

Supplementary material

Mata, C.; González, B.A.; Donoso, D.; Fuentes-Allende, N.; Estades, C.F.; Malo, J.E. Ecological Connectivity of Vicuña (*Vicugna vicugna*) in a Remote Area of Chile and Conservation Implications. *Land* 2024, 13.

Panel 1. Model building Environmental suitability analysis

First, a habitat suitability model for the vicuña was constructed for each season with the sighting records and a selection of environmental variables. The spatial resolution for all variables was the same, 1km² grid cells (raster layers of 113x261 cells and presence data per km², regardless of the number of sightings obtained in the grid cell).

1st Step: variable selection

Nineteen climate variables from the WorldClim database (www.worldclim.org) were considered and a first screening was performed to discard those that presented a high cross-correlation with other climatic variables ($R > 0.85$; [69]). In this drop-off step, simple climatic variables were retained when possible.

Six topographic variables extracted from the ASTER GDEM (METI & NASA) 75 m resolution digital terrain model were also included in this step: altitude, slope and roughness, considering mean and standard deviation of each one of them. Slope and roughness were computed using the "Surface Analysis" tool of ArcGis 9.3 (ESRI 2008). Similarly, the distances of the observations to the nearest ravine and to populated areas (including mining settlements) were included as explanatory variables. Finally, vegetation was incorporated from the classification of land use established by the Servicio Agrario y Ganadero from the Government of Chile (Table S1).

Boosted Regression Trees (BRT) were then used to reduce the number of variables before modeling the distribution of the species, thus reducing the risk of over-parameterizing the model and obtaining more robust models and reliable results [70]. This method requires presence and absence data, so we extracted 145 control points evenly distributed throughout the study area [24]. BRT models were fitted and evaluated with R statistical software [71], using the gbm package [72]. Parameter selection was done using a learning rate of 0.005, a tree complexity of 5 and a training/validation ratio of 0.5 [70,73]. In the final selection, we followed the basic rule of not introducing more than one variable for every 10 presences.

The final model fitted by the BRTs to predict vicuña presence showed a good fit with 800 regression trees ($AUC \pm \text{Standard Error} = 0.940 \pm 0.014$).

2nd Step: Model building

Once the most relevant variables from the BRTs were defined, a series of potential distribution models were built using MaxEnt version 3.3.3.k [74]. Different algorithm parameters of the program were varied, such as the regularization parameter [75] and

the functions of environmental variables [76] to improve final model. We compared two different sets of feature classes: the default “autofeatures” option (which allows all possible features), and allowing only linear, quadratic, and product (LQP) features. The model showing the best fit was selected using the ENM Tools and the Akaike AIC information criterion [48, 77].

The ENMTools software [48] was then used to compare habitat suitability models of each season using the niche overlap tool. The program automatically measures overlap using three different statistics – Schoener’s D (Schoener 1968), the I statistic [47], and relative rank (RR, [77]). Values obtained for all statistics were high: D = 0.811; I = 0.961 and RR = 0.808.

The model finally selected was built for all sightings jointly by cross-validation with 10 partitions.

The importance of each of the different explanatory environmental variables used to build the models was evaluated by the jackknife method. In addition, the AUC (*Area Under the Curve*) index was used to measure the consistency of the models. This index is derived from the area under the Receiver Operating Characteristics (ROC) curve statistic [38]. In addition, a logistic output was obtained for each variable to facilitate interpretation [78].

3rd Step: Maps of probability of presence

Once the models were built, two different cutoff thresholds were used in the selected model. Thus, to establish potential vicuña distribution areas we used the value that maximizes sensitivity plus specificity (MaxSS; [37,38]) and the average of the values of all prediction pixels (AvPP; [39]).

Table S1. Comprehensive list of the original variables used to build the habitat suitability models (HSM). In bold selected climatic variables introduced to Boosted Regression Trees after cross-correlated ones (Spearman rank correlation $R < 0.85$) were dropped from analyses.

