, “Protecting the Greater Chaco Landscape: Native Voices,” scheduled for Saturday afternoon, at which a panel of Native American speakers will convey the deep spiritual importance of the Greater Chaco Landscape and will discuss their views of the best management practices for its preservation.

I will be participating as a discussant in the #MeToo in Archaeology panel on Saturday afternoon, where a selection of representative narratives, anonymously submitted, will be read aloud to provide a platform for people to share their stories of sexual misconduct, sexual harassment, and sexual violence directly experienced on archaeological projects and/or within the archaeological community.

2019 SAA Elections

Please check your e-mail for a link to the 2019 SAA candidate statements and digital ballot and vote for the colleagues you would like to have represent you in the governance of our professional society. Your votes must be received by January 31, 2019.
It is a great honor to announce a completely new research funding opportunity, the H. and T. King Grant for Pre Columbian Archaeology. Thanks to the generosity of these donors, SAA will award up to $60,000 each year for five years to early career and senior archaeologists who have completed their advanced academic education and need support to conduct research, laboratory, collections, or fieldwork that will promise transformative contributions to the understanding of these early indigenous civilizations. Over 50% of the grants are dedicated to help early career archaeologists (those within five years of completion of the doctorate or Licenciado). Read more about this stupendous opportunity at https://www.saa.org.

www.saa.org

Speaking of our website, I would like to thank the incredible SAA staff effort to migrate content from the old site to the new; saa.org is now easier to navigate, faster to update, and as visually exciting as the field itself. The new website offers responsive design, which makes it easier to read on mobile phones. I also thank two member taskforces, who advised on navigation, content, and design. I thank these SAA members for helping to realize a new digital home for the Society. Check out the Preliminary Program on the new Annual Meeting web page!

Join Us in Albuquerque, New Mexico, April 10–14, 2019

In 2019, the SAA Annual Meeting sets up its tent in the Southwestern United States. What a perfect inauguration for me to meet the members of the Society for American Archaeology—in a city palpably enriched with Native American heritage and surrounded by a landscape where archaeological sights—and sites—abound. Thanks to our Local Programming Chair, Matthew Schmader, SAA will offer tours to Bandelier National Monument and Acoma Pueblo, among others. Visit one of these breathtaking destinations by signing up for a tour at saa.org.

SAA will bring a trove of archaeological knowledge into the Albuquerque Convention Center. The preliminary program is posted on saa.org. The lineup showcases over 450 sessions, symposia, special events, and workshops.

Some things can’t be found within the program. Albuquerque’s Downtown is a pleasant walk of less than one mile from the Convention Center and provides a bounty of eateries; Old Town is a short bus ride west on Central Ave.; and Nob Hill (next to the University) is a short bus ride east on Central Ave. You can buy an unlimited one-day pass for $2.00 and plan your bus trips at http://planyourride.cabq.gov.

Whichever way you head, I believe you will find a few microbreweries. One 2017 report tallies more microbreweries in Albuquerque than in Portland, Oregon! I hope I’ll see you at the meeting.

E-Communities

Exchanging information with colleagues is a vital attraction of the Annual Meeting. SAA also offers members additional opportunities to connect on a more flexible schedule. To this effect, each Interest Group of the SAA has been offered the chance to create an e-Community—a digital environment where members of the Interest Group can share information, post questions, provide advice, and meet others who share that group’s special interest.

Members can access any e-Communities to the Interest Groups they have joined. Visit saa.org and select the “e-Communities” option under the Member Center Login tab.

Renew Your Membership

Not least, the Society can only exist but for its members. Members receive discounts to the Annual Meeting as well as access to the new e-Communities. Your dues enable the organization’s defense of the Antiquities Act, its vociferous condemnation of looting, and its work to protect the future of the archaeological record. Your membership ensures that the Society can continue to amplify your voice on behalf of archaeology.

For those who have already paid your 2019 dues, I thank you for continuing to support SAA. I am very proud of our organization and its efforts to ensure that archaeological knowledge is available for future generations. I am also interested in ways SAA can do more, to help members stay in the Society and remain in the field that they love. I am always here for any questions or ideas you want to share: oona_schmid@saa.org.

Oona Schmid

Oona Schmid is the executive director of the Society for American Archaeology.
SAA ANTI-HARASSMENT POLICY

MESSAGE FROM THE SAA PRESIDENT

The SAA Board has recently adopted the following anti-harassment policy that pertains to any SAA-sponsored conference, meeting, or workshop. The policy goes into effect immediately and pertains to everyone in attendance at the upcoming Annual Meeting in Albuquerque, including presenters, students, guests, staff, contractors, and exhibitors.

SAA is proud of our diverse membership and wants to ensure that our conference symposia, poster sessions, meetings, social events, and informal gatherings are safe spaces where all members can participate without feeling threatened or intimidated and where ideas can be exchanged in a respectful, inclusive atmosphere.

As part of our new anti-harassment measures, SAA Staff and Officers will wear green “Talk to Me” buttons so that they can be easily identified at the conference. If you are harassed or witness harassment, whether it is speech or deed, we urge you to report to one of these safe authorities so that prompt and appropriate action can be taken. Acts of sexual violence will be reported to the authorities. While informants will understandably prefer that SAA limit disclosure of information to those on a “need to know” basis, we cannot guarantee anonymity, and we need sufficient level of detail (for instance, location, time, name, and witnesses) to respond.

While ours is not a perfect community, the Board hopes this policy will further the goals of the SAA Annual Meeting as a place where all archaeologists feel safe and can freely share ideas with each other.

SAA Anti-Harassment Policy (adopted November 2018)
The SAA is dedicated to providing a harassment-free meeting experience for everyone, regardless of sex, gender, identity and expression, sexual orientation, disability, physical appearance, ethnicity, religion, or age. Harassment is unwanted attention that a recipient experiences as offensive or disruptive to their wellbeing. Harassment not only sabotages the individual; it also damages the SAA's community by discouraging participation in the Society and compromising the exchange of ideas that is at the center of SAA's mission to promote and stimulate interest and research in the archaeology of the Americas.

Sexual harassment is behavior that demeans, humiliated, or threatens an individual on the basis of their sex or gender and can include crude behavior (such as offensive statements, jokes, or gestures); dismissive or insulting modes of address (such as referring to a woman not by her first name but as “babe”); unwelcome sexual attention (such as unwanted touching or repeated requests for dates); and coercion. Sex-based harassment also takes nonsexual forms when an individual is targeted because of their gender expression. It singles out some members of the community as acceptable targets and as unworthy of respect.

All of the spaces into which SAA's professional meetings extend are professional, and the values of respect, equity, multicultural pluralism, and non-discrimination should inform conduct in formal sessions, meetings, and informal conversations over coffee and over drinks. All members should aspire to treat each member as having an equally valuable contribution to make. All members should remember our society is enriched from multicultural differences.

This policy applies to all attendees of SAA-sponsored conferences, meetings, or workshops including presenters, students, guests, staff, contractors, and exhibitors throughout the conference space whether participating in the program, tours, meetings, social event, or other function. The SAA Principles of Archaeological Ethics equally apply.

However, should an incident occur while at an SAA-sponsored conference, meeting, workshop, tour, or social event, or other function, the SAA President, the SAA Executive Director, SAA Staff, or any SAA Officer may be considered safe authorities with whom incidents can be discussed. The SAA will have mechanisms at each Annual Meeting to keep our conference a respectful environment for all its participants.
Visitors to New Mexico often find themselves enchanted by many things—the landscape, the architecture, the timeless cultural diversity. This is partly why the state is called the Land of Enchantment. First-time visitors will be enthralled that such an exotic place can be found in this country. Those who are returning will relive the excitement of having been here before. Many who came with the intent of a short visit found themselves never leaving, even decades later.

An integral part of the New Mexico experience is its world-famous cuisine. Aficionados of Mexican food from the southern border states all claim their version is the best. Tex Mex is heavier, uses more tomatoes, and is bolder while Cal Mex is lighter, uses less cheese, and leans towards crispy shells for tacos. These subtle differences are wiped away like a stained napkin when compared to the “real best,” which is clearly New Mex. Our centuries-long fusion across the artificial US–Mexico border, along with native influences, has produced a truly authentic blend like no other: borrowing where needed, adapting where wanted, and always innovative. This food comes with its own vernacular. A good plato combinación features chiles rellenos, carne adovada, tamales, soft tacos, and creamy enchiladas, all topped with a delectable sauce of green chile and a side of sopaipillas. Note that the right spelling is not “chili,” which is Texan beans and ground beef, but “chile,” a heady concoction of chopped green peppers or a caribe sauce made from ground dried red peppers. In fact, New Mexico may be the only state in the land with an official state question: “Red or Green?,” referring to your choice of accompanying chile sauce (for the ambivalent, or those who just want the best of both worlds, there is “Christmas”—a dose of both red and green). Be prepared with an answer for your food server to the red-or-green question.

I go to these lengths just to highlight some of the many tasty treasures you will want to seek out, since archaeologists are known for their love of food! Besides the obvious local foods, there is a wide variety of ethnic cuisine that reflects Albuquerque’s location as a geographic and cultural crossroads, and its growing immigrant population. Thai, Vietnamese, Turkish, Persian, West African, Brazilian, and Caribbean are but a few choices to augment standard American fare. With luck, some of the city’s ever-growing food truck offerings will be set up near the convention center. A great site to visit for citywide dining offerings is alibi.com/media/special_publications/Chowtown Fall 2018. If you truly want to nail down your New Mexico encounter, get a great plate of New Mexican food. And wash it down with an offering from one of the many top-quality microbrews now found in Albuquerque. Some of our breweries have recently pulled in national honors. There are 58 taprooms in the city at last count, 6 of them within blocks of the conference hotels. These breweries are plotted out in the handy NM Beer map: https://nmbeer.org/beermap/—check it out.

After satiating your various food and drink appetites, be sure to indulge your sight-seeing and shopping side. Albuquerque is a modern western city grown within the confines of eighteenth-century Spanish colonial roots. Founded as a villa real (royally sanctioned settlement) in 1706, it remained a smaller outpost until the arrival of the railroad in the early 1880s. Its various growth spurts throughout the 1900s made it one of the largest metropolitan areas in the Southwest, which also means that most of the things worth doing require a car to reach its many spread-out attractions. Albuquerque has always been a settlement at the
crossroads—between the high mountains and the great plains, or the Rio Grande Rift valley and the Chihuahuan Desert—and our cultural history reflects these edges coming together. The intersection of the Pan-American Highway and the Intercontinental Freeway system is an overlay onto the earlier Royal Road or Camino Real that wound from Zacatecas, Mexico, to Santa Fe, and the Mother Road, or early Route 66. Albuquerque still bears remnants of these venerable corridors, especially its long stretch of neon down Central Avenue, one of the longest intact urban swaths of Route 66 left in the country. Conference-goers will be just a block’s walking distance from Central Avenue and can easily get from downtown to Old Town, the charming original plaza built around the early Spanish villa, replete with souvenir shops and the picturesque Gothic Revival and Territorial-style San Felipe de Neri church (built starting in 1793). On another historic note the conference hotel, the downtown Hyatt Regency, was built on top of “Hell’s Half Acre,” the city’s former early 1900s red light district.

It’s worth setting aside at least a day to drive in any direction, whether north to Santa Fe, or to any of the nearby pueblos, several national monuments and state parks, and a wide variety of museums and nature areas. All are reachable in a drive of less than 75 minutes. A reminder too, about the time of year and the climate: Albuquerque is a mile high in elevation and is in the high desert. This means that April is an unpredictable month, being the shoulder between late spring and the warm-up of early summer. With 278 days of sunshine a year, expect bright days but very changeable weather that can be cold at night and quite windy as the spring breezes arrive. Bring layers of clothing and be sure to put them on or take them off as you need. In a way, this will emulate the layers of experience you’re sure to have at the next SAA Annual Meeting!

ALBUQUERQUE 2019

The 84th Annual Meeting marks a major milestone in SAA’s history as well as a strange coincidence for me. The 2019 meeting will be the first time in 30 years that the annual meeting has taken place in the American Southwest. The last time was in 1988 with the 53rd Annual Meeting held in Phoenix. And, for that meeting, one of my mentors and closest friends, Arleyn W. Simon, chaired the program committee with Sylvia Gaines.

Arleyn is recently retired from Arizona State University, where she had an amazingly successful career and mentored hundreds of students who are now professional archaeologists all over the world. If you want to congratulate Arleyn, be sure to attend the back-to-back symposia she and Glen Rice have organized called Why Platform Mounds?, which bring together archaeologists from Arizona State, Desert Archaeology, Statistical Research, and SWCA who participated in the Roosevelt Dam Project (also 30 years ago!), one of the largest salvage projects ever undertaken in the Southwest. The sessions are on Friday morning and afternoon in Ballroom C and, with 800 seats, there’s plenty of room for everyone! I know I will be there.

Times have changed since the 53rd Annual Meeting. In 1988, Arleyn and Sylvia created a conference program with about 850 presentations. Arleyn recalls that they used “cutting-edge technology” to organize the program: Sylvia’s new AT machine running DOS and an early version of R-based software. They printed out strips of each session, arranged them on large fiberboards, and then moved them around until they solved the Rubik’s Cube. It was the first time computers were used to organize the sessions. Flash forward three decades and this year we have over 3,500 presentations! To organize the sessions, I used SAA’s custom software along with Excel and the help of 54 wonderful volunteers who made up the program committee. I won’t list them all here, but I ask that everyone attending the meetings be sure to look at the list of names in the final program and, if you happen to run into one or more of them, please thank them for their service. They worked long and hard, often with last-minute requests late at night and on weekends. I am very grateful to each and every one of them for their help. I am also very grateful to Anthony Tricarico, my program assistant, who did the lion’s share of the most mind-numbing tasks.
NOTES FROM THE LOCAL AND PROGRAM CHAIR

After working on the program, I can see that there is going to be a lot of love in Albuquerque. I have been attending the SAA meetings for nearly 25 years and I have never seen so many toasts and roasts in one place. Colleagues and friends are honoring the following: J. Stephen Athens, Anna Kerttula, Ben Nelson, Stephen Houston, David W. Anthony, Keith Kintigh, Elinor Ostrom, Frederick W. Lange, Bradley J. Parker, Polly Schaafsma, Patricia Urban and Edward Schortman, Ann F. Ramenofsky, Julie K. Stein, John Rick, M. Steven Shackley, James M. Skibo, Cecelia Klein, Lawrence L. Loendorf, Alan H. Simmons, and Luis Alberto Borrero. Whew!

If you are one of the few SAA members not attending any one of those sessions, there are plenty of other sessions and activities to choose from. Here I will mention just a few that piqued my interest. First, there is a forum that made its debut at the 2018 AAA meetings, #MeToo in Archaeology, which “provide[s] a platform for people to anonymously share their stories of sexual misconduct, sexual harassment, and sexual violence directly experienced on archaeological projects and/or within the archaeological community.” Members of the session's panel will read selections of the narratives aloud and then open the room for discussion. Another is Protecting the Greater Chaco Landscape: Native Voices, an SAA Presidential Sponsored Session with a panel of Native American speakers who will discuss their views on best management practices for preservation of the Chaco landscape. Finally, the AAA Archaeology Division is sponsoring the electronic symposium Sins of Our Ancestors (and of Ourselves): Confronting Archaeological Legacies, which examines the lives and legacies of early archaeologists in order to confront today's sociopolitical and ethical struggles in the discipline. I am told this session will be catered with good food and drink—come early and stay late!

Several sessions also deal with the relevance of archaeology to contemporary problems:

- During the electronic symposium Advancing Public Perceptions of Sustainability through Archaeology, “participants will outline the contributions their research makes to our understanding of sustainability in the past, and then shift to a discussion of specific and creative strategies that their research could generate for communicating sustainability science to the public.”
- Archaeology Out-of-the-Box: Investigating the Edge of the Discipline showcases “efforts to make the discipline germane and relevant in untraditional ways.”
- The forum From “Saving the Past for the Future” to “Saving the Future with the Past” is designed to “explore, with the audience, how we can build more persuasive arguments for the relevance of our knowledge of the long-term past for understanding the present and how that knowledge might bring unique insights that can genuinely benefit public policy.”

Finally, I would be remiss if I did not draw your attention to three staples of the Annual Meeting, which always impress. The opening session this year, Presidential Forum: Learning from the Past, Looking Towards the Future: Archaeological Ethics and the SAA (Wednesday at 6:30–8:30 p.m. in the Kiva Auditorium), will provide SAA members with an opportunity to discuss ethical concerns and how these might be addressed in the revised Ethical Principles. The ever-popular Ethics Bowl takes place on Thursday at 1:00–3:00 p.m. in Galisteo. And, with nearly 200 presentations (!), Posters After Hours (Thursday 5:00–7:00 p.m. in Hall 3) this year focuses on two major themes: archaeological science/experimental archaeology and community/applied archaeology.

