



ELSEVIER

Contents lists available at ScienceDirect

MethodsX

journal homepage: www.elsevier.com/locate/mex

Method Article

Integrating faunal and botanical remains using multivariate statistics to reconstruct (pre)historic subsistence developments



Shyama Vermeersch^{a,b,*}, Simone Riehl^{a,b,c}, Britt M. Starkovich^{a,b,c},
Jens Kamlah^{a,d}

^aSFB 1070 ResourceCultures, University of Tübingen, Tübingen, Germany

^bInstitute for Archaeological Sciences, University of Tübingen, Tübingen, Germany

^cSenckenberg Centre for Human Evolution and Palaeoenvironment at the University of Tübingen, Tübingen, Germany

^dInstitute of Biblical Archaeology, University of Tübingen, Tübingen, Germany

A B S T R A C T

Archaeological faunal and botanical remains are often treated and published separately to understand past subsistence practices. This distinction is an arbitrary one based on methodological differences, especially since we know from ethnological sources that animal husbandry and crop cultivation are usually interdependent in agricultural systems. Here, we use correspondence, detrended correspondence, and canonical correspondence analyses to integrate these different lines of evidence. We customise this method by:

- Adjusting criteria to select and prepare data for integration.
- Including independent parameters such as chronology and mean annual precipitation to study relationships.
- Presenting additional visualisations of data to aid interpretation.

The customised method we present can be applied to any time period, geographical region or research question, as long as botanical and faunal data are available. By analysing these data in an integrative way, we can improve our knowledge of subsistence and agriculture, which in turn can provide a context to better understand social and political changes in past societies.

© 2021 The Author(s). Published by Elsevier B.V.

This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>)

A R T I C L E I N F O

Method name: Correspondence Analysis

Keywords: Animal husbandry, Archaeology, Zooarchaeology, Archaeobotany, Correspondence analysis, Agriculture, Past societies, Subsistence

Article history: Received 19 January 2021; Accepted 31 March 2021; Available online 7 April 2021

DOI of original article: [10.1016/j.quascirev.2020.106776](https://doi.org/10.1016/j.quascirev.2020.106776)

* Corresponding author at: Institute for Archaeological Sciences, University of Tübingen, Tübingen, Germany.

E-mail address: shyama.vermeersch@uni-tuebingen.de (S. Vermeersch).

<https://doi.org/10.1016/j.mex.2021.101336>

2215-0161/© 2021 The Author(s). Published by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>)

Specifications Table

Subject Area	
More specific subject area	Archaeology
Method name	Correspondence Analysis
Name and reference of original method	Correspondence Analysis Smith, A., Munro, N.D. [44]. A Holistic Approach to Examining Ancient Agriculture: A Case Study from the Bronze and Iron Age Near East. <i>Curr. Anthropol.</i> 50, 925–936. https://doi.org/10.1086/648316
Resource availability	Any statistical software able to run multivariate statistics (e.g., Canoco 5, SPSS, PAST)

Method details

Data selection and preparation

Before performing multivariate analyses to integrate archaeological faunal and botanical remains, analysts need to select and prepare these data. The criteria we use in our customised method are based on those established by Smith and Munro [44] but we elaborate on them. The created dataset should be a cross table, representing taxa (variables) and samples (cases). Whether taxa are represented in rows or tables will depend on the statistical software used. In Canoco 5, both options are possible. We recommend publishing the obtained dataset in the supplementary information so readers can replicate the results. Here, we provide specific recommendations based on our research question to investigate general patterns in subsistence from the Bronze through Iron Age in the southern and central Levant. Analysts should note parameters can differ depending on their research question.

First, analysts must decide whether to use quantitative (abundance measures) or binary (presence/absence) data. Advantages and disadvantages of different data types heavily depend on the primary research question and are discussed in various archaeobotanical reports (e.g., [2,3]). When using quantitative data, we recommend using NISP (number of identified specimens) for faunal remains and seed/chaff counts for botanical remains. We believe that, at present, NISP is the best suited counterpart to seed count since both represent primary data which reflect observed specimens [9,32,33]. These two quantitative measures are also most frequently provided in archaeological reports. When selecting data from published reports for one's dataset, make sure they represent the same types of contexts, i.e., only compare samples from household contexts when looking for an overall dietary or economic pattern or only use data from ritual or burial contexts from different sites when looking for regionally diverse ritual practice. Additionally, only include reports which present data for both wild and domesticated taxa when trying to obtain a complete understanding of subsistence (this is a criterion we added to those established by Smith and Munro [44]). Furthermore, try to preferably use data that have been achieved through standardised methods of sampling and sample processing.

Second, analysts need to decide how to classify their data: for example, cases (samples) per relative dating (e.g., Early Bronze Age), absolute dating (3600–2000 BCE), or function (urban vs. rural), variables (taxa) per biological, ecological, or economic characteristics. In the dataset we provide here as an example (raw data see SI 1), we classified our data using relative dating.

Third, as a part of data manipulation, analysts need to broaden taxonomic categories to account for the different levels of taxa identification between analysts since they will identify specimens to a different taxonomic level. An example in our dataset is to merge *Dama dama*, *Dama mesopotamica*, and *Dama dama mesopotamica* to *Dama* sp. Similarly, archaeobotanists use a broad range of individual taxonomies to compensate for diverse uncertainties during the identification process, resulting in an immense number of taxa in large datasets with very low overall ubiquities. To receive interpretable patterns, one would need to amalgamate taxa names that are beyond the species level. When using correspondence analyses, different levels of taxonomic identifications are possible, so the dataset can have specimens identified to the species levels and, for example, family level.

