

Final report:

"Effectiveness of the protected areas of Chile to represent the native freshwater fish species distribution"

Student:
CRISTIAN CAMILO MARTÍNEZ GONZÁLEZ

ccmartinez2@uc.cl

Advisor: PATRICIO PLISCOFF

Course: UNIDAD DE INVESTIGACIÓN II BIO4016

DOCTORADO EN CIENCIAS BIOLÓGICAS, MENCIÓN EN ECOLOGÍA PONTIFICIA UNIVERSIDAD CATÓLICA DE CHILE 2022

ABSTRACT

In this *Research Unit-II*, I made Habitat-Suitability models to estimate the current distribution patterns of freshwater fish species in Chile. I compared the distribution areas of the species in their natural ranges and in the protected areas system (PA); for this, I used the specific environment variables and fragmentation scenarios for freshwater ecosystems previously identified in the *Research Unit-I*. I evaluate the effectiveness of Protected Areas to represent the potential distribution of native freshwater fish species in Chile. Eight species considered Vulnerable and Endangered are also underrepresented in the PA of Chile (0.1-3% of their range distribution).

There are no records of an investigation of this type, and I hope that these results can be used as a tool for the conservation and management of native fish species in Chile, as well as, I expect that the study developed here will be useful in future research related to my doctoral thesis.

INTRODUCTION

Understanding the spatial distribution patterns of species is of great ecological importance considering the transformations in the structure and dynamics of ecosystems caused by human activities (Baessler & Klotz 2019). The current scenario of water scarcity, ecosystem fragmentation, and contamination of continental aquatic ecosystems have most of Chile's hydrographic basins in a state of high vulnerability (MMA 2017). The freshwater fish populations have been one of the biological groups most affected by the modifications of the water bodies, the construction of hydroelectric dams, and the introduction of different exotic species, left in a state of threat to most of the native freshwater species of Chile (Lacy et al. 2017).

The threats afore-mentioned are acting concomitantly with a system of Protected Areas (PA) that scarcely represent the freshwater ecosystems in Chile, from their conceptualization to implementation the (PA) were planned to the protection of the biodiversity of terrestrial ecosystems, coast, and marine wetlands (Pauchard & Villarroel 2002); Although there are no studies evaluate the representativeness of continental aquatic ecosystems in the PA, in this the representativeness of terrestrial way, ecosystems has been evaluated in the Chilean protected areas system (Pliscoff & Fuente-Castillo 2011), I expect a similar or lesser degree of representativeness trend of the freshwater ecosystems in Chile in the PA.

The main objective of this Research Unit II was to make models that predict accurately the current distribution areas of freshwater fish species in Chile. The distribution areas were mapped and contrasted with the protected area system (AP) and with the habitat fragmentation scenarios of freshwater ecosystems made in the *Research Unit I*, here, I assessed the effectiveness of protected areas to represent the potential distribution of native freshwater fish species in Chile.

The current state of conservation of freshwater fish species in Chile.

The geomorphology and climatic history of Chile have contributed to the development of unique fish fauna, characterized by a high degree of endemism (Habit et al. 2006). The Andes mountain range to the east, the Pacific Ocean to the west, and the Atacama desert in the north of the country have biogeographically isolated continental waters in Chile (Vila & Habit 2015); This isolation has generated contrasting climatic regimes and precipitation gradients as a result of latitudinal differences, resultant in a unique fauna with ancestral freshwater fish characteristics and restricted distribution ranges, with specific hydraulic and feeding requirements (Vila et al. 1999, Habit et al. 2006).

The taxonomy and systematics of the Chilean freshwater fish fauna have changed in the last twenty years and reviews of the systematic and biogeographical situation based on phylogenetic relationships report 43 species, in 7 Orders, 10 Families, and 19 Genus. Additionally, there are 2 species of lampreys (1 Order, 2 Families, and 2 Genus) that carry out part of their life cycle in continental waters. Considering all the species, except for one species considered functionally extinct, *Diplomystes chilensis* (Arratia & Quezada-Romegialli 2017) and a series of local extinctions (Habit et al. 2010), 42% of the genera and 70% of the species are endemic to Chile

(Dyer 2000, Vila et al. 2011, Alò et al. 2013, Habit et al. 2019).

