

remBoot: An R package for Random Encounter Modelling

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Software

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Summary

The Random Encounter Model (REM) allows researchers to calculate population densities from camera trap data for species which do no exhibit individually-identifiable markings (Rowcliffe et al. 2008) such as tapir (*Tapirus terrestris*; (Oliveira-Santos et al. 2010), pine marten (*Martes martes*; (Manzo et al. 2012), and hares (*Lepus* sp.; (Caravaggi et al. 2016)).

Density (D) is linearly scaled with trapping rate, based on two biological variables and two camera characteristics: g = average animal group size; y = number of detections; t = survey effort (i.e. camera hours); v = average distance travelled by the species in 24 hours; r = radial distance to the animal; and, theta = zone of detection (Fig. 1; (Rowcliffe et al. 2008)).

remBoot is the first package to implement REM calculations in R. The package also contains functions which allow the calculation of variance (standard deviation [SD] and/or 95% confidence intervals [CI]; Fig. 2). These calculations are computationally inexpensive and can be applied to datasets of considerable size. Densities and associated variances can be calculated for one or more sites concurrently, streamlining the analytical process.

Acknowledgments

Thanks to Kevin Keenan for his work on implementing REMs in R early on, when the language was still very new to me, and to Bryce Mecum (@amoeba) for his efforts in reviewing this package.

Figure 1. Data inputs (y and t) and parameters (r, v and theta) required for the calculation of population density estimates from camera trap data by the Random Encounter Model (REM). g = average animal group size; y = number of detections; t = survey effort (i.e. camera hours); v = average distance travelled by the species in 24 hours; r = radial distance to the animal; and, theta = zone of detection.

Figure 2. Animal densities (individuals.km2) with associated variances (SD) calculated via Random Encounter Models, using remBoot.

References

Caravaggi, Anthony, Marco Zaccaroni, Francesco Riga, Stephanie C. Schai-Braun, Jaimie T.A. Dick, W. Ian Montgomery, and Neil Reid. 2016. "An Invasive-Native Mammalian



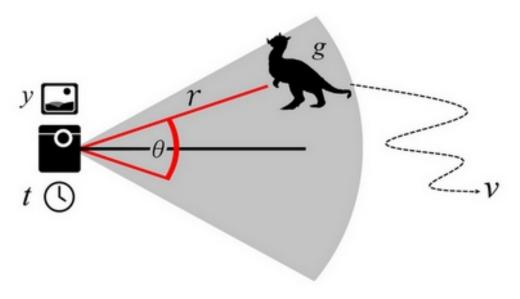


Figure 1: REM diagram

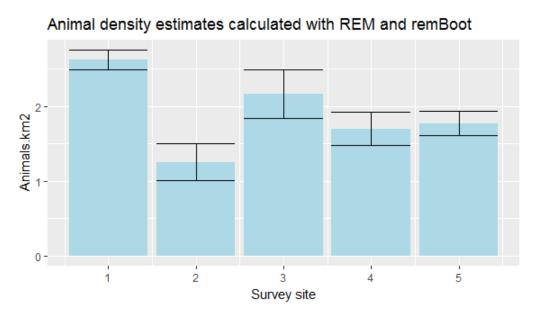


Figure 2: Density plot



Species Replacement Process Captured by Camera Trap Survey Random Encounter Models." Remote Sensing in Ecology and Conservation 2 (1): 45–58. doi:10.1002/rse2.11.

Manzo, Emiliano, Paola Bartolommei, J. Marcus Rowcliffe, and Roberto Cozzolino. 2012. "Estimation of Population Density of European Pine Marten in Central Italy Using Camera Trapping." *Acta Theriologica* 57 (2): 165–72. doi:10.1007/s13364-011-0055-8.

Oliveira-Santos, Luiz Gustavo R., Carlos André Zucco, Pamela Castro Antunes, and Peter G. Crawshaw Jr. 2010. "Is It Possible to Individually Identify Mammals with No Natural Markings Using Camera-Traps? A Controlled Case-Study with Lowland Tapirs." *Mammalian Biology - Zeitschrift Für Säugetierkunde* 75 (4): 375–78. doi:http://dx.doi.org/10.1016/j.mambio.2009.08.005.

Rowcliffe, J. Marcus, Juliet Field, Samuel T. Turvey, and Chris Carbone. 2008. "Estimating Animal Density Using Camera Traps Without the Need for Individual Recognition." $Journal\ of\ Applied\ Ecology\ 45\ (4)$. Blackwell Publishing Ltd: 1228–36. doi:10.1111/j.1365-2664.2008.01473.x.