## 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

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

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

Note that there are multiple parameters corresponding to different scales and incorporating of evenness; these include:

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

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

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

You can refer to the “Assumptions, Pros, Cons” dropdown above to see relevant information for all three.

```{figure} ../03\_images/03\_image\_files/pyron\_2010\_fig1\_clipped.png

:align: center

:scale: 60%

```

\*\*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.

:::

## Advanced

:::{note}

This section is still in progress

:::

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

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

## Study design

### Number of cameras

The optimal number of cameras required will be influenced by factors such as landscape heterogeneity, [survey](/09\_gloss\_ref/09\_glossary.md#survey) duration and spatial scale, species rarity and desired level of precision ({{ colyn\_et\_al\_2018 }}; {{ rovero\_et\_al\_2013 }}). For example, Kays et al. (2020) found that 25–35 cameras were needed for precise estimates of species richness, depending on the spatial scale of the [survey](/09\_gloss\_ref/09\_glossary.md#survey) and landscape diversity. In general, deploying more cameras and/or for longer durations always results in more precise estimates; however, users can consider rotating cameras across multiple sites for shorter durations (if feasible).

### Duration - Camera days per camera location

For measures of species richness or diversity, it is presumed that a camera is active long enough to detect rare species that may occur at a specific location ({{ wearn\_gloverkapfer\_2017 }}). If this is not the case, the results will indicate that the species was not present when it was (i.e., a “false negative”). False negatives may also be problematic for other measures, such as [\*\*relative abundance indices\*\*](/09\_gloss\_ref/09\_glossary.md#mods\_relative\_abundance) (count data, with or without [zero-inflation](/09\_gloss\_ref/09\_glossary.md#mods\_zero\_inflation) and/or [overdispersion](/09\_gloss\_ref/09\_glossary.md#mods\_overdispersion)), even if the model type used can account for [imperfect detection](/09\_gloss\_ref/09\_glossary.md#imperfect\_detection) explicitly (e.g., combined occurrence/[relative abundance](/09\_gloss\_ref/09\_glossary.md#mods\_relative\_abundance); [N-mixture models](/09\_gloss\_ref/09\_glossary.md#mods\_n\_mixture)).

### Number of cameras vs. Camera days per camera location

If a user must choose between more cameras \*vs.\* fewer cameras with longer [surveys](/09\_gloss\_ref/09\_glossary.md#survey), Chatterjee et al. (2021) suggested that for rare species, the optimal precision can be obtained by increasing the number of sites, whereas for common species, increasing the number of samples is more effective. For measuring species richness, Si et al. (2014) found that rotating cameras to new sites was more efficient than leaving cameras at fewer sites for longer periods. O'Connor et al. (2017) also recommended utilizing more cameras \*vs\*. increasing study length to increase [detection probabilities](/09\_gloss\_ref/09\_glossary.md#detection\_probability). In general, regardless of species and [objective](/09\_gloss\_ref/09\_glossary.md#survey\_objectives), increasing the number of [survey](/09\_gloss\_ref/09\_glossary.md#survey) locations or the [survey](/09\_gloss\_ref/09\_glossary.md#survey) length improved precision ({{ chatterjee\_et\_al\_2021 }}).

Analysis

Note that there are multiple parameters corresponding to different scales and incorporating of evenness; these include:

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

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

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

Its important to note the difference in \*\*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  :::{dropdown}  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\_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\_fig6\_clipped.png | \*\*Gotelli & Chao (2013) – Fig. 6\*\* Diversity profile for assemblages of differing evenness.  :::{dropdown}  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.  ::: | gotelli\_chao\_2013 |
|  | 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 |
|  | figure5\_filename.png | figure5\_caption | figure5\_ref\_id |
|  | figure6\_filename.png | figure6\_caption | figure6\_ref\_id |
|  | figure7\_filename.png | figure7\_caption | figure7\_ref\_id |
|  | figure8\_filename.png | figure8\_caption | figure8\_ref\_id |
|  | figure9\_filename.png | figure9\_caption | figure9\_ref\_id |
|  | figure10\_filename.png | figure10\_caption | figure10\_ref\_id |
|  | figure11\_filename.png | figure11\_caption | figure11\_ref\_id |
|  | figure12\_filename.png | figure12\_caption | figure12\_ref\_id |

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\_2020a |
| 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

