## INFO ENTRY - QUESTION INFO

ENTRY NOTES:

* green = does not need to be editted
* yellow = info for the inputter
* ref\_id = “refs\_glossary\_2024-08-09.xls > “references” tab
  + if the reference not present, either add it (if you’re confident that you can follow the format), or add a comment in this doc with the info and I will adjust
* **images – file name in** “refs\_glossary\_2024-08-09.xls > “references” tab
* Ignore everything in the “POPULATE MARKDOWN” section
* Size of columns in tables and text format do not matter; see note on bold and italize below
* Any content with “glue}`` prefix or surrounded by “{{ “ / “ }}” indicates where text will be inserted from the keys
* You may see “<br>” throughout, you can ignore these
* additional formatting notes (optional)
  + \*\***bold**\*\*
  + \**italics*\*
* **Topic Info**
  + If the topic is NOT related to a question, you can leave “question” as NULL
  + “question” here is more for your reference
* **Assumptions, Pros, Cons**
  + Only for modelling approaches; can ignore otherwise (leave table here)
  + [WILL BE HERE, BUT INSERTED DIRECTLY FROM CSV FILE (THUS NO INPUT NEEDED)]
* **Advanced**
  + If the topic doesn’t warrant inclusion, you can leave as NULL
* **Figures**
  + Placeholders here as “filename” can leave in if not <5 images
* **Video**
  + no “<” before the URL text and a “>” after URL in this case
  + ref\_id in this example is not correct, just for illustrative purposes
* **Analytical tools & resources**
  + The ref\_id should be included in the reference column (and the full text reference in the master reference file). If you aren’t sure if the reference is in the master doc, add the full text ref as a comment.
  + Please add a “<” before the URL text and a “>” after (e.g., <http://www.somesitelink.com>)
  + Type can be something similar to: Article, App/Program, R package
* **References / Glossary** 
  + items in-text above (IGNORE FOR NOW)
* **Notes**
  + (future ref / not included in markdown conversion)

## Topic Info

|  |  |
| --- | --- |
| info\_id | mod\_divers\_rich |
| question | NULL |

## Assumptions, Pros, Cons – if modelling approach

|  |  |  |
| --- | --- | --- |
| Assumptions | Pros | Cons |
|  |  |  |

## Overview

“Species richness\*\* is simply “the total number of species in an assemblage or a sample” ({{ ref\_intext\_gotelli\_chao\_2013 }}.

Species richness in an assemblage is difficult to estimate reliably from sample data because it is very sensitive to the number of individuals and the number of samples collected. Species richness is a diversity of order 0 (which means it is completely insensitive to species abundances).

Species diversity is more complex, and includes a measure of the number of species in a community, and a measure of the abundance of each species. Species diversity is usually described by an index, such as Shannon's Index H'.” {{ ref\_intext\_pyron\_2010 }}

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:::{note}

This section is still in progress

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Rarefaction:

“A statistical interpolation method of rarefying or thinning a reference sample by drawing random subsets of individuals (or samples) in order to standardize the comparison of biological diversity on the basis of a common number of individuals or samples” ({{ ref\_intext\_gotelli\_chao\_2013 }})

Species accumulation curve:

“A curve of rising biodiversity in which the x-axis is the number of sampling units (individuals or samples) from an assemblage and the y-axis is the observed species richness. The species accumulation curve rises monotonically to an asymptotic maximum number of species.” ({{ ref\_intext\_gotelli\_chao\_2013 }})

Species richness:

The total number of species in an assemblage or a sample. Species richness in an assemblage is difficult to estimate reliably from sample data because it is very sensitive to the number of individuals and the number of samples collected. Species richness is a diversity of order 0 (which means it is completely insensitive to species abundances). ({{ ref\_intext\_gotelli\_chao\_2013 }})

“Species diversity”

A measure of diversity that incorporates both the number of species in an assemblage and some measure of their relative abundances. Many species diversity indices can be converted by an algebraic transformation to Hill numbers.

