

RH: dispRity package.

dispRity : a modular R package for measuring disparity.

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Abstract

1. Biological data is multivariate in essence: many traits in organisms co-vary with each other in space and time. This causes biologists to either reduce these variables in a manageable number of variables or, increasingly, to use multivariate toolkits. One such toolkit is based on creating a multidimensional space where the variables are the axis of this space. It is then possible to use a summary metrics for measuring some properties of this space for some group of species and compare them. For example, if studying morphology, one can create a morphospace for two groups of species, measure some aspect of these groups (such as their spread in the space - often termed disparity) and then test whether they have a different disparity.

2. There are as many definition of these multidimensional spaces, metrics and tests as there are questions that can be tackled with such methods. Many of these methods are implemented in specific software or R packages. However, the definition of the space, metric and test is often dependent on the software/package's author's point of view or specific question. This can unfortunately hamper researchers to apply different methods that suits best their specific questions.

3. Here I present the `dispRity` package, a flexible R package for running multidimensional analysis. This package allows users to define each step of the analysis (whether it is the space, the metric or the test) through a highly modular architecture where each definition can be passed as a function. It also provides a tidy interface through the `dispRity` object, allowing to easily run

24 reproducible multivariate analysis.

25 4. The `disPRity` package also comes with an extend manual regularly updated
26 following users questions or suggestions. Furthermore, the package contains
27 some simulation tools (e.g to simulate complex multidimensional space or
28 morphological data). Finally it also contains a suit of utilities to work with
29 `disPRity` objects aimed at helping users to develop their own
30 multidimensional metrics and/or tests.

31 (Keywords: disparity, ordination, multidimensionality, disparity-through-time,
32 palaeobiology, ecology)

INTRODUCTION

Biological data are complex. To understand the ecology and evolution of species we must use multiple variables that inevitably covary with each other through time and space. One solution to this problem is to analyse these data in a multivariate framework (e.g. Price et al., 2015; Díaz et al., 2016). Such analyses aim to capture the complex multidimensionality of biological data, while still providing outputs that are interpretable in our physical world restricted to three dimensions. These multivariate analyses can be used to investigate changes in morphological diversity through time (Close et al., 2015), competitive replacement scenarios (Brusatte et al., 2008), relationships among form and function (Díaz et al., 2016) and even to describe the entirety of possible shapes for a group of organisms (Raup, 1966). The biological variables in such analyses are equally diverse, including morphological traits (discrete traits like the presence or absence of a character, e.g. Brusatte et al. 2012; and continuous traits such as lengths, e.g. Price et al. 2015), life history traits (e.g. Díaz et al., 2016), or even ecosystem properties (e.g. Donohue et al., 2013).

In all these analysis, each set of multivariate traits forms a multidimensional space, usually represented as matrices where the columns are the dimensions (or some transformation thereof) and rows are the elements (often species or individuals) within this space. These multidimensional spaces can be defined in many ways, for example as a pairwise distance matrix (Close et al., 2015), or as outputs from a principal coordinates analysis (PCO; Brusatte et al., 2008), a principal components analysis (PCA;

Zelditch et al., 2012), or a multidimensional scaling (MDS; Donohue et al., 2013), among others. The name we give to the multidimensional space tends to vary with the kinds of traits used to construct it. For example, when using morphological traits the multivariate space will be a morphospace, when using ecological traits it may be referred to as an ecospace or trait space. Once the multidimensional space is defined it is then possible to measure a specific aspect of it. This specific measurement (hereafter referred to as a “disparity metric”) can in turn be defined in many different ways depending on the specific question being investigated (e.g. Wills, 2001; Ciampaglio et al., 2001; Foth et al., 2012; Donohue et al., 2013; Hughes et al., 2013; Finlay and Cooper, 2015; Close et al., 2015, or combinations thereof). Finally, all these different multidimensional spaces and their associated disparity metrics can be used in an equal variety of statistical tests such as non-parametric multivariate analyses of variance (e.g. Brusatte et al., 2008), multidimensional permutation tests (e.g. Díaz et al., 2016) or even simply by looking at the confidence interval overlaps between disparity measurements (e.g. Halliday and Goswami, 2016). In summary, there are many different ways to perform each step of a multidimensional analysis, making analyses of complexity ever more complex.

