

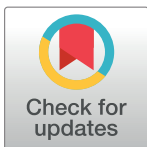
CORRECTION

Correction: Cryptic chytridiomycosis linked to climate and genetic variation in amphibian populations of the southeastern United States

Ariel A. Horner, Eric A. Hoffman, Matthew R. Tye, Tyler D. Hether, Anna E. Savage

There is an error in the first sentence of the “Genetic and environmental disease modeling” subsection of the Methods section. The correct sentence is: For species that tested positive for *Bd* or *Rv* in multiple populations, we used general linear models (GLMs) weighted based on population size to predict pathogen prevalence (with binomial error; [51]) and the natural log of intensity based on genetic and environmental variables, as well as location.

There is an error in [Fig 1](#). Panels C and D appear in the incorrect order and the caption contains spelling errors. Please see the corrected [Fig 1](#) and its caption here.



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Citation: Horner AA, Hoffman EA, Tye MR, Hether TD, Savage AE (2017) Correction: Cryptic chytridiomycosis linked to climate and genetic variation in amphibian populations of the southeastern United States. PLoS ONE 12(10): e0186066. <https://doi.org/10.1371/journal.pone.0186066>

Published: October 3, 2017

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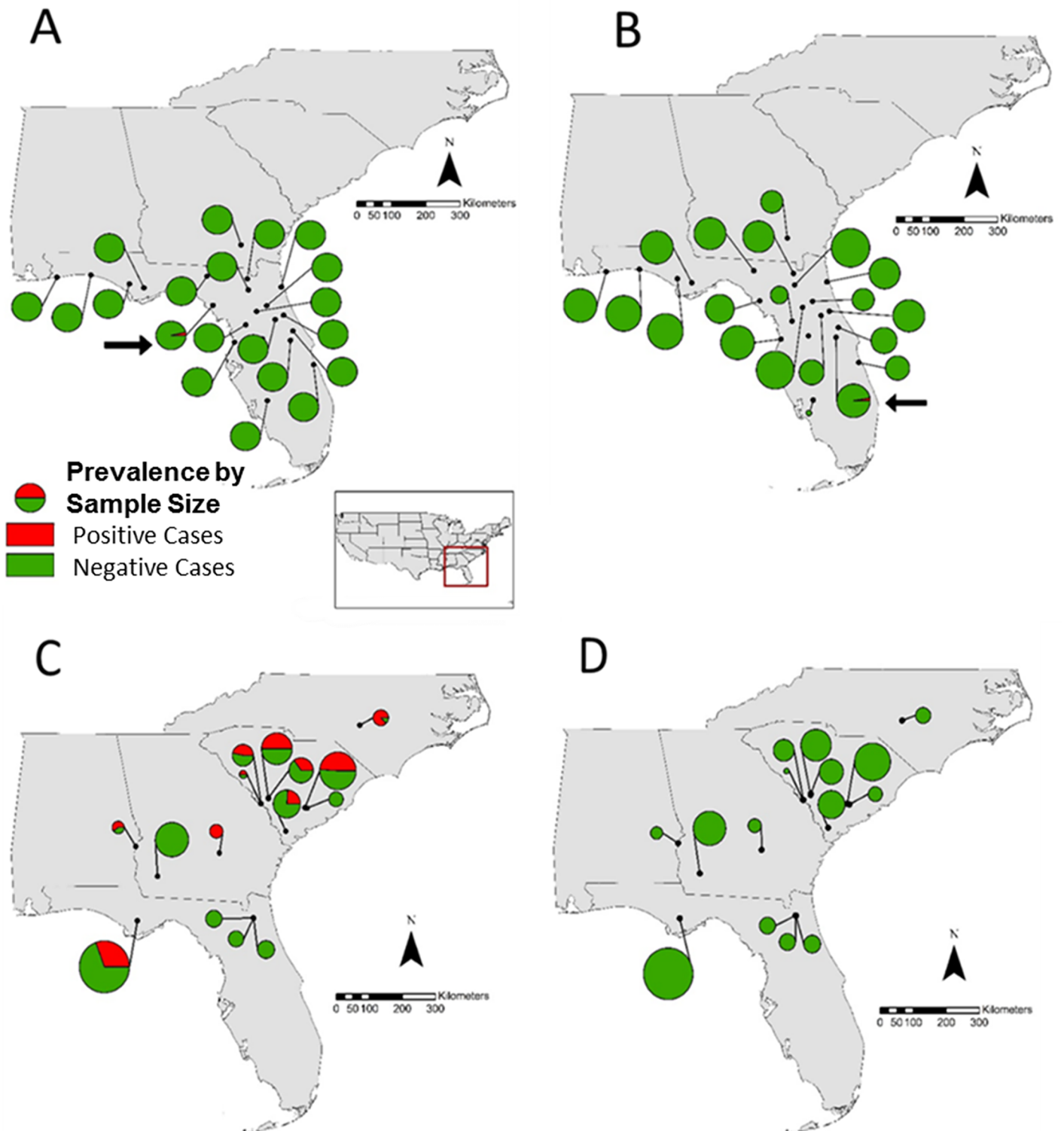


Fig 1. Map of sample localities and (A) *Bd* prevalence in *Hyla squirella*, (B) *Rv* prevalence in *H. squirella*, (C) *Bd* prevalence in *Pseudacris ornata* and (D) *Rv* prevalence in *P. ornata*. Circle size is proportional to sample size. Arrows point to infected *H. squirella* populations. Green represents proportion of negative cases of the indicated pathogen while red represents proportion of positive cases.

<https://doi.org/10.1371/journal.pone.0186066.g001>

Reference

1. Horner AA, Hoffman EA, Tye MR, Hether TD, Savage AE (2017) Cryptic chytridiomycosis linked to climate and genetic variation in amphibian populations of the southeastern United States. *PLoS ONE* 12(4): e0175843. <https://doi.org/10.1371/journal.pone.0175843> PMID: 28448517