

# **Biodiverse Calculations and Indices**

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# 1 Overview

This is a listing of the indices available in Biodiverse, ordered by the calculations used to generate them. It is generated from the system metadata and contains all the information visible in the GUI, plus some additional details.

Most of the headings are self-explanatory. For the others:

- The *Subroutine* is the name of the subroutine used to call the function if you are using Biodiverse through a script.
- The *Index* is the name of the index in the SPATIAL\_RESULTS list, or if it is its own list then this will be its name. These lists can contain a variety of values, but are usually lists of labels with some value, for example the weights used in an endemism calculation. The names of such lists typically end in “LIST”, “ARRAY”, “HASH”, “LABELS” or “STATS”.
- *Grouping?* states whether or not the index can be used to define the grouping for a cluster or region grower analysis. A blank value means it cannot be used for either.
- The *Minimum number of neighbour sets* dictates whether or not a calculation or index will be run. If you specify only one neighbour set then all those calculations that require two sets will be dropped from the analysis. (This is always the case for calculations applied to cluster nodes as there is only one neighbour set, defined by the set of groups linked to the terminal nodes below a cluster node). Note that many of the calculations lump neighbour sets 1 and 2 together. See the [SpatialConditions](#) page for more details on neighbour sets.

Note that some calculations can provide different numbers of indices depending on the nature of the BaseData set used. This currently applies to the hierarchically partitioned endemism calculations (both [central](#) and [whole](#)).

For space reasons, columns are not shown if all cells are empty.

## 2 Table of calculations and indices

*Generated GMT Sat Feb 7 06:47:44 2026, Biodiverse version 5.0.*

- Element Properties
  - Group property Gi\* statistics
  - Group property data
  - Group property hashes
  - Group property quantiles
  - Group property summary stats
  - Label property Gi\* statistics
  - Label property Gi\* statistics (local range weighted)
  - Label property data
  - Label property hashes
  - Label property hashes (local range weighted)
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  - Endemism central hierarchical partition
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- Hierarchical Labels
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- Lists and Counts

- Element arrays
- Element counts
- Element lists
- Label counts
- Label counts not in sample
- Local range lists
- Local range summary statistics
- Non-empty element counts
- Rank relative sample counts per label
- Redundancy
- Richness
- Sample count lists
- Sample count quantiles
- Sample count summary stats
- Matrix
  - Compare dissimilarity matrix values
  - Matrix statistics
  - Rao's quadratic entropy, matrix weighted
- Numeric Labels
  - Numeric label data
  - Numeric label dissimilarity
  - Numeric label harmonic and geometric means
  - Numeric label quantiles
  - Numeric label statistics
  - Numeric labels  $G_i^*$  statistic
- PhyloCom Indices
  - NRI and NTI expected values
  - NRI and NTI, abundance weighted
  - NRI and NTI, local range weighted
  - NRI and NTI, unweighted
  - Net VPD expected values
  - Net variance of pair-wise phylogenetic distances, unweighted
  - Phylogenetic and Nearest taxon distances, abundance weighted
  - Phylogenetic and Nearest taxon distances, local range weighted
  - Phylogenetic and Nearest taxon distances, unweighted
- Phylogenetic Endemism Indices
  - Corrected weighted phylogenetic endemism
  - Corrected weighted phylogenetic endemism, central variant
  - Corrected weighted phylogenetic rarity



- PD-Endemism
- PE clade contributions
- PE clade loss
- PE clade loss (ancestral component)
- Phylogenetic Endemism
- Phylogenetic Endemism central
- Phylogenetic Endemism central lists
- Phylogenetic Endemism lists
- Phylogenetic Endemism single
- RWiBaLD
- Phylogenetic Indices
  - Count labels on tree
  - Evolutionary distinctiveness
  - Evolutionary distinctiveness per site
  - Evolutionary distinctiveness per terminal taxon per site
  - Labels not on tree
  - Labels on tree
  - Last shared ancestor properties
  - PD clade contributions
  - PD clade loss
  - PD clade loss (ancestral component)
  - Phylogenetic Abundance
  - Phylogenetic Diversity
  - Phylogenetic Diversity (local)
  - Phylogenetic Diversity node list
  - Phylogenetic Diversity terminal node count
  - Phylogenetic Diversity terminal node list
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  - Relative Phylogenetic Endemism, type 1
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  - Hurlbert richness estimation
  - ICE
- Taxonomic Dissimilarity and Comparison
  - Beta diversity
  - Bray-Curtis non-metric
  - Bray-Curtis non-metric, group count normalised
  - Jaccard
  - Kulczynski 2
  - Nestedness-resultant
  - Range weighted Sorenson
  - Rao's quadratic entropy, taxonomically weighted
  - S2
  - Simpson and Shannon
  - Sorenson

## 2.1 Element Properties

### 2.1.1 Group property Gi\* statistics

**Description:** List of Getis-Ord Gi\* statistics for each group property across both neighbour sets

**Subroutine:** `calc_gpprop_gistar`

**Reference:** Getis and Ord (1992) Geographical Analysis

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
GPPROP_GISTAR_LIST	List of Gi* scores	1

### 2.1.2 Group property data

**Description:** Lists of the groups and their property values used in the group properties calculations. Returns one list for each property, so if your data have properties named ‘GPROP1’ and ‘GPROP2’ then it will return two lists named ‘GPPROP\_STATS\_GPROP1\_DATA’ and ‘GPPROP\_STATS\_GPROP2\_DATA’, respectively.

**Subroutine:** calc\_gpprop\_lists

**Indices:**

- Data set dependent

### 2.1.3 Group property hashes

**Description:** Hashes of the groups and their property values used in the group properties calculations. Hash keys are the property values, hash values are the property value frequencies. Returns one list for each property, so if your data have properties named ‘GPROP1’ and ‘GPROP2’ then it will return two lists named ‘GPPROP\_STATS\_GPROP1\_HASH’ and ‘GPPROP\_STATS\_GPROP2\_HASH’, respectively.

**Subroutine:** calc\_gpprop\_hashes

**Indices:**

- Data set dependent

### 2.1.4 Group property quantiles

**Description:** Quantiles for each group property across both neighbour sets

**Subroutine:** calc\_gpprop\_quantiles

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
GPPROP_QUANTILE_LIST	List of quantiles for the label properties (05 10 20 30 40 50 60 70 80 90 95)	1

### 2.1.5 Group property summary stats

**Description:** List of summary statistics for each group property across both neighbour sets

**Subroutine:** calc\_gpprop\_stats

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
GPPROP_STATS_LIST	List of summary statistics (count mean min max median sum sd iqr)	1

### 2.1.6 Label property Gi\* statistics

**Description:** List of Getis-Ord Gi\* statistic for each label property across both neighbour sets

**Subroutine:** calc\_lbprop\_gistar

**Reference:** [Getis and Ord \(1992\) Geographical Analysis](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
LBPROP_GISTAR_LIST	List of Gi* scores	1

### 2.1.7 Label property Gi\* statistics (local range weighted)

**Description:** List of Getis-Ord Gi\* statistic values for each label property across both neighbour sets (local range weighted)

**Subroutine:** calc\_lbprop\_gistar\_abc2

**Reference:** [Getis and Ord \(1992\) Geographical Analysis](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
LBPROP_GISTAR_LIST_ABC2	List of Gi* scores	1

**2.1.8 Label property data**

**Description:** Lists of the labels and their property values used in the label properties calculations. Returns one list for each property, so if your data have properties named ‘PROP1’ and ‘PROP2’ then it will return two lists named ‘LBPROP\_STATS\_PROP1\_DATA’ and ‘LBPROP\_STATS\_PROP2\_DATA’, respectively.

**Subroutine:** calc\_lbprop\_data

**Indices:**

- Data set dependent

**2.1.9 Label property hashes**

**Description:** Hashes of the labels and their property values used in the label properties calculations. Hash keys are the property values, hash values are the property value frequencies. Returns one hash for each property, so if your data have properties named ‘PROP1’ and ‘PROP2’ then it will return two lists named ‘LBPROP\_STATS\_PROP1\_HASH’ and ‘LBPROP\_STATS\_PROP2\_HASH’, respectively.

**Subroutine:** calc\_lbprop\_hashes

**Indices:**

- Data set dependent

**2.1.10 Label property hashes (local range weighted)**

**Description:** Hashes of the labels and their property values used in the local range weighted label properties calculations. Hash keys are the property values, hash values are the property value frequencies. Returns one hash for each property, so if your data have properties named ‘PROP1’ and ‘PROP2’ then it will return two lists named ‘LBPROP\_STATS\_PROP1\_HASH2’ and ‘LBPROP\_STATS\_PROP2\_HASH2’, respectively.

**Subroutine:** calc\_lbprop\_hashes\_abc2

**Indices:**

- Data set dependent

### 2.1.11 Label property lists

**Description:** Lists of the labels and their property values within the neighbour sets. Returns one list for each property, so if your data have properties named ‘PROP1’ and ‘PROP2’ then it will return two lists named ‘LBPROP\_LIST\_PROP1’ and ‘LBPROP\_LIST\_PROP2’, respectively.

