



Potential habitat modelling methodology

Queensland Herbarium 2021

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Version history

The Queensland Herbarium has developed Potential Habitat Models since 2010, releasing Version 1 Potential Habitat Models via the Queensland Government Open Data Portal in 2012. This document describes an updated methodology associated with the release of Version 2 Potential Habitat Models and associated products.

Front cover images clockwise from left:

Glossy black-cockatoo *Calyptorhynchus lathami* (Vulnerable) female, Blackdown Tableland National Park (I.C. Gynther); Cascade treefrog *Litoria pearsoniana* (Vulnerable) male, Springbrook National Park (A.H. McCall); Brush-tailed rock-wallaby *Petrogale penicillata* (Vulnerable), Gambubal Section of Main Range National Park (J. Rowland); Key's Boronia *Boronia keysii* (Vulnerable) flowering post-fire, Great Sandy National Park (M.T. Mathieson).



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Introduction

Regional ecosystems (REs) have proved an effective surrogate for mapping biodiversity across Queensland since the 1990s (Neldner *et al.* 2020). RE mapping allows us to visualise, quantify and understand a great deal about the distribution of Queensland's native biodiversity.

Crucially, RE mapping provides information about the distribution of ecosystems across Queensland prior to the impact of land clearing, as well their remnant distribution in the current landscape. Together, pre-clearing and remnant RE mapping equip us with a robust understanding of ecosystem change in Queensland and provide guidance for the restoration of ecosystems. The mapping also tracks trends in recent habitat loss and land use change, as the distribution of remnant vegetation is remapped at regular, biannual intervals using aerial photography, satellite imagery and ground-truthing. These RE mapping products are vital to informing Queensland's biodiversity policy, planning and management.

RE mapping has improved our understanding of the distribution of biodiversity at the community level, but biodiversity manifests at many other scales, from Earth's biomes through ecosystems to genes. Species-level information, especially for threatened species, is vital for managing and protecting Queensland's biodiversity. Unfortunately, our understanding of species distributions across a state as large, complex, and inaccessible as Queensland is far from comprehensive.

Flora and fauna specimens and distribution data have long been collected in Queensland and for some species we can be confident in our understanding of their distribution and habitat requirements. For many species, however, we know that our records likely under-represent their distribution and therefore the habitats they occupy. This is particularly the case for range-restricted species, species with lifecycles linked to unpredictable weather events and for cryptic species difficult to detect or identify. These factors can be particularly important for threatened species listed under Queensland's *Nature Conservation Act 1992*.

One way to extrapolate species' distributions from point data is to apply a buffer (e.g. 1 km) around a presence record to capture its key habitat features and any additional individuals. In cases where

few records exist, this is the primary data-driven approach used to put a species 'on the map' and capture some of its habitat requirements. We acknowledge that in many cases, this is likely to greatly underestimate the distribution of these species, but equally in heterogeneous landscapes, it is unlikely that the entire buffered area will provide habitat. An alternative to simply applying a defined buffer around records is to utilise expert knowledge of the species' distribution and translate this into spatial surrogates, including RE, broad vegetation group (Neldner *et al.* 2021) or land zone (Wilson and Taylor 2012) mapping. That is, to use expert opinion to 'join the dots' and delineate the likely distribution of habitat.

In each case, the potential for error must be considered and minimised. This approach relies upon experts having a comprehensive knowledge of a species' requirements, tolerances and lifecycle, information that is unfortunately unknown for many species. It is also a slow process.

Habitat maps constructed from expert opinion are a form of species distribution model (SDM), but most SDMs are quantitative, data-driven, computer algorithms. SDMs are a proven tool for understanding and mapping the distribution of species and their habitat requirements. Commonly used in the fields of ecology, biogeography, and evolutionary biology, SDMs are vital to species management and conservation planning (Liu *et al.* 2013). SDMs combine data on species presence (and/or absence in the case of some modelling frameworks) at a site with mapped or modelled data on habitat variables to build a statistical understanding of a species' habitat requirements. The probability that a species has suitable habitat distributed beyond its known locations can then be extrapolated and mapped. The statistical weight, or contribution of environmental variables in driving a species' distribution model can also be examined.

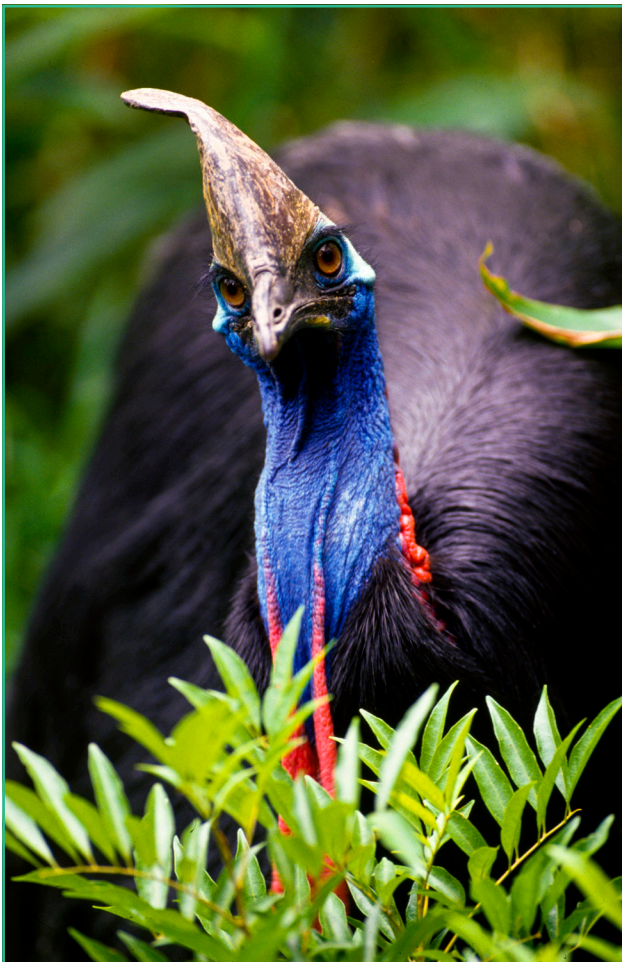
While many species distribution modelling frameworks are available, the Queensland Herbarium utilises maximum entropy (Maxent) modelling (Phillips *et al.* 2006) to produce pre-clearing potential habitat models for priority terrestrial flora and fauna habitat across the state.