	Variables		units
Climatic	Annual Mean Temperature	Bio1	
	Mean Diurnal Range (Mean of monthly (max temp - min temp))	Bio2	°C
	Isothermality (Bio2/Bio7)	Bio3	-
	Temperature Seasonality (standard deviation)	Bio4	
	Max Temperature of Warmest Month	Bio5	
	Min Temperature of Coldest Month	Bio6	
	Temperature Annual Range (BIO5-BIO6)	Bio7	°C
	Mean Temperature of Wettest Quarter	Bio8	
	Mean Temperature of Driest Quarter	Bio9	
	Mean Temperature of Warmest Quarter	Bio10	
	Mean Temperature of Coldest Quarter	Bio11	
	Annual Precipitation	Bio12	
	Precipitation of Wettest Month	Bio13	mm
	Precipitation of Driest Month	Bio14	
	Precipitation Seasonality (Coefficient of Variation)	Bio15	%
	Precipitation of Wettest Quarter	Bio16	
	Precipitation of Driest Quarter	Bio17	mm
	Precipitation of Warmest Quarter	Bio18	
	Precipitation of Coldest Quarter	Bio19	
Topographic	Mean altitude		m
	standard deviation of altitude		
	Mean gradient		%
	standard deviation of gradient		
	Mean roughness		%
	standard deviation of roughness		
Location	Distance to ravines		m
	Distance to settlements		m
Lan use and vegetation	Bare rock		
	Without vegetation		
	Salt marshes		
	Agriculture areas		
	Wetlands (Vegas): <i>Festuca nardifolia</i> , <i>Distichilis humilis</i> , <i>Deschampsia cespitosa</i>		
	Bofedales: <i>Oxychloe andina</i> , <i>Distichilis humilis</i>		
	Altiplanic steppe: <i>Stipa ichu</i> , <i>Baccharis</i> spp, <i>Deyeuxia</i> , <i>Azorella</i>		
	Very open shrub: <i>Queñoa</i> , <i>lampaya</i> , <i>Stipa</i> spp., <i>Baccharis</i>		
	Prairie-shrub: <i>Stipa</i> spp, <i>pulika</i>		
	Open shrubs: <i>Parastrephia lepidophylla</i> (<i>Pulika</i>), <i>Stipa frigida</i>		
	Leaf-succulent shrubs: <i>Pesco tola</i> , <i>Grinde tarapa</i> , <i>Corryo brevis</i>		
	Succulent: <i>Browningia candelaris</i> , <i>Ambrosia</i> , <i>Corryo brevis</i>		
	Permanent snow		

Table S2. Results of variable screening using boosted regression trees (BRT). The contribution of each one and main results of this model are shown, after fitting final gbm model with a fixed number of 800 trees. Selected variables marked in bold.

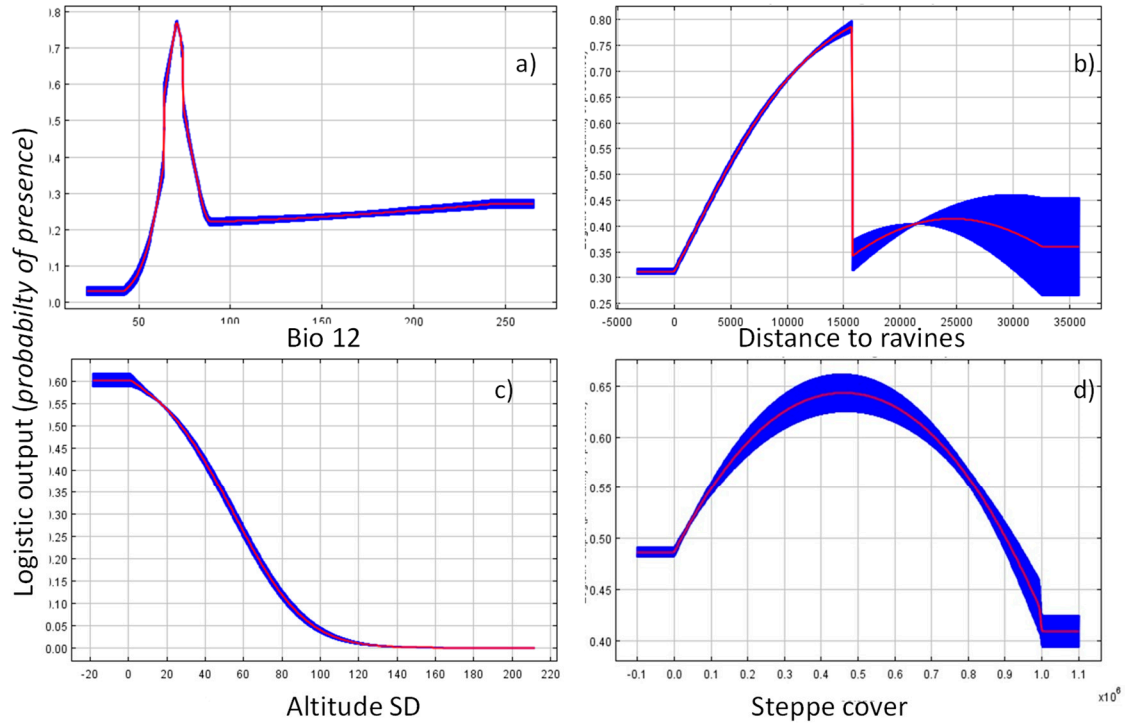
mean total deviance = 1.29
mean residual deviance = 0.32
estimated cv deviance = 0.611 ; se = 0.069
training data correlation = 0.915
cv correlation = 0.768 ; se = 0.035
training data ROC score = 0.992
cv ROC score = 0.94 ; se = 0.014

