The Niche of an Invasive Species, *Polyommatus icarus*

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Introduction

Introduced Species and *Polyommatus icarus*

Introduced species are species that are moved purposely or accidentally from their native habitat to a new one, where they may become established and widespread. Human activities have and continue to lead to the introduction of new species into new habitats worldwide (1). If the introduced species spreads widely in its new home and damages or dominates the new habitat, it is labeled an invasive species (3). *Polyommatus icarus (P. icarus)* (Rottemburg) has all the hallmarks of an invasive species. In 2005, *P. icarus,* known as the common blue butterfly, was introduced into North America, specifically, into the Montreal area of Quebec (2). The native habitat of *P. icarus* is widespread across mainland Europe, North Africa, and parts of Asia (4). The common blue's caterpillar is a herbivore, eating mainly legumes like the bird's foot trefoil (5). This particular legume has also been introduced into North America and has spread widely (4). *P. icarus* is a butterfly that can live in a variety of habitats, many of which resemble those found in North America. These points demonstrate that *P. icarus* has a solid basis to spread in North America and become a dominant invasive species.

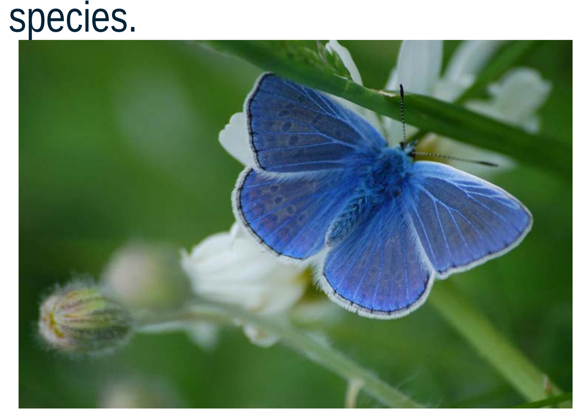

Figure 1. *Polyommatus icarus* is a blue butterfly that is widely distributed throughout Europe. (6)

Figure 3. *Polyommatus icarus* was recently introduced into the Montreal area of Quebec.

The overarching objective of this project is to create a random parameterized (spreading dye) model of the common blue's future distribution in North America. To do this, it is necessary to have information on the niche of the common blue and to know the environmental parameters that control its distribution within its native range. Therefore, this part of the project's purpose was to create a niche model to determine the niche and the most important variables that control the common blue's distribution in its native range.

Niche models

The (fundamental) niche of an organism is the set of environmental factors in which a species can exist. Niche models are used to predict a species' niche. This is done by linking the species' presence or absence to environmental factors. This will result in a model showing the range of the species in its native habitat. This model will also determine which variables affect the distribution of the species control its range the most. To create the model, the modelling program Maxent will be used. The benefit of using Maxent is that it does not need to link species absence to certain environmental variables. It can create a model by linking only species presence data to environmental variables.

However, a niche model by its self cannot be used to predict the future distribution of a species in a new environment. This is because the niche model assumes that a species is in equilibrium with the climate of the habitat that its niche is being modeled in. When a species is introduced into a new habitat, it is not in equilibrium with the climate, but is constantly expnanding. To predict the distribution in a new habitat, a random parameterized (spreading dye) model has to be used. These models can be created with a set dispersal capacity, which constricts them to only a certain amount of range expansion per period of time. They can also be created with range restrictions, which are derived from the niche predicted by the niche model. These range restrictions prevent the model from surpassing certain environmental limits while expanding. This, in the end, should provide a prediction of how *P. icarus* will spread in its new North American habitat.

Materials and Methods

Data Collection

The species distribution data was downloaded from the Global Biodiversity Information Facility (GBIF) Data Portal (4).

↓

Any occurrence that did not have a longitude or latitude entry or had a coordinate precision value of less than 20 Km was omitted.

Environmental data was downloaded from the BIOCLIM section of WORLDCLIM in the ESRI grid format with a grain size of 10 arc minutes (~20km x 20km) (7).

↓

Data was then clipped to an extent that had the following limits: 75^0 north, 140^0 west, -17^0 east, and 20^0 south and converted to ASCII format for use with MaxEnt.

Table 1. The names of the environmental variables that were downloaded from BIOCLIM.

Variable Name
Annual mean temperature
Maximum temperature of the warmest month
Minimum temperature of the coldest month
Meant temperature of the warmest quarter
Annual precipitation
Precipitation seasonality (coefficient of variation)

Creating Models

The species distribution data was inserted into the Samples field, while the environmental variables files were inserted into the Samples with Data Sets field.

