# 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**
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## Topic Info

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| **info\_id** | mod\_tte |
| **question** | NULL |

## Assumptions, Pros, Cons – if modelling approach

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| **Assumptions** | **Pros** | **Cons** |
| - {{ mod\_tte\_assump\_01 }}  - {{ mod\_tte\_assump\_02 }}  - {{ mod\_tte\_assump\_03 }}  - {{ mod\_tte\_assump\_04 }}  - {{ mod\_tte\_assump\_05 }}  - {{ mod\_tte\_assump\_06 }}  - {{ mod\_tte\_assump\_07 }}  - {{ mod\_tte\_assump\_08 }} | - {{ mod\_tte\_pro\_01 }} | - {{ mod\_tte\_con\_01 }} |

## Overview

Add some info here

## Advanced

:::{note}

\*\*This content was adapted from\*\*: The Density Handbook, "[Using Camera Traps to Estimate Medium and Large Mammal Density: Comparison of Methods and Recommendations for Wildlife Managers](https://www.researchgate.net/publication/368601884\_Using\_Camera\_Traps\_to\_Estimate\_Medium\_and\_Large\_Mammal\_Density\_Comparison\_of\_Methods\_and\_Recommendations\_for\_Wildlife\_Managers)" (Clarke et al.. 2024)

:::

Time-to-event (TTE) analysis is used in many disciplines to estimate the rate at which an event occurs, by repeatedly measuring the time that elapses before said event takes place ({{ ref\_intext\_loonam\_et\_al\_2021b }}). A TTE model might be used in medicine, for example, to approximate time from diagnosis until remission or death ({{ ref\_intext\_clark\_et\_al\_2003 }}). Moeller et al. (2018) developed an extension of the TTE framework to estimate animal density using camera trap data, where the “event” of interest is an animal detection, and the rate of interest is animals per viewshed area – density ({{ ref\_intext\_loonam\_et\_al\_2021b }}). Their version capitalizes on the fact that, at a randomly deployed motion-triggered camera, the time it takes to capture an image of an animal is a function of animal movement speed, detection probability and population size ({{ ref\_intext\_jennelle\_et\_al\_2002 }}, {{ ref\_intext\_moeller\_et\_al\_2018 }}, {{ ref\_intext\_parsons\_et\_al\_2017 }}). When movement speed is known and detection probability is perfect, population size can be estimated by measuring the time from an arbitrary starting point until an image of an animal is captured ({{ ref\_intext\_lukacs\_2021 }}; {{ ref\_intext\_moeller\_et\_al\_2018 }}).

The equation for camera data-based density estimation using TTE is:

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where \*𝜆\* is the average number of animals in the viewshed, given the time until an animal is detected, and \*𝑎\* is the average viewshed area. \*𝑎\* is calculated using the equation:

```{figure} ../03\_images/03\_image\_files/clarke\_et\_al\_2023\_eqn\_tte2\_ste1.png

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where \*𝑟\* is the trigger distance (i.e., the maximum distance from which an animal can reliably trigger a camera’s motion sensor), and \*𝜃\* is the angle of the camera lens in degrees ({{ ref\_intext\_moeller\_et\_al\_2018 }}).

To illustrate how \*𝜆\* is calculated, let’s take a simple example. We begin by dividing the total time cameras are active into sampling occasions, then sampling periods (Figure 10; {{ ref\_intext\_moeller\_et\_al\_2018 }}). We might choose to define a sampling occasion as a day, and a sampling period as one of 24 one-hour intervals in a day ({{ ref\_intext\_moeller\_et\_al\_2018 }}). The images collected at a camera station can now be grouped by occasion and period to generate a detection history, and the number of sampling periods (i.e., \*𝑘\* out of 24) until an image of an animal is encountered can be determined for each sampling occasion ({{ ref\_intext\_moeller\_et\_al\_2018 }}). The detection history at a given camera after 7 days might look something like {NA, NA, 7, NA, 22, 1, NA}, where NA indicates no animal detections for that day. Inputting this information into a likelihood equation generates the average number of animals in the viewshed, \*𝜆\* ({{ ref\_intext\_moeller\_et\_al\_2018 }}).