“Species richness plays a fundamental role in much of modern ecological theory, and features in one of ecology’s few laws, the species-area relationship (Lomolino 2000)” ({{ ref\_intext\_wearn\_gloverkapfer\_2017 }})

## Advanced

:::{note}

This section is still in progress

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Parameters:

- \*\*α-richness (alpha richness)\*\*: species richness at the level of an individual camera location {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}

- \*\*γ-richness (gamma richness)\*\*: species richness across a whole study area {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}

- \*\*β-diversity (betadiversity)\*\*: the differences between the communities or, more formally, the variance among the communities {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}

<br>

\*\*Observed \*vs\* estimated species richness\*\* (from {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}):

- \*\*Observed species richness\*\*: the sum of the number of species seen (e.g. {{ ref\_intext\_kitamura\_et\_al\_2010 }}; {{ ref\_intext\_pettorelli\_et\_al\_2010 }}; {{ ref\_intext\_ahumada\_et\_al\_2011 }}; {{ ref\_intext\_samejima\_et\_al\_2012 }})

- Observed species richness will not, in general, be a reliable index of actual species richness because, even if sampling effort is strictly controlled, the detectability of species will vary across samples

- \*\*Estimated species richness\*\*: when the “sum of the number of species seen” is adjusted based on corrections for “imperfect detection” (i.e. the fact that some species in a given sample may have been missed)

- (e.g. {{ ref\_intext\_tobler\_et\_al\_2008 }}; {{ ref\_intext\_kinnaird-&-obrien-2012 }}; {{ ref\_intext\_brodie\_et\_al\_2015 }}; {{ ref\_intext\_yue\_et\_al\_2015 }}; {{ ref\_intext\_wearn\_et\_al\_2016 }})

- The \*\*two principal ways of estimating species richness from remote camera data \*\* are (from {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}):<br>

- non-parametric estimators ({{ ref\_intext\_gotelli\_chao\_2013 }}), which use information about the rarest species in the sample to provide a minimum estimate of the number of true species (e.g. {{ ref\_intext\_tobler\_et\_al\_2008 }}),

- or 2) occupancy models ({{ ref\_intext\_mackenzie\_et\_al\_2006 }})

