AUSTRALIAN ARCHAEOLOGY
2024, VOL. 90, NO. 3, 299–318
https://doi.org/10.1080/03122417.2024.2402586

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ARTICLE

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Beyond hinges and spires: A critical examination of archaeomalacological quantification methodologies using coral reef molluscan assemblages from Jiigurru (Lizard Island Group), northern Great Barrier Reef

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ABSTRACT

Quantification, as one of the pillars of the zooarchaeological subdiscipline, is an invaluable component of the toolkit researchers use to study past people-animal interactions. Despite being the subject of rigorous (zoo)archaeological debate, the calculation of Minimum Number of Individuals (MNI) values remains one of the main methods of quantifying the relative abundance of taxa within faunal assemblages. Choosing the appropriate quantification protocol to calculate the MNI of archaeological invertebrate assemblages can be challenging due to regional taxonomic considerations and the myriad of quantification methodologies and frameworks available in the global archaeomalacological literature. In an Australian context, methodologies for quantifying coral reef molluscan assemblages have not been explicitly evaluated. Using archaeological molluscan assemblages from two midden sites (Freshwater Bay Midden and Mangrove Beach Headland Midden) on the northern Great Barrier Reef island group of Jiigurru (the Lizard Island Group), we critically examine two commonly adopted archaeomalacological quantification methodologies: the NRE MNI and tMNI protocols. The NRE MNI methodology uses one to two non-repetitive elements (NREs) of molluscs, whilst the tMNI protocol includes a wider range of elements akin to vertebrate MNI quantification methodologies. Through a comparison of taxa abundances and statistical analyses, results show that the tMNI protocol, with some modification, is best suited for the Jiigurru assemblages. Higher MNI values and an increased assemblage diversity, evenness, and richness were recorded for the molluscan assemblages at both midden sites when the tMNI protocol was applied. This study foregrounds the importance of data transparency when reporting quantification protocols and outcomes to ensure the highest degree of data quality, replicability, and usability.

ARTICLE HISTORY
Received 3 July 2024
Accepted 6 September 2024

KEYWORDS
Data transparency; invertebrates; middens; minimum number of individuals; non-repetitive elements; tMNI; zooarchaeology

Introduction

Quantification in zooarchaeology, or the process of counting and measuring faunal remains, is integral to the subdiscipline. Quantification is necessary to understand relative abundances of taxa within and between archaeological faunal assemblages (Grayson 1984; Reitz and Wing 1999) and to generate data that can, in turn, be used to understand past subsistence regimes and forager decision-making. Three main methods of quantification are commonly employed in modern zooarchaeological research: Number of Identified Specimens (NISP), Minimum Number of Individuals (MNI), and weight. The application of these methods has been subject to international archaeological debate for decades with proponents and opponents for NISP, MNI, and weight (e.g. Claassen 1998, 2000; Giovas 2009; Glassow 2000; Grayson 1984; Harris et al. 2015; Lambrides and Weisler 2016; Lyman 1994, 2008, 2019; Mason et al. 1998, 2000; Reitz and Wing 1999; Rowland 1982; Szabó 2009). There is no international consensus or standardised protocol that determines the application of quantification methodologies due to local, regional, and global differences in zooarchaeological assemblage compositions and research foci, which prevent the application of a one-size-fits-all approach. These factors complicate

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cross-comparison between sites within regions and studies from different regions.

Australian archaeology is no different, with a wide range of quantification protocols having been applied since the surge of zooarchaeology in Australian research in the 1960s (Cosgrove 2002). The application of different protocols makes cross-comparison of results complex; however, the problem is compounded when identification and quantification methodologies are not transparently reported. To continue to undertake best-practice research, the principles of quality assurance and quality control, as named by Wolverton (2013) and inspired by Driver (1992), remain integral, yet are often underutilised. This study contributes to the debate on quantification and data transparency through the comparison of two archaeomalacological MNI quantification protocols, the NRE MNI (Claassen 1998) and tMNI protocols (Harris et al. 2015), to assess the outcomes for Australian coral reef molluscan assemblages. The modified tMNI protocol introduced and explicated in this study has been adapted from the original methodology to aid (zoo)archaeologists working in Australia with identifications of Australian coral reef molluscan assemblages.

The NRE MNI and tMNI quantification protocols were applied to two sites on the northern Great Barrier Reef island group of Jiigurru (Lizard Island Group) to test the efficacy of both methodologies and assess broader implications for other Australian archaeological sites dominated by coral reef species. The most efficacious quantification protocol for molluscan assemblages is the protocol that most accurately reflects true assemblage diversity and richness and best reveals the complexity of past marine foraging strategies through results expressing the breadth of species foraged and the range of habitats targeted. In this study, efficacy is tested using differences in total MNI values, rank order abundances, standard zooarchaeological statistical analyses, element frequencies, and habitat comparison between the two protocols.

First, a literature review of archaeomalacological quantification in Australia contextualises this study. Second, different archaeomalacological quantification protocols are discussed, followed by an introduction to Jiigurru and the archaeological sites of Freshwater Bay Midden and Mangrove Beach Headland Midden. Next, a tMNI quantification protocol modified for Australian coral reef assemblages is introduced. Following this, the efficacy of the NRE MNI and tMNI protocols is tested using the methods mentioned above. Lastly, results are discussed through the use of habitat as a case study to explore how the application of different quantification protocols can influence the results of zooarchaeological analyses and interpretations.

Archaeomalacological quantification in Australia

The first published accounts on Australian shell middens can be traced back to the nineteenth century and feature qualitative descriptions of shell middens and their contents. Studies from middens along the shores of Tasmania (Gunn 1842) and in the deltas of the Clarence, Richmond, and Brunswick Rivers in New South Wales (Statham 1892) show that interest was primarily focused on identification of molluscan taxa rather than quantifying their abundances. In the 1960s, quantitative studies of shell midden sites increased, alongside the development of a more formalised Australian zooarchaeology and archaeomalacology. Three main phases can be seen in the development of archaeomalacological quantification in Australia: (1) the use of weights; (2) the introduction of MNI; and (3) the (re)introduction of NISP in addition to MNI.

The earliest quantitative studies of Australian shell midden contents focused on the use of weights to understand differences in relative abundances between taxa and between stratigraphic sequences. Examples include research into the New South Wales Durras North rockshelter (Lampert 1966), the Burrill Lake and Currarong middens (Lampert 1971), the Western Australian rockshelter site of Mandu Mandu Creek (Morse 1988), and the seminal ethnographic work of Meehan (1982) in Arnhem Land.

The application of MNI, and more broadly quantification as a topic in Australian zooarchaeological literature, gained traction in the late 1970s and 1980s with publications on shell middens from around Australia, such as the Richmond River middens in New South Wales (Bailey 1975), Cave Bay Cave in Tasmania (Bowdler 1984), and Nara Inlet 1 on Hook Island, Queensland (Barker 1989). As Cosgrove (2002) points out in his review of Australian zooarchaeology from the 1960s to early 2000s, this period aligned with a time of international debate around the most suitable quantification protocols (e.g. Claassen 1998, 2000; Glassow 2000; Grayson 1984; Lyman 1994; Mason et al. 1998, 2000; Reitz and Wing 1999). The combined application of weights and MNI continues to this day as one of the main methods of shell quantification throughout Australia. For example, research from Kurturniaiwak in the Torres Strait (David and Weisler 2006), studies of Shoalwater Bay, the Whitsundays, and Jiigurru along the Great Barrier Reef (Barker 2004; Lentfer et al. 2013; McNiven et al. 2014), Alligator Rivers middens

in Western Arnhem Land (Mowat 1995), and Cape Duquesne in Victoria (Richards 2012).

The incorporation of NISP appears to have had a recent resurgence with specialists moving away from a more traditional NRE MNI protocol and integrating or formalising archaeomalocological quantification protocols developed for archaeological sites outside Australia (e.g. Giovas 2009; Harris et al. 2015). The added value of reporting NISP for invertebrate assemblages can be seen in the calculation of fragmentation ratios and indices which use NISP alongside other measures to understand the nature of archaeological assemblages (e.g. Faulkner 2010; Gutiérrez Zugasti 2011). Publications over the past two decades have utilised weight, NISP, and MNI in conjunction, such as studies on Barrow Island in Western Australia (Veth et al. 2017), Blue Mud Bay (Faulkner 2013) and the Alligator Rivers region in the Northern Territory (Brockwell et al. 2020a), freshwater middens along the Murray River in northwestern Victoria (Garvey 2017), the southeast Queensland coast (Smith 2016; Smith and McNiven 2019) and along the Great Barrier Reef on the southern Curtis Coast (Ulm 2006), Mazie Bay (Aird 2020), Yindayin rockshelter (Wright 2018), and Mangrove Beach Headland Midden (Lambrides et al. 2020).

Quantification of archaeological faunal remains: Minimum number of individuals (MNI)

Minimum Number of Individuals (MNI), as a method of quantification, has a lengthy history tightly connected with natural sciences and has been used by palaeontologists since the early twentieth century. White (1953) has oftentimes been credited with introducing MNI from North American palaeontology to zooarchaeology (e.g. Grayson 1984:27; Nikita and Lahr 2011:629; Reitz and Wing 1999:21). Recent research suggests other archaeologists applied the same techniques before White (e.g. Hilzheimer 1941); regardless, the seminal work of White (1953) had a significant role in popularising the use of MNI in the subdiscipline of zooarchaeology (Lyman 2016:99–128).

Traditional (vertebrate) MNI

Concerned with questions regarding past subsistence and relative abundances of taxa, White (1953) aimed to understand meat weights by determining the least number of individuals that would have been present in an archaeological assemblage. Using the most prolific elements of each species in an archaeological assemblage and separating these into left, right, and axial elements, White (1953) used the highest count value of non-repetitive elements to calculate what we refer to as the MNI value today. Despite the age of the publication, the basics of the traditional MNI are, to this day, consistently applied in modern vertebrate zooarchaeological research (Grayson 1984; Reitz and Wing 1999).

