

## What is BioLink modelling?

BioLink modelling is used to estimate or predict the likely range of a taxon based on known collecting localities. This is an implementation of the methods developed by Drs Henry Nix and John Busby (see Nix, H. A. 1986. A biogeographic analysis of Australian elapid snakes. Pp. 4–15 in R. Longmore (ed.). Atlas of Elapid Snakes of Australia. Australian Flora and Fauna Series No. 7. Australian Government Publishing Service, Canberra; and Busby, J.R. 1991. BIOCLIM—a bioclimate analysis and prediction system. Plant Protection Quarterly 6: 8–9) and Andy Gillison (see Carpenter, G., Gillison, A.N. and Winter, J. 1993. DOMAIN: a flexible modelling procedure for mapping potential distributions of plants and animals. Biodiversity and Conservation 2: 667–680). Both of these programs use the same basic techniques but differ in the statistical method implemented. For details of these (and related) models see Carpenter (1993, full citation above), <http://cres.anu.edu.au/software/anuclim.html> (for BIOCLIM) and [http://www.cgiar.org/cifor/research/intro\\_d.html](http://www.cgiar.org/cifor/research/intro_d.html) (for DOMAIN).

## Running an analysis

1. Open the Predictive Distribution Model window by selecting the **Modelling** command from the **Tools** menu.
2. Add training points for the taxon/taxa to be modelled. This can be done in one of two ways. If specimens have been entered in BioLink Material, drag their taxon name from the Taxon Explorer and drop it in the Training Points window. This will retrieve all geocoded sites for the selected taxon (and any of its children). The second method is to prepare a text file with latitude/longitude pairs, in decimal degrees (positive for north and east, negative for south and west), longitude first, latitude second and separated with a tab, for each location. Load this file using the **Load Point File** button.
3. Add data layers to be used in the model. To add these layers, click the Data Layers tab and use the **Add** button to open the Add File dialog where the required files can be specified. A number of demonstration layers are found on the BioLink CD-ROM\*. (For information on purchasing additional layers see <http://cres.anu.edu.au/software/anuclim.html> or contact [biolink@ento.csiro.au](mailto:biolink@ento.csiro.au).)
4. Click the Single Model tab and select the model to run and set its options. If the results are to be mapped using BioLink select the Generate Bitmap checkbox and enter the number of class intervals and cut off level (for the Gower Metric model) and the colours to use (for both models). Once set, press the **Start Model** button.

If the Generate Bitmap option was selected the Mapping Assistant will load and the predicted distribution will be displayed. This map can then be manipulated using the features and tools available for the Mapping Assistant.

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