In theory, this multitude of ways to generate and define multidimensional spaces, measure disparity within and analyse these metrics is not an issue, in fact, it allows researchers to choose both the most appropriate method for their question or data, or even to test their question using multiple methods (such as Matzke, 2013, for

biogeography). In practice, however, this is hampered by existing software implementations. Although many software packages exist for multidimensional analysis (e.g. Bouxin, 2005; De Caceres et al., 2007; Oksanen et al., 2007; Adams and Otárola-Castillo, 2013; Lloyd, 2015; Adams et al., 2017), package maintainers/software developers choose their preferred definition of multidimensional space and disparity metric and then enforce this on users by allowing little to no flexibility. For example, in the excellent and widely used geomorph package, morphological disparity analysis uses the morphol.disparity function that defines the multidimensional space as the ordination of the Procrustes transform of morphometric data, the disparity metric as the Procrustes variance, and uses a permutation tests to test hypotheses (Zelditch et al., 2012; Adams and Otárola-Castillo, 2013; Adams et al., 2017). This is ideal in some cases, but in others may not be the most appropriate analysis. This can lead to inappropriate analyses by users confined by the existing software implementations.

The aim of the disPRity package is to solve such problems by providing a completely flexible framework for studying multidimensional data. This package is based on a highly modular architecture where each crucial decision in multidimensional analysis (which data, which metric and which test) can be provided by the user. It implements many commonly used metrics and definitions of disparity, as well as providing a simple interface for users to implement their own disparity functions. The package is described here for the use of discrete morphological data diversity analysis but can be generalised to any type of multidimensional data (see the

96 package vignette for more examples).

97 DESCRIPTION

98 In brief, the package takes a `matrix` object (the multidimensional space), calculates
99 some aspect of it (the disparity metric) and allows users to analyse the resulting
100 `disprity` object (see Manuals and Vignettes below). Some additional functions modify
101 the multidimensional space, for example by dividing it by groups or through time
102 and/or bootstrapping it (see Fig. 1 and Table 1).

103 *Measuring disparity*

104 The `disprity` function measures disparity of any multidimensional space (of class
105 `matrix` or `data.frame`) where the columns correspond to the dimensions and the rows
106 correspond to the elements present in the space. The disparity metric (i.e. the aspect of
107 interest of the space) is passed through the `metric` argument and is defined by the user
108 as any function or combination of functions that can either transform the matrix into:

- 109 • Another matrix (a dimension-level 3 function - e.g. a variance-covariance matrix;
110 `stats::cor`)
- 111 • A vector (a dimension-level 2 function - e.g. the variance of each dimension;
112 `disprity::variances` - see below)
- 113 • A single value (a dimension-level 1 function - e.g. the overall standard deviation;
114 `stats::sd`)