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 |
| resource8\_type | resource8\_name | resource8\_note | resource8\_url | resource8\_ref\_id |
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| resource14\_type | resource14\_name | resource14\_note | resource14\_url | resource14\_ref\_id |
| resource15\_type | resource15\_name | resource15\_note | resource15\_url | resource15\_ref\_id |

## References / Glossary

|  |  |
| --- | --- |
| ref\_id |  |
| {{ 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\_chao\_2013 }}  {{ 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\_2022a }}  {{ ref\_bib\_riffomonas\_project\_2022b }}  {{ ref\_bib\_samejima\_et\_al\_2012 }}  {{ ref\_bib\_styring\_2020a }}  {{ ref\_bib\_styring\_2020b }}  {{ 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 }} |  |

## Notes

“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). ({{ ref\_intext\_gotelli\_chao\_2013 }}.

“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 }})

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. ({{ ref\_intext\_gotelli\_chao\_2013 }})

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 }}

\*\*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\_2024-09-14 – MODS (ADJUST DIVERS\_RICH)

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jupytext:

formats: md:myst

text\_representation:

extension: .md

format\_name: myst

format\_version: 0.13

jupytext\_version: 1.16.4

kernelspec:

display\_name: Python 3

language: python

name: python3

editor\_options:

markdown:

wrap: none

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(i\_mod\_divers\_rich)=

# {{ name\_mod\_divers\_rich }}

::::::{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 }}

:::

:::{grid-item-card} Pros

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

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

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

:::

:::{grid-item-card} Cons

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

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

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

:::

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:::::

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

::::{grid}

:::{grid-item-card} Assumptions

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

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

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

:::

:::{grid-item-card} Pros

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

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

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

:::

:::{grid-item-card} Cons

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

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

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

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

::::{grid}

:::{grid-item-card} Assumptions

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

- {{ 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 }}

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

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

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

\*\*{{ term\_ }}\*\*: {{ term\_def\_ }}

Add some info here

#### ::::::

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

Occupancy models describe spatial patterns of animal occurrence ({{ ref\_intext\_sollmann\_et\_al\_2018 }}) and have been proposed as a proxy for abundance ({{ ref\_intext\_noon\_et\_al\_2012 }}). They ask: what proportion of a study area is inhabited by a population – that is, at how many camera sites do one or more individuals of a species occur ({{ ref\_intext\_mackenzie\_et\_al\_2017 }})? The basic equation for occupancy is: <br><br>

```{figure} ../03\_images/03\_image\_files/clarke\_et\_al\_2023\_eqn\_occupancy1.png

:align: center

```

where \*𝜓\* is the probability a site is occupied, \*𝑥̂\* is the estimated number of occupied sites (i.e., the count of sites where animals were detected, corrected for detection probability) and 𝑠 is the total number of sites surveyed ({{ ref\_intext\_mackenzie\_et\_al\_2017 }}). Unlike simple measures of presence-absence, occupancy models account for imperfect detection ({{ ref\_intext\_sollmann\_et\_al\_2018 }}). They attempt to differentiate between absence – animals truly not present – and nondetection – animals present but not detected – by repeatedly sampling sites over time. The central assumption of basic occupancy models is that repeated samples occur during a period in which the site is closed to changes in occupancy (i.e., occupancy status – present or absent – does not change during the sampling period). Thus if a species is detected during one of three sampling occasions, it is assumed that it was present during all three occasions but undetected during two. <br>

<br>

In theory, occupancy and abundance share a predictable relationship. As population size increases, the number of sites occupied by members of that population should also increase (until all sites are occupied); likewise, a decrease in population size should lead to a decrease in the number of sites used ({{ ref\_intext\_gaston\_et\_al\_2000 }}; {{ ref\_intext\_royle\_dorazio\_2008 }}). This is called an occupancy-abundance relationship, and – because of it – occupancy can be used as an index of abundance. <br>

<br>

Advantages of occupancy as an index of abundance include: <br>

<br>

- Occupancy studies may be easier to implement than some abundance or density estimators ({{ ref\_intext\_noon\_et\_al\_2012 }}; {{ ref\_intext\_sollmann\_et\_al\_2018 }}).

- Occupancy-abundance relationships appear to be robust to territoriality, group travelling behaviour and other biological traits (

{{ ref\_intext\_steenweg\_et\_al\_2018 }}).