Archaeomalacological (invertebrate) MNI

Vertebrate individuals are associated with high numbers of skeletal elements, for example, a cow has more than 200 bones, in contrast to invertebrates, which are composed of very few elements. Molluscan remains can consist of a single valve (Gastropoda), two valves (Bivalvia), or up to eight valves (Polyplacophora). This makes calculating the MNI of molluscs less susceptible to the problems of vertebrate MNI quantification, such as 'division into aggregates' (Grayson 1984; Szabó 2009:187). Additionally, the effects of taphonomic processes on invertebrate remains, such as divergent patterns of fragmentation and the leaching of calcium carbonate, may result in biased NISP and weight values for molluscan assemblages. Many invertebrate zooarchaeologists therefore prefer MNI as their main method of quantification over NISP and weight (Harris et al. 2015), whereas some vertebrate zooarchaeologists advocate for the use of NISP over the use of MNI to calculate taxonomic abundances (Grayson 1984; Lyman 1994, 2008, 2019). The inherent differences between vertebrate and invertebrate remains and research led to the development of tailored archaeomalacological methodologies for calculating MNI values of molluscs, such as NRE MNI (Claassen 1998) and more recently tMNI (Harris et al. 2015).

NRE MNI

NRE MNI, or the minimum number of individuals based on non-repetitive elements, is a commonly applied quantification method for invertebrate assemblages. Non-repetitive elements are those which are characteristically different and occur only once per animal, allowing for the researcher to identify the element, as well as quantify the minimum number of individuals needed to account for the number of non-repetitive elements present in an assemblage (Claassen 1998:104; Mason et al. 1998). The non-repetitive elements commonly identified and quantified using this protocol, consisting of one to two NREs per taxon, are detailed in the methods section below. The NRE MNI protocol and variations of it have been applied globally in archaeomalacological research from Africa (e.g. Hunt et al. 2011; Jerardino 1997), Asia (e.g. Brockwell et al.

2020b), Europe (e.g. Hood and Melsæther 2016; Kurzawska et al. 2021), Oceania (e.g. Campbell and Schmidt 2001; Litster et al. 2020), and the Americas (e.g. Barron et al. 2024; Creamer et al. 2011).

In traditional (vertebrate) MNI the results of identification determine the range of NREs present in the assemblage, whereas when applying the NRE MNI methodology, the NREs to-be-counted during identification and quantification are predetermined before the start of the laboratory analysis (Claassen 1998:104; Giovas 2009:1558). By solely focusing on these preselected NREs, other fragments of shell with retained NREs are not included in aggregated counts. This difference in the quantification methods between vertebrate and invertebrate fauna also raises questions as to how comparable these assemblages are within a site when different analytical protocols have been adopted. Since Claassen (1998) proposed the NRE MNI quantification protocol, researchers have critiqued the methodology and proposed innovative new quantification protocols to address some of these limitations.

Giovas (2009) proposed a part-scoring system where, before identification, each type of mollusc shell is subdivided into parts or zones and assigned a code. Using this part-scoring system, multiple parts are considered during quantification resulting in a more detailed frequency count and subsequent MNI value calculation. More recently, Harris et al. (2015) proposed tMNI, a formalised NRE-based quantification protocol expanding upon the original foundations as laid out by NRE MNI. Due to this close relationship between the protocols, NRE MNI and tMNI were selected as the two methodologies compared in this study.

tMNI

Harris et al. (2015) combined elements from the traditional (vertebrate) MNI as popularised by White (1953) and the NRE MNI method to propose a new protocol for molluscan quantification named tMNI. This protocol was developed to aid identification and quantification efforts in the Pacific and Harris et al. (2015) encouraged researchers in other areas to adapt and tailor the tMNI protocol to suit their assemblages. Several studies in Africa, Australia, Europe, and the Pacific have applied and critically examined tMNI since its publication in 2015 (e.g. Faulkner et al. 2022; Lyman 2019; Rogers and Weisler 2021, 2022; Thomas and Mannino 2017; Veth et al. 2017; Weisler and Rogers 2021; Wright 2018; Wright et al. 2023).

The tMNI quantification protocol differs from NRE MNI in three ways: (1) tMNI favours the use of multiple NREs to reflect the assemblage more completely. Harris et al. (2015) detail seven NREs for Gastropoda and five for Bivalvia (see Methods below); (2) during analyses, the entire assemblage is analysed and all NREs are recorded for each taxon; and (3) tMNI calculates MNI values per taxon based on the most frequently occurring NRE after the entire assemblage has been identified and has been divided into site appropriate, mutually exclusive, aggregates, such as stratigraphic layers or cultural phases. Using the tMNI methodology, researchers can directly compare invertebrate to vertebrate remains as both the traditional MNI and tMNI use the most frequently occurring NREs for quantification.

Archaeological and environmental context

Jiigurru (Lizard Island Group)

Jiigurru (Lizard Island Group) is an offshore island group located 33 km off the coast of Cape Flattery, Queensland (Figure 1). The island group has a tropical climate and is surrounded by fringing and barrier reefs, formed during the Holocene. Separating the shores of the islands and islets of Jiigurru is a central tidal lagoon, with a maximum depth of 10 m (Hamylton et al. 2014; Lambrides et al. 2020; Leon et al. 2013; Rees et al. 2006; Saunders et al. 2015; Ulm et al. 2024).

Nearshore ecosystems around Jiigurru include seagrass meadows, coral rubble beds, mangroves, sandy and rocky beaches, and the reef flat of the lagoon, supporting a wide range of intertidal and subtidal marine fauna (Hamylton et al. 2014; McKenzie et al. 1997; Saunders et al. 2015). Molluscan fauna includes bivalves, such as giant clams (Tridacninae), oyster (Ostreidae), scallops (Pectinidae), and venus clams (Veneridae), alongside gastropods, such as top shells (Tegulidae and Trochidae), nerites (Neritidae), conch shells (Strombidae), cowries (Cypraeidae), and cone snails (Conidae) (Braley 2023; Lambrides et al. 2020; Robertson 1981). Additionally, surveys indicate the presence of a wide variety of cephalopods, such as chambered nautiluses (Nautilidae), cuttlefish (Sepiidae), ram's horn squid (Spirulidae), and octopuses (Octopodidae), and several families of Polyplacophora (including Chitonidae and Schizochitonidae) (Robertson 1981; Roper and Hochberg 1987).

Jiigurru, unlike many of its northern Great Barrier Reef counterparts, has been the subject of extensive archaeological inquiry, spanning the past 50 years (Beaton 1973, 1978; Fitzpatrick et al. 2018; Lambrides et al. 2020; Lentfer et al. 2013; Mills 1992; Specht 1978; Tochilin et al. 2012; Ulm et al. 2019, 2024). The earliest surveys were undertaken by Beaton (1973) as part of broader investigations into islands of the northern Great Barrier Reef; surveys continue to be undertaken under the banner of the Lizard Island Archaeological Project, set up by Ulm and McNiven with Dingaal and Nguurruumungu