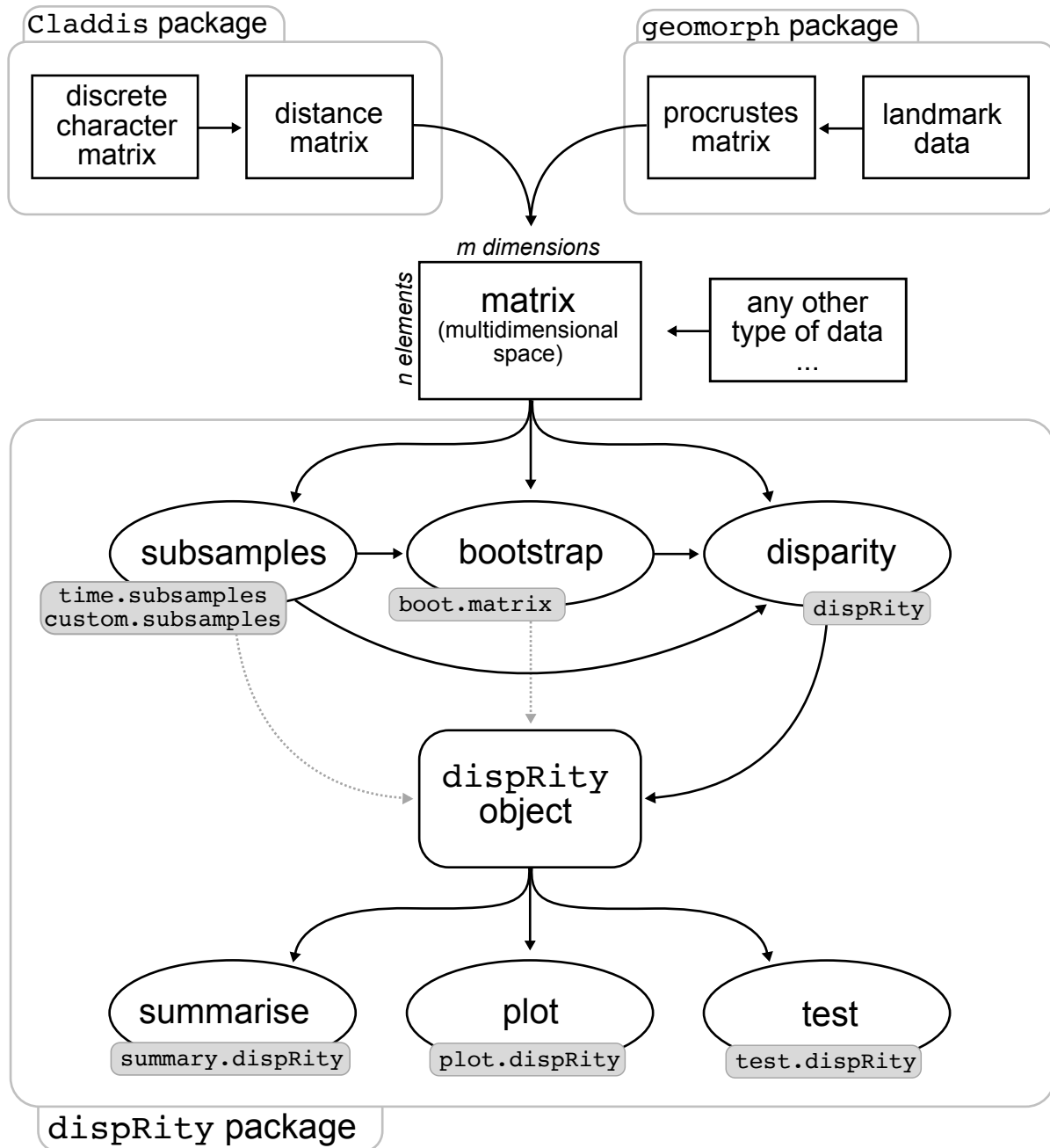


Figure 1: dispRity package workflow: rectangles represent matrices; ellipses represent functions; plain black arrows indicate input/output; dashed grey arrows indicate output (though the summary, plot, and test function cannot be applied if no disparity has been calculated).

Function	Description
<code>geomorph.ordination</code>	Imports data from the <code>geomorph</code> package.
<code>Claddis.ordination</code>	Imports data from the <code>Claddis</code> package.
<code>custom.subsamples</code>	Separates data into custom subsamples.
<code>time.subsamples</code>	Separates data into time subsamples.
<code>boot.matrix</code>	Bootstraps and rarefies a matrix or a <code>dispRity</code> object.
<code>dispRity</code>	Calculates disparity from an matrix or a <code>dispRity</code> object.
<code>summary.dispRity</code>	Summarises a <code>dispRity</code> object.
<code>plot.dispRity</code>	Plots a <code>dispRity</code> object.
<code>test.dispRity</code>	Applies statistical tests to a <code>dispRity</code> object.
<code>dispRity.per.group</code>	Pipeline for disparity within groups analysis.
<code>dispRity.through.time</code>	Pipeline for disparity-through-time analysis.

Table 1: Main functions in the `dispRity` package.

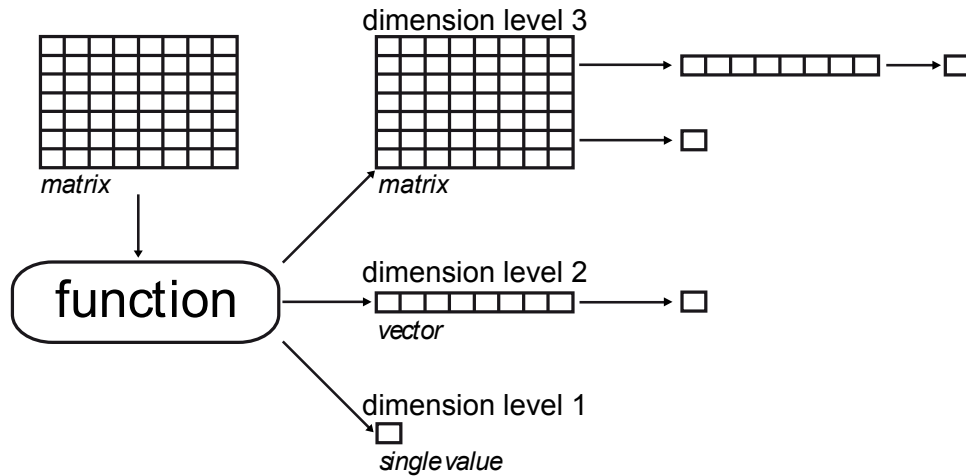


Figure 2: Illustration of the different metric dimension-levels in the dispRity package. In this example, each cell correspond to a single value (e.g. a 8×7 matrix or a vector of eight elements).

The disparity metrics can be functions from other packages, defined by the user or from the dispRity package (see Table 2 for the currently implemented metrics). When multiple functions are passed to the `metric` argument, the functions are sorted by dimension-level and applied in decreasing order to the data. For example, if the metric is defined as `metric = c(mean, range)`, the range function (dimension-level 2) is first applied to the data and the function mean is then applied to the result (e.g. `mean(range(data))`). There is no limitation on the metric dimensions only that at least one dimension-level 2 or 1 function must be present in the metric definition (i.e. disparity can only be defined as distribution or a single value).