## Figures

|  |  |  |  |
| --- | --- | --- | --- |
| Image | file\_name | Caption (if applicable) | ref\_id |
|  | pyron\_2010\_fig1\_clipped.png | \*\*Pyron (2010) – Fig. 1\*\*: Species evenness and species richness for animalcule communities  <!-- Both communities contain five species of animalcules. Species richness is the same. The community on the left is dominated by one of the species. The community on the right has equal proportions of each species. Evenness is higher when species are present in similar proportions. Thus the community on the left has higher species diversity, because evenness is higher. --> | pyron\_2010 |
|  | gotelli\_and\_colwell\_2011\_fig4\_1\_clipped.png | \*\*Gotelli & Colwell (2011) – Fig. 4.1\*\* Species accumulation and rarefaction curves. The jagged line is the species accumulation curve for one of many possible orderings of 121 soil seedbank samples, yielding a total of 952 individual tree seedlings, from an intensive census of a plot of Costa Rican rainforest (Butler & Chazdon 1998). The cumulative number of tree species (y-axis) is plotted as a function of the cumulative number of samples (upper x-axis), pooled in random order. The smooth, solid line is the sample-based rarefaction curve for the same data set, showing the mean number of species for all possible combinations of 1, 2, . . . , m∗, . . . , 121 actual samples from the dataset—this curve plots the statistical expectation of the (sample-based) species accumulation curve. The dashed line is the individual-based rarefaction curve for the same data set—the expected number of species for (m∗) (952/121) individuals, randomly chosen from all 952 individuals (lower x-axis). The black dot indicates the total richness for all samples (or all individuals) pooled. The sample-based rarefaction curve lies below the individual-based rarefaction curve because of spatial aggregation within species. This is a very typical pattern for empirical comparisons of sample-based and individual-based rarefaction curves. | gotelli\_colwell\_2011 |
|  | vandooren\_2016\_fig1\_clipped.png | \*\*Vandooren (2016) – Fig. 1\*\*: Species accumulation curves. Species richness is the asymptote of a species accumulation curve, which expresses the dependence on sampling effort of the number of species sampled from an assemblage….  <!-- In CA2013, sampling effort is given by the number of records from which the number of species is calculated. For illustrative purposes, an example with three arbitrary samples (for 10000, 5000 and 2000 records, labeled from one to three) is drawn. For sample one, a predicted species accumulation curve is added that gradually increases from one species sampled to the predicted species richness for that assemblage (full line). Such curves are constructed on the basis of interpolation and extrapolation. For samples two and three only segments of extrapolated curves are drawn (dotted lines). For sample two, a curve that crosses the species accumulation curve of sample one is sketched. For samples one and three species accumulation curves are more or less proportional. The way in which the species richness differences between samples are assessed in CA2013 is illustrated by indicating on the species accumulation curves at which numbers of records pairwise comparisons would be made between two sample pairs (1 vs. 2 and 1 vs. 3). The number of species of the sample with the smallest number of records is extrapolated to the number expected at three times the number of records. When the number of records of the other sample is still larger than that, the number of species of the second sample is interpolated (rarefied), otherwise it is extrapolated as well. --> | vandooren\_2016 |
|  | molloy\_2018\_fig9.png | NULL | molloy\_2018 |
| Species accumulation and rarefaction curves. Species accumulation curves show the number of species obtained by successively censusing either individual organisms (individual-based accumulation curves) or samples (sample-based accumulation curves). Smoothed species rarefaction curves represent the statistical expectation of the corresponding accumulation curves. Credit: Rob Colwell, after Gotelli and Colwell (2001) | loreau\_2010\_fig4\_clipped.png | \*\*Loreau et al. (2010) – Fig. 4.\*\* Species accumulation and rarefaction curves. Species accumulation curves show the number of species obtained by successively censusing either individual organisms (individual-based accumulation curves) or samples (sample-based accumulation curves). Smoothed species rarefaction curves represent the statistical expectation of the corresponding accumulation curves. Credit: Rob Colwell, after Gotelli and Colwell (2001) | loreau\_2010 |
|  | loreau\_2010\_fig3.png | \*\*Loreau et al. (2010) – Fig. 3.\*\* The various levels of organisation and components that define the multiple facets  of biodiversity | loreau\_2010 |
|  | gotelli\_chao\_2013\_fig1\_clipped.png | \*\*Gotelli & Chao (2013) – Fig. 1\*\* Species richness sampling in a hypothetical walk through the woods. Each different symbol represents one of 20 distinct species, and each row contains 20 characters, representing the first 20 individual trees that might be encountered in a random sample. Community A is maximally even, with each of the 20 species comprising 5% of the total abundance. In this assemblage, the two samples of 20 individual trees yielded 15 and 13 species, respectively. Community B is highly uneven, with one species (the open circle) representing 81% of the total abundance, and the remaining 19 species contributing only 1% each. In this assemblage, the two samples of 20 individual trees yielded only three and four species, respectively. | gotelli\_chao\_2013 |
|  | gotelli\_chao\_2013\_fig4\_clipped.png | \*\*Gotelli & Chao (2013) – Fig. 4\*\* Standardized comparison of species richness for two individual-based rarefaction curves. The data represent summary counts of carabid beetles that were pitfall-trapped from a set of young pine plantations (o20 years old; upper curve) and a set of old pine plantations (20–60 years old; lower curve). The solid lines are the rarefaction curves, calculated from eqn [2], and the shaded polygons are the 95% confidence intervals, calculated from the unconditional variance eqn [5]. The young plantation samples contained 243 individuals representing 31 species, and the old plantation samples contained 63 individuals representing nine species. The dashed and dotted vertical line illustrates a species richness comparison standardized to 63 individuals, which was the observed abundance in the smaller of the two data sets. Data from Niemel ̈a J, Haila Y, Halme E, et al. (1988) The distribution of carabid beetles in fragments of old coniferous taiga and adjacent managed forest. Annales Zoologici Fennici 25: 107–199. | gotelli\_chao\_2013 |
|  | gotelli\_chao\_2013\_fig6\_clipped.png | \*\*Gotelli & Chao (2013) – Fig. 6\*\* Diversity profile for assemblages of differing evenness. The x-axis is the order \*q\* in the Hill number (eqn [23a]), and is illustrated for values of \*q\* from 0 to 5. The y-axis is the calculated Hill number (the equivalent number of equally abundant species). Each of the four assemblages has exactly 100 species and 500 individuals, but they differ in their relative evenness: (1) completely even assemblage (black solid line): each species is represented by five individuals; (2) slightly uneven assemblage (red dashed line): 50 species each represented by seven individuals and 50 species each represented by three individuals (this structure is denoted as {50 x 7, 50 x 3}); (3) moderately uneven assemblage (green dotted line): {22 x 10, 28 x 5, 40 x 3, 10 x 2}; (4) highly uneven assemblage (blue dash–dot line): {1 x 120, 1 x 80, 1 x 70, 1 x 50, 3 x 20, 3 x 10, 90 x 1}. For \*q\*=0, the Hill number is species richness, which is equal to 100 for all assemblages. Because Hill numbers represent the equivalent number of equally abundant species, the curve for the perfectly even assemblage (black solid line) does not change as q is increased. Larger values of q place progressively more weight on common species, so the equivalent number of equally abundant species is much lower for the more uneven assemblages than for more even assemblages. |  |
|  |  |  |  |