**Subroutine:** calc\_lbprop\_lists

**Indices:**

- Data set dependent

### 2.1.12 Label property quantiles

**Description:** List of quantiles for each label property across both neighbour sets

**Subroutine:** calc\_lbprop\_quantiles

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
LBPROP_QUANTILES	List of quantiles for the label properties: (05 10 20 30 40 50 60 70 80 90 95)	1

### 2.1.13 Label property quantiles (local range weighted)

**Description:** List of quantiles for each label property across both neighbour sets (local range weighted)

**Subroutine:** calc\_lbprop\_quantiles\_abc2

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
LBPROP_QUAN- TILES_ABC2	List of quantiles for the label properties: (05 10 20 30 40 50 60 70 80 90 95)	1

### 2.1.14 Label property summary stats

**Description:** List of summary statistics for each label property across both neighbour sets

**Subroutine:** calc\_lbprop\_stats

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
LBPROP_STATS	List of summary statistics (count mean min max median sum skewness kurtosis sd iqr)	1

### 2.1.15 Label property summary stats (local range weighted)

**Description:** List of summary statistics for each label property across both neighbour sets, weighted by local ranges

**Subroutine:** calc\_lbprop\_stats\_abc2

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
LBPROP_STATS_ABC2	List of summary statistics (count mean min max median sum skewness kurtosis sd iqr)	1

## 2.2 Endemism

### 2.2.1 Absolute endemism

**Description:** Absolute endemism scores.

**Subroutine:** calc\_endemism\_absolute

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
END_ABS1	Count of labels entirely endemic to neighbour set 1		1
END_ABS1_P	Proportion of labels entirely endemic to neighbour set 1		1
END_ABS2	Count of labels entirely endemic to neighbour set 2		1
END_ABS2_P	Proportion of labels entirely endemic to neighbour set 2		1
END_ABS_ALL	Count of labels entirely endemic to neighbour sets 1 and 2 combined	region grower	1
END_ABS_ALL_P	Proportion of labels entirely endemic to neighbour sets 1 and 2 combined		1

### 2.2.2 Absolute endemism lists

**Description:** Lists underlying the absolute endemism scores.

**Subroutine:** calc\_endemism\_absolute\_lists

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
END_ABS1_LIST	List of labels entirely endemic to neighbour set 1	1
END_ABS2_LIST	List of labels entirely endemic to neighbour set 1	1
END_ABS_ALL_LIST	List of labels entirely endemic to neighbour sets 1 and 2 combined	1



### 2.2.3 Endemism central

**Description:** Calculate endemism for labels only in neighbour set 1, but with local ranges calculated using both neighbour sets

**Subroutine:** calc\_endemism\_central

**Reference:** [Crisp et al. \(2001\)](#) J Biogeog; [Laffan and Crisp \(2003\)](#) J Biogeog

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
ENDC_CWE	Corrected weighted endemism	1	$= \frac{ENDC\_WE}{ENDC\_RICHNESS}$	
ENDC_RICH- NESS	Richness used in ENDC_CWE (same as index RICH-NESS_SET1)	1		
ENDC_SINGLE	Endemism unweighted by the number of neighbours. Counts each label only once, regardless of how many groups in the neighbourhood it is found in. Useful if your data have sampling biases and best applied with a small window.	1	$= \sum_{t \in T} \frac{1}{R_t}$ where $t$ is a label (taxon) in the set of labels (taxa) $T$ in neighbour set 1, and $R_t$ is the global range of label $t$ across the data set (the number of groups it is found in, unless the range is specified at import).	<a href="#">Slatyer et al. (2007)</a> J. Biogeog

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
ENDC_WE	Weighted endemism	1	$= \sum_{t \in T} \frac{r_t}{R_t}$ where $t$ is a label (taxon) in the set of labels (taxa) $T$ in neighbour set 1, $r_t$ is the local range (the number of elements containing label $t$ within neighbour sets 1 & 2, this is also its value in list ABC2_LA- BELS_ALL), and $R_t$ is the global range of label $t$ across the data set (the number of groups it is found in, unless the range is specified at import).	

#### 2.2.4 Endemism central hierarchical partition

**Description:** Partition the endemism central results based on the taxonomic hierarchy inferred from the label axes. (Level 0 is the highest).

**Subroutine:** calc\_endemism\_central\_hier\_part

**Reference:** [Laffan et al. \(2013\)](#) J Biogeog

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ENDC_HPART_0	List of the proportional contribution of labels to the endemism central calculations, hierarchical level 0	1
ENDC_HPART_1	List of the proportional contribution of labels to the endemism central calculations, hierarchical level 1	1
ENDC_HPART_C_0	List of the proportional count of labels to the endemism central calculations (equivalent to richness per hierarchical grouping), hierarchical level 0	1
ENDC_HPART_C_1	List of the proportional count of labels to the endemism central calculations (equivalent to richness per hierarchical grouping), hierarchical level 1	1
ENDC_HPART_E_0	List of the expected proportional contribution of labels to the endemism central calculations (richness per hierarchical grouping divided by overall richness), hierarchical level 0	1
ENDC_HPART_E_1	List of the expected proportional contribution of labels to the endemism central calculations (richness per hierarchical grouping divided by overall richness), hierarchical level 1	1

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ENDC_HPART_OME_0	List of the observed minus expected proportional contribution of labels to the endemism central calculations , hierarchical level 0	1
ENDC_HPART_OME_1	List of the observed minus expected proportional contribution of labels to the endemism central calculations , hierarchical level 1	1

### 2.2.5 Endemism central lists

**Description:** Lists used in endemism central calculations

**Subroutine:** calc\_endemism\_central\_lists

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ENDC_RANGELIST	List of ranges for each label used in the endemism central calculations	1
ENDC_WTLIST	List of weights for each label used in the endemism central calculations	1

### 2.2.6 Endemism central normalised

**Description:** Normalise the WE and CWE scores by the neighbourhood size. (The number of groups used to determine the local ranges).

**Subroutine:** calc\_endemism\_central\_normalised

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
ENDC_CWE_NORM	Corrected weighted endemism normalised by groups	1	$= \frac{ENDC\_CWE}{EL\_COUNT\_ALL}$
ENDC_WE_NORM	Weighted endemism normalised by groups	1	$= \frac{ENDC\_WE}{EL\_COUNT\_ALL}$

### 2.2.7 Endemism whole

**Description:** Calculate endemism using all labels found in both neighbour sets

**Subroutine:** calc\_endemism\_whole

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
ENDW_CWE	Corrected weighted endemism		1	$= \frac{ENDW\_WE}{ENDW\_RICHNESS}$	
ENDW_RICH- NESS	Richness used in ENDW_CWE (same as index RICH- NESS_ALL)	region grower	1		

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
ENDW_SIN- GLE	Endemism unweighted by the number of neighbours. Counts each label only once, regardless of how many groups in the neighbour- hood it is found in. Useful if your data have sampling biases and best applied with a small window.	region grower	1	$= \sum_{t \in T} \frac{1}{R_t}$ where $t$ is a label (taxon) in the set of labels (taxa) $T$ across neighbour sets 1 & 2, and $R_t$ is the global range of label $t$ across the data set (the number of groups it is found in, unless the range is specified at import).	<a href="#">Slatyer et al. (2007) J. Biogeog</a>

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
ENDW_WE	Weighted endemism	region grower	1	$= \sum_{t \in T} \frac{r_t}{R_t}$ <p>where <math>t</math> is a label (taxon) in the set of labels (taxa) <math>T</math> across both neighbour sets, <math>r_t</math> is the local range (the number of elements containing label <math>t</math> within neighbour sets 1 &amp; 2, this is also its value in list ABC2_LA- BELS_ALL), and <math>R_t</math> is the global range of label <math>t</math> across the data set (the number of groups it is found in, unless the range is specified at import).</p>	

### 2.2.8 Endemism whole hierarchical partition

**Description:** Partition the endemism whole results based on the taxonomic hierarchy inferred from the label axes. (Level 0 is the highest).

**Subroutine:** calc\_endemism\_whole\_hier\_part

**Reference:** [Laffan et al. \(2013\)](#) J Biogeog

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ENDW_HPART_0	List of the proportional contribution of labels to the endemism whole calculations, hierarchical level 0	1
ENDW_HPART_1	List of the proportional contribution of labels to the endemism whole calculations, hierarchical level 1	1
ENDW_HPART_C_0	List of the proportional count of labels to the endemism whole calculations (equivalent to richness per hierarchical grouping), hierarchical level 0	1
ENDW_HPART_C_1	List of the proportional count of labels to the endemism whole calculations (equivalent to richness per hierarchical grouping), hierarchical level 1	1
ENDW_HPART_E_0	List of the expected proportional contribution of labels to the endemism whole calculations (richness per hierarchical grouping divided by overall richness), hierarchical level 0	1
ENDW_HPART_E_1	List of the expected proportional contribution of labels to the endemism whole calculations (richness per hierarchical grouping divided by overall richness), hierarchical level 1	1



<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ENDW_HPART_OME_0	List of the observed minus expected proportional contribution of labels to the endemism whole calculations , hierarchical level 0	1
ENDW_HPART_OME_1	List of the observed minus expected proportional contribution of labels to the endemism whole calculations , hierarchical level 1	1

### 2.2.9 Endemism whole lists

**Description:** Lists used in the endemism whole calculations

**Subroutine:** calc\_endemism\_whole\_lists

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ENDW_RANGELIST	List of ranges for each label used in the endemism whole calculations	1
ENDW_WTLIST	List of weights for each label used in the endemism whole calculations	1

### 2.2.10 Endemism whole normalised

**Description:** Normalise the WE and CWE scores by the neighbourhood size. (The number of groups used to determine the local ranges).

**Subroutine:** calc\_endemism\_whole\_normalised

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
ENDW_CWE_NORM	Corrected weighted endemism normalised by groups	1	$= \frac{ENDW\_CWE}{EL\_COUNT\_ALL}$
ENDW_WE_NORM	Weighted endemism normalised by groups	1	$= \frac{ENDW\_WE}{EL\_COUNT\_ALL}$

## 2.3 Hierarchical Labels

### 2.3.1 Ratios of hierarchical labels

**Description:** Analyse the diversity of labels using their hierarchical levels. The A, B and C scores are the same as in the Label Counts analysis (calc\_label\_counts) but calculated for each hierarchical level, e.g. for three axes one could have A0 as the Family level, A1 for the Family:Genus level, and A2 for the Family:Genus:Species level. The number of list elements generated depends on how many axes are used in the labels. Axes are order from zero as the highest level in the hierarchy, so index 0 is the top level of the hierarchy.

Note that this calculation produces lists since version 4.99\_002 so one can no longer use the SUMRAT indices for clustering. This can be re-enabled if there is a need.

**Subroutine:** calc\_hierarchical\_label\_ratios

**Reference:** [Jones and Laffan \(2008\) Trans Philol Soc](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
HIER_A	A score for each level	2
HIER_ARAT	Ratio of A scores between adjacent levels	2
HIER_ASUM	Sum of shared label sample counts	2
HIER_ASUMRAT	1 - Ratio of shared label sample counts between adjacent levels	2
HIER_B	B score for each level	2
HIER_BRAT	Ratio of B scores between adjacent levels	2
HIER_C	C score for each level	2

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
HIER_CRAT	Ratio of C scores between adjacent levels	2

## 2.4 Lists and Counts

### 2.4.1 Element arrays

**Description:** Arrays of elements used in neighbour sets 1 and 2. These form the basis for all the spatial calculations.