I have been fortunate to have the opportunity to interact with many SAA members while organizing the conference program, and I wish to thank all of you for your courtesy and politeness, even when you discovered that your paper on European Neolithic burials was included in a session on ancient Maya pottery, or some other such peculiar combination. I also wish to thank Tobi Brimsek, Oona Schmid, and most specially Cheng Zhang for their tireless help and abundant patience. SAA staff is, and will always be, the backbone of the society and we owe them our deepest gratitude and respect.

Please refer to the final program for dates, times, and locations of all Annual Meeting sessions.
The Archaeological Collections Consortium (ACC) includes representatives from the Society for American Archaeology (SAA), the Society for Historical Archaeology (SHA), and the American Cultural Resources Association (ACRA), who are focused on the use, preservation, and management of archaeological collections. A key ACC goal is to develop and act upon a common platform of objectives that seek to benefit the discipline and ultimately the public for whom archaeological collections are curated in the public trust.

The ACC is concerned about the growing trends of no-collection, in-field artifact analyses, and collections reburial. The use of these practices is driven by several factors, including limited availability of collections storage space, costs of curation, pressure among agencies to reduce overall project costs, and concerns among some Tribal Historic Preservation Officers (THPOs) and tribes about how their patrimonies are being treated by others once archaeological objects are removed from a site. These practices negatively impact the types and breadth of archaeological collections available for present and future research, interpretation, and education. They impede the archaeologist’s ability to analyze existing artifacts by using future research designs and methods and independently verifying results, actions which are critical to the credibility of an archaeological project and the scientific process in general. They also run counter to the professional ethics of the organizations participating in the ACC.

Furthermore, these strategies are not justified in law and are rarely included in federal or state standards and guidelines, and very little has been published on these topics. Statutory authority for recovery of archaeological material remains on federal land primarily comes from Sections 106 (compliance) and 110 (resource management) of the National Historic Preservation Act (NHPA) and the Archaeological Resources Protection Act (ARPA). These federal laws were enacted in recognition of the need to preserve and research the enormous historic, cultural, and scientific value of archaeological materials for the benefit of the American people. By specifying that such items located on federal land are the property of the federal government, and by systematizing the procedures for the excavation and handling of covered objects, ARPA sought to 1) protect the items from pillage, and 2) by doing so, better enable the American people to learn about and appreciate the lives of those who came before them. Likewise, the NHPA ensures that development considerations are balanced with preservation values, and confirms the public’s interest in heritage preservation. Compliance agreements under Section 106 of NHPA require management considerations, which in many cases include archaeological data recovery and curation of the recovered collections. ARPA permits also govern archaeological data recovery and curation of the recovered collections. The federal regulations 36 CFR Part 79 (Curation of Federally-Owned and Administered Archaeological Collections) then ensure that the recovered and analyzed collection is deposited in a repository that meets certain standards. Burial in the ground does not meet those standards.

The ACC is not aware of any published studies that explore the relative costs of no-collection and in-field analysis versus long-term curation to determine where the most significant expenses/savings occur when both follow professional ethics and guidelines. No-collection strategies might actually cost agencies more than curation if sites must be revisited and reevaluated because collections are not available to verify artifact identifications and the specific attributes of those artifacts. Additionally, even when artifacts are not collected during a project, the associated records, whether hard copy or digital, should be assembled as a collection and may be subject to curation fees (Childs et al. 2010; Drew 2010; Kintigh and Altschul 2010).

Various combinations of no-collection and in-field identification and analysis have been implemented, particularly in the western United States. It is unclear whether these practices were developed using datasets and studies about their benefits and drawbacks, or whether an assessment was made of how these practices may run counter to historic preservation laws. The effectiveness and reproducibility of these practices and their impacts on the archaeological record and future research should be carefully considered by archaeologists and other stakeholders involved in an archaeological investigation.
BEST PRACTICES FOR NO-COLLECTION PROJECTS AND IN-FIELD ANALYSIS IN THE UNITED STATES

Therefore, for all of the reasons stated above, the ACC strongly discourages the use of no-collection, in-field analysis, and collections reburial until further study can be done, with exceptions for the use of no-collection and in-field analysis in the following circumstances: when a site is subject to a HAZMAT situation (e.g., harmful contamination) and for projects that conform to selected types of surface survey only (e.g., water lines, culverts, power lines, pump houses, microwave towers). For these few instances when the applications may be appropriate, the ACC offers the following best practices to provide guidance to stakeholders. The goal of these guidelines is to ensure that no-collection and in-field identification and analysis methods—when agreed upon, documented, and adopted—are implemented with appropriate care and ethical consideration. The ACC decided not to provide best practices on reburial at this time because the reasons for reburial and the methods used seem to be widely varied, unevaluated, and unpublished in the United States (an exception is Williams 2011 on reburial for conservation).

These best practices should be considered interim until more research is conducted on the history, legal foundations, and long-term impacts of no-collection and in-field identification and analysis on the archaeological process (see Moving Forward section below). Primary stakeholders for these guidelines include government (federal, tribal, state, and local) archaeologists and resource managers, descendant communities, cultural resource management companies, academic archaeologists, students, and professional societies, all of which might participate in developing archaeological research designs.

The ACC also considers these best practices to provide a framework that can be adjusted to specific archaeological projects and, perhaps, state policies and guidelines. There is considerable regional variation in how prehistoric and historical archaeological investigations are undertaken across the United States, especially during survey projects, which can affect these practices. Factors such as local flora, topography, and soil type(s) should be considered when choosing appropriate archaeological field methods, as should the guidelines presented below.

Best Practices for No-Collection and In-Field Analysis

- **Determine if a no-collection and/or in-field analysis and identification strategy is appropriate for the project.** Consider the following instances when these field methods might not be appropriate:
  - Projects where the discovered sites will yield artifacts that are difficult to identify, are unique, and/or will require precise artifact identification, such as chemical or microscopic analysis, to answer the research questions established for the project.
  - Projects where accurate artifact identification is critical to determine the eligibility of a site for listing in the National Register of Historic Places.
  - Projects where one or more sites are at high risk of being destroyed through natural (e.g., erosion or climate change) or human (e.g., development or mitigation) causes.
  - Testing and data recovery projects, since the long-term research value of the well-documented contextual associations for these collections will be lost. Exceptions might be if a site contains burials or hazardous materials.

- **Prepare to curate the project records.** Field notes, maps, photographs, artifact data, background research, and other records associated with any archaeological project are a crucial part of the resulting collection. For a no-collection project, the associated records will constitute the entire collection and therefore should be curated in a repository just like records that have associated artifacts. The associated digital records, including all the data about the artifacts found but not collected, should be curated in a repository that has well-established procedures for long-term preservation, management, and accessibility of digital records and data. For federal and many state projects, the collections must be curated in a repository that meets the standards in 36 CFR Part 79, and the repository must be identified prior to the start of fieldwork. It is strongly recommended that the repository be identified in the project report.

- **Consider no-collection and in-field analysis methods in agency or other program planning.** The use of no-collection and/or in-field analysis is usually decided during project scoping and is identified in a Request for Proposal for a contracted archaeological project or Scope of Work/Performance Work Statement. However, the efficacy of no-collection and/or in-field analysis needs to be considered at a programmatic level and should be addressed in agency/installation/university planning documents (i.e., Integrated Cultural Resources Management Plans). Agencies and university programs, in particular, should find opportunities to engage stakeholders in discussion and meaningful consultation regarding the merit of these methods, including during Section 106 consultation under the National Historic Preservation Act, to inform scoping of specific projects. Any positions of agreement and disagreement should be recorded in writing, used for future planning, and curated with the project’s associated records. The following considerations related to no-collection and/or in-field analysis should be assessed by stakeholders during any opportunities for consultation:
  - The results of background research to identify the potential for archaeological resources, including previous land use;
geomorphological processes that have affected the project area; previous archaeological investigations in the project area and surrounding area; and, when appropriate, historical sources (e.g., original maps, deeds, birth records). If no archaeological project has been done in the area, then carefully consider whether no-collection and/or in-field identification and analysis is appropriate at all.

- The results of examining existing collections from the project and surrounding area, if available, to determine the range of potential artifact classes and corresponding cultural time periods. If several artifacts were difficult to identify in the existing collections, then this information should be factored into the appropriateness of no-collection and/or in-field identification and analysis for the new project.

- The proposed collection strategy (i.e., collection, no-collection, limited no-collection when diagnostics are kept, or no-collection with some sampling at a complex site) to be used, including the reasons for collecting versus not collecting artifacts that are appropriate to the project at hand.

- Details about the documentation process. This should include the qualifications of those who will be responsible for field analysis and artifact identification; the process that will be used to record the presence/absence and identification of the artifacts; and the standardized information that will be recorded about each artifact found.

- The location where artifact identification and documentation will be performed during the project (e.g., at the location of discovery, field laboratory, or non-field laboratory). A dedicated laboratory—a separated space away from the site itself—is recommended for artifact identification, analysis, and documentation to ensure that the process is performed accurately. Discuss the relative benefits of in-field versus laboratory analysis, if the former is intended to be used.

- The method to be used to test the accuracy of in-field artifact identification and analysis (see “Verify research results” below).

- Final disposition of the recovered artifacts, including the rationale for, and location where they will be relocated at the site, if no-collection and/or in-field identification and analysis are used.

- Develop a contingency plan. All project scopes of work designed with a no-collection and/or in-field identification and analysis method should have a contingency if, during the project, it becomes clear that the method(s) is not appropriate. For example, a survey anticipating late prehistoric sites might encounter an early Paleoindian component, which might justify modification of collection strategies. Therefore, project scopes of work should include the following:

  - Criteria that identify when no-collection and/or in-field identification and analysis should be reevaluated.
  - A clause in the Scope of Work and/or contract that allows the archaeologist performing the work to recommend a change in scope and, when applicable, allows the project proponent to modify the scope.
  - An alternate plan for collection recovery that would be triggered in these circumstances, including consideration of an appropriate budget and how funding would be acquired to carry out collection recovery, analysis, and curation.
  - Define appropriate in-field analysis procedures. Many government agencies and some cultural resource management firms have a technical field manual for archaeological investigations. Such manuals should include the following information for projects involving no-collection surveys and/or in-field identification and analysis:
    - Explicit information on how to identify and record the potential artifact types, especially for prehistoric and early historical period sites (e.g., pre-industrial). Since artifact types vary by region across the United States, pertinent resources to assist with this step are available through State Archaeologists, State Historic Preservation Offices, Tribal Historic Preservation Offices, state historical societies, and others. Provide a full citation to any books or articles from which typological definitions are derived.
    - Standardized forms for each anticipated artifact type for field technicians to record key information about each artifact found, including but not limited to provenience, including descriptive information about context (e.g., high-density artifact concentration; on top of a visible feature); description; dimensions; diagnostic/decorative elements; and degree of fragmentation.
    - Standardized procedures for photographing cleaned artifacts using current technology appropriate for the project. A representative percentage of artifacts should be photographed using a sampling strategy that is appropriate to the project goals. A dimensional scale should be used to ensure that future researchers, resource managers, and persons conducting background research about the site and region have enough information to make appropriate decisions about the artifact type. The manual should include explicit information on how to decide which artifacts to photograph when there are many comparable examples; how to select a representative sample size of an artifact type; the number of faces of the artifact to photograph based on the artifact type; and how to record the photographs in standardized photo logs and/or by metadata tagging.
    - A strategy for identifying and documenting artifacts that are difficult to classify. Identify the qualified material culture specialist(s) and/or institutions who will consult on artifact
Identification. Provide the procedure to follow if unexpected diagnostics or other artifacts are found when no one on the crew is qualified to identify them. Define circumstances when diagnostics and/or other artifacts will be retained for curation and which material culture specialist(s) will make that decision (see “Develop a contingency plan” above).

- **Train field technicians.** Prior to fieldwork, it is critical to train all field technicians to identify and record artifact types specific to the survey area, region, and cultural time periods expected to be represented. The training should complement the information in the technical manual provided and include the following:
  - How to operate any hand-held devices that are used to record artifact location and conduct artifact identification.
  - How to clean artifacts, whether in the field or lab, to ensure that artifact identification is accurate and photo documentation is good-to-excellent quality.
  - How to accurately identify artifacts using replicable artifact classifications and standardized forms.
    - Develop an exercise to test field technicians on artifact identification prior to starting fieldwork. The exercise should be overseen by appropriate material culture specialists.
  - Who to go to with questions about identifying particular artifacts. If possible or practical, discuss the use of mobile devices to take photos and who to send them to for identification.
  - How to accurately photograph artifacts using appropriate, current technology for permanent documentation purposes and how to complete a photo log or to record metadata about the photographs.

- **Verify research results.** Within the first few days of the project, the accuracy and adequacy of in-field artifact identification/documentation should be tested by each person tasked with the work. Any inaccuracies must be corrected in the forms already completed, and new training should be initiated to correct the procedures to ensure standardization and accuracy. Periodic testing of the accuracy of in-field artifact analysis should occur to ensure consistent procedures and accurate data collection.

**Moving Forward**

The ACC and others (Heilen and Altschul 2013) advocate for more research on no-collection and in-field identification and analysis practices across the United States. Some critical topics to explore, which are ripe for dissertation or thesis work, include the following:

- The driving forces or reasons behind the use of these practices to better understand how pervasive they are. The ACC recognizes that limited availability of collections storage space; high curation costs; pressure from government agencies at all levels to reduce overall project costs; and tribal feedback and concern are some of the reasons, but are there others? How do the reasons break down across stakeholder groups and in different regions of the United States? How are those reasons impacting the frequency of the practices across the country?
  - How and when were these practices developed by different stakeholder groups? Were considerations given to the effects of these practices on future research potential or replicability of the data created and interpreted at different types of sites, or by project phases (i.e., survey, testing, and data recovery)?
  - Other than the study by Heilen and Altschul (2013), has any research been done to determine the accuracy of the data created during projects using no-collection and/or in-field artifact identification by different stakeholder groups or by region? Are there any other testing strategies that compare and evaluate the data from no-collection projects with data from projects that collected artifacts to identify if there are meaningful differences in the information recovered? If there are meaningful differences, what are some recommended solutions?
  - Where are these practices codified in law, regulation, policy, and/or guidance with a breakdown by stakeholder group (e.g., federal, tribal, state, and local agencies; academia; private developers)? What is the range of variation in the methods prescribed and what might be motivating any variation found?
  - How can in-field artifact identification and analysis be further improved through training, technology, or other means to increase the accuracy and reproducibility of the data and the interpretation of the sites that rely on those data?
  - What are the relative costs of no-collection and in-field analysis versus the costs of long-term curation of both artifacts and associated records, including digital records, when all are done appropriately and follow professional ethics and guidelines? How does this vary by region of the United States? How does the cost of curation compare to the cost of revisiting a site when questions arise, and artifacts are not available to verify conclusions?
  - What are the possible impacts of no-collection and in-field artifact identification and analysis on the dissemination of the results of the archaeological investigation, as well as public outreach and education for investigations that use these strategies? Consideration needs to be given to the future number and types of artifacts available for exhibition and research in museums and other venues for public outreach and education.
  - What are the possible effects of no-collection strategies on the commercialization of the archaeological record? If fewer artifacts are curated, how might the laws of supply and demand affect the commercial value of artifacts obtained either legally or illegally? Will this encourage or discourage looting of archaeological sites?
  - Artifact reburial is often associated with no-collection and in-field artifact identification and analysis. Research related to reburial is needed on a number of topics. These include the reasons for arti-
The ACC is not including immediate reburial of large organic objects.


ACRA’s February Monthly Member Update (2017).

ACRA's February Monthly Member Update (2017).


BEST PRACTICES FOR NO-COLLECTION PROJECTS AND IN-FIELD ANALYSIS IN THE UNITED STATES

In conclusion, the ACC contends that the practices of no-collection, in-field analysis, and collections reburial run counter to historic preservation laws and professional ethics. In only two circumstances—the event of a hazardous situation and for some kinds of surface survey—does the ACC recognize that no-collection and in-field analysis could be utilized. Additional comparative studies on this topic are needed; the few that exist clearly demonstrate that no-collection and in-field analyses cannot match analysis completed in the laboratory, in terms of replicability and accuracy. However, given that no-collection projects are proceeding without clear answers to the questions outlined above, the ACC offers these best practices for no-collection projects and in-field artifact identification and analysis as interim guidance. When further research into the legality, legitimacy, and cost-effectiveness of these archaeological field strategies is completed, this guidance can be amended. In drafting these initial best practices, the ACC is making an effort to fill an informational void for those who undertake such projects while trying to preserve a breadth of archaeological collections available for present and future research, interpretation, and education.

Notes

1. The current ACC members and authors of this article are Ralph Bailey, Danielle Benden, S. Terry Childs, Jenna Domieschel, Julia King, Teresita Majewski, Heather Olson, Sarah Rivers Cofield, Michael “Sonny” Trimble, and Mark Warner.

2. Several of the terms used in this document are defined by the ACC in a compendium of definitions jointly published in The SAA Archaeological Record ([2016, 16(1):41–43]), SHA Newsletter ([2015, 48(4):4–6]), and ACRA’s February Monthly Member Update (2017).


