# 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** | sp\_hr\_size |
| **question** | **Question:** Is home range size information available for your Target Species (can be taken from the literature)? If so, enter the home range diameter (in metres)  Home range data - importance for site selection |

## Overview

Check the linked table from "HomeRange: A global database of mammalian home ranges" ({{ ref\_in\_text\_broekman\_et\_al\_2022 }}) or see if you can find similar information on home range sizes online or elsewhere.

\*\*Why does this matter?\*\*

Home range size information should, ideally, be chosen to reflect the conditions of your study (as closely as possible). For example, using data on home range size from a study that only reported home range size for one season (e.g., summer home range size) might bias placement if your study aims to evaluate occupancy over the entire year of a species whose movement highly varies between seasons (e.g., moves more in summer).

::: {note}

The size of species’ home has implicatons for many modelling approaches.

For example, home range size “has implications for the interpretation of occupancy. If animals range over a much larger area than a single site, then a) they may conceivably be unavailable for capture during a sampling occasion, and b) the “occupancy” of a site is more related to the ranging patterns and habitat preferences of an individual, rather than the coarse-scale distribution of a species” (Wearn & Glover-Kapfer, 2017).

::: {note}

:::

## Advanced

Add some info here

## Figures

|  |  |  |  |
| --- | --- | --- | --- |
| **Image** | **file\_name** | **Caption (if applicable)** | **ref\_id** |
|  | figure1\_filename.png | figure1\_caption | figure1\_ref\_id |
|  | figure2\_filename.png | figure2\_caption | figure2\_ref\_id |
|  | figure3\_filename.png | figure4\_caption | figure3\_ref\_id |
|  | figure4\_filename.png | figure4\_caption | figure4\_ref\_id |
|  | figure5\_filename.png | figure5\_caption | figure5\_ref\_id |
|  | figure6\_filename.png | figure6\_caption | figure6\_ref\_id |

## Video

|  |  |  |
| --- | --- | --- |
| **caption** | **URL (no < / > before/after URL** | **ref\_id** |
| vid1\_caption | vid1\_url | vid1\_ref\_id |
| vid2\_caption | vid2\_url | vid2\_ref\_id |
| vid3\_caption | vid3\_url | vid3\_ref\_id |
| vid4\_caption | vid4\_url | vid4\_ref\_id |
| vid5\_caption | vid5\_url | vid5\_ref\_id |
| vid6\_caption | vid6\_url | vid6\_ref\_id |

## Analytical tools & resources

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Type** | **Name** | **Note** | **URL** | **ref\_id** |
| Database | HomeRange: A global database of mammalian home range | HomeRange, a global database with 75,611 home- range values across 960 different species of mammals, including terrestrial, aquatic and aerial species | Article - <<https://onlinelibrary.wiley.com/doi/epdf/10.1111/geb.13625> >  <<https://github.com/SHoeks/HomeRange>>  <<https://shoeks.github.io/HomeRange/>> | resource1\_ref\_id |
| resource2\_type | resource2\_name | resource2\_note | resource2\_url | resource2\_ref\_id |
| resource3\_type | resource3\_name | resource3\_note | resource3\_url | resource3\_ref\_id |
| resource4\_type | resource4\_name | resource4\_note | resource4\_url | resource4\_ref\_id |
| resource5\_type | resource5\_name | resource5\_note | resource5\_url | resource5\_ref\_id |
| resource6\_type | resource6\_name | resource6\_note | resource6\_url | resource6\_ref\_id |
| resource7\_type | resource7\_name | resource7\_note | resource7\_url | resource7\_ref\_id |
| resource8\_type | resource8\_name | resource8\_note | resource8\_url | resource8\_ref\_id |
| resource9\_type | resource9\_name | resource9\_note | resource9\_url | resource9\_ref\_id |
| resource10\_type | resource10\_name | resource10\_note | resource10\_url | resource10\_ref\_id |
| resource11\_type | resource11\_name | resource11\_note | resource11\_url | resource11\_ref\_id |
| resource12\_type | resource12\_name | resource12\_note | resource12\_url | resource12\_ref\_id |
| resource13\_type | resource13\_name | resource13\_note | resource13\_url | resource13\_ref\_id |
| 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** | **glossary\_keys** |
| Refs | keys\_here |