Images in

* Colwell, RK, A Chao, NJ Gotelli, SY Lin, CX Mao, RL Chazdon, and JT Longino. “Models and Estimators Linking Individual-Based and Sample-Based Rarefaction, Extrapolation and Comparison of Assemblages.” *JOURNAL OF PLANT ECOLOGY* 5, no. 1 (March 2012): 3–21. <https://doi.org/10.1093/jpe/rtr044>.
* Gotelli, Nicholas J., and Anne Chao. “Measuring and Estimating Species Richness, Species Diversity, and Biotic Similarity from Sampling Data.” In *Encyclopedia of Biodiversity*, 195–211. Elsevier, 2013. <https://doi.org/10.1016/B978-0-12-384719-5.00424-X>.

## Video

|  |  |  |
| --- | --- | --- |
| caption | URL (no < / > before/after URL | ref\_id |
| Abundance, species richness, and diversity | https://www.youtube.com/embed/ghhZClDRK\_g?si=khprL1u5NJrFduTb | project\_dragonfly\_2019 |
| Species accumulation and rarefaction curves | https://www.youtube.com/embed/4gcmAUpo9TU?si=\_S-JYDDskR8QbHs5 | mecks100\_2018 |
| Using vegan to calculate alpha diversity metrics within the tidyverse in R (CC196) | https://www.youtube.com/embed/wq1SXGQYgCs?si=Re5tglERblfkCNhDl | riffomonas\_project\_2022a |
| Species abundance tools in Genstat | https://www.youtube.com/embed/wBx7f4PP8RE?si=D6mtAMNMLlk3aH8H | vsn\_international\_2022 |
| Species Diversity and Species Richness | https://www.youtube.com/embed/UXJ0r4hjbqI?si=gYR6rOmIMgyibyvR | baylor\_tutoring\_center\_2021 |
| Field Ecology - Diversity Metrics in R | https://www.youtube.com/embed/KBByV3kR3IA?si=RPcG1lFQ-v0Shwaw | styring\_2020 |
| Generating a rarefaction curve from collector's curves in R within the tidyverse (CC198) | https://www.youtube.com/embed/ywHVb0Q-qsM?si=\_xJ5jbFc6MDEQlAh | riffomonas\_project\_2022b |
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## Shiny

Shiny name = iNext Online

Shiny caption =  Software for interpolation and extrapolation of species diversity Rarefied Species Accumulation Curves (the simple way) tutoriall

Shiny URL = https://chao.shinyapps.io/iNEXTOnline

Shiny name = \*\*Visualizing Biodiversity in \[U.S.\] National Parks\*\*

Shiny caption =

Shiny URL = <https://abenedetti.shinyapps.io/bioNPS/>

<!-- https://shiny.posit.co/r/gallery/life-sciences/biodiversity-national-parks/-->