**Subroutine:** calc\_element\_lists\_used\_as\_arrays

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
EL_ARRAY_ALL	Array of elements in both neighbour sets	2
EL_ARRAY_SET1	Array of elements in neighbour set 1	1
EL_ARRAY_SET2	Array of elements in neighbour set 2	2

### 2.4.2 Element counts

**Description:** Counts of elements used in neighbour sets 1 and 2.

**Subroutine:** calc\_elements\_used

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
EL_COUNT_ALL	Count of elements in both neighbour sets	region grower	1
EL_COUNT_SET1	Count of elements in neighbour set 1		1
EL_COUNT_SET2	Count of elements in neighbour set 2		2

### 2.4.3 Element lists

**Description:** [DEPRECATED] Lists of elements used in neighbour sets 1 and 2. These form the basis for all the spatial calculations. The return types are inconsistent. New code should use `calc_element_lists_used_as_arrays`

**Subroutine:** `calc_element_lists_used`

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
EL_LIST_ALL	List of elements in both neighbour sets	2
EL_LIST_SET1	List of elements in neighbour set 1	1
EL_LIST_SET2	List of elements in neighbour set 2	2

### 2.4.4 Label counts

**Description:** Counts of labels in neighbour sets 1 and 2. These form the basis for the Taxonomic Dissimilarity and Comparison indices.

**Subroutine:** `calc_abc_counts`

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
ABC_A	Count of labels common to both neighbour sets	region grower	2
ABC_ABC	Total label count across both neighbour sets (same as RICHNESS_ALL)	region grower	2
ABC_B	Count of labels unique to neighbour set 1		2
ABC_C	Count of labels unique to neighbour set 2		2

### 2.4.5 Label counts not in sample

**Description:** Count of basedata labels not in either neighbour set (shared absence) Used in some of the dissimilarity metrics.

**Subroutine:** calc\_d

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ABC_D	Count of labels not in either neighbour set (D score)	1

### 2.4.6 Local range lists

**Description:** Lists of labels with their local ranges as values. The local ranges are the number of elements in which each label is found in each neighbour set.

**Subroutine:** calc\_local\_range\_lists

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ABC2_LABELS_ALL	List of labels in both neighbour sets	2
ABC2_LABELS_SET1	List of labels in neighbour set 1	1
ABC2_LABELS_SET2	List of labels in neighbour set 2	2

### 2.4.7 Local range summary statistics

**Description:** Summary stats of the local ranges within neighbour sets.

**Subroutine:** calc\_local\_range\_stats

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ABC2_MEAN_ALL	Mean label range in both element sets	1
ABC2_MEAN_SET1	Mean label range in neighbour set 1	1
ABC2_MEAN_SET2	Mean label range in neighbour set 2	2

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ABC2_SD_ALL	Standard deviation of label ranges in both element sets	2
ABC2_SD_SET1	Standard deviation of label ranges in neighbour set 1	1
ABC2_SD_SET2	Standard deviation of label ranges in neighbour set 2	2

#### 2.4.8 Non-empty element counts

**Description:** Counts of non-empty elements in neighbour sets 1 and 2.

**Subroutine:** calc\_nonempty\_elements\_used

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
EL_COUNT_NONEMPTY_ALL	Count of non-empty elements in both neighbour sets	1
EL_COUNT_NONEMPTY_SET1	Count of non-empty elements in neighbour set 1	1
EL_COUNT_NONEMPTY_SET2	Count of non-empty elements in neighbour set 2	2

#### 2.4.9 Rank relative sample counts per label

**Description:** Find the per-group percentile rank of all labels across both neighbour sets, relative to the processing group. An absence is treated as a sample count of zero.

**Subroutine:** calc\_label\_count\_quantile\_position

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
LA-BEL_COUNT_RANK_PCT	List of percentile ranks for each label's sample count	1

### 2.4.10 Redundancy

**Description:** Ratio of labels to samples. Values close to 1 are well sampled while zero means there is no redundancy in the sampling

**Subroutine:** calc\_redundancy

**Reference:** [Garcillan et al. \(2003\)](#) J Veget. Sci

**Formula:**  $= 1 - \frac{\text{richness}}{\text{sum of the sample counts}}$

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
REDUN-DANCY_ALL	for both neighbour sets	region grower	1	$= 1 - \frac{RICHNESS\_ALL}{ABC3\_SUM\_ALL}$
REDUN-DANCY_SET1	for neighbour set 1		1	$= 1 - \frac{RICHNESS\_SET1}{ABC3\_SUM\_SET1}$
REDUN-DANCY_SET2	for neighbour set 2		2	$= 1 - \frac{RICHNESS\_SET2}{ABC3\_SUM\_SET2}$

### 2.4.11 Richness

**Description:** Count the number of labels in the neighbour sets

**Subroutine:** calc\_richness

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
RICHNESS_ALL	for both sets of neighbours	region grower	1
RICHNESS_SET1	for neighbour set 1		1
RICHNESS_SET2	for neighbour set 2		2

### 2.4.12 Sample count lists

**Description:** Lists of sample counts for each label within the neighbour sets. These form the basis of the sample indices.

**Subroutine:** calc\_local\_sample\_count\_lists

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ABC3_LABELS_ALL	List of labels in both neighbour sets with their sample counts as the values.	2
ABC3_LABELS_SET1	List of labels in neighbour set 1. 1. Values are the sample counts.	1
ABC3_LABELS_SET2	List of labels in neighbour set 2. 2. Values are the sample counts.	2

### 2.4.13 Sample count quantiles

**Description:** Quantiles of the sample counts across the neighbour sets.

**Subroutine:** calc\_local\_sample\_count\_quantiles

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
ABC3_QUANTILES_ALL	List of quantiles for both neighbour sets	2
ABC3_QUANTILES_SET1	List of quantiles for neighbour set 1	1
ABC3_QUANTILES_SET2	List of quantiles for neighbour set 2	2

### 2.4.14 Sample count summary stats

**Description:** Summary stats of the sample counts across the neighbour sets.

**Subroutine:** calc\_local\_sample\_count\_stats

**Indices:**



<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
ABC3_MEAN_ALL	Mean of label sample counts across both element sets.		2
ABC3_MEAN_SET1	Mean of label sample counts in neighbour set1.		1
ABC3_MEAN_SET2	Mean of label sample counts in neighbour set 2.		2
ABC3_SD_ALL	Standard deviation of label sample counts in both element sets.		2
ABC3_SD_SET1	Standard deviation of sample counts in neighbour set 1.		1
ABC3_SD_SET2	Standard deviation of label sample counts in neighbour set 2.		2
ABC3_SUM_ALL	Sum of the label sample counts across both neighbour sets.	region grower	2
ABC3_SUM_SET1	Sum of the label sample counts across both neighbour sets.		1
ABC3_SUM_SET2	Sum of the label sample counts in neighbour set2.		2

## 2.5 Matrix

### 2.5.1 Compare dissimilarity matrix values

**Description:** Compare the set of labels in one neighbour set with those in another using their matrix values. Labels not in the matrix are ignored. (This calculation assumes a matrix of dissimilarities and uses 0 as identical, so take care).

**Subroutine:** calc\_compare\_dissim\_matrix\_values

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
MXD_COUNT	Count of comparisons used.		2
MXD_LIST1	List of the labels used from neighbour set 1 (those in the matrix). The list values are the number of times each label was used in the calculations. This will always be 1 for labels in neighbour set 1.		2
MXD_LIST2	List of the labels used from neighbour set 2 (those in the matrix). The list values are the number of times each label was used in the calculations. This will equal the number of labels used from neighbour set 1.		2
MXD_MEAN	Mean dissimilarity of labels in set 1 to those in set 2.		2
MXD_VARIANCE	Variance of the dissimilarity values, set 1 vs set 2.	cluster metric	2

## 2.5.2 Matrix statistics

**Description:** Calculate summary statistics of matrix elements in the selected matrix for labels found across both neighbour sets. Labels not in the matrix are ignored.

**Subroutine:** calc\_matrix\_stats

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
MX_KURT	Kurtosis		1
MX_LABELS	List of the matrix labels in the neighbour sets		1
MX_MAXVALUE	Maximum value	region grower	1
MX_MEAN	Mean		1
MX_MEDIAN	Median		1
MX_MINVALUE	Minimum value		1
MX_N	Number of samples (matrix elements, not labels)		1
MX_PCT05	5th percentile value		1
MX_PCT25	First quartile (25th percentile)		1
MX_PCT75	Third quartile (75th percentile)		1
MX_PCT95	95th percentile value		1
MX_RANGE	Range (max-min)		1
MX_SD	Standard deviation		1
MX_SKEW	Skewness		1
MX_VALUES	List of the matrix values		1

### 2.5.3 Rao's quadratic entropy, matrix weighted

**Description:** Calculate Rao's quadratic entropy for a matrix weights scheme. BaseData labels not in the matrix are ignored

**Subroutine:** calc\_mx\_rao\_qe

**Formula:**  $= \sum_{i \in L} \sum_{j \in L} d_{ij} p_i p_j$  where  $p_i$  and  $p_j$  are the sample counts for the i'th and j'th labels,  $d_{ij}$  is the matrix value for the pair of labels  $ij$  and  $L$  is the set of labels across both neighbour sets that occur in the matrix.

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
MX_RAO_QE	Matrix weighted quadratic entropy	1

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
MX_RAO_TLABELS	List of labels and values used in the MX_RAO_QE calculations	1
MX_RAO_TN	Count of comparisons used to calculate MX_RAO_QE	1

## 2.6 Numeric Labels

### 2.6.1 Numeric label data

**Description:** The underlying data used for the numeric labels stats, as an array. For the hash form, use the ABC3\_LABELS\_ALL index from the ‘Sample count lists’ calculation.

