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Ecological niche modelling in
triatomines – *abusus non tollit
usum*: a reply to Gutiérrez (2016)

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In [1], the vectorial risk of Chagas disease transmission was estimated from the climatic suitability expected for *Rhodnius prolixus* and *Triatoma infestans* by year 2050 in Argentina and Venezuela using ecological niche modelling (ENM), and Gutierrez [2] claimed that the nature of the data and the study regions might invalidate the conclusions. Although this warning is fit and welcomed, in triatomines and for particular goals the use of ENM, though not complying with some methodological prescriptions, can be justified.

In [1], data quality controls were applied: *R. prolixus* was deleted from Bolivia and southern Amazonia, *T. infestans* was pooled with *T. melanosoma*, and extended in Bolivia; coordinates were deleted using a database with georeferenced water bodies. Elevational false positives claimed by Gutierrez [2] are not such (by mistake, Medone *et al.* [1] reported the altitudinal limits given by Carcavallo *et al.* [3] instead of the ones of the data used). Other false positives mentioned by Gutierrez [2] were *R. prolixus* in Costa Rica (though its presence there has been confirmed [4,5]), and in Panama, the latter an historical taxonomic error.

Lack of prediction errors from the use of confirmed occurrences was criticized by Gutierrez [2]; however, MAXENT was not run with confirmed presence data: only predictions from range maps with confirmed presences were checked. We apologize for not reporting the geographical projection of the models, which was the Americas, between 44 N and –47 S, and –34 E and –125 E.

The study regions should not include areas that cannot be accessed due to dispersal problems, but there are some caveats in triatomines: (i) triatomines are detectable in restricted time/space-windows (time of day or year, type of habitat), affecting the pseudo-presence/pseudo-absence problem more than inaccessible areas; (ii) sampling triatomines is biased: most sampling is associated with rural houses in detriment to sylvatic habitats ('biased in environmental dimensions' [6]), inducing more noise than the pseudo-presence problem; (iii) the use of domiciliated microhabitats dampens climatic effects [7,8], minimizing pseudo-presences (areas nearby confirmed presence have a higher possibility of being pseudo-absence than pseudo-presence); and (iv) in addition to their own dispersal capacities, triatomines are also transported by humans and animals, resulting in range shifts that outweigh the pseudo-presence/pseudo-absence problems.

The pseudo-presence and background problems raised by Gutierrez [2] are possibly the strongest criticism to [1], regardless of the use of surveys and range maps to estimate richness results in under- and overestimation, respectively [9]. Is not complying with the use of confirmed occurrences a serious violation in triatomines? In *T. infestans* using the average first nearest-neighbour distance (between confirmed occurrences and random coordinates from [3]) was 29.1 km (26.4–31.9 km 95% CI; $n = 640$). Checking the geographical autocorrelation for six bioclimatic predictors on arbitrary 'transects' running along longitudes and 'crossing' through various latitudes, in plain and mountainous regions in Argentina, Colombia and Venezuela, there was a significant spatial autocorrelation of 100–300 and 50–80 km in the plain and mountainous areas, respectively. With the nearest-neighbour distances within the spatial

autocorrelation scale of the bioclimatic variables the use of random coordinates from the range maps would not invalidate the conclusions of Medone *et al.* [1].

The shapes of BAM diagrams [6,10] depend upon the species' eco-physiological and behavioural characteristics and the abiotic and biotic environments; triatomine BAM diagrams (TBAM) are different to classical BAM diagrams for triatomines are characterized by: (i) a high mobility (active + passive) so factor M in the TBAM includes factors A and B (and is close to their union, $A \cup B$); (ii) an eclectic diet, so B overlaps closely with A; and (iii) a selective microhabitat use, so components A, B and M are extremely close to the geographic area (G). Using the shape of the Americas as G, *T. infestans* shows a disjoint BAM, while *R. prolixus* shows a more 'classical' BAM, but for both species the M 'envelope' encompasses practically the whole of A and B regions. This peculiar TBAM justifies a large modelling background that includes almost all of the Americas.

Range maps are scale-dependent abstractions of species distributions [9], with resolutions less than 2° (≈ 200 km) usually overestimating the occupancy area of individual species [11]; as the purpose was to link environmental suitability to epidemiological risk, Medone *et al.* [1] preferred to err towards an overestimation rather than to an underestimation. Exceptions to the recommended methodology (such as using confirmed occurrences in MAXENT) are regularly published when a specific objective justifies them [12,13].

The large M area of *T. infestans* and *R. prolixus* is also influenced by the B region; triatomine presence is mainly

determined by the host species (pathogens, parasites, predators and competitors have a much smaller role), and a lack of negative interactions across G makes the B area smaller than or equal to abiotic G_A [6]. As the performance of MAXENT is sensitive to the size of the background, this results in a conundrum for triatomines, because the large M area would justify using a large background.

An ongoing analysis of three triatomine species [14], where confirmed occurrences for *Panstrongylus geniculatus*, *P. megistus* and *T. guasayana* (with 189, 593 and 90 coordinates, respectively) were compared with a random selection of range maps from [3] using MAXENT and GARP software, showed no statistically significant differences in the suitability predictions between the two datasets using three methods of evaluation (average AUC curves from 10 replicates, threshold-dependent kappa and True Skill Statistics).

Being the first application of a methodology to convert suitability predictions into epidemiological risk, Medone *et al.* [1] stated that results should not be taken as a policy guide. Owing to the short space available for this reply, details on the statistical tests and full arguments here used will appear in a full paper that is underway. Nevertheless, I consider that the observations and caveats posed in [2] are valid in general, and I thank this author for pointing out some incomplete descriptions in [1]; I believe that his observations about potentially dangerous applications of the MAXENT software, if used inadequately, will be welcomed by readers and practitioners, particularly if they keep in mind 'abusus non tollit usum' (misuse does not remove use).

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