Strengths and limitations of potential habitat modelling

All methods used to predict the distribution of species habitat, including SDMs, are accompanied by a set of assumptions, advantages, and disadvantages. Choosing the method which best utilises the available data while reducing unwanted outcomes is paramount. Maxent has been selected to produce potential habitat models for Queensland as it utilises both the state's existing high-resolution spatial products and high-precision presence records for flora and fauna. Some of the strengths and limitations identified for Queensland's potential habitat models are discussed below.

Further information on Maxent and its utility can be found in publications including Phillips *et al.* 2006, Phillips *et al.* 2017, Elith and Leathwick 2009; Elith *et al.* 2011 and Merow *et al.* 2013.

A detailed tutorial on the use of Maxent can also be found online (Phillips 2017): https://biodiversityinformatics.amnh.org/open_source/maxent/Maxent_tutorial2017.pdf



Habitat suitability vs. habitat occupancy

Potential habitat models aim to predict the probable distribution of suitable species habitat based on input variables likely to test their biological tolerance limits. Potential habitat models are unable to predict if the modelled habitat is currently occupied by that species, however. Habitat occupancy for any species will be influenced by a multitude of factors including local microclimate, soil type, habitat condition, connectivity and many others which vary at scales finer than we can map. Individual species traits may further limit occupancy, for example, reliance on large tree hollows for breeding, time required between fires or reliance on mycorrhizal fungal associations.

Potential habitat models can, however, be used to inform on-ground surveys aimed at confirming occupancy or to refine our understanding of a species' habitat requirements.

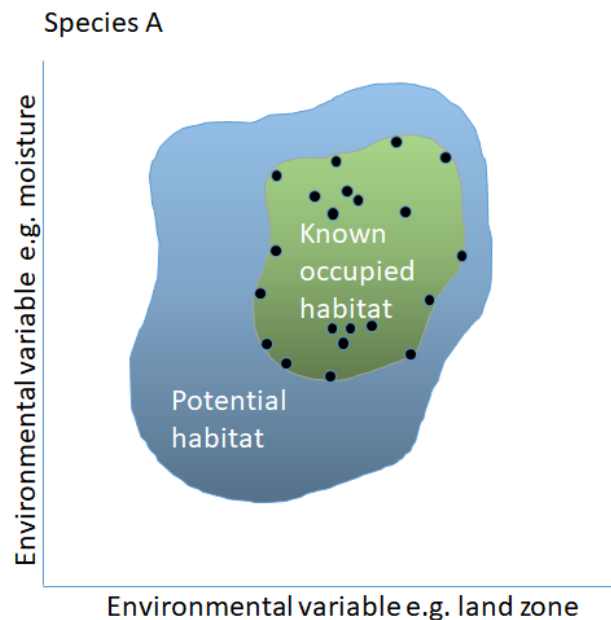


Image left: The southern cassowary (*Casuarius casuarius johnsonii*) is an Endangered species because of land clearing, urban settlement, road development, etc. The Queensland Herbarium has mapped southern cassowary habitat which can be used when assessing future plans by state and local governments to protect its habitat

Non-remnant habitat

Potential habitat models aim to predict the probable pre-clearing distribution of a species' habitat. In fragmented landscapes, some modelled potential habitat will no longer be in remnant condition. While some flora and fauna species may be able to utilise non-remnant vegetation, for many species the extent to which this is true is not well understood. Threatening processes such as habitat degradation, loss of habitat connectivity, disease, predation, invasive species, grazing and inappropriate fire management place significant additional pressure on threatened fauna in both remnant and non-remnant habitat. For this reason, caution must be exercised when considering the extent of potential habitat in non-remnant landscapes. As a result, we consider remnant modelled habitat to be a conservative estimate of current habitat availability.

Modelling extent

SDMs have been prepared for a selection of priority species at a national scale by a range of government agencies, universities, and conservation organisations. National level modelling has the advantage of being able to utilise known records from across a species entire range and to model habitat distributions without consideration of state boundaries. This approach allows mapping and analysis at a national level and is vital for informing policy and planning, particularly useful in the case

of species listed as threatened under the federal *Environment Protection and Biodiversity Conservation Act 1999* (EPBC Act).

Unfortunately modelling at a national scale restricts the list of candidate input variables to those available at the national scale, generally coarse grids of geology or climate data. The spatial resolution of the modelling produced is limited to the spatial resolution of these coarse spatial layers resulting in models of ≥ 1 km grid resolution. Finer scale spatial layers available for individual states generally cannot be utilised (e.g. vegetation mapping) as different scales and methodologies have been used. As a result, national scale models may not be suitable for local scale analysis or area-based calculations (Australian Government 2021).

A constraint of Queensland's potential habitat modelling program is that only records from Queensland are considered when producing models and for some species with broader distributions, data from their entire known range are not used to train the model. This geographic filter is necessary, however, because our chosen modelling framework, Maxent, requires all input variables to have the same spatial extent. Our high-resolution spatial products of pre-clearing broad vegetation group and land zone are available only for Queensland. This trade-off results in high resolution potential habitat model allowing detailed analysis and mapping while acknowledging that not all records have been considered.