```{figure} ../03\_images/03\_image\_files/clarke\_et\_al\_2023\_fig10\_clipped.png

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\*\*Clarke et al. (2023) - Fig. 10\*\* Adapted from Moeller et al. (2018). Visualization of how total sampling time at a camera station is broken down into sampling occasions and then sampling periods.

To account for movement, the sampling period is set as the average time animals take to pass through the camera viewshed ({{ ref\_intext\_moeller\_et\_al\_2018 }}). Thus, practitioners need measures of animal movement speed.

**## Simulations and Field Experiments**

Simulations show that:

- The TTE model tends to underestimate population density. In both walk ({{ ref\_intext\_loonam\_2019 }}) and random walk simulations ({{ ref\_intext\_moeller\_et\_al\_2018 }}), the TTE yielded density estimates below the true value, whether populations were large or small, or animals moved quickly or slowly. Estimates were, however, particularly low for slow-moving species.

- The TTE is sensitive to movement speed. Indeed, Loonam et al.’s (2021b) simulations showed that over- or underestimating movement rate biases density estimates. For example: a 50% underestimation of movement speed resulted in a density estimate 40% lower than the true density; overestimating movement speed by 200% resulted in density estimates that were over 85% higher than actual ({{ ref\_intext\_loonam\_et\_al\_2021b }}). Taken together, these results suggest that the integrity of TTE estimates depends on the movement behaviour of the focal species, and obtaining accurate measures of animal movement speed.

- The TTE model performs best when cameras are deployed randomly on the landscape. Setting cameras to maximize detections (i.e., targeted deployment) resulted in considerable over- or underestimates of density in walk simulations ({{ ref\_intext\_loonam\_et\_al\_2021b }}). Of the sampling designs tested in Grosklos’ (in preparation) simulations, random camera placement produced the best results. Thus, practitioners using the TTE model are advised to deploy their camera networks randomly to minimize model bias.

The TTE is robust to population openness and territoriality. Population openness is a violation of assumption 1 (population closure); territoriality is a violation of assumption 5 (animals are Poisson distributed across the landscape; {{ ref\_intext\_moeller\_et\_al\_2018 }}). Neither appeared to impact TTE estimates – indicating that the model applies well to actual populations, which often violate these assumptions ({{ ref\_intext\_loonam\_et\_al\_2021b }}).

It is worth noting that in all of Loonam et al.’s (2021b) simulations, the precision of TTE estimates was inflated – that is, estimates were calculated to be more precise than they actually were. Practitioners should keep this in mind when evaluating reported values of precision, as they may be artificially high.

In the field: the TTE has produced density estimates similar to established censusing techniques. Moeller et al., (2018) piloted the TTE on a population of elk in Idaho, and found that the model produced a density estimate comparable to an aerial survey of the same area – even though cameras were not deployed randomly. In this system, the TTE produced higher estimates of population density than either of its sister models (space-to-event (STE) and instantaneous sampling (IS); see below). For cougars – a low-density species – TTE-based estimates were actually more precise than both genetic mark-recapture and random encounter model (REM; see *2.2.3 Random Encounter Model*) estimates, and similarly or more consistent across years, respectively ({{ ref\_intext\_loonam\_et\_al\_2021a }}). Density estimates could have been biased and misleadingly precise, however, because of non-random camera placement ({{ ref\_intext\_loonam\_et\_al\_2021a }}, {{ ref\_intext\_morin\_et\_al\_2022 }}).