- Occupancy can be modelled as a function of site- and sampling-specific covariates to better understand which factors predict animal occurrence ({{ ref\_intext\_sollmann\_et\_al\_2018 }}). <br>

<br>

However, many researchers have cautioned against the use occupancy as an index. As with relative abundance (RA; see above), there is no consistent, long-term relationship between occupancy and abundance ({{ ref\_intext\_efford\_dawson\_2012 }}). Occupancy can change with abundance, but also with survey duration, species home range size, animal movement, etc., muddling occupancy-abundance relationships and thus inferences about population size ({{ ref\_intext\_neilson\_et\_al\_2018 }}; {{ ref\_intext\_steenweg\_et\_al\_2018 }}). While occupancy is a powerful stand-alone metric, Sollmann (2018) says it should not be “misinterpreted” as an index of abundance. <br>

<br>

Despite its widespread use, occupancy may be particularly problematic for camera trap studies due to the violation of the closure assumption. Burton et al. (2015) highlighted that many camera trap studies using occupancy do not explicitly define the “site,” although is often implicitly given as some larger area around a camera trap. Since camera trap studies typically target mammal species with relatively large home ranges, the site closure assumption is almost certainly violated in most cases. Many camera trappers therefore assume that “occupancy” is in fact “use” of a site (i.e., the site is not closed), and that detection probability also includes availability for detection. Mackenzie et al. (2017) suggested that estimates should be unbiased if movements in and out of a site are random, but this assumption is rarely tested. And where occupancy estimates have been tested using realistic mammal movements, they have generally performed poorly ({{ ref\_intext\_neilson\_et\_al\_2018 }}; {{ ref\_intext\_stewart\_et\_al\_2018 }}).

#### ::::::

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

##### :::::{grid} 3

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###### ::::{grid-item-card} {{ ref\_intext\_murray\_et\_al\_2021 }}

```{figure} ../03\_images/03\_image\_files/murray\_et\_al\_2021.jpg

:class: img\_grid

```

\*\*Murray et al. (2021) - Fig. 1.\*\* Schematic of our multi- state occupancy model to estimate the occurrence of coyotes and mange. We used images of coyotes collected along transects following an urban gradient in the Chicago metro area in a standard single-species multi-season model with a stacked design. Following the coyote occupancy model, our mange model estimates the distribution of coyote with sarcoptic mange conditional on the distribution of coyote, mangy or otherwise, using by-image variation in the presence of mange signs and the quality of the image

###### ::::

###### ::::{grid-item-card} {{ ref\_intext\_southwell\_et\_al\_2019 }}

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:class: img\_grid

```

\*\*Southwell et al. (2019) - Fig. 1.\*\* Structure of the spatially explicit power analysis framework for multiple species in dynamic landscapes.

###### ::::

###### ::::{grid-item-card} {{ ref\_intext\_clarke\_et\_al\_2023 }}

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###### ::::

##### :::::

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```{figure} ../03\_images/03\_image\_files/chatterjee\_et\_al\_2021\_table2\_clipped.png

:class: img\_grid

```

\*\*Chatterjee et al. (2021) - Table 2.\*\* Broad classifications of mammals based on occupancy and detection probabilities.