Splitting the multidimensional space into subsets

name	description	dimension level	definition	source
ellipse. volume ¹	The volume of the ellipsoid	1	$\frac{\pi^{k/2}}{\Gamma(\frac{k}{2}+1)} \prod_{i=1}^k (\lambda_i^{0.5})$	Donohue et al. (2013)
convhull. surface	The surface of the convex hull	1	NA	geometry::convhulln
convhull. volume	The volume of the convex hull	1	NA	geometry::convhulln
diagonal	The greatest Euclidean distance	1	$\sqrt{\sum_{i=1}^k \max(k_i) - \min(k_i) }$	dispRity::diagonal
mode.val	The modal value	1	NA	dispRity::mode.val
ranges	The absolute ranges of each dimension	2	$ \max(k_i) - \min(k_i) $	dispRity::ranges
variances	The variance of each dimension	2	$\sigma^2 k_i$	dispRity::variances
centroids	The distance between each element and a fixed point ² of the space	2	$\sqrt{\sum_{i=1}^n (k_n - \text{Centroid}_k)^2}$	dispRity::centroids

Table 2: Where k is the number of dimensions, n the number of elements, λ_i is the eigenvalue of each dimensions, σ^2 is their variance and Centroid_k is their mean. ¹ this function uses a fast estimation of the eigenvalue that only works in an ordinated space based on MDS or PCO/PCoA (*not* PCA); ² by default that point is the centroid of the elements.

Prior to calculating disparity, the multidimensional space can be subdivided into subsamples, typically to be compared to each other. For example, one may be interested in seeing how the disparity of a specific subsample of the space compares to another (e.g. difference among groups) or, how different subsamples change sequentially (e.g. through time). In essence, the original space corresponds to the overall space (e.g. a morphospace contains all the possible observed morphologies). Conversely, subsamples correspond to parts of the space with pooled characteristics (i.e. only a subset of the total morphospace).

This splitting can be done using the `custom.subsamples` or `time.subsamples` functions. The first takes as argument the matrix defining the multidimensional space and a list of elements to group into different subsamples. The second also takes a matrix and arguments giving the age of the taxa (a phylogeny and/or a table containing the first and last occurrence data for all/some elements - this allows species with a longer timespan to be present in multiple time subsamples for example) and which subsamples to create: (1) discrete time subsamples (or time-binning) or (2) continuous time subsamples (or time-slicing).

The time-binning method groups elements by specific age range. The time-slicing method works by using a phylogeny and looking at which taxa are present at any specific point in time. This method thus requires the nodes to be part of the multidimensional space, a dated phylogeny (chronogram) and which model to use when slicing through branches rather than tips and nodes. When a slice occurs not on a

tip or a node, four methods are available to select either the descendent or the ancestor's node/tip as an element for this time slice:

- "acctrans" (accelerated transformation) where the data chosen along the branch is always the one of the descendant
- "deltrans" (delayed transformation) where the data chosen along the branch is always the one of the ancestor
- "punctuated" where the data chosen along the branch is randomly chosen between the descendant or the ancestor
- "gradual" where the data chosen along the branch is either the descendant or the ancestor depending on branch length

Bootstrapping and rarefying

Disparity measurement can be influenced by sampling (Butler et al., 2012). To take this source of bias into account, it is common practice to bootstrap the multidimensional space (to minimise the effect of outliers) or/and to rarefy the data (to minimise the effect of different sample sizes in different subsamples). Additionally, if disparity is defined as a dimension-level 1 metric, it can be useful to measure it on bootstrapped data to obtain a distribution on which to perform statistical analyses.

Bootstrapping can be achieved by using the `boot.matrix` function which pseudo-replicates the multidimensional space following two algorithms (1) the "full"

algorithm where the bootstrapping is entirely stochastic (n elements are replaced by any m elements drawn from the data) and (2) the “single” algorithm where only one random element is replaced for each pseudo-replicate (somewhat akin to jackknife resampling).

Similarly, rarefaction can be achieved through the same `boot.matrix` function. Rarefaction can be useful when looking at the effect of reducing the number of elements on the results of an analysis or for allowing the comparisons of subsamples with the same number of elements in each. In practice, rarefaction limits the number of elements to be drawn for each bootstrap replication: only $n - x$ elements are selected at each bootstrap replicate (where x is the number of non-sampled elements).

Interpreting results

The functions above all generate a `disPRity` object that can be summarised or plotted using the S3 method functions `summary.disPRity` and `plot.disPRity` (provided disparity was calculated). These results can then be analysed using the `test.disPRity` function for comparing subsamples or testing hypotheses.