**Subroutine:** calc\_numeric\_label\_data

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
NUM_DATA_ARRAY	Numeric label data in array form. Multiple occurrences are repeated based on their sample counts.	1

### 2.6.2 Numeric label dissimilarity

**Description:** Compare the set of numeric labels in one neighbour set with those in another.

**Subroutine:** calc\_numeric\_label\_dissimilarity

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
NUMD_AB-SMEAN	Mean absolute dissimilarity of labels in set 1 to those in set 2.	cluster metric	2	$\frac{\sum_{l_{1i} \in L_1} \sum_{l_{2j} \in L_2} \text{abs}(l_{1i} - l_{2j})(w_{1i} \times w_{2j})}{n_1 \times n_2}$ <p>where <math>L_1</math> and <math>L_2</math> are the labels in neighbour sets 1 and 2 respectively, and <math>n_1</math> and <math>n_2</math> are the sample counts in neighbour sets 1 and 2</p>
NUMD_COUNT	Count of comparisons used.		2	$= n_1 * n_2$ <p>where values are as for <i>NUMD_ABSMEAN</i></p>
NUMD_VARI-ANCE	Variance of the dissimilarity values (mean squared deviation), set 1 vs set 2.	cluster metric	2	$\frac{\sum_{l_{1i} \in L_1} \sum_{l_{2j} \in L_2} (l_{1i} - l_{2j})^2 (w_{1i} \times w_{2j})}{n_1 \times n_2}$ <p>where values are as for <i>NUMD_ABSMEAN</i></p>

### 2.6.3 Numeric label harmonic and geometric means

**Description:** Calculate geometric and harmonic means for a set of numeric labels.

**Subroutine:** calc\_numeric\_label\_other\_means

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
NUM_GMEAN	Geometric mean	1
NUM_HMEAN	Harmonic mean	1

### 2.6.4 Numeric label quantiles

**Description:** Calculate quantiles from a set of numeric labels. Weights by samples so multiple occurrences are accounted for.

**Subroutine:** calc\_numeric\_label\_quantiles

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
NUM_Q005	5th percentile	1
NUM_Q010	10th percentile	1
NUM_Q015	15th percentile	1
NUM_Q020	20th percentile	1
NUM_Q025	25th percentile	1
NUM_Q030	30th percentile	1
NUM_Q035	35th percentile	1
NUM_Q040	40th percentile	1
NUM_Q045	45th percentile	1
NUM_Q050	50th percentile	1
NUM_Q055	55th percentile	1
NUM_Q060	60th percentile	1
NUM_Q065	65th percentile	1
NUM_Q070	70th percentile	1
NUM_Q075	75th percentile	1
NUM_Q080	80th percentile	1
NUM_Q085	85th percentile	1
NUM_Q090	90th percentile	1
NUM_Q095	95th percentile	1

### 2.6.5 Numeric label statistics

**Description:** Calculate summary statistics from a set of numeric labels. Weights by samples so multiple occurrences are accounted for.

**Subroutine:** calc\_numeric\_label\_stats

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
NUM_CV	Coefficient of variation (NUM_SD / NUM_MEAN)		1
NUM_KURT	Kurtosis		1
NUM_MAX	Maximum value (100th quantile)	region grower	1

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
NUM_MEAN	Mean		1
NUM_MIN	Minimum value (zero quantile)		1
NUM_N	Number of samples	region grower	1
NUM_RANGE	Range (max - min)		1
NUM_SD	Standard deviation		1
NUM_SKEW	Skewness		1

### 2.6.6 Numeric labels Gi\* statistic

**Description:** Getis-Ord Gi\* statistic for numeric labels across both neighbour sets

**Subroutine:** calc\_num\_labels\_gistar

**Reference:** [Getis and Ord \(1992\) Geographical Analysis](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
NUM_GISTAR	List of Gi* scores	1

## 2.7 PhyloCom Indices

### 2.7.1 NRI and NTI expected values

**Description:** Expected values used in the NRI and NTI calculations. Derived using a null model without resampling where each label has an equal probability of being selected (a null model of even distribution). The expected mean and SD are the same for each unique number of labels across all neighbour sets. This means if you have three neighbour sets, each with three labels, then the expected values will be identical for each, even if the labels are completely different.

**Subroutine:** calc\_nri\_nti\_expected\_values

**Reference:** [Webb et al. \(2008\) <https://doi.org/10.1093/bioinformatics/btn358>](#), [Tsirogiannis et al. \(2012\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PHYLO_NRI_NTI_SAM- PLE_N	Number of random resamples used	1
PHYLO_NRI_SAM- PLE_MEAN	Expected mean of pair-wise distances	1
PHYLO_NRI_SAM- PLE_SD	Expected standard deviation of pair-wise distances	1
PHYLO_NTI_SAM- PLE_MEAN	Expected mean of nearest taxon distances	1
PHYLO_NTI_SAM- PLE_SD	Expected standard deviation of nearest taxon distances	1

### 2.7.2 NRI and NTI, abundance weighted

**Description:** NRI and NTI for the set of labels on the tree in the sample. This version is -1\* the Phylocom implementation, so values >0 have longer branches than expected. Abundance weighted.

**Subroutine:** calc\_nri\_nti3

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PHYLO_NRI3	Net Relatedness Index, abundance weighted	1
PHYLO_NTI3	Nearest Taxon Index, abundance weighted	1

### 2.7.3 NRI and NTI, local range weighted

**Description:** NRI and NTI for the set of labels on the tree in the sample. This version is -1\* the Phylocom implementation, so values >0 have longer branches than expected. Local range weighted.

**Subroutine:** calc\_nri\_nti2

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PHYLO_NRI2	Net Relatedness Index, local range weighted	1
PHYLO_NTI2	Nearest Taxon Index, local range weighted	1



## 2.7.4 NRI and NTI, unweighted

**Description:** NRI and NTI for the set of labels on the tree in the sample. This version is -1\* the Phylocom implementation, so values >0 have longer branches than expected. Not weighted by sample counts, so each label counts once only.

**Subroutine:** calc\_nri\_ntil

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_NRI1	Net Relatedness Index, unweighted	1	$NRI = \frac{MPD_{obs} - mean(MPD_{rand})}{sd(MPD_{rand})}$
PHYLO_NTI1	Nearest Taxon Index, unweighted	1	$NTI = \frac{MNTD_{obs} - mean(MNTD_{rand})}{sd(MNTD_{rand})}$

## 2.7.5 Net VPD expected values

**Description:** Expected values for VPD, analogous to the NRI/NTI results

**Subroutine:** calc\_vpd\_expected\_values

**Reference:** [Warwick & Clarke \(2001\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PHYLO_NET_VPD_SAM- PLE_MEAN	Expected mean of pair-wise variance (VPD)	1
PHYLO_NET_VPD_SAM- PLE_N	Number of random resamples used to calculate expected pair-wise variance scores(will equal PHYLO_NRI_NTI_SAM- PLE_N for non-ultrametric trees)	1
PHYLO_NET_VPD_SAM- PLE_SD	Expected standard deviation of pair-wise variance (VPD)	1

### 2.7.6 Net variance of pair-wise phylogenetic distances, unweighted

**Description:** Z-score of VPD calculated using NRI/NTI resampling Not weighted by sample counts, so each label counts once only.

**Subroutine:** calc\_net\_vpd

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PHYLO_NET_VPD	Net variance of pair-wise phylogenetic distances, unweighted	1

### 2.7.7 Phylogenetic and Nearest taxon distances, abundance weighted

**Description:** Distance stats from each label to the nearest label along the tree. Compares with all other labels across both neighbour sets. Weighted by sample counts (which currently must be integers)

**Subroutine:** calc\_phylo\_mpd\_mntd3

**Reference:** [Webb et al. \(2008\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PMPD3_MAX	Maximum of pairwise phylogenetic distances		1	

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PMPD3_MEAN	Mean of pairwise phylogenetic distances		1	$MPD = \frac{\sum_{t_i=1}^{n_t-1} \sum_{t_j=1}^{n_t} d_{t_i \leftrightarrow t_j}}{(n_t-1)^2}, i \neq j$ <p>where <math>d_{t_i \leftrightarrow t_j} = \sum_{b \in B_{t_i \leftrightarrow t_j}} L_b</math> is the sum of the branch lengths along the path connecting <math>t_i</math> and <math>t_j</math> such that <math>L_b</math> is the length of each branch in the set of branches <math>B</math></p>
PMPD3_MIN	Minimum of pairwise phylogenetic distances		1	
PMPD3_N	Count of pairwise phylogenetic distances		1	
PMPD3_RMSD	Root mean squared pairwise phylogenetic distances		1	

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PMPD3_VARI- ANCE	Variance of pairwise phylogenetic distances, similar to Clarke and Warwick (2001; <a href="http://dx.doi.org/10.3354/meps216265">http://dx.doi.org/10.3354/meps216265</a> ) but uses tip-to-tip distances instead of tip to most recent common ancestor.		1	
PNTD3_MAX	Maximum of nearest taxon distances	region grower	1	
PNTD3_MEAN	Mean of nearest taxon distances		1	
PNTD3_MIN	Minimum of nearest taxon distances		1	
PNTD3_N	Count of nearest taxon distances		1	
PNTD3_RMSD	Root mean squared nearest taxon distances		1	
PNTD3_VARI- ANCE	Variance of nearest taxon distances		1	

### 2.7.8 Phylogenetic and Nearest taxon distances, local range weighted

**Description:** Distance stats from each label to the nearest label along the tree. Compares with all other labels across both neighbour sets. Weighted by sample counts

**Subroutine:** `calc_phylo_mpd_mntd2`

**Reference:** [Webb et al. \(2008\)](#)

# Indices:

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PMPD2_MAX	Maximum of pairwise phylogenetic distances		1	
PMPD2_MEAN	Mean of pairwise phylogenetic distances		1	$MPD = \frac{\sum_{i=1}^{n_t-1} \sum_{j=1}^{n_t} d_{t_i \leftrightarrow t_j}}{(n_t-1)^2}, i \neq j$ <p>where <math>d_{t_i \leftrightarrow t_j}</math> is the sum of the branch lengths along the path connecting <math>t_i</math> and <math>t_j</math> such that <math>L_b</math> is the length of each branch in the set of branches <math>B</math></p>
PMPD2_MIN	Minimum of pairwise phylogenetic distances		1	
PMPD2_N	Count of pairwise phylogenetic distances		1	
PMPD2_RMSD	Root mean squared pairwise phylogenetic distances		1	

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PMPD2_VARI- ANCE	Variance of pairwise phylogenetic distances, similar to Clarke and Warwick (2001; <a href="http://dx.doi.org/10.3354/meps216265">http://dx.doi.org/10.3354/meps216265</a> ) but uses tip-to-tip distances instead of tip to most recent common ancestor.		1	
PNTD2_MAX	Maximum of nearest taxon distances	region grower	1	
PNTD2_MEAN	Mean of nearest taxon distances		1	
PNTD2_MIN	Minimum of nearest taxon distances		1	
PNTD2_N	Count of nearest taxon distances		1	
PNTD2_RMSD	Root mean squared nearest taxon distances		1	
PNTD2_VARI- ANCE	Variance of nearest taxon distances		1	

### 2.7.9 Phylogenetic and Nearest taxon distances, unweighted

**Description:** Distance stats from each label to the nearest label along the tree. Compares with all other labels across both neighbour sets.