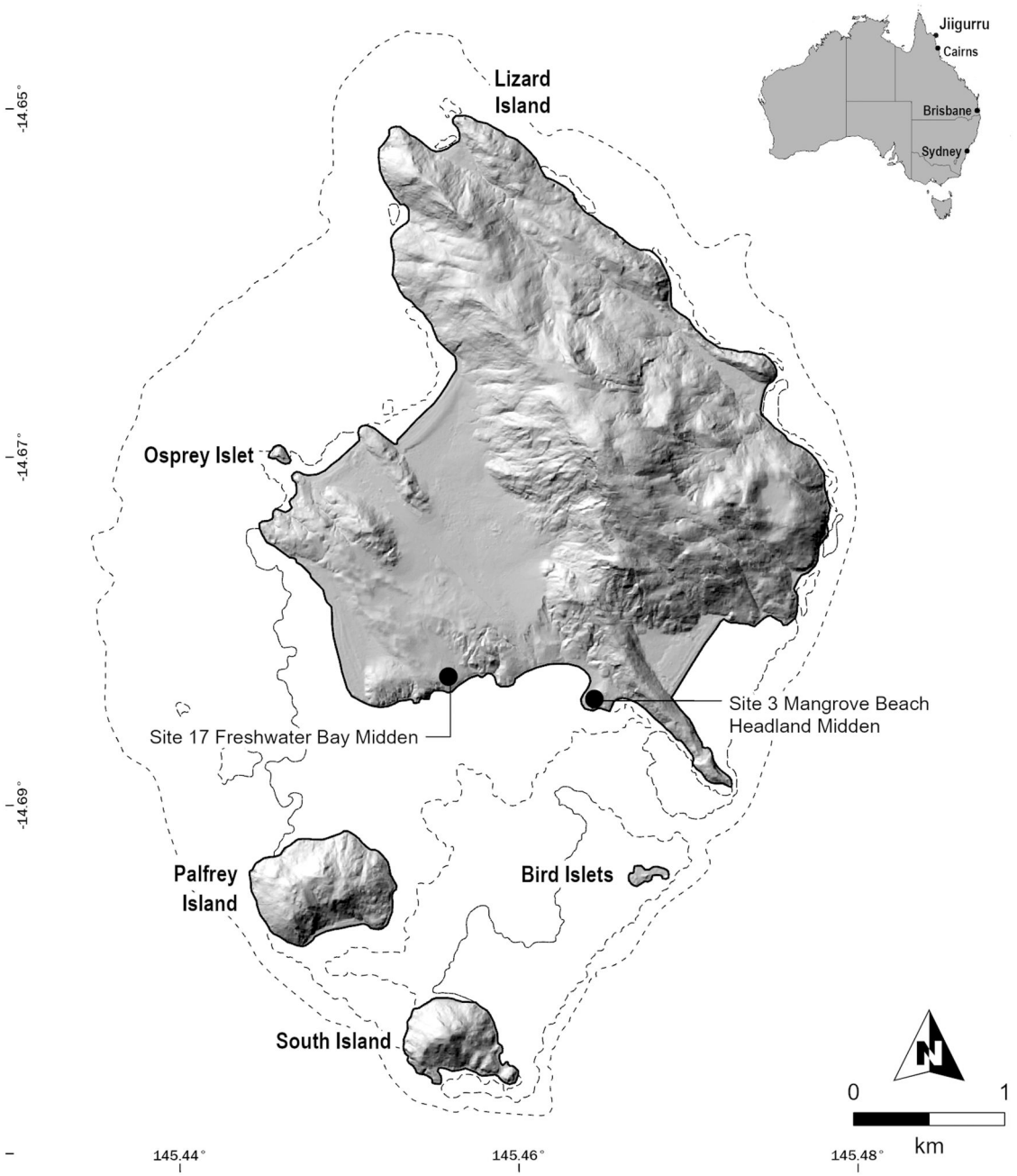

Figure 1. Map of Jiigurru (Lizard Island Group) showing the locations of Site 17 Freshwater Bay Midden (FBM) and Site 3 Mangrove Beach Headland Midden (MBHM).

Traditional Owners in 2012 (Lambrides et al. 2020; Ulm et al. 2024).

Three midden sites have been excavated across Jiigurru: Site 3 Mangrove Beach Headland Midden (Lambrides et al. 2020) and Site 17 Freshwater Bay Midden (Lentfer et al. 2013; Mills 1992; this study) on Lizard Island and South Island Headland Midden on South Island (Ulm et al. 2024). Molluscan assemblages from the sites of Mangrove Beach Headland Midden and Freshwater Bay Midden are the materials used in this study (Figure 1).

Site 3 Mangrove Beach Headland Midden

Site 3 Mangrove Beach Headland Midden (MBHM) is located on the southern side of Lizard Island, close to the lagoon (Figure 1). In 2013, Mangrove Beach Headland Midden was excavated as part of the Lizard Island Archaeological Project (Figure 2) (Lambrides et al. 2020). A 1 m x 1 m square was excavated to a depth of 1.52 m in 59 excavation units (arbitrary layers of c.2 cm). A total of six stratigraphic units were determined. During excavation, efforts were made to separate stratigraphic units with excavation units, however, blurred boundaries between stratigraphic units complicated this separation. All excavated material was weighed and dry and wet sieved using a 2.36 mm mesh. Radiocarbon ages available for MBHM show occupation at the site between c.4,000 and c.500 years ago (Lambrides et al. 2020:52). The molluscan assemblage was first used in Ulm et al. (2019) and

Figure 2. Jiigurru (Lizard Island Group) site photos. (A) Site 3 Mangrove Beach Headland Midden (MBHM) excavation in 2013. Photograph taken during the excavation (XU1), camera facing west towards Mangrove Beach and Site 17 Freshwater Bay Midden (FBM) (Photograph: Ian McNiven, 2013). (B) Site 17 Freshwater Bay Midden (FBM) excavation in 2022. Drone photograph taken at completion of excavation, drone camera facing south towards Blue Lagoon, Palfrey Island (top right), and South Island (top middle) (Photograph: Joshua Connelly, 2022).

later published in Lambrides et al. (2020). The MBHM identification and quantification results, as published by Lambrides et al. (2020), will be used in this study.

Site 17 Freshwater Bay Midden

Site 17 Freshwater Bay Midden (FBM) is also located on the southern side of Lizard Island, about a kilometre to the west of MBHM. Freshwater Bay Midden has been the subject of extensive archaeological inquiry with excavations taking place in 1992 (Mills 1992) and 2009 (Lentfer et al. 2013). More recently, a 1 m x 1 m square was excavated to a depth of 1.34 m in 62 excavation units in 2022 (Figure 2). A total of seven stratigraphic units were determined. Similarly to MBHM, blurred boundaries between stratigraphic units made efforts to separate stratigraphic units with excavation units difficult. All excavated material was weighed and dry and wet sieved using a 2.36 mm mesh. Radiocarbon ages from the 1992 and 2009 excavations of FBM show the earliest evidence for discard of cultural activity at the site c.3500 years ago with the surface of the

site dating to the recent past (Lentfer et al. 2013:145; Mills 1992:66–67). The molluscan assemblage used in this study is the assemblage excavated during the 2022 field season and has not previously been reported.

Methods

Identification protocols

Identifications of the molluscan remains were undertaken using the Tropical Archaeology Research Laboratory mollusc reference collection at the James Cook University Nguma-bada campus in Cairns. In cases of species gaps in the reference collection, Food and Agriculture Organisation (FAO) manuals were consulted to aid identifications (Carpenter and Niem 1998). Taxonomic identifications use binomial nomenclature in accordance with the online World Register of Marine Species (WoRMS) database (Bernot et al. 2024).

Quantification protocols

The following NRE MNI and tMNI quantification protocols were applied to the molluscan assemblage from FBM and MBHM to test their efficacy for Jiigurru molluscan assemblages. To ensure exclusivity when quantifying specimens to the level of species, genus, and family, the same NREs are used between potentially overlapping taxonomic categories (i.e. *Tridacna* and *Tridacna maxima*) for both the NRE MNI and tMNI methodology.

NRE MNI quantification protocol

The NRE MNI methodology applied in this study combines the traditionally used NREs as outlined in Claassen (1998:106–107) and Giovas (2009:1558). Gastropoda were identified according to their apices, the umbo and hinge were used for Bivalvia, as well as the posterior and anterior valves for Polyplacophora (Figure 3). To be included in the quantification, an NRE needs to be >50% complete. MNI was calculated using the most frequently occurring NRE per taxon.

tMNI quantification protocol

The tMNI quantification protocol applied in this study broadly follows the conventions outlined in Harris et al. (2015), which has a focus on Pacific taxa, with several additions to suit the Australian coral reef assemblages from FBM and MBHM.

The original non-repetitive elements for Gastropoda included in Harris et al. (2015) are: (1) spire; (2) anterior notch/canal; (3) posterior notch/canal; (4) outer lip; (5) aperture; (6) operculum; and (7) umbilicus (Figure 4). Harris et al. (2015) describe additional NREs for the families Cypraeidae and Neritidae. For Neritidae, these NREs include (8) intersection of the anterior columellar deck and the outer lip; and (9) intersection of the posterior columellar deck and the outer lip (Figure 4). For Cypraeidae, the base and labum have been identified as NREs (not represented in Figure 4). For Bivalvia, the following non-repetitive elements were proposed: (1) umbo; (2) posterior hinge; (3) anterior hinge; (4) posterior adductor muscle scar; and (5) anterior adductor muscle scar (Figure 5).

Note the absence of the anterior adductor muscle scar in Figure 5 as the species depicted are monomyarian in nature, possessing only the posterior adductor muscle and associated muscle scar. Figures 4 and 5 have been redrawn to illustrate species forms more commonly found in Australian coral reef assemblages.

Newly designated NREs for Australian coral reef assemblages are detailed further below and include the stromboid notch for the gastropod family Strombidae, the anterior, intermediate, and posterior valves for Polyplacophora, the umbilicus, outer lip,

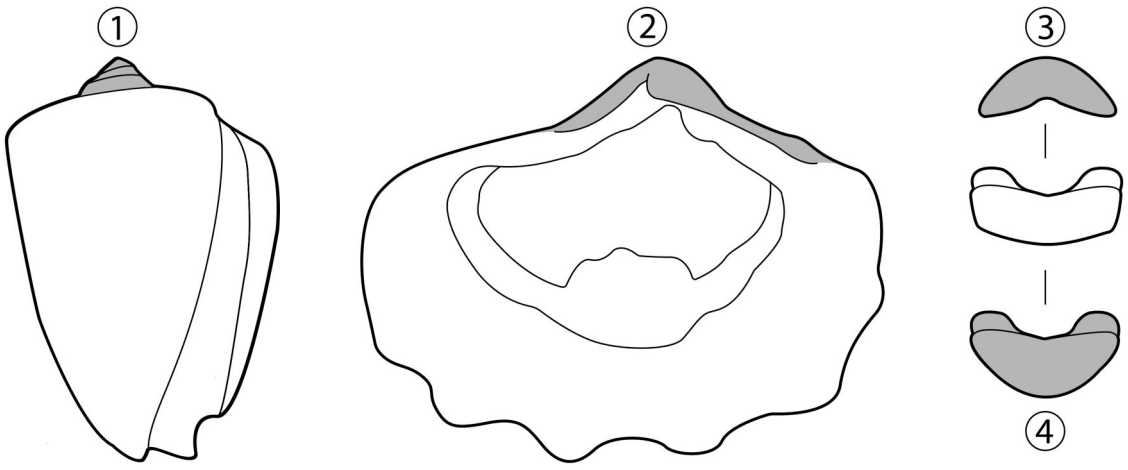

Figure 3. Non-repetitive elements used for the NRE MNI quantification protocol. Left: Gastropoda NRE (1 = spire) (ventral view), middle: Bivalvia NRE (2 = umbo/hinge) (right valve, ventral view), and right: Polyplacophora NRE (3 = anterior valve; 4 = posterior valve) (distal view).