The TTE has also performed poorly in natural populations. A study on snowshoe hare found that the TTE tended to overestimate density compared with the REM and the random encounter and staying time model (REST; see *2.2.4 Random Encounter and Staying Time*; {{ ref\_intext\_jensen\_et\_al\_2022 }}). Out of the three camera-based models, the TTE was also the least consistent with live-trapping spatial capture-recapture (SCR; see *2.1.2 Spatial Capture-Recapture*; {{ ref\_intext\_jensen\_et\_al\_2022 }})

## Figures

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| --- | --- | --- | --- |
| **Image** | **file\_name** | **Caption (if applicable)** | **ref\_id** |
| A black and white math equation  Description automatically generated with medium confidence | clarke\_et\_al\_2023\_eqn\_tte1.png | \*\*Clarke et al. (2023) - Eqn TTE\*\*:  The equation for camera data-based density estimation using TTE, where \*𝜆\* is the average number of animals in the viewshed, given the time until an animal is detected, and \*𝑎\* is the average viewshed area. | clarke\_et\_al\_2023 |
| A mathematical equation with numbers  Description automatically generated | clarke\_et\_al\_2023\_eqn\_tte2\_ste1.png | \*\*Clarke et al. (2023) - Eqn TTE \*𝑎\*\*\*:The equation for \*𝑎\* in camera data-based density estimation using TTE (refer to “Clarke et al. (2023) - Eqn TTE”). | clarke\_et\_al\_2023 |
| A screenshot of a computer  Description automatically generated | clarke\_et\_al\_2023\_fig10\_clipped.png | \*\*Clarke et al. (2023) - Fig. 10\*\* Adapted from Moeller et al. (2018). Visualization of how total sampling time at a camera station is broken down into sampling occasions and then sampling periods. | clarke\_et\_al\_2023 |
|  | clarke\_et\_al\_2023\_fig11\_clipped.png | \*\*Clarke et al. (2023) - Fig. 11\*\* Simple diagrams showing dispersed, clumped and Poisson-distributed animals (red dots) in space. | clarke\_et\_al\_2023 |
| A diagram of a process flow  Description automatically generated | moeller\_lukacs\_2022\_fig1.png | \*\*Moeller & Lukacs (2022)\*\* The spaceNtime workflow for count data. The user will go through five major steps for STE, TTE, and IS analyses. If the user has presence/absence (0 and 1) data instead of count data, the IS analysis is not appropriate, and the IS pathway should be removed from the flowchart. | moeller\_lukacs\_2022 |
|  | moeller\_et\_al\_2018\_fig1\_clipped.png | \*\*Moeller et al. (2018) - Fig. 1\*\* Schematic of sampling periods and occasions for the time to event model. At camera \*i\* = 1, 2, . . ., \*M\*, sampling occasion \*j\* = 1, 2, . . ., \*J\* is broken into several sampling periods \*k\* = 1, 2, . . ., \*K\*. Here, \*J\* = 2 and \*K\* = 3. | moeller\_et\_al\_2018 |
|  | moeller\_et\_al\_2018\_fig2\_clipped.png | \*\*Moeller et al. (2018) - Fig. 2. Conceptual diagram of the time to event (TTE) model.  :::{dropdown}  The circular sector is the viewshed of a single camera \*i\* on a single occasion \*j\* divided into three successive sampling periods (a–c). The black dots represent randomly placed animals. The observed TTE Tij is equal to the period \*k\* in which the camera first contains an animal. There are no animals in the camera in (a) \*k\* = 1 or (b) \*k\* = 2, but there is an animal in the camera in (c) \*k\* = 3, so for this camera and sampling occasion, T\*<sub>ij</sub>\* = 3.  ::: | moeller\_et\_al\_2018 |
|  | figure8\_filename.png | figure8\_caption | figure8\_ref\_id |
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## Video

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## Shiny

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## Analytical tools & resources

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| **Type** | **Name** | **Note** | **URL** | **ref\_id** |
| R package | spaceNtime: an R package for estimating abundance of unmarked animals using camera-trap photographs | free and open-source R package designed to assist in the implementation of the STE and TTE models, along with the IS estimator | <https://github.com/annam21/spaceNtime;<br><https://link.springer.com/article/10.1007/s42991-021-00181-8> | moeller\_lukacs\_2022 |
| resource2\_type | resource2\_name | resource2\_note | resource2\_url | resource2\_ref\_id |
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## References / Glossary