The information currently available is mostly based on taxonomic studies and morphological descriptions, although studies have recently been carried out on the effects of hydroelectric barriers on gene flow in native fish populations (Valenzuela-Aguayo et al. 2020). The knowledge of the ecology of fishes in Chile is still incomplete and requires updated studies; the knowledge gaps constitute serious limitations for the development of effective conservation and recovery strategies for freshwater fish communities in Chile (Peredo-Parada et al. 2009, Habit et al. 2019), the foregoing becomes more important given the current anthropic pressures on aquatic ecosystems in the country (Vila & Habit 2015).

Different studies document a significant decrease in the abundance and diversity of Chilean native fish species, worsening their already weakened conservation status (Pringle et al. 2000, Vila & Habit 2015), as a result of the effects of multiple stressors on the species, such as the modification of the hydrological regime due to channeling and damming of rivers for hydroelectric purposes (Vila et al. 2001), extraction of water for irrigation and livestock (Habit et al. 2006a), the introduction of exotic species, the mining, changes in land use, effluents and anthropogenic pollution, aquaculture and recreational fishing, which destroy the physical habitat of freshwater species in Chile (Vila et al. 2001, Habit et al. 2006, Habit et al 2010).

The Chilean freshwater fish fauna has increased by almost 50% with the presence of 22 introduced species (Dyers 2000), Chile is one of the six global "hotspots" of freshwater fish invasions (Leprieur et al. 2008), showing patterns of significant homogenization of the fish fauna (Villéger et al. 2011). The salmonids introduced in 1903 in most freshwater ecosystems in Chile seem to have affected the species composition, trophic interactions, and nutrient dynamics (Soto et al. 2001, Iriarte et al. 2005), influencing the distribution patterns, diversity, and the life history of native fishes (McDowall, 2006, Soto et al. 2007, Pascual & Ciancio 2007), currently introduced species dominate in terms of abundance and total biomass in some of the Chilean aquatic ecosystems (Ruiz 1993, Behnke 2002, Soto et al. 2006, Habit et al. 2010). There is no evidence of biotic resistance of native species to the expansion of salmonids (Habit et al. 2012), perhaps, for this reason, the 43 native freshwater species are considered threatened (CONAF 1993); However, studies are required to quantify the effects of introduced fish species on the decline of native fish populations (Dyers 2000, Soto et al. 2006). This information is of vital importance when adopting appropriate conservation measures for each native species and watershed (Habit et al. 2006).

Even though the Chilean continental ichthyofauna is poor in species, it has a high systematic, biogeographical, and conservation value (Habit et al. 2006). However, there is little information on reproductive times and strategies, age cohorts, locomotor capacity, migrations, trophic niche, Spatio-temporal distribution at micro, meso, and macroscale of freshwater fish populations in Chile (Habit et al. 2006), to fill this knowledge gaps, more research is needed to understand the different factors of life history, evolution and ecology that are influencing the population decline of migratory and endemic fish species in Chile (Alò et al. 2020). It is necessary

implement mitigation and management measures against the threats that keep a high number of these species at risk of extinction (Habit et al. 2006).

SNASPE

The National System of Protected Wilderness Areas of the State SNASPE (Sistema Nacional de Áreas Silvestres Protegidas del Estado) protects the natural ecosystems of Chile, this network of protected areas is administrated by the CONAF (Corporación Nacional Forestal). The SNASPE is an in situ conservation system with the conservation objective of the of the environmental heritage, preserve of nature, and safeguarding biological diversity; international preservation and conservation standards.