Variable	Contribution (%)
BIO12	41.306
BIO4	12.892
BIO1	8.004
BIO7	7.883
Distance to ravine slopes	5.893
Distance to settlements	4.646
BIO2	4.282
Mean altitude	3.794
Shrub steppes	3.193
Mean gradient	2.260
Steppe	2.175
standard deviation of altitude	1.701
BIO3	1.336
shallow wetlands (Bofedal)	0.608
BIO17	0.020
BIO19	0.008
standard deviation of gradient	0.000
Prairies with shrub	0.000
Very open shrub	0.000

Table S3. Main results of the model selection process carried out with ENMtools and based on the Akaike Information Criteria (AIC). Features for each model include the regularization parameters and functions of environmental variables. The selected Maxent model is shown in bold.

Model features	Log Likelihood	Parameters	Sample Size	AIC score	AICc score	BIC score
$\beta=3$ and Autofeatures (AUTO)	-1221.531	45	149	2533.063	2573.257	2668.241
$\beta=2$ and linear, quadratic, and product (LQP) features	-1219.470	49	149	2536.941	2586.436	2684.134
$\beta=3$ and LQP	-1229.553	48	149	2555.106	2602.146	2699.296
$\beta=2$ and AUTO	-1220.271	53	149	2546.542	2606.795	2705.752
$\beta=1$ and LQP	-1214.702	57	149	2543.403	2616.063	2714.628
$\beta=1$ and AUTO	-1154.795	85	149	2479.591	2711.654	2734.926

Figure S1. Response probability of vicugna presence according to the variables included in the model (Table 1, variables marked in bold). To facilitate interpretation, figures correspond to Maxent models created using only the corresponding variable. (a) annual precipitation (BIO 12, mm), (b) distance to ravines (m), (c) standard error of altitude, and (d) cover of steppe (proportion 0-1 $\times 10^6$). The curves show mean responses of the 10 Maxent replicates (red) \pm SD (blue).



Panel 2. Computation of distance equivalences

From the effective resistance values obtained with the Circuitscape software, the corresponding (real) Euclidean distances in the landscape have been calculated. Thus, a linear regression between the effective resistance and the Euclidean distance, taking into account the average dispersion capacity of the species (10.4 km), yielded the following equivalences:

For MaxSS threshold:

$$R^2 = 0.860; F = 36867.46; p < 0.0001$$

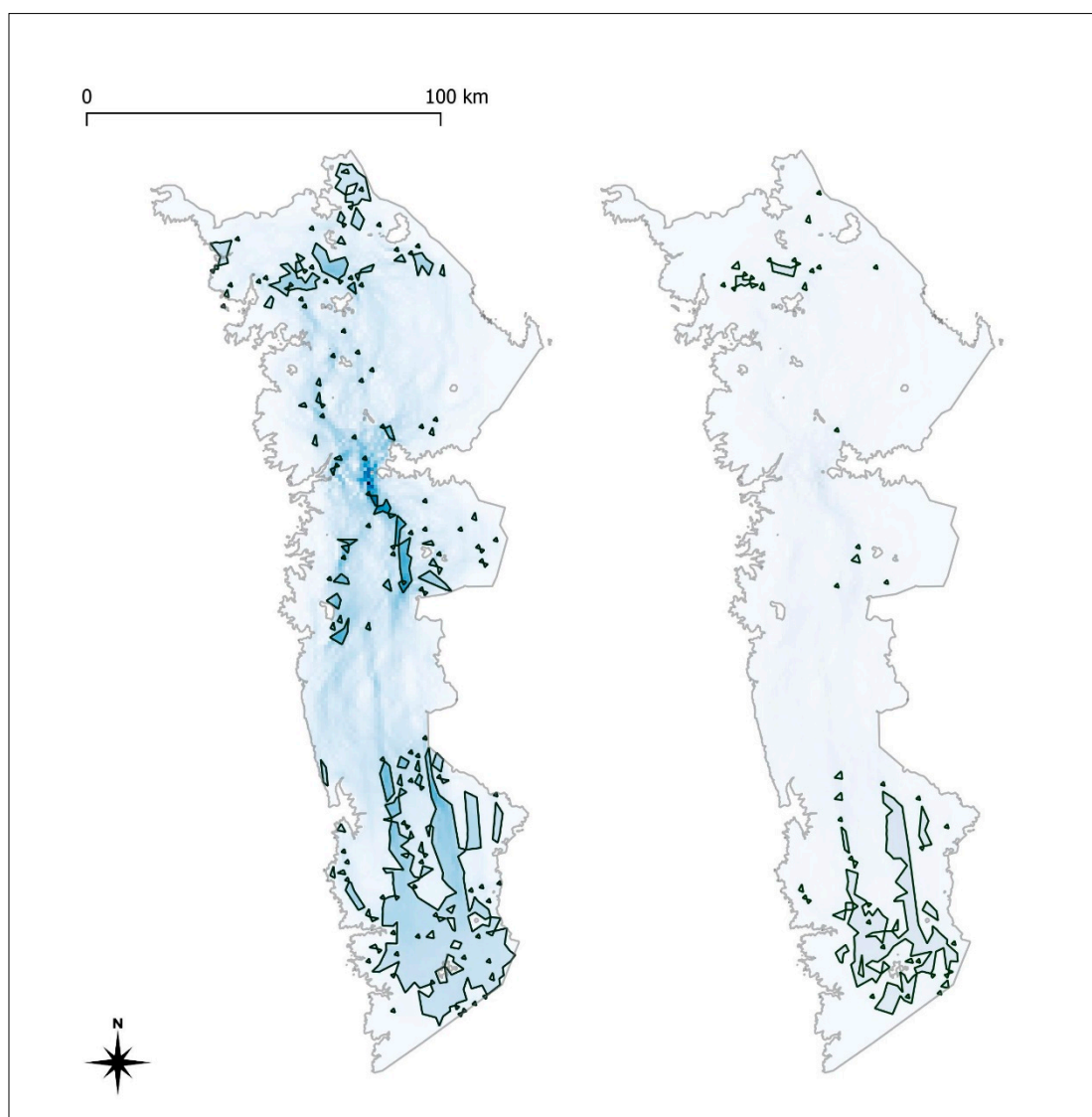
$$\text{Effective resistance (Circuitscape)}_{\text{threshold MaxSS}} = 3.0749 + 0.0002 \times 10.41 = 5.16$$