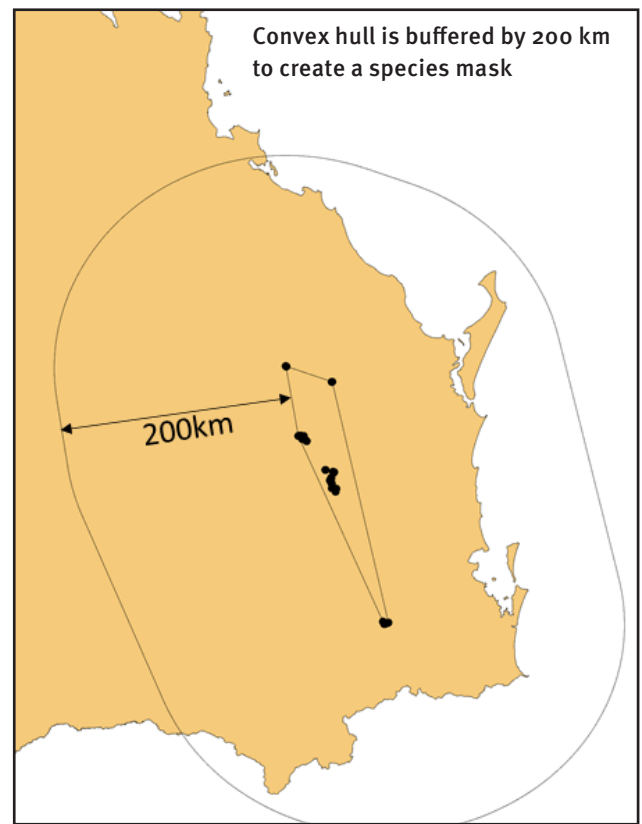
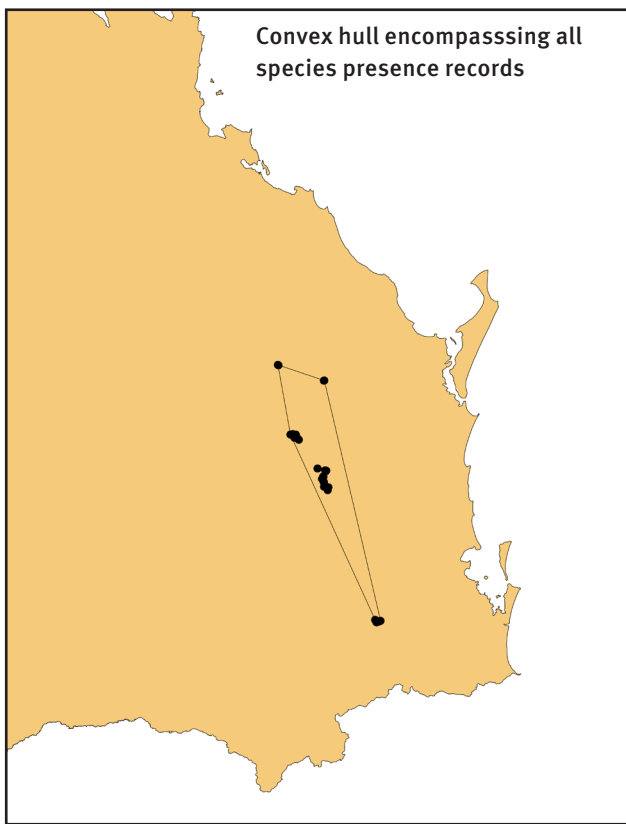


Image: Protected plants can be difficult to find and identify, like this *Commersonia pearnii* (*Critically Endangered*), which was only described in 2005. It has extremely limited distribution, and occurs in open-forest growing to a metre in height
Photographer: P. Forster

Occurrence mask

Models are constrained within an occurrence mask for each species, defined by a buffer of 200km around the smallest polygon that encompasses all species presence records. These masks are used by Maxent to restrict the selection of background points to the region of species presence and have important implications for model performance (Van Der Waal *et al.* 2009).

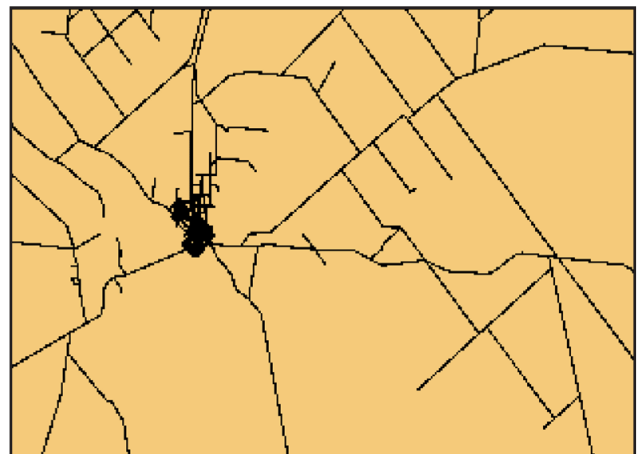
A mask of 200 km was also considered to reflect a balance between any modest range extensions for a majority of species whilst not over-predicting habitat distribution. To this end, model outputs are restricted to the mask extent, and this can be seen in some model outputs.

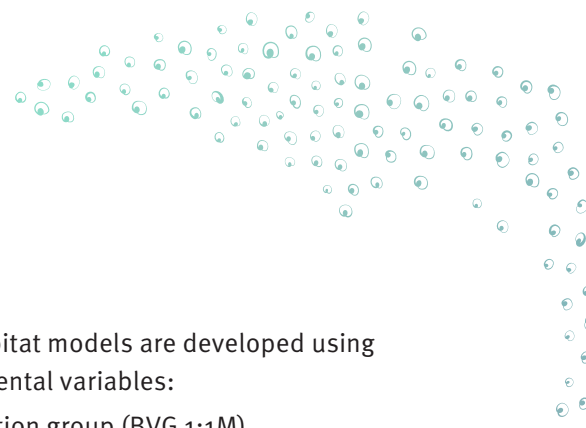


Example: *Phebalium distans* (Critically Endangered Nature Conservation Act 1992)

Collection bias

Records of species occurrence are rarely collected in a systematic fashion and tend to be biased toward accessible parts of the landscape. To address this collection bias, we used a mask of Queensland's road network to down-weight species records collected within 50m of roads to have half the value of records collected further away from a road. The bias file is loaded into Maxent's settings menu prior to modelling.





Multiple species records with the same coordinates or within a single grid cell can also bias model outputs. Duplicate records can be excluded from the modelling process by using the default option to ‘remove duplicate presence records’ within Maxent’s settings to address this source of bias.

We acknowledge that other sources of data bias are likely to remain within our methodology and we will seek to address these as they are identified.