The SNASPE protects 107 of the 127 terrestrial ecosystems present in Chile, of which 35 protected areas achieve the *Aichi Biodiversity Targets* (Juffe-Bignoli et al. 2016), while 72 are under these goals. Currently, the SNASPE covers an area of 18,620,139.08 hectares, an area totaling 106 protected areas (42 National Parks, 46 National Reserves, and 18 Natural Monuments) distributed in all administrative regions of Chile.

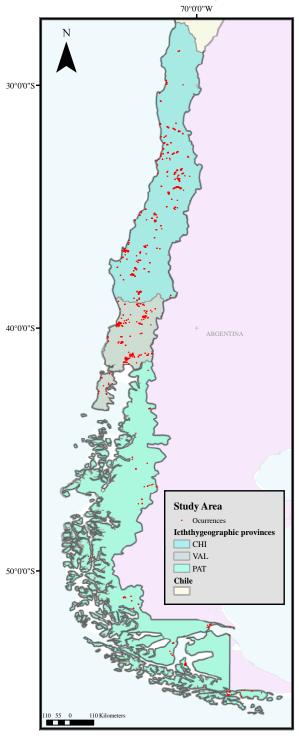
METHODS

Study Area

delimited the study area to the Ichthyogeographic provinces within the Chilean territory described by Abell et al. (2008). These freshwater ecoregions are defined as large areas encompassing one or more freshwater basins and body systems; based on patterns biogeographical, phylogenetic,

palaeogeographical, and ecological similarity of freshwater fish communities (Dinerstein et al. 1995).

Figure 1. Ichthyogeographic provinces and occurrences in this study.



The research was restricted to three of the six Ichthyogeographic provinces in Chile: Central Andean Basins (CHI), Los Lagos Region -Valdivia (VAL), and Patagonia (PAT). In each one of the provinces the water systems will drain, their flows towards the ocean (exorheic basins) (see Fig. 1); The provinces of Atacama, Titicaca, and Mar Chiquita provinces were excluded, due to the low number of occurrences and extreme endemism of the freshwater fish species in these provinces (see Genus Orestias Supplementary material S1). Each of the selected provinces is a geospatial unit that represents the patterns of environmental and ecological variables that influence on the large-scale biodiversity distribution of freshwater fishes (Groves 2002).

Biological Data and sampling design

To get occurrence data for the freshwater fish species reported in the country and using the R package *spocc: Interface to Species Occurrence Data Sources*, the research was conducted in different georeferenced databases, like museum specimens reports and published and

unpublished records from 1989 to 2021 (*e.x:* VerNet; FishBase; iNat; iDigBio; GBIF, AMHN and ZMH museums).

I acquired reliable information about 43 native species in Chile. The taxonomy status (Scientific names, authors, years, family, and synonyms) of the species were checked in the *Eschmeyer's Catalog of Fishes* (Fricke et al. 2022. *See Supplementary material* S1). Of the 43 species, only 18 species (42%) had enough records on their distribution range (+2 Basins) to filter and snap the occurrences into the gridded hydroclimatic variables of the Ichthyogeographic provinces and the protected areas system (SNASPE) (*See Supplementary material* S2 and S3).

Environmental variables

To model the distribution area of the freshwater fish species, I used the predictor variables from EarthEnv in 1km² of cell-size resolution (Domisch, et al. 2015) and the hydrologic network dataset of RiverATLAS (Linke et al. 2019). The network was cut by the current

Table 1. Information of the freshwater predicts variables used in this study, with their respective variation numbers, units, and forms of measurement.