Fourth, analysts need to establish a threshold for the presence of taxa in their dataset [8]. This threshold can vary between 5 and 10% and will depend on how many samples there are in the dataset

[8]. Establishing such a threshold is important since rare taxa will introduce strong numerically based patterns into the biplot of the correspondence analyses that reduce the visibility of associations of the better represented taxa, i.e., we see patterns that are based on the lack of presence rather than on meaningful contextual relationships. In our dataset, we used a 5% threshold for the presence of a taxon in all samples.

Finally, when using abundance data and working with a dataset with many samples, analysts need to establish a threshold for the total number of specimens per sample. For botanical remains we recommend samples have a minimum of ten taxa and a minimum abundance of a 100 seed counts. Higher thresholds are better [48], but are frequently not provided in archaeobotanical studies. For faunal remains, we recommend running some test biplots for correspondence analyses in 100 NISP increments until a threshold is reached where samples with too little data are eliminated but the trends in the data are still visible. Alternatively, when dealing with a small dataset, one can drop the abundance threshold in favour of gaining more comparative material, which we did for the dataset provided here. There are no fixed ruled for establishing this threshold.

Once analysts have selected and prepared their data, they should prepare several specific datasets depending on their research question and parameters. For example, in our dataset we investigate general subsistence practices, so we made three datasets: a domesticated, wild, and all available taxa dataset. The domesticated taxa dataset allows to investigate agricultural patterns and practices, and the wild taxa dataset allows to investigate the environment and the role of hunting, agricultural techniques via weeds, and fodder. The dataset with all available taxa combines these data and provides an in-depth look into subsistence practices in their entirety. Note that when making the domesticated and wild taxa dataset, analysts might have to re-evaluate the presence and abundance thresholds. Analysts should also choose some known parameters or classifiers to explore their dataset. One possibility would be to group cases (samples) according to such parameters following point two in data preparation (e.g., relative dating). Other examples are mean annual precipitation or elevation. Finally, once analysts have chosen their classifiers, it is important to check the distribution of samples within these, i.e., whether the samples evenly contribute to these set categories. Establishing this can help interpret the integrative data, by knowing which, for example, zones of mean annual precipitation are underrepresented in your data.

Types of correspondence analysis

Multivariate statistics consist of a wide range of methods. For our integrative analyses, we focus on correspondence analysis (CA), detrended correspondence analysis (DCA), and canonical correspondence analysis (CCA). These types of statistical analyses are useful to recognise patterns in larger datasets and provide several benefits, outlined by Ter Braak [47]:

- Both quantitative and binary data are accepted.
- large numbers of taxa are allowed (10–500 taxa).
- Allows a dataset containing many zero values.
- Manages to show a non-linear, unimodal relationship between taxa and quantitative environmental parameters.

CA, DCA, and CCA are visualised by a biplot. The first axis (the horizontal axis) represents the greatest amount of variance within the data, whereas the second axis (the vertical axis) represents lesser variance [25]. It is important to remember correspondence analyses are multivariate statistics, meaning these two axes only manage to give a two-dimensional view of results. It is good practice to check the biplots represented by other axes (the third and fourth axis), especially when patterns are unclear.

Sometimes, when running a CA, analysts will see the points in the biplot are scattered in the shape of an arch, which is called the 'arch effect' [21]. Whenever this occurs, analysts should run a DCA, which will remove the arch by detrending the data using polynomials or segments [46]. We recommend first trying to detrend data using polynomials, and if this does not work, to use segments. For example, in our dataset, we use second-order polynomials for detrending.

CCA helps recognizing patterns against known parameters, it does this by constraining the ordination axes to assess the effect they have on the data [45]. Analysts are free to choose any parameter but should publish the criteria for these parameters. For example, in our dataset we use chronology and mean annual precipitation as parameters, so we need to provide these data either as raw data or by a representative map. The advantage of CCA is that its results can be tested for the statistical significance of the null hypothesis by performing a Monte Carlo permutations test.

Data interpretation

The results of the correspondence analyses are expressed in a biplot which shows both taxa (variables) and samples (cases). It is important to check the explained cumulative variation of the correspondence analysis for the first and second axis (or the other appropriate axes) to see how much variation is explained by the two axes. There are no statistical tests which can provide the significance of the results for CA and DCA, so it relies on a critical, visual assessment of the data. It is useful to visually classify the samples per parameter to aid in interpretation. For example, in our dataset, we give samples with a different relative dating a different symbol (Fig. 1). The closer a taxon is located to the origin of the biplot (the point where the two axes cross), the more common it is throughout all samples and as such is not ideal to differentiate between samples. Samples with similar taxa composition and proportions will plot in close vicinity to each other, essentially forming a group or cluster. When outliers are present, so samples plotting separately or far from other samples or clusters, analysts should investigate why they are different and then create a biplot leaving these outliers out. Sometimes, this will change the way your samples plot, other times it will not change anything. When interpreting the biplot it is important to also check the raw data of the dataset and reread the original reports. Often, this will help to understand the observed clustering of samples or will enable the analysts to explain outliers. The biplot of a CCA should be interpreted similarly, although the software amalgamates samples of one category (Fig. 2). We recommend always running a CCA since this can test the statistical significance and help you recognise which groups cluster together, followed by a (D)CA where one can see more details on what taxa are associated with what samples or clusters.