**Subroutine:** `calc_phylo_mpd_mntd1`

**Reference:** [Webb et al. \(2008\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PMPD1_MAX	Maximum of pairwise phylogenetic distances		1	
PMPD1_MEAN	Mean of pairwise phylogenetic distances		1	$MPD = \frac{\sum_{t_i=1}^{n_t-1} \sum_{t_j=1}^{n_t} d_{t_i \leftrightarrow t_j}}{(n_t-1)^2}, i \neq j$ <p>where <math>d_{t_i \leftrightarrow t_j}</math> is the sum of the branch lengths along the path connecting <math>t_i</math> and <math>t_j</math> such that <math>L_b</math> is the length of each branch in the set of branches <math>B</math></p>
PMPD1_MIN	Minimum of pairwise phylogenetic distances		1	
PMPD1_N	Count of pairwise phylogenetic distances		1	
PMPD1_RMSD	Root mean squared pairwise phylogenetic distances		1	

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PMPD1_VARI- ANCE	Variance of pairwise phylogenetic distances, similar to Clarke and Warwick (2001; <a href="http://dx.doi.org/10.3354/meps216265">http://dx.doi.org/10.3354/meps216265</a> ) but uses tip-to-tip distances instead of tip to most recent common ancestor.		1	
PNTD1_MAX	Maximum of nearest taxon distances	region grower	1	
PNTD1_MEAN	Mean of nearest taxon distances		1	
PNTD1_MIN	Minimum of nearest taxon distances		1	
PNTD1_N	Count of nearest taxon distances		1	
PNTD1_RMSD	Root mean squared nearest taxon distances		1	
PNTD1_VARI- ANCE	Variance of nearest taxon distances		1	

## 2.8 Phylogenetic Endemism Indices

### 2.8.1 Corrected weighted phylogenetic endemism

**Description:** What proportion of the PD is range-restricted to this neighbour set?

**Subroutine:** `calc_phylo_corrected_weighted_endemism`



**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
PE_CWE	Corrected weighted endemism. This is the phylogenetic analogue of corrected weighted endemism.	1	$PE_{WE}/PD$	

**2.8.2 Corrected weighted phylogenetic endemism, central variant**

**Description:** What proportion of the PD in neighbour set 1 is range-restricted to neighbour sets 1 and 2?

**Subroutine:** calc\_pe\_central\_cwe

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PEC_CWE	Corrected weighted phylogenetic endemism, central variant	1
PEC_CWE_PD	PD used in the PEC_CWE index.	1

**2.8.3 Corrected weighted phylogenetic rarity**

**Description:** What proportion of the PD is abundance-restricted to this neighbour set?

**Subroutine:** calc\_phylo\_corrected\_weighted\_rarity

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
PHYLO_RAR- ITY_CWR	Corrected weighted phylogenetic rarity. This is the phylogenetic rarity analogue of corrected weighted endemism.	1	$AED_T/PD$	

## 2.8.4 PD-Endemism

**Description:** Absolute endemism analogue of PE. It is the sum of the branch lengths restricted to the neighbour sets.

**Subroutine:** calc\_pd\_endemism

**Reference:** See [Faith \(2004\) Cons Biol.](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
PD_ENDEMISM	Phylogenetic Diversity Endemism	region grower	1
PD_ENDEMISM_P	Phylogenetic Diversity Endemism, as a proportion of the whole tree	region grower	1
PD_EN- DEMISM_WTS	Phylogenetic Diversity Endemism weights per node found only in the neighbour set		1

### 2.8.5 PE clade contributions

**Description:** Contribution of each node and its descendents to the Phylogenetic endemism (PE) calculation.

**Subroutine:** calc\_pe\_clade\_contributions

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PE_CLADE_CONTR	List of node (clade) contributions to the PE calculation	1
PE_CLADE_CONTR_P	List of node (clade) contributions to the PE calculation, proportional to the entire tree	1
PE_CLADE_SCORE	List of PE scores for each node (clade), being the sum of all descendent PE weights	1

### 2.8.6 PE clade loss

**Description:** How much of the PE would be lost if a clade were to be removed? Calculates the clade PE below the last ancestral node in the neighbour set which would still be in the neighbour set.

**Subroutine:** calc\_pe\_clade\_loss

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PE_CLADE_LOSS_CONTR	List of the proportion of the PE score which would be lost if each clade were removed.	1
PE_CLADE_LOSS_CONTR_P	As per PE_CLADE_LOSS but proportional to the entire tree	1
PE_CLADE_LOSS_SCORE	List of how much PE would be lost if each clade were removed.	1

### 2.8.7 PE clade loss (ancestral component)

**Description:** How much of the PE clade loss is due to the ancestral branches? The score is zero when there is no ancestral loss.

**Subroutine:** calc\_pe\_clade\_loss\_ancestral

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PE_CLADE_LOSS_ANC	List of how much ancestral PE would be lost if each clade were removed. The value is 0 when no ancestral PE is lost.	1
PE_CLADE_LOSS_ANC_P	List of the proportion of the clade's PE loss that is due to the ancestral branches.	1

### 2.8.8 Phylogenetic Endemism

**Description:** Phylogenetic endemism (PE). Uses labels across both neighbourhoods and trims the tree to exclude labels not in the BaseData object.

**Subroutine:** calc\_pe

**Reference:** [Rosauer et al \(2009\) Mol. Ecol](#); [Laity et al. \(2015\)](#); [Laffan et al. \(2016\)](#)

**Formula:**  $PE = \sum_{\lambda \in \Lambda} L_{\lambda} \frac{r_{\lambda}}{R_{\lambda}}$  where  $\Lambda$  is the set of branches found across neighbour sets 1 and 2,  $L_{\lambda}$  is the length of branch  $\lambda$ ,  $r_{\lambda}$  is the local range of branch  $\lambda$  (the number of groups in neighbour sets 1 and 2 containing it), and  $R_{\lambda}$  is the global range of branch  $\lambda$  (the number of groups across the entire data set containing it).

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PE_WE	Phylogenetic endemism	region grower	1	

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PE_WE_P	Phylogenetic weighted endemism as a proportion of the total tree length	region grower	1	$PE\_WE/L$ where L is the sum of all branch lengths in the trimmed tree

### 2.8.9 Phylogenetic Endemism central

**Description:** A variant of Phylogenetic endemism (PE) that uses labels from neighbour set 1 but local ranges from across both neighbour sets 1 and 2. Identical to PE if only one neighbour set is specified.

**Subroutine:** calc\_pe\_central

**Reference:** [Rosauer et al \(2009\)](#) Mol. Ecol

**Formula:**  $PEC = \sum_{\lambda \in \Lambda} L_{\lambda} \frac{r_{\lambda}}{R_{\lambda}}$  where  $\Lambda$  is the set of branches found across neighbour set 1 only,  $L_{\lambda}$  is the length of branch  $\lambda$ ,  $r_{\lambda}$  is the local range of branch  $\lambda$  (the number of groups in neighbour sets 1 and 2 containing it), and  $R_{\lambda}$  is the global range of branch  $\lambda$  (the number of groups across the entire data set containing it).

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
PEC_WE	Phylogenetic endemism, central variant	region grower	1
PEC_WE_P	Phylogenetic weighted endemism as a proportion of the total tree length, central variant	region grower	1

### 2.8.10 Phylogenetic Endemism central lists

**Description:** Lists underlying the phylogenetic endemism central indices. Uses labels from neighbour set one but local ranges from across both neighbour sets.

**Subroutine:** calc\_pe\_central\_lists

**Reference:** [Rosauer et al \(2009\)](#) Mol. Ecol

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PEC_LOCAL_RANGELIST	Phylogenetic endemism local range lists, central variant	1
PEC_RANGELIST	Phylogenetic endemism global range lists, central variant	1
PEC_WTLIST	Phylogenetic endemism weights, central variant	1

### 2.8.11 Phylogenetic Endemism lists

**Description:** Lists used in the Phylogenetic endemism (PE) calculations.

**Subroutine:** calc\_pe\_lists

**Reference:** [Rosauer et al \(2009\)](#) Mol. Ecol

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PE_LOCAL_RANGELIST	Local node ranges used in PE calculations (number of groups in which a node is found)	1
PE_RANGELIST	Node ranges used in PE calculations	1
PE_WTLIST	Node weights used in PE calculations	1

### 2.8.12 Phylogenetic Endemism single

**Description:** PE scores, but not weighted by local ranges. This is the strict interpretation of the formula given in Rosauer et al. (2009), although the approach has always been implemented as the fraction of each branch's geographic range that is found in the sample window (see formula for PE\_WE).

**Subroutine:** calc\_pe\_single

**Reference:** [Rosauer et al \(2009\)](#) Mol. Ecol

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
PE_WE_SINGLE	Phylogenetic endemism unweighted by the number of neighbours. Counts each label only once, regardless of how many groups in the neighbourhood it is found in. Useful if your data have sampling biases. Better with small sample windows.	region grower	1
PE_WE_SIN- GLE_P	Phylogenetic endemism unweighted by the number of neighbours as a proportion of the total tree length. Counts each label only once, regardless of how many groups in the neighbourhood it is found. Useful if your data have sampling biases.	region grower	1

### 2.8.13 RWiBaLD

**Description:** Range weighted branch length differences. Values are spatially constant, only the subsets change

**Subroutine:** calc\_rwibald

**Reference:** Mishler et al. (in review)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
RWIBALD_CODES	RWiBaLD codes, 1=palaeo, 2=neo, 3=meso	1
RWIBALD_CODE_COUNTS	Counts of branches in each RWiBaLD category	1
RWIBALD_DIFFS	RWiBaLD scores (continuous differences)	1
RWIBALD_METADATA	General metadata for the RWiBaLD calculations	1
RWIBALD_RR_DIFFS	RWiBaLD scores for the range restricted subset (continuous differences)	1

## 2.9 Phylogenetic Indices

### 2.9.1 Count labels on tree

**Description:** Count the number of labels that are on the tree

**Subroutine:** calc\_count\_labels\_on\_tree

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
PHYLO_LABELS_ON_TREE_COUNT	The number of labels found on the tree, across both neighbour sets	region grower	1

### 2.9.2 Evolutionary distinctiveness

**Description:** Evolutionary distinctiveness metrics (AED, ED, ES) Label values are constant for all neighbourhoods in which each label is found.