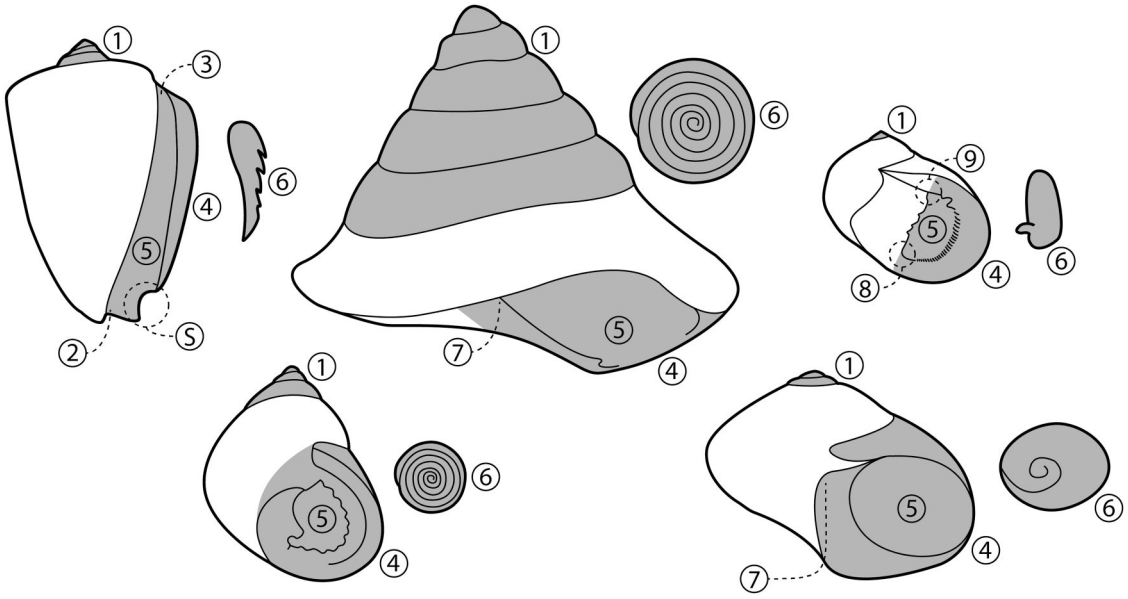

Figure 4. Non-repetitive elements for Gastropoda per the tMNI quantification protocol (1 = spire; 2 = anterior notch/canal; 3 = posterior notch/canal; 4 = outer lip; 5 = aperture; 6 = operculum; 7 = umbilicus; 8 = intersection anterior columellar deck/outer lip; 9 = intersection posterior columellar deck/outer lip; S = stromboid notch). The species depicted (ventral view) are *Conomurex luhuanus* (top left), *Rochia nilotica* (top middle), *Nerita undata* (top right), *Monodonta labio* (bottom left), and *Lunella cinerea* (bottom right).

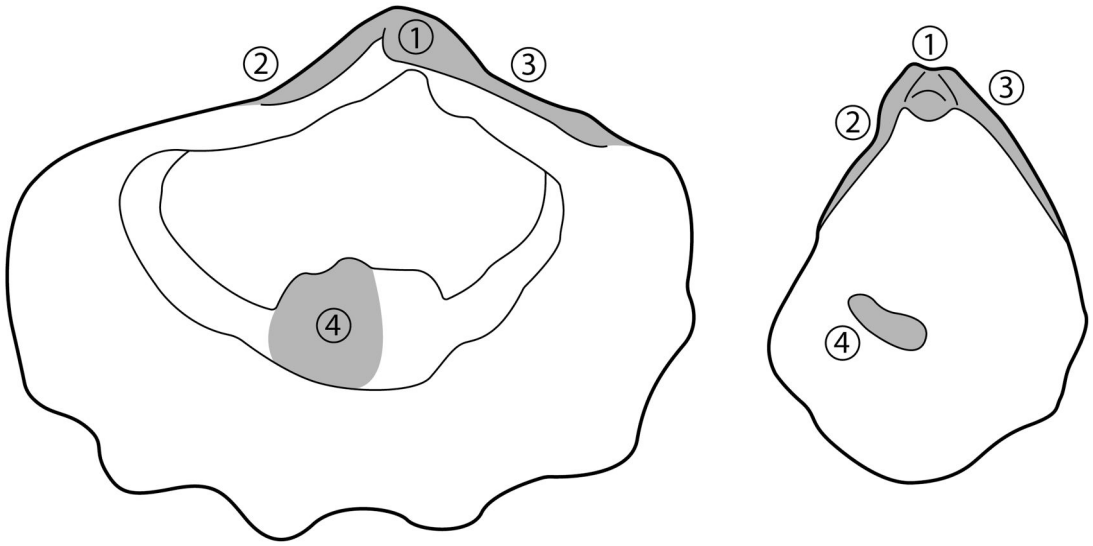

Figure 5. Non-repetitive elements for Bivalvia per the tMNI quantification protocol (1 = umbo; 2 = posterior hinge; 3 = anterior hinge; 4 = posterior adductor muscle scar). Note the absence of the anterior adductor muscle scar in this figure as the species depicted are monomyarian. The species depicted (right valve, ventral view) are *Tridacna maxima* (left) and *Saccostrea cucullata* (right).

and aperture for Nautilidae, and the anterior-ventral portion and posterior-ventral cones and spine for Sepiidae cuttlebone.

Newly designated NREs for Australian coral reef assemblages

Strombidae

Stromboid Notch: Most adolescent and adult specimens of species in the family Strombidae have an additional notch along the outer lip, close to the anterior canal, known as the stromboid notch. This notch allows for the shorter right eye stalk of the organism to extend from the shell (Beesley et al. 1998). As the stromboid notch is part of the outer lip, another NRE utilised by Harris et al. (2015) in the quantification of gastropods, the counts for Strombidae might be duplicated with both NRE being recorded; however, without the stromboid notch, outer lips for these taxa will generally be unidentifiable, minimising this issue. The stromboid notch needs to be whole and intact for this NRE to be counted for MNI (Figure 4).

Polyplacophora

Polyplacophora, more commonly known as chitons, are a molluscan Class that are exclusively marine-based and are found in intertidal and shallow subtidal zones, and in the deep sea. The shell of Polyplacophora consists of eight overlapping calcareous plates, embedded in the mantle or girdle by the apophyses (two lobed extensions on the anterior of the valve), which serve as protection from potential predators while remaining flexible enough for movement across rocky surfaces (Ruppert et al. 2004:292–298). Valve terminology separates the eight valves into the anterior valve, six intermediate valves, and the posterior valve (Schwabe 2010). These terms align with the NREs designated below (Figure 6).

Anterior valve: The anterior valve, also known as the head valve and valve i, is the valve closest to the mouth of the organism and tends to be recognisable in species as the only valve without apophyses, by its usually crescent-like to semi-circular shape, and by the posterior presence of a raised apex or semi-circular notch (Giovas 2009; Schwabe 2010). More than 50% of the anterior valve needs to be present and must include the posterior apex or notch to be counted for MNI (Figure 6).

Intermediate valves: The intermediate valves, also known as valves ii-vii, are the six valves covering the organism between the anterior valve and the posterior valve. These can be recognised by their shape, the presence of oblique muscle scars, and by the presence of two apophyses (Giovas 2009; Schwabe 2010). The valve needs to be >50% complete and must include the area between apophyses or jugal laminae to be identified, however, these valves cannot directly contribute to MNI as it is difficult to distinguish between most of the intermediate valves (Figure 6).

For some species, including the frequently encountered giant gem chiton (*Acanthopleura gemmata*) the second valve, or valve ii, can be diagnostic, as this valve is the only valve to have a w-shaped central callus and jugal area. If this characteristic is identified and the element is >50% complete, the valve can be counted towards MNI (Figure 6).

Posterior valve: The posterior valve, also known as the tail valve and valve viii, is the valve closest to the anus of the organism and is the only valve to grow from a central point outward. This central point is usually still present on the posterior valve in the shape of a small protrusion known as the mucro (Giovas 2009; Schwabe 2010). Additionally,

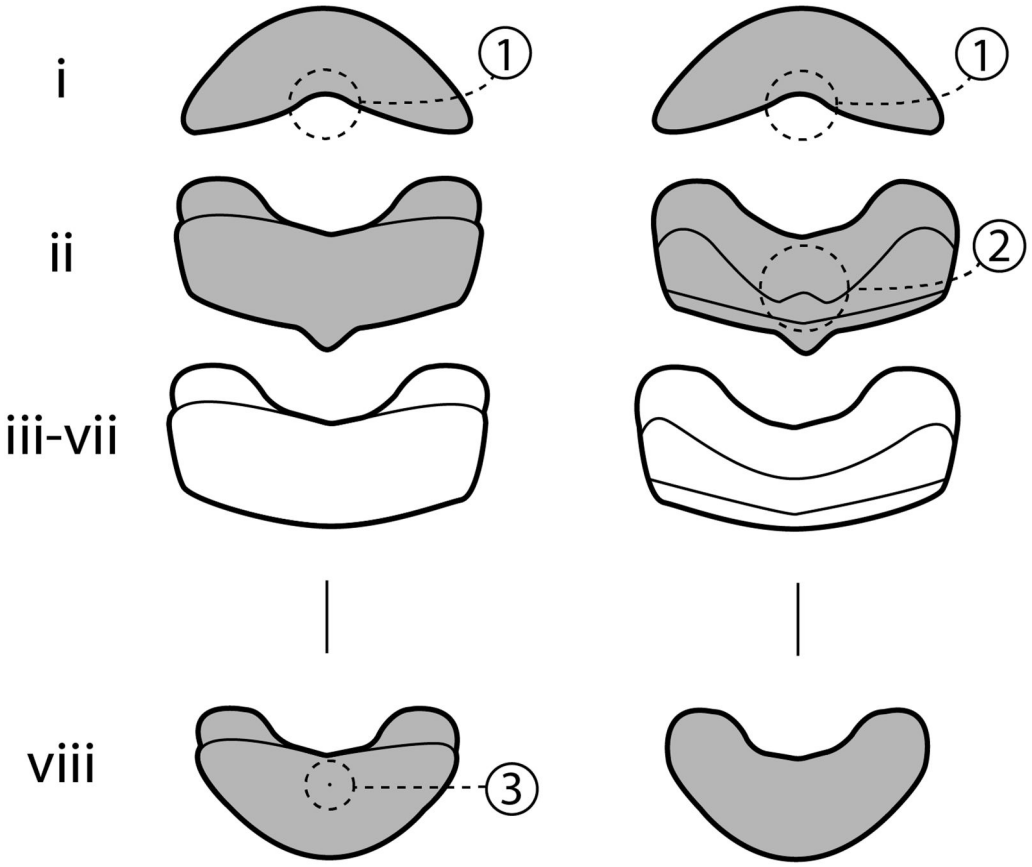

Figure 6. Non-repetitive elements for Polyplacophora per the tMNI quantification protocol (1 = posterior apex/notch of the anterior valve; 2 = w-shaped central callus and jugal area; 3 = mucro of the posterior valve). Species depicted (left column distal view, right column ventral view) is *Acanthopleura gemmata*. Valve i represents the anterior valve, valves ii-vii represent the intermediate valves, and valve viii represents the posterior valve.

the posterior valve can be identified by the presence of two apophyses. More than 50% of the valve, including the mucro, needs to be present to count the valve for MNI (Figure 6).