Variables	Number of layers	Units	Measure	Source
Hydroclimatic variables	19	[°C] * 10 / [mm] Hydroclim_weighted_average	Weighted sum	Worldkin
Elevation	2	M	Elevation and slope of the ground surface derived from	HydroSHEDS
Slope	2	[°] * 100	digital elevation measurement (DEM CGIAR-CSI SRTM v4.1)	HydroSHEDS
Flow Accumulation	1	Count of upstream stream grid cells	# of cells (1 km²) of the upflow grid, # of cells (1 km²) of	HydroSHEDS
Flow Length	1	Number of upstream catchment grid cells	the upstream catchment water network	HydroSHEDS
Land Cover	1	Herbaceous vegetation	Range	CLC
Geology	1	Water	Weighted sum	USGS

scenario of fragmentation and loss of connectivity previously identified and selected in *Research Unit I* (*see* **Table 1**.) The variables and the hydrologic network provide the most realistic current scenario; this environment exhibits the hydroclimatic, topographic, land cover, and geologic variation of the continental freshwaters of Chile (*Research Unit I*).

I transform the set of Hydroclimatic variables (see **Table 1**.) into Rasters-PCA to obtain a workable environment for the distribution modeling process. This orthogonal transformation (Rasters-PCA) is analogous to a conventional Principal Component Analysis (PCA), where, the principal components are images with large information in each of the pixels (Leutner et al. 2019); 3 Rasters-PCA summarize the 93.5% variance of the set of hydroclimatic variables.

Mapping the SNASPE

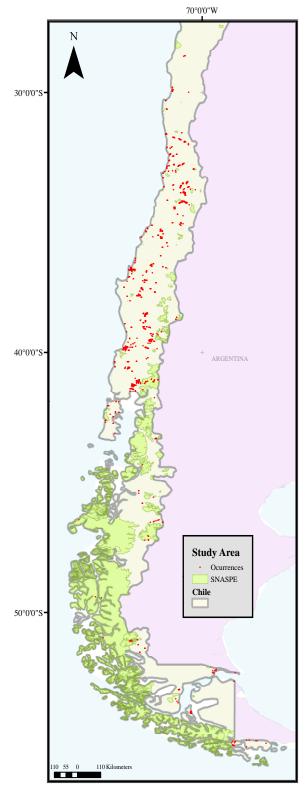
I acquired the georeferenced location of the National System of Protected Wilderness Areas of the State (SNASPE) on the Geospatial Database Infrastructure of Chile, IDE Chile (www.ide.cl); the 96 protected areas in the country were mapped (see Fig. 2); the type, categories, regions, locations, and size of each protected area are related in Supplementary Material S4. With this data, I evaluated the effectiveness of the protected area system (SNASPE) to represent the potential distribution of native freshwater fish species.

Models' Assessment

Using the Species Distribution Models (SDM), I bring the occurrences of the species with the environmental variables using of three different mathematical algorithms (Support vector

machines - SVM (Tax & Duin 2004, Karatzoglou

Figure 2. SNASPE and occurrences in this study.



et al. 2006), Random Forest - RF (Breinman et al. 1984), and Maximum entropy - MaxEnt (Phillips et al. 2006), to predict the Suitability of habitats in sites (Icththyo-geographic provinces or protected areas SNASPE) i.e estimates the possible freshwater fish species ranges (Peterson et al. 2012, Franklin 2013). The joined use of these algorithms increases the accuracy of predictions of rare species distribution, species with few samples in large undersampled areas, and improve the range predictions of species with different niche tolerances (Araújo & New 2007, Diniz-Filho et al. 2009). Each one of these algorithms was run 100 times per each species using the R packages "dismo" (Hijmans et al. 2015), and "kernlab" (Karatzoglou al et. 2004) in the R environment program (R Core Team, 2019).

Models' evaluation

To evaluate the resulting models, I used the bootstrap technique (Efron 1979). Briefly, for each species, I divided random occurrences into two groups, 75% to generate models and 25% to test them (Guisan & Zimmermann 2000). I used the occurrence test group to check for omission or commission errors (Fielding & Bell 1997), i.e. the ability of the model to predict each observation of the test group. Using the Area Under Curve (AUC), I assessed the model sensitivity - the proportion of presences accurately predicted, and the model specificity - the proportion of absences accurately predicted (Allouche et al. 2006). I selected the models that had an AUC value equal to or greater than 0.75.