## Analytical tools & resources

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Type | Name | Note | URL | ref\_id |
| R package | Chapter 9 Community composition | \- | <https://bookdown.org/c\_w\_beirne/wildCo-Data-Analysis/composition.html#estimated-richnes> | wildco\_lab\_2021b |
| R package | R package “vegan | \- | <https://cran.r-project.org/web/packages/vegan/index.html> | oksanen\_et\_al\_2024 |
| Program | EstimateS | Dedicated software for estimating diversity, using asymptotic or rarefaction methods. Mac version available | <https://www.robertkcolwell.org/pages/1407> | colwell\_2022 |
| R package | Package ‘iNEXT’ - Interpolation and Extrapolation for Species Diversity | The [iNext package](https://cran.r-project.org/web/packages/iNEXT/) (INterpolation and EXTrapolation of species richness) - is both easy to use and rapid to compute. It also comes with a wealth of plotting functions - see the [iNext Quick Introduction](https://cran.r-project.org/web/packages/iNEXT/vignettes/Introduction.pdf) for a great walk through tutorial. Its core functionality is based on: [Chao, Anne, et al. “Rarefaction and extrapolation with Hill numbers: a framework for sampling and estimation in species diversity studies.” Ecological monographs 84.1 (2014): 45-67.](https://esajournals.onlinelibrary.wiley.com/doi/10.1890/13-0133.1) | <https://cran.r-project.org/web/packages/iNEXT/iNEXT.pdf> | chao\_et\_al\_2016 |
| Exercise/Tutorial | 2.2: Measuring Species Diversity | Easy to interpet explanation of species richness vs evenness, species area curves, rarefaction, and how to calculate diversity | <https://bio.libretexts.org/Courses/University\_of\_California\_Davis/BIS\_2B%3A\_Introduction\_to\_Biology\_-\_Ecology\_and\_Evolution/02%3A\_Biodiversity/2.02%3A\_Measuring\_Species\_Diversity> | gerhartbarley\_nd |
| R package / Tutorial | Species Accumulation Curves with vegan, BiodiversityR and ggplot2 | Software for interpolation and extrapolation of species diversity | <https://rpubs.com/Roeland-KINDT/694021> | roeland\_2020 |
| resource7\_type | resource7\_name | resource7\_note | resource7\_url | resource7\_ref\_id |

## References / Glossary

|  |  |
| --- | --- |
| ref\_id | glossary\_keys |
| {{ ref\_bib\_ahumada\_et\_al\_2011 }}  {{ ref\_bib\_baylor\_tutoring\_center\_2021 }}  {{ ref\_bib\_brodie\_et\_al\_2015 }}  {{ ref\_bib\_chao\_et\_al\_2016 }}  {{ ref\_bib\_chao\_et\_al\_2014 }}  {{ ref\_bib\_colwell\_2022 }}  {{ ref\_bib\_gerhartbarley\_nd }}  {{ ref\_gotelli\_chao\_2013 }}  {{ ref\_bib\_gotelli\_colwell\_2001 }}  {{ ref\_bib\_gotelli\_colwell\_2010 }}  {{ ref\_bib\_hsieh\_et\_al\_2015 }}  {{ ref\_bib\_iknayan\_et\_al\_2014 }}  {{ ref\_bib\_kinnaird\_obrien\_2012 }}  {{ ref\_bib\_kitamura\_et\_al\_2010 }}  {{ ref\_bib\_mackenzie\_et\_al\_2006 }}  {{ ref\_bib\_mecks100\_2018 }}  {{ ref\_bib\_oksanen\_et\_al\_2024 }}  {{ ref\_bib\_pettorelli\_et\_al\_2010 }}  {{ ref\_bib\_project\_dragonfly\_2019 }}  {{ ref\_bib\_pyron\_2010 }}  {{ ref\_bib\_riffomonas\_project\_2022 }}  {{ ref\_bib\_samejima\_et\_al\_2012 }}  {{ ref\_bib\_styring\_2020 }}  {{ ref\_bib\_tobler\_et\_al\_2008 }}  {{ ref\_bib\_vsn\_international\_2022 }}  {{ ref\_bib\_wearn\_et\_al\_2016 }}  {{ ref\_bib\_wildco\_lab\_2021b }}  {{ ref\_bib\_yue\_et\_al\_2015 }} | keys\_here |

## Notes

\*\*Pyron (2010) - Figure 1\*\*:

“Species richness” can be thought of as the sum of different species seen in a particular area during a particular time period

Pg 62 wearn

6-2 Community variance or β-diversity

When considering two (or more) communities, it is possible to calculate a state variable which reflects the differences between the communities or, more formally, the variance among the communities. We sometimes call this community variance “β-diversity” (betadiversity). This is useful, for example, for assessing the degree to which communities subject to different management differ (e.g. comparing an old-growth site, a selectively-logged site and a plantation forest site). This is sometimes called “across-site” β-diversity, because it is being used to assess community variance across heterogeneous habitat types.

β-diversity measures can also be used to assess community variance within single habitat types, at a smaller scale. This is sometimes called “within-site” β-diversity (although the distinction from across-site β-diversity may not always be clear-cut). This can be important because changes in community variance within a study site may reflect changes in the fundamental processes which generate biodiversity at local scales (such as habitat heterogeneity and the connectivity of populations).