**Subroutine:** calc\_phylo\_aed

**Reference:** [Cadotte & Davies \(2010\)](#)



**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Reference</i>
PHYLO_AED_LIST	Abundance weighted ED per terminal label	1	<a href="#">Cadotte &amp; Davies (2010)</a>
PHYLO_ED_LIST	“Fair proportion” partitioning of PD per terminal label	1	<a href="#">Isaac et al. (2007)</a>
PHYLO_ES_LIST	Equal splits partitioning of PD per terminal label	1	<a href="#">Redding &amp; Mooers (2006)</a>

**2.9.3 Evolutionary distinctiveness per site**

**Description:** Site level evolutionary distinctiveness

**Subroutine:** calc\_phylo\_aed\_t

**Reference:** [Cadotte & Davies \(2010\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Reference</i>
PHYLO_AED_T	Abundance weighted ED_t (sum of values in PHYLO_AED_LIST times their abundances). This is equivalent to a phylogenetic rarity score (see phylogenetic endemism)	region grower	1	<a href="#">Cadotte &amp; Davies (2010)</a>

## 2.9.4 Evolutionary distinctiveness per terminal taxon per site

**Description:** Site level evolutionary distinctiveness per terminal taxon

**Subroutine:** calc\_phylo\_aed\_t\_wtlists

**Reference:** [Cadotte & Davies \(2010\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Reference</i>
PHYLO_AED_T_WTLISTS	Abundance weighted ED per terminal taxon (the AED score of each taxon multiplied by its abundance in the sample)	1	<a href="#">Cadotte &amp; Davies (2010)</a>
PHYLO_AED_T_WTLISTS_P	Proportional contribution of each terminal taxon to the AED_T score	1	<a href="#">Cadotte &amp; Davies (2010)</a>

## 2.9.5 Labels not on tree

**Description:** Create a hash of the labels that are not on the tree

**Subroutine:** calc\_labels\_not\_on\_tree

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
PHYLO_LA- BELS_NOT_ON_TREE	A hash of labels that are not found on the tree, across both neighbour sets		1
PHYLO_LA- BELS_NOT_ON_TREE_N	Number of labels not on the tree	region grower	1
PHYLO_LA- BELS_NOT_ON_TREE_P	Proportion of labels not on the tree		1

### 2.9.6 Labels on tree

**Description:** Create a hash of the labels that are on the tree

**Subroutine:** calc\_labels\_on\_tree

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PHYLO_LA- BELS_ON_TREE	A hash of labels that are found on the tree, across both neighbour sets	1

### 2.9.7 Last shared ancestor properties

**Description:** Properties of the last shared ancestor of an assemblage. Uses labels in both neighbourhoods.

**Subroutine:** calc\_last\_shared\_ancestor\_props

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
LAST_SHARED_ANCE- TOR_DEPTH	Depth of last shared ancestor from the root. The root has a depth of zero.	1
LAST_SHARED_ANCE- TOR_DIST_TO_ROOT	Distance along the tree from the last shared ancestor to the root. Includes the shared ancestor's length.	1
LAST_SHARED_ANCE- TOR_DIST_TO_TIP	Distance along the tree from the last shared ancestor to the furthest tip in the sample. This is calculated from the point at which the lineages merge, which is the branch end further from the root	1
LAST_SHARED_ANCE- TOR_LENGTH	Branch length of last shared ancestor	1

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
LAST_SHARED_ANCESTOR_POS_REL	Relative position of the last shared ancestor. Value is the fraction of the distance from the root to the furthest terminal. This uses the point at which the lineages merge, and is the branch end further from the root	1

### 2.9.8 PD clade contributions

**Description:** Contribution of each node and its descendents to the Phylogenetic diversity (PD) calculation.

**Subroutine:** calc\_pd\_clade\_contributions

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PD_CLADE_CONTR	List of node (clade) contributions to the PD calculation	1
PD_CLADE_CONTR_P	List of node (clade) contributions to the PD calculation, proportional to the entire tree	1
PD_CLADE_SCORE	List of PD scores for each node (clade), being the sum of all descendent branch lengths	1

### 2.9.9 PD clade loss

**Description:** How much of the PD would be lost if a clade were to be removed? Calculates the clade PD below the last ancestral node in the neighbour set which would still be in the neighbour set.

**Subroutine:** calc\_pd\_clade\_loss

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PD_CLADE_LOSS_CONTR	List of the proportion of the PD score which would be lost if each clade were removed.	1
PD_CLADE_LOSS_CONTR_Rs	Rs per PD_CLADE_LOSS but proportional to the entire tree	1
PD_CLADE_LOSS_SCORE	List of how much PD would be lost if each clade were removed.	1

**2.9.10 PD clade loss (ancestral component)**

**Description:** How much of the PD clade loss is due to the ancestral branches? The score is zero when there is no ancestral loss.

**Subroutine:** calc\_pd\_clade\_loss\_ancestral

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PD_CLADE_LOSS_ANC	List of how much ancestral PE would be lost if each clade were removed. The value is 0 when no ancestral PD is lost.	1
PD_CLADE_LOSS_ANC_P	List of the proportion of the clade's PD loss that is due to the ancestral branches.	1

**2.9.11 Phylogenetic Abundance**

**Description:** Phylogenetic abundance based on branch lengths back to the root of the tree. Uses labels in both neighbourhoods.

**Subroutine:** calc\_phylo\_abundance

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
PHYLO_ABUN DANCE	Phylogenetic abundance	region grower	1	$= \sum_{c \in C} A \times L_c$ <p>where <math>C</math> is the set of branches in the minimum spanning path joining the labels in both neighbour sets to the root of the tree, <math>c</math> is a branch (a single segment between two nodes) in the spanning path <math>C</math>, and <math>L_c</math> is the length of branch <math>c</math>, and <math>A</math> is the abundance of that branch (the sum of its descendant label abundances).</p>	
PHYLO_ABUN DANCE_BRANCH FLASH	Phylogenetic abundance per branch		1		

### 2.9.12 Phylogenetic Diversity

**Description:** Phylogenetic diversity (PD) based on branch lengths back to the root of the tree. Uses labels in both neighbourhoods.

**Subroutine:** calc\_pd

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
PD	Phylogenetic diversity	region grower	1	$= \sum_{c \in C} L_c$ where $C$ is the set of branches in the minimum spanning path joining the labels in both neighbour sets to the root of the tree, $c$ is a branch (a single segment between two nodes) in the spanning path $C$ , and $L_c$ is the length of branch $c$ .	<a href="#">Faith (1992)</a> <a href="#">Biol. Cons</a>

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>	<i>Reference</i>
PD_P	Phylogenetic diversity as a proportion of total tree length	region grower	1	$= \frac{PD}{\sum_{c \in C} L_c}$ where terms are the same as for PD, but $c$ , $C$ and $L_c$ are calculated for all nodes in the tree.	
PD_P_per_taxon	Phylogenetic diversity per taxon as a proportion of total tree length		1	$= \frac{PD\_P}{RICHNESS\_ALL}$	
PD_per_taxon	Phylogenetic diversity per taxon		1	$= \frac{PD}{RICHNESS\_ALL}$	

### 2.9.13 Phylogenetic Diversity (local)

**Description:** Phylogenetic diversity (PD) based on branch lengths back to the last shared ancestor. Uses labels in both neighbourhoods.

**Subroutine:** calc\_pd\_local

**Indices:**



<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PD_LOCAL	Phylogenetic diversity calculated to last shared ancestor	region grower	1	$= \sum_{c \in C} L_c$ where $C$ is the set of branches in the minimum spanning path joining the labels in both neighbour sets to the last shared ancestor, $c$ is a branch (a single segment between two nodes) in the spanning path $C$ , and $L_c$ is the length of branch $c$ .
PD_LOCAL_P	Phylogenetic diversity as a proportion of total tree length	region grower	1	$= \frac{PD}{\sum_{c \in C} L_c}$ where terms are the same as for PD, but $c$ , $C$ and $L_c$ are calculated for all nodes in the tree.

#### 2.9.14 Phylogenetic Diversity node list

**Description:** Phylogenetic diversity (PD) nodes used.

**Subroutine:** calc\_pd\_node\_list

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PD_IN- CLUDED_NODE_LIST	List of tree nodes included in the PD calculations	1

### 2.9.15 Phylogenetic Diversity terminal node count

**Description:** Number of terminal nodes in neighbour sets 1 and 2.

**Subroutine:** calc\_pd\_terminal\_node\_count

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PD_INCLUDED_TERMINAL_NODE_COUNT	Count of tree terminal nodes included in the PD calculations	1

### 2.9.16 Phylogenetic Diversity terminal node list

**Description:** Phylogenetic diversity (PD) terminal nodes used.

**Subroutine:** calc\_pd\_terminal\_node\_list

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PD_INCLUDED_TERMINAL_NODE_LIST	List of tree terminal nodes included in the PD calculations	1

## 2.10 Phylogenetic Indices (relative)

### 2.10.1 Labels not on trimmed tree

**Description:** Create a hash of the labels that are not on the trimmed tree

**Subroutine:** calc\_labels\_not\_on\_trimmed\_tree

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PHYLO_LA- BELS_NOT_ON_TRIMMED_TREE	A hash of labels that are not found on the tree after it has been trimmed to the basedata, across both neighbour sets	1
PHYLO_LA- BELS_NOT_ON_TRIMMED_TREE	Number of labels not on the trimmed tree	1
PHYLO_LA- BELS_NOT_ON_TRIMMED_TREE	Proportion of labels not on the trimmed tree	1

### 2.10.2 Labels on trimmed tree

**Description:** Create a hash of the labels that are on the trimmed tree

**Subroutine:** calc\_labels\_on\_trimmed\_tree

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
PHYLO_LA- BELS_ON_TRIMMED_TREE	A hash of labels that are found on the tree after it has been trimmed to match the basedata, across both neighbour sets	1

### 2.10.3 Relative Phylogenetic Diversity, type 1

**Description:** Relative Phylogenetic Diversity type 1 (RPD1). The ratio of the tree's PD to a null model of PD evenly distributed across terminals and where ancestral nodes are collapsed to zero length. You probably want to use RPD2 instead as it uses the tree's topology.

