



# Macroecological perspectives on the competition between the native and invasive bumblebees in southern South America under climate change

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**Abstract** A handful of known bumble bee species (*Bombus*) have been transported worldwide and introduced in non-native regions for crop pollination, leading to long-lasting biological invasions. The introductions and invasions of European *Bombus terrestris* and, previously, of *Bombus ruderatus* in southern South America have been associated with sharp population declines of the giant Patagonian bumblebee,

*Bombus dahlbomii*. We gathered a comprehensive database of occurrence records for *B. dahlbomii*, *B. ruderatus*, and *B. terrestris* from museums and citizen science sources. Multivariate bioclimatic niche analyses and species distribution models were used to determine the extent of climatic niche overlap between invasive and native species and the potential effects of current and future climatic scenarios on the distribution of these bumblebees. We found extensive pairwise niche overlap between the three bumble bee species, *B. terrestris* versus *B. ruderatus* (67%), *B. terrestris* versus *B. dahlbomii* (61%), and *B. ruderatus* versus *B. dahlbomii* (46%). Compared to its historical records, the current distribution of *B. dahlbomii* is narrowing and is expected to shrink even more under the most climatically pessimistic future scenario, while that of *B. terrestris* shows an extensive, still expanding distribution. However, the models show that in the case of a climatic pessimistic future scenario, *B. terrestris* will also slow down its expansion on the continent. Finally, we discuss the consequences of the large niche overlap between the introduced bumble bee species and endangered *B. dahlbomii* and the effect of climate change on these three species of bumble bees in South America.

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## Introduction

Biological invasions are considered one of the paramount threats to biodiversity (Clavero and García-Berthou 2005). Invasive species can affect the composition and function of invaded communities, often exacerbated by anthropic effects (Kolar and Lodge 2001; Lodge 1993; Mack et al. 2000; Mooney and Hobbs 2000). Such processes could trigger the extinction of native species, homogenization of the local biota, and disruption of ecological interactions (Simberloff et al. 1997; Traveset and Richardson 2006). Also, the economic losses in agriculture and fisheries due to invasive species have cost billions of dollars due to lost productivity and the expenses of controlling them (Diagne et al. 2021; Jackson 2015; Pimentel et al. 2000; Vitousek et al. 1996).

Despite the recognized negative impacts of invasive species, incomplete knowledge of their present and future geographical distribution and biotic interactions in the invaded regions curtail possibilities for correct impact evaluation. These knowledge limitations are known as the “Wallacean” and “Eltonian” shortfalls. The Wallacean shortfall is the absence of information about species distribution, and the Eltonian shortfall is the lack of knowledge about interactions among species groups (Hortal et al. 2015). Wallacean and Eltonian shortfalls are particularly prominent among non-native species because of the novelty of new environments (Wallacean) and the evolutionary time context (Eltonian). Additionally, these shortfalls are a significant barrier to assessing the impact and effective control of the introduced species (Whittaker et al. 2005). However, species distribution models (SDMs) and citizen science data can be valuable tools for addressing these Wallacean and Eltonian shortfalls and aid in identifying suitable areas for occupation by exotic species (Hinojosa-Díaz et al. 2005, 2009; Silva et al. 2014; Faleiro et al. 2015). Citizen science tracks bumble bees in several world regions (Suzuki-Ohno et al. 2017; Falk et al. 2019; MacPhail et al. 2019). For example, SDMs combining citizen science data have helped track invasive *B. terrestris* in Japan and some other regions of East Asia (Acosta et al. 2016; Montalva et al. 2017; Suzuki-Ohno et al. 2017; Naeem et al. 2018; Morales et al. 2022).