Another useful type of biplot to help interpret the dataset, is to plot the taxa as pie charts to see their contribution to your chosen sample categories (e.g., mean annual precipitation) instead of plotting the samples (Fig. 3). These biplots are more intuitive to interpret, since one only need to look at the proportions reflected by the different sections of the pie diagram to see in where the taxon occurs most frequently. We recommend using quantitative data for making these biplots. We suggest making these plots for taxa which seem promising or are regarded as important for past subsistence. It can also be used to verify trends where one taxon lost popularity in favour for another.

Finally, attribute plots of a taxon or several taxa can be helpful for interpreting your data (Fig. 4). Our recommendations are similar to those for the biplots expressing taxa as pie diagrams, namely using quantitative data and taxa which are of interest. These biplots are easy to interpret, the bigger the symbol, the more frequent the taxon appears in the sample. Analysts will notice the position of the samples in the attribute plot is the same as in the (D)CA biplot.

Method validation

We first applied the methodology described here to investigate developments in subsistence practices from the Early Bronze Age through the Iron Age (3600–586 BCE) in the central and southern Levant. We investigated how the results of the correspondence analyses for the integrative dataset compared to those of the separate faunal and botanical datasets [49]. In this paper, we will use the same integrative dataset but instead of quantitative data, we will apply binary data to show that using either quantitative or binary data will usually yield similar results. The dataset uses a 5% taxa presence threshold and consists of 24 samples representing 15 sites (Table 1), which we have selected and prepared using the guidelines described earlier. We also provide the distribution of the parameters used in our dataset (Table 2). The raw data we used for the correspondence analyses and the legend of the sites can be found in SI 1.

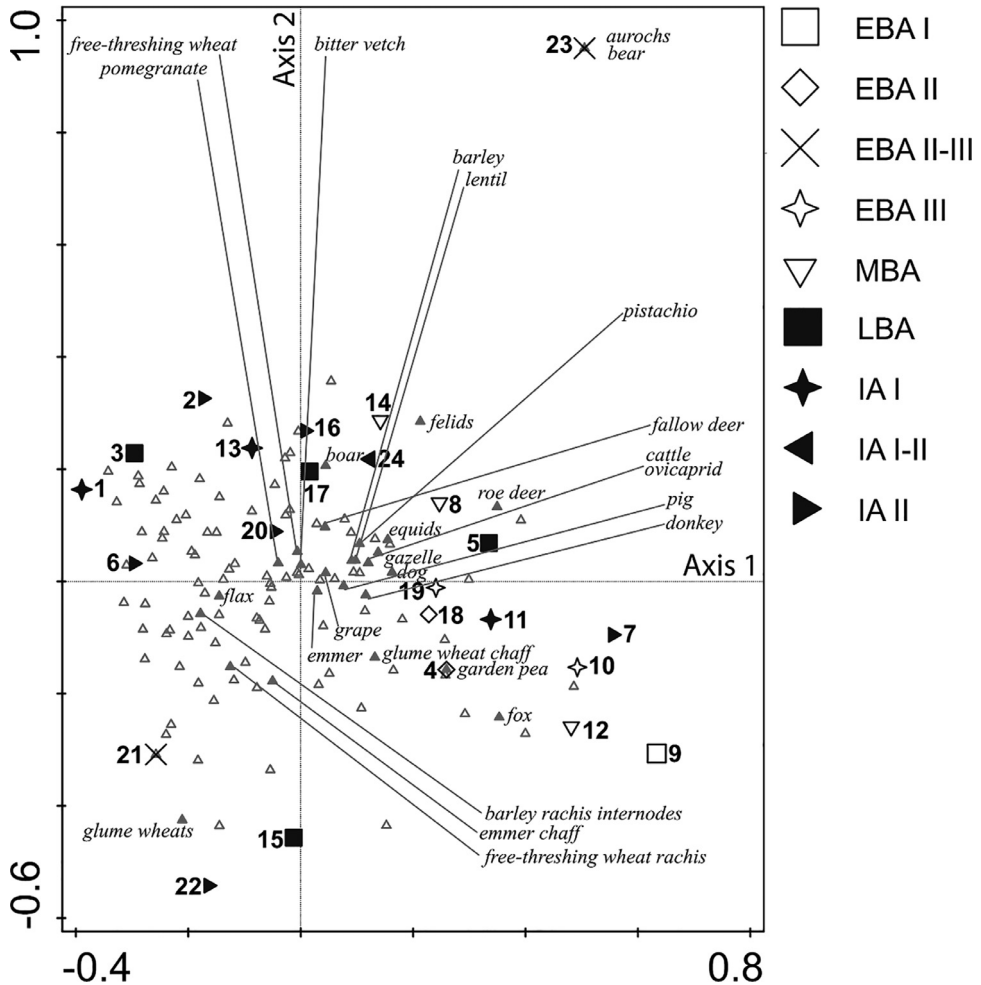


Fig. 1. DCA biplot of our integrative dataset, showing an explained cumulative variation of 13.02% on axis 1 and 22.63% on axis 2. The eigenvalues of axis 1 and 2 are 0.2799 and 0.2065, respectively.