Cephalopoda

Cephalopod remains are rare in archaeological deposits due to taphonomic processes or foraging preferences, but their presence can inform our understanding of foraging strategies, cultural practices, and targeted habitats. The hard part remains of cephalopods can be classified broadly into three categories: (1) external structures, such as Nautilidae shell; (2) internal structures including Sepiidae cuttlebone and the shell of *Spirula spirula*; and (3) chitin beaks and gladia, or pens, like ones found in other Decapodiformes (Somerville et al. 2017:217). The designated NREs attributed in this paper will focus on the external and internal structures of Nautilidae and Sepiidae.

Nautilidae

Nautilidae is a family of ectocochleate (external shell-bearing) cephalopods comprising the genera *Allonautilus* and *Nautilus* (Ward and Saunders 1997). All members of Nautilidae have an external shell consisting of a body chamber, where the organism resides, and the phragmocone, the internal chambered portion of the shell, which allows for the regulation of buoyancy of the organism through the exchange of gases and fluids between phragmocone chambers (Ruppert et al. 2004:346–348). Due to similarities between the shell morphology of Nautilidae and Gastropoda, the same terminology is used for both taxa. Three NREs were designated for Nautilidae shell: (1) umbilicus; (2) outer lip; and (3) aperture (Figure 7).

Umbilicus: The umbilicus in Gastropoda is a depression where the shell coils around the central columella. What differentiates the umbilicus of Nautilidae from that of Gastropoda is the presence of a left and right umbilicus due to the lateral symmetry of the Nautilus shell. For this NRE to be counted, not only will at least one umbilicus have to be present, more than 50% of the internal phragmocone structure between both umbilici will have to be present as well (Figure 7).

Outer Lip: The outer lip is the edge along the opening of Gastropoda and Nautilidae shells. Though the outer lip of gastropods might have additional structure, the Nautilidae shell is thin and smooth. More than 50% of the outer lip needs to be present to be able to count the NRE for MNI (Figure 7).

Aperture: The aperture is the opening of the shell, which includes the outer lip and the body chamber up until the second chamber in the Nautilus shell. To be able to count the aperture as an NRE for MNI, at least 50% of the outer lip and body chamber needs to be present. While this NRE includes the outer lip NRE noted above, Harris et al. (2015) note that recording the aperture of Gastropoda can aid in taphonomic studies (Figure 7).

Sepiidae

The endocochleate (internal shell-bearing) family Sepiidae (cuttlefish) has a calcareous internal shell, known as the cuttlebone or sepion, which allows for regulation of buoyancy for cuttlefish through gas and fluid regulation in the inner sepion chambers (Ruppert et al. 2004:343–367). Despite critiques on the possibility of using cuttlebone to identify species due to intraspecies variation in cuttlebone (Lu 1998), the method remains commonly used to assist species identification in the absence of soft parts of the animal (Jereb and Roper 2005; Neige 2006; Salvador et al. 2021). Two NREs were designated for the sepion: (1) the anterior-ventral portion; and (2) the posterior-ventral cones and spine, whenever present (Figure 8).

The anterior-ventral portion: The anterior-ventral portion generally consists of a thin outer cone and the last loculus above the striated zone and varies widely in shape. To count this NRE for MNI, at least 50% of the outer curvature of the anterior portion of the sepion and the anterior tip of the cuttlebone needs to be present (Figure 8).

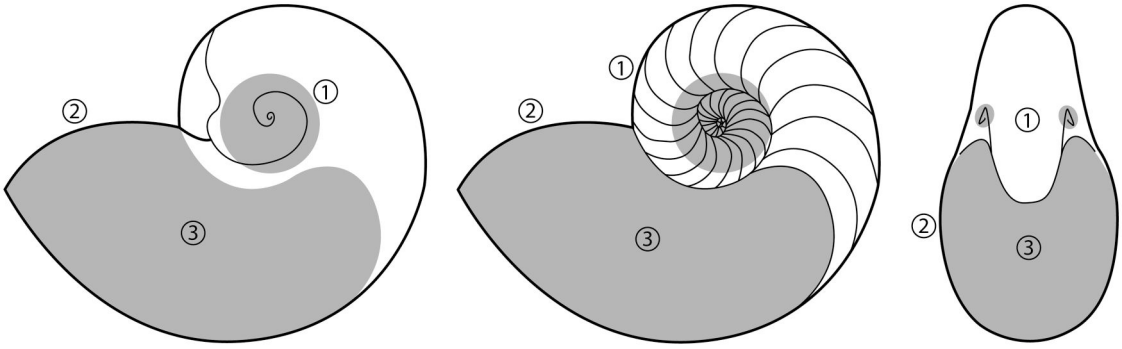

Figure 7. Non-repetitive elements for Nautilidae shell per the tMNI quantification protocol (1 = umbilicus; 2 = outer lip; 3 = aperture). Left (lateral view), middle (lateral cross-section with internal phragmocone structure exposed), and right (ventral view).

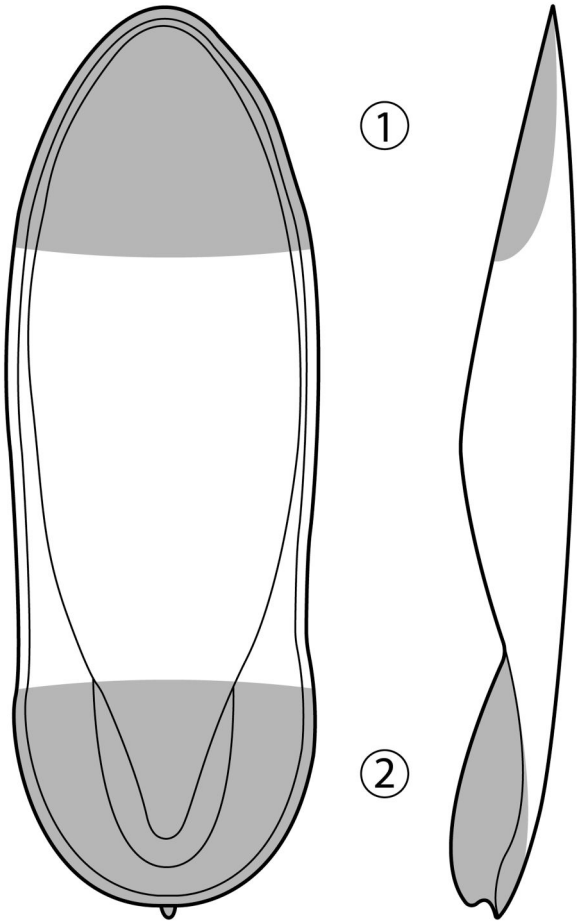

Figure 8. Non-repetitive elements for Sepiidae sepion per the tMNI quantification protocol (1 = anterior-ventral portion; 2 = posterior-ventral cones and rostrum). Left (ventral view) and right (lateral view).

The posterior-ventral inner cone, outer cone, and rostrum: The posterior-ventral portion of the sepion commonly consists of an inner and outer cone which are considered as diagnostic for species identification. Greater than 50% of the curvature of the inner and outer cone needs to be present for this NRE to count. Several cuttlefish species have an additional spine, or rostrum, on the posterior end of the cuttlebone which should be included if present in the species (Figure 8).

Testing efficacy

To determine whether the NRE MNI or the tMNI quantification protocol was the more efficacious protocol for Jiigurru molluscan assemblages, differences in total MNI values, rank order abundances, statistical analyses, element frequencies, and a habitat comparison are used.

Through the application of both protocols to the two assemblages, total MNI values for the site were calculated. Using these values, rank order abundances were created. Comparisons between the rank order abundances show the degree of influence quantification protocols have over relative abundances.

Species diversity, evenness, and richness were calculated using NTAXA and several statistical analyses using PAST software (version 4.17). NTAXA (number of taxa) tests the species richness, or the number of identified taxa in the assemblages, by using the highest common taxonomic level per taxon to ensure the results are not inflated by taxa which might be easier to identify. An example would be to use Strombidae instead of separately using *Conomurex luhuanus, Lambis lambis*, and Strombidae.