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| **ref\_id** | **glossary\_keys** |
| {{ ref\_bib\_clark\_et\_al\_2003 }}  {{ ref\_bib\_clarke\_et\_al\_2023 }}  {{ ref\_intext\_jennelle\_et\_al\_2002 }}  {{ ref\_bib\_jensen\_et\_al\_2022 }}  {{ ref\_bib\_loonam\_et\_al\_2021a }}  {{ ref\_bib\_loonam\_et\_al\_2021b }}  ({{ ref\_bib\_lukacs\_2021 }}  {{ ref\_bib\_moeller\_lukacs\_2021 }}  {{ ref\_bib\_moeller\_et\_al\_2018 }}  {{ ref\_bib\_morin\_et\_al\_2022 }} | keys\_here |

## Notes

# Markdown

## File from = 00\_00\_template-master\_2024-09-29.docx

**POPULATE MARKDOWN \_2024-09-28** - MODS

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formats: md:myst

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jupytext\_version: 1.16.4 <!-- 6.5.4-->

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name: python3

editor\_options:

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**Error! Reference source not found.**:::::

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

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::::{grid-item-card} Assumptions

- {{ mod\_rai\_assump\_01 }}

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::::{grid-item-card} Pros

- {{ mod\_rai\_pro\_01 }}

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

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::::::{tab-item} In-depth

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\*\*This content was adapted from\*\*: The Density Handbook, "[Using Camera Traps to Estimate Medium and Large Mammal Density: Comparison of Methods and Recommendations for Wildlife Managers](https://www.researchgate.net/publication/368601884\_Using\_Camera\_Traps\_to\_Estimate\_Medium\_and\_Large\_Mammal\_Density\_Comparison\_of\_Methods\_and\_Recommendations\_for\_Wildlife\_Managers)" (Clarke et al., 2024)

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In ecology, relative abundance (RA) is any count of animals or animal sign (e.g., number of deer sighted, number of bird vocalizations per unit time, number of moose tracks per kilometer of transect) that is assumed to correlate with absolute abundance ({{ ref\_intext\_obrien\_2011 }}). RA is a controversial index for two reasons: 1) there is often no documented relationship between the number of animals or signs observed and population size (i.e., index validation), and 2) detection probability is assumed to be constant between the areas, times or species being compared ({{ ref\_intext\_obrien\_2011 }}; {{ ref\_intext\_thompson\_et\_al\_1998 }}).

To the first point: the relationship between the number of animals or signs and abundance is rarely established ({{ ref\_intext\_burton\_et\_al\_2015 }}). Researchers often assume that counts and population size scale linearly – but many other kinds of relationships are possible. When the assumed relationship between counts and abundance diverges from the actual relationship, inferences from RA are not very meaningful ({{ ref\_intext\_thompson\_et\_al\_1998 }}). Validating a count-abundance relationship requires comparison with a robust, accurate estimate of absolute density (e.g., {{ ref\_intext\_krebs\_et\_al\_1987}}; {{ ref\_intext\_rovero\_marshall\_2009 }}; {{ ref\_intext\_villette\_et\_al\_2016 }}).

To the second point: consider the canonical equation,

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where \*𝑁\* is population size, \*𝐶\* is the count of animals or signs and \*𝑝\* is detection probability ({{ ref\_intext\_anderson\_2001 }}; {{ ref\_intext\_brennan\_2019 }}). This equation underlies many estimators of abundance, including capture-recapture (CR; see {bdg-link-primary-line}`Capture-recapture (CR) / Capture-mark-recapture (CMR)<https://ab-rcsc.github.io/rc-decision-support-tool\_concept-library/02\_dialog-boxes/03\_10\_mod\_cr\_cmr.html>`) and distance sampling (DS; see {bdg-link-primary-line}`Distance sampling<https://ab-rcsc.github.io/rc-decision-support-tool\_concept-library/02\_dialog-boxes/03\_20\_mod\_ds.html>`) methods ({{ ref\_intext\_obrien\_2011 }}). RA comparisons assume that detection probability \*𝑝\* is constant across space, time or species, and can therefore be ignored ({{ ref\_intext\_anderson\_2011 }}; {{ ref\_intext\_obrien\_2011 }}; {{ ref\_intext\_sollmann\_et\_al\_2013b }}), such that:

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so count essentially becomes a surrogate for population size.