4. For exceptions, see Butler (1979); Griset and Kodack (1999); Heilen (2013); Heilen and Altschul (2013); Heilen et al. (2008); and Williams (2011). Only Butler (1979) and Heilen and Altschul (2013) are in peer-reviewed publications.

5. The ACC is not including immediate reburial of large organic objects for preservation purposes in its consideration of artifact reburial.

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BONES AND CHROMOSOMES: THE ANCIENT DNA REVOLUTION IN ARCHAEOLOGY (PART 1)

Matthew Piscitelli

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INTRODUCTION

Our special section is the first of a two-part series entitled “Bones and Chromosomes: The Ancient DNA Revolution in Archaeology.” These articles were inspired by the National Geographic Society’s efforts to grapple with the rapidly changing landscape of genetic anthropology while staying true to its funding of cutting-edge scientific research, particularly in archaeology. Part 1 of the series describes the basics of ancient DNA research, including how results have both advanced and complicated our understanding of the past.

Matthew Piscitelli highlights tensions between archaeologists and geneticists through playful dialogue reminiscent of how “The Golden Marshalltown” has allowed countless graduate students to more easily digest archaeological theory through literary caricature. Courtney Hofman and Christina Warinner have adapted their widely successful SAA Online Seminar for The SAA Archaeological Record and have added a useful shortlist of commonly used software tools and programs. Jakob Sedig leverages his archaeology background and position at the Reich Laboratory of Medical and Population Genetics to assuage common concerns and demonstrate the power of ancient DNA to illuminate our collective past. John Terrell’s unique contribution questions the promise of new technological methods for gathering biological data about our past by way of medical diagnosis. Lastly, John Hawks reflects on why media outlets seem so enamored with ancient DNA research and offers recommendations for archaeologists to achieve better public relations.

THE OFFICE ODD COUPLE

Note: The following story is fictional and does not depict any actual person or event. Nevertheless, similar scenarios are undoubtedly taking place in anthropology departments and museums across the globe.

A tall man with dingy cargo pants and a faded hiking shirt opened the door and plopped down behind his desk. He moved aside a stack of dusty library books and placed his coffee mug atop a dozen other brown, ring-shaped stains. He turned on his laptop and launched his browser. He opened the homepage, cringed at the flashing “100” signaling way too many e-mails in his inbox, and instead focused his gaze on the day’s headlines.

“Ancient DNA reveals complex migrations of the first Americans” (https://www.nationalgeographic.com/science/2018/11/ancient-dna-reveals-complex-migrations-first-americans/). Although the article was only a seven-minute read, he stopped at the second paragraph and turned to his office mate, who had been quietly watching and sipping tea in the opposite corner as if expecting this exact moment.

“’The trio of new papers—published today in the journals Science, Cell, and Science Advances—dramatically increases the number of sequenced whole genomes from South America’s indigenous peoples, both living and ancient.’ How unbelievable?!”

“Good morning to you too, Michael. And I know. It essentially rewrites our understanding of the peopling of the Americas.” The other, slightly older man wore a freshly pressed oxford shirt and navy khakis. He put down his tea cup and picked up a PDF of the Cell article, which he had printed earlier that morning.
“I was actually referring to the fact that as an archaeologist I can only dream of having my research published in the likes of *Nature* or *Science*, and it seems that every other month there is an ancient DNA study featured in some high-impact journal.” Shaking his head, Mateo navigated back to his homepage only to find that a new headline had popped up, this one for a *New York Times* article (https://www.nytimes.com/2018/11/08/science/prehistoric-migration-americas.html) similarly commenting on the recently published research.

Mateo, the tea-sipping genetic anthropologist, looked up from his PDF. “I think it’s something about the lab coat. It’s as if science performed in a lab has a bit more credibility, unless you’re a climate scientist,” he chuckled.

“Ha! Kind of like the British accent and documentaries. Richard Attenborough could tell me the world was flat and I’d believe him. No, I don’t think that necessarily applies to peer-reviewed publications. However, I did read an article by Ann Horsburgh where she describes what she calls ‘molecular chauvinism.’ Due to the investment and cost required to run genetic analyses, the results are privileged over other sources of data.”

“But those costs have been greatly reduced, especially since the development of high quality, high-throughput sequencing, according to Shendure and colleagues.”

“True,” Michael replied, “but why is the general public so fascinated by ancient DNA? The *New York Times* just published an online article on the results.”

“Perhaps it’s the simplicity of the presentation? Archaeologists like yourself have fought over the peopling of the Americas for decades, arguing over notching on arrowheads and tempers used in pots. With advances in genetic technologies we can draw these big bold arrows across a map of the Western Hemisphere and illuminate several waves of migration.”

Michael cringed and shook his head. “Ugh. Don’t use the m-word.”

“What, map?” Mateo quipped.

“No, migration.” Michael shot back a dirty look. “Decades ago, archaeologists finally realized that pots are pots, not people. A drastic change in material culture didn’t necessarily represent the movement of a new group in kicking the old one out. The past is complex. The past is nuanced. We don’t want to repeat Kossinna’s mistake.”

“Who’s Kossinna?” Mateo asked.

“Gustaf Kossinna was an early twentieth-century archaeologist,” said Michael. “He said that the people associated with Corded Ware pottery replaced the Neolithic groups of Western Europe. His perspectives on prehistory gave rise to settlement archaeology.”
Mateo looked confused. “So what’s wrong with that?”

Michael continued his lesson in archaeology history. “Kossinna connected the Corded Ware culture with modern Germany. His thoughts on the past were incorporated into Nazi ideology. They’re the guys that Indiana Jones is always punching.”

“Whenever we talk I have to go home and watch at least one of those films. That’s the only way I can understand where you’re coming from.” Michael rolled his eyes.

“But how can geneticists make such grandiose interpretations with such small samples? I know that ancient DNA is incredibly rare from a preservation perspective and subject to all sorts of contamination. While these three studies compare 229 genomes from across the Americas—which is more than Reich and colleagues had to draw up the Denisovans—how can you tell the story of thousands of individuals over tens of thousands of years from such a small sample size?”

“Think about it this way.” Mateo sat up a bit straighter as if to deliver a brief lecture. “Each genome is made up of millions of base pairs essentially magnifying the sample. Therefore, a single toe bone, under the right conditions, can tell the story of an entire species.”

“I still think that we need to be careful,” Michael warned. “Archaeologists have a tendency to get overexcited about new technologies—radiocarbon dating, isotopic analysis, LiDAR—and latch on without fully understanding the baseline assumptions behind the methodologies or the interpretations sometimes thrust upon them by the specialist. I think at the end of the day we’re all scientists who want to tell the story of the past, but we do so in slightly different languages.”

“Closer collaboration certainly can’t hurt and I already know that it’s happening. However, we can probably do a better job at the research design stage. Maybe archaeologists need to be in the driver’s seat when we set the agenda.”

“Really?! Does that mean I can be first author on your next paper?”

“Don’t get too crazy.” Mateo’s computer chirped, signaling the arrival of a new e-mail, which he immediately opened. “Oh look! I’m a co-author on another paper that was accepted in Nature.” Michael just grumbled and opened the first of his 100 e-mails.

**Further Reading:**

A great deal has changed in the field of ancient DNA (aDNA) over the past decade. High quality high-throughput sequencing (HTS) first became commercially available on a wide scale in the early 2010s, and since then, the application of this technology to archaeological questions has revolutionized our understanding of the past—upending previous narratives of human ancestry (Meyer et al. 2012; Prüfer et al. 2014), migration (Allentoft et al. 2015; Haak et al. 2015; Olalde et al. 2018; Posth et al. 2018), domestication (Daly et al. 2018; Gaunitz et al. 2018; Ní Leathlobhair et al. 2018), historical ecology (Star et al. 2017; Thomson et al. 2014), historical epidemics (Bos et al. 2014; Vågene et al. 2018), and the microbiome (Warinner et al. 2014).

Because so much has changed so rapidly, it can be difficult to stay up to date on the latest techniques and terminology. Here we provide a brief guide to the basics of aDNA and explain some of the most important recent changes and new possibilities in the field of paleogenomics. To help the reader navigate the increasingly complex and jargon-laden methods sections of paleogenomics articles, we provide a list of commonly used DNA analysis tools, along with descriptions and links, at the end of this article (Box 1). Finally, for those looking to integrate paleogenomics approaches into their own research, we provide information on the costs and infrastructure required and offer advice on how to set up a successful collaboration with an aDNA laboratory.

**Fundamentals of aDNA**

Just as the field of paleogenomics has grown dramatically over the last decade, so has our understanding of the molecular structure and biochemistry of aDNA. Although it may seem remarkable today, it was not until very recently that we learned just how fragmented and chemically damaged aDNA actually is. During life, DNA is organized into very long, delicate strands, called chromosomes. Bacteria typically have a single circular chromosome that ranges in length from about one to three million base pairs (bp). Eukaryotic cells, which include humans, plants, and animals, generally have many linear chromosomes in their nucleus, as well as small circular chromosomes in their mitochondria (and chloroplasts in the case of plants). The length of eukaryotic chromosomes can vary widely. The human nuclear genome contains 23 pairs of chromosomes, numbered sequentially in order of length. Chromosome 1 is the longest at ~250 million bp, while chromosome 22 measures the shortest at ~50 million bp. The last pair, the sex chromosomes X and Y, are ~156 and ~57 million bp, respectively. The human mitochondrial genome contains 23 pairs of chromosomes, numbered sequentially in order of length. Chromosome 1 is the longest at ~250 million bp, while chromosome 22 measures the shortest at ~50 million bp. The last pair, the sex chromosomes X and Y, are ~156 and ~57 million bp, respectively. The human mitochondrial genome, measuring only ~16,500 bp, is orders of magnitude smaller than the nuclear chromosomes, but it is found in thousands of copies per cell.

After death, these long strands of DNA are no longer repaired and maintained by cellular enzymes, and they begin to break down in predictable ways. Damage begins with sporadic DNA depurination—the loss of some adenine (A) and guanine (G) bases in the DNA molecule. This makes the DNA susceptible to nicking of the DNA backbone at these sites, which over time leads to fragmentation. Before the HTS era, most researchers estimated that aDNA fragments were around 100 bp long, but today the length of DNA can be measured more directly, and we now know that most DNA in a given archaeological sample is closer to 50 bp or less.

In retrospect, knowing this explains why earlier methods, such as targeted Polymerase Chain Reaction (PCR), had so
often failed in early aDNA studies. Targeted PCR cannot be reliably applied to DNA sequences shorter than ~100 bp, and therefore most ancient DNA fragments are inaccessible by PCR. Additionally, long DNA fragments tend to be contaminants, and thus PCR strongly biases towards the recovery of contaminant DNA. By contrast, there is no lower limit on DNA length for HTS, and the enhanced recovery of ultrashort DNA fragments has led to the realization that many archaeological samples contain far more aDNA, and especially endogenous aDNA, than originally thought.

In addition to depurination and fragmentation, aDNA also accumulates damage in the form of cytosine (C) deamination to uracil (U), which is incorrectly sequenced as a thymine (T). Such damage occurs orders of magnitude faster on the single-stranded overhangs at the ends of DNA fragments than in the double-stranded interiors (Briggs et al. 2007), and this excess of damage at the ends of DNA fragments is used by programs such as mapDamage2 to authenticate aDNA (see Box 1). The ability to authenticate aDNA sequences using damage patterns is an enormous advantage of HTS over PCR, and filtering datasets to retain only damaged DNA is a powerful means of contamination removal that has been instrumental in recovering genomes from heavily contaminated samples, including from archaic hominins (Skoglund et al. 2014).

Sources of aDNA
Ancient DNA has been successfully recovered from a wide range of archaeological materials, including bone, teeth, desiccated and mummified soft tissues, paleofeces, dental calculus, seeds and other plant material, cultural objects, and sediments, among others (Figure 1). During the PCR era, cortical bone of the femur was usually the bone of choice in studies of host DNA, but HTS has revealed that the otic capsule within the petrous portion of the temporal bone contains far more (>100-fold) endogenous DNA than other bones (Pinhasi et al. 2013), leading to a veritable run on petrous bones in museums across the world. However, the otic capsule is not the solution for every question. Teeth are also a relatively good source of host DNA, and importantly they are also the best source of ancient pathogen DNA, whereas petrous bone retains little to no information about infections during life. And with 32 teeth per dentition, teeth are a more abundant resource than the two tiny otic capsules present in the petrous portions of each individual. In terms of total DNA, however, neither can compare with dental calculus (calcified dental plaque), which typically contains 10–1,000-fold more DNA than bones or teeth and is the richest known source of aDNA in the archaeological record. However, dental calculus is in short supply, with only milligrams available per individual, and the vast majority (>99.9%) of the DNA in dental calculus derives from the human oral microbiome rather than the human genome (Mann et al. 2018). In addition, different labs have their own preferences and set protocols for different source materials, which could also influence which material is used. In all cases, the goal of the study should be taken into account when selecting appropriate sources of DNA for analysis.

Sources of Contamination
Contamination is non-endogenous DNA that accumulates in archaeological samples through a variety of postmortem processes. Contamination can itself be ancient (e.g., early bacteria that invade the body shortly after death and burial) or recent (e.g., human DNA and skin bacteria from archaeologist hands), and it can originate from myriad sources, including the burial environment, people who excavate and handle the material, post-excavation treatment (washing and consolidants), storage conditions, and the laboratory environment. During the PCR era, contamination was a near-intractable problem for two main reasons: first, it could not be easily distinguished from aDNA, and second, PCR-based methods are strongly biased towards the recovery of modern DNA over aDNA. Together, these two problems sank many early aDNA studies.

Fortunately, HTS to a large extent overcomes both of these problems, and, depending on the contamination source and age, much of it can be identified and removed using current technologies. Nevertheless, it is always best to try to minimize contamination before it happens, and a set of best practices has been developed for the field and laboratory (Key et al. 2017; Llamas et al. 2017). Gloves should be worn when handling materials that might be used for biomolecular analysis, and the materials should never be licked—an outdated practice that was once done to distinguish porous bone fragments from stone. Exposure to sunlight, water, and heat should be avoided, and materials should be stored in a clean, dark, dry, and cool place. Care should also be taken when cleaning and consolidating materials, as both of these practices are notorious for introducing contaminating DNA from unclean water sources and animal glues. In the lab, aDNA work should be performed only in a dedicated aDNA laboratory (Figure 1) that has rigorous cleaning procedures, personal protective equipment, decontamination protocols, and contamination monitoring methods for reagents and facilities.

Recent Laboratory Advances in Paleogenomics
Many things have changed in aDNA laboratories over the past decade, but there are five major technological advancements that have truly transformed the field. First was the development of an extremely efficient protocol for recovering ultrashort DNA fragments from archaeological bone (Dabney et al.
2013). Published almost in passing in a study on Pleistocene cave bears, it showed that by massively increasing the volume of binding buffer used with silica spin columns, much higher aDNA recovery could be achieved. With a few other minor tweaks, this highly efficient protocol capped off a decade of intensive research on DNA extraction protocol improvement.

The second major advancement was the development of aDNA-optimized HTS library construction protocols, including robust protocols for preparing both double-stranded (Meyer and Kircher 2010) and single-stranded (Gansauge and Meyer 2013) DNA libraries, as well as the use of dual-indexing to mitigate “index hopping” in multiplexed sequencing (Kircher et al. 2012). Note that here “library” refers not to a room full of books, but rather to the end product of a suite of synthetic modifications made to the DNA in order to make it “readable” by HTS instruments. Quick and easy, double-stranded library preps are suitable for most archaeological samples with average to good preservation. Single-stranded library preps are significantly more expensive and difficult, but they do recover more endogenous DNA. However, because of the difficulty and expense, they are usually reserved for only very marginal samples from warm climates or deep time.

The third important advancement was the development of uracil-DNA glycosylase (UDG; Briggs et al. 2010) and UDG-half (Rohland et al. 2015) protocols to selectively remove damaged sections of aDNA. Such damage removal enables more accurate DNA sequencing, as well as microbial species identification and genome reconstruction. The use of UDG also has the side benefit of enabling the identification of epigenetic (acquired “imprinting”) modifications in ancient genomes.

The fourth major advancement was the development and adaptation of targeted enrichment methods (also known as DNA sequence capture) to selectively recover genomic regions of interest from ancient samples. First developed on solid arrays and later in solution, this technique works on a principle similar to PCR, but on a massively expanded scale and without the drawbacks of classical PCR amplification. Both PCR and capture are often likened to fishing—however, in this metaphor the former is a lone fly fisherman and the latter is a ship trawling millions of “baited” hooks. The goal of capture is to “fish out” desired DNA sequences from a sea of unwanted (usually environmental) DNA so that less sequencing effort and cost is needed to obtain the desired genetic information. Depending on its size, a well-designed capture system can increase the proportion of on-target (desired) DNA in a sample by more than a thousand-fold. Capture systems can be designed at small, medium, or large scales, ranging from the recovery of whole mitochondrial genomes (Maricic et al. 2010), to whole bacterial genomes (Vågene et al. 2018), to genome-wide panels of more than a million genetic markers (Posth et al. 2018).

Finally, the fifth major advancement was the development of HTS technologies (see the review in Shendure et al. 2017), and in particular Illumina’s sequencing by synthesis. Developed during the race to sequence the human genome, Illumina (formerly Solexa) was initially a latecomer to the HTS revolution, but by the early 2010s it had edged out most of its competitors. Unlike the previous generation of sequencing technology, known as chain-termination sequencing (or Sanger sequencing, after its inventor), Illumina’s “Next-Generation” sequencing by synthesis enabled DNA sequencing on a massively parallel scale—meaning it enabled the sequencing of not one but billions of DNA sequences simultaneously, by eliminating the problem of multiple DNA strands crowding a reading frame and making it unreadable. And, as an additional bonus for the aDNA field, it works best on very short DNA fragments.

Today, Illumina sequencing instruments are the workhorses of paleogenomics, generating terabytes of data on several different sequencing platforms including the HiSeq, NextSeq and MiSeq models, which differ in size, cost, runtime, and amount of data generated. Project scale and the amount of required data determine which platform is optimal for a particular set of samples and questions. In addition to Illumina sequencing, there are exciting new so-called “third generation” sequencing technologies on the horizon, but not all are applicable to degraded short DNA fragments. PacBio and Oxford Nanopore instruments are designed to sequence very long fragments of DNA, but they have limited utility for paleogenomics. Instead these third generation sequencing technologies are likely to make the biggest impact in the field of de novo genome sequencing and assembly.
BONES AND CHROMOSOMES: THE ANCIENT DNA REVOLUTION IN ARCHAEOLOGY (PART 1)

Recent Advances in Data Analysis and Bioinformatics

The effect of HTS on aDNA data analysis has been profound and cannot be adequately summarized here. It is the sheer volume of genetic sequence data (terabytes and terabytes) that has made the most difference. During the PCR era, for example, a single instrument could only generate a few hundred sequences a day, perhaps a thousand if run at maximum capacity. Today, the data output of a single day of sequencing on an Illumina HiSeq4000 is more than 5 billion sequences (~250 billion bp), and sequencing a million DNA sequences from an ancient sample is now considered merely “routine screening.” The benefit of having so much data is that very powerful statistical tools and inference methods can be applied to answer complex questions ranging from the population history of a continent to the virulence factors present in a historic pathogen. Rather than attempt to summarize the ever-growing software toolkit available for aDNA data analysis, we instead provide a short list of key tools and programs commonly used in paleogenomics, together with a brief description of each resource and links to the source code (Box 1).

Costs and Benefits

It is difficult to compare the costs of projects based on conventional PCR and HTS technologies because such projects are carried out at vastly different scales and for different purposes. Using PCR and Sanger sequencing, only a very small portion of a genome (typically only ~100 bp for ancient samples) can be sequenced at a time. Although this can be done relatively quickly and cheaply, it is not scalable, and with genome sizes ranging from millions (e.g., bacteria) to billions (e.g., humans) of base pairs, such an approach quickly exhausts both sample material and bank accounts. Using a fundamentally different approach, HTS sequences millions of genomic DNA fragments simultaneously at a fraction of the cost per base pair; however, the per sample up-front costs are high, and the procedure can only be performed at high volume, making it economical only at a large scale and essentially at the level of genomes. While these differences are stark, the cost-benefit assessment for a given project really depends on the question. For simple questions, such as sample screening for DNA preservation or basic faunal identifications, Sanger sequencing is often sufficient and more economical than HTS. It is also a low-risk way to introduce students to laboratory methods because the entry costs are low and the price of failure for a given analysis is on the order of tens—rather than tens of thousands—of dollars. However, HTS is a much more powerful technology, and going forward most interesting archaeological questions will require data generation at this scale.

Many people want to know how much HTS aDNA analysis costs, but getting a straightforward answer can be difficult, and if you have ever shopped around, you have probably noticed that price quotes can differ widely from lab to lab. The reality is that there are many factors that influence the cost of aDNA research, and these factors differ from institution to institution, and even from lab to lab. For example, some universities subsidize their core facilities, thereby artificially lowering instrument costs and sequencing fees. Some laboratories charge for technician labor, while others save costs by using student volunteers and interns, or cover these costs in other ways. University stockrooms charge labs overheads for ordering supplies, which for a typical aDNA lab can number in the hundreds of products. Prices for each of these products change regularly, as do the shipping fees, and consequently labs often order in bulk to save money. In addition to paying for consumables, labs also have to pay maintenance and service contracts on equipment, as well as for repairs on instruments out of warranty. Delays and repeat analyses must also be budgeted in, and all the other little things add up. Although a full accounting of these costs can be difficult to calculate, a well-run lab will take all of these institution-specific factors into account when drawing up a project budget.

Infrastructure and Personnel

One of the primary challenges of paleogenomics research—and HTS in general—is that highly specialized facilities, resources, and skills are required. The best ancient DNA laboratories are specifically designed to meet rigorous cleanroom standards that simply cannot be met in an ordinary genetics laboratory and should not be attempted, no matter how deeply it is cleaned. The large amounts of airborne amplified PCR products routinely generated in a standard genetics lab can easily overwhelm the small amounts of degraded DNA present in ancient samples, leading to costly errors and faulty data. When ancient DNA research is attempted outside of lab space specifically designed for this purpose, contamination and false positives are very likely and it may be challenging to publish the resulting data. This applies not only to studies of human DNA, but to plant, animal, and bacterial DNA as well. Ancient DNA is most vulnerable to laboratory contamination during DNA extraction and HTS library steps prior to indexing PCR amplification. Subsequent post-PCR steps can be performed in more typical genetics labs or even core or commercial facilities, but the initial steps must be performed in a dedicated ancient DNA laboratory.

Paleogenomics research also requires significant investment in computational resources for both data storage and analysis. Across the board in genetics, there has been a systematic shift in how researchers spend their time—with fewer hours in the lab and many more in front of a computer. Competency in programming languages, such as Python and R, and a background in evolutionary theory and statistical analysis are critical skills for any downstream analysis or data interpretation.
Establishing a Successful Research Partnership

Paleogenomics is by its nature a highly interdisciplinary field that bridges archaeology, genetics, and the broader biological sciences to answer novel questions about the past. For archaeologists and geneticists wishing to collaborate, we offer three points of advice to help get your project off to a good start:

- Build a good team around your project. Paleogenomics is team science. As an archaeologist, selecting the right research partner is a critical step in establishing a successful project. Different aDNA labs specialize in different areas (e.g., population genetics, pathogen genetics, domestication, etc.), and it is important to seek out specialists with the right expertise for your questions. Invest time in this process and keep your lines of communication open. Also, remember that a research collaboration is a long-term relationship. Because paleogenomics projects generally take about two to three years to complete, choose research partners with whom you can work productively over the long term. Before approaching a lab, look up their previous publications and make sure they are a good fit for your questions. Do not hesitate to contact their past coauthors to ask about their collaboration experiences.

- Have a frank conversation about project priorities and resources. Archaeologists and geneticists operate in different disciplines with different goals, evaluation metrics, incentive structures, and research agendas. Find out up front what is most important to your research partner, and explain what is most important to you. Topics you should discuss at the onset include authorship, project funding, student participation, training (if relevant), and level of involvement in data interpretation and manuscript preparation. Discuss the research timeline for the project in advance, and set clear goals and milestones to keep the project on track. Specific questions to ask include the following:
  1. What methods and analyses will be used?
  2. What type of sample is best (petrous, tooth, pathological lesion, etc.)?
  3. Why those particular methods?
  4. Who will work on the samples?
  5. What will be the final product?
  6. How will writing and authorship work?
  7. Will the samples/data be used in other studies?
  8. What happens to the samples/DNA after the project is complete?
  9. What is the expected timeline for the project?

- Develop the research questions together. Genetic analyses rely on complex analytical frameworks centered on hypothesis testing, and consequently open-ended and exploratory questions are difficult to address. Even seemingly simple anthropological questions can prove challenging to translate into experiments that can be tested using genetic data, and on the flip side, some questions that interest geneticists are of little value or use to archaeologists. Communicate early and often with your research partners to establish clear research questions and goals. If possible, do this even before fieldwork or sample collection begins. Never start a project with the goal of simply “doing the DNA.” Ancient DNA research must have a goal and testable hypotheses in mind if it is to be successful. Your project and your collaboration will greatly benefit from having an explicit research question.

We are living in the golden age of paleogenomics. The field has advanced enormously over the past decade, and although many of the recent changes can at times feel confusing and bewildering, do not get discouraged. There has never been a better time for doing aDNA research.

Box 1. A shortlist of commonly used software tools and programs used in paleogenomics.

Bioinformatic approaches change rapidly as new software programs become available. The following list is not exhaustive, but represents tools available at the time of writing that are routinely used in aDNA data analysis.

Multipurpose GUI platforms
- **Geneious** is a commercially available software suite for analyzing genomic data. ([https://www.geneious.com](https://www.geneious.com))
- **CLC Genomics Workbench** is a commercially available software suite for analyzing genomic data. ([https://www.qiagenbioinformatics.com/products/clc-genomics-workbench/](https://www.qiagenbioinformatics.com/products/clc-genomics-workbench/))

Initial data handling and quality assessment
- **EAGER (Efficient Ancient GenomE Reconstruction)** is a GUI wrapper software for quality filtering and mapping sequence data to a reference sequence. ([https://eager.readthedocs.io/en/latest/](https://eager.readthedocs.io/en/latest/))
- **PALEOMIX** is a pipeline for quality filtering and mapping ancient DNA data to a reference sequence. ([https://github.com/MikkelSchubert/paleomix](https://github.com/MikkelSchubert/paleomix))
- **preseq** is a tool that estimates DNA library complexity, essentially allowing users to model the costs and genome recovery potential of a given archaeological sample. ([https://github.com/smithlabcode/preseq](https://github.com/smithlabcode/preseq))
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DNA sequence alignment
- **BWAn** (Burrows-Wheeler Aligner) aligns DNA sequences to a reference sequence. BWAn can manipulate and analyze DNA sequences from various sources. (https://bitbucket.org/tguen/dna-index-sources)
- **BWA** (Burrows-Wheeler Aligner) aligns DNA sequences to a reference sequence. BWAn is commonly used in high-throughput sequencing. (https://bitbucket.org/bowtie-bio/bowtie2/index.shtml)
- **Bowtiez** aligns DNA sequences to a reference sequence. (http://bowtie-bio.sourceforge.net/bowtie2/) and can be used to model changes in effective population size through time. (https://github.com/chrchang/eigensoft/blob/master/POPGEN/README)
- **icMLkin** (Maximum Likelihood Estimation of Relatedness) uses genotype likelihoods to infer genetic relatedness from low coverage sequencing data. (https://github.com/COMBINE-lab/icMLkin)
- **AdmixTools** is a toolkit for inferring admixture. It is used to calculate f_3-, 
  ^- populations and evolutionary history
- **BEAST2** is a Bayesian phylogenetic analysis software package used to date population divergence between samples of known ages, and it is also used to model changes in effective population sizes through time. (http://www.beast2.org)
- **MEGA** is a multifunction software suite for analyzing sequence data, including phylogenetic tree-building. (https://www.megasoftware.net/)
- **RevBayes** is a modeling, simulation, and Bayesian inference software for phylogenetic analysis. (https://revbayes.github.io)
- **SIMCOAL2** is a coalescent modeling program for simulating recombination patterns under different demographic models, including migration events. (http://mpg.unibe.ch/software/simcoal2/)
- **Bayesian Serial SimCoal (BayeSSC)** is a modification of SIMCOAL that allows flexible coalescent modeling from different priors. It can incorpo-
rate ancient datasets to estimate the timing and magnitude of past demographic events. ([http://web.stanford.edu/group/haddylab/ssc/](http://web.stanford.edu/group/haddylab/ssc/))

- **PSMC** (Pairwise Sequentially Markovian Coalescent) infers population size history from a diploid genome. ([https://github.com/lh3/psmc](https://github.com/lh3/psmc))

- **MSMC** (Multiple Sequentially Markovian Coalescent) infers population size history and gene flow from multiple genomes. ([https://github.com/stschiff/msmc](https://github.com/stschiff/msmc))

- **RAxML** (Randomized Accelerated Maximum Likelihood) infers phylogeny for large datasets using maximum likelihood. ([https://sco.h-its.org/exelixis/software.html](https://sco.h-its.org/exelixis/software.html))


- **DIAMOND** is an ultrafast DNA aligner that aligns translated DNA sequences to a protein sequence database. ([http://ab.inf.uni-tuebingen.de/software/diamond/](http://ab.inf.uni-tuebingen.de/software/diamond/))

- **MALT** (MEGAN ALignment Tool) rapidly aligns DNA sequences to a reference database. It is especially useful for large metagenomic datasets. ([http://ab.inf.uni-tuebingen.de/software/malt/](http://ab.inf.uni-tuebingen.de/software/malt/))

- **MEGAN** is a multifunction software suite for analyzing metagenomic data. ([http://ab.inf.uni-tuebingen.de/software/megan6/](http://ab.inf.uni-tuebingen.de/software/megan6/))

- **QIIME** (Quantitative Insights Into Microbial Ecology) is a popular multifunction software suite for analyzing 16S rRNA gene microbial profiles. ([https://qiime2.org](https://qiime2.org))

- **MIDAS** (Metagenomic Intra-Species Diversity Analysis System) utilizes a database of single copy genes, representative genes, and pan genomes to profile microbial communities from metagenomics datasets. ([https://github.com/snyayfach/MIDAS](https://github.com/snyayfach/MIDAS))

- **MetaPhlAn2.0** uses marker genes from reference genomes to profile microbial communities in metagenomic data. ([http://luettenhower.sph.harvard.edu/metaphlan2](http://luettenhower.sph.harvard.edu/metaphlan2))

- **SPARSE** (Strain Prediction and Analysis using Representative Sequences) is a tool for identifying pathogen sequences in ancient metagenomics datasets. ([https://github.com/zheminzhou/SPARSE](https://github.com/zheminzhou/SPARSE))

- **metaBIT** is a taxonomic profiling and visualization software for metagenomics datasets. ([https://bitbucket.org/Glouvel/metabit](https://bitbucket.org/Glouvel/metabit))

**Visualization tools**

- **Krona** is a visualization tool that allows hierarchical data to be explored through interactive, multilayered pie charts. It is especially useful for visualizing taxonomically assigned metagenomics data. ([https://github.com/marbl/Krona/wiki](https://github.com/marbl/Krona/wiki))

- **GrapeTree** is an interactive tree visualization program that supports manipulation of tree layout and metadata. ([https://github.com/achtman-lab/GrapeTree](https://github.com/achtman-lab/GrapeTree))

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In this article I discuss how ancient DNA (aDNA) has the potential to provide powerful new insights into humanity’s past. It may seem odd for such comments to come from someone who considers himself an American Southwest archaeologist; however, my role in the Reich Laboratory of Medical and Population Genetics as a liaison between geneticists and archaeologists has allowed me to critically examine the relationship between these two fields and to explore how they work together.

The Power of aDNA

Perhaps the most well-known example of the power of aDNA involves ancient hominins. As is likely the case for many readers of this piece, I initially learned of aDNA’s capabilities with the publication of the Neanderthal genome. The ability to recover aDNA from a Neanderthal was astounding in and of itself, but these data also confirmed that Neanderthals and modern humans interbred. Possibly even more astonishing was the discovery of a new group of hominins (Denisovans) from a single finger-bone. These were incredible findings, but they also felt remote. Ancient DNA seemed confined to paleoanthropological research and not directly relevant to my own archaeological research interests. It soon became apparent, though, that aDNA would permeate archaeology.

Data from a few ancient hominins demonstrated how aDNA can reshape our understanding of human history at the global scale. Once archaic genomes were decoded, it became possible to identify segments of them in modern populations. Researchers discovered that Neanderthal and Denisovan DNA is virtually absent in sub-Saharan African populations, highest in Australo-Papuan populations, and intermediate in European, East Asian, and Native American groups (Reich 2018). The presence of archaic genome segments in non-Africans is interesting in its own right, but also constrains possible scenarios for the history of the peopling of particular regions. For example, since modern Australian Aborigines have Denisovan/Neanderthal DNA, these populations must have arrived in Australia after intermixing occurred, which is genetically dated to 54–49 kya for the Neanderthal admixture and 49–44 kya for the Denisovan admixture (Reich 2018). Yet some archaeological studies (Clarkson et al. 2017) claim evidence of human occupation in Australia by at least 65 kya, meaning that if the 65 kya dates are indeed accurate and correspond to human settlements, then they must reflect people who contributed little if anything to present-day Australian Aborigines. This discrepancy has yet to be resolved, but it is clear that future research into the initial populating of Australia must take aDNA data into consideration.

In addition, aDNA studies in both Remote Oceania and the Americas have demonstrated that there was no single “founder event” from which modern groups solely derive their ancestry. Ancient DNA has revealed that the first inhabitants of Remote Oceania, associated with the Lapita archaeological culture, were almost entirely of mainland East Asian/Taiwan aboriginal related ancestry, and later mixed with groups carrying Papuan ancestry (Lipson et al. 2018a; Skoglund et al. 2016). In the Americas, aDNA from an ~12,600-year-old infant skeleton in Montana (Anzick-1) was found to be more similar to modern-day Central and South American populations (Rasmussen et al. 2014) than to northern North American groups (Cree, Ojibwa, and Algonquin), which suggests that northern-southern lineage population structure in the Americas is at least as old as the Anzick-1 infant. An additional unexpected discovery is that some present-day Amazonian groups have significant genetic similarities to Australo-Papuans and Andaman Islanders (Skoglund and Reich 2016), as well as to a Paleolithic Chinese individual dating to ~40,000 years ago (Yang et al. 2017), a pattern that can only be explained by a genetically diverse
population contributing to the ancestors of present-day South Americans (multiple pulses of movement from Asia). Potential evidence of this “population Y” was only recently found in very ancient individuals (approximately 10,400–9,800 BP) from Lagoa Santa, Brazil (Moreno-Mayer et al. 2018). However, this signal has yet to be found in any other more recent samples, and thus serves as a good example of how genetic data can generate new testable hypotheses.

The power of aDNA is not limited to examinations of the spread of Homo sapiens into previously uninhabited areas. Ancient DNA can also shed light on the transformations of specific archaeological cultures through time. One of the starkest examples of this was the virtually complete replacement of English Neolithic farmers by mainland Europeans associated with the Bell Beaker archaeological culture around 2000 BC (Olalde et al. 2018). Ancient DNA has also helped elucidate the spread of farming populations into Europe and southeast Asia (Haak et al. 2015; Lipson et al. 2018b). In each of these instances there is robust genetic evidence of previously distinct local groups mixing with incoming agricultural and/or pastoralist groups.

Such genetic insights add nuance to the archaeological record and can be used to reassess assumptions engrafted in archaeology. Pots don’t equal people, but aDNA at least allows researchers to examine if the efflorescence of a new type of pottery (or any cultural practice) correlates with the arrival of a new group of people. Ancient populations were not static; people moved, migrated, and interacted with one another constantly. With very little variation, modern groups in a particular area or region are genetically different from the people who lived there one thousand years ago. Thus, we must think of archaeological cultures as fluid, not as homogeneous entities bounded by time and geography.

Although some of the most notable aDNA research has elucidated global- or continental-scale transformations, ancient genomes can be just as powerful for addressing regional or site-specific archaeological questions. Y chromosome and mitochondrial DNA haplogroups, genetically inferred sex, and proportions of ancestry from divergent source populations are all data that are normally generated during aDNA analysis and can be very informative for specific archaeological questions. These data can be used to identify relatives and/or familial lineages at particular sites or in particular regions. Hundreds of first- and second-degree relatives have been identified in data analyzed at the Reich Laboratory. In some instances, we have been able to identify related individuals from sites kilometers apart, such as an English Bell Beaker-associated father-daughter pair (Olalde et al. 2018). There was no prior archaeological indication that these individuals were related—in fact, archaeologists had initially assessed the father-daughter as being from two different archaeological cultures. Such examples from aDNA demonstrate the truly arbitrary nature of archaeological boundaries. These two individuals, from different sites, previously seemed like bounded, discrete entities. Yet when we consider them as father-daughter, these boundaries melt away.

Combining aDNA with isotopic and archaeological data also allows archaeologists to examine social organization in more detail than ever before. For example, data could be used to determine if individuals from certain room blocks or neighborhoods at a particular site were closely related to each other, or if social organization was more heterogeneous. It could also be used to determine if particular familial lineages had more power than others. Archaeologists can produce rich life-histories for individuals and should now be able to determine if a person lived and died in the same place, who their closest relatives were, what they ate, and multiple other fine-grained details.

A study conducted by Corina Knipper and colleagues (2017) is an excellent example of how multiple techniques can be combined to create new insight into the social organization of a particular place. Using isotopic, genetic, and archaeological data from Late Neolithic Bell Beaker and early Bronze Age individuals of Germany’s Lecht Valley, researchers were able to determine that the majority of adult females were non-locals (whereas males and juveniles were locals), that local individuals tended to share mtDNA haplogroups while the mtDNA haplogroups of non-locals were heterogeneous, that non-locals were buried similarly to locals, and that non-local females arrived around the age of 16. Knipper and colleagues used these findings to argue that inhabitants of these Lecht Valley sites practiced a patrilocal residential system with female exogamy. While studies of whether particular groups were patriarchal, matrilineal, exogamous, etc., certainly are not new to archaeology and have been examined without aDNA, at the very least, aDNA can help confirm or deny previous hypotheses. As the work by Knipper and colleagues demonstrates, however, combining aDNA with other techniques can provide powerful new understandings of ancient social practices.

Explaining aDNA Practices

The explosive growth of research in aDNA over the last few years (Figure 1) has been extraordinarily exciting, but it has also justifiably created some anxiety. As an archaeologist embedded in one of the world’s most active aDNA laboratories, I would like to speak to some concerns and explain some aDNA practices so that readers can better understand how aDNA laboratories operate and how aDNA research is conducted.

Any insights gained from aDNA undeniably come at a price—a price that is by no means solely financial. Perhaps
the most obvious is the conversion of skeletal elements into powder from which aDNA is then extracted (Figure 2). While destructive analysis is required for various biomolecular techniques (e.g., radiocarbon dating and isotope analysis), much of the trepidation surrounding aDNA largely stems from the processing of the petrosal portion of the temporal bone to access and obtain aDNA from the cochlea (Figure 3). Studies have demonstrated that cochlea
yield up to 100x more endogenous human DNA per unit of powder than other skeletal elements (Gamba et al. 2014; Pinhasi et al. 2015). This has allowed for the acquisition of aDNA from archaeological contexts which were previously virtually unobtainable (particularly in hot, humid regions), and for a higher overall acquisition success rate. Since each person has only two petrous/cochlea, these are much rarer than some other skeletal elements (like ribs or teeth) and destructive analysis is therefore more impactful. Yet the amount and quality of aDNA data that can be recovered from the petrous/cochlea often justifies destructive analysis of this element.

The focus on the petrous/cochlea, along with the exponentially increasing number of aDNA studies, has led to concerns about destructive sampling of these skeletal elements. Ancient DNA labs should take every measure to ensure that destructive analysis is as slight as possible, and we endeavor to do that in the Reich Laboratory. Methods are constantly being refined to minimize destructive impact. We also try, where possible, to analyze individuals who have both petrous/cochlea present, so that one can remain morphologically intact.

A complementary concern that I have seen expressed involves data access. This issue certainly is not limited to aDNA; open access publications, online public databases, and article preprints are just a few indicators that sharing of data has become an integral aspect of scholarly work. Regarding aDNA specifically, I have heard archaeologists express worry that genetic data will be kept from them and that skeletal samples will be locked up in aDNA labs, making the samples inaccessible to other archaeologists or paleoanthropologists. Speaking from my experience, however, this is an area where I believe that archaeologists should have few concerns. The aDNA community has extremely high standards of data sharing, and researchers in this community share all data through open access third-party databases as a condition of publication (Figure 4). In fact, gaining access to aDNA data often seems easier than archaeological data, which can be buried in “gray literature,” remain unpublished for decades in incomplete site reports, or is sometimes inaccessible for independent examination even after publication.

There is also a concern that, at this point, most of the world’s aDNA data have been produced by a handful of laboratories; for example, about half the world’s published human aDNA
data (measured by the number of samples with genome-scale data) have been published by the Reich Laboratory (see Figure 1). It is important that laboratories in this field do not hold skeletal samples longer than is needed to queue and process them. In the Reich Laboratory, we aim to process any skeletal elements we receive and return them to the archaeologists or anthropologists who shared them with us within a year of receipt. This was an aspiration until recently, but it is now a goal that we are achieving for most samples that we process.

Another feature of aDNA research that archaeologists may find odd is that there are (currently) no for-fee service aDNA labs, and thus the laboratory relationships that archaeologists are familiar with (e.g., radiocarbon laboratories) are not the right models. Some of the misunderstandings between archaeologists and aDNA laboratories may stem from this. Similar to for-fee chronometric laboratories, aDNA technicians and analysts process samples provided by archaeologists, and therefore should expediently report those results to them. However, aDNA labs have their own research programs to which the samples they are studying need to contribute, and are not just providing a service to archaeologists. Geneticians in aDNA labs tend to be most interested in population-level research questions that span vast geographic regions and segments of time, whereas the data and results archaeologists most often request from laboratories focus on particular individuals, features, or sites. Thus, archaeologists should expect the collaborations formed with aDNA labs to be atypical of collaborations with other for-fee laboratories, and the goal should be to work with geneticists to generate papers that produce findings of interest to both communities. I have seen multiple positive examples of these kinds of outcomes during my time in the Reich Laboratory.

Concerns with aDNA Analysis

As aDNA studies have become more common, archaeologists have also raised broader questions about the limits of what aDNA can tell us about the past and how data can be applied to the archaeological record; such discussion is absolutely necessary to advance the field.

Some of the most pointed critiques of aDNA, especially from archaeologists who work in Eurasia, have focused on studies that find evidence of migration and significant population transformations over time. Many of these critiques about aDNA and migration have previously been addressed and discussed in public forums, especially European archaeological journals (Furholt 2017; Johannsen et al. 2017; Klejn et al. 2017), but it is valuable to briefly summarize the discussions here. Some archaeologists have argued that it is inappropriate to make strong claims with relatively few samples—data from a few individuals within a particular archaeological culture are seemingly used to represent everyone from that time and place. Concerns about low sample sizes have been ameliorated, however, as aDNA data from tens or even hundreds of individuals are now examined for regional/continental-scale studies. Other archaeological concerns center on the idea of migration in general. “Migration” was heavily criticized within archaeology in the 1970s–1990s. During that time, archaeologists became focused on the small-scale and deconstructed the idea that shared material culture represented homogeneous social entities. An obviously related concern is that aDNA studies attempt to link specific archaeological cultures with biological populations. Thus, it may seem that aDNA researchers are chasing the ghosts of archaeology’s past by studying migration, and that aDNA is removing nuance from the archaeological record.

While the field of archaeology may have moved away from migration, the population-level questions geneticists and aDNA analysts address should not be constrained by archaeological theoretical trends. Data cannot be ignored simply because it does not fit en vogue theories. However, I do not mean to flippantly dismiss archaeological data in favor of aDNA—aDNA alone cannot answer all the questions in which archaeologists are usually most interested. Returning to the English Neolithic-Bell Beaker replacement example, although it is evident genetically that dramatic population replacement occurred, why this happened cannot be answered solely with aDNA. Did Neolithic Britons welcome continental Bell Beakers with open arms? Or were the Britons brutally subdued? “Typical” conquest—maurding groups of males killing local adult males and claiming women as their slaves, captives, and wives—seems unlikely, since both Y and mtDNA haplogroups were replaced, but this cannot be ruled out entirely through genetics. Indeed, with this new genetic evidence, archaeologists can reevaluate previous archaeological findings for unnoticed or understudied aspects of the material record that may relate to this replacement. Archaeologists and geneticists therefore must collaborate so that results in both fields can be synthesized.

Another concern that has been articulated regarding aDNA stems from the fact that most of the work in this field has been carried out by European and American researchers, and that aDNA studies of European cultures far outnumber those from the rest of the world (Marciniak and Perry 2017; Pendergast and Sawchuk 2018). This asymmetry largely reflects the fact that it is in Europe where most of the aDNA technology was invented, and it is in Europe where some of the best-preserved skeletal samples are available for research; the field is so new that most of the studies have remained focused on European contexts based on sample sets collected several
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years ago. Laboratories, including the one in which I work, increasingly include researchers and samples from non-European contexts, but the imbalances are far from rectified, and addressing these issues will be an important challenge for the aDNA field to solve over the coming years.

Engagement and outreach with indigenous communities is a particular issue in aDNA that needs to be given special consideration and should be an integral aspect of research (Bardill et al. 2018). The question of how best to conduct outreach with indigenous communities—especially when samples cannot be connected in a clear way to any living group—is a challenge, and there is not yet a clear consensus about how best to do it. Studies in the last few years have addressed these issues through approaches ranging from direct and repeated engagements between geneticists and large numbers of local tribal groups, to no direct engagements at the request of museums that held the collections (Kennett et al. 2017; Rasmussen et al. 2011; Rasmussen et al. 2014; Rasmussen et al. 2015). It is increasingly clear that some direct engagement between geneticists and indigenous peoples should happen, and aDNA projects do appear to be taking engagement more seriously, as demonstrated by two recent publications on the spread of humans through the Americas (Moreno-Mayer et al. 2018; Posth et al. 2018; see also Malaspina et al. 2016; Scheib et al. 2018; Tobler et al. 2017). Yet continued engagement is necessary—for example, even if a study meets the letter of the law for the Native American Graves Protection and Repatriation Act, that law has not yet had time to catch up to community practice and expectations. The range of reasonable solutions is still being explored and is an issue we all need to work on collaboratively over the coming years.

Conclusion

While some major differences in approaches exist between archaeologists and aDNA specialists, it is incumbent on archaeologists and geneticists to find a shared language that allows them to work together with shared values. Ancient DNA is most powerful when hundreds of individuals from multiple time periods, sites, and regions can be studied in synthesis—this is the population level at which geneticists work. However, this large, population-level scale is not what many archaeologists are accustomed to. Archaeologists, including myself, often research a particular site, or particular features at a site. Thus, researchers on both sides need to better appreciate the different approaches and research questions addressed by the respective fields.

To help ameliorate any tensions, more open communication between archaeologists and geneticists is needed. Fortunately, efforts to build bridges between genetics and archaeology are occurring more regularly. Along with this issue, there was an excellent SAA Online Seminar on aDNA in December 2017 led by Drs. Christina Warinner and Courtney Hofman, and there is a growing number of aDNA symposia at archaeology and genetic conferences. It is also important to carry out more student training—students interested in population genetics must learn about ancient cultures and about how archaeologists interpret the past, and aDNA research methods must be incorporated into archaeology classes.

Keeping up with the speed of aDNA research can be overwhelming. Some of the research mentioned in this issue will undoubtedly be out of date by the time of publication. Ancient DNA is rapidly revolutionizing what we know about the past, from the spread of our hominin ancestors, to the social organization of specific archaeological groups. As with other technologies that have revolutionized the field (e.g., radiocarbon dating, GIS analysis, LiDAR), it seems likely that future generations will find it difficult to imagine a time when aDNA wasn’t an integral part of archaeological research.

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SHOW-AND-TELL GENETICS: DIAGNOSIS AND TREATMENT

John Edward Terrell

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If you have ever searched for medical information on the Internet, chances are you have come across the webpages of the famed Mayo Clinic. The patient care and health information available from their website is detailed, beautifully presented, and informative. Academics could learn a thing or two from how well this clinic gets its messages across. Our students might rate us more highly if we did.

Like many, I have no doubts about the promise and at least some of the already achieved results of the new technological ways of gathering biological data about our species’ past. As John Hawks has said previously, accessing such paleogenetic information has already achieved something remarkable. Who would have ever thought that we would be reading a headline like this one for a blog post John published back on 17 February 2016: “Earlier Mixture from Modern Populations into Neanderthal Populations”? Perhaps you are too young to do a double-take when reading these words, but it wasn’t all that long ago when paleoanthropology saw Neanderthals as an archaic species of *Homo* with whom anatomically modern humans could never ever have successfully mated, even if those on one side of this particular species boundary had been able to give those on the other side the right kind of come-hither look (Figure 1).

Since then, of course, the complexity of trying to come to grips with human genetic diversity and the biological prehistory of our kind of creature has grown with each new development in our technological access to the particulars of what it means to be human, genetically speaking, around the world (Yang and Fu 2018). Case in point: not everyone finds the genetic evidence convincing that we did in fact mate with Neanderthals in the past (see Amos 2018).

What I find even more astonishing, however, is that despite today’s technological superiority over what we had available as research tools half a century ago when I was a graduate student, many today who ought to know better are still falling short in elementary ways when it comes to theory development, plausibility analysis, statistical sampling, and hypothesis testing. Because I don’t want to single out anyone in particular as exhibiting such scientific shortcomings, I want to offer you instead a few observations about show-and-tell genetics, a rarefied but globally distributed form of what in recent years I have come to call plug & play dementia—a generalized type of research disability observable not only in the scholarly arena of molecular genetics, but in modern archaeology, evolutionary biology, and other disciplines, too.

Please do not be too hasty to conclude that this is one affliction you do not need to be worried about. This cognitive disability is far more common than you may think. Yet if caught early enough, there is a good chance most of its more deleterious effects can be avoided.
Plug & Play Dementia

Plug & play dementia isn’t a specific disease. Instead, this designation describes a group of symptoms affecting empirical rationality and social relevance severely enough to interfere with long-term scientific productivity and scholarly functioning. The major defining characteristic of plug & play dementia is the willingness to fit (or “plug”) new information (data) into a preexisting explanation (“play”) without evaluating the plausibility of that favored explanation, and without weighing the likelihood that alternative explanations may be of similar or greater plausibility.

Subcategory: Show-and-tell genetics

Plug & play dementia symptoms vary depending on the cause, but judging by the ancient DNA (aDNA) research now available, common signs and symptoms of show-and-tell genetics include the following:

Symptoms

Sense of entitlement

As my mother used to say to her four kids when we were young, “just because you can, doesn’t mean you should.” The corollary for aDNA studies is that just because we now have the technological tools needed to retrieve paleogenetic information from human remains does not mean we should, or more to the point, that we are entitled to do so. Issues of privacy, informed consent, etc., still apply. And they do so even if instead of seeking direct signed permission from the dead we must ask their living descendents, direct or collateral, to assure that any information we glean, however robust or questionable, will be in their best interests, not just in our own.

WARNING: The exploitation of personal information harvested behind the scenes from more than ~87 million Facebook accounts during the 2016 presidential election in the United States shows how easily information nowadays (e.g., “big data”) can be misused. Anyone familiar with the history of the eugenics movement and its current global manifestations knows the fear that “if they can, some will” isn’t foolish. Access to and use of personal DNA sequences stored digitally must be carefully regulated and monitored in perpetuity as to use.

Memory loss (usually observed by others)

I don’t know whether history actually repeats itself, but there is certainly nothing new about saying that when it comes to human genetics, great caution must be observed. In 1975, for example, I gave a talk titled “The Savage and the Innocent: Sophisticated Techniques and Naive Theory in the Study of Human Population Genetics in Melanesia” at the Plenary Session of the 44th Annual Meeting of the American Association of Physical Anthropologists in Denver. My paper was later published as the lead paper in the Association’s Yearbook of Physical Anthropology for that year (Terrell and Fagan 1975).

My take-home message was that human genetics research in the southwestern Pacific had failed to make substantial contributions either to history or science because the research questions considered had been poorly formulated, the alternative hypotheses examined were often trivial, and generally speaking insufficient attention had been given to nongenetic variables affecting the development, maintenance, and stability of biological similarities and differences among people in this part of the Pacific.

Difficulty reasoning or solving problems

Conventional Wisdom. The influential twentieth-century evolutionist C. H. ("Wad") Waddington had his own name for it: COWDUNG, his almost acronym for “Conventional Wisdom of the Dominant Group” (Waddington 1977). Despite their scientific training and accomplishments, a surprising number of scholars even nowadays, for instance, continue to make use of such old-fashioned folk notions as (1) the belief that races are real (but to sound scientific, please be sure to call them groups, populations, lineages, tribes, and the like), and (2) observed similarities between such supposedly collective entities must be either (a) traits they have inherited from the same common ancestor, or (b) traits they have picked up from one another through something generally left up to the reader’s imagination called “admixture” (Terrell 2013). Currently, however, the similarly vague term “introgression” seems to be giving “admixture” a run for its money (see Hawks 2016).

Imaginary Players and Events. Just as children are sometimes observed to be playing with imaginary friends, those suffering from this form of dementia may try to explain what they are seeing in the patterning of human genetic variation in space and time using imaginary or insufficiently characterized actors and events such as the popular combo commonly labeled populations, migrations, and admixture (Furholt 2018).

Revealing characteristics of this trio of supposed actors and their actions are the convictions that human “population mixtures” are recent (say, within the last 5,000 years or so; Terrell 2018a); that before then, people lived in some (unstat- ed, but presumably modest) number of more or less separate and isolated populations; and even in the case of today’s many “admixed populations,” something meaningful and primordial still can be captured statistically as “averages” expressing...
substantial genetic differences among populations however “mixed” they may currently be.

**Polarization and False Analogies.** One of the most diagnostic symptoms of this form of plug & play dementia is the willingness to pose complex issues as if they can be reduced to a choice between two (and simply two) alternative interpretations (Terrell 2000). Another highly diagnostic characteristic is the willingness to report analytical findings (i.e., “show”) and then state how they are to be interpreted (“tell”) without offering further in-depth explanation or explicit testing of alternative hypotheses (e.g., Bolnick et al. 2016; Nielsen et al. 2017). Much in the spirit of “if it looks like a duck and walks like a duck,” it is apparently easy to believe that how the patterning of genetic variation manifests itself tells us more or less directly how to explain the patterning observed just because what we are seeing may look a lot like something we have seen before.

Consider, however, the old cliché that there is more than one way to skin a cat. Another way of saying this is a pattern is not a process. However worded, as Ludwig von Bertalanffy and his predecessor Hans Driesch famously observed, in open systems an end state (or pattern) can be reached by many potential means—a pesky truth about historical causation formally called equifinality (Novembre and Stephens 2008; Terrell 2009).

**Explanatory Naïveté.** Just as there are those who forget simple truths, such as the absence of evidence is not evidence of absence, and a correlation is not a cause, so too, by not dealing with the problem of equifinality, those suffering from plug & play dementia may come to believe the patterning of genetic variation in space and time can be effectively self-explanatory. More crippling still, they may think this patterning is all they need to know to plug their new data into existing explanations (Terrell 2018b) supplied by those working in other research fields (in the case of aDNA, commonly archaeologists and more conventional bioanthropologists).

**Difficulty with planning and organization**

**Data Fishing.** As a curator at one of the world’s largest natural history museums, I have long been fielding requests from scholars and others who want access to our collections (about 98% of what we are caring for is not on public display) to see if what we have “in storage” is something they could turn into something awe-inspiring. We museum types have a name for this kind of vague inquiry: fishing. And given that we don’t charge for research access to our collections, “goin’ fishin’” means we would need to invest staff time and effort to accommodate such unfocused “research visits.” Therefore, we rarely consent to fishing expeditions in our collections, even by world-famous researchers who promise on Scout’s Honor that their powerful new gizmos and gadgets will let them discover truths about the world and its mysteries hitherto hidden for generations in plain sight on our storeroom shelves. Sorry, Charlie, museums are not fishing shoals. And if a researcher wants to perform some kind of destructive analysis on what we have responsibility for maintaining, we will require a formal and detailed research proposal worthy of the National Science Foundation.

**Inadequate Plausibility Analysis.** No modern historian would assert that witches can fly, people are able to change themselves into animals and then back again, or kingdoms fall due to an unfavorable alignment of the planets. Modern understandings of physical reality so utterly preclude these possibilities that such explanations for what has happened in history can no longer be maintained or mentioned by scholars except as quaint ideas once upon a time held to be credible by medieval and earlier savants as well as by the average laborer in the field at that time. But what about explanations and events that
are less extreme, less improbable? How are we to draw the line between the impossible and the plausible?

While much has been written about Bayesian statistical probability, tests of significance, p-values, and the like, surprisingly little has yet been codified about how to evaluate the prior plausibility of research models and hypotheses despite the enduring interest of philosophers in the proper characteristics of a good argument—sometimes referred to as subjective probability theory or confirmation theory. This is not the place to go into this issue, but a significant part of avoiding or overcoming plug & play dementia rests on tackling the plausibility of your ideas and hunches directly in your own research work before you explore them further (e.g., Terrell 1986, 2018c).

**Poor Sampling.** While reading aDNA research reports, I have at times wondered whether those involved have ever met a bone they didn’t like if it held out the promise of containing extractable stuff. Like archaeology, too, in the popular imagination, paleogenetics can have the appeal of a treasure hunt. That’s fine if one is producing a Discovery Channel half hour or so, but of course, this is not the way good science is done however much at the mercy of serendipity researchers may be.

In any case, all bones are not alike, and not just because they may or may not contain useful aDNA. Researchers need samples that are large enough to be representative (but of what, pray tell?). They also must have confidence that they can tell how relevant, reliable, and necessary every individual included in a sample genuinely is. Grabbing a bone off a museum shelf simply won’t do.

Furthermore, just because high-throughput (“next-generation”) sequencing is making it cost-effective to build huge online databases of genetics information does not mean the old saying “garbage in, garbage out” no longer applies. The same concerns just noted for aDNA apply equally well to DNA obtained from the living. It is nonsense, for example, to think that a handful of sequences collected at various times for various reasons, good or poor, at one or even a few places (e.g., urban hospitals), can be used to characterize human genetic variation on New Guinea, the second-largest island on earth (Terrell 2006).

It is also long past the time when those reporting aDNA results should have stopped kidding themselves and others that they are studying populations, however ancient or modern. They aren’t, as any statistician will tell them. Even under the best of conditions, they are studying samples, not populations. And their samples are drawn from an almost entirely unknown historical universe.

As they say in a certain popular sport, therefore, it is a flag on the field if while reading a paper reporting aDNA research you come across the term “population” (e.g., Browning et al. 2018). Cross it out. Write in “sample” instead. This makes it so much easier to not be bamboozled by claims about ancient migrations, contacts, dispersals, etc. Samples, after all, are rarely said to move about, fornicate, or engage in other forms of reproductive hanky-panky.

**Treatment**

Even in cases where plug & play dementia cannot be cured, there are ways to manage your symptoms without necessarily resorting to prescription or over-the-counter medications. Such non-drug approaches to dealing with show-and-tell genetics include the following:

- **Don’t fall for wishful thinking.** Just because we are now able to do something remarkable like extracting and then sequencing aDNA does not guarantee that any of us will be able to make much sense of what is being recovered. Like it or not, it is a form of academic wishful thinking to believe that “getting data,” however old-fashioned or newfangled, inevitably leads to scientifically meaningful results.

- **Be sure you know what you are looking for and why, not just how to find it.** Science has its proper protocols and doesn’t begin with dropping a fishing line off the back of a boat. Furthermore, remember what my mother said. Just because you can doesn’t mean you should. You not only need to know what you are looking for, but why anyone else on earth should give a damn.

- **Partner with those who may be affected.** Avoid taking on paleogenetic investigations solely on your own reconnaissance or that of your research team. Even if you are a member of the descent source community involved, seek the support and collaboration of others who may be affected by public disclosure of your research findings before proceeding (Bolnick et al. 2016).

- **Stop thinking categorically, and start thinking relationally instead** (e.g., Emirbayer and Goodwin 1994; Terrell 2018d).

- **Do a thorough plausibility analysis to find what may be the most likely explanations** (e.g., Shipman 2015; Terrell 2018c).

- **Develop testable hypotheses based on these several alternative plausible explanations** (e.g., Terrell 2010).

- **Admit that you need adequate samples** (see above) and stop pretending you can use genetic information about single individuals or incredibly small samples from here, there, or elsewhere to successfully read the elusive and complex tea leaves of human biological diversity and history.
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- Admit to yourself that trying to discover the timing and number of “admixture events” in the past is nonsensical, particularly if all you have for information about the past is just a handful of genetic profiles from an opportunistic sample of individuals. The notion that today we can somehow pinpoint how often people, however archaic or modern, “did it” with one another in the past is ludicrous.

- Use the right software for the job. Do not rely on current software programs such as STRUCTURE (https://web.stanford.edu/group/pritchardlab/structure.html), PAUP (http://phylosolutions.com/paup-test/), FastNGSadmix (http://www.popgen.dk/software/index.php/FastNGSadmix), and other approaches that presuppose genetic similarities among people are to be attributed to such ill-defined “causes” as ancestry, migration, and admixture (aka introgression) between allegedly isolated and more or less discrete groups, populations, lineages, etc. (Winther 2014). To do so is, as they say, putting the analytical cart before the horse. Although formal methods for implementing plausibility analysis and dynamic networks research are still largely under development, visualization tools are already in hand that can be used to show, for example, how human genetic variation may be structured by isolation-by-distance and constrained by social networks that are in turn (and in part) constrained by geography (e.g., Petkova et al. 2016; Terrell 2010).

Coping and Support

Receiving a diagnosis of some form of plug & play dementia such as show-and-tell genetics can be devastating. Many details need to be considered to ensure that you and those around you are as prepared as possible for dealing with a condition that can be unpredictable and progressive.

- Stay active and involved.
- Seek out others who can help you learn to recognize the symptoms of show-and-tell genetics in yourself and in others whose research findings apparently support the conclusions you favor.
- Find new ways to express yourself.
- Delegate help with decision-making to someone you trust.

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FROM THE SAA PRESS

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Using and Curating Archaeological Collections
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All archaeologists have responsibilities to support the collections they produce, yet budgeting for and managing collections over the length of a project and beyond is not part of most archaeologists’ training. While this book highlights major challenges that archaeologists and curators face with regards to collections, it also stresses the values, uses, and benefits of collections. It also demonstrates the continued significance of archaeological collections to the profession, tribes, and the public and provides critical resources for archaeologists to carry out their responsibilities. Many lament that the archaeological record is finite and disappearing. In this context, collections are even more important to preserve for future use, and this book will help all stakeholders do so.

Preorder at the Discounted Advance Order Price by visiting the Marketplace at www.saa.org

Oaxaca: Arqueología de una Región Mesoamericana
POR NELLY M. ROBLES GARCÍA
Este libro ofrece una visión general de la arqueología de la región oaxaqueña, abordada desde sus orígenes, con los científicos del siglo XIX, hasta los estudios mas recientes en la época moderna. Ubicada en el sur de México, esta región mesoamericana ha sido considerada como cuna de civilizaciones debido a su ininterrumpido desarrollo cultural, desde la prehistoria hasta nuestros días. El libro se presenta organizado en una manera cronológica, a fin de que el lector pueda comprender el desarrollo de las antigüas culturas que han convivido a lo largo de varios siglos en este agreste territorio. Ofrece una compilación de los conocimientos emanados de los varios proyectos arqueológicos que se han realizado permanentemente en Oaxaca, que han permitido ir construyendo la historia de los grupos humanos asentados desde la etapa lítica hasta la llegada de la conquista europea en las diversas sub-regiones. Muestra también los diversos enfoques de la arqueología mexicana y norteamericana que la han modelado, y que se han complementado de manera afortunada para hacer de Oaxaca una de las regiones más estudiadas de Mesoamérica.
ancient DNA (aDNA) research fascinates the public. The attraction is not hard to understand. Ancient DNA evidence has resolved some 150-year-old scientific problems, has uncovered surprising new evidence of populations previously unguessed at by archaeologists, and has brought a fresh wave of young researchers into prehistoric research. Some of the leaders in this field of science have told their own stories in popular books (e.g. Pääbo 2014; Reich 2018; Shapiro 2015) or in articles written for the public. More broadly, many of the world’s leading science writers and documentarians have brought aDNA discoveries to the interested public.

Still, it is easy to find media outlets that espouse aDNA sensationalism, spreading myths and misunderstandings. How can researchers help to improve media coverage of this new area of science?

This is a question I think a lot about. For the past 20 years, I have been fortunate to work not only as a scientist and professor but also as a public communicator, consultant for documentary productions, blogger, and media commentator. During this same time, aDNA evidence has grown from its infancy into a major research area. My laboratory does not perform extraction or sequencing of DNA from ancient bone samples, but much of my research has relied strongly upon aDNA data, and I maintain active collaborations with aDNA specialists. One of my foremost goals as a science communicator has been to provide accurate and understandable accounts of ancient DNA for the media, as well as for professional anthropologists and archaeologists for whom this area of research may seem impenetrable (e.g., Hawks 2013, 2014).

A few notable discoveries helped kickstart public interest in aDNA—especially the discovery that Neanderthals contributed a fraction of the ancestry of living human populations. Such discoveries helped generate a demand for more, equally groundbreaking news. At the same time, general scientific journals like Nature and Science, whose editorial decisions are based in part on news interest, have increased the pace of publication of aDNA evidence. Ancient DNA research now outweighs all other published articles on human population history in such general interest journals. These editorial decisions have sustained a supply of news in the form most trafficked by mass media outlets: embargoed scientific papers and press releases. This media cycle has helped to draw resources and researchers into aDNA. At the same time, many workers who study the past using other methodologies may feel bypassed or alienated by the idea that aDNA is “revolutionizing” the field.

I begin by noting three aspects of aDNA research that are genuinely transformational:

1. Ancient DNA research is at the forefront of bringing open data access into anthropology. A culture of data accessibility and reuse has been part of human genetics since the 1990s, codified under the Bermuda Principles and Fort Lauderdale Agreement. Data accessibility means that new sequence data are not a dead-end means of testing a single hypothesis. New data enter the public domain, building an enduring foundation that supports hundreds, or even thousands of researches who often have no formal relationship with aDNA laboratories. Data accessibility vastly increases the citations that accrue to new sequence analyses, a currency highly valued under traditional measures of scientific productivity. From the standpoint of media and public interest, data accessibility enables scientists and communicators to incorporate real observations into their public engagement and outreach activities. Few aspects of Neanderthal sequencing research have had the public impact that the 23andMe “Neanderthal ancestry” calculator has had, and this was made possible by the open sharing of aDNA sequence results. The open approach contrasts strongly with many areas of human evolution research, which have a long and well-earned reputation for secrecy and lack of data accessibility.
2. The collaborative model of research in aDNA has been effective in building teams to address “big questions” of prehistoric research. For example, in a 2015 study in Nature, 29 authors applied aDNA, archaeological, and linguistic evidence to examine the initial spread of Indo-European languages in Europe (Haak et al. 2015). Few problems have had greater interdisciplinary resonance in archaeology than this one, dating to the 1700s. Other “big questions,” like the origins of dog domestication, the geographic origin of the initial inhabitants of the Americas, and the composition of the early Polynesian dispersal, have likewise been addressed by large interdisciplinary teams.

3. Ancient DNA researchers continue to generate novel discoveries that were never predicted from other forms of evidence. For the media and public, these new discoveries have created a continuing narrative of scientific advance, not an endless volley among scientists holding entrenched positions. For example, the initial sequencing of Neanderthal genome data from Vindija, Croatia (Green et al. 2010) provided a newsworthy test of earlier suggestions of gene flow or genetic introgression from Neanderthal populations into modern humans (e.g., Hawks and Cochran 2006; Smith et al. 2005; Wolpoff et al. 2001). That finding alone might have merely remained a static outcome, but the sequence data rapidly gave rise to further, never-expected observations: East Asians carry more Neanderthal ancestry than Europeans, the X chromosome has only one-fifth the Neanderthal contribution of the autosomes, and Neanderthal genes contribute to immune system function in living people.

What these research strengths share is that they relate to the process of science, not the particular results of a single study. This process tends to broaden the representation of people doing the science, both by facilitating the involvement of specialists from many disciplines and by giving valuable roles to early career researchers. It is not only this new form of evidence but also the hundreds of fresh minds entering the field that have broadened the scope of questions we can ask about prehistory.

These strengths are not unique to aDNA research. For example, the projects surrounding the discovery and analysis of Australopithecus sediba and Homo naledi in South Africa have incorporated open data accessibility as well as collaboration among more than a hundred scientists, and have yielded a series of surprising discoveries not predicted from other data. The continuing media and public interest in these projects follows a trend similar to aDNA research. In other words, media and public interest in aDNA has followed genuine, newsworthy changes to the scientific process and our knowledge of the past.

But the media is not monolithic, and nobody can deny that press officers, journalists, and irresponsible researchers sometimes sensationalize the results of research. Ancient DNA research is no exception to this rule. Institutional press offices, media, and researchers themselves have sometimes failed in their responsibility to communicate accurately to the public.

One case from early 2018 helps to illustrate the complexity of media-researcher interactions and the media ecosystem related to aDNA. Geneticists from Stanford and the University of California-San Francisco published aDNA sequence results from the so-called “Ata” fetal skeleton from Chile (Bhattacharya et al. 2018). The media involvement with this story was elaborate and occurred over several phases. Initially, the producers of a documentary film, Sirius, approached researchers about the skeleton, and these producers ultimately provided radiographs and tissue samples for the study (Bhattacharya et al. 2018; Nolan and Butte 2018). The documentary pursued the pseudoscientific claim that the skeleton might represent an extraterrestrial life form, and expert analysis of the skeleton debunked this claim. A journalist from Science wrote about the research on the skeleton at an early stage (Stone 2013), including comment from other researchers external to the study. Later, in 2018, Genome Research published a study of the Ata skeleton, with both genomic data and assertions about how novel mutations may relate to features of the skeleton interpreted as developmental abnormalities (Bhattacharya et al. 2018). The publication of this research study was accompanied by a press release, giving rise to stories in more than 100 media outlets worldwide (e.g., Zimmer 2018a), which were shared by countless individuals on social media. Scientists in Chile reading these stories responded strongly, at first on social media and then in traditional media (Dorador and Harrod 2018). These scientists and others raised objections ranging from the possible illegality of exhumation, purchase, and export of human skeletal remains, the lack of consultation or permit from Chilean authorities, and the exploitation of a fetal skeleton from a twentieth-century burial without attempt to locate or obtain permission from next of kin. Journalists in the US then covered the ethical concerns with the research (e.g., Zimmer 2018b). Later in the year, a group of anthropologists published an academic article in the International Journal of Paleopathology that refuted several of the scientific claims made in the Genome Research article and commented on the ethics of the original study (Halcrow et al. 2018). Looking at the multiple factors that contributed to sensationalism in this case helps to illustrate the many different stages of research and publication where failures of accurate communication occur. The media originated this research, recruited some of the scientists who pursued aDNA examination of the...
specimen, and provided samples and other documentation. The scientists may have felt motivated by the desire to debunk pseudoscientific claims, but the objective effect of their involvement was to greatly extend the dissemination of these pseudoscientific ideas. *Science* magazine, widely considered an “elite” venue for scientific reporting, also helped to legitimize these questions by covering the research in 2013. *Science*’s reporting failed to investigate the basic ethical problems that should have been evident: the lack of permit, the lack of IRB or heritage oversight, the possible illegal origin of the remains. This reporting gave life to the false idea that debunking extraterrestrials is a legitimate application of destructive sampling of skeletal remains. When it was published in 2018, the *Genome Research* paper (Bhattacharya et al. 2018) was subject to worldwide press attention, largely driven by credulous journalists and media organizations who repeated claims from a press release. Very few science writers who had previous experience with aDNA covered the story. Yet it was very widely shared on social media, becoming one of the most prominent archaeology stories of 2018. Scientists and self-styled “skeptics” were among the biggest social sharers of these articles, often commenting that science “proves once again” that ancient aliens did not exist. Social sharing was also driven by a single unscaled photograph of the skeleton, from the *Genome Research* publication and press release. This photograph portrays the fetal skeleton in a non-standard orientation without scale or context, and social media comments often centered on its “weird” appearance.

Many archaeologists might want to shrug off this massive case of public misinformation as an example of irresponsible media sensationalizing science. But I emphasize that researchers and “bystander” archaeologists and anthropologists are ultimately responsible. Looking at the many failures of professional practice in this case, from study design and sampling all the way to press release design and social media sharing, I encourage archaeologists to consider five concrete recommendations for better media and public interactions.

1. **Responsible practice is ethical practice.** Many anthropologists and professional human geneticists employ aDNA methods in their work on skeletal samples. These specialists have been trained in the study of ancient skeletal material, including appropriate methods of photo documentation, curation, respectful treatment, and legal regulations governing human skeletal material and destructive sampling. Accurately communicating these professional obligations is an important part of maintaining public trust in anthropological and archaeological science. As aDNA methods become cheaper and more widespread, a broader set of researchers unfamiliar with the ethical standards of anthropological research have started to use aDNA to answer questions. I have personally had countless conversations with students, postdoctoral scientists, and others involved in aDNA sampling who do not understand the basic professional obligations of anthropologists, archaeologists, and curators. Ethics should be part of the training for all workers involved in human skeletal remains, and all of us must work to ensure that the ethical practices of the field are reflected in media reporting on this work.

2. **Involve descendant communities.** Many ancient populations have descendant communities that exist today, and aDNA researchers too often ignore or overlook these communities. In some cases, researchers have evaded human subject protocols or other ethical review by studying aDNA from historic specimens in the place of DNA samples from living people. A few aDNA researchers have taken their case to the media, complaining about indigenous communities who choose not to participate in research or who choose to rebury ancient remains. These developments have contributed to the mistrust that many indigenous populations bear toward human geneticists and anthropologists. Anthropological geneticists have recently made progress toward meaningful involvement of indigenous communities in genomic research, for example, the Summer Internship for Indigenous Peoples in Genomics (described in Wade 2018). Ancient DNA researchers should learn from these efforts and join them, giving indigenous communities a real voice in their research design and sampling decisions.

3. **Genetic observations are not ethnic, linguistic, or material culture observations.** Ancient DNA researchers have often been motivated by archaeological or ethnolinguistic questions, for example, the “origin of Indo-Europeans,” or the relationship between the Harappan archaeological tradition and Vedic scriptures. But framing genetic studies around such questions can be very misleading. The biological relationships of ancient peoples may indeed be relevant to such ethnolinguistic and cultural questions, but only under certain assumptions about population dynamics and culture change. The complexity of the relationship between migration, population growth, culture, and linguistics has been well discussed by both geneticists (e.g., Richards 2003) and archaeologists, but nuances and uncertainty expressed in research papers are often absent from media and public discussion of new results.

4. **Scientists must vet their press releases.** Ancient DNA research is now carried out by large interdisciplinary teams in which the archaeologists and curators may not be principal investigators. Press releases often come from the institutions of the primary investigator, or from the journal that publishes a paper. Press officers who compose a
release may not speak to the archaeologists who are co-authors. This is not an ethical practice. We must hold scientists responsible for misstatements, exaggerations, and errors in the press releases for their papers, regardless of which institution has issued them. Archaeologists need to ensure that press releases reflect the research study accurately and convey appropriate professional practices.

5. Social media matters. When a scientist shares a story on social media, journalists and others notice. Many archaeologists do not realize that they are not mere consumers of stories on social media; their actions actually influence the scope of media coverage of the field. The Ata skeleton became a massive worldwide story in part because archaeologists shared it, imagining that they were helping to debunk “ancient alien” pseudoscience. We all now have a responsibility to exercise professional judgments on the stories we share. Just as a professional archaeologist should not bring unethical research into the classroom, we should not share unethical research on social media without an appropriate professional response.

In communicating the importance of aDNA research, I often emphasize ways that the science is still developing. Results are almost never completely definitive. The questions anthropologists and archaeologists ask of ancient populations are rarely those that can be answered by DNA alone. When aDNA establishes that interbreeding occurred between ancient groups, it may say little about the circumstances of contact and mixture. When aDNA establishes a large demographic turnover between earlier and later time periods within a region, it may say little about the economic, climatic, or conflict conditions that gave rise to the turnover. It is a major step to establish what happened in demographic terms, but leaves much work to understand why and how demographic changes took place, and whether they left material or linguistic traces.

What is most inspiring about aDNA research is that it can empower scientists and the public to ask these “why” and “how” questions. In doing so, anthropologists and archaeologists may discover common patterns of change that shed light on the evolution and diversification of our species.

Let me finish by adding a few words about why positive media engagement is important to the future of our science.

Many of my old friends respond with cynicism to aDNA findings. Having lived through the 1970s, 1980s, and 1990s, they have seen confident pronouncements of genetic results from several generations of human geneticists that turned out to be premature or exaggerated. Media framing of genetics as a revolution influenced the direction of science through funding and publication decisions. The aggressive public demeanor of participants in high-profile scientific debates discouraged many talented students from careers in archaeology and anthropology.

Archaeological science is bigger today than it has ever been. The areas of the field that are expanding are those that have become more open, more collaborative, and more interdisciplinary. There is much to be said for the increasingly rigorous tradition of data collection and reporting that developed during the twentieth century. But the scientific advances of the twenty-first century have been those that express rigor with transparency. The future of archaeological science lies in those areas that have adopted a mode of publication and public engagement that builds a foundation for effective interdisciplinary work.

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CALENDAR

JANUARY 24, 2019
Online Seminar: Metals Managed: Using X-radiography to Identify, Document, and Sample Corroded Iron
2:00 p.m.–3:00 p.m. EST
FREE and for SAA Members Only

JANUARY 30, 2019
SAA Annual Meeting: SAA 2019 Member Participant Renewal Deadline

JANUARY 31, 2019
2019 SAA Election Ballot Closes.
Must be a paid 2019 Member for your vote to count.

FEBRUARY 7, 2019
Online Seminar: How to Prepare for a Job in CRM
2:00 p.m.–3:00 p.m. EST
FREE and for SAA Members Only

FEBRUARY 26, 2019
Online Seminar: Addressing Orphaned Collections: A Practical Approach
2:00 p.m.–4:00 p.m. EST

MARCH 5, 2019
Online Seminar: Grant and Research Proposal Writing for Archaeologists
2:00 p.m.–4:00 p.m. EST

APRIL 10–14, 2019
SAA’s 84th Annual Meeting in Albuquerque, NM

MAY 1, 2019
Submissions for SAA’s 85th Annual Meeting in Austin, TX Opens

To learn more about the Online Seminars and to register, visit www.saa.org/OnlineSeminars/.
REPORT TO THE BOARD OF DIRECTORS OF THE SOCIETY FOR AMERICAN ARCHAEOLOGY

TASK FORCE ON REVISIONS OF THE SAA PRINCIPLES OF ARCHAEOLOGICAL ETHICS: STAGE ONE

September 5, 2018

Task Force Members

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Eldon Yellowhorn (Simon Fraser University, Canada, member)

Task Force Board Liaison

Jane Baxter (DePaul University, USA)

At the Spring 2018 Society for American Archaeology (SAA) Board meeting, this Task Force (TF) was created and charged with the following task:

Task Force Charge

140-28.1 [D°] Motion 140-28.1 – The Board establishes the Task Force on Revisions of the SAA Principles of Archaeological Ethics: Stage One. The Board charges the Task Force with recommending a process to revise and update the current SAA Principles of Archaeological Ethics that will engage, gather input from, and inform the membership. The Task Force will be comprised of four members and a chair. The Task Force will produce a final report for the Board by the Fall 2018 meeting.

Co-chairs Douglass and Rakita, upon receiving their appointments as co-chairs and the TF charge, selected and invited TF members to ensure that different stakeholders and geographic diversities within SAA membership were included. Luckily, everyone who was invited agreed to serve. TF members' employment sectors include academia (in the US and abroad), public outreach, government agency, and the private sector. TF members reside and work in three countries in the Americas (Argentina, Canada, and the United States). In addition, TF members belong to a wide range of other archaeological and anthropological organizations and networks. This diversity helped ensure that there were conscious inclusions of a wide variety of stakeholders in considering the implementation of the TF charge.

TF Data Gathering

At the initial TF conference call on May 7, 2018, TF members engaged in some initial brainstorming, discussed possible processes, and agreed upon a strategy for data collection to implement the TF charge. TF members reached out to their networks across the Americas to determine which organizations they knew had undertaken either establishment or revision of ethical principles. For those they identified, TF members agreed to reach out to leadership and find out what those experiences were like. Questions included the following:

- What was the general process undertaken by the organization?
- What forms of stakeholder feedback did the organization receive and use?
- How was stakeholder feedback collected? What forms of media were used?
- What were the pitfalls that the organization encountered?
- What were the most efficient choices that the organization made during the process?
- Did the organization use one TF/committee for the entire process, or was it phased, with different participants in each phase?
- How long did the process take from start to finish?
- How might the organization have proceeded differently, with 20/20 hindsight?
After this initial TF meeting, co-chairs Douglass and Rakita collected information from TF members regarding organizations that had gone through this process in recent years. These organizations included:

- American Anthropological Association (AAA)
- Linguistic Society of America (LSA)
- National Association for the Practice of Anthropology (NAPA)
- Society for Historical Archaeology (SHA)
- Canadian Archaeological Association (CAA)

Co-chairs Douglass and Rakita, along with TF members, followed up with members of these organizations who were a part of establishing or revising ethical principles. In addition, they spoke with individuals from the SAA who have been a part of collecting such data from other organizations over the years. In a series of individual phone calls, conference calls, and e-mails between June and August, co-chairs Douglass and Rakita and TF members spoke with the following people:

- Alex Barker (University of Missouri, President of AAA, AAA Ethics Committee revisions co-chair, and SAA member)
- Meg Conkey (UC Berkeley, SAA Committee on Ethics member)
- Lise Dobrin (University of Virginia, AAA and LSA member, helped revise both organizations' ethical principles)
- Ray Hayes (Retired physician, SHA Gender and Minority Affairs Committee member)
- Scott Hutson (University of Kentucky, former AAA Ethics Committee member, and SAA member)
- Chad Morris (Roanoke College, AAA Ethics Committee revisions co-chair, also NAPA Ethics Committee chair)
- Dena Plemmons (University of California Riverside, AAA Ethics Committee revisions co-chair)
- Niel Tashima (LTG Associates, NAPA Sub-Committee on Ethics revisions chair)
- Della Scott-Ireton (FPAN and Advisory Council of Underwater Archaeology)
- Barbara Clark (FPAN and currently enrolled in Public Administration MA program with emphasis on ethics)
- Emily Jane Murray (FPAN and Florida Anthropological Society [FAS] Board)
- Florie Bugaren (Howard University, SHA Gender and Minority Affairs Committee chair)
- Michael Deal (CAA President) and Gary Warrick (CAA Vice President)

Task Force members held another conference call on August 23 to review the results of data collection over the summer and discuss general recommendations. Co-chairs Douglass and Rakita developed a draft report and TF members provided feedback, ideas, and edits on the draft. The cumulative result of these efforts constitutes this report.

At the request of President Chandler, the Task Force co-chairs organized the President’s Forum for Wednesday night, April 10, at the 2019 Annual Meeting in Albuquerque, New Mexico. The forum, entitled Learning from the Past, Looking Towards the Future: Archaeological Ethics and the SAA, will be chaired by Alex Barker, past SAA Board member and current President of AAA. Invited discussants include Meg Conkey, Bonnie Pitblado, Joe Watkins, Luis Jaime Castillo Butters, and Arlen Chase. This forum will provide an opportunity for the Society’s members to engage in a discourse on which ethical concerns the membership wishes to consider as part of the process of evaluating and revising its ethical principles.