Summarising and plotting.— The `summary.disPRity` and `plot.disPRity` functions allow users to set which central tendency and which quantiles should be represented. Additionally, the `plot.disPRity` function graphically represents the summarised results using different representations: (1) “continuous” for displaying continuous disparity curves (in the case of disparity-through-time analysis for example) and (2)

“box”, “lines”, or “polygons” to display them using boxplots, confidence interval lines or polygons respectively. Additional arguments specific to `dispRity` objects can also be used such as `observed` to display the observed disparity (i.e. non-bootstrapped) or `rarefaction` to only plot the disparity for a certain number of elements (i.e. the rarefaction level). The function can also take any additional graphic arguments (`main`, `xlab`, `col`, etc...) from base R.

Testing hypotheses.— The `test.dispRity` function allows users to test hypotheses on the disparity data (e.g. by comparing the different subsamples to each other). Similarly to the `dispRity` function described above, this function can take any test defined by the user or from other R packages. The `comparison` arguments indicates in which order (if any) the tests should be applied to the subsamples: (1) “pairwise” for pairwise comparisons; (2) “referential” for comparing the first subsample to all the others; (3) “sequential” for comparing subsamples sequentially (e.g. first against second, second against third, etc.); (4) “all” for comparing all the subsamples simultaneously (i.e. $\text{disparity} \sim \text{subsamples}$ - this can be used for `lm` or `glm`) or (5) any list of pairs (or more) of subsamples to compare.

Some tests are implemented within the package such as the Bhattacharyya Coefficient (`bhatt.coeff`; Bhattacharyya, 1943; Guillerme and Cooper, 2016) or a permutation test based on null hypothesised multidimensional space following Díaz et al. (2016) (`null.test`). Additionally, this function also allows additional arguments such as `rarefaction` (as described above) or `correction` to adjust p-values when using

multiple parametric tests.

EXAMPLES

Multivariate analysis can be really useful for looking multiple aspects of organisms diversity together. For example, one classic univariate trait used in ecology and evolution can be the sheer number of species present in an ecosystem or/and through time. This trait can be useful to test whether some ecosystems or/and time periods have more species diversity than others. In this case one can then test some hypothesis such as: environments with bigger altitudes gradients contain more species.

Conversely, in the case of species diversity, one can also look at another independent multivariate trait: the diversity of morphologies (or disparity; Ruta et al., 2013). Using disparity, it is then also possible to assess whether one ecosystem or/and time period display more morphological variation. Following the previous example, if disparity is also higher with bigger altitudes gradients, one could argue that the species richness is caused by an increased number of morphologies adapted to more ecological niches (or something akin).

The following example is based on a classical palaeobiology morphological disparity analysis. Note that more examples are available in the package manual (https://rawgit.com/TGuillerme/disPRity/master/inst/gitbook/_book/index.html).

disPRity data.— The package contains a dataset that is a subset from Beck and Lee

(2014) and includes:

- BeckLee_mat50: an ordinated matrix for 50 mammals based on the distance between discrete morphological characters.
- BeckLee_mat99: the same matrix BeckLee_mat50 but also containing the reconstruction of their 49 ancestors.
- BeckLee_tree: a chronogram with the 50 mammal species present in BeckLee_mat50 and BeckLee_mat99.
- BeckLee_ages: the first and last occurrence data for 14 of the mammal species present in BeckLee_mat50 and BeckLee_mat99.
- disparity: a pre-made dispRity object based on the data above.

In this example, the multidimensional space is defined as a morphospace: the ordination of the distances among discrete morphological characters for 50 mammal species (from Beck and Lee, 2014). Additionally, we can define disparity as the sum of the variances on each dimension (Wills et al., 1994) that will represent an aspect of the the volume of the morphospace (i.e. a large sum of variances approximates a large morphospace and vice versa).

Typical disparity among groups analysis

One typical question with such analysis would be to test whether two groups of species have a different disparity. For example, using the data described above, we can test

245 whether the crown mammals (the living mammals and their descendants) are more
246 diverse in term of morphology than the stem mammals (the fossil mammals with no
247 living descendants). In other words, whether the approximation of the volume within
248 the morphospace (the disparity as defined above) is different in crown or stem
249 mammals.

250 These two groups can be defined as follows (where the integers are the row number of
251 the species in the matrix):

```
252 > mammal_groups <- list('crown' = c(16, 19:41, 45:50), 'stem' = c(1:15,  
253 17:18, 42:44))
```

254 It is then possible to measure the disparity between the two groups as follows:

```
255 > disparity <- dispRity.per.group(data = BeckLee_mat50, group =  
256 mammal_groups, metric = c(sum, variances))
```

257 Note that this function is a wrapper function that is the equivalent to:

```
258 > subsamples <- custom.subsamples(data = BeckLee_mat50, group =  
259 mammal_groups)  
260 > bootstraps <- boot.matrix(subsamples)  
261 > disparity <- dispRity(bootstraps, metric = c(sum, variances))
```

262 Which allows a finer tuning of the optional arguments in each function. The three
263 arguments here are defined as follows: data = BeckLee_mat50 is our definition of the
264 multidimensional space, group = mammal_groups indicates which mammals belong to
265 which group and metric = c(sum, variances) is our definition of disparity.