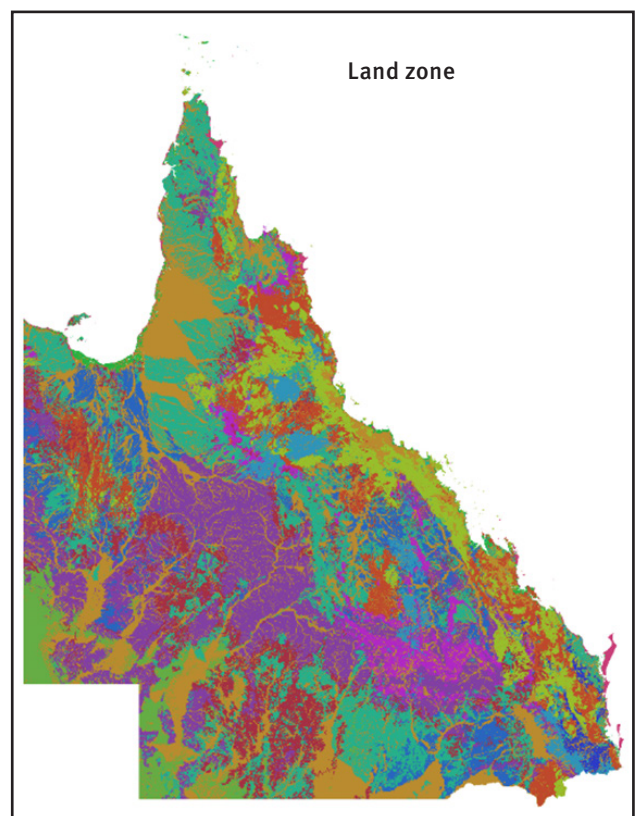
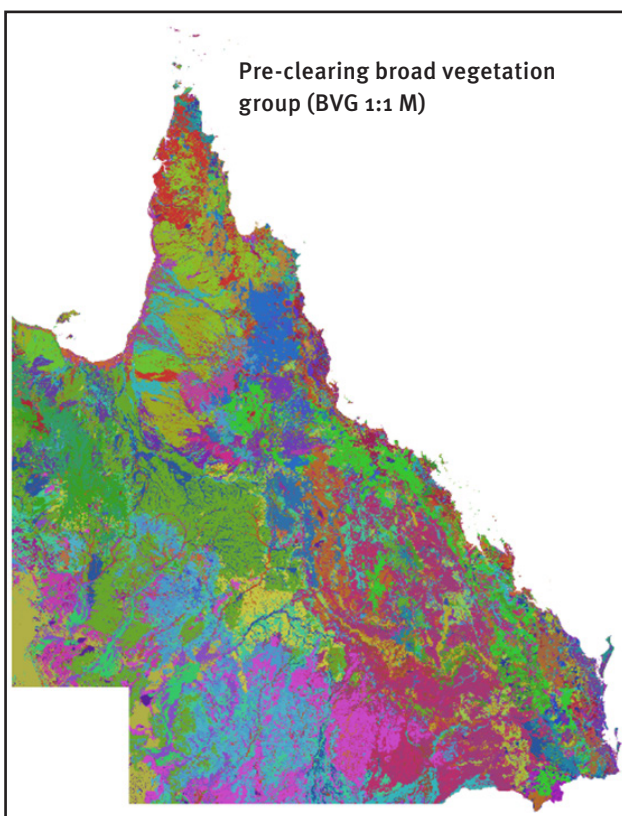
Variable selection

Experts were asked to nominate a selection of model input variables expected to test the biological tolerance limits and distribution of Queensland’s flora and fauna species. Maxent performs best when a minimum set of uncorrelated variables is used (Phillips *et al.* 2006). Highly correlated variables were removed via testing until a minimum set of input variables was identified for Queensland.

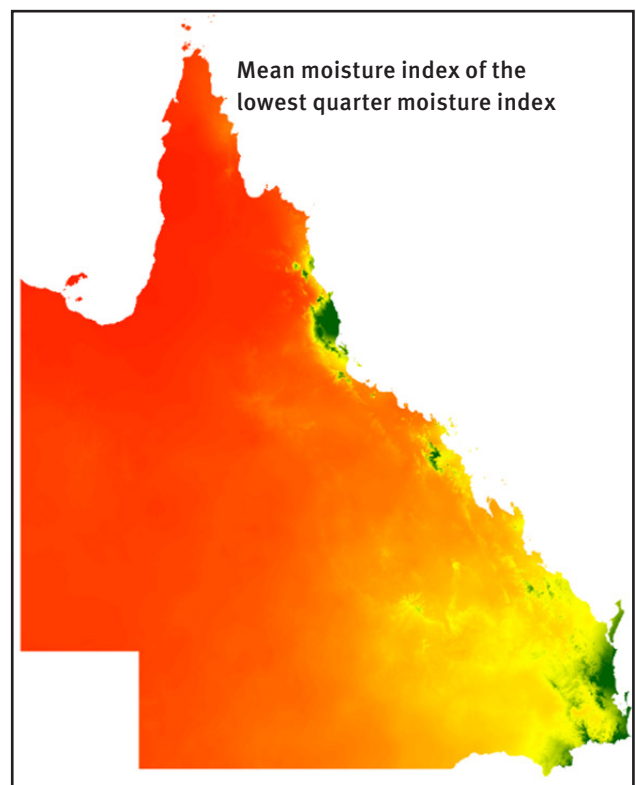
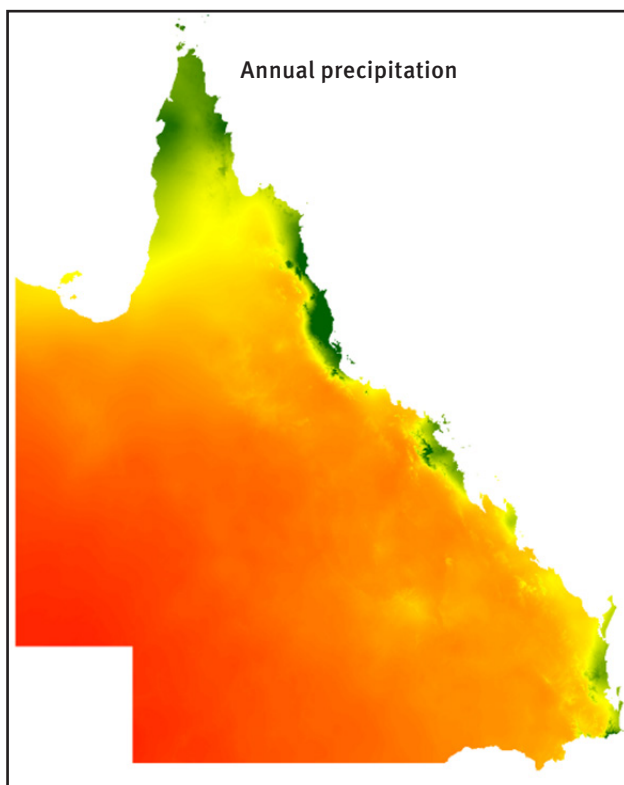
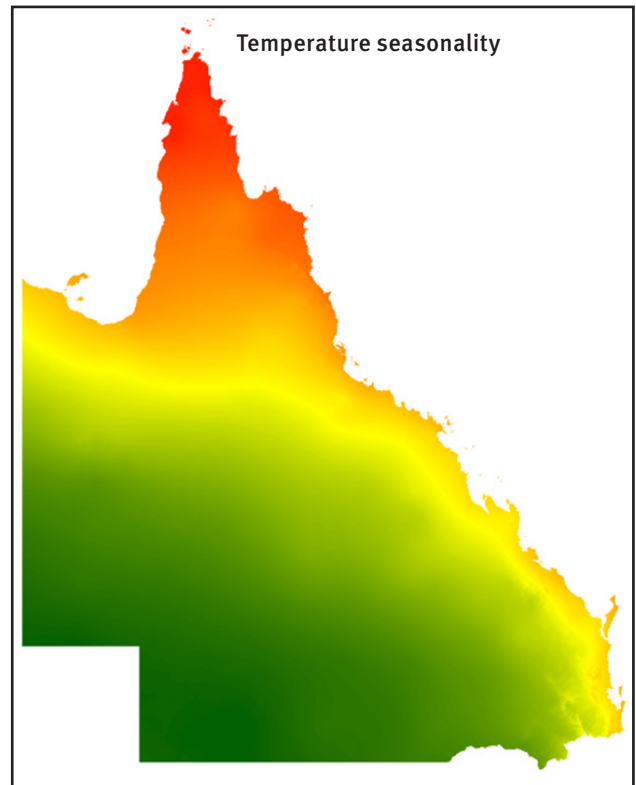
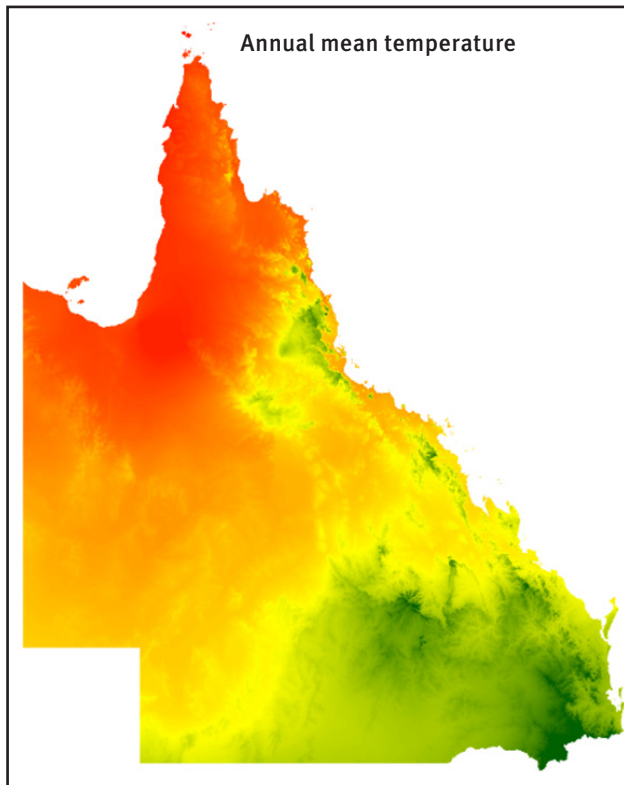
All potential habitat models are developed using seven environmental variables:

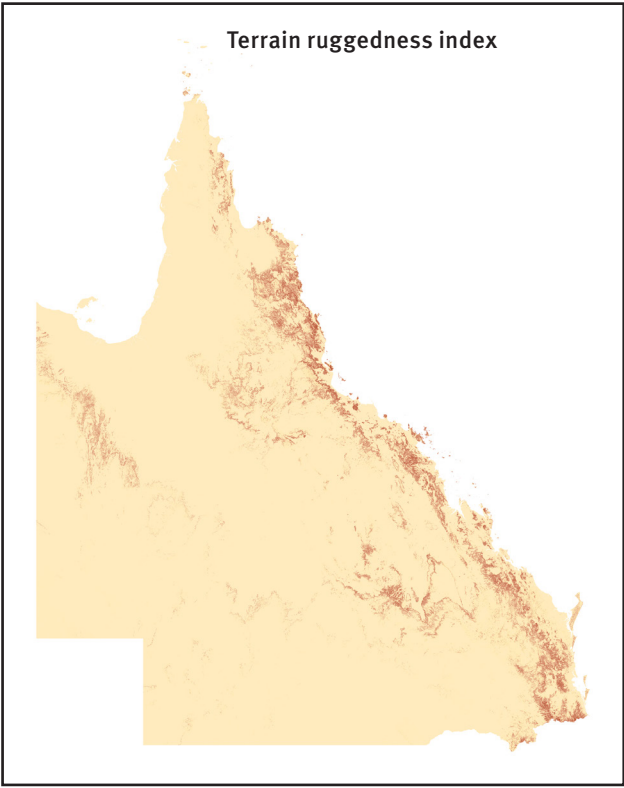
1. Broad vegetation group (BVG 1:1M)
2. Land zone:
3. Annual mean temperature
4. Temperature seasonality (coefficient of variation)
5. Annual precipitation
6. Mean moisture index of the lowest quarter moisture index
7. Terrain ruggedness index.

Two categorical variables, pre-clearing broad vegetation group (1:1M) and land zone, were derived from pre-clearing RE mapping for use in the potential habitat models. Land zone provides a high-level classification of substrate and geomorphology into twelve groups ranging from marine sediments through to ancient igneous substrates (Wilson and Taylor 2012) and broad vegetation group is a high-level classification of vegetation composition at the 1:1M scale (Neldner *et al.* 2021).