Diversity and evenness were tested using several diversity indices including Simpson's index of dominance (1-*D*), the Shannon-Weiner index of diversity (H'), Shannon's index of evenness (E), and Fisher's alpha (α). Simpson's index of dominance measures the degree of dominance by a single species with values ranging between 0 and 1, with values closer to 0 representing a molluscan assemblage dominated by a single species and values closer to 1 indicating an assemblage with a more even spread of taxa (Magurran 2004:114–116). The Shannon-Weiner index of diversity reflects the diversity and richness within an assemblage and has values ranging between 0 and 5, with values most commonly falling between 1.5 and 3.5. Values closer to 0 reflect a lower diversity and richness within an assemblage and values closer to 5 reflecting the opposite, a higher diversity and richness (Reitz and Wing 1999:102–106). Shannon's index of evenness has values ranging between 0 and 1 and is similar to Simpson's index of dominance, with values closer to 0 representing an assemblage dominated by a single taxon, however, values closer to 1 differ by reflecting a more even spread of many taxa with similar numbers of individuals (Reitz and Wing 1999:102–106). Fisher's α tests the diversity of an assemblage, independently from sample size, by foregrounding taxa represented by a single individual, with higher α values reflecting more diverse assemblages (Harris et al. 2016:224; Hayek and Buzas 2010:290–296). Through random permutation tests, the significance of the results between FBM and MBHM was tested.

Lastly, NRE element frequencies were calculated to understand the degrees of information each quantification protocol provides.

Results

Close to 20,000 molluscan fragments were recovered from the excavation of FBM in 2022 ($n = 7{,}248$) and MBHM in 2013 ($n = 11{,}127$). Following taxonomic identification, a NISP of 1,380 was determined for the FBM assemblage and 5,827 for the MBHM

assemblage. Both sites are dominated by the same marine gastropod species, *Conomurex luhuanus*.

During the identification of the molluscan assemblages from FBM and MBHM, several taxa were identified based on elements that could not be designated as a NRE, such as surface sculpture and morphology. These taxa, though present in the assemblage, were unable to be quantified per the two outlined NRE-based MNI protocols included in this study and are therefore not attributed an MNI value. For FBM, the taxa Vermetidae, Volutidae, *Anadara antiquata*, and *Tridacna* were excluded from the analyses. For MBHM, families Vermetidae, Muricidae, and Sepiidae, and species *Hippopus hippopus* and *Periglypta puerpera* were excluded.

To maintain exclusivity in the aggregated counts, several taxa had to be excluded from the below MNI analyses; these consist of the specimens identified to the family-level taxon Strombidae for the FBM assemblage and the specimens identified to the family-level taxon Strombidae and genus-level taxon *Nerita* for the MBHM assemblage.

Total MNI

The total MNI values of the FBM and MBHM assemblages were calculated using the NRE MNI and tMNI protocols by aggregating at the square level (i.e. a single aggregation unit to ensure comparability between sites). Based on site level total MNI values, an overall increase of around 3% can be seen in the assemblages when the tMNI protocol is applied (Table 1). Total MNI values per Class show that applying tMNI to both sites results in either the same or higher MNI values when compared to NRE MNI (Table 1). The dominance of Gastropoda in both FBM and MBHM is evident, coinciding with the highest disparity between total MNI values per Class identified for Gastropoda.

Table 1. MNI per class and total MNI for the NRE MNI and tMNI protocols for the FBM and MBHM assemblages when aggregated to the level of the excavation square.

	FBM		MBHM	
Class	NRE MNI	tMNI	NRE MNI	tMNI
Gastropoda	885	905	1,242	1,279
Bivalvia	4	9	16	16
Polyplacophora	1	1	1	1
Cephalopoda	0	0	0	1
Total	890	915	1,259	1,297

Rank order abundances

The rank order abundance tables (Tables 2 and 3) show a more marked difference between the application of the NRE MNI and tMNI quantification protocols. All taxa, aside from the excluded ones, identified and quantified are represented in the rank order abundance tables with a maximum of 9 ranks.

Table 2. Rank order abundance table showing the rank orders for the FBM assemblage using NRE MNI and tMNI protocols.

NRE MNI			tMNI		
Rank	Taxon	MNI	Rank	Taxon	MNI
1	*Conomurex luhuanus*	646	1	*Conomurex luhuanus*	646
2	Subulinidae	200	2	Subulinidae	200
3	Helicarionidae	12	3	Helicarionidae	12
4	Pupillidae	11	4	*Monodonta labio*	11
5	Camaenidae	8		Pupillidae	11
6	*Rochia nilotica*$^{\vee}$	4	5	*Rochia nilotica*$^{\wedge}$	8
	Lambis lambis$^{\wedge}$	4		Camaenidae	8
7	Mytilidae$^{\wedge}$	2	6	Ostreidae	4
8	*Acanthopleura* sp.$^{\wedge}$	1	7	*Lambis lambis*$^{\vee}$	3
	Hippopus hippopus$^{\wedge}$	1	8	*Lambis* sp.	2
	Tridacna maxima$^{\wedge}$	1		Mytilidae$^{\vee}$	2
			9	*Acanthopleura* sp.$^{\vee}$	1
				Turbinidae	1
				Nerita sp.	1
				Conidae	1
				Rhytididae	1
				Saccostrea scyphophilla	1
				Hippopus hippopus$^{\vee}$	1
				Tridacna maxima$^{\vee}$	1

Light shading indicates a shift in rank order between the two protocols. Dark shading indicates a taxon not documented by the NRE MNI protocol. The symbol $^{\vee}$ indicates a shift downwards compared to the other protocol, whereas the symbol $^{\wedge}$ indicates a shift upwards compared to the other protocol.

Table 3. Rank order abundance table showing the rank orders for the MBHM assemblage using NRE MNI and tMNI protocols.

NRE MNI			tMNI		
Rank	Taxon	MNI	Rank	Taxon	MNI
1	*Conomurex luhuanus*	1,201	1	*Conomurex luhuanus*	1,201
2	*Rochia nilotica*	20	2	*Rochia nilotica*	44
3	*Tridacna maxima*	10	3	*Lambis* sp.$^{\wedge}$	10
4	*Lambis lambis*$^{\wedge}$	9		*Tridacna maxima*	10
5	*Nerita polita*	5	4	Tegulidae	6
6	Rhytididae	3	5	*Nerita polita*	5
	Tridacna crocea	3		*Lambis lambis*$^{\vee}$	5
7	*Acanthopleura gemmata*	1	6	Rhytididae	3
	Monodonta labio	1		*Tridacna crocea*	3
	Nerita costata	1	7	*Acanthopleura gemmata*	1
	Lambis sp.$^{\vee}$	1		*Monodonta labio*	1
	Conus sp.	1		*Nerita costata*	1
	Ostreidae	1		*Thais* sp.	1
	Tridacna gigas	1		*Conus* sp.	1
	Tridacna sp.	1		Conidae	1
				Ostreidae	1
				Tridacna gigas	1
				Tridacna sp.	1
				Nautilus sp.	1

Light shading indicates a shift in rank order between the two protocols. Dark shading indicates a taxon not documented by the NRE MNI protocol. The symbol $^{\vee}$ indicates a shift downwards compared to the other protocol, whereas the symbol $^{\wedge}$ indicates a shift upwards compared to the other protocol.

Rank order abundance—Freshwater Bay Midden

The application of the tMNI protocol to the FBM assemblage causes a slight shift in the rank order abundance, partially due to higher MNI values for *Rochia nilotica*, as seen below (Table 2). Additionally, several families ($n = 4$), genera ($n = 2$), and species ($n = 2$) were only reported when the

tMNI methodology was applied, albeit in limited quantities ranging between 1 and 11 specimens. The application of the tMNI methodology results in a similar or higher MNI for most identified taxa.

Rank order abundance—Mangrove Beach Headland Midden

Applying the tMNI protocol for the MBHM assemblage resulted in a smaller shift in the rank order abundance compared to the FBM assemblage. A total of two taxa reported altered rank-order abundance (Table 3). Several families ($n = 2$) and genera ($n = 2$) only had MNI recorded using the tMNI protocol. Similar to the rank order abundance trend seen for the FBM assemblage, the application of tMNI shows the same or higher MNI values for most taxa.

Species evenness and richness

Significant differences between the application of NRE MNI and tMNI quantification protocols at both sites are apparent when statistical analyses are applied (Table 4).

For the FBM assemblage, NTAXA, the Shannon-Weiner index of diversity, and the Fisher's α index show a statistically significant increase in diversity and richness using the tMNI protocol. It is important to note that the Shannon-Weiner index values between 1.5 and 3.5 are the most common; both the NRE MNI and tMNI values for FBM are below 1, highlighting the dominant nature of *Conomurex luhuanus* in the assemblage.

For the MBHM assemblage, the results of the diversity indices present values correlated with a more even and diverse assemblage where the tMNI protocol is applied. NTAXA and Fisher's α show a relative, not statistically significant, increase in diversity and evenness, whereas Simpson's index of dominance, the Shannon-Weiner index of diversity, and Shannon's index of evenness show a statistically significant increase in assemblage diversity, evenness, and richness. The assemblage itself remains dominated by *Conomurex luhuanus*, however, the application of tMNI over NRE MNI shows the assemblage to be slightly more even, with more taxa represented and a higher abundance of unique taxa (i.e. taxa represented by single individuals).

Table 4. Results of diversity indices [NTAXA, Simpson's index of dominance (1-*D*), Shannon-Weiner index of diversity (*H'*), Shannon's index of evenness (*E*), and Fisher's α] detailing species diversity, evenness, richness for FBM and MBHM.

	FBM			MBHM		
	NRE MNI	tMNI	*p*	NRE MNI	tMNI	*p*
NTAXA	11	17	0.0156	11	13	0.4705
1-*D*	0.5778	0.5469	0.1904	0.9105	0.8592	0.004
H'	0.808	0.9467	0.0154	0.2667	0.3785	0.0106
E	0.3369	0.3341	0.9124	0.1112	0.1476	0.0291
α	1.767	2.964	0.0145	1.658	2.009	0.3612

Shading indicates statistical significance (*p*), tested using random permutation tests.