Assuming constant detection probability \*𝑝\* is problematic, since the likelihood an animal or sign is counted during a survey will vary with observational, environmental, and habitat- and species-specific factors, which in turn can vary with time ({{ ref\_intext\_anderson\_2001 }}). For example: at site A, animals may be difficult to spot in dense vegetation, while at site B, animals may be easy to spot in open grassland; and the effects of vegetation on observability may differ seasonally. If the effects of vegetation on detectability are not accounted for, how can we be sure that differences in animal counts at site A and B are due to true differences in abundance, and not simply artefacts of detection bias ({{ ref\_intext\_sollmann\_et\_al\_2013b }})?

In a camera trapping context, RA is the comparison of detection rates across space, time or species – where detection rates are typically reported as the number of images per 100 trap days, but can also be reported in terms of the total number of detections, other units of effort (e.g., camera trap hours), proportion of stations with detections, etc. ({{ ref\_intext\_burton\_et\_al\_2015 }}). As with other kinds of RA surveys, comparisons of camera trap detection rates can confound abundance with animal behaviour and observability ({{ ref\_intext\_anderson\_2001 }}; {{ ref\_intext\_burton\_et\_al\_2015 }}).

RA has been criticized as an abundance estimator. Anderson (2001) condemned the index as “unprofessional,” while O’Brien (2011) called it a “metric of last resort.” Sollmann et al. (2013b) used simulations to determine that camera trap RA analyses did not detect changes in big cat density, and called use of the index for wildlife management “alarming.” Nevertheless, some researchers have had success with the method and/or have argued for its conceptual and practical advantages (e.g., {{ ref\_intext\_rovero\_carbone\_et\_al\_2001, {{ ref\_intext\_johnson\_2008 }}; {{ ref\_intext\_palmer\_et\_al\_2018 }}; {{ ref\_intext\_rovero\_marshall\_2009 }}). Broadley et al. (2019) used simulations to show that RA could be sensitive to density-dependent movement, but generally tracked abundance well. Banks-Leite (2014) emphasized the importance of careful sampling design and protocols to control for variation in detectability, arguing that researchers should not solely rely on statistical corrections.

Ultimately, there is no “silver bullet” and researchers must carefully consider their inferential objectives and potential sources of sampling and estimation bias when choosing response variables and modelling frameworks for camera trap data.

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

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Modified from Gilbert et al. (2022) - Figure 3.

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::::{grid-item-card} {{ ref\_intext\_denes\_et\_al\_2015 }}

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\*\*Dénes et al. (2015) - Fig. 1.\*\* Mechanisms that cause different types of zero observations in count surveys and how species rarity, detectability and sampling effort affect them.

:::{dropdown}

(a) False zeroes are due to either imperfect detection or temporary absence. True zeroes can occur when the sample unit is unoccupied by the species, due to demographic stochasticity or due to ecological mechanisms such as unsuitable habitat or interspecific competition. (b) For common and detectable species (lower right), the majority of zeroes can be expected to result from ecological processes. As species detectability decreases, new false zeroes arise due to detection error (lower left). Species rarity results in fewer detections (dark green bars), additional true zeroes arise from unoccupied sample units (white bars) and increased demographic stochasticity (beige bars). (c) When the area sampled and/or the time of visit are small/ short relative to the species home range or movements, individuals may not be available for detection during the survey, resulting in additional false zeroes and fewer non-zero observations.

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::::{grid-item-card} {{ ref\_intext\_blasco\_moreno\_et\_al\_2019 }}

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\*\*Blasco-Moreno et al. (2019) - Fig 1.\*\* Different sources of zeros that could emerge in count data.