For AvPP (Average) threshold:

$$R^2 = 0.934; F = 8959.109, p < 0.001$$

$$\text{Effective resistance (Circuitscape)}_{\text{threshold Averageprob}} = 0.0492 + 0.0002 \times 10.41 = 2.13$$

Figure S2. ‘Current map’ showing potential connection fluxes between core habitat patches for vicuña. Marked polygons correspond to node areas according to both thresholds, MaxSS (left panel) and AvPP (right panel). Darker blue indicates areas (connectors) with higher ‘current’ (potential flux) density.



References

47. Warren, D.L.; Glor, R.E.; Turelli, M. ENMTools: A toolbox for comparative studies of environmental niche models. *Ecography* **2010**, *33*, 607–611.
48. Warren, D.L.; Glor, R.E.; Turelli, M. Environmental niche equivalency versus conservatism: Quantitative approaches to niche evolution. *Evolution* **2008**, *62*, 2868–2883.
69. Elith, J.; Graham, C.H.; Anderson, R.P.; Dudík, M.; Ferrier, S.; Guisan, A.; Hijmans, R.J.; Huettmann, F.; Leathwick, J.R.; Lehmann, A.; et al. Novel methods improve prediction of species' distributions from occurrence data. *Ecography* **2006**, *29*, 129–151.
70. Elith, J.; Leathwick, J.R.; Hastie, T. A working guide to boosted regression trees. *J. Anim. Ecol.* **2008**, *77*, 802–813.
71. R Core Team. *R: A Language and Environment for Statistical Computing*; R Foundation for Statistical Computing: Vienna, Austria, 2014. Available online: <http://www.R-project.org/> (accessed on 26 March 2018).
72. Ridgeway, G. Generalized Boosted Models: A guide to the gbm package. Update, 2007, vol. 1, no 1, p. 2007.
73. Elith, J., & Leathwick, J. Boosted Regression Trees for ecological modeling. R Documentation. 2017. Available online: <https://cran.r-project.org/web/packages/dismo/vignettes/brt.pdf> (accessed on 26 March 2018).
74. Phillips, S.J.; Anderson, R.P.; Schapire, R.E. Maximum entropy modeling of species geographic distributions. *Ecol. Model.* **2006**, *190*, 231–259.
75. Radosavljevic, A.; Anderson, R.P. Making better Maxent models of species distributions: Complexity, overfitting and evaluation. *J. Biogeogr.* **2014**, *41*, 629–643.
76. Merow, C.; Smith, M.J.; Silander, J.A. A practical guide to MaxEnt for modeling species' distributions: What it does, and why inputs and settings matter. *Ecography* **2013**, *36*, 1058–1069. <https://doi.org/10.1111/j.1600-0587.2013.07872.x>.
77. Warren, D.L.; Seifert, S.N. Ecological niche modeling in Maxent: The importance of model complexity and the performance of model selection criteria. *Ecol. Appl.* **2011**, *21*, 335–342.
78. Phillips, S.J.; Dudík, M. Modeling of species distributions with Maxent: New extensions and a comprehensive evaluation. *Ecography* **2008**, *31*, 161–175.