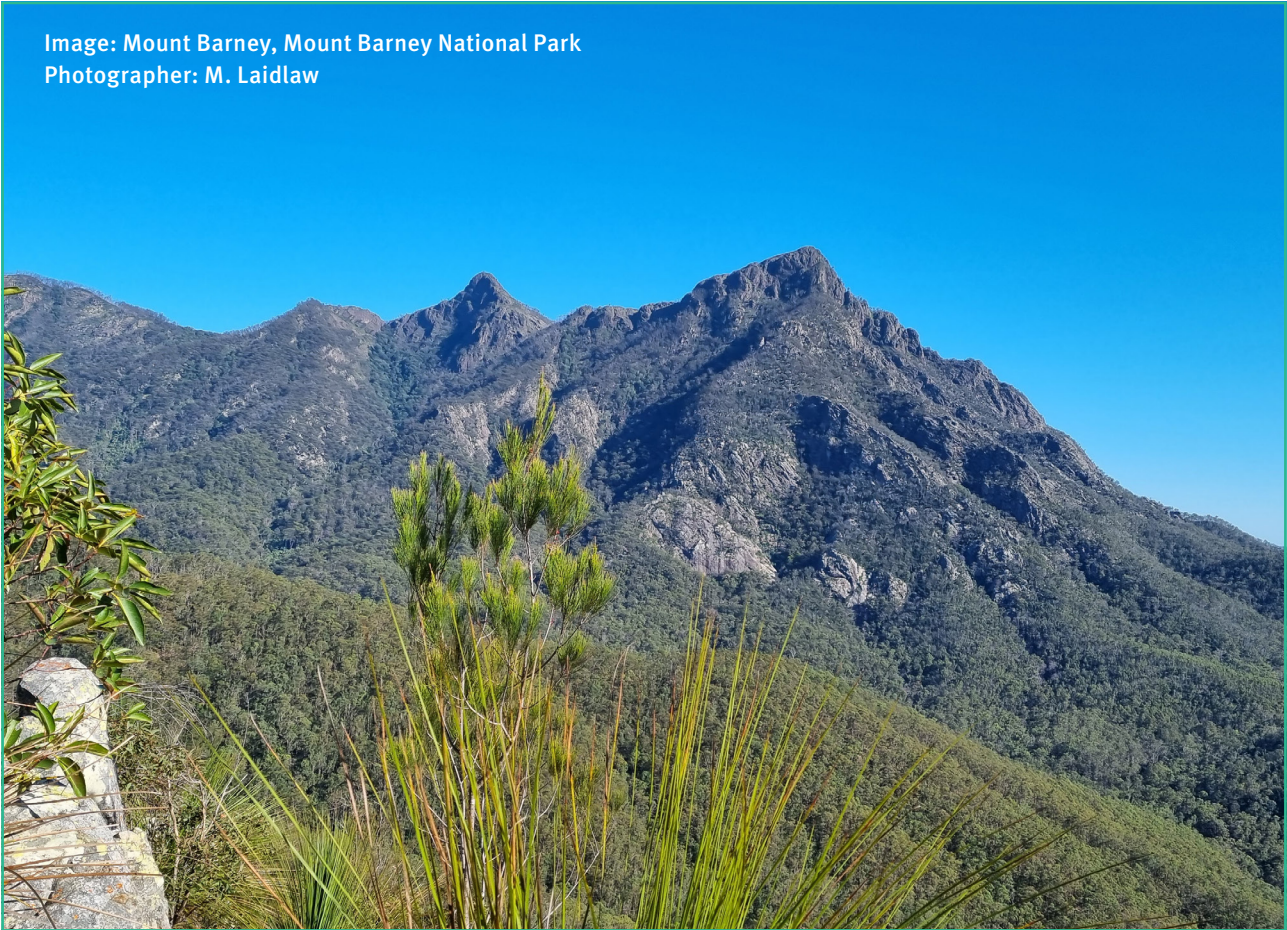


Four climate variables were modelled from Australian monthly mean climate values nominally centred on 1990 (1976–2005) using Anuclim Version 6.1 software (Xu and Hutchinson 2011) applied to a SRTM-derived 3 Second Digital Elevation Model (DEM) (Geoscience Australia 2019).





Finally, an index of terrain ruggedness was derived from the DEM using the methodology of Riley *et al.* (1999) and indicates the change in elevation between adjacent cells across Queensland.



Maxent settings

Maxent model settings can be customised to suit the data used, desired tests, plots and grids. In most cases Queensland's potential habitat models have been generated using the default Maxent options for iterations, background points, features and thresholds (Appendix A). Exceptions related to the handling of bias and test data have already been discussed above. Maxent outputs have been transformed using logistic transformation, however the default format option in the latest iteration of Maxent is cloglog transformation (Phillips *et al.* 2017). The impact of this change on modelling potential habitat for Queensland's threatened species is currently being investigated.

Model testing

For species with an abundance of presence data, a sub-set of records is often set-aside from model development to be used for testing. In the case of many threatened species, however, limited presence records often mean this approach is not possible and other statistical methods need to be used. In this case, the setting to nominate a 'random test percentage' is set to zero. Instead, models are independently tested by comparing the model AUC with the 95th percentile AUC from 1000 null models for each species created by randomly selecting locations from under the species' mask (Raes and ter Steege 2007). Species failing this test are further assessed against the 95th percentile AUC from 1000 null models created by randomly selecting locations from under the minimum convex hull formed by presence records. This step is largely required for range-restricted species with a limited environmental envelope. Only models with an AUC exceeding the 95th percentile null model AUC are accepted.

Individual species models may fail performance testing for various reasons. For example, the number of presence records may be inadequate relative to the environmental variation captured by their distribution, or none of the chosen input variables may reflect the dominant driver for that species, or the species may be a habitat generalist, having many presence records over a large geographic area incorporating a large amount of habitat variation.

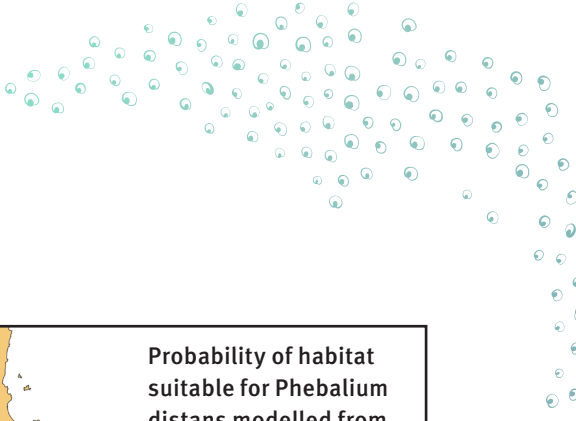
In the latter case it is difficult for Maxent to identify the relationship between presence records and the input variables.

Finally, draft potential habitat models are assessed by experts for feasibility and to identify if any post-hoc refinement of the modelled distribution is required. Some species may be known with a high degree of confidence to have specific habitat requirements not incorporated into the development of the model. Where spatial products are available, e.g., discrete soil types, models can be clipped to produce a more refined product.