The number of replicates was set to 10, the maximum number of background points was set to 10000, the random seed option was selected, the random test percentage was set to 20%. The rest of the settings were left in their default state.

MaxEnt was run, and 10 test models were generated as well as a composite model that was the average of the 10 test models.

Results

Native Range Distribution

Hypothesis: Considering the present knowledge about *P. icarus,* we expect it to be very well distributed throughout its native range.

The composite model created by Maxent to predict the distribution of *P. icarus* over its native range showed that the species has a wide distribution across Europe and parts of the Middle East and North Africa. The 10 runs that were used to create the composite model had an average AUC (Area Under Rate of Occurrence Curve) of 0.880 and a standard deviation of 0.005. This is a good AUC value, and it is given strength and meaning by the fact that the model successfully predicts where the species has documented occurrences and where the species is believed or reported to exist but there has been no documentation of its occurrence. The dataset that contributed the most to the composite model was the precipitation seasonality, with a 39.1 % contribution, meaning that it has the greatest influence on the range of *P. icarus* in this model. Below is a graphic of the model that was generated:

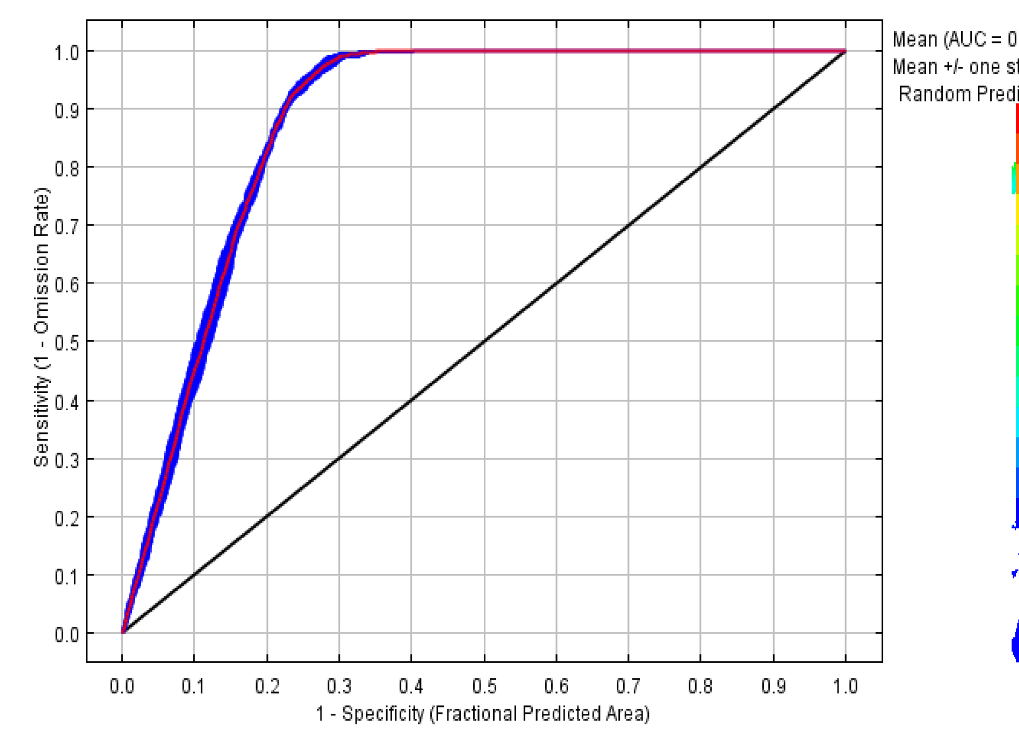

Figure 4. Graph of Specificity vs. Sensitivity for the spatial model predicting the distribution of *P. icarus* in it's native range. The Area Under Rate of Occurrence Curve corresponds to the ability of the model to predict the occurrence of the butterfly. If the area is 0.5 or less (denoted by the black line), then the model's predictions are not better than chance.

