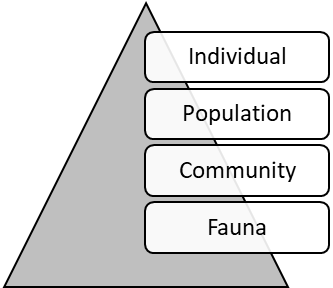
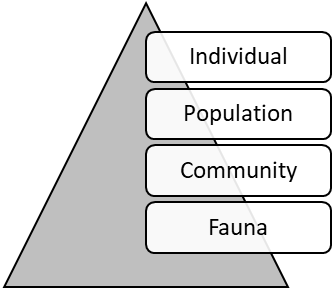
**1 | INTRODUCTION**

**[PAR1]** Despite often being neglected in ecological studies (Morley, 2012; Scholz & Choudhury, 2014), parasites are key components of natural communities and ecosystem Functioning (Dobson & Hudson, 1986; Frainer et al., 2018; Lafferty et al., 2008; Marcogliese, 2004; Minchella & Scott, 1991; Pascal et al., 2020; Poulin, 1999). Given their dependence and co-evolution with their free-living hosts, some species are inherently vulnerable to the same environmental changes that threaten biodiversity globally (Gandon et al., 2008; Mostowy & Engelstädter, 2010). Yet, their spatial distribution patterns and networks are still misunderstood as general rules are hard to uncover (Poulin, 2007). One of the first steps to clarify these context-dependencies is to address the importance of spatial scaling for the estimation of infection parameters such as the prevalence of infection in biotic communities.

**[PAR2]** Infection patterns within a population or community can vary across taxa, time and/or space making it difficult to understand and model the drivers of infection within ecological systems (Happel, 2019; Poulin, 2006; Poulin & Dick, 2007; Thieltges & Reise, 2007; Villalba-Vasquez et al., 2018; Young & Maccoll, 2017). Indeed, the literature currently fails to disentangle the processes explaining variation in parasite infection across scales as metacommunities’ species filtering is widely scale-dependent (Bolnick et al., 2020). Scaling is especially relevant in parasite ecology given the hierarchical organization of both the parasite and host component (Fig1). For example…. Considering the complexity of host-parasite systems, there are still many biological scale combinations that need to be investigated. For example, component communities (see Bush et al., 1997) of metazoan parasites in fish host-populations have been the focus of many studies in the past decades regarding spatiotemporal patterns (e.g. Carney & Dick, 2000; González & Poulin, 2005; Pérez-del-Olmo et al., 2009; Villalba-Vasquez et al., 2018). Conversely, species-specific infection patterns in host-communities remain largely unexplored in fish species across spatial scales. Thus, host-parasite associations are well-suited models to investigate the implications of scaling on infection estimates.



Parasite

Host

Fig1.

As a matter of fact, scale-dependance has been raised on abundance and distribution patterns of metazoan parasite infection in freshwater (Poulin, 1998).

