## Topic Info

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| **info\_id** | mod\_cr\_cmr |

## Note banner

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## Overview

```{include} include/00\_coming\_soon.md

```

## In-depth

```{include} include/note\_adapted\_clarke\_et\_al\_2023.md

```

Of all the modelling frameworks discussed in this document, capture-recapture (CR) also called capture-mark-recapture or mark-recapture – is perhaps the most wellknown. Since the 19th century, CR has been used to measure population size by capturing, marking, releasing and recapturing individuals ({{ rtxt\_lecren\_1965 }}, {{ rtxt\_otis\_et\_al\_1978 }}). For species or populations that are challenging to physically trap and mark, CR can also be applied to DNA, acoustic and camera trap data ({{ rtxt\_royle\_et\_al\_2014 }}). Here, we will discuss camera trap CR.

:::{figure} ../03\_images/03\_image\_files/clarke\_et\_al\_2023\_fig11\_clipped.png

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> \*\*Clarke et al. (2023) - Fig. 11\*\* Adapted from Royle (2020). A detection history matrix for an example population. For each individual (1 through \*𝑛\*) during each sampling occasion (1 through \*𝐾\*), a value of 1 is assigned if that individual was detected at a camera trap and a value of 0 is assigned if it was not detected at a camera trap. Note that we do not detect individuals \*𝑛\* + 1, \*𝑛\* + 2…\*𝑁\* (0s for every sampling occasion), but they are still present and able to be detected.

To estimate density using camera trap CR, we must first estimate population size \*𝑁\*. CR models use individuals’ detection histories – that is, the record of when each individual was photographed or not photographed (i.e., (re)captured or not (re)captured) – to solve for \*𝑁\* (Figure 3; Royle, 2020). Population-level detection histories look like a matrix of 1s and 0s, where 1s signify that an individual was captured during a given sampling occasion \*𝑘\*, and 0s signify that the individual was not captured during that occasion ({{ rtxt\_royle\_2020 }}, {{ rtxt\_royle\_et\_al\_2014 }}). The number of individuals photographed at least once over the course of the study (i.e., the count of animals captured) is \*𝑛\*.

Importantly, the count of animals is not the same as the size of the population (i.e., \*𝑛\* ≠ \*𝑁\*). Some individuals will never be photographed during a study, even though they are present and able to be detected (i.e., they are in \*𝑁\* but not in \*𝑛\*; {{ rtxt\_royle\_2020 }}). Using the matrix of detection histories, we must therefore calculate the likelihood animals will be detected by an array of camera traps – that is, detection probability \*p\* ({{ rtxt\_royle\_2020 }}).

Taking this information together, we can calculate population size \*𝑁\* as:

:::{figure} ../03\_images/03\_image\_files/clarke\_et\_al\_2023\_eqn\_cr1.png

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which is often referred to as the canonical estimator of population size ({{ rtxt\_royle\_2020 }}). Population size \*𝑁\* can then be divided by an estimate of the area of the sampling frame \*𝐴\* to obtain density.

CR models have important limitations – notably that they do not consider the spatial configuration of camera traps or the spatial pattern of animal detections. This gives rise to two major issues:

1. The sampling frame \*𝐴\* is not known ({{ rtxt\_chandler\_royle\_2013 }}). In other words: the true area animals occupy is never measured, only approximated using adhoc approaches (e.g., using a buffer strip around the trap array; {{ rtxt\_rich\_et\_al\_2014 }}, {{ rtxt\_sollmann\_2018 }}). Consequently, density cannot be calculated explicitly ({{ rtxt\_chandler\_royle\_2013 }}), and CR-derived density estimates are somewhat arbitrary and difficult to compare across studies ({{ rtxt\_green\_et\_al\_2020 }}, {{ rtxt\_royle\_et\_al\_2014 }}, {{ rtxt\_sollmann\_2018 }}).

2. Detection probability is assumed to be the same across all individuals and sampling occasions, even though the likelihood a given individual is detected at a given camera trap will change with its proximity to that trap. An animal that occupies territory far away from a trap is less likely to be detected there than one that lives nearby, for example ({{ rtxt\_morin\_et\_al\_2022 }}).

The standard CR model has largely been phased out with the advent of spatially-explicit CR models (see {bdg-link-primary-line}`Spatial capture-recapture (SCR) / Spatially explicit capture recapture (SECR)<https://ab-rcsc.github.io/rc-decision-support-tool\_concept-library/02\_dialog-boxes/03\_11\_mod\_scr\_secr.html>`); {{ rtxt\_burton\_et\_al\_2015 }}, {{ rtxt\_sollmann\_2018 }}), which address the shortcomings of CR and have been shown to produce more accurate density estimates (e.g., {{ rtxt\_blanc\_et\_al\_2013 }}, {{ rtxt\_obbard\_et\_al\_2010 }}, {{ rtxt\_sollmann\_et\_al\_2011 }}).

## Figures

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| **Image** | **file\_name** | **Caption (if applicable)** | **ref\_id** |
| A black background with a white arrow  Description automatically generated | clarke\_et\_al\_2023\_fig11\_clipped.png | \*\*Clarke et al. (2023) – **Fig. 3\*\*** Adapted from Royle (2020). A detection history matrix for an example population.  :::{dropdown}  For each individual (1 through \*𝑛\*) during each sampling occasion (1 through \*𝐾\*), a value of 1 is assigned if that individual was detected at a camera trap and a value of 0 is assigned if it was not detected at a camera trap. Note that we do not detect individuals \*𝑛\* + 1, \*𝑛\* + 2…\*𝑁\* (0s for every sampling occasion), but they are still present and able to be detected.  ::: | clarke\_et\_al\_2023 |
| A number of letters and numbers  Description automatically generated with medium confidence | clarke\_et\_al\_2023\_eqn\_cr1.png |  | clarke\_et\_al\_2023 |
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|  | figure6\_filename.png | figure6\_caption | figure6\_ref\_id |

## Video

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## Analytical tools & resources

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| CAPTURE | resource2\_name | resource2\_note | resource2\_url | resource2\_ref\_id |
| R package | ‘multimark’: Capture-Mark-Recapture Analysis using Multiple Non-Invasive Marks | Linked package version 2.1.6 updated as of 2023 | <https://cran.r-project.org/web/packages/multimark/index.html> | mcclintock\_et\_al\_2015 |
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## References / Glossary

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## Notes

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**::::::{tab-item} Overview**  
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**::::::{tab-item} In-depth**  
```{include} include/note\_adapted\_clarke\_et\_al\_2023.md

```

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:::{figure} ../03\_images/03\_image\_files/clarke\_et\_al\_2023\_fig11\_clipped.png

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Taking this information together, we can calculate population size \*𝑁\* as:

:::{figure} ../03\_images/03\_image\_files/clarke\_et\_al\_2023\_eqn\_cr1.png

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

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\*\*Clarke et al. (2023) – **Fig. 3\*\*** Adapted from Royle (2020). A detection history matrix for an example population.

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For each individual (1 through \*𝑛\*) during each sampling occasion (1 through \*𝐾\*), a value of 1 is assigned if that individual was detected at a camera trap and a value of 0 is assigned if it was not detected at a camera trap. Note that we do not detect individuals \*𝑛\* + 1, \*𝑛\* + 2…\*𝑁\* (0s for every sampling occasion), but they are still present and able to be detected.

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**:::::{tab-item} Analytical** tools & Resources  
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