We use the Canoco 5 software to perform a detrended correspondence analysis on our integrative dataset and classify our data using relative chronology. The biplot presented here (Fig. 1) has been cleaned and is not the original output from the Canoco 5 software (we provide a step-by-step manual on how to use Canoco 5 most efficiently in the additional information section of this paper). First, we try to observe clustering of samples, or relationships in the biplot representing the first two axes. We see that the samples of the Early Bronze Age (EBA) and Middle Bronze Age (MBA) tend to plot on the right side of the first axis and on the negative part of the second axis. These samples are associated with the main animal domesticates (pig, cattle, ovicaprids), equids and fox. If we look at the botanical taxa driving this association, we see garden pea, glume wheats, lentil, and wild pistachio are determining EBA and MBA samples. However, two outliers are present in this group, Hirbet ez-Zeraqon (21) and Sidon (23) for which we must find an explanation. This should be done by looking at the raw data and rereading the original reports. When we do this, we see Hirbet ez-Zeraqon has a high diversity (i.e., the number of taxa represented in the sample) and has high frequencies of emmer chaff, wild botanical taxa, fox, and equids. Sidon has a low diversity, and a high frequency of bear,

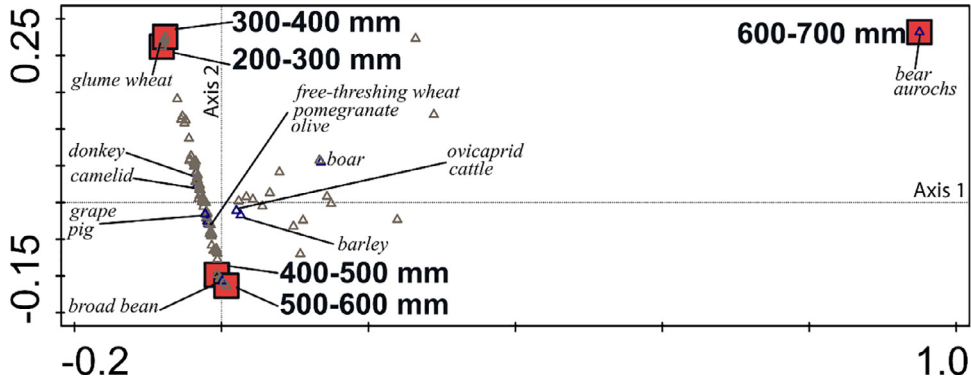


Fig. 2. CCA biplot of our integrative dataset, showing an explained cumulative variation of 8.82% on axis 1 and 15.97% on axis 2. The eigenvalues of axis 1 and 2 are 0.1896 and 0.1538, respectively.

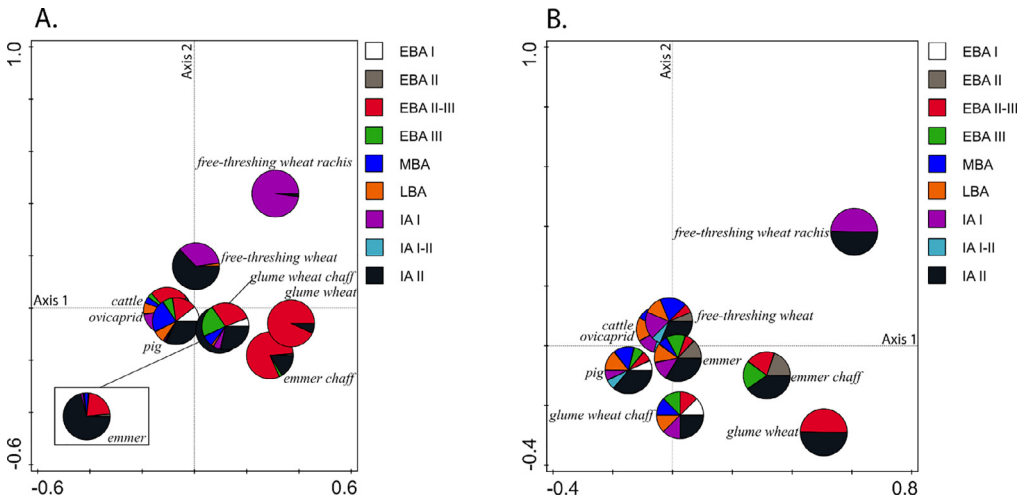


Fig. 3. Biplots representing the most common domesticated taxa as pie diagrams, which reflect the division of the parameter relative chronology. 3A: CA biplot with quantitative data, showing an explained cumulative variation of 36.37% on axis 1 and 61.52% on axis 2. The eigenvalues of axis 1 and 2 are 0.2414 and 0.1670, respectively. 3B: DCA biplot with binary data, showing an explained cumulative variation of 31.65% on axis 1 and 50.94% on axis 2. The eigenvalues of axis 1 and 2 are 0.2467 and 0.1504, respectively.

aurochs, and barley which causes this sample to plot separately. Samples classified to the Late Bronze Age (LBA) plot heterogeneously which suggests a lot of variety in the taxonomic composition for these samples. Samples classified to the Iron Age mostly cluster together on the left side of the first axis and on the positive part of the second axis. These samples are mainly associated with boar, felids, free-threshing wheat, pomegranate, grape and bitter vetch. Once clusters of samples and trends have been recognised, we need to put these trends in their socio-political contexts. We refrain from doing this here since data interpretation will differ between time periods, geographical context, and research question.