Non-repetitive element frequencies

Results show the most frequently occurring non-repetitive element in the FBM molluscan assemblage is the spire for Gastropoda, the posterior adductor muscle scar for Bivalvia, and the intermediate valve for Polyplacophora. When compared to the NREs that the NRE MNI protocol uses to establish MNI values, tMNI results for the FBM assemblage show that the spire is indeed the most prolific of gastropod elements to be preserved, however solely using the spire excludes taxa, such as *Monodonta labio*, Turbinidae, *Nerita*, Conidae, and Rhytididae from the NRE MNI protocol results (Table 5). For bivalves in the FBM assemblage, the posterior adductor muscle scar is most frequently counted, meaning the Ostreidae family, and specifically *Saccostrea scyphophilla*, would have been underrepresented using an NRE MNI approach (Table 6). Polyplacophora itself is not influenced by the use of either NRE MNI or tMNI methodology as the MNI value for both protocols remains 1 (Table 7).

Results for the MBHM molluscan assemblage show the most frequently occurring non-repetitive element being the spire for Gastropoda, the posterior hinge for Bivalvia, the anterior valve for Polyplacophora, and the umbilicus for Cephalopoda (Nautilidae) (Tables 5–8). The spire is, again, the most abundant NRE element found using both the NRE MNI and tMNI approaches, however Tegulidae, *Nerita*, *Thais*, and Conidae specimens would not have been reported using a traditional NRE MNI approach due to the absence of associated spires in the assemblage. Bivalve and chiton MNI results would have been the same regardless of the quantification protocol applied. The Nautilidae umbilicus would not have been included in the analyses if an NRE MNI protocol were to be applied, as it would not have been a predetermined NRE.

Table 9 shows the difference in the number of identified NREs for the FBM and MBHM assemblage when using the NRE MNI and tMNI protocols; results show more information is recorded when the tMNI protocol is applied at both sites (Table 9). This information can, in turn, be used to inform other analyses, such as studies on taphonomy and differential fragmentation between taxa.

Table 5. Identified non-repetitive elements of Gastropoda from the FBM and MBHM assemblages using the NRE MNI and modified tMNI protocols.

FBM											
Taxon	NRE MNI	tMNI	NISP	SPI	ANC	PNC	OUL	APE	OPE	UMB	STN
Conomurex luhuanus	646	646	650	646	291	141	45	4	0	–	0
Subulinidae	200	200	217	200	191	192	191	187	–	–	–
Strombidae	5	48	198	5	0	0	48	0	0	–	48
Helicarionidae	12	12	13	12	–	–	6	6	–	12	–
Monodonta labio	0	11	26	0	–	–	11	0	0	1	–
Pupillidae	11	11	12	11	11	11	11	10	–	0	–
Rochia nilotica	4	8	54	4	–	–	6	1	0	8	–
Camaenidae	8	8	8	8	–	–	5	5	–	8	–
Lambis lambis	4	3	11	4	3	1	3	1	0	–	0
Lambis sp.	0	2	8	0	0	1	2	0	0	–	0
Turbinidae	0	1	1	0	–	–	0	0	1	0	–
Nerita sp.	0	1	1	0	0	0	1	0	0	–	–
Conidae	0	1	1	0	1	0	0	0	0	–	–
Rhytididae	0	1	1	0	–	–	0	0	–	1	–

MBHM											
Taxon	NRE MNI	tMNI	NISP	SPI	ANC	PNC	OUL	APE	OPE	UMB	STN
Conomurex luhuanus	1,201	1,201	1,726	1,201	421	316	195	177	0	–	0
Rochia nilotica	20	44	65	20	–	–	20	20	0	44	–
Lambis lambis	9	5	26	9	5	12	13	8	0	–	0
Lambis sp.	1	10	71	1	10	1	1	2	0	–	0
Strombidae	8	8	119	8	8	0	0	0	0	–	0
Tegulidae	0	6	2,946	0	–	–	0	0	0	6	–
Nerita polita	5	5	8	5	3	2	2	2	0	–	–
Rhytididae	3	3	7	3	–	–	1	1	–	3	–
Nerita spp.	0	2	9	0	2	2	2	1	0	–	–
Monodonta labio	1	1	14	1	–	–	0	0	0	0	–
Nerita costata	1	1	1	1	0	0	0	0	0	–	–
Thais sp.	0	1	2	0	1	0	1	1	0	–	–
Conus sp.	1	1	1	1	1	0	0	0	0	–	–
Conidae	0	1	1	0	1	0	0	0	0	–	–

SPI: spire; ANC: anterior notch/canal; PNC: posterior notch/canal; OUL: outer lip; APE: aperture; OPE: operculum; UMB: umbilicus; STN: stromboid notch.
Shading indicates the exclusion of the taxon from the MNI and habitat analyses.

Table 6. Identified non-repetitive elements of Bivalvia from the FBM and MBHM assemblages using the NRE MNI and modified tMNI protocols.

FBM								
Taxon	NRE MNI	tMNI	NISP	UMB	POH	ANH	PAM	AAM
Ostreidae	0	4	57	0	0	0	8	–
Mytilidae	2	2	3	2	2	2	3	2
Saccostrea scyphophilla	0	1	4	0	0	0	1	–
Hippopus hippopus	1	1	1	0	0	1	0	–
Tridacna maxima	1	1	1	1	1	1	1	–

MBHM								
Taxon	NRE MNI	tMNI	NISP	UMB	POH	ANH	PAM	AAM
Tridacna maxima	10	10	24	12	16	13	7	–
Tridacna crocea	3	3	4	4	4	4	2	–
Ostreidae	1	1	19	1	1	1	2	–
Tridacna gigas	1	1	1	1	1	1	0	–
Tridacna sp.	1	1	173	0	1	0	0	–

UMB: umbo; POH: posterior hinge; ANH: anterior hinge; PAM: posterior adductor muscle scar; AAM: anterior adductor muscle scar.

Table 7. Identified non-repetitive elements of Polyplacophora from the FBM and MBHM assemblages using the NRE MNI and modified tMNI protocols.

FBM							
Taxon	NRE MNI	tMNI	NISP	AV	IV	IVii	PV
Acanthopleura sp.	1	1	3	0	2	0	1

MBHM							
Taxon	NRE MNI	tMNI	NISP	AV	IV	IVii	PV
Acanthopleura gemmata	1	1	1	1	0	0	0

AV: anterior valve; IV: intermediate valve; IVii: second intermediate valve; PV: posterior valve.

Table 8. Identified non-repetitive elements of Cephalopoda, specifically Nautilidae, from the MBHM assemblage using the NRE MNI and modified tMNI protocols.

Taxon	NRE MNI	tMNI	NISP	OUL	APE	UMB
Nautilus sp.	0	1	1	0	0	1

OUL: outer lip; APE: aperture; UMB: umbilicus.

Table 9. Non-repetitive element frequencies per quantification protocol for the FBM and MBHM assemblages.

		FBM		MBHM	
Class	Non-repetitive Element (NRE)	NRE MNI	tMNI	NRE MNI	tMNI
Gastropoda	Spire	890	890	1,250	1,250
	Anterior canal	n/a	497	n/a	452
	Posterior canal	n/a	346	n/a	333
	Outer lip	n/a	329	n/a	234
	Aperture	n/a	214	n/a	211
	Operculum	n/a	1	n/a	0
	Umbilicus	n/a	30	n/a	53
	Stromboid notch	n/a	48	n/a	0
Bivalvia	Umbo	3	3	18	18
	Posterior hinge	3	3	23	23
	Anterior hinge	4	4	19	19
	Posterior adductor muscle scar	n/a	13	n/a	11
	Anterior adductor muscle scar	n/a	2	n/a	0
Polyplacophora	Anterior valve	0	0	1	1
	Intermediate valve	n/a	2	n/a	0
	Intermediate valve ii	n/a	0	n/a	0
	Posterior valve	1	1	0	0
Cephalopoda	Nautiloidea outer lip	n/a	0	n/a	0
	Nautiloidea aperture	n/a	0	n/a	0
	Nautiloidea umbilicus	n/a	0	n/a	1
Total		901	2,383	1,311	2,606

n/a values in the NRE MNI column highlights the elements not investigated using the NRE MNI protocol.

Discussion

Comparative results of the NRE MNI and tMNI quantification protocols show significant differences between the protocols. This includes an overall increase in general MNI values, around 3%, when the tMNI protocol is applied to both the FBM and MHBM molluscan assemblages. The largest increases can be seen in the Gastropoda from both sites.

Rank order abundances show differences between the NRE MNI and tMNI protocols at FBM and MBHM, especially for the FBM assemblage. Both sites are dominated by *Conomurex luhuanus* in all rank order abundance tables. Multiple families, genera, and species were underrepresented when an NRE MNI protocol was applied to the sites. MNI values calculated per taxa using the tMNI protocol record mostly similar or higher values when compared to those of the NRE MNI protocol.

Statistical analyses show relative differences between quantification protocols, with most diversity indices indicating a relative increase in diversity, evenness, and richness at both sites when the tMNI protocol is applied. Several of the differences between NRE MNI and tMNI protocol results were deemed to be statistically significant.

NRE frequencies show that the non-repetitive elements commonly used for NRE MNI protocols tend to be the most abundant ones in the assemblages, however solely using these predetermined NREs, the true diversity and richness of the excavated assemblages appear underrepresented.

To visualise differences between the NRE MNI and tMNI quantification protocols, and to allow for another comparison between FBM and MBHM site assemblages, each taxon identified in the FBM and MBHM molluscan assemblages was attributed to an aggregated and generalised habitat descriptor to understand the impact different quantification protocols have on habitat information and the ways quantification protocols may influence interpretations about people-reef interactions (Table 10) (habitat and foraging assignments following: Carpenter and Niem 1998; Lambrides et al. 2020; Wright 2018).