###### ::::

###### ::::{grid-item-card} {{ ref\_intext\_figure5\_ref\_id }}

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figure5\_caption

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figure6\_caption

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figure7\_caption

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figure8\_caption

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figure9\_caption

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figure10\_caption

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:class: img\_grid

```

figure11\_caption

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figure12\_caption

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###### ::::{grid-item-card} {{ ref\_intext\_cove\_2020a }}

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Occupancy Modeling Video 1 -- Sampling Techniques for Mammals

###### ::::

###### ::::{grid-item-card} {{ ref\_intext\_cove\_2020b }}

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Occupancy Modeling Video 2 -- Introductory Statistical Review

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Occupancy Modeling Video 3 -- What are Occupancy Models and What are the Applications?

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allowfullscreen>

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Occupancy Modeling Video 4 -- How to Run and Interpret the Models in PRESENCE

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###### ::::{grid-item-card} {{ ref\_intext\_vid5\_ref\_id }}

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frameborder="0"

allow="accelerometer; autoplay; clipboard-write; encrypted-media; gyroscope; picture-in-picture"

allowfullscreen>

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Occupancy modelling - more than species presence/absence! (Darryl MacKenzie)

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###### ::::{grid-item-card} {{ ref\_intext\_vid6\_ref\_id }}

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allowfullscreen>

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https://www.youtube.com/watch?v=rpjVrFI\_dr8

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

Check back in the future!

<!--

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shiny\_caption

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

| Type | Name | Note | URL |Reference |

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

| rJAGS/R code | mfidino/multi-state-occupancy-models | Mason Fidino's GitHub | <https://github.com/mfidino/multi-state-occupancy-models> | {{ ref\_bib\_fidino\_2021 }} |

| JAGS/R code | mfidino/integrated-occupancy-model” | Mason Fidino's GitHub | <https://github.com/mfidino/integrated-occupancy-model> | {{ ref\_bib\_fidino\_2021 }} |

| JAGS code | mfidino/auto-logistic-occupancy | Mason Fidino's GitHub | <https://github.com/mfidino/auto-logistic-occupancy> | {{ ref\_bib\_resource3\_ref\_id }} |

| R package | R package - “autoOcc” | An R package for fitting autologistic occupancy models | <https://github.com/mfidino/autoOcc> | {{ ref\_bib\_resource4\_ref\_id }} |

| R code | mfidino/periodicity | Using Fourier series to predict periodic patterns in dynamic occupancy models | <https://github.com/mfidino/periodicity> | {{ ref\_bib\_resource5\_ref\_id }} |

| resource13\_type |

|

| < > | {{ ref\_bib\_resource6\_ref\_id }} |

| R code/Tutorial | “An Introduction to Camera Trap Data Management and Analysis in R > Chapter 11 Occupancy” | | <https://bookdown.org/c\_w\_beirne/wildCo-Data-Analysis/occupancy.html> | {{ ref\_bib\_wildco\_lab\_2021c }} |

| Program | “PRESENCE” | "Relatively simple, but comprehensive, software dedicated to occupancy estimation. Linux version available. Can also be used for occupancy-based species richness estimation." (Wearn & Glover-Kapfer, 2017) | \*\*Software\*\*: <www.mbr-pwrc.usgs.gov/ software/presence.html>;<br>\*\*Help forum\*\*: <www.phidot.org>| {{ ref\_bib\_resource8\_ref\_id}} |

| R package | R package - “RPresence” | “The R counterpart to Presence. Cross-platform (Windows, Mac and Linux)." (Wearn & Glover-Kapfer, 2017) | <https://www.mbr-pwrc.usgs.gov/software/presence.shtml> | {{ ref\_bib\_resource9\_ref\_id }} |

| R package | R package "unmarked” | "Implements a wide variety of occupancy and count-based abundance models (the latter are mostly not appropriate for camera-trapping). Actively being developed and supported by a community of users. Cross-platform (Windows, Mac and Linux)." (Wearn & Glover-Kapfer, 2017) | <https://cran.r-project.org/web/packages/unmarked/index.html>;<br><https://groups.google.com/g/unmarked> | {{ ref\_bib\_resource10\_ref\_id }} |

| R code/Tutorial | “Multi-season Occupancy Models” | Mason Fidino's GitHub | <https://darinjmcneil.weebly.com/multi-season-occupancy.html> | {{ ref\_bib\_resource11\_ref\_id }} |

| R package | R package for analyzing wildlife data with detection error | resource12\_note | resource12\_url | {{ ref\_bib\_resource12\_ref\_id }} |

| resource13\_type | resource13\_name | resource13\_note | resource13\_url | {{ ref\_bib\_resource13\_ref\_id }} |

| resource14\_type | resource14\_name | resource14\_note | resource14\_url | {{ ref\_bib\_resource14\_ref\_id }} |

| resource15\_type | resource15\_name | resource15\_note | resource15\_url | {{ ref\_bib\_resource15\_ref\_id }} |

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

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

{{ ref\_bib\_cove\_2020a }}

{{ ref\_bib\_cove\_2020b }}

{{ ref\_bib\_cove\_2020c }}

{{ ref\_bib\_cove\_2020d }}

{{ ref\_bib\_efford\_dawson\_2012 }}

{{ ref\_bib\_gaston\_et\_al\_2000 }}

{{ ref\_bib\_gimenez\_2023 }}

{{ ref\_bib\_mackenzie\_et\_al\_2017 }}

{{ ref\_bib\_murray\_et\_al\_2021 }}

{{ ref\_bib\_neilson\_et\_al\_2018 }}

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{{ ref\_bib\_royle\_dorazio\_2008 }}

{{ ref\_bib\_sollmann\_et\_al\_2018 }}

{{ ref\_bib\_southwell\_et\_al\_2019 }}

{{ ref\_bib\_steenweg\_et\_al\_2018 }}

{{ ref\_bib\_stewart\_et\_al\_2018 }}

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