Next, we present a CCA biplot using our integrative dataset expressed with binary data against the known parameter of mean annual precipitation (Fig. 2). Using this analysis, we can check whether subsistence significantly changes between zones of mean annual precipitation. As mentioned before, this can be done using a Monte Carlo permutations test. Here, it indicates a significant difference

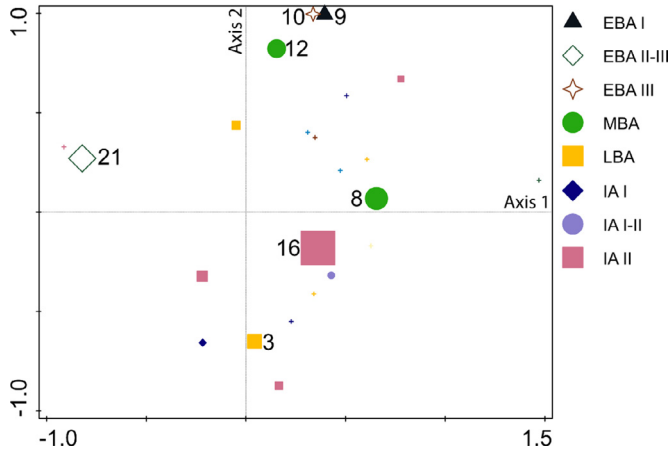


Fig. 4. Attribute plot of pig against the parameter of relative chronology. Small “+” signs indicate absence of pigs.

Table 1

Sites used for our integrative analyses with their references.

Site	Reference
Aphek	[13,17,30]
Arad	[16,26]
Ashdod	[12,35,37]
Ashkelon	[15,52]
Bet-Shean	[18,30]
Hirbet el-Mudeyine el-'Aliye	[7,28,38]
Hirbet ez-Zeraqon	[6,40]
Manahat	[19,23]
Megiddo	[1,31,42,51]
Qubur el-Waleyide	[34,39] + Orendi unpublished data
Shiloh	[14,24,29]
Sidon	[5,50]
Tel Burna	[11,43] + Orendi unpublished data
Tell es-Safi	[22,27,36]
Tell Yarmuth	[4,41]

Table 2

Distribution of the parameters relative dating and mean annual precipitation in our dataset.

Parameter	Number of samples
Relative Dating	
Early Bronze Age I	1
Early Bronze Age II	2
Early Bronze Age II-III	2
Early Bronze Age III	2
Middle Bronze Age	3
Late Bronze Age	4
Iron Age I	3
Iron Age I-II	1
Iron Age II	6
Mean Annual Precipitation	
200–300 mm	3
300–400 mm	3
400–500 mm	8
500–600 mm	9
600–700 mm	1

between different zones of mean annual precipitation (pseudo- $F = 1.6$, $p = 0.002$). The interpretation of the CCA is like that of the (D)CA. We see three clusters of precipitation zones: 200–400 mm, 400–600 mm, and 600–700 mm. The lower precipitation zones are amongst other taxa associated with glume wheat, donkey, and camelid. The latter is particularly known to be adapted to dry climates. The 400–600 mm precipitation zone is characterised by a range of taxa including grape, pig, broad bean but also ovicaprid, cattle, and barley. The wettest precipitation zone is distinguished by the frequencies of bear, aurochs, and boar. Although the CCA biplot is informative and can be tested statistically, we recommend comparing its results with those of the (D)CA biplot to obtain a more in-depth look regarding samples.

It is also possible to represent taxa as pie diagrams in the biplot, the pie diagram representing the proportion of a specific parameter (in this example, relative chronology). We choose to represent the most common domesticates in the past diet of the people of the Bronze and Iron Age in the southern and central Levant: ovicaprids, cattle, pig, free-threshing wheat, glume wheat, and emmer. The first biplot uses quantitative data (Fig. 3A) where we observe emmer occurring more often in the Early Bronze Age II-III, whereas free-threshing wheat occurs most frequently in the Iron Age. Note, there is still a large quantity of emmer during Iron Age II. This needs to be explained and could be related to the different functionalities of chaff and grain. The high frequency of emmer grains comes from the Ashkelon Iron Age II sample. If we return to the raw data and original report, we see the authors considered this to be exceptional, and emmer was used as a food staple at the site or was imported from inland sites. We now compare these results to a biplot using binary data (Fig. 3B). Here, we see similar results as in the previous biplot (i.e., a shift from emmer to free-threshing wheat) but the trend is less clear, because it reflects the number of sites in which a taxon is present and our dataset used for this example contains only 15 sites, i.e., is comparatively small. Hence, both taxa will still be present in the sample. Note the dominance of the Iron Age II in the pie diagram for emmer is not as noticeable as it was in the previous biplot. We recommend using quantitative data for biplots expressing taxa as pie diagrams in particular if site or sample numbers are low, and to compare the results with a biplot using binary data, which helps to discover differences in taxa abundance and frequency. Visually, we see the pie diagrams for ovicaprid and cattle overlap in both biplots (Fig. 3A and 3B) but since these taxa appear in all time periods, we did not create a pop-out window for these taxa.

Finally, a last visualisation option are attribute biplots representing a taxon (or taxa) following a classification using quantitative data. Attribute plots can help analysts understand in what category or parameter a taxon is more prominent, which can aid in explanations of the integrative data. Here, we create an attribute plot for pigs classified per relative chronology (Fig. 4). Notice the samples plot similarly to the CA biplot containing all data. These biplots are intuitive to understand: the bigger the symbol, the more frequent the taxon appears in the sample. Generally, pigs are more present in earlier time periods (i.e., the Early and Middle Bronze Age) but we see one notable exception: the Iron Age II sample of Tell es-Safi. In consulting the original report, we see that Tell es-Safi is identified as having a Philistine culture where pig consumption was higher than in contemporary settlements [27].