Applying the NRE MNI and tMNI quantification protocols to the assemblage of FBM present different results when habitat is attributed to the quantified taxa (Figure 9). Reef flat species are the most abundant, followed by terrestrial and intertidal taxa for both methodologies. The differences in abundance might be slight, but when applying the tMNI protocol, a higher percentage of taxa is attributed to the intertidal zone, possibly reflecting a higher degree of foraging efforts focused on intertidal species. Spires of *Monodonta labio* were not encountered in the assemblage and this taxon would not have been represented if the NRE MNI protocol was used. Despite these intertidal taxa consisting of only 1.42% of the excavated molluscan assemblage of FBM, their presence indicates that foraging strategies were likely not to have been solely concentrated on the lagoonal reef flats of Jiigurru.

The habitat analysis of the MBHM assemblage shows minor differences when the NRE MNI and tMNI quantification results are compared (Figure 9). Similar to FBM, reef flat species represent the vast majority of the assemblage. Unlike FBM, the second largest category, excluding varied taxa, consists of

Table 10. Identified taxa from FBM and MBHM categorised into generalised habitats with the accompanying foraging strategies per habitat.

Habitat	Foraging strategies	Taxon
Intertidal—hard substrate	Hand collection	*Acanthopleura* sp.
		Acanthopleura gemmata
		Monodonta labio
		Nerita costata
		Nerita polita
		Thais sp.
		Saccostrea scyphophilla
Reef flat	Hand collection, wading, and diving	*Rochia nilotica*
		Conomurex luhuanus
		Lambis lambis
		Lambis sp.
		Hippopus hippopus
		Tridacna crocea
		Tridacna gigas
		Tridacna maxima
		Tridacna sp.
Reef slope	Diving/hand collection from beach	*Nautilus* sp.
Terrestrial	Hand collection/natural inclusion	Pupillidae
		Subulinidae
		Rhytididae
		Helicarionidae
		Camaenidae
Varied	Varied	Tegulidae
		Turbinidae
		Nerita sp.
		Strombidae
		Conus sp.
		Conidae
		Mytilidae
		Ostreidae

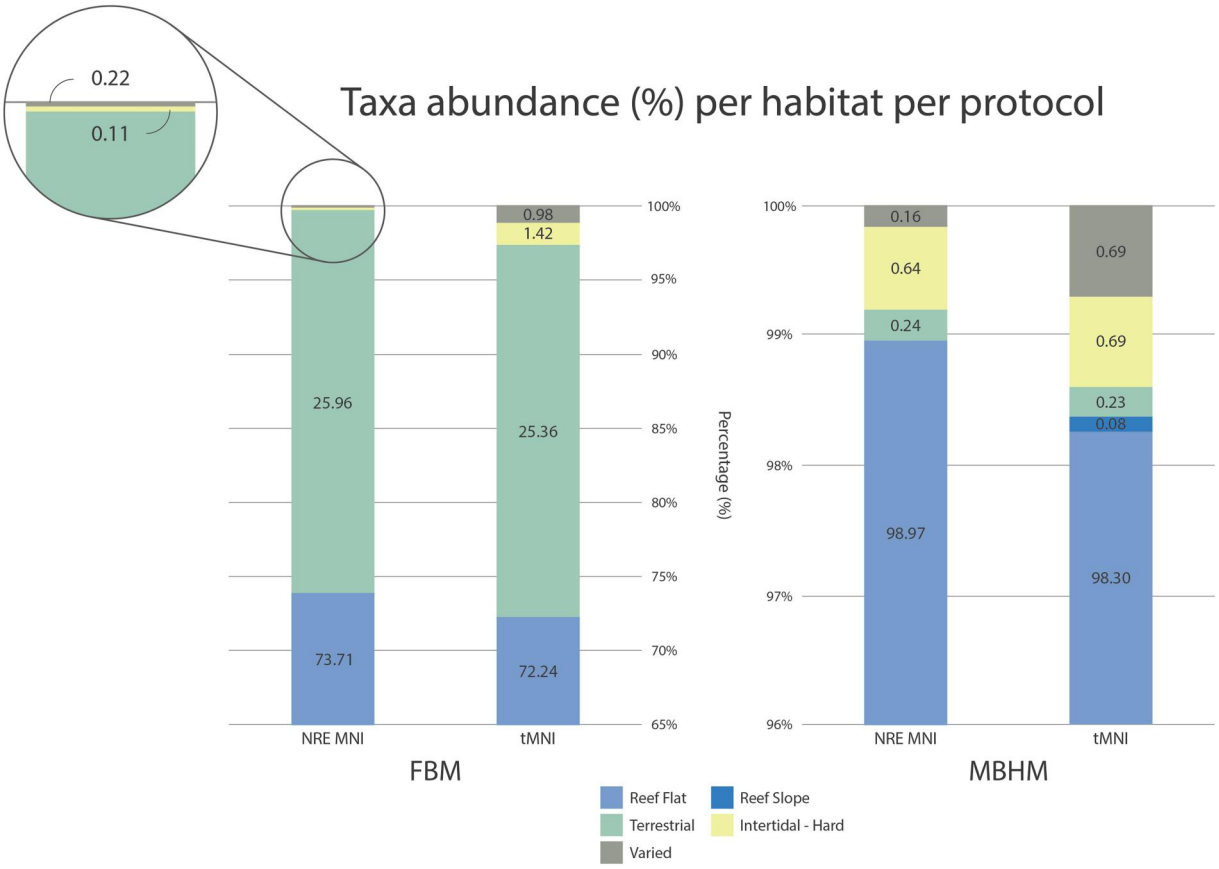

Figure 9. Graphs showing taxa categorised by habitat for the FBM and MBHM molluscan assemblages for the NRE MNI and tMNI quantification protocols.

intertidal taxa, followed by terrestrial and reef slope taxa. The only major difference between the two quantification protocols is the inclusion of the reef slope habitat in the tMNI results. This category is included due to the presence of the Nautilidae umbilicus in the assemblage and might reflect collection of

washed-up *Nautilus* shell from the beach or the potential inclusion of the reef slope as a targeted foraging habitat.

What is important to note is that both the NRE MNI and tMNI quantification protocols are valid methodologies useful for quantification, with different protocols serving different goals. The NRE MNI protocol is easy to apply, does not need a highly skilled specialist, is less time-consuming as only the designated NREs need to be analysed, and is, therefore, more cost-effective. The downside is that NRE MNI might result in an underrepresentation of taxa, especially those that are prone to fragmentation. The tMNI protocol is more time consuming and requires a higher level of skill, yet, as shown in this study and the study by Harris et al. (2015), results in more comprehensive outcomes that might more accurately reflect the true reality of the invertebrate taxa at the site. tMNI is worth the time investment if research questions and funding allow for it.

As mentioned in the results, several taxa from both sites were unable to be included in this study due to the absence of identifiable NREs. The inclusion of these taxa would have slightly influenced the results of this study, especially *Anadara antiquata* and *Periglypta puerpera*. These species would have led to the inclusion of intertidal sandy and muddy habitats in the habitat analysis to a limited degree. The application of the tMNI methodology is the best fit for the Jiigurru assemblages and reflects the true assemblage diversity and richness most accurately, however, it has its limitations as a NRE-based quantification protocol. This raises an interesting point; quantification protocols are made to aid the archaeologist but must be carefully applied so as not to entrap and limit the researcher. Quantification protocols, whether they include MNI (NRE MNI or tMNI), NISP, weight, or not, need to be applied and modified on a site-specific basis and care must be taken to ensure the applied methodologies are properly described in publications to allow for replicability. Archaeologists need to be transparent in the ways they record and analyse their data and strive to gain the most from their assemblage in terms of data quality.

Conclusion

This study revealed the utility of the tMNI protocol for the assemblages of Jiigurru and other Australian coral reef molluscan assemblages, highlighting its capacity to develop more refined narratives of past people-reef interactions when compared to the NRE MNI protocol. Significantly, the application of the tMNI protocol resulted in an overall increase in MNI in both assemblages, alongside marked differences in both rank order abundance and statistical analyses. This study additionally revealed that several taxa were obscured by the NRE MNI methodology, with a habitat analysis of quantified taxa presenting a more nuanced picture of assemblage diversity when the tMNI methodology is applied. Despite this, both the NRE MNI and the tMNI quantification protocols were shown to have their limitations. Outcomes of this study highlight the importance of carefully selecting the methodology that best suits the characteristics of the archaeological molluscan assemblage on a case-by-case basis based on research questions, research-related logistics including available funding and time, and laboratory facilities. This is essential to ensure accurate reconstruction of assemblage diversity, past forager decision-making, and to increase (zoo)archaeological data replicability, comparability, and transparency for future research.

Acknowledgements

We acknowledge the Dingaal and Nguurruumungu Aboriginal communities as partners in this research. We extend a special thanks to Dr. Anne Hoggett and Dr. Lyle Vail for hosting us at the Australian Museum's Lizard Island Research Station during fieldwork, and to Joshua Connelly for the drone imagery.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

This research was supported by the Australian Research Council Centre of Excellence for Australian Biodiversity and Heritage (project number CE170100015) and the Australian Research Council Centre of Excellence for Indigenous and Environmental Histories and Futures (project number CE230100009). A.J.B.L. is the recipient of an Australian Research Council Early Career Researcher Award (DE210101087) and Sir John & Laurine Proud Research Fellowship from the Lizard Island Reef Research Foundation. Fieldwork on Lizard Island was conducted under Queensland Government Department of Environment and Heritage Protection Permit Number P-PTUKI-100112747.

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