Ensemble forecasting approach.

Each model selected by the AUC predicts

slightly different scenarios, generating uncertainty about estimates of Habitat-Suitability of the species analyzed (Diniz-Filho et al. 2009). To avoid this uncertainty and minimize errors, I used the ensemble forecasting technique, which, used the previous models that obtained the AUC value ≥ 0.75. AUC is an effective, thresholdindependent model evaluation indicator and is also independent of the prevalence (i.e. the frequency of occurrence approach) of the species. The ensemble forecasting approach provides the consensus result of multiple models reducing both uncertainty and errors (Araújo & New 2007).

Threshold and binary maps

I used the frequency of predictions that indicated, as species were present in each grid; the projections were calculated after transforming each probability map into binary values (presence/absence). The binary maps (0 for absence and 1 for presence) are based on the results of the ensemble models of the Habitat-Suitability of each species; for this, I transform continuous frequencies of the ensemble models outputs, into binary outputs. I applied the threshold: 20th Percentile Training Presence (PTP), this threshold omits all regions with habitat suitability lower than the suitability values for the lowest 20% of occurrence records. This threshold omits a larger region than the Lowest Presence Threshold (LPT) and threshold 10th PTP, i.e, it is more conservative in the predictions; this scenario is more realistic in the potential area range distribution of the species with a low number of occurrences, endemics or with limited dispersal aptitude (case of fishes between the basins), for this reason, the 20th PTP threshold is widely used in conservation. Other authors have used successfully the 20th PTP to avoid bias by outlying records (Pearson et al. 2007; Wisz et al. 2008).

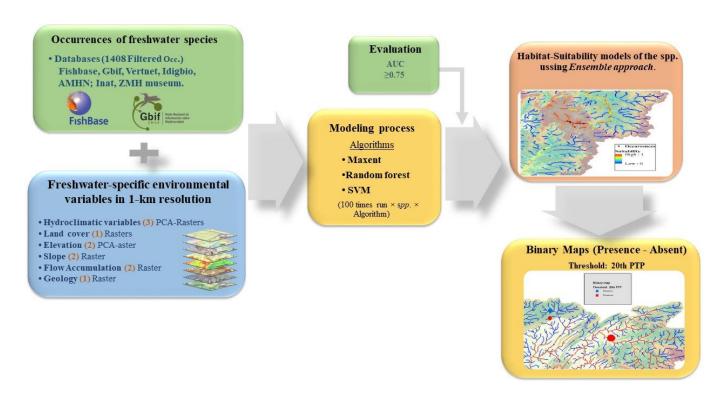
Analysis of habitat suitability maps

To perform a comparative analysis of the effectively protected area for the freshwater fish species, I extract the suitability values, for each cell in 1km² resolution in-stream distance for all water bodies in the study area, from the frequency ensemble models (Presences). This has been done using the tools "Spatial Analyst Tools" from ArcToolbox, and the "XToolsPro" in the work environment Arc-Map of the software ArcGIS® 10.8. I extract the in-stream habitat-suitability values of the fish species in the natural range (Ichthyogeographic provinces) and the values in the SNASPE.

Statistical and graphical analyzes were performed in the integrated development environment RStudio, for Software in R®, version 3.6.1, using the packages caret, colorRamps, complot, factoextra, FactoMineR, psych, raster, tidyverse, usdm, Viridis and dplyr.

The **Fig. 3.** summarizes the approach that I used to estimate the range distribution predictions and the maps of habitat-suitability of the freshwater fishes in the study area.

Figure 3. The general schematic process was used to model the distribution ranges of the species in this study.



RESULTS

In *Supplementary material* **S5** the Habitat-Suitability maps of all species analyzed in this study are available, as well as the evaluations of the algorithms (MaxEnt, Random Forest -RF and Support Vector Machine - SVM) and the AUC metrics used to construct the ensemble of the models. The binary maps indicating suitable habitats in their natural range and the suitable habitats on the SNASPE for all species using the threshold: 20th Percentile Training Presence (PTP) are also found in *Supplementary material* **S5**.