Pitfalls

The methods presented here are not without issues. A first problem, which might seem trivial, is the aesthetics of the biplots produced. When working with large datasets containing many samples and numerous taxa, it can be difficult to interpret the data, but more importantly, to present the biplot clearly to the reader. We recommend labelling samples with numbers and providing a corresponding legend, and only labelling those taxa which affect the trends and clusters in the biplot. When plotting taxa as pie diagrams representing a category or specific parameter, quite often pie diagrams will overlap. In this case, some editing of the biplot using visualisation software is necessary.

A more pressing issue is the methodological challenges faced when trying to integrate archaeological botanical and faunal remains. We described these in depth previously [49] but summarise the main issues here.

- Different qualities as placeholders for living plants and animals

Archaeological faunal material is represented by fragments from specific animal bones (quantified as NISP) [10], so we can reconstruct the MNI (minimum number of individuals). Archaeological botanical material, however, is represented by parts of the reproduction unit and - at present - we cannot reconstruct the number of individuals [20]. This means, although we use NISP and seed count to integrate these two lines of evidence, inherently they do not represent equivalent values.

- Different functionality
Faunal remains generally represent cooking or household refuse and most often indigestible food debris, whereas plant remains can derive from multiple activities, such as crop processing, storage, cooking, the use of dung or animal feed. Whereas faunal remains typically have been consumed by humans, botanical remains typically are not (except for human faeces or gut contents).
- Different taxonomic representations
Faunal analysts tend to publish results on macrofauna (i.e., larger mammals), fish, molluscs, reptiles, birds, and microfauna separately. Adding to this, quite often only the macrofauna of a site is published, although this situation is rapidly improving thanks to proper recovery methods being employed at excavations. In contrast, archaeobotanists publish all botanical remains in a single report. Besides this, faunal remains tend to be dominated by domestic taxa, specifically ovicaprids and cattle, whereas plant remains have a broader taxonomic diversity which will reflect environmental conditions better.
- Potential bias in clustering
Clustering of samples of multi-period sites in the biplots should always be treated carefully. Sometimes, this can be related to biases introduced by either excavators or analysts, caused by, for example, stratigraphic difficulties or limited laboratory resources.
- Weaker patterns
Biplot using integrative data tend to show trends weaker than biplots using only faunal or plant data. This is because faunal and botanical remains may have contradictory trends which will be amalgamated in the final output, where the more dominant remain group will lead the clustering.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

We thank the University of Tübingen (Germany) for supporting us by granting us the Open Access Publishing Fund. We would like to thank the project members of the SFB 1070 A05 project for helping us compile the faunal and botanical reports and checking the chronology of the sites, Andrea Orendi, Adriano Orsinger, and Effrosyni Roditi.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:[10.1016/j.mex.2021.101336](https://doi.org/10.1016/j.mex.2021.101336).

References

- [1] K. Borovic, The archaeobotanical finds, in: I. Finkelstein, D. Ussishkin, B. Halpern (Eds.), *Megiddo IV: The 1998-2002 Seasons* (Eds.), Emery and Claire Yass Publications in Archaeology, Tel Aviv, 2006.
- [2] S. Colledge, Identifying pre-domestication cultivation in the archaeobotanical record using multivariate analysis: presenting the case for quantification, in: R.T.J. Cappers, S. Bottema (Eds.), *The Dawn of Farming in the Near East, Ex Oriente*, Berlin, 2002, pp. 141-152.
- [3] S. Colledge, J. Conolly, S. Shennan, Archaeobotanical evidence for the spread of farming in the Eastern Mediterranean, *Curr. Anthropol.* 45 (2004) S25-S58, doi:[10.1086/422086](https://doi.org/10.1086/422086).