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The example shows the presence (>0) or absence (0) of herbivores on a plant species. Zeros due to the lack of experience of the observer (a–b) or resulting from a poor experimental design (c–h) are called False Zeros and should be minimized when performing the experiment. Structural Zeros, that is, zeros related to the ecological system under study (i–k), and Random Zeros emerging from the sampling variability (l) are known as True Zeros. Classifying a zero as a design error or structural zero depends on whether the event is part of the hypotheses tested. Only when the study includes the possibility of a zero value as part of the hypotheses (e.g. the study aims to test whether the interaction is occurring) the resulting zeros would be structural and should be included in the statistical analysis. The following text explains different scenarios that would result in a zero value, and, in brackets, how errors due to false zeros can be minimized: (a) the insects or the damage exerted are so small that the observer cannot detect them [sample when the insects are expected to be well developed]; (b) the observer does not see the herbivore (e.g. it is mistaken for a seed) or the damage is associated to other causes not related to herbivory (e.g. mechanical damage during sampling, pathogens, etc.) [the observer should be trained properly]; (c) the distributional areas of herbivores and plants are not coincident [know the species distribution before sampling]; (d) a herbivore is not present in a certain location within its distributional area, for example due to the microclimatic conditions [sample in habitats with adequate environmental conditions for a herbivore, or perform replicate surveys in different areas]; (e) a single survey is conducted, and is not coincident with the herbivore phenology [know the herbivore life cycle or perform long‐term surveys]; (f) a long‐term survey is conducted, but the low sampling frequency does not enable capture of the presence of the herbivore [sample on a more frequent basis]; (g) herbivores are not found because they are absent at the time of sampling [record plant damage instead of the presence of insects]; (h) herbivores are so infrequent that the design cannot capture their presence [perform extensive sampling with a high number of replicates]; (i) phenology of plants and herbivores are not completely coincident at a temporal level; (j) herbivores do not recognize a plant as a potential host; (k) herbivores recognize a plant as a host but prefer to feed on another species and (l) the herbivore population is not large enough to saturate the available plant resources.

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\*\* Denes et al. (2015) - Fig. 2\*\* Summary of the main modelling approaches for estimating abundance of unmarked animal populations described in the text.

:::{dropdown}

Red boxes represent important model assumptions (in bold) and sampling design requirements (in italic), green boxes represent the types of input data used by each model, lilac and orange ellipses represent established and emerging methods, respectively, and blue diamonds represent additional parameters estimated. w indicates models that estimate potential occupancy probability, / indicates models that estimate probability of temporary emigration from the sample unit, and q indicates models that account for correlation in detection of individuals. p is site-level detection probability, c and x are arrival rate and survival probability parameters, respectively, r is the spatial correlation in counts, and Ω is the probability that a species is present in the supercommunity.

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

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https://www.mdpi.com/2673-4591/39/1/38

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figure8\_caption

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figure11\_caption

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Using Hurdle Models to Analyze Zero-Inflated Count Data

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Hurdle models

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::::{grid-item-card} {{ ref\_intext\_tilestats\_2021 }}

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Zero-inflated Poisson (ZIP) regression

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Poisson Regression Review

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Poisson Regression: Zero Inflation (Excessive Zeros)

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::::{grid-item-card} {{ ref\_intext\_russel\_2020 }}

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</div>

Fitting Poisson and zero-inflated Poisson models.

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

Check back in the future!

<!--::::{dropdown}-->

:::::{card} Microbiome Analysis: Relative Abundance Boxplots

A Shiny app allows you to visualize data by using R scripts without having to interact with the R script itself. This Shiny app will allow you to plot your **Relative Abundance** microbiome data in an easy-to-view format. If this is your first time utilizing this Shiny app, follow the step below to start visualising your data now!