**[PAR3]** Since current literature lacks consistency, it remains unclear whether infection patterns result from stochastic events (i.e….) or determinist filtering (i.e. xxx) (Carney & Dick, 2000; González & Poulin, 2005; Kennedy, 2009; Poulin, 2007; Poulin & Valtonen, 2002). Studies have shown that both biotic and abiotic components can be correlated to variation in infection metrics at various spatial scales (Altman & Byers, 2014; Falke & Preston, 2021; Lagrue et al., 2011; Lagrue & Poulin, 2015; Poulin & Morand, 1999; Thieltges et al., 2008). Individual host characteristics such as sex (Zuk & McKean, 1996), age/size (Marcogliese et al., 2001; Poulin, 2000) and genetics (Williams-Blangero et al., 2012) drive host susceptibility leading to sources of variation in infection estimates and population-level patterns. On a larger scale, community properties such as species richness and host population density can create a “dilution effect” by reducing a parasite’s encounter rates with hosts or success of infection (Ahn & Goater, 2021; Buck & Lutterschmidt, 2017; Dargent et al., 2013; Lagrue & Poulin, 2015). Local habitat characteristics have also been correlated to variation in parasitological metrics in host communities. In American eels (*Anguilla rostrata*), parasite diversity decreases when water pH is below 5.4, with some parasite families such as digenean trematodes being absent below pH 4.7 (Marcogliese & Cone, 1997). Similarly, lentic water bodies with dense vegetation display higher prevalence and abundance of *Posthodiplostomum cuticola* paraites in host fish than rivers and reservoirs with steep banks (Ondrackova et al., 2004), suggesting that local habitat and morphometry of the water body are drivers of encounter filtering. Furthermore, spatial features of an ecosystem (e.g., watershed, connectivity) act as large scale filtering by limiting dispersal (Bolnick et al., 2020) thus creating infection patchiness in the landscape level. Happel (2019) provided evidence for consistent geographical patterns in prevalence of the black spot disease between watersheds. Bolnick et al. (2020) also found a small effect of waterways distance between waterbodies on parasite communities of threespine stickleback (*Gasterosteus aculeatus*). With this in mind, a complete ecological perspective on host-parasite systems must incorporate abiotic, biotic and spatial drivers to highlight mechanism shaping patterns as some filters are scale-dependent (Bolnick et al., 2020; Cohen et al., 2016). Still, we lack crucial information on how patterns and predictors of infection parameters change across scale to properly monitor and manage parasitic disease.

**[PAR4]** Here, we test the effect of spatial scale on infection prevalence estimates across different sampling methods using data on the black spot disease in littoral fish communities across 15 lakes varying in morphometric attributes and local conditions. We analyze infection prevalence data at the host-community level for scaling-dependencies through three spatial scale levels (regional, local and fine-scale) in order to investigate **(i)** the effect of random sampling effort on regional prevalence estimation through different sampling methods **(ii)** the distribution of observed local prevalence estimations and **(iii)** the importance of ecological predictors on infection prevalence on a manageable scale (i.e., transect).

**[PAR5]** For regional scale estimates, we used random prevalence accumulation curves by resampling across lakes. This approach allows us to compare regional-scale prevalence estimates (and associated variance) among different sampling methods along a gradient of increasing sampling effort (or area sampled). Akin to interpretations of species-area relationships, the accumulation curves can show evidence for scale-invariance (“flat curve” – infection prevalence does not change with increasing sampled area because it is well mixed across samples) or for spatial patchiness (“non-linear curve” – the number of infected individuals sampled and the number of individual sampled increase at different rates). Observed estimates in wild fish populations can be influenced by sampling design elements such as sample size (Poulin, 2013), sampling method (Wilson et al., 1993) and timing of sampling (Hutchins et al., 2021). Consequently, sampling design elements must be considered when studying scale-dependencies of infection estimates. Patterns of regional-scale estimates from random sampling can be caused by different underlying local patterns of infection. For instance, a regional prevalence of 20% could be caused by all lakes having the same prevalence with no variance (i.e. all lakes at 20%) or by the average prevalence of all lakes being at 20% with large inter-lake variance (e.g., half at 0% and half at 40%). Thus, investigating local-scale patterns is important to bring the necessary nuances on the regional-scale estimates and to infer processes properly. For example, frequency distributions of infection parameters are useful to understand infection dynamics in the landscape (Hess et al., 2002; McGeoch & Gaston, 2002). The final step was to test a suit of deterministic environmental predictors underlying scale-dependent processes to understand the observed infection prevalence and explore whether some indicators could be useful for the management of parasite infection in fish communities. Investigating wide-ranging predictors has the potential to enlighten processes driving infection patchiness (herein infection hotspots) within a system that appears homogenous (Bolnick et al., 2020). The shapes and strength of the relationships between infection parameters and drivers are a key element to better understand the mechanisms behind infection patterns (Poulin et al., 2011). Our goal here was not to make predictions on spatial distribution of the parasitic infection but rather to disentangle how patterns are shaped through a scaling perspective to facilitate the monitoring and management of parasitic infection in freshwater systems.

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