- [4] S.J.M. Davis, The Mammal Bones: tel Yarmuth 1980-1983, in: P. de Miroschedji (Ed.), Yarmouth : Rapport Sur Les Trois Premières Campagnes de Fouilles à Tel Yarmouth (Israel)(1980 - 1982), éditions Recherche sur les civilisations, 1988, pp. 143-149. Éd. Recherche sur les Civilisations, Paris.
- [5] D. de Moulins, A. Marsh, Sidon: plant remains from the middle bronze age, *Archaeol. Hist. Leban.* (2011) 236-258.
- [6] B. Dechert, Faunal remains from Hirbet-ez Zeraqon, in: H. Buitenhuis, H.P. Uerpmann (Eds.), *Archaeozoology of the Near East II*, Backhuys, Leiden, 1994, pp. 79-87.
- [7] A. Farahani, B.W. Porter, H. Huynh, B.E. Routledge, Crop storage and animal husbandry at early iron age Khirbat al-Mudayna al-'Aliya (Jordan): a paleoethnobotanical approach, in: K. McGeough (Ed.), *The Archaeology of Agro-Pastoralist Economies in Jordan*, American Schools of Oriental Research, Boston, 2016, pp. 27-89. *Annual of the American Schools of Oriental Research*.
- [8] H.G. Gauch, *Multivariate Analysis in Community Ecology*, Cambridge University Press, Cambridge, 1982.
- [9] D. Gifford-Gonzalez, *An Introduction to Zooarchaeology*, Springer, Cham, 2018.
- [10] D.K. Grayson, *Quantitative Zooarchaeology: Topics in the Analysis of Archaeological Faunas*, Academic Press, Orlando, Florida, 1984.
- [11] T. Greenfield, C. McKinny, I. Shai, 18. i can count all my bones": a preliminary report of the late bronze faunal remains from area B1 at Tel Burna, Israel, in: J. Lev-Tov, P. Hesse, A. Gilbert (Eds.), *The Wide Lens in Archaeology: Honoring Brian Hesse's Contributions to Anthropological Archaeology*, Lockwood Press, Atlanta, 2017, pp. 419-441.
- [12] D. Hakker-Orion, P. Nahshoni, The faunal remains, in: *A Thirteenth-Century BCE Site on the Southern Beach of Ashdod*, Atiqot, 2013, pp. 59-122. pp.
- [13] S. Hellwing, Faunal Remains, in: M. Kokhavi, P. Beck, E. Yadin (Eds.), *Aphek-Antipatris I: Excavation of Areas A and B : The 1972-1976 Seasons*, Tel Aviv University and Sonia and Marco Nadler Institute of Archaeology, Tel Aviv, 2000, pp. 293-314.
- [14] S. Hellwing, M. Sade, V. Kishon, Faunal remains, in: I. Finkelstein (Ed.), *Shiloh : The Archaeology of a Biblical Site*, Institute of Archaeology of Tel Aviv University, Tel Aviv, 1993, pp. 309-349.
- [15] B. Hesse, D.N. Fulton, P. Wapnish, Animal remains, in: L.E. Stager, D.M. Master, J.D. Schloen (Eds.), *Ashkelon 3: The Seventh Century B.C., Eisenbrauns, Winona Lake, Indiana*, 2011, pp. 615-644. (Final Reports of The Leon Levy Expedition to Ashkelon).
- [16] Strata V.I. M. Hopf, Plant remains, in: R. Amiran (Ed.), *Early Arad: The Chalcolithic Settlement and Early Bronze City*, Israel Exploration Society, Jerusalem, 1978, pp. 64-82.
- [17] L.K. Horwitz, Terrestrial fauna, in: Y. Gadot, E. Yadin (Eds.), *Aphek-Antipatris II: The Remains On the Acropolis: The Moshe Kochavi and Pirhiya Beck Excavations*, Emery and Claire Yass Publications in Archaeology, Tel Aviv, 2009, pp. 526-561.
- [18] L.K. Horwitz, Mammalian Remains from Areas, H, L, P and Q, in: A. Mazar (Ed.), *Excavations at Tell Beth-Shean 1989-1996, Vol 1 : From the Late Bronze Age IIB to the Medieval Period*, Israel Exploration Society, 2006, pp. 689-710. , Jerusalem.
- [19] L.K. Horwitz, The faunal remains, in: G. Edelstein (Ed.), *Villages, Terraces and Stone Mounds : The Rephaim Valley Project; Excavations at Manahat*, Jerusalem, 1987 - 1989, Israel Antiquities Authority, Jerusalem, 1998, pp. 104-112.
- [20] S. Jacomet, C. Brombacher, M. Dick, Archäobotanik am Zürichsee. Ackerbau, Sammelwirtschaft Und Umwelt von Neolithischen Und Bronzezeitlichen Seeufersiedlungen im Raum Zürich, Orell Füssli, Zürich, 1989.
- [21] R.H. Jongman, C.J. ter Braak, O.F.R. Van Tongeren, *Data Analysis in Community and Landscape Ecology*, Pudoc, Wageningen, 1987.
- [22] R. Kehati, A. Dagan, L.K. Horwitz, Iron age animal husbandry at tell es-Şāfi/gath: notes on the fauna from area D, *Near East. Archaeol.* 81 (2018) 41-44.
- [23] M. Kislev, Impact of pig husbandry vs. goat browsing on ancient oak forest in Israel, in: G. Edelstein, I. Milevski, S. Aurant (Eds.), *Villages, Terraces and Stone Mounds. Excavations at Manahat*, Jerusalem, 1987-1989, Israel Antiquities Authority, Jerusalem, 1987.
- [24] M.E. Kislev, I. Finkelstein, S. Bunimovitz, Z. Lederman, in: *Food remains*, in: Shiloh. *The Archaeology of a Biblical Site*, University of Tel Aviv University, Tel Aviv, 1993, pp. 354-361. Publications.
- [25] J. Leps, P. Smilauer, *Multivariate Analysis of Ecological Data Using CANOCO*, Cambridge University Press, Cambridge, 2003.
- [26] H. Lernau, Faunal Remains, Strata III-I, in: R. Amiran (Ed.), *Early Arad: The Chalcolithic Settlement and Early Bronze City, 1st-5th Seasons of Excavations, 1962-1966*, Israel Exploration Society, Jerusalem, 1978, pp. 83-113.
- [27] J.S.E. Lev-Tov, A preliminary report on the late bronze and iron age faunal assemblage from Tell es-Safi/Gath, in: A.M. Maeir (Ed.), *Tell Es-Safi/Gath I: The 1996 -2005 Seasons*, Harrassowitz, Wiesbaden, 2012, pp. 589-612.
- [28] Lev-Tov J.S., B.W. Porter, B.E. Routledge, Measuring local diversity in early iron age animal economies: a view from Khirbat al-Mudayna al-'aliya (Jordan), *Bulletin of the American Schools of Oriental Research* 361 (1) (2011) 67-93, doi:10.1016/j.jthermalsci.2009.02.006.
- [29] N. Liphshitz, Palaeobotanical remains, in: I. Finkelstein, S. Bunimovitz, Z. Lederman (Eds.), *Shiloh: The Archaeology of a Biblical Site*, Tel Aviv University, Institute of Archaeology, Tel Aviv, 1993, pp. 351-353.
- [30] N. Liphshitz, Plant economy and diet in the Early Bronze Age in Israel: a summary of present research, in: P. de Miroschedji (Ed.), *L'Urbanisation de La Palestine al'Age Du Bronze Ancien. Bilan et Perspectives Des Recherches Actuelles*, B.A.R, Oxford, 1989, pp. 269-277.
- [31] N. Liphshitz, I. Finkelstein, D. Ussishkin, B. Halpern, Wood remains, Megiddo IV: The 1998-2002 Seasons, Emery and Claire Yass Publications in Archaeology, Tel Aviv, 2006.
- [32] R. Lyman, Observations on the history of zooarchaeological quantitative units: why NISP, then MNI, then NISP again? *J. Archaeol. Sci. Rep.* 18 (2018) 505-518, doi:10.1016/j.jasrep.2017.12.051.
- [33] R.L. Lyman, *Quantitative Paleoecology*, Cambridge Manuals in Archaeology, Cambridge University Press, Cambridge, 2008.
- [34] E.F. Maher, Late iron age faunal remains from Qubur al-Walaydah, *Welt Orient.* 40 (2010) 268-272.
- [35] E.F. Maher, The faunal remains, in: M. Dothan, D. Ben-Shlomo (Eds.), *Ashdod VI. The Excavations of Areas H and K (1968 -1969)*, Israel Antiquities Authority, Jerusalem, 2005, pp. 283-290.
- [36] Y. Mahler-Slasky, M.E. Kislev, Preliminary Archaeobotanical Research at Tell es-Safi/Gath-The 1997-2002 Seasons, in: A.M. Maeir (Ed.), *Tell Es-Safi/Gath I: The 1996-2005 Seasons. Vol. 1: Text*, Harrassowitz, Wiesbaden, 2012, pp. 579-587.
- [37] Y. Melamed, Botanical remains from the excavation on the southern beach of Ashdod, *Atiqot* 74 (2013) 127-131.