## Notes

* “Home range size is used as a means to control spacing between detectors when point sampling, but it is not related to the occupancy-abundance relationship and the potential for bias in estimates of occupancy. Rather, the importance of home range size to control spacing is related to bias in the standard errors if the independence of occupancy status assumption (e.g., sites are closed to changes in the state of occupancy for the duration of sampling) is violated. Investigators choose grain size, yet many studies fail to report justification for the selected grain size (Devarajan et al., 2020), and frequently use grid cell size to space traps/detectors under aerial sampling in discrete space and point sampling in continuous space. A final concern related to the site grainsize and assumptionthat the occupancy states across sites are independent relates to spatial correlation in the occupancy process. If individual home ranges overlap more than one point detector (e.g., point sampling of use), there is potential for spatial correlation in neighboring site occupancy states that could lead to false positives in testing hypotheses about ψ, as for example,in incorrectly concluding that occupancy changed (increased or decreased) over time. The outcome of spatial correlation in the occupancy process is that measures of precision will be overestimated (MacKenzie et al., 2017). To our knowledge, these types of false positive errors have not been formally investigated in occupancy models. The choice of grain is therefore an important consideration in occupancy studies since that choice will affect model assumptions and interpretation and is dependent on whether the study involves areal or point sampling (Efford and Dawson, 2012). Finally, point sampling in continuous space may result in unmodeled site-level heterogeneity in detection, resulting in underestimates in both ψ in occupancy models and site-level abundance in Royle-Nichols models (Efford and Dawson, 2012). This form of heterogeneity may arise because the probability of detecting an individual should increase with increasing overlap of its home range and a detector, and the number of individuals varies among occupied sites; the probability of detecting the species given presence may therefore be heterogeneous due to both variation in home-range overlap with sites and abundance at sites, while Royle-Nichols models only account for variation in abundance across sites..” ([Fuller et al., 2022, p. 4](about:blank)) ([pdf](about:blank))

# POPULATE MARKDOWN

---

jupytext:

formats: md:myst

text\_representation:

extension: .md

format\_name: myst

format\_version: '1.16'

jupytext\_version: 1.16.1

kernelspec:

display\_name: Python 3

language: python

name: python3

editor\_options:

markdown:

wrap: none

---

(i\_mod\_divers\_rich)=

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

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

:::

:::{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 }}

:::

::::

:::::

:::::{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 }}

:::

::::

:::::

:::::{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 }}

:::

:::{grid-item-card} Pros

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

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

:::

:::{grid-item-card} Cons

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

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

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

:::

::::

:::::

### ::::::

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

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

:align: center

:scale: 60%

```

#### ::::::

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

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

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

:gutter: 1

:padding: 0

:margin: 0

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

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

:height: 300px

:align: center

```

\*\*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 }}

```{figure} ../03\_images/03\_image\_files/gotelli\_and\_colwell\_2011\_fig4\_1.png

:width: 300px

:align: center

```

NULL

###### ::::

###### ::::{grid-item-card} {{ ref\_intext\_vandooren\_2016 }}

```{figure} ../03\_images/03\_image\_files/vandooren\_2016\_fig1.png

:width: 300px

:align: center

```

\*\*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….

###### ::::

##### :::::

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

:gutter: 1

:padding: 0

:margin: 0

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

```{figure} ../03\_images/03\_image\_files/molloy\_2018\_fig9.png

:width: 300px

:align: center

```

NULL

###### ::::

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

```{figure} ../03\_images/03\_image\_files/loreau\_2010\_fig4.png

:width: 300px

:align: center

```

\*\*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)

###### ::::

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

```{figure} ../03\_images/03\_image\_files/loreau\_2010\_fig3.png

:width: 300px

:align: center

```

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

of biodiversity

###### ::::

##### :::::

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

:gutter: 1

:padding: 0

:margin: 0

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

<iframe

width="300"

height="200"

src="https://www.youtube.com/embed/ghhZClDRK\_g?si=khprL1u5NJrFduTb"

frameborder="0"

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

allowfullscreen>

</iframe>

Abundance, species richness, and diversity

###### ::::

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

<iframe

width="300"

height="200"

src="https://www.youtube.com/embed/4gcmAUpo9TU?si=\_S-JYDDskR8QbHs5"

frameborder="0"

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

allowfullscreen>

</iframe>

Species accumulation and rarefaction curves

###### ::::

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

<iframe

width="300"

height="200"

src="https://www.youtube.com/embed/wq1SXGQYgCs?si=Re5tglERblfkCNhDl"

frameborder="0"

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

allowfullscreen>

</iframe>

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

###### ::::

##### :::::

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

:gutter: 1

:padding: 0

:margin: 0

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

<iframe

width="300"

height="200"

src="https://www.youtube.com/embed/wBx7f4PP8RE?si=D6mtAMNMLlk3aH8H"

frameborder="0"

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

allowfullscreen>

</iframe>

Species abundance tools in Genstat

###### ::::

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

<iframe

width="300"

height="200"

src="https://www.youtube.com/embed/UXJ0r4hjbqI?si=gYR6rOmIMgyibyvR"

frameborder="0"

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

allowfullscreen>

</iframe>

Species Diversity and Species Richness

###### ::::

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

<iframe

width="300"

height="200"

src="https://www.youtube.com/embed/KBByV3kR3IA?si=RPcG1lFQ-v0Shwaw"

frameborder="0"

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

allowfullscreen>

</iframe>

Field Ecology - Diversity Metrics in R

###### ::::

##### :::::

#### ::::::

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

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

\*\* iNEXTOnline \*\*

shiny\_caption

<iframe

width="100%"

height="900"

src="https://chao.shinyapps.io/iNEXTOnline"

frameborder="0"

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

allowfullscreen>

</iframe>

##### :::::

#### ::::::

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

**Error! Not a valid filename.**

| 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\_hsieh\_et\_al\_2015 }} |

| 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 }} |

::::::

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

<font size="3">

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

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

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

{{ chao\_et\_al\_2016 }}

{{ 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 }}

</font>\

#### ::::::

### :::::::

### :::::::::