266 This function returns a `dispRity` object that summarises the disparity analysis:

267 `> disparity`

268 ---- `dispRity` object ----

269 2 customised subsamples for 50 elements with 48 dimensions:

270 `crown, stem.`

271 Data was bootstrapped 100 times (method:"full").

272 Disparity was calculated as: `c(sum, variances).`

273 As indicated, the `dispRity` object contains two customised subsamples (called
274 “crown” and “stem”) from a morphospace made of 50 elements for 48 dimensions. The
275 `dispRity` object also displays information on the number and method of the bootstrap
276 replicates as well as the definition of disparity. To visualise the actual disparity values,
277 one can use the `summary` or/and `plot` options (Table 3 and Fig. 3):

278 `> summary(disparity)`

	subsamples	n	obs	bs.median	2.5%	25%	75%	97.5%
1	crown	30	2.00	1.93	1.87	1.92	1.95	1.98
2	stem	20	1.72	1.63	1.53	1.60	1.66	1.69

Table 3: Summarising a `dispRity` object (disparity per groups). *n* is the number of elements per subsamples, *obs* the observed disparity (not bootstrapped), *bs.median* is the median bootstrapped disparity (here the median of the sum of ranges) and the 2.5, 25, 75 and 95% are the confidence intervals.

279 > plot(disparity)

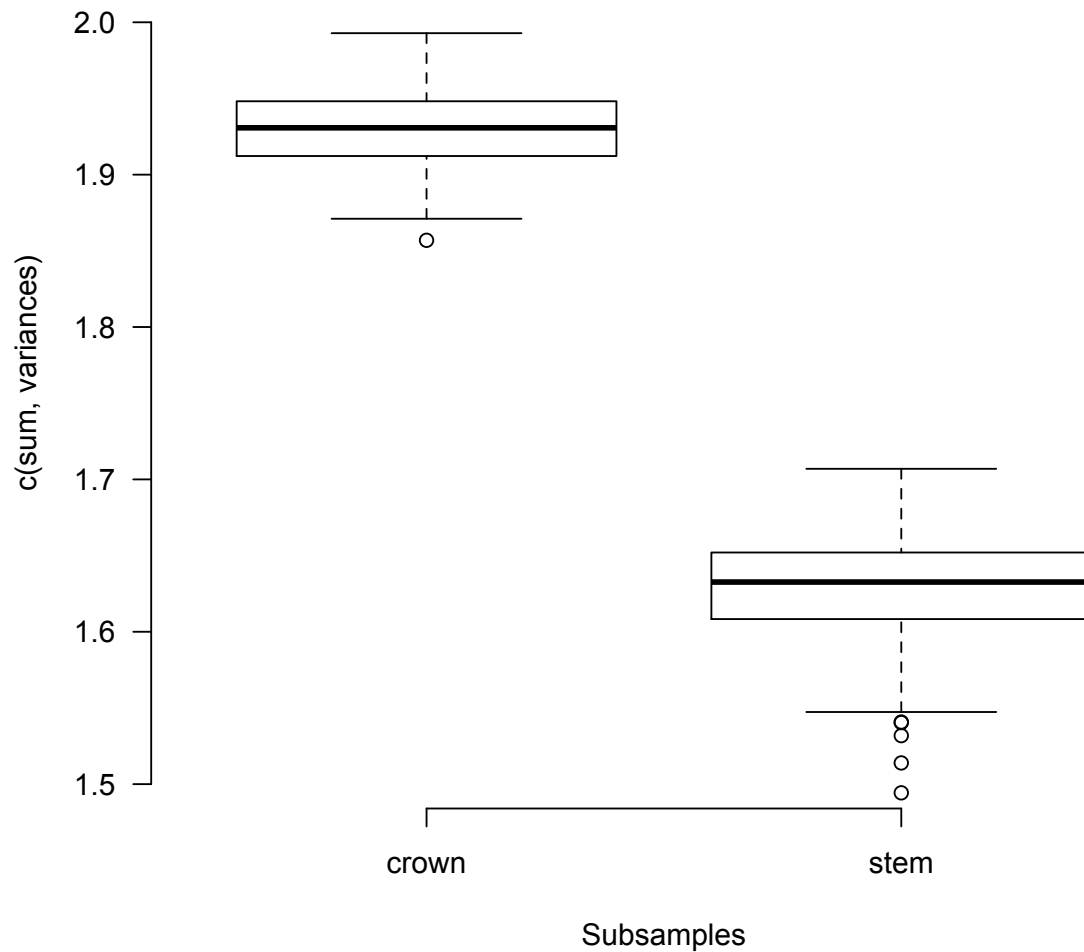


Figure 3: dispRity plot of disparity differences between groups.