**Subroutine:** calc\_phylo\_rpd1

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_RPD1	RPD1		1	
PHYLO_RPD_DIFF1	How much more or less PD is there than expected, in original tree units.		1	$= tree\_length \times (PD\_P - PHYLO\_RPD\_NULL1)$
PHYLO_RPD_NULL1	Null model score used as the denominator in the RPD1 calculations	region grower	1	

#### 2.10.4 Relative Phylogenetic Diversity, type 2

**Description:** Relative Phylogenetic Diversity (RPD), type 2. The ratio of the tree's PD to a null model of PD evenly distributed across all nodes (all branches are of equal length).

**Subroutine:** calc\_phylo\_rpd2

**Reference:** [Mishler et al. \(2014\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_RPD2	RPD2		1	
PHYLO_RPD_DIFF2	How much more or less PD is there than expected, in original tree units.		1	$= tree\_length \times (PD\_P - PHYLO\_RPD\_NULL2)$
PHYLO_RPD_NULL2	Null model score used as the denominator in the RPD2 calculations	region grower	1	

### 2.10.5 Relative Phylogenetic Endemism, central

**Description:** Relative Phylogenetic Endemism (RPE). The ratio of the tree's PE to a null model where PE is calculated using a tree where all branches are of equal length. Same as RPE2 except it only uses the branches in the first neighbour set when more than one is set.

**Subroutine:** calc\_phylo\_rpe\_central

**Reference:** [Mishler et al. \(2014\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_RPEC	Relative Phylogenetic Endemism score, central	1	
PHYLO_RPE_DIFFC	How much more or less PE is there than expected, in original tree units.	1	$= tree\_length \times (PE\_WEC\_P - PHYLO\_RPE\_NULLC)$
PHYLO_RPE_NULLC	Null score used as the denominator in the PHYLO_RPEC calculations	1	

### 2.10.6 Relative Phylogenetic Endemism, type 1

**Description:** Relative Phylogenetic Endemism, type 1 (RPE1). The ratio of the tree's PE to a null model of PD evenly distributed across terminals, but with the same range per terminal and where ancestral nodes are of zero length (as per RPD1). You probably want to use RPE2 instead as it uses the tree's topology.

**Subroutine:** calc\_phylo\_rpe1

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_RPE1	Relative Phylogenetic Endemism score		1	

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_RPE_DIFF1	How much more or less PE is there than expected, in original tree units.		1	$= tree\_length \times (PE\_WE\_P - PHYLO\_RPE\_NULL1)$
PHYLO_RPE_NULL1	Null score used as the denominator in the RPE calculations	region grower	1	

### 2.10.7 Relative Phylogenetic Endemism, type 2

**Description:** Relative Phylogenetic Endemism (RPE). The ratio of the tree's PE to a null model where PE is calculated using a tree where all non-zero branches are of equal length.

**Subroutine:** calc\_phylo\_rpe2

**Reference:** [Mishler et al. \(2014\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_RPE2	Relative Phylogenetic Endemism score, type 2		1	
PHYLO_RPE_DIFF2	How much more or less PE is there than expected, in original tree units.		1	$= tree\_length \times (PE\_WE\_P - PHYLO\_RPE\_NULL2)$

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_RPE_NUM	Phylo score used as the denominator in the RPE2 calculations	region grower	1	

## 2.11 Phylogenetic Turnover

### 2.11.1 Phylo Jaccard

**Description:** Jaccard phylogenetic dissimilarity between two sets of taxa, represented by spanning sets of branches

**Subroutine:** calc\_phylo\_jaccard

**Reference:** [Lozupone and Knight \(2005\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_JACCARD	Phylo Jaccard score	cluster metric	2	$= 1 - (A / (A + B + C))$ where A is the length of shared branches, and B and C are the length of branches found only in neighbour sets 1 and 2

### 2.11.2 Phylo Range weighted Turnover

**Description:** Phylo Range weighted Turnover

**Subroutine:** calc\_phylo\_rw\_turnover

**Reference:** [Laffan et al. \(2016\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
PHYLO_RW_TURNOVER	Weighted turnover	cluster metric	2
PHYLO_RW_TURNOVER_A	Weighted turnover, shared component	region grower	2
PHYLO_RW_TURNOVER_B	Weighted turnover, component found only in nbr set 1		2
PHYLO_RW_TURNOVER_C	Weighted turnover, component found only in nbr set 2		2

### 2.11.3 Phylo S2

**Description:** S2 phylogenetic dissimilarity between two sets of taxa, represented by spanning sets of branches

**Subroutine:** calc\_phylo\_s2

**Indices:**



<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_S2	Phylo S2 score	cluster metric	2	$= 1 - (A/(A + \min(B, C)))$ where A is the sum of shared branch lengths, and B and C are the sum of branch lengths found only in neighbour sets 1 and 2

#### 2.11.4 Phylo Sorenson

**Description:** Sorenson phylogenetic dissimilarity between two sets of taxa, represented by spanning sets of branches

**Subroutine:** calc\_phylo\_sorenson

**Reference:** [Bryant et al. \(2008\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
PHYLO_SOREN- SON	Phylo Sorenson score	cluster metric	2	$1 - (2A/(2A + B + C))$ where A is the length of shared branches, and B and C are the length of branches found only in neighbour sets 1 and 2

### 2.11.5 Phylogenetic ABC

**Description:** Calculate the shared and not shared branch lengths between two sets of labels

**Subroutine:** calc\_phylo\_abc

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
PHYLO_A	Sum of branch lengths shared by labels in nbr sets 1 and 2	region grower	2
PHYLO_ABC	Sum of branch lengths associated with labels in nbr sets 1 and 2	region grower	2
PHYLO_B	Sum of branch lengths unique to labels in nbr set 1		2
PHYLO_C	Sum of branch lengths unique to labels in nbr set 2		2

## 2.12 Rarity

### 2.12.1 Rarity central

**Description:** Calculate rarity for species only in neighbour set 1, but with local sample counts calculated from both neighbour sets. Uses the same algorithm as the endemism indices but weights by sample counts instead of by groups occupied.

**Subroutine:** calc\_rarity\_central

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
RAREC_CWE	Corrected weighted rarity	1	$= \frac{RAREC\_WE}{RAREC\_RICHNESS}$

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
RAREC_RICHNESS	Richness used in RAREC_CWE (same as index RICHNESS_SET1).	1	
RAREC_WE	Weighted rarity	1	$= \sum_{t \in T} \frac{s_t}{S_t}$ where $t$ is a label (taxon) in the set of labels (taxa) $T$ across neighbour set 1, $s_t$ is sum of the sample counts for $t$ across the elements in neighbour sets 1 & 2 (its value in list ABC3_LA- BELS_ALL), and $S_t$ is the total number of samples across the data set for label $t$ (unless the total sample count is specified at import).

### 2.12.2 Rarity central lists

**Description:** Lists used in rarity central calculations

**Subroutine:** calc\_rarity\_central\_lists

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
RAREC_RANGELIST	List of ranges for each label used in the rarity central calculations	1
RAREC_WTLIST	List of weights for each label used in the rarity central calculations	1

### 2.12.3 Rarity whole

**Description:** Calculate rarity using all species in both neighbour sets. Uses the same algorithm as the endemism indices but weights by sample counts instead of by groups occupied.

**Subroutine:** calc\_rarity\_whole

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
RAREW_CWE	Corrected weighted rarity		1	$= \frac{RAREW\_WE}{RAREW\_RICHNESS}$
RAREW_RICH- NESS	Richness used in RAREW_CWE (same as index RICH- NESS_ALL).	region grower	1	
RAREW_WE	Weighted rarity	region grower	1	$= \sum_{t \in T} \frac{s_t}{S_t}$ where $t$ is a label (taxon) in the set of labels (taxa) $T$ across both neighbour sets, $s_t$ is sum of the sample counts for $t$ across the elements in neighbour sets 1 & 2 (its value in list ABC3_LA- BELS_ALL), and $S_t$ is the total number of samples across the data set for label $t$ (unless the total sample count is specified at import).

## 2.12.4 Rarity whole lists

**Description:** Lists used in rarity whole calculations

**Subroutine:** calc\_rarity\_whole\_lists

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
RAREW_RANGELIST	List of ranges for each label used in the rarity whole calculations	1
RAREW_WTLIST	List of weights for each label used in the rarity whole calculations	1

## 2.13 Richness estimators

### 2.13.1 ACE

**Description:** Abundance Coverage-based Estimator of species richness

**Subroutine:** calc\_ace

**Reference:** [Chao and Lee \(1992\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
ACE_CI_LOWER	ACE lower confidence interval estimate	region grower	1
ACE_CI_UPPER	ACE upper confidence interval estimate	region grower	1
ACE_ESTIMATE	ACE score	region grower	1
ACE_ESTI- MATE_USED_CHAO	Set to 1 when ACE cannot be calculated and so Chao1 estimate is used		1
ACE_INFRE- QUENT_COUNT	Count of infrequent species	region grower	1

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
ACE_SE	ACE standard error		1
ACE_UNDETECTED	Estimated number of undetected species	region grower	1
ACE_VARIANCE	ACE variance		1

### 2.13.2 Chao1

**Description:** Chao1 species richness estimator (abundance based)

**Subroutine:** calc\_chao1

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Reference</i>
CHAO1_CI_LOWER	Lower confidence interval for the Chao1 estimate	region grower	1	
CHAO1_CI_UPPER	Upper confidence interval for the Chao1 estimate	region grower	1	
CHAO1_ESTIMATE	Chao1 index	region grower	1	NEEDED
CHAO1_F1_COUNT	Number of singletons in the sample	region grower	1	
CHAO1_F2_COUNT	Number of doubletons in the sample	region grower	1	

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Reference</i>
CHAO1_META	Metadata indicating which formulae were used in the calculations. Numbers refer to EstimateS equations at <a href="https://www.robertk-colwell.org/media_files/63">https://www.robertk-colwell.org/media_files/63</a>		1	
CHAO1_SE	Standard error of the Chao1 estimator [= sqrt(variance)]	region grower	1	
CHAO1_UNDETECTED	Estimated number of undetected species	region grower	1	
CHAO1_VARIANCE	Variance of the Chao1 estimator	region grower	1	