<iframe

width="100%"

height="900"

src="https://guthub.org/shiny/sample-apps/absboxplot/ "

frameborder="0"

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

allowfullscreen>

</iframe>

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

| Type | Name | Note | URL |Reference |

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

| R resource | abmi.camera.extras: Animal Density from Camera Data > Probabilistic gaps | | Main resource page: <https://mabecker89.github.io/abmi.camera.extras/index.html>;<br>[Probabilistic gaps]<https://mabecker89.github.io/abmi.camera.extras/articles/gaps.html> | {{ ref\_bib\_becker\_et\_al\_2020 }} |

| App/Program | Introduction to Camera Trap Data Management and Analysis in R > Chapter 12 Activity | | <https://bookdown.org/c\_w\_beirne/wildCo-Data-Analysis/activity.html> | {{ ref\_bib\_wildco\_lab\_2021d }} |

| App/Program | R package “activity” | Provides functions to express clock time data relative to anchor points (typically solar); fit kernel density functions to animal activity time data; plot activity distributions; quantify overall levels of activity; statistically compare activity metrics through bootstrapping; evaluate variation in linear variables with time (or other circular variables). | <https://cran.r-project.org/web/packages/activity/index.html> | {{ ref\_bib\_rowcliffe\_2023 }} |

| R package | R package “overlap” | Estimates of Coefficient of Overlapping for Animal Activity Patterns | <https://cran.r-project.org/web/packages/overlap/index.html> | {{ ref\_bib\_campbell\_2024 }} |

| Tutorial | Chapter 6 Modeling Relative Abundance | | <https://cornelllabofornithology.github.io/ebird-best-practices/abundance.html> | {{ ref\_bib\_strimasmackey\_et\_al\_2023 }} |

| R package | glmmTMB: Generalized Linear Mixed Models using Template Model Builder | resource6\_note | <https://cran.r-project.org/web/packages/glmmTMB/index.html> | {{ ref\_bib\_resource6\_ref\_id }} |

| R package | R package “zicounts” | Counts data models: zero-inflation as well as interval icensored | <https://github.com/cran/zicounts> | {{ ref\_bib\_resource7\_ref\_id }} |

| R package | R package “DHARMa” | Can be used to assess goodness-of-fit of a mixed effect model via quantile–quantile (Q–Q) plots of standardized residuals | <https://CRAN.R-project.org/package=DHARMa>| {{ ref\_bib\_hartig\_2019}} |

| R package | R package “Pscl” | resource9\_note | < https://cran.r-project.org/web/packages/pscl/index.html> | {{ ref\_bib\_jackman\_2024 }} |

| R package | R package “countreg” | Can be used to assess goodness-of-fit of a mixed effect hurdle model via rootograms ({{ ref\_intext\_kleiber\_zeileis\_2016 }}) | <https://rdrr.io/rforge/countreg/><br>

https://rdrr.io/rforge/countreg/f/inst/doc/countreg.pdf><br><https://www.zeileis.org/papers/Kleiber+Zeileis-2016.pdf> | {{ ref\_bib\_zeileis\_et\_al\_2008 }} |

| resource11\_type | A guide to modeling outcomes that have lots of zeros with Bayesian hurdle lognormal and hurdle Gaussian regression models | resource11\_note | <https://www.andrewheiss.com/blog/2022/05/09/hurdle-lognormal-gaussian-brms> | {{ ref\_bib\_resource11\_ref\_id }} |

| resource12\_type | resource12\_name | resource12\_note | resource12\_url | {{ ref\_bib\_resource12\_ref\_id }} |

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{{ ref\_bib\_anderson\_2001 }}

{{ ref\_bib\_banksleite\_2014 }}

{{ ref\_bib\_blasco\_moreno\_et\_al\_2019 }}

{{ ref\_bib\_brennan\_2019 }}

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

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

{{ ref\_bib\_carbone\_et\_al\_2001 }}

{{ ref\_bib\_cao\_2021 }}

{{ ref\_bib\_clark\_et\_al\_2003 }}

{{ ref\_bib\_dectre\_accel\_2016 }}

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{{ ref\_bib\_heilbron\_1994 }}

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{{ ref\_bib\_krebs\_et\_al\_1987 }}

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{{ ref\_bib\_thompson\_et\_al\_1998 }}

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

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

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

+check others

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