Predicting the Spread of Invasive Species using GARP Models and Time-Series Data

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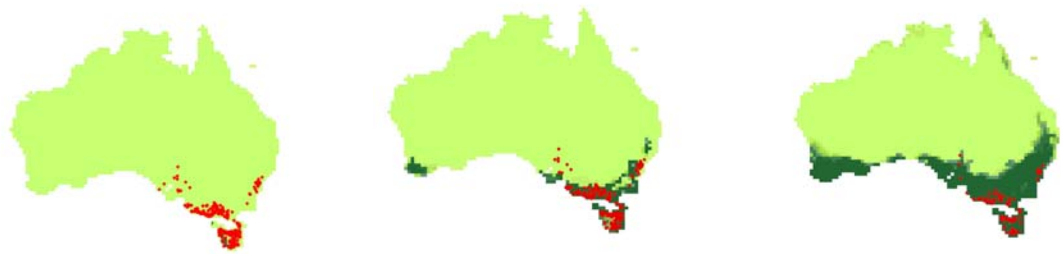
Introduction:
An understanding of the potential distribution of biological invaders contributes to the evaluation of the environmental, economic and social costs of invasive species. Ecological modelling of invasive species allows the identification of suitable habitat for an invader. It is common practice to build models with data from the invaders native range and project the habitat suitability model onto the invaded region. It is less common to use data from the invaded range to make predictions about the potential distribution of the invader.

The invasive New Zealand mudsnail, *Potamopyrgus antipodarum*, has spread widely in south-eastern Australia since its initial introduction in the late-nineteenth century, and its range may still be expanding. The mudsnail was first found in North America 20 years ago, and since then it has been rapidly spreading in the western USA and has been reported in the Great Lakes. In North America, the New Zealand mudsnail has been reported to occur in densities of up to 800,000 per m^2, and may out-compete native macroinvertebrates for resources and have ecosystem-level impacts.

Method:
To assess the potential distribution of the snail in Australia and North America, I used the Genetic Algorithm for Rule-set Production (GARP) modelling framework. GARP performs a spatially explicit, ecological niche modelling analysis to predict the potential distribution of a species, based on known records of the species occurrence. Models were built using distributional datasets from the snail's native range in New Zealand and contrasted with models built from its range of invasion in Australia and North America.

Results:
The models built for Australia with the native range data from New Zealand were found to be making statistically significant, although weak predictions (AUC = 0.686, $p <$ 0.0001) (Fig. 1a). By using data from early in the invasion sequence in Australia (pre-1915), current distributions were predicted well (AUC = 0.879, $p < 0.0001$) (Fig. 1b).

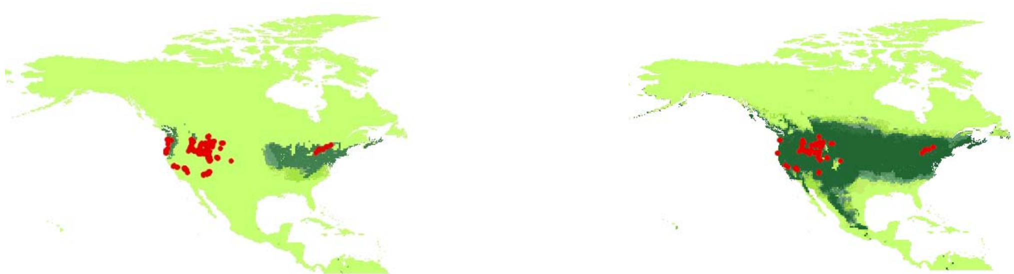
Models built with 'current' post-1980 Australian data made the strongest predictions (AUC = 0.969, $p < 0.0001$) (Fig. 1c).



a). b). c).

Figure 1: GARP predictions on the potential distribution of *Potamopyrgus antipodarum* in Australia built using the a). New Zealand, b). pre-1915 Australian and c). post-1980 Australian datasets. The green color range indicates the intersection of various models sets, dark shades representing the intersection of all ten best subset models and the light shades the intersection of fewer models or no models at all. The red colored circles on the map represent known point occurrences of *P. antipodarum.*

The models built for North America with the native range data from New Zealand made weak predictions (AUC = 0.528, $p = 0.017$) (Fig 2a). When the current North American data was used the predictions were very accurate (AUC = 0.877, $p < 0.0001$) (Fig 2b).



a). b).

Figure 2: GARP predictions on the potential distribution of *Potamopyrgus antipodarum* in North America built using the a). New Zealand, and b). North American datasets. The green color range indicates the intersection of various models sets, dark shades representing the intersection of all ten best subset models and the light shades the intersection of fewer models or no models at all. The red colored circles on the map represent known point occurrences of *P. antipodarum.*

Discussion

The spatial distribution models forecast an expansion in the New Zealand mudsnail's range in both Australia and North America. The broad environmental tolerances of *P. antipodarum* allow the snail to thrive in environmental conditions found outside of New Zealand. The small geographical size of New Zealand compared with the Australian and North American continents means in the native-range models were built with a relatively narrow range of environmental conditions. When an invader originates from a small, limited environmental range, and is transported to a larger, more heterogeneous location, its potential range may be underestimated. In these cases ecological models built with data from the range of invasion may be more accurate.