The movement and trade of crop pollinators are increasing sources of biological invasions. *Bombus*

*runderatus* (Fabricius, 1775) and *B. terrestris* (Linnaeus, 1758) are two European bumble bee species introduced for crop pollination in Chile (Aizen et al. 2019; Montalva et al. 2011; Smith-Ramírez et al. 2018). Queens of *B. ruderatus*, previously naturalized in New Zealand, were introduced near Temuco in the south of Chile in 1982–1983 to pollinate *Trifolium pratense* (red clover), a livestock forage crop (Arretz and Macfarlane 1986). Later, this species was first reported in Argentina in 1993 (Roig Alsina and Aizen 1996). European *B. terrestris* (buff-tailed bumble bee) is the leading commercial bumblebee species and has been introduced in several countries worldwide (Dafni et al. 2010; Kadoya and Washitani 2010; Matsumura et al. 2004; Naeem et al. 2018). *Bombus terrestris* was first introduced to central Chile in 1997 (Montalva et al. 2011), and since then, more than a million colonies have been imported into the country (Aizen et al. 2019; Smith-Ramírez et al. 2018). The continuous and massive importation of *B. terrestris* into Chile maximizes propagule pressure. Consequently, it has spread throughout Chile, reaching the Atacama Desert in the north (Montalva et al. 2017) and the subarctic island of Navarino in the south (Rendoll-Carcamo et al. 2017). *Bombus terrestris* was reported in Argentina in 2006, and its current distribution extends throughout Patagonia (Acosta et al. 2016; Torretta et al. 2006a; Morales et al. 2013).

The impact of these two invasive species on native South American ecosystems should concern researchers and land managers alike. Both European bumble bee species are now feral in Chile and parts of Argentina and are blamed for the decline of the Patagonian giant bumble bee, *B. dahlbomii* Guérin-Ménéville 1835 (Aizen et al. 2019; Morales et al. 2016; Smith-Ramírez et al. 2018). Although there may be competition for floral resources between exotic and native species (Vergara et al. 2023), introducing diseases is the most relevant cause of decline (Aizen et al. 2019; Smith-Ramírez et al. 2018). Different studies have revealed the presence of European parasites in Chile, likely carried by European bumble bees, contributing to the decline of *B. dahlbomii* populations (Arbetman et al. 2013; Arismendi et al. 2016, 2021; Schmid-Hempel et al. 2014). In less than 20 years (or since the introduction of *B. terrestris*), the distribution of *B. dahlbomii* has shrunk considerably (Montalva et al. 2015; Morales et al. 2016). *Bombus dahlbomii* is now listed as endangered by both the International Union

for the Conservation of Nature (IUCN) Red List and the Chilean Ministerio de Medio Ambiente (MMA) (Montalva et al. 2015; Morales et al. 2016). According to a recent related study (Morales et al. 2022), climate change (CC) cannot be pointed out as a primary driver of population declines in *B. dahlbomii* observed in the last decades, with the role of invasive bumblebees still being the hypothesis with considerable support.

This research aimed to ascertain the potential for ecological interactions among these three species over space and time under the premise that these interspecific interactions can take place where the climatic niches of the species overlap. Specifically, we sought to answer the following questions: (1) Is there extensive climatic niche overlap among these *Bombus* species? (2) How will the current predicted distribution of the species change under expected future climatic scenarios? We applied multivariate bioclimatic niche analyses (Broennimann et al. 2012) and SDMs to answer these questions and evaluate the relationship between the distributions of the two European bumble bee species and native *B. dahlbomii*. Therefore, we calculated the pairwise overlap of species niches in geographic and climatic space to determine the potential threat of European species to native endangered species. We also used SDMs to predict the current and future distributions of these three bumble bee species in South America.

## Methods

### Species occurrence dataset

We gathered a comprehensive database of occurrence records for *B. dahlbomii*, *B. ruderatus*, and *B. terrestris* from the Global Biodiversity Information Facility (GBIF; <https://www.gbif.org>; *B. dahlbomii* DOI: <https://www.gbif.org/species/1340388>, *B. ruderatus* DOI: <https://www.gbif.org/species/1340383>, *B. terrestris* DOI: <https://www.gbif.org/species/1340503>) online database and records from the Citizen Science initiative “Salvemos Nuestro Abejorro” (Save our Bumble bee; <https://salvemosnuestroabejorro.wordpress.com/>). From GBIF, we aggregated museum records (data from museum Pontificia Universidad Católica de Valparaíso; American Museum of Natural History New York; Museo Nacional de

Historia Natural Chile; Instituto de Entomología de la Universidad Metropolitana de Ciencias de la Educación; Institute Miguel Lillo, Argentina; Museo Argentino de Ciencias Naturