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Discriminating Paleoindian point types from Florida using landmark geometric morphometrics

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A B S T R A C T

Traditional artifact typologies are typically poorly defined. While several attributes usually help define a "type," shape is invariably the most important. Here I report on a study that uses landmark-based geometric morphometrics to better define three Paleoindian point types from Florida: Suwannees, Simpsons, and Transitional Side Notched. Bilaterally symmetric specimens were created from the original artifacts to capture the presumed ideational forms of the points. The shapes of the bases and the entire points were tested to determine whether the types could be discriminated, and if so which shape was best at discriminating the types. The results show that the base configurations were best at discriminating the groups in two different jackknife allocation tests. The entire point shape was less robust due to the variability in blade shape. The study demonstrates that the three point types can be rigorously defined in ways that are usable in daily archaeological practice, and that base shape, rather than the entire shape, is a better discriminator. Further, the study demonstrates the utility of using several freeware programs for processing and analyzing shape data.

1. Introduction

North American prehistoric archaeologists routinely discuss the use of hafted bifaces (referred to here as "points") as cultural historical markers (Justice, 1987). These points are often the only evidence used to identify many archaeological sites and strata. The use of points as "type fossils" is ubiquitous in both academic research and cultural resource management. Unfortunately many of the types are so poorly and broadly defined that the utility of these definitions is doubtful (Dunbar and Hemmings, 2004; Lenardi and Merwin, 2010). In many cases the definitions were compiled from isolated artifacts in the 1950's and 1960's (Bell, 1958, 1960; Bullen, 1975; Cambron and Hulse, 1975; Perino, 1968, 1976; Ritchie, 1971) or single sites (Broyles, 1966; Coe, 1964) using general descriptive terms. Quantitative descriptions are rare and limited to a few measurements (e.g., maximum length, width, thickness). Types based on limited samples of isolated specimens usually fail to capture the variation in point form due to manufacturing variability and resharpening. Appending suffixes such as "-oid" (ex., Folsomoid) or "-like" emphasize the variability but do not hone the definitions. Even though these problems are apparent and occasionally discussed (e.g., Kimball, 1996), archaeology as a discipline has an inertia that keeps it dependent on "type specimens" and traditional point descriptions. Q2

In this paper I examine the problem of ambiguous point definitions using three Paleoindian point types from Florida: the Suwannee, Simpson, and Transitional Side Notched (TSN). TSN encompasses several varieties, including Greenbrier and Union Side Notched. These will be referred to as points with the understanding they could have been used as projectile tips, knives, or both. The resharpening trajectory for a point is rarely defined, and the final shape of a point may have little obvious relationship to its pristine shape (e.g., Goodyear, 1974; Hoffman, 1985). The resharpening trajectory has not been described for Suwannee, Simpson, or TSN points so the shape of these points at exhaustion is unknown, making their identification problematic.

My working hypothesis is that the best way to define a point type is to focus on the haft, because that is least likely to have been altered from its original form since manufacture (Ahler, 1971; Goodyear, 1974; Hoffman, 1985; Thulman, 2006). By "original form" I mean the form of the point when it was manufactured, which would capture the intent of the point's maker. The null hypothesis here is that there is no significant difference between the three point types under comparison. That is, variation among these point types is continuous and that types cannot be discriminated in statistically significant ways. The test of this hypothesis depends both on finding significant differences among groups and correctly

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allocating points to each group. I examined this hypothesis by using landmark-based geometric morphometrics (LGM; Adams et al., 2004; Zelditch et al., 2004) to define the shape of 50 whole points that were identified to type. Different configurations of landmarks were used to determine whether the symmetric shape of the base or entire point was better at correctly assigning points to their identified types. The effectiveness of category assignment was tested through discriminant function analysis (DFA) and canonical variates analysis (CVA) for each configuration. Although all types were significantly different from one another, jackknife tests of the performance of the categories showed that the base configuration was far superior for correct assignation of specimens. The discriminatory power of the entire outline was likely less discriminatory because the blade shapes were not statistically distinct.

2. Materials and methods

2.1. *The allocation of specimens to type*

Along with fluted Clovis points, Suwannee and Simpson points are the most common types associated with the Paleoindian period by professionals in Florida, although none have been recovered in a dated context. TSNs are fewer in number in Florida, and unambiguous examples have never been reported in a professional excavation. Suwannees, Simpsons, and TSNs are lanceolates that are typically unfluted, with concave bases that are ground in the concavity and along the lateral edges. The standard definitions of these points are found in Bullen (1975), although others have commented on them (Daniel and Wisenbaker, 1987; Goodyear et al., 1983; Purdy, 1981) or proposed new definitions (Dunbar and Hemmings, 2004). They are known mostly from isolated finds and rarely from an unmixed stratified site (Daniel and Wisenbaker, 1987; Dunbar and Hemmings, 2004; Dunbar and Vojnovski, 2007). Simpsons appear to be rarer than Suwannees, although that scarcity is impressionistic. Simpsons have been proposed as an interim form between Clovis and Suwannee, but they have been excavated with Suwannee points (Daniel and Wisenbaker, 1987).

Bullen's (1975) descriptions of the three groups illustrate the limitations of traditional typologies. All the descriptions are accompanied by 1–3 simple line drawings (without scale) and a range of measurements for length, width, and thickness.

> <u>Suwannee</u>: A usually large and fairly heavy, lanceolate shaped, slightly waisted point with concave base, basal ears, and basal grinding of bottom and waisted parts of sides. Basal thinning and suggestions of fluting are but rarely present. Workmanship varies from good to poor. This definition is more specific than previous contexts (Bullen, 1975:55)
>
> <u>Simpson</u>: A wide bladed, relatively narrow waisted, fairly thin, concave based, medium to large sized point with grinding on bottom and waisted edges. Basal ears are present but are not as developed as in the Suwannee point. Basal thinning is present but, also, is not well developed. Workmanship is good to fair. (Bullen, 1975:56)
>
> <u>Greenbriar</u> (TSN variety): A heavy (thick), relatively broad, usually medium sized, dominantly bifacially beveled, side notched, trianguloid point with straight or slightly concave or convex base. … Width of base is equal to, or greater than, width of blade. Blades are slightly excurvate but may be straight. … Length of hafting area is about one-quarter of the total length of the point. Basal corners tend to be rounded or eared. … (Bullen, 1975:53)
>
> <u>Union Side Notched</u> (TSN variety): A fairly thick, medium sized, bifacially beveled, lanceolate shaped point with shallow side notches immediately above rounded basal corners and grinding of basal edges and of notches. (Bullen, 1975:54)

In the 30-plus years since Bullen's work, there has been little progress made on refining these types and making definitive statements about what is truly similar and different between Suwannee and Simpson points. For example, I asked eight professional and avocational archaeologists with experience in differentiating these point forms to sort 65 actual-size color images of lanceolate points found in isolated contexts as "Suwannee," "Simpson," or "Other." On only a few of the points was there complete agreement, so type designations were made based on a clear majority of opinion. Twenty-six points were identified as Suwannee, 17 as Simpson, five as Other, which, based on comments of some of the analysts, I grouped within the general definition of TSN. No agreement was reached on 15 of the points, and these were designated "Unknown." The images were drawn from a set of about 750 images of unfluted Paleoindian points from Florida, most of which were broken (Thulman, 2006). The images were collected from private and public collections in Florida using a flatbed scanner, which had an error of <0.1 mm (Thulman, 2006). Images were scanned at 600 dpi. The lengths of lateral grinding were measured to the nearest millimeter, and thickness along the midline and location were also recorded.

While point typology is based on several factors, the most important is shape, and the analysts commented that they relied on such aspects of shape as the shape of the ears, depth of the basal concavity, and the relationship between the shapes of the haft and blade. I focused this analysis on three parts of the point shape: the entire outline, the haft, and the blade (Fig. 1). The definition of "the haft" is not necessarily self-evident, so here the distal terminus of lateral grinding marked the transition from the base to the blade (landmarks 1 and 11 in Fig. 1). Points were used that were relatively well preserved. Points were rarely perfectly preserved; most have some damage, such as a missing ear tip or blade tip or flakes

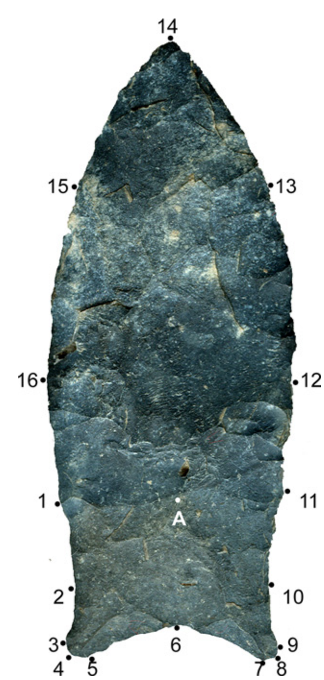

Fig. 1. Landmark locations used in the analyses. Entire point outline configuration: LMs 1–16; base configuration: 1–11; blade configuration 1 and 11–16.

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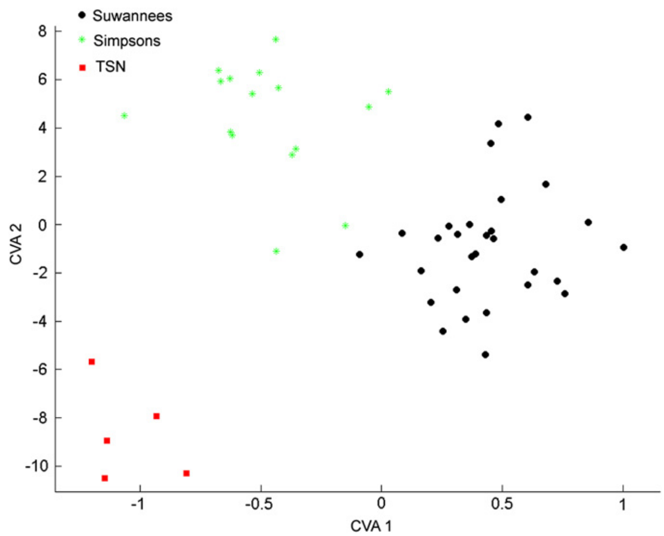

Fig. 2. CVA plot of the entire point configuration.

removed from the blade margin. Thus, some compensation was made in digitizing the specimens to remedy obvious damage by estimating the location of the edge without the damage (described in section 2.3). Further, the grinding length was rarely the same on both basal edges, and sometimes they were substantially different (i.e., >5 mm). I decided that only specimens that differed 5 mm or less in the lengths of lateral grinding would be included.[1,2] Thus, on specimens with grinding of different lengths, the limits of the haft would not likely to have been perpendicular to the bilateral axis of the point. (It is possible the haft limit could be perpendicular if one ear was shorter than another.) This difference was eliminated by creating bilaterally symmetric specimens, as described in Section 2.4.

2.2. Landmark geometric morphometrics

The development of LGM over the last two decades has focused on the analysis of biological systems, mainly understanding ontology, speciation, and evolutionary processes. Most of the explanatory literature and methodologies were developed to work with biological and paleontological specimens (e.g., Hammer and Harper, 2006; Zelditch et al., 2004). The foundation of LGM lies in the theory of shape developed by Kendall (1984), Bookstein (1991), and others (Adams et al., 2004). A specimen of interest can be characterized in two or three dimensions as a combination of shape, size, rotation, and position, so prior to analysis of shape all information related to size, shape, rotation, and position must be removed. The shape of a specimen (biological or archaeological) lies in a curved multi-dimensional "shape space" that contains all shapes of the same dimension. The shapes in shape space are compared mathematically by alignment through superimposition, which eliminates the non-shape components, and projected onto a linear (flat) tangent plane (Rohlf, 1999). The projection is a linear approximation of the shape in shape-space but allows the use of Euclidean geometry and standard mathematics, including traditional multivariate statistical analysis of the shapes (Slice, 2005).

Several approaches to capturing and analyzing entire two dimensional shapes have been used by archaeologists, including elliptical Fourier transformations (Ioviţă, 2009, 2010), eigenshape analysis (Costa, 2010; Tompkins, 1993), and landmark-based analyses (Buchanan, 2006; Buchanan and Collard, 2007; Lenardi and Merwin, 2010). In the last few years, archaeologists have begun using LGM more frequently for a variety of purposes (e.g., Archer and Braun, 2010; Buchanan, 2006; Buchanan and Collard, 2010; Buchanan et al., 2011; Cardillo, 2009, 2010; Lenardi and Merwin, 2010; Lycett et al., 2006; Monnier and McNulty, 2010; Shott and Trail, 2010; Smith and Smallwood, 2011), and its use should become more common for several reasons. It is relatively easy to do. Most of the statistical analyses in this research were facilitated in user-friendly freeware programs that do not require "steep learning curves" to use (Hammer, 2010:357). Several freeware computer programs are readily available and well documented that facilitate the use of LGM for artifact analysis. All of the digitizing and image analysis in this paper was done with freeware computer programs: the *tps* program suite, developed by F. James Rohlf; *IMP* suite (Integrated Morphometric Program v.7), developed by H. David Sheets (Zelditch et al., 2004); and *MorphJ* v. 1.03c, developed by C. P. Klingenberg (2011).[3] The software can analyze the shapes and illustrate the results in ways that are intuitive. Thus, the analyst can see how shapes differ through thin plate spline deformations, average images, and graphical displays of superimpositions. However, while it is easy to generate data and produce results LGM should not be approached without an understanding of its theoretical underpinnings and limitations (Zelditch et al., 2004).

2.3. Landmark placement

Comparing shapes in LGM requires the designation of homologous points on each specimen. The choice of landmarks (LM) in biological specimens has been extensively discussed (Bookstein, 1991, 1997; Zelditch et al., 2004). Zelditch et al. (2004) describe five criteria for choosing proper landmarks. Foremost, the landmarks must be homologous. In addition, their relative position among specimens should not change, and they must lie in the same plane, provide adequate coverage of the shape, and be reliably repeatable.

Archaeologists have noted the difficulty in identifying homologous points on artifacts, which typically do not have many unambiguous landmarks and rarely have homologous points interior to the outline of the object (Ioviţă, 2010; Lycett and Chauhan, 2010; Shott and Trail, 2010). Two landmark schemes commonly used by biologists (Bookstein, 1991; Dryden and Mardia, 1998) rank the quality of landmarks, in part, on the biological significance of the location, such as the juncture of different tissues (e.g., suture intersections) that arise from a common evolutionary patterning. Both schemes for biological landmarks have limitations when applied to artifacts (Barceló, 2010), and analysts should focus on locations of cultural significance that have structural correspondence between and within groups, which usually are limited to one or more salient aspects of shape (e.g., functional attributes (Shott and Trail, 2010:199)). While biological specimens can often be adequately described with landmarks on the interior and edge of the specimen, archaeological specimens are usually better conceptualized as a combination of curves and landmarks on only the outline. Curves without identifiable landmarks can be

[1] The differential grinding length implies that this was intentional and probably functional. On some points it is apparent they were used as knives with the binding backing the blade. The implications of this configuration are presently being explored with some replication blades, handles, and hafts.

[2] The difference in the length of lateral grinding was clearly intentional. Points with different grinding lengths most likely served as knives rather than projectile tips.

[3] All these programs (and many others) can be downloaded from the SUNY Stony Brook morphometrics website http://life.bio.sunysb.edu/morph/index.html.

Table 1
LM placement on a typical specimen. The LMs were placed in *TpsDIG2* on the edge of the image.

LM #	Location
1 & 11	At the distal extent of lateral grinding
2 & 10	Defines the minimum basal width
3 & 9	Widest points on the ears
4 & 8	Distal points of the ears
5 & 7	The point at which the ear meets the basal curve
6	Equidistant between points 3 & 9
12 & 16	Defines the maximum blade width
14	Blade tip
13 & 15	Equidistant between tip and points 16 & 12
A	Temporary point to define axis of bilateral symmetry

incorporated into LGM with semi-landmarks that define the curve, although that approach was not employed here. The curve, rather than its points, becomes the homologous structure (Sheets et al., 2006). Unlike biological specimens, few artifact landmarks will be single loci – they will more likely define a dimension (maximum or minimum width), the endpoints of a curve, or intersection of two curves – and virtually all landmarks will lie on the outline of the artifact.

In this research, the salient aspects of the outlines were captured with the LM locations indicated on Fig. 1 are described in Table 1. These LMs would be classified as Bookstein LM Types II or III. The proper classification of LMs seems less important than ensuring they adequately define the structures of interest and are replicable (Shott and Trail, 2010:199). Using a single LM configuration to characterize shape for all projectile point types might be ideal but may not be possible or appropriate for all research designs. For example, Buchanan and Collard (2007) and Buchanan et al. (2011) used the shareware program *MakeFan* to place evenly spaced LMs along the outline of Paleoindian lanceolate points, setting primary LMs at the tip and junction of the blade and base edges. However, I found that the *MakeFan* approach used by those researchers did not adequately capture the more complex shapes of the points in my study. Two additional considerations will be commonly encountered with archaeological specimens: damaged outlines and ideational forms. Since edges and tips of tools are commonly damaged or missing, it may be appropriate to infer where the LM would have been placed but for the damage. Because I am interested in how the points differed when made, rather than how they were used (Buchanan and Collard, 2007), I focused on the ideational form, i.e., the maker's mental template (Deetz, 1996), of which the specimens are approximations. I assume the ideational form was bilaterally symmetric, so I created symmetric forms of the hafts, blades, and entire outlines.

Here, LMs were placed on the images using the freeware *tpsDig2* v.2.16 (Rohlf, 2010). As Table 1 illustrates the location of LMs can be ambiguous, which can adversely affect the requirement for homology and replication. Sixteen LM were used for the entire outline, seven for the blade, and eleven for the base (LMs 1 & 11 were used for both the blade and base configurations; Fig. 1).[4] Visual inspection of the points and comments from the analysts indicated salient variation was present in the shape and orientation of the basal ears, so several landmarks were placed to capture that variation (LMs 3, 4, 5 and 7, 8, 9 in Fig. 1). Also, the curves that define the basal and lateral margins of the haft and curve of the blade seemed significant, so I placed landmarks at and intermediate to the maximum and minimum loci of those curves. Once the entire outlines were completed, *tpsUtil* v.1.46 (Rohlf, 2010) was used to reorder the arrangements of LMs for the blade and base. The distal end of the base (and the proximal end of the blade) was defined by the extent of lateral grinding. Then, artifacts in the three configurations (entire outlines, bases, and blades) were superimposed through generalized Procrustes analysis, which preserves the shapes but eliminates size, rotation, and translation (Rohlf, 1999). All the analyses were conducted on these data without further transformation, other than to create bilaterally symmetric points.

2.4. Bilateral symmetry

I created symmetric points by reflecting the LMs across the axis of symmetry and averaged the LM locations (Mardia et al., 2000), which created symmetric outlines. Using symmetric shapes is justified here, because a fundamental assumption in this research is that for these points, the makers intended to create bisymmetrical tools, even though perfectly bisymmetric tools may never have been made. That assumption would not be appropriate in other research designs, and I do not advocate its use in all instances.

Symmetry is created by orienting the shapes along a midline. In this case the midlines were defined by LMs 6 & 14 for the entire outline, 6 & A for the base, and 14 & A for the blade (Fig. 1). In essence the shape is reflected across the midline "by multiplying one of the coordinates of all landmarks by −1 (e.g., all x-coordinates)" (Savriama et al., 2010:45). The corresponding LM coordinates are averaged, and a new, symmetric shape is created. In this case, the corresponding LMs are listed in Table 1 and connected by an ampersand (ex., LMs 1 & 11). Both *lmedit7a* (an IMP program) and *MorphoJ* will produce symmetric specimens with average LM coordinates.[5] Using symmetric points eliminates the problems that could be caused by asymmetric specimens and small sample sizes. For example, if by chance the images of asymmetric specimens were oriented so that the longer ears were all on the left side of the image, the analysis might find statistically significant differences among groups that captured that anomaly of digitization, rather than culturally significant aspects of shape. Creating symmetry can smooth out irregularities in the outlines caused by damage. In this case it also eliminated the potential problem in the delineation of the extent of the haft and blade caused by differential lateral grinding. In sum, LM placement and whether to capture asymmetry in the outline or "fix" it by making the image symmetric depends on the research question.

An option, not pursued here, that avoids the need to create bilaterally symmetric images would be to use half-images in the analysis (e.g., LMs 6–14 in Fig. 1 for the entire outline configuration). However, this would require choosing the most "representative" half of the specimen, which is not always obvious. Nevertheless, using half-images would allow the inclusion of broken specimens that could not otherwise be used. A second option would use only half the created symmetric image.

2.5. Statistical analysis

Several tests were implemented to determine which outline best discriminated the *a priori* groups and was most successful in correctly allocating specimens to the appropriate group. First, the groups were analyzed through a canonical variates analysis (CVA)

[4] Several different combinations of LMs were tested for the base (18, 17, and 13), but 11 LMs performed best at correctly discriminating these types.

[5] *lmedit7a* requires that two endpoints of the axis of symmetry be designated. LM *A* in Fig. 2 filled that requirement. Once a symmetric specimen was created, LM *A* was deleted and the analyses were run on the 11 LM configuration for the base and 7 LM configuration for the blade.

Table 2
Results from the significant Bartlett's tests for differences among Suwannee, Simpson, and TSN for the three configurations.

Configuration	Axes	Wilk's Λ	X^2	df	*p*-value
Entire Outline	Not significant for the first axis				
	2	0.0400	107.8303	56	0.0000
Base Outline	1	0.0559	111.0308	36	0.0000
	2	0.3952	35.7427	17	0.0049
Blade Outline	Not significant for the first axis				
	2	0.3465	45.0476	20	0.0011

and discriminant function analysis (DFA) to evaluate the cohesiveness of the grouping. Bartlett's test, which is based on a MANOVA testing the hypothesis of differences among the groups, was run on the initial group allocations to determine the number of significant CVA axes (Zelditch et al., 2004). The efficacy and robustness of the groupings were evaluated through a bootstrapping assignment and cross-validation methodology. Finally, the 15 points classified as "Unknown" were examined with CVA and tested through the bootstrapping assignment methodology.

Both DFA and CVA maximize the separation between groups identified by the analyst, but the results are not necessarily statistically significant. DFA identifies the linear combination of multivariate data that maximizes separation between the groups and projects the result onto a single axis in the form of a histogram. DFA determines group membership by measuring the distance of an individual specimen from the group mean. Thus, while the group means may be statistically different in a MANOVA, there may not be a good separation of groups in DFA because the within-group variance is large. In short, a good separation of groups in DFA does not mean the groups are significantly different in multivariate means or that significantly different means will give good separation in DFA. The same is true for CVA, which is DFA for more than two groups.

The effectiveness of groupings of artifacts is only partly tested by a MANOVA, since the within-group variability of artifacts defining the group can be large. The test of effectiveness for DFA and CVA is their ability to properly allocate specimens by measuring their distance (usually using Mahalanobis distances) to the group means (Sheets et al., 2006). Here, the CVA analysis was done in *CVAGen7a*, which computes the partial warp scores to the common references (the average of all members of the group), conducts the MANOVA

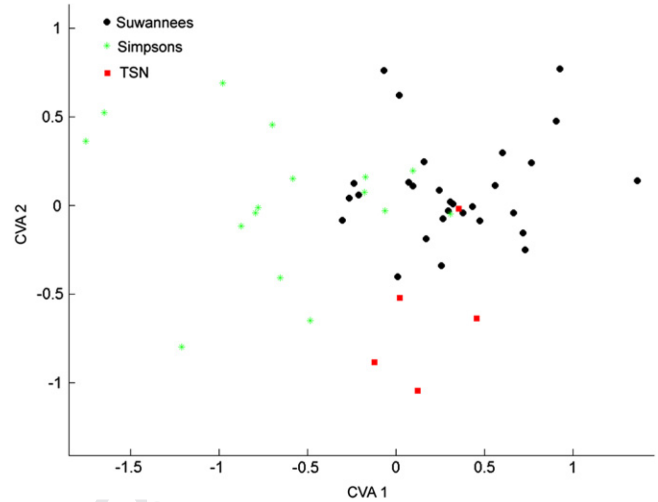

Fig. 4. CVA plot of the blade configuration.

and calculates the Mahalanobis distances from the partial warp scores of the individuals. The initial validation test simply measures the distances of all specimens to the group means and reports the allocations. This tends to inflate the effectiveness of the CVA since the member specimens were used in calculating the mean. A second approach uses a jackknife procedure that removes one specimen from the dataset, recalculates the means, treats the removed specimen as an "unknown," and assigns it to the closest group mean. The results of this jackknife procedure are reported in Section 3.

An assignments test is available in *CVAGen7a* that assesses the probability of the group assignment of a single specimen (Nolte and Sheets, 2005). A Monte Carlo simulation is employed to create a model of random variation around the group mean, and this model is used to determine the likelihood that a specimen's distance from the group mean is consistent with the null hypothesis of random variation around the mean. A *p*-value of <0.05 means the assignment is doubtful. Here, the assignments test was used to iteratively reallocate specimens until the group membership became stable (i.e., the assignments test no longer

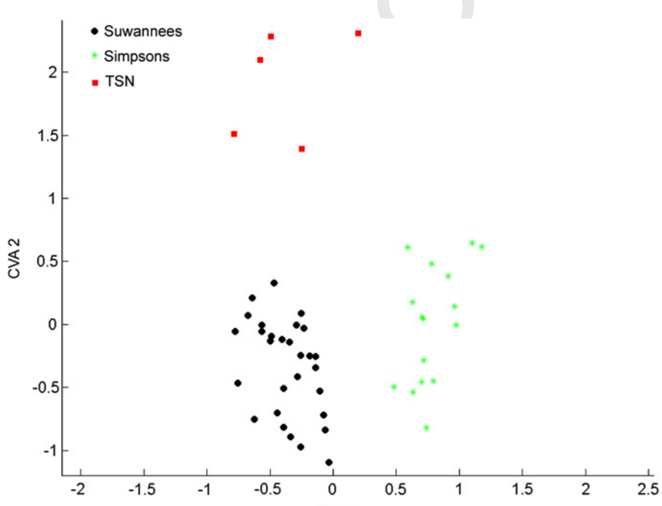

Fig. 3. CVA plot of the base configuration.

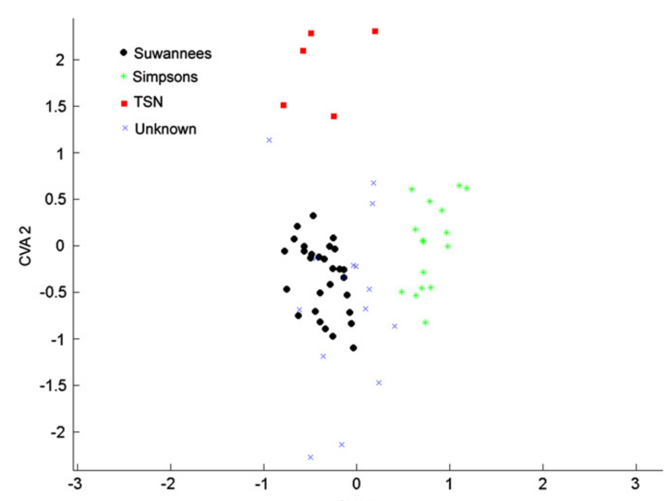

Fig. 5. CVA plot of the blade configuration with the 15 Unknown points plotted based on their CVA scores.

Table 3
Results for the Mahalanobis distance between means of the TSN–Suwannee, and TSN–Simpson groups for the blade configuration.

	TSN–Suwannee	TSN–Simpson	Suwannee–Simpson
Mahalanobis distance:	1.8338	2.0641	1.7659
T^2:	14.2673	16.4609	32.9873
p-value:	0.0563	0.0638	0.0003

found that a specimen was misallocated). For example, if the first assignments test indicated that a specimen designated as "Suwannee" was closer to the "Simpson" mean shape, then that specimen was reallocated to the Simpson group, and the assignment test was run again. Stable groups were reached within two iterations, meaning the assignments test for each configuration was run no more than twice before group members no longer needed to be reallocated. The assignment test can also estimate the probability of group membership of unknown specimens, which was used here for the 15 Unknown points in the initial group allocation. The test assigns the Unknown points to one of the *a priori* groups or to a Group 0, which means the specimen was highly unlikely (p-value < 0.001) to belong to any of the designated groups.

A second jackknife test is available in *CVAGen7a* to evaluate the effectiveness of the assignments test, which allows more than one specimen to be removed at a time. By sequentially removing larger percentages of the specimens (ex., 1%, 10%, 30%, 50%) the cohesiveness of the group can be assessed. If a LM configuration continues to correctly identify specimens as more specimens as removed, then we can infer it is robust. The results of the second jackknife test are reported as: % correct and significant, % correct and insignificant, % incorrect and significant, and % incorrect and insignificant. The insignificant results reflect outliers that were nonetheless assigned to a group.

3. Results

CVAs were run on all LM configurations. The Bartlett's test found significant differences among the initial three group membership allocations for the base configuration, but the entire outline and blade configurations were not significant for both axes (Table 2). The distinction among the groups can be seen in the CVA plots (Figs. 3–5). Of the three plots, the base configuration (Fig. 3) best discriminated the groups, while there was no clear discrimination based on blade shape (Fig. 4). The DFA results of the three groups showed the blade configuration did not distinguish between TSNs and Suwannees or Simpsons (Table 3; Fig. 4).

The jackknife replacement test results for all LM configurations on the initial group membership assignments show the relative efficacy of the ability of the groups to accurately allocate membership (Tables 4–6). Of note are the overall success rates of the entire point and base configurations; the entire point configuration had an overall success rate of 78%, whereas the overall success rate of the base configuration was 66%. The jackknife replacement tests were re-run based on the final stable group assignments, and the results are reported in Tables 7 and 8. With stable groups, the overall successful allocation rate for the base configuration rose to 90%, whereas the overall success rate for the entire point configuration fell to 70%. The change in percentages represents an increase of 17 correct identifications for the base configuration and a decrease of 4 correct identifications for the entire point configuration.

Jackknife assignment tests were run on the entire point and base configurations. Tables 9 and 10 show the results for 1000 jackknife iterations for the 1, 10, 30 and 50% removals. Several things are apparent. For the base configuration, significant successful results for the 1% removal (five specimens at a time) is in good agreement with the single-specimen jackknife removal test (Table 5): 88.2% and 90%, respectively. In contrast, the entire point configuration is in fair agreement with the single-specimen jackknife removal test (Table 6): 61.8% and 70%, respectively. Second, the predictive power of the entire point configuration (measured by the percent of successful significant assignments) drops more quickly as larger percentages of the group are removed and the mean recalculated. At the 30% removal rate, the entire point configuration has a significant success rate of only 23%. In contrast, the base configuration generally maintains its significant success rate past the 30% removal rate. Even when half the specimens are removed, the base configuration has better predictive power than the entire point configuration at the 30% removal. Similarly, the significant false allocations are minimized in the base configuration, almost half the number for the entire point configurations. Finally, the

Table 4
Jackknife replacement results for base configuration, with 66% overall correct assignments.

Type	Suwannee	Simpson	TSN	% correct
Suwannee	17	8	1	65%
Simpson	7	12	0	63%
TSN	1	0	4	80%

Table 5
Jackknife replacement results for entire point configuration and the initial group membership assignments. 78% overall correct assignments.

Type	Suwannee	Simpson	TSN	% correct
Suwannee	22	3	1	85%
Simpson	4	14	1	74%
TSN	1	1	3	60%

Table 6
Jackknife replacement results for blade configuration and the initial group membership assignments. 54% overall correct assignments.

Type	Suwannee	Simpson	TSN	% correct
Suwannee	14	5	7	54%
Simpson	4	12	3	63%
TSN	3	1	1	20%

Table 7
Jackknife replacement results for base configuration and the final stable group membership assignments. 90% overall correct assignments.

Type	Suwannee	Simpson	TSN	% correct
Suwannee	28	0	1	100%
Simpson	2	13	1	81%
TSN	1	0	4	80%

Table 8
Jackknife replacement results for base configuration and stable membership assignment. 70% overall correct assignments.

Type	Suwannee	Simpson	TSN	% correct
Suwannee	18	8	1	67%
Simpson	4	13	1	72%
TSN	1	0	4	80%

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Table 9
Jackknife estimates of assignment performance for entire outline (1000 replications).

% left out in jackknife	1	10	30
% correct	61.8	55.7	23.3
% correct n.s.	13.7	14.9	32.5
% false	17.2	21.0	20.8
% false n.s.	7.3	8.4	23.4

Table 10
Jackknife estimates of assignment performance for base outline (1000 replications).

% left out in Jackknife	1	10	30	50
% correct	88.2	86.5	72.7	35.7
% correct n.s.	2.0	2.9	9.9	28.8
% false	9.8	10.0	13.8	17.6
% false n.s.	0.0	0.6	3.7	17.9

non-significant allocations are also informative, since they represent correctly or incorrectly allocated outliers. The number of non-significant results is kept to a minimum in the base configuration, indicating less variance among the group members (i.e., fewer outliers).

Fig. 5 is the CVA for the base configuration including the 15 Unknown points. The CVA results are confirmed in the assignment test, which assigned one to TSN, eight to Suwannees, zero to Simpsons, and six as unaffiliated. A review of the images of the unaffiliated Unknowns supports most of the allocations in Fig. 5; points that are located between the Suwannee and Simpson groups have shape aspects that are intermediate between those types. Further, several of the unaffiliated Unknowns are unlike specimens from the *a priori* groups.

4. Discussion

The jackknife assignment tests reveal that the base configuration better discriminates the three groups of Paleoindian points than the entire point configuration. In addition, the base configuration is more cohesive than the entire point configuration, meaning there is less within-group variation, and it remains a better predictor of proper group assignment, even with smaller data sets. The reason appears to lie in the wide overlap in blade shape among the groups (Fig. 4). When blades are resharpened, the ratio of length to width typically changes (i.e., the blade get shorter at a faster rate than its width), modifying their shapes in addition to their sizes. Further, almost half the time the blades were misallocated to group. Additionally, the variation is high within the entire point configuration (as demonstrated by the drop in significant correct allocations and high percentage of insignificant allocations in Table 9). Thus, the working hypothesis that the base should be the best predictor of shape is supported by these analyses.

The day-to-day utility of the method employed here depends on whether archaeologists can use the results as a handy reference for point identification. CVA plots and assignment tests are not practical for quickly performed point identifications. However, averaged images of group specimens can be created and do provide a workable reference for the average or typical point shape in a group. Fig. 6 illustrates averaged images of the artifacts for each group, using the base configuration. The images were created in *tpsSuper* v. 1.14. Only the bases were superimposed so the blade sizes are variable. These figures also illustrate the earlier conclusion that variable blade shapes affected the utility of the entire point configuration for accurate member allocation. Regardless, the method is a vast improvement on the traditional impressionistic artifact descriptions and cursory linear measurements, angles, and ratios (Shott and Trail, 2010).

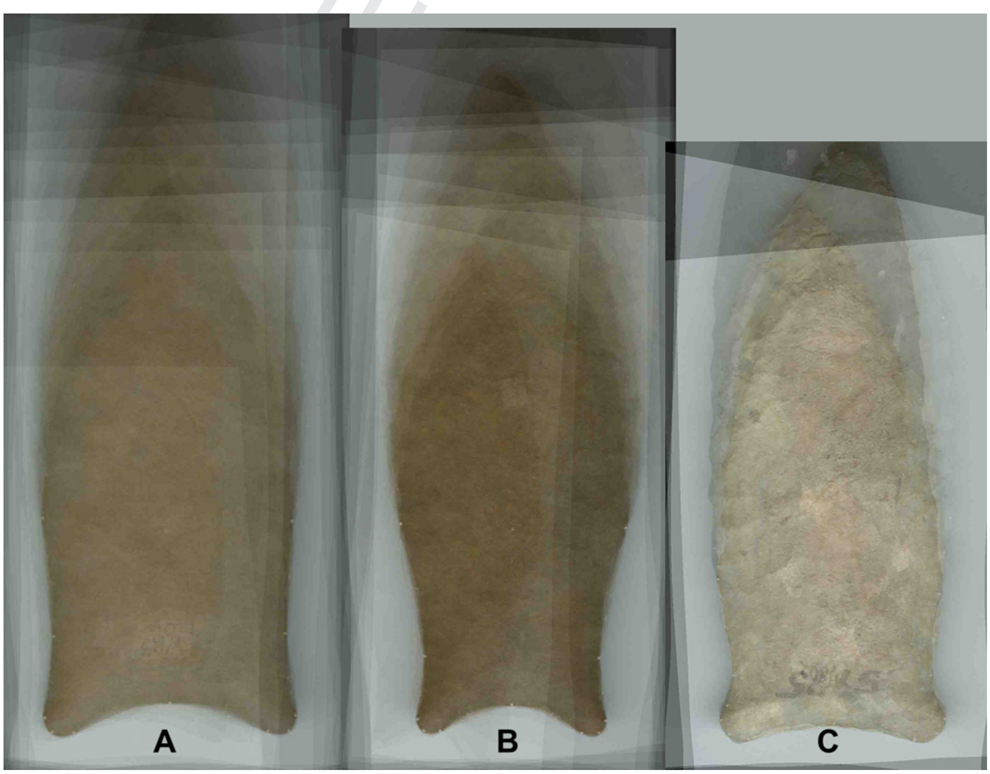

Fig. 6. Average images created in *tpsSuper* using the base configurations. Suwannee (A), Simpson (B), TSN (C).

5. Conclusion

The process employed here demonstrates the ability to investigate three issues that are integral to establishing more definitive typologies. First, the LGM method provides a means to determine whether in fact two or more groups of points, or other artifacts distinguished by shape, can be rigorously distinguished. Rather than relying on impressionistic descriptions and traditional measurements, artifact shapes can be defined in a way that allows unknown specimens to be assigned. Second, the use of symmetric specimens created from images of artifacts that were presumably intended to be bilaterally symmetric better captures the maker's ideational model and eliminates asymmetries introduced into shape by damage and manufacturing errors. Third, the jackknife and assignments tests allow exploration of culturally important issues of difference and affiliation. This level of analysis would not likely be possible using typical standard morphometric measures. The Unknown assignments present a cautionary note, however: the allocations based on LGM should not be slavishly accepted. LGM can identify significant differences in artifact shapes, but it cannot determine whether the differences have cultural significance.

Regardless of the ease of use of the freeware capable of analyzing artifact shapes, analysts must use caution, since they are all specifically developed for analysis of biological specimens. The general rules of LM choice cannot be strictly applied to artifact analysis. The choice to create symmetric specimens will depend on the research questions. Nevertheless, traditional morphometric analysis has been limited to linear measurements, angles, ratios, areas, principle components, and the like (Adams et al., 2004). These traditional descriptors are frustratingly limited in their ability to capture all the relationships in a shape through univariate and multivariate statistics. Frequently, an analyst can see differences in morphology but cannot find the appropriate measures to define that difference in a way that allows for statistical analysis. Geometric morphometrics has the promise of overcoming the limitations in traditional morphometrics by capturing and describing shape in a way that allows mathematical analysis of the data and visualization of the ways that shapes differ (Adams et al., 2004; Lycett and Chauhan, 2010). It can also help analysts parse large datasets and create usable group definitions based on criteria that have cultural salience and are statistically rigorous, rather than impressionistic.

The analysis presented here does not resolve questions of chronology or function (Rink et al., in press) for these points. However, it does confirm that the variation is not continuous in the specimens, i.e., that these traditional point types can be defined as three statistically significant different groups that can be discerned from specimens that vary in blade length and blade shape. Additionally, LGM provides useful tools for visualizing these shape groups (Fig. 6) and statistically sound approaches to the allocation of unknown specimens to known groups.

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