280 As we can see from the summary table (Table 3) and the plot (3), there seems to
281 be a significant difference in morphospace volume occupied between the two groups. It
282 is possible to test this hypothesis by using, for example, a non-parametric Wilcoxon test

```

283 (stats::wilcox.test):
284 > test.dispRity(disparity, test = wilcox.test)
285 [[1]]
286 statistic
287 crown : stem 10000
288 [[2]]
289 p.value
290 crown : stem 2.562144e-34

```

291 As indicated by the p value, there is a significant difference in disparity between
 292 the groups. Relating back to our question: yes, crown mammals display a higher
 293 diversity in morphologies than their stem counterparts (in this example and dataset!).

294 *Typical disparity-through-time analysis.*— A following up question to this observation
 295 could be to test whether this difference is due to an overall change in disparity through
 296 time or not. In other words, did disparity increased through time in mammals globally
 297 or is it only between stem and crown mammals. Using the same definition of the
 298 multidimensional space and disparity as in the previous example, we can measure, for
 299 example, changes in disparity through time between the Late Cretaceous (100.5 to 66.0
 300 million years ago - Mya), the Paleocene (66.0 to 56.0 Mya) and the Eocene (56.0 to 33.9
 301 Mya).

```

302 > time_bins <- c(100.5, 66, 56, 33.9)

```

303 It is then possible to measure disparity-through-time using the following

304 function:

```
305 > disparity <- dispRity.through.time(data = BeckLee_mat50, tree =  
306 BeckLee_tree, time = time_bins, metric = c(sum, variances))
```

307 Note that this function is a wrapper function that is the equivalent to:

```
308 > subsamples <- time.subsamples(data = BeckLee_mat50, tree = BeckLee_tree,  
309 time = time_bins, method = 'discrete')  
310 > bootstraps <- boot.matrix(subsamples)  
311 > disparity <- dispRity(bootstraps, metric = c(sum, variances))
```

312 The arguments `data = BeckLee_mat50` and `metric = c(sum, variances)` are the same
313 as in the example above. However, in this type of analysis, we also need to have
314 additional arguments: the `time = time_bins` indicates the boundaries of the different
315 time bins, the `tree = BeckLee_tree` argument provides information on the age of each
316 element and `method = 'discrete'` indicates that the data is time-binned.

317 Again, the resulting `dispRity` object can be summarised and plotted (Table 4 and
318 Fig. 4):

```
319 > summary(disparity)  
320 > plot(disparity, type = 'continuous')
```

321 Note that many plot options specific to `dispRity` objects are available such as plotting
322 disparity in a “continuous” fashion (inferring disparity between the time bins).

323 From the plot and the summary, disparity seems to change (increase) through
324 time from the Cretaceous to the Eocene. Similarly to the example above, it is also