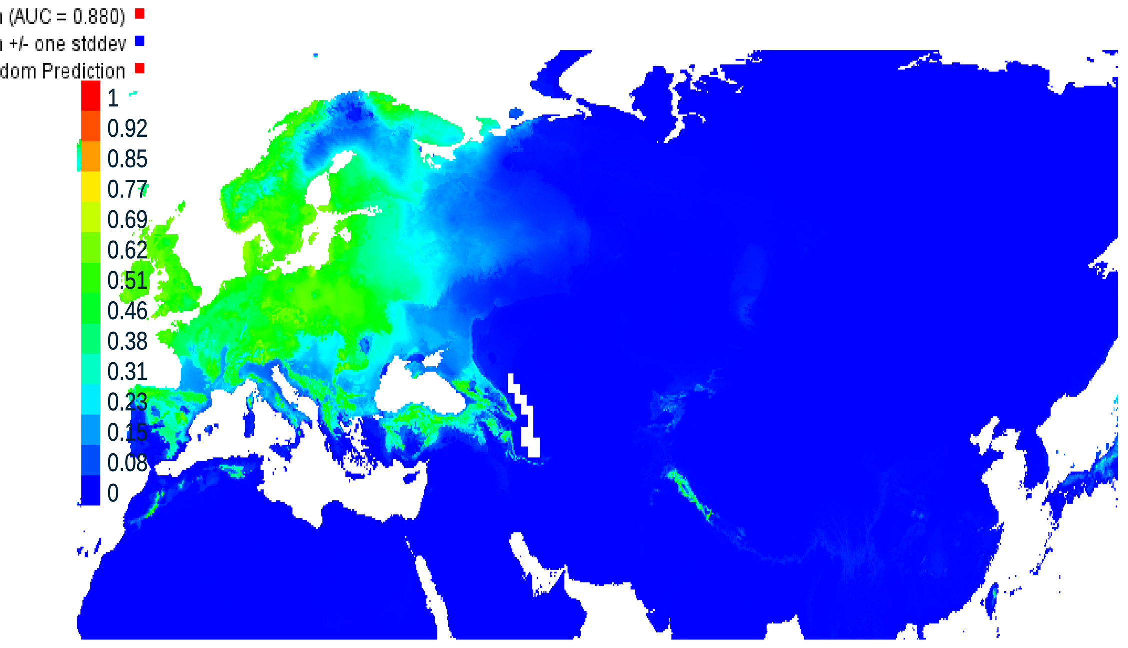

Figure 5. Spatial model showing the probability of distribution of *P. icarus* in its native range. The black dots indicate areas where there have been recorded sightings of the butterfly.

Table 2. The environmental variables that had the greatest contribution to the composite nice model. These are the variables that control the range of the common blue in its native range.

Variable	Percent contribution
Precipitation seasonality (coefficient of variation)	35.6
Minimum temperature of the coldest month	26.9
Annual precipitation	22.3
Meant temperature of the warmest quarter	12.5
Maximum temperature of the warmest month	2.1
Annual Mean Temperature	0.6

Future studies

- In the future, it would be interesting to include human parameters in the models to see the impact of human land use and population density on the butterfly's distribution.
- The main project can continue. A spreading dye model can be created and used to predict the future distribution of *P. icarus.* The model should be fairly accurate in predicting the future spread of *P. icarus* if the correct set dispersal capacity and range restrictions are used. The range restrictions would be based on the niche, which we have reason to believe was predicted accurately.

References

[1] Vitousek et. al "Introduced Species: A Significant component of Human-Caused Global Change". Newzealand Journal of Ecology 21. 1 (1997). 1-16.
[2] Hall, Peter. "The European Common Blue *Polyommatus icarus*: A New Alien Butterfly Close to Vermont". VES News. Vermont Entomological Society. Winter 2007-2008. Web. March 15, 2011.
[3] Heutte, T., and E. Bella. 2003. Invasive plants and exotic weeds of Southeast Alaska. Anchorage, AK: USDA Forest Service. Website: http://akweeds.uaa.alaska.edu/pdfs/literature/se_inv_plnt_guide.pdf
[4] Biodiversity occurrence data published by: Museum of Zoology University of Navarra, Baekdu Mountain, Lepidopterological Society of Finland, Biologiezentrum Linz (Accessed through GBIF Data Portal, data.gbif.org, 2011-02-11)
[5] "Common Blue (Male)". Butterfly Conservation: Saving Butterflys, Moths and Our Environment. Butterfly Conservation. n.d. Web. March 12, 2011.
[6] Lilly M. Plyommatus icarus . 2006. http://commons.wikimedia.org/wiki/File:Polyommatus_icarus_001.JPG
[7] WorldClim: Global Climate Data. Version 1.4 (release 3). n.d. Web. February 11, 2011.

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