Summary of Findings

Speaking to members and chairs of TFs and committees from other organizations, as well as members of particular committees within the SAA, has been very helpful in thinking about the process for the SAA. Experiences of and thoughts on these numerous conversations include the following:

- Twice in the past decade, the AAA has updated its ethical principles, in part as a reaction to a crisis within the organization. The SAA was commended on being proactive in considering revising its principles. That said, on multiple occasions, TF members were cautioned that a static statement of principles is vulnerable to becoming less useful and perhaps even divisive in the face of new, unexpected ethical crises. It was recommended that the SAA consider a “living document” that includes statements of ethical principles that are embedded within contextualizing materials, examples, dialogue, and historical background. For example, some organization websites have ongoing and regularly updated scenarios and practical applications of ethical principles to help guide and educate membership. In addition, some organizations publish regular columns that are focused on real-life examples of ethical dilemmas, how they are considered, and how they were resolved. While core ethical principles may in some ways be viewed as timeless, perspectives and situations sometimes change with time. A living document approach seeks to avoid these problems in the future, as “timeless” is hard to do well.

- One key for future TFs is to determine what sort of philosophy of ethical principles the SAA and its membership want to undertake, i.e., specific prescriptions/prohibitions or overarching principles. There are positives and negatives to each. With prohibitions, anything not listed is implicitly permissible. Future
TFs must think about this early on in the process. Currently, the SAA has overarching principles, while the RPA (Register of Professional Archaeologists)—of which the SAA is a sponsoring organization—has specific prohibitions and also accountability. How will revised SAA ethical principles complement/align/connect with the RPA? The members of this Task Force believe that it is still appropriate (especially given the Society’s relationship with the RPA) to maintain “aspirational” rather than “prescriptive” ethical principles. In addition, it is clear that there should be decisive and purposeful dialogue between the RPA and the SAA in thinking about revising the SAA’s Principles of Archaeological Ethics.

- Providing sequential and regular communications to SAA members throughout the process of considering and revising its Principles of Archaeological Ethics is critical, as is an initial “setting the stage” so that membership and stakeholders feel that they are engaged in the process.

- Stakeholder input was collected by organizations using various media, including face-to-face forums at annual and regional meetings, surveys, and organization website interfaces, such as a blog. Networking between TF and committee members from other organizations was critical, as was ensuring diversity of the TF and committees to ensure accurate stakeholder representation. Sustained and consistent opportunities for members to comment throughout the process were viewed as essential. Forums and panels at both regional and annual meetings, social media, blogs, an SAA YouTube channel, massive open online courses (MOOCs), and other media were all recommended.

- The concept of stakeholder, given the international nature of the SAA, is important to fully consider. Reaching out to tribes (THPOs in the US), descendant communities, interest groups, and international anthropological institutes (traditionally in Latin America) is vital to a successful strategy. Defining the stakeholders is a difficult undertaking, as in some ways it may categorize people in ways they wish not to be. Based on discussions, these are some aspects of stakeholder diversity to consider:
  - Descendant community members
  - SAA members from different generations who hold different attitudes and opinions
  - SAA committees and interest groups
  - People who have had a variety of experiences, interests, and specialties in archaeology, including avocational archaeologists and the public
  - Individuals of/from different countries and cultures
  - Members from a wide variety of employment backgrounds
  - Those who are engaged in and confronted with issues of ethics on a regular basis

- The process to be undertaken by the SAA, based on other similar organizations, will take several years and several rounds of back-and-forth with membership at key stages/milestones. This will allow the TFs to have an iterative, interactive way to work with membership step by step.

- While input from membership and stakeholders throughout the process ought to be incorporated, input from standing SAA committees has recently been received by the Committee on Ethics. This input should be considered as part of the process, although we acknowledge that committee membership may have changed since that input was originally solicited and thoughts may have changed in the interim. Reaching out again to standing committees to gather input may be appropriate.

- As subsequent TF work proceeds, review of similar national and international archaeological and anthropological organizations’ ethical principles and their presentation to the public may be useful to understand the range of possibilities for the SAA.

- Once a new set of ethical principles is in place, it will be important for the Board of Directors to contemplate how to keep membership engaged in implementing and living/practicing them. How, in the everyday life of archaeologists, can the SAA prompt members to consider the implementation of these principles? Some organizations saw their role in ethics as educational and thus set up specific processes to keep ethics at the forefront of members’ attention. The following ideas were suggested:
  - Create a prompt when renewing membership to acknowledge the ethical principles, much like that for submitting abstracts for the Annual Meeting.
  - Feature a regular column in The SAA Archaeological Record on practical applications of the ethical principles through case studies of ethical dilemmas, how the SAA Principles of Archaeological Ethics may apply, and how these situations were resolved.
  - Send semiregular e-mail blasts on ethics and different viewpoints and perspectives based on different stakeholders (similar to the Government Affairs Committee regular e-mail blasts).
  - Create a blog or other informational and interactive online resource to allow regular and easily facilitated interaction with membership on issues of ethics. The Committee on Ethics may be able to coordinate and run this.
  - Engage Board members more regularly in pondering ethical dilemmas. As part of this, have several members of the Board on the Ethics Bowl panel each year to heighten awareness of this important event at the Annual Meeting.
  - Should there be regular review of ethical principles by the Board or Society? If so, what would be the schedule and process
for this? Some organizations viewed their principles as living documents, which may help in aiding this potential process.

**Recommendations for a Process to Revise and Update the SAA Principles of Archaeological Ethics**

**General Process Structure**

Per the co-chairs’ discussion with the Board and President Chandler, and based on our TF’s investigations, we recommend two sequential Task Forces that will follow ours.

**Task Force – Stage Two** (TF-2) is envisioned as gathering input and feedback from the membership and stakeholder groups on the existing ethical principles. We expect the volume of this feedback to be considerable, thus this group will also distill and synthesize this feedback and provide both their raw data and their summary to the next Task Force.

**Task Force – Stage Three** (TF-3) will be guided by the summary of TF-2 and on that basis will complete the revisions of the principles. They will present a draft revision to the Board for consideration and if acceptable, will disseminate the draft to the membership for a comment period, subsequent revision, and a vote.

Given our discussions and recommendations from those non-SAA groups we spoke with, our TF recommends that the timeline for the subsequent two Task Forces be considerable.

**Task Force – Stage Two**

Charge: TF-2 should be charged with gathering feedback, comments, and ideas from the membership, standing committees, interest groups, and stakeholders, and synthesizing those materials.

Composition: TF-2 needs to be large (12–15 members), with a diverse group of representatives and experts on ethical issues. TF-2 need not have a member from all possible stakeholder groups, but members need to be open, inclusive, and aware of all these groups. It should include experts in surveys and ethnographic data collection (both qualitative and quantitative data). Expertise in ethics may be demonstrated in a variety of ways (publishing, service, job setting), but however demonstrated, TF-2 should include people who have been actively grappling with the practical application of ethical principles. We recommend identifying individuals who have demonstrated the capacity to compromise and to show flexibility. TF-2 membership should include representatives from a range of generations with some skew towards younger members, as they are the next generation of the SAA. The SAA Committee on Ethics could be asked for recommendations of possible members. At least one member of TF-2 should be a former member of TF-1 to maintain continuity and transfer of history/knowledge.

Tasks: Develop and deploy a survey to the Society membership soliciting their feedback on the current ethical principles and their suggestions for revision. Organize and hold forums/listening sessions, regional town-hall-style meetings, calls for comments, interactive blogs, and/or other efforts to collect public comments on the revision of the Society’s ethical principles. Actively engage the membership in discussions regarding ethics. Collaborate with the Society’s Committee on Ethics as appropriate on the revision efforts as well as efforts to develop materials and methods to make the statement a living document.

Funding & Support: We recommend funding to support a graduate student or similar assistant to aid in the processing of survey results, etc.

**Annual Meeting Milestones and Timing:** It would be advantageous to have the TF-2 chair identified at the Fall 2018 Board meeting, subsequent to this report being received, and TF-2 members identified well prior to the 2019 Albuquerque Annual Meeting to begin their initial work. The topic for the President’s Forum at that Annual Meeting will be the revision of the Society’s ethical principles. It would be advantageous to enable the TF-2 members and chair to attend, observe, and listen to feedback from membership during the forum. Between the 2019 and 2020 Annual Meetings, it is expected that a survey and online media will be implemented by TF-2 to receive public comments on the current Principles of Archaeological Ethics. The 2020 Austin Annual Meeting would be an ideal setting for a forum or series of forums to receive face-to-face input from membership and also to provide an update on progress. Given the timing, it is unclear to us if the Fall 2020 or Spring 2021 board meeting would be an appropriate deadline for the TF-2 report.

Although the TF suggests a lengthy incubation period for TF-2 to do its work, this is in part because of logistical concerns. As one example, creating a survey on ethics, having it approved by the Board, submitting it to membership, receiving responses, and reviewing and incorporating responses all will take considerable time. The survey creation alone could take months. In addition, the timing of a face-to-face forum hosted by TF-2 at an Annual Meeting is constrained by timing. The 2019 Annual Meeting will likely be premature given that TF-2 may be created only months before that meeting; as a result, the 2020 Annual Meeting would be the best venue for such an event. Receiving those responses and incorporating them, again, will take time. As a result, while there may be some Board members who wish to see a more streamlined, one-year period for TF-2 to conduct its important work, the logistics of a survey and a face-to-face forum will require a longer time span than might otherwise be desired.

Duration: We recommend TF-2 be given a minimum of a year (and likely two years) to gather input and synthesize their find-
ing board for these Task Forces as they go about their business. The Committee on Ethics may act as an important sounding board for TF-2 and TF-3. The Committee on Ethics represents a dedicated, energetic, and engaged group of members for whom archaeological ethics are not simply an interest but a passion.

We recommend that the Board consider incorporating the expertise of the Committee on Ethics in this future work of the Society. Over the last several years, the Committee on Ethics received comments and feedback from a number of standing committees on the ethical principles, and those comments ought to be leveraged and used along with any new comments that would be collected. One or more members from the Committee on Ethics may be assigned to TF-2 and TF-3. The Committee on Ethics may act as an important sounding board for these Task Forces as they go about their business. The natural continuity of the Committee on Ethics membership will be maintained and charge

**Task Force – Stage Three**

**Charge:** TF-3 should be charged with implementing the revision or rewriting of the Society’s ethical principles statement. The Task Force should take serious consideration of and heed the recommendations, data, ideas, and themes provided to them by TF-2.

**Composition:** TF-3 needs to be small (approximately 5 people). We recommend well-respected and above-reproach members who will garner trust and buy-in from the membership. These individuals should have some experience with ethical dilemmas, but need not be ethical “experts.” They will need to be able to devote considerable and focused time to this project. They should be able to take the deliverables of TF-2 and craft from them a workable draft statement of ethical principles. At least one member of TF-3 (perhaps two) should be a former member of TF-2 to maintain continuity and transfer of history/knowledge.

**Tasks:** Accept the information provided by TF-2 and craft a new Statement of Principles of Archaeological Ethics for the Society. Upon Board approval, disseminate the draft statement to the membership for feedback, edit accordingly, and submit the final draft for a vote to the membership.

**Funding & Support:** Should TF-3 deem it advisable, funding and support should be provided for one or two retreat events. These retreats can be used to hammer out details of the principles and the writing process and to facilitate a final writing push.

**Annual Meeting Milestones and Timing:** We expect that the TF-2 report will be ready for the Board by the Fall 2020 or the Spring 2021 Board meeting. At that point, the TF-3 chair could be identified and the small number of TF-3 members convened. A draft statement and report may be ready for the Board at their Spring 2022 meeting, with a rollout by the President and the Board soon afterwards to membership for response. Subsequent to a membership comment and revisions period, TF-3 may be able to submit the final revised Principles on Archaeological Ethics to the Board, for subsequent vote by membership, by the Spring 2023 meeting.

**Duration:** We recommend TF-3 be given at least a year for writing a draft statement of ethical principles and another year for the subsequent Board review, membership comment period, and revisions based on that feedback, submission of final statement, and subsequent final vote.

**Deliverables:**

1. Brief account of activities
2. A draft statement of ethical principles for Board review
3. Recommendations to the Board on a method for gathering member feedback on the draft
4. Gathering of member feedback on the draft
5. A final draft (i.e., revisions to the draft statement in response to member feedback)

**Additional Recommendations**

The Society’s Committee on Ethics already has a considerable workload. It previously provided the Board with feedback on the SAA Principles, which spurred Board action on them. The Committee on Ethics represents a dedicated, energetic, and engaged group of members for whom archaeological ethics are not simply an interest but a passion.

We recommend that the Board consider incorporating the expertise of the Committee on Ethics in this future work of the Society. Over the last several years, the Committee on Ethics received comments and feedback from a number of standing committees on the ethical principles, and those comments ought to be leveraged and used along with any new comments that would be collected. One or more members from the Committee on Ethics may be assigned to TF-2 and TF-3. The Committee on Ethics may act as an important sounding board for these Task Forces as they go about their business. The natural continuity of the Committee on Ethics membership will be

**Deliverables:**

1. Brief account of activities and efforts to engage the membership on the Society’s Principles of Archaeological Ethics
2. Raw data of membership discourse on principles (e.g., survey methods and results, notes from forums, recommendations from other SAA committees and interest groups)
3. Synthesis of key and overarching themes from discourse, including ideas on both the content and structure of the revised principles
4. Recommendations to TF-3 regarding the advisability of a revision of the existing Principles of Archaeological Ethics or a wholesale rewriting of them
5. Recommendations (in conjunction with the Committee on Ethics) for specific ways that the Society can develop the new principles statement into a living document with historical context, case studies, and venues for ongoing dialogue between members (e.g., a series of articles in *Advances in Archaeological Practice* or a regular column in *The SAA Archaeological Record*, a series of blog posts, handouts/flyers, curricula, etc.). Members need to be continually (re)-engaged on ethical quandaries.
6. Recommendations to the Board regarding TF-3 composition and charge
one source of continuity for the sequential Task Forces. We recommend the Committee on Ethics be asked to review raw data collected by TF-2 and provide feedback and comments (thus helping with the distillation process). TF-2 could also coordinate with the Committee on Ethics on events, forums, and sessions at the meetings. For example, we see considerable potential in using the annual Ethics Bowl during the revision process. Perhaps certain topics or issues that TF-2 are learning about and starting to consider (i.e., 3-D printing of artifacts, remote sensing) could be selected as topics for the Ethics Bowl. Additionally, it might be possible to encourage university groups to work on ethical problems outside of the Annual Meeting and publish them in The SAA Archaeological Record. The Committee on Ethics should be prepared to implement some of the action items developed by TF-2 regarding the development of an ongoing dialogue within the membership on ethical issues. TF-3 could use the Committee on Ethics as a sounding board and source of commentary on draft principles statements as they are prepared.

Final Points

• The Society needs to take this opportunity to not only consider how to revise the principles but also to use this as leverage to structurally keep ethical principles in the forefront of members’ minds into the future.

• Revision of our statement of ethical principles will take considerable time and should not be rushed.

• It is critical that both member and nonmember stakeholders have a chance to participate in the dialogue surrounding the revision and that their voices are heard (and that they feel their voices are heard).

Suggested Resources for TF-2 and TF-3

• CAA ethics page, with links: https://canadianarchaeology.com/caa/about/ethics

• NAPA ethics page, with links: http://practicinganthropology.org/practicing-anthro/ethics/

• SHA Ethics Committee webpage, with links: https://sha.org/committees/ethics-committee/


• AAA ethics resources page, with links: http://www.americananthro.org/ParticipateAndAdvocate/Content.aspx?ItemNumber=1895

• LSA ethics webpage, with links: https://www.linguisticsociety.org/resource/ethics

• Advisory Council on Underwater Archaeologists (ACUA) blog post with link to press kit: https://acuaonline.org/deep-thoughts/a matter-of-ethics-by-della-scott-ireton/


• HMS Florida application requires adherence to FAS code of ethics: https://docs.google.com/forms/d/e/1FAIpQLScRH-H6JLVppkwVli6z5_kWjbDXK-Ba_w1eVrC3If82VOBX-pw/viewform?c=0&w=1

• Southeastern Archaeological Conference (SEAC) links to SAA’s code of ethics for membership requirement: https://www.southeasternarchaeology.org/membership/membership-options/

• SEAC also has page with links dedicated to sexual harassment policies, posters, and papers: https://www.southeasternarchaeology.org/sexual-harassment-task-force/

• RPA’s Archaeological Ethics Database—codes, papers, journal articles—an in-depth resource: http://archaeologicalethics.org/


SHOW OFF YOUR STATE!

Submit your state’s poster to the 2019 SAA Archaeology Celebration Poster Contest

Instructions for submissions available at:
https://www.saa.org/career-practice/awards/awards-detail/state-archaeology-celebration-poster-award

Deadline for submissions is March 1. Meeting participants will vote on their favorite posters in the Poster Hall at the annual meeting in Albuquerque, NM in April. The top three winners will be announced at the SAA business meeting on Friday, April 12, 2019. Winning posters will be displayed on the SAA website.