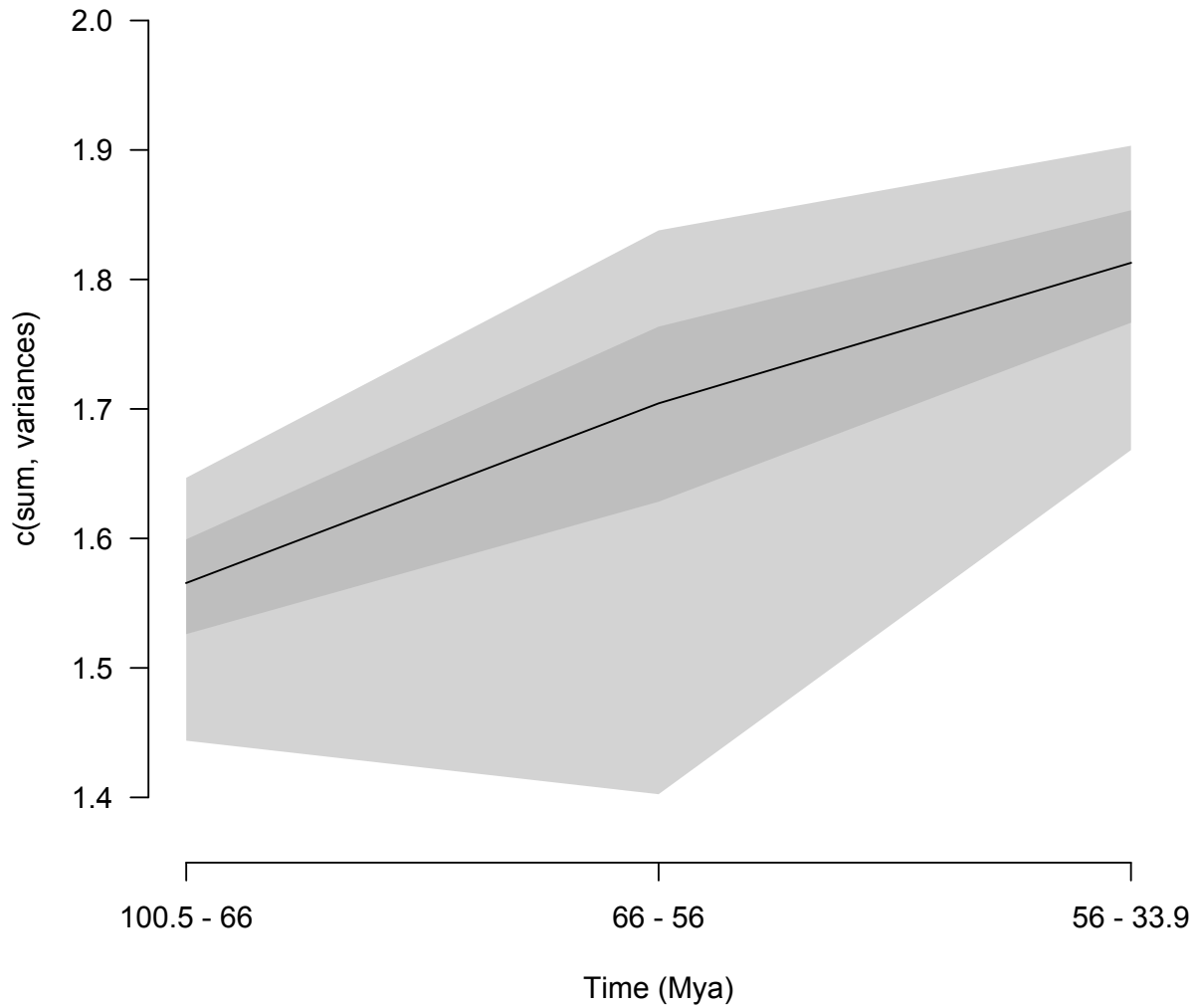


Figure 4: dispRity plot of disparity-through-time. The black line represents the median disparity (median sum of variances), the dark grey and light surfaces represent respectively the 50% and 95% confidence intervals.

	subsamples	n	obs	bs.median	2.5%	25%	75%	97.5%
1	100.5 - 66	15	1.67	1.55	1.40	1.51	1.58	1.65
2	66 - 56	9	1.88	1.69	1.43	1.63	1.77	1.83
3	56 - 33.9	13	1.96	1.83	1.62	1.77	1.86	1.90

Table 4: Summarising a `dispRity` object (disparity through time). *n* is the number of elements per subsamples, *obs* the observed disparity (not bootstrapped), *bs.median* is the median bootstrapped disparity (here the median of the sum of ranges) and the 2.5, 25, 75 and 95% are the confidence intervals.

possible to statistically test this hypothesis using, for example, an ANOVA (Table 5):

```
> anova(test.dispRity(disparity, test = lm, comparisons = 'all'))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
subsamples	2	3.14	1.57	177.84	0.0000
Residuals	297	2.62	0.01		

Table 5: ANOVA performed on a `dispRity` object.

To answer our specific question above: yes there is an effect of time on morphological disparity (an increase) in this dataset.

ADDITIONAL INFORMATION

Manuals and vignette

Supplementary information about the package is available on the project page (<https://TGuillerme/dispRity>). Information concerning each function can be found in R in the individual function manuals and a package manual with more detailed information is available online (https://rawgit.com/TGuillerme/dispRity/master/inst/gitbook/_book/index.html). This manual contains substantially more information and detailed examples including a tutorial for a “classic” disparity analysis in palaeobiology as well as an introduction to the use of this package in ecology or other disciplines.

Data simulations

This package also contains functions for simulating random discrete morphological matrices (`sim.morpho`) or random multidimensional spaces (`space.maker`). These functions are based on a similar modular architecture as that used by the `dispRity` functions, allowing users to provide their own distribution parameters for the simulations. For example, `stats::rnorm` can be provided as an argument for drawing normal characters rates with `sim.morpho` or normally distributed multidimensional space with `space.maker`. The discrete morphological data simulations are based on protocols from Guillerme and Cooper (2016), O'Reilly et al. (2016) and Puttick et al. (2017). The multidimensional space simulations are based on the methods from Díaz et al. (2016). Both functionalities are described in more details in the package manual.

CONCLUSION

The `disprity` package is based on a highly modular architecture allowing researchers to simply define both their multidimensional space and their disparity metric to efficiently analyse multivariate data. The `disprity` object allows users to easily pipeline disparity analysis from the data input (the matrix) to publication standard results (tables, plots, hypothesis testing). With the help of this package, researchers will be able to run multivariate analysis in an easy way while still allowing the flexibility necessary to such analyses.

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