β-diversity should also play an important role in spatial conservation planning, for example in designing networks of reserves. All else being equal, if β-diversity is high, it will be important to establish a network of reserves so that all species in the landscape are covered. On the other hand, if β-diversity is low and communities are similar across space, then a single large reserve may be the best option.

Communities can also be compared across time, rather than across space, giving rise to temporal β-diversity. This can be used to track how much, and how quickly, communities are changing at a single site over time.

Camera trap studies typically sample a large number of locations, making them highly suitable for quantifying β-diversity, but this has rarely been done (but see: Wearn et al. 2016). At least in part, this is probably because the importance of β-diversity is poorly appreciated amongst wildlife biologists and conservationists. In addition, there are many different ways β-diversity can be calculated, each with their own strengths and weaknesses, with no single best measure. This can be confusing and lead to “analysis paralysis”. In common with species richness, β-diversity is also dependent on spatial scale (Olivier & Aarde 2014). For example, some habitats such as logged forests may show high β-diversity (rapid community turnover) at fine spatial scales, but low β-diversity (homogenous communities) at coarse spatial scales (Wearn et al. 2016). Finally, interpreting and communicating measures of β-diversity can be hard, because they are often in meaningless units, or because they do not lend themselves directly to comparisons across different studies.

# POPULATE MARKDOWN

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### :::::::::{div} full-width

### ::::::{dropdown} Assumptions, Pros, Cons

:::::{dropdown} Species richness (Alpha diversity)

::::{grid}

:::{grid-item-card} Assumptions

- {{ mod\_divers\_rich\_alpha\_assump\_01 }}

- {{ mod\_divers\_rich\_alpha\_assump\_02 }}

- {{ mod\_divers\_rich\_alpha\_assump\_03 }}

- {{ mod\_divers\_rich\_alpha\_assump\_04 }}

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:::{grid-item-card} Pros

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- {{ mod\_divers\_rich\_alpha\_pro\_03 }}

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:::{grid-item-card} Cons

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- {{ mod\_divers\_rich\_alpha\_con\_02 }}

- {{ mod\_divers\_rich\_alpha\_con\_03 }}

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:::::{dropdown} Species diversity (Beta diversity)

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- {{ mod\_divers\_rich\_beta\_assump\_03 }}

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:::{grid-item-card} Pros

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- {{ mod\_divers\_rich\_beta\_pro\_02 }}

- {{ mod\_divers\_rich\_beta\_pro\_03 }}

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:::{grid-item-card} Cons

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- {{ mod\_divers\_rich\_beta\_con\_02 }}

- {{ mod\_divers\_rich\_beta\_con\_03 }}

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:::::{dropdown} Species diversity (Gamma diversity)

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- {{ mod\_divers\_rich\_gamma\_assump\_02 }}

- {{ mod\_divers\_rich\_gamma\_assump\_03 }}

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:::{grid-item-card} Pros

- {{ mod\_divers\_rich\_gamma\_pro\_01 }}

- {{ mod\_divers\_rich\_gamma\_pro\_02 }}

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:::{grid-item-card} Cons

- {{ mod\_divers\_rich\_gamma\_con\_01 }}

- {{ mod\_divers\_rich\_gamma\_con\_02 }}

- {{ mod\_divers\_rich\_gamma\_con\_03 }}

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### ::::::

### :::::::{tab-set}

#### ::::::{tab-item} Overview

\*\*{{ term\_mod\_divers\_rich }}\*\*: {{ term\_def\_mod\_divers\_rich }}

<br>

“Species richness is simply the number of species in an area ({{ ref\_intext\_wearn\_gloverkapfer\_2017 }})

Species diversity is more complex, and includes a measure of the number of species in a community, and a measure of the abundance of each species. Species diversity is usually described by an index, such as Shannon's Index H'.” {{ ref\_intext\_pyron\_2010 }}

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#### ::::::

#### ::::::{tab-item} Advanced

:::{note}

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Parameters:

- \*\*α-richness (alpha richness)\*\*: species richness at the level of an individual camera location {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}

- \*\*γ-richness (gamma richness)\*\*: species richness across a whole study area {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}