Potential habitat extent

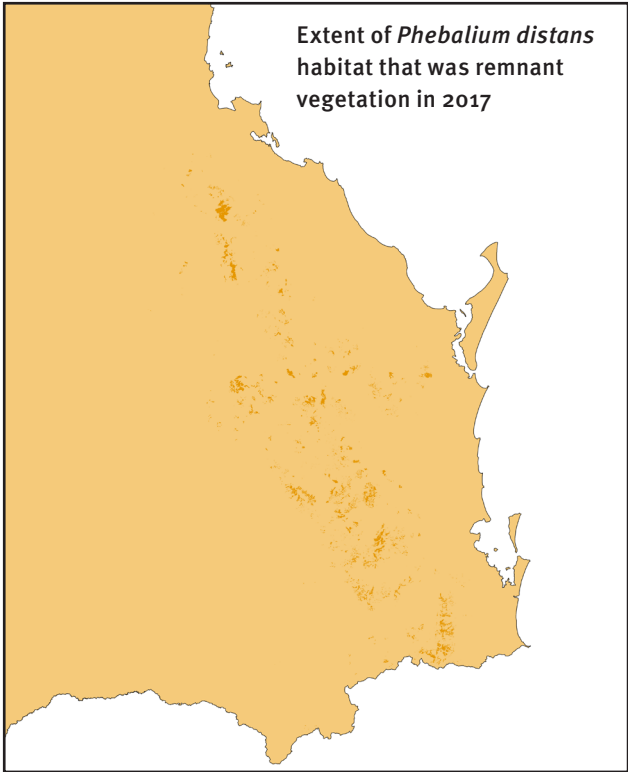
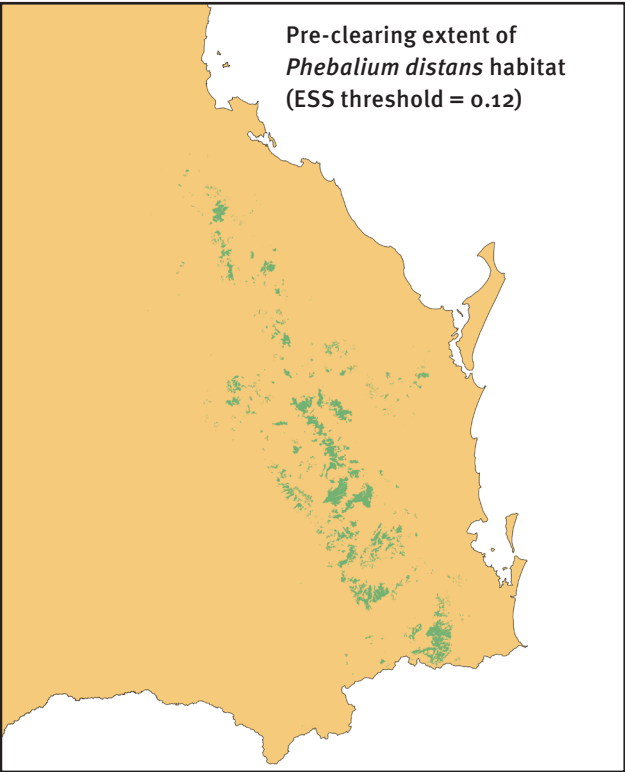
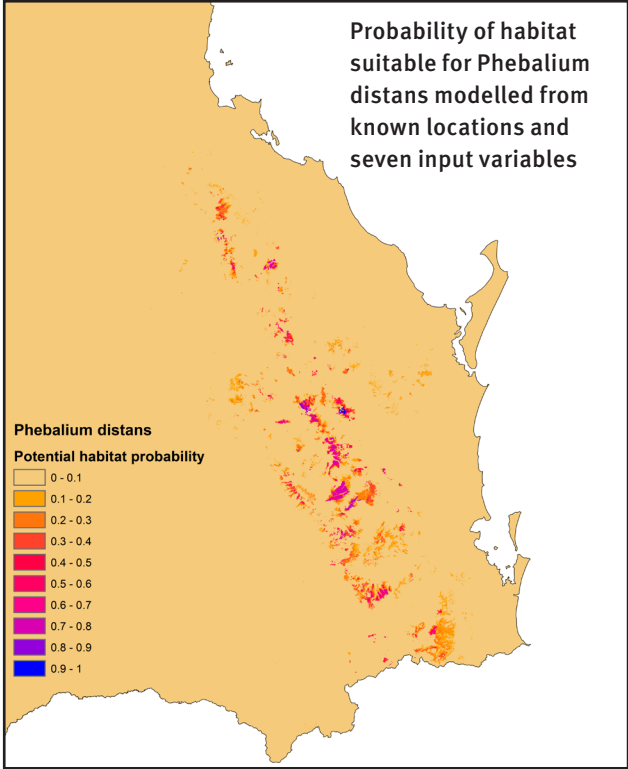
Maxent produces a grid of continuous values from zero to one, analogous to the probability that suitable habitat, based on the input variables, is present. The ascii output is converted to raster format and classified to show the spread of values as shown on page 13. Depending on the question being addressed by the modelling, probability thresholds may need to be applied to convert the continuous probability output into a binary prediction of 'potential' habitat extent. For example, models developed for the calculation of habitat area or to inform targeted surveys for a threatened species could have a high threshold applied to focus survey efforts towards the most likely habitat, whereas a lower threshold could be suitable if trying to locate non-remnant habitat areas suitable for rehabilitation. In all cases, it is important to note that it is the probability of suitable habitat which is being modelled and not the probability that it is occupied by the species.

Where the area of potential habitat or trends in habitat extent must be calculated, each species' continuous probability map is converted to a binary map of potential habitat extent by applying the 'equal training sensitivity and specificity logistic threshold (ESS)'. This conservative threshold is used in recognition that the available presence records for many species, and threatened species in particular, are likely to under-sample their range. Other thresholds can be applied for purposes where a higher degree of certainty is required.



Any presence records that are excluded from the modelled distribution resulting from the application of this conservative threshold are dissolved back into the output following the application of a 1 km radius buffer. The resulting output is further restricted to the extent of the species' mask to allow for up to a 200km range extension beyond known locations. The output is also simplified using a majority filter algorithm to remove single 'orphan' cells from the output.

Example: *Phebalium distans* (Critically Endangered Nature Conservation Act 1992)—prior to land clearing, 456,380 ha of *Phebalium distans* habitat is modelled for Queensland. By 2017, only 175,755 ha remained as remnant vegetation. This suggests that 61% of pre-clear habitat for *Phebalium distans* had been cleared by 2017



Potential habitat that is remnant vegetation

While potential habitat models are prepared based on pre-clearing vegetation distribution, models may be clipped to remnant vegetation mapping available for the period 1997 to 2019.

Remnant mapping has been used to quantify the impacts of land clearing on Queensland's threatened species and to track habitat loss over time. A full analysis of land clearing impacts on threatened species in Queensland is available via the Queensland State of the Environment reports 2015 to 2020 and in Neldner *et al.* 2017.

As previously mentioned, it should be noted that while some threatened fauna species may be able to utilise non-remnant vegetation, threatening processes such as habitat degradation, loss of habitat connectivity, disease, predation, invasive species, grazing and inappropriate fire management place significant additional pressure on threatened fauna in both remnant and non-remnant habitat. As a result, we consider remnant modelled habitat to be a conservative estimate of habitat availability.