- [38] P.R.W. Popkin, The Society and Economy of Iron Age Transjordan: a Contextual Zooarchaeological Analysis, University College London, *Bulletin of the American Schools of Oriental Research* 361 (1) (2009) 67–93.
- [39] S. Riehl, *Archäobotanische Funde aus der Kampagne 2009 in Qubur al-Walaydah, Welt Orient.* 40 (2010) 259–267.
- [40] S. Riehl, Archaeobotany at the early bronze age settlement of Hîrbet ez-Zeraqôn: a preliminary report, *Z. Dtsch. Paläst. Ver.* 120 (2004) 101–122.
- [41] A. Salavert, Olive cultivation and oil production in Palestine during the early Bronze Age (3500–2000 BC): the case of Tel Yarmouth, Israel, *Veg. Hist. Archaeobotany* 17 (2008) 53–61.
- [42] A. Sasson, Faunal remains from the iron age levels, in: I. Finkelstein, D. Ussishkin, E.H. Cline (Eds.), *Megiddo V: The 2004–2008 Seasons*, Eisenbrauns, Winona Lake, 2013, pp. 1131–1209. Volume III.
- [43] I. Shai, J. Uziel, Addressing survey methodology in the southern Levant: applying different methods for the survey of Tel Burna, Israel, *Isr. Explor. J.* 64 (2014) 172–190.
- [44] A. Smith, N.D. Munro, A holistic approach to examining ancient agriculture: a case study from the bronze and iron age near East, *Curr. Anthropol.* 50 (2009) 925–936, doi:10.1086/648316.
- [45] C.J. ter Braak, Canonical community ordination. Part I: basic theory and linear methods, *Ecoscience* 1 (1994) 127–140.
- [46] Ter Braak, C.J., Smilauer, P., 2012. *Canoco reference manual and user's guide: software for ordination*, version 5.0.
- [47] C.J.F. ter Braak, *Unimodal Models to Relate Species to Environment*, Biological Mathematics Group, Wageningen, 1996.
- [48] M. van der Veen, N. Fieller, Sampling seeds, *J. Archaeol. Sci.* 9 (1982) 287–298.
- [49] S. Vermeersch, S. Riehl, B.M. Starkovich, J. Kamlah, Developments in subsistence during the Early Bronze Age through the Iron Age in the southern and central Levant: integration of faunal and botanical remains using multivariate statistics, *Quat. Sci. Rev.* 253 (2021) 106776, doi:10.1016/j.quascirev.2020.106776.
- [50] E. Vila, *Etude de la faune du Bronze ancien à Sidon*, in: C. Doumet-Serhal (Ed.), *The Early Bronze Age in Sidon: "College Site" Excavations*, Institut français du Proche-Orient, Beirut, 2006, pp. 301–338. (1998–2000–2001).
- [51] P. Wapnish, B. Hesse, Mammal remains from the early bronze sacred compound, in: I. Finkelstein, D. Ussishkin, B. Halpern (Eds.), *Megiddo III: The 1992–1996 Seasons*, Monograph Series of the Institute of Archaeology of Tel Aviv University, Emery and Claire Yass Publications in Archaeology, Tel Aviv, 2000, pp. 429–462.
- [52] E. Weiss, M.E. Kislev, Y. Mahler-Slasky, Plant remains, in: L.E. Stager, D.M. Master, J.D. Schloen (Eds.), *Ashkelon 3: The Seventh Century B.C.*, Eisenbrauns, Winona Lake, 2011, pp. 591–613. (Final Reports of the Leon Levy Expedition to Ashkelon).