- \*\*β-diversity (betadiversity)\*\*: the differences between the communities or, more formally, the variance among the communities {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}

<br>

\*\*Observed \*vs\* estimated species richness\*\* (from {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}):

- \*\*Observed species richness\*\*: the sum of the number of species seen (e.g. {{ ref\_intext\_kitamura\_et\_al\_2010 }}; {{ ref\_intext\_pettorelli\_et\_al\_2010 }}; {{ ref\_intext\_ahumada\_et\_al\_2011 }}; {{ ref\_intext\_samejima\_et\_al\_2012 }})

- Observed species richness will not, in general, be a reliable index of actual species richness because, even if sampling effort is strictly controlled, the detectability of species will vary across samples

- \*\*Estimated species richness\*\*: when the “sum of the number of species seen” is adjusted based on corrections for “imperfect detection” (i.e. the fact that some species in a given sample may have been missed)

- (e.g. {{ ref\_intext\_tobler\_et\_al\_2008 }}; {{ ref\_intext\_kinnaird-&-obrien-2012 }}; {{ ref\_intext\_brodie\_et\_al\_2015 }}; {{ ref\_intext\_yue\_et\_al\_2015 }}; {{ ref\_intext\_wearn\_et\_al\_2016 }})

- The \*\*two principal ways of estimating species richness from remote camera data \*\* are (from {{ ref\_intext\_wearn\_gloverkapfer\_2019 }}):<br>

- non-parametric estimators ({{ ref\_intext\_gotelli\_chao\_2013 }}), which use information about the rarest species in the sample to provide a minimum estimate of the number of true species (e.g. {{ ref\_intext\_tobler\_et\_al\_2008 }}),

- or 2) occupancy models ({{ ref\_intext\_mackenzie\_et\_al\_2006 }})

#### ::::::

#### ::::::{tab-item} Visual resources

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```

\*\*Pyron (2010) - Figure 1\*\*: Species evenness and species richness for animalcule communities

<!-- Both communities contain five species of animalcules. Species richness is the same. The community on the left is dominated by one of the species. The community on the right has equal proportions of each species. Evenness is higher when species are present in similar proportions. Thus the community on the left has higher species diversity, because evenness is higher. -->

###### ::::

###### ::::{grid-item-card} {{ ref\_intext\_gotelli\_colwell\_2011 }}

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\*\*Vandooren (2016) – Figure 1\*\*: Species accumulation curves. Species richness is the asymptote of a species accumulation curve, which expresses the dependence on sampling effort of the number of species sampled from an assemblage….

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\*\*Loreau et al. (2010) – Figure 4.\*\* Species accumulation and rarefaction curves. Species accumulation curves show the number of species obtained by successively censusing either individual organisms (individual-based accumulation curves) or samples (sample-based accumulation curves). Smoothed species rarefaction curves represent the statistical expectation of the corresponding accumulation curves. Credit: Rob Colwell, after Gotelli and Colwell (2001)

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###### ::::{grid-item-card} {{ ref\_intext\_loreau\_2010 }}

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\*\*Loreau et al. (2010) – Figure 3.\*\* The various levels of organisation and components that define the multiple facets

of biodiversity

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Abundance, species richness, and diversity

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###### ::::{grid-item-card} {{ ref\_intext mecks100\_2018 }}

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Species accumulation and rarefaction curves

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###### ::::{grid-item-card} {{ ref\_intext riffomonas\_project\_2022a }}

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Using vegan to calculate alpha diversity metrics within the tidyverse in R (CC196)

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###### ::::{grid-item-card} {{ ref\_intext vsn\_international\_2022 }}

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Species abundance tools in Genstat

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###### ::::{grid-item-card} {{ ref\_intext\_baylor\_tutoring\_center\_2021 }}

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Species Diversity and Species Richness

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###### ::::{grid-item-card} {{ ref\_intext\_styring\_2020 }}

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Field Ecology - Diversity Metrics in R

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Generating a rarefaction curve from collector's curves in R within the tidyverse (CC198)

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#### ::::::{tab-item} Shiny apps/Widgets

##### :::::{card}

\*\*iNext Online\*\*

Software for interpolation and extrapolation of species diversity Rarefied Species Accumulation Curves (the simple way) tutoriall

<iframe

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#### ::::::