### 2.13.3 Chao2

**Description:** Chao2 species richness estimator (incidence based)

**Subroutine:** calc\_chao2

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Reference</i>
CHAO2_CI_LOWER	Lower confidence interval for the Chao2 estimate	region grower	1	

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Reference</i>
CHAO2_CI_UP- PER	Upper confidence interval for the Chao2 estimate	region grower	1	NEEDED
CHAO2_ESTI- MATE	Chao2 index	region grower	1	
CHAO2_META	Metadata indicating which formulae were used in the calculations. Numbers refer to EstimateS equations at <a href="https://www.robertk-colwell.org/media_files/63">https://www.robertk-colwell.org/media_files/63</a>		1	
CHAO2_Q1_COUNT	Number of uniques in the sample	region grower	1	
CHAO2_Q2_COUNT	Number of duplicates in the sample	region grower	1	
CHAO2_SE	Standard error of the Chao2 estimator [= sqrt (variance)]	region grower	1	
CHAO2_UNDE- TECTED	Estimated number of undetected species	region grower	1	
CHAO2_VARI- ANCE	Variance of the Chao2 estimator	region grower	1	

#### 2.13.4 Hurlbert richness estimation

**Description:** Hurlbert estimated species richness scores for given number of samples.



**Subroutine:** calc\_hurlbert\_es

**Reference:** [Hurlbert, S.H. \(1971\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
HURLBERT_ES	List of Hurlbert estimated species richness scores for given number of samples	1

### 2.13.5 ICE

**Description:** Incidence Coverage-based Estimator of species richness

**Subroutine:** calc\_ice

**Reference:** [Gotelli and Chao \(2013\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
ICE_CI_LOWER	ICE lower confidence interval estimate	region grower	1
ICE_CI_UPPER	ICE upper confidence interval estimate	region grower	1
ICE_ESTIMATE	ICE score	region grower	1
ICE_ESTI- MATE_USED_CHAO	Set to 1 when ICE cannot be calculated and so Chao2 estimate is used		1
ICE_INFRE- QUENT_COUNT	Count of infrequent species	region grower	1
ICE_SE	ICE standard error		1
ICE_UNDE- TECTED	Estimated number of undetected species	region grower	1
ICE_VARIANCE	ICE variance		1

## 2.14 Taxonomic Dissimilarity and Comparison

### 2.14.1 Beta diversity

**Description:** Beta diversity between neighbour sets 1 and 2.

**Subroutine:** calc\_beta\_diversity

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
BETA_2	The other beta	cluster metric	2	$= \frac{A+B+C}{\max((A+B), (A+C))} - 1$ <p>where <math>A</math> is the count of labels found in both neighbour sets, <math>B</math> is the count unique to neighbour set 1, and <math>C</math> is the count unique to neighbour set 2. Use the <a href="#">Label counts</a> calculation to derive these directly.</p>

### 2.14.2 Bray-Curtis non-metric

**Description:** Bray-Curtis dissimilarity between two sets of labels. Reduces to the Sorenson metric for binary data (where sample counts are 1 or 0).

**Subroutine:** calc\_bray\_curtis

**Formula:**  $= 1 - \frac{2W}{A+B}$  where  $A$  is the sum of the sample counts in neighbour set 1,  $B$  is the sum of sample counts in neighbour set 2, and  $W = \sum_{i=1}^n \min(\text{sample\_count\_label}_{i_{\text{set1}}}, \text{sample\_count\_label}_{i_{\text{set2}}})$  (meaning it sums the minimum of the sample counts for each of the  $n$  labels across the two neighbour sets),

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
BC_A	The A factor used in calculations (see formula)		2
BC_B	The B factor used in calculations (see formula)		2
BC_W	The W factor used in calculations (see formula)	region grower	2
BRAY_CURTIS	Bray Curtis dissimilarity	cluster metric	2

**2.14.3 Bray-Curtis non-metric, group count normalised**

**Description:** Bray-Curtis dissimilarity between two neighbourhoods, where the counts in each neighbourhood are divided by the number of groups in each neighbourhood to correct for unbalanced sizes.

**Subroutine:** calc\_bray\_curtis\_norm\_by\_gp\_counts

**Formula:**  $= 1 - \frac{2W}{A+B}$  where  $A$  is the sum of the sample counts in neighbour set 1 normalised (divided) by the number of groups,  $B$  is the sum of the sample counts in neighbour set 2 normalised by the number of groups, and  $W = \sum_{i=1}^n \min(\text{sample\_count\_label}_{i_{set1}}, \text{sample\_count\_label}_{i_{set2}})$  (meaning it sums the minimum of the normalised sample counts for each of the  $n$  labels across the two neighbour sets),

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
BCN_A	The A factor used in calculations (see formula)		2
BCN_B	The B factor used in calculations (see formula)		2
BCN_W	The W factor used in calculations (see formula)	region grower	2

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
BRAY_CUR-TIS_NORM	Bray Curtis dissimilarity normalised by groups	cluster metric	2

#### 2.14.4 Jaccard

**Description:** Jaccard dissimilarity between the labels in neighbour sets 1 and 2.

**Subroutine:** calc\_jaccard

**Formula:**  $= 1 - \frac{A}{A+B+C}$  where  $A$  is the count of labels found in both neighbour sets,  $B$  is the count unique to neighbour set 1, and  $C$  is the count unique to neighbour set 2. Use the [Label counts](#) calculation to derive these directly.

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
JACCARD	Jaccard value, 0 is identical, 1 is completely dissimilar	cluster metric	2

#### 2.14.5 Kulczynski 2

**Description:** Kulczynski 2 dissimilarity between two sets of labels.

**Subroutine:** calc\_kulczynski2

**Formula:**  $= 1 - 0.5 \times (\frac{A}{A+B} + \frac{A}{A+C})$  where  $A$  is the count of labels found in both neighbour sets,  $B$  is the count unique to neighbour set 1, and  $C$  is the count unique to neighbour set 2. Use the [Label counts](#) calculation to derive these directly.

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
KULCZYNSKI2	Kulczynski 2 index	cluster metric	2

### 2.14.6 Nestedness-resultant

**Description:** Nestedness-resultant index between the labels in neighbour sets 1 and 2.

**Subroutine:** calc\_nestedness\_resultant

**Reference:** [Baselga \(2010\)](#) Glob Ecol Biogeog.

**Formula:**  $= \frac{|B-C|}{2A+B+C} \times \frac{A}{A+\min(B,C)} = SORENSON - S2$  where  $A$  is the count of labels found in both neighbour sets,  $B$  is the count unique to neighbour set 1, and  $C$  is the count unique to neighbour set 2. Use the [Label counts](#) calculation to derive these directly.

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
NEST_RESULTANT	Nestedness-resultant index	cluster metric	2

### 2.14.7 Range weighted Sorenson

**Description:** Range weighted Sorenson

**Subroutine:** calc\_rw\_turnover

**Reference:** [Laffan et al. \(2016\)](#)

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
RW_TURNOVER	Range weighted turnover	cluster metric	2
RW_TURNOVER_A	Range weighted turnover, shared component		2
RW_TURNOVER_B	Range weighted turnover, component found only in nbr set 1		2
RW_TURNOVER_C	Range weighted turnover, component found only in nbr set 2		2

### 2.14.8 Rao's quadratic entropy, taxonomically weighted

**Description:** Calculate Rao's quadratic entropy for a taxonomic weights scheme. Should collapse to be the Simpson index for presence/absence data.

**Subroutine:** calc\_tx\_rao\_qe

**Formula:**  $= \sum_{i \in L} \sum_{j \in L} d_{ij} p_i p_j$  where  $p_i$  and  $p_j$  are the sample counts for the i'th and j'th labels,  $d_{ij}$  is a value of zero if  $i = j$ , and a value of 1 otherwise.  $L$  is the set of labels across both neighbour sets.

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>
TX_RAO_QE	Taxonomically weighted quadratic entropy	1
TX_RAO_TLABELS	List of labels and values used in the TX_RAO_QE calculations	1
TX_RAO_TN	Count of comparisons used to calculate TX_RAO_QE	1

### 2.14.9 S2

**Description:** S2 dissimilarity between two sets of labels

**Subroutine:** calc\_s2

**Reference:** [Lennon et al. \(2001\) J Animal Ecol.](#)

**Formula:**  $= 1 - \frac{A}{A + \min(B, C)}$  where  $A$  is the count of labels found in both neighbour sets,  $B$  is the count unique to neighbour set 1, and  $C$  is the count unique to neighbour set 2. Use the [Label counts](#) calculation to derive these directly.

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
S2	S2 dissimilarity index	cluster metric	2

### 2.14.10 Simpson and Shannon

**Description:** Simpson and Shannon diversity metrics using samples from all neighbourhoods.

**Subroutine:** calc\_simpson\_shannon

**Formula:** For each index formula,  $p_i$  is the number of samples of the  $i$ 'th label as a proportion of the total number of samples  $n$  in the neighbourhoods.

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Minimum number of neighbour sets</i>	<i>Formula</i>
SHANNON_E	Shannon's evenness ( $H / HMAX$ )	1	$Evenness = \frac{H}{HMAX}$
SHANNON_H	Shannon's H	1	$H = -\sum_{i=1}^n (p_i \cdot \ln(p_i))$
SHANNON_HMAX	maximum possible value of Shannon's H	1	$HMAX = \ln(richness)$
SIMPSON_D	Simpson's D. A score of zero is more similar.	1	$D = 1 - \sum_{i=1}^n p_i^2$

### 2.14.11 Sorenson

**Description:** Sorenson dissimilarity between two sets of labels. It is the complement of the (unimplemented) Czechanowski index, and numerically the same as Whittaker's beta.

**Subroutine:** calc\_sorenson

**Formula:**  $= 1 - \frac{2A}{2A+B+C}$  where  $A$  is the count of labels found in both neighbour sets,  $B$  is the count unique to neighbour set 1, and  $C$  is the count unique to neighbour set 2. Use the [Label counts](#) calculation to derive these directly.

**Indices:**

<i>Index</i>	<i>Description</i>	<i>Grouping metric?</i>	<i>Minimum number of neighbour sets</i>
SORENSEN	Sorenson index	cluster metric	2