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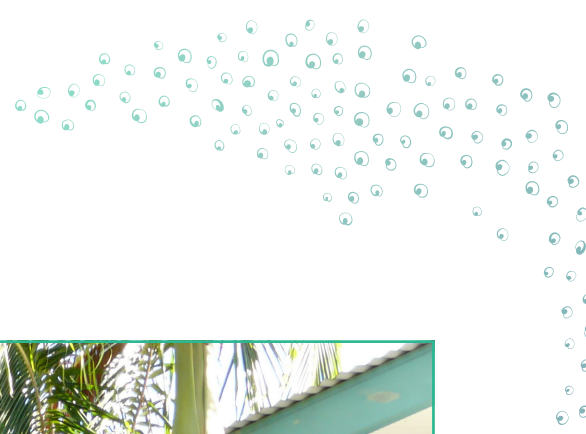
Appendix A: Maxent configuration

Flag	Maxent default	Potential habitat modelling	Meaning
response curves	FALSE	TRUE	Create graphs showing how predicted relative probability of occurrence depends on the value of each environmental variable.
pictures	TRUE	TRUE	Create a .png image for each output grid.
jackknife	FALSE	TRUE	Measure importance of each environmental variable by training with each environmental variable first omitted, then use in isolation.
output format	cloglog	logistic	Representation of probabilities used in writing output grids.
output file type	asc	asc	File format for writing output grids.
random seed	FALSE	FALSE	If selected, a different random seed will be used for each run, so a different random test/train partition will be made and a different random subset of the background will be used, if applicable.
log scale	TRUE	TRUE	If selected, all pictures of models will use a logarithmic scale for colour coding.
warnings	TRUE	TRUE	Pop-up windows to warn about potential problems with input data. Regardless of this setting, warnings are always printed to the log file.
tool tips	TRUE	TRUE	Show messages that explain various parts of the interface.
ask overwrite	TRUE	TRUE	If output files already exist for a species being modeled, pop up a window asking whether to overwrite or skip. Default is overwrite.
skip if exists	FALSE	FALSE	If output files already exist for a species being modeled, skip the species without remaking the model.
remove duplicates	TRUE	TRUE	Remove duplicate presence records. If environmental data are in grids, duplicates are records in the same grid cell. Otherwise, duplicates are records with identical coordinates.
write clamp grid	TRUE	TRUE	Write a grid that shows the spatial distribution of clamping. At each point, the value is the absolute difference between prediction values with and without clamping.
write mess	TRUE	TRUE	A multi-dimensional environmental similarity surface (MESS) shows where novel climate conditions exist in the projection layers. The analysis shows both the degree of novelty and the variable that is most out of range at each point.
random test point	0	0	Percentage of presence localities to be randomly set aside as test points, used to compute AUC, omission, etc.
beta multiplier	1	1	Multiply all automatic regularisation parameters by this number. A higher number gives a more spread out distribution.
maximum background	10000	10000	If the number of background points/grid cells is larger than this number, then this number of cells is chosen randomly for background points.
replicates	1	1	Number of replicate runs to do when cross-validating, bootstrapping or doing sampling with replacement runs
replicate types	cross-validate	cross-validate	If replicates >1, do multiple runs of this type. Cross-validate: samples divided into replicates folds; each fold in turn used for test data. Bootstrap: replicate sample sets chosen by sampling with replacement. Subsample: replicate sample sets chosen by removing random test percentage without replacement to be used for evaluation.
per species results	FALSE	TRUE	Write separate maxentResults file for each species
write background predictions	FALSE	FALSE	Write .csv file with predictions at background points.



Flag	Maxent default	Potential habitat modelling	Meaning
response curves exponent	FALSE	FALSE	Instead of showing the logistic value for the y-axis in response curves, show the exponent (a linear combination of features).
linear	TRUE	TRUE	Allow linear feature to be used.
quadratic	TRUE	TRUE	Allow quadratic features to be used.
product	TRUE	TRUE	Allow product features to be used.
threshold	FALSE	FALSE	Allow threshold features to be used.
hinge	TRUE	TRUE	Allow hinge features to be used.
add samples to background	TRUE	TRUE	Add to the background any sample for which has a combination of environmental values that are already present in the background.
add all samples to background	FALSE	FALSE	Add all samples to the background, even if they have combinations of environmental values that are already present in the background.
autorun	FALSE	FALSE	Start running as soon as the program starts up.
write plot data	FALSE	TRUE	Write output files containing the data used to make response curves, for import into external plotting software.
fade by clamping	FALSE	FALSE	Reduce prediction at each point in projects by the difference between clamped and non-clamped output at that point.
extrapolate	TRUE	TRUE	Predict to regions of environmental space outside the limits encountered during training.
visible	TRUE	TRUE	Make the Maxent user interface visible.
auto feature	TRUE	TRUE	Automatically select which feature classes to use, based on number of training samples.
do clamp	TRUE	TRUE	Apply clamping with projecting.
output grids	TRUE	TRUE	Write output grids. Turning this off when doing replicate runs causes only the summary grids (average, std deviation, etc.) to be written, not those for the individual runs.
plots	TRUE	TRUE	Write various plots for inclusion in .html output.
append to results file	FALSE	FALSE	If false, maxentResults .csv file is re-initialised before each run.
maximum iterations	500	500	Stop training after this many iterations of the optimisation algorithm.
convergence threshold	1.00E-05	1.00E-05	Stop training when the drop in log loss per iteration drops below this number.
adjust sample radius	0	0	Add this number of pixels to the radius of white/purple dots for samples on pictures of predictions. Negative values reduce size of dots.
threads	1	1	Number of processor threads to use. Matching this number to the number of cores on your computer speeds up some operations, especially variable jackknifing.
lq2lqpt threshold	80	80	Number of samples at which product and threshold features start being used.
l2lq threshold	10	10	Number of samples at which quadratic features start being used.
hinge threshold	15	15	Number of samples at which hinge features start being used.
beta threshold	-1	-1	Regularisation parameter to be applied to all threshold features; negative value enables automatic setting.
beta categorical	-1	-1	Regularisation parameter to be applied to all categorical features; negative value enables automatic setting.

Flag	Maxent default	Potential habitat modelling	Meaning
beta lqp	-1	-1	Regularisation parameter to be applied to all linear, quadratic and product features; negative value enables automatic setting.
beta hinge	-1	-1	Regularisation parameter to be applied to all hinge features; negative value enables automatic setting.
log file	maxent.log	maxent.log	File name to be used for writing debugging information about a run in output directory.
cache	TRUE	TRUE	Make a .mxe cached version of ascii files, for faster access.
default prevalence	0.5	0.5	Default prevalence of the species:probability of presence at ordinary occurrence points.
apply threshold rule		ESS logistic threshold	Apply a threshold rule, generating a binary output grid in addition to the regular prediction grid. Use the full name of the threshold rule in Maxent's html output as the argument. For example, 'applyThresholdRule=Fixed cumulative value 1'.
verbose	FALSE	FALSE	Gives detailed diagnostics for debugging.
allow partial data	FALSE	FALSE	During model training, allow use of samples that have nodata values for one or more environmental variables.
no data	-9999	-9999	Value to be interpreted as nodata values in SWD sample data.





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