#### ::::::{tab-item} Analytical tools & resources

| Type | Name | Note | URL |Reference |

|:----------------|:---------------------------------------|:----------------------------------------------------------------|:----------------------------------------------------------------|:----------------------------------------------------------------|

| R package | Chapter 9 Community composition | \- | <https://bookdown.org/c\_w\_beirne/wildCo-Data-Analysis/composition.html#estimated-richnes> | {{ ref\_bib\_wildco\_lab\_2021b }} |

| R package | R package “vegan | \- | <https://cran.r-project.org/web/packages/vegan/index.html> | {{ ref\_bib\_oksanen\_et\_al\_2024 }} |

| Program | EstimateS | Dedicated software for estimating diversity, using asymptotic or rarefaction methods. Mac version available | <https://www.robertkcolwell.org/pages/1407> | {{ ref\_bib\_colwell\_2022 }} |

| R package | Package ‘iNEXT’ - Interpolation and Extrapolation for Species Diversity | The iNext package (INterpolation and EXTrapolation of species richness) - is both easy to use and rapid to compute. It also comes with a wealth of plotting functions - see the iNext Quick Introduction for a great walk through tutorial. Its core functionality is based on: Chao, Anne, et al. “Rarefaction and extrapolation with Hill numbers: a framework for sampling and estimation in species diversity studies.” Ecological monographs 84.1 (2014): 45-67. | <https://cran.r-project.org/web/packages/iNEXT/iNEXT.pdf> | {{ ref\_bib\_chao\_et\_al\_2016 }} |

| Exercise/Tutorial | 2.2: Measuring Species Diversity | Easy to interpet explanation of species richness vs evenness, species area curves, rarefaction, and how to calculate diversity | <https://bio.libretexts.org/Courses/University\_of\_California\_Davis/BIS\_2B%3A\_Introduction\_to\_Biology\_-\_Ecology\_and\_Evolution/02%3A\_Biodiversity/2.02%3A\_Measuring\_Species\_Diversity> | {{ ref\_bib\_gerhartbarley\_nd }} |

| R package / Tutorial | Species Accumulation Curves with vegan, BiodiversityR and ggplot2 | Software for interpolation and extrapolation of species diversityRarefied Species Accumulation Curves (the simple way) | <https://rpubs.com/Roeland-KINDT/694021> | {{ ref\_bib\_resource6\_ref\_id }} |

| resource7\_type | resource7\_name | resource7\_note | resource7\_note | {{ ref\_bib\_resource7\_ref\_id }} |

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#### ::::::{tab-item} References

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{{ ref\_bib\_ahumada\_et\_al\_2011 }}

{{ ref\_bib\_baylor\_tutoring\_center\_2021 }}

{{ ref\_bib\_brodie\_et\_al\_2015 }}

{{ ref\_bib\_chao\_et\_al\_2016 }}

{{ ref\_bib\_chao\_et\_al\_2014 }}

{{ ref\_bib\_colwell\_2022 }}

{{ ref\_bib\_gerhartbarley\_nd }}

{{ ref\_bib\_gotelli\_colwell\_2001 }}

{{ ref\_bib\_gotelli\_colwell\_2010 }}

{{ ref\_bib\_hsieh\_et\_al\_2015 }}

{{ ref\_bib\_iknayan\_et\_al\_2014 }}

{{ ref\_bib\_kinnaird\_obrien\_2012 }}

{{ ref\_bib\_kitamura\_et\_al\_2010 }}

{{ ref\_bib\_mackenzie\_et\_al\_2006 }}

{{ ref\_bib\_mecks100\_2018 }}

{{ ref\_bib\_oksanen\_et\_al\_2024 }}

{{ ref\_bib\_pettorelli\_et\_al\_2010 }}

{{ ref\_bib\_project\_dragonfly\_2019 }}

{{ ref\_bib\_pyron\_2010 }}

{{ ref\_bib\_riffomonas\_project\_2022 }}

{{ ref\_bib\_samejima\_et\_al\_2012 }}

{{ ref\_bib\_styring\_2020 }}

{{ ref\_bib\_tobler\_et\_al\_2008 }}

{{ ref\_bib\_vsn\_international\_2022 }}

{{ ref\_bib\_wearn\_et\_al\_2016 }}

{{ ref\_bib\_wildco\_lab\_2021b }}

{{ ref\_bib\_yue\_et\_al\_2015 }}

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