I achieve the objective proposed in this *Research Unit II*, by integrating the environmental variables and habitat fragmentation made in *Research Unit I*, to determine the distribution patterns of the main freshwater fishes o_i in their natural range and in the protected area system in Chile (SNASPE).

The remaining result is observed in *table 2*., here, is a comparison of the potential distribution areas predicted by the Habitat-Suitability models, between the natural distribution range of the species and the distribution range of the species in the protected areas by the SNASPE.

Table 2. Percentage of the natural distribution range of the native freshwater fish species in Chile protected by the SNASPE, using the estimates of Habitat-Suitability models.

ID	Notive appeies	Natural	Range in the	% A ² of range
ID	Native species	Range/Km ²	SNASPE/Km ²	protected by SNASPE
1	Aplochiton taeniatus Jenyns 1842	43 741	10 121	23.14 %
2	Aplochiton zebra Jenyns 1842	54 936	12 237	22.28 %
3	Basilichthys microlepidotus (Jenyns 1841)	25 133	768	3.06 %
4	Brachygalaxias bullocki (Regan 1908)	21 567	610	2.83 %
5	Bullockia maldonadoi (Eigenmann 1928)	6 568	2	0.03 %
6	Cheirodon australe Eigenmann 1927	57 166	10 778	18.85 %
7	Cheirodon galusdae Eigenmann 1927	8 899	9	0.10 %
8	Cheirodon pisciculus Girard 1855	20 908	177	0.85 %
9	Galaxias maculatus (Jenyns 1842)	64 553	13 250	20.53 %
10	Galaxias platei Steindachner 1898	35 019	10 335	29.51
11	Geotria australis Gray 1851	34 078	4 661	13.68
12	Mordacia lapicida (Gray 1851)	27 507	3 700	13.45
13	Nematogenys inermis (Guichenot 1848)	12 070	24	0.20 %
14	Odontesthes mauleanum (Steindachner 1896)	23 589	6 89	2.92 %
15	Percichthys melanops Girard 1855	12 755	19	0.15 %
16	Percichthys trucha (Valenciennes 1833)	38 194	5 857	15.33 %
17	Percilia gillissi Girard 1855	1 263	746	59.07 %
18	Trichomycterus areolatus Valenciennes 1833	39 275	5 693	14.50 %
	Total	527 221	191 788	36.38 %

DISCUSSION AND CONCLUSIONS

The models created here don't show the realized niche of the native freshwater fishes (i.e. interactions with introduced species above mentioned and population dynamics are ignored) (Davis et al. 1998), but the Habitat-Suitability models (fundamental niche) shown by the models, can be a useful tool for the conservation management of the studied species (Peterson et al. 2011). In this sense, it is important to highlight that the worst represented species (8 species) in the protected areas in Chile (SNASPE) according to this study (0.1-3%, **Table. 2**), are those the same species that are in a degree of threat (Vulnerable Endangered), according to the conservation status of the freshwater fishes of Chile by Campos et al. (1998), (See details Supplementary Material **S6**).

Although works such as those by Zamorano et al. (2019) consider the effect of fish size is important when modeling the distribution of the fish species, their study was made on a small scale (1 or 2 basins in southern Chilean rivers); here I don't consider this relevant factor in the distribution of species on large scale (This study).

I expect the results obtained here can be a useful tool for prioritizing areas for the integrated and sustainable management of hydrobiological resources and freshwater species and facilitate the future stages of my research (Thesis) serving as criteria and justification to use the Refuges for Climate Change approach in the establishment of protected areas in freshwater ecosystems.

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- the complete report and the Supplementary Material have already been sent to the teacher; however, due to the maximum capacity of 5MB that the BioSaga platform allows sending, this report is the summarized version without SM.