NEXT-GENERATION SEROLOGY: INTEGRATING CROSS-SECTIONAL AND CAPTURE–RECAPTURE APPROACHES TO INFER DISEASE DYNAMICS

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Study Description

Two approaches have been classically used to estimate epidemiological parameters from field studies: cross-sectional sampling from unmarked individuals and longitudinal capture–mark–recapture setups, which generally involve more limited numbers of individuals due to cost and logistical constrains. Inspired by recent method developments in quantitative ecology, we explored the benefits of integrating together these two approaches and compared the performances of cross-sectional, longitudinal, and integrated designs to estimate epidemiological parameters. Our results highlight that host species life history, antibody persistence, and the availability of reliable a priori knowledge of demographic and epidemiologic parameters are key elements to determine optimal sampling designs.

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Photo 1: Longitudinal approaches based on repeated sample collection from marked individuals in a capture–recapture framework are especially efficient to estimate eco-epidemiological parameters in host species exhibiting long lifespan and high breeding site faithfulness such as albatrosses, especially when considering infectious agents eliciting long-lived immune responses, and this even with limited a priori knowledge on demographic and epidemiologic parameters. This picture features an Indian yellow-nosed albatross (*Thalassarche carteri*) marked as part of a study on *Pasteurella multocida* epidemiology in subantarctic seabird communities. Photo credit: Thierry Boulinier, IPEV.

Photo 2: Cross-sectional approaches based on sample collection from unmarked individuals perform well to estimate eco-epidemiological parameters when host lifespan and/or antibody level maintenance are short relatively to delay between sampling occasions, as it is the case when studying interannual dynamics in rodent populations, or when reliable a priori knowledge on demographic and epidemiologic parameters is available. This picture features a natal multimammate mouse (*Mastomys natalensis*) sampled to study the dynamics of arenaviruses in the populations Photo credit: Benny Borremans.

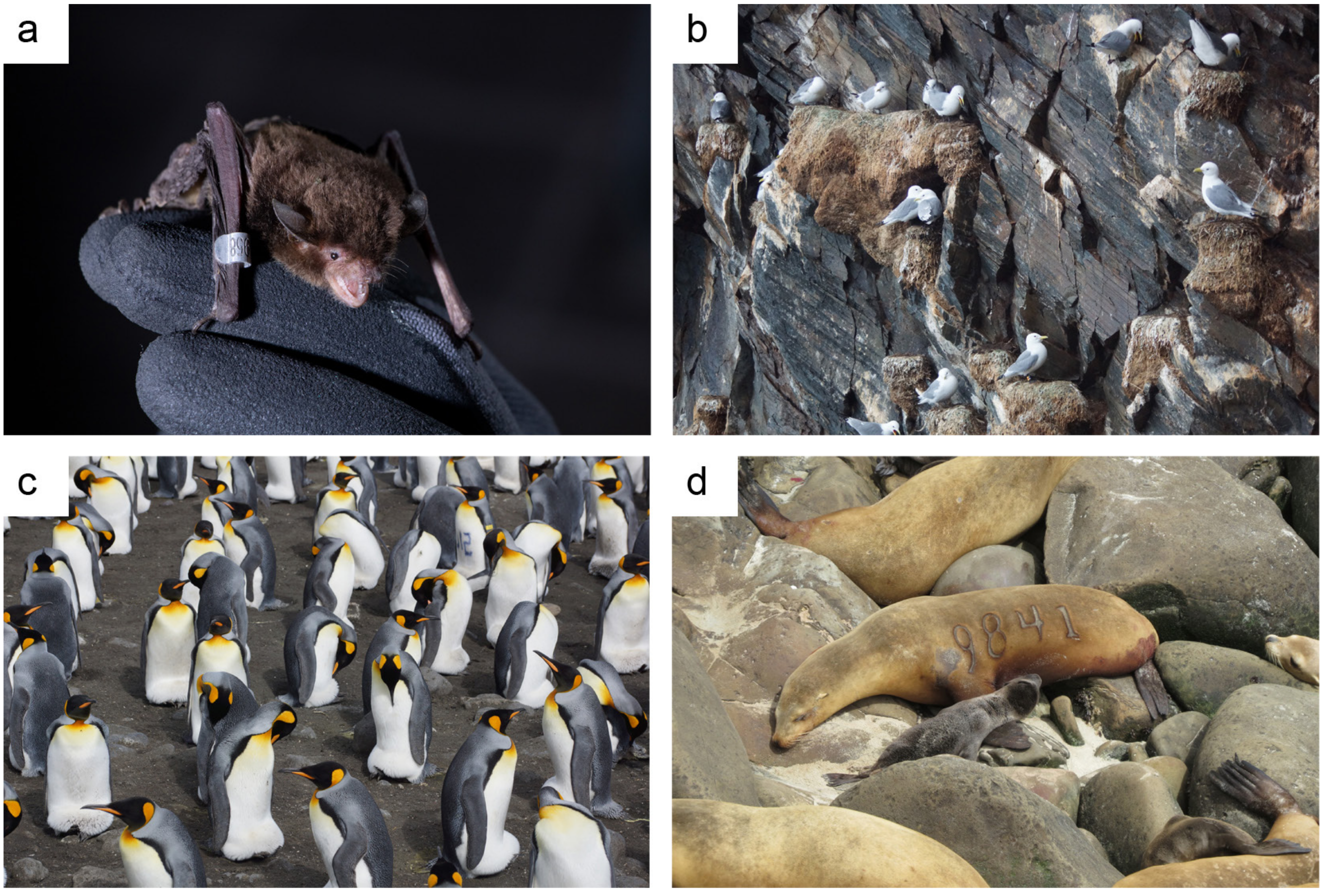

Photo 3: Integrating cross-sectional and longitudinal data using the novel framework we propose offers the opportunity to efficiently estimate eco-epidemiological parameters when host lifespan is intermediate and/or marked individuals are difficult to recapture because of non-negligible dispersal probabilities (such as bats or small gulls), low individual resighting probability (such as densely breeding penguins marked with internal tags), or low individual recapture probability (such as pinnipeds, which are intrinsically difficult to capture). The pictures feature (a) a yellowish myotis (*Myotis levis*) marked and sampled notably to study herpesvirus genetic structuration among bat populations, (b) black-legged Kittiwakes (*Rissa tridactyla*) marked and monitored as part of a study on Lyme disease *Borrelia* epidemiology in seabirds, (c) king penguins (*Aptenodytes patagonicus*), potentially including pit-tagged individuals, and (d) California sea lion (*Zalophus californianus*) marked as part of a study on the impact of *Leptospira* spp. outbreaks on the population. Photo credit: Germán Botto Nuñez (a), Amandine Gamble (b, c, d), IPEV (b, c), NOAA AFSC Marine Mammal Laboratory (d).

These photographs illustrate the article “Next-generation serology: integrating cross-sectional and capture-recapture approaches to infer disease dynamics” by A. Gamble, R. Garnier, T. Chambert, O. Gimenez and T. Boulinier, published in Ecology. https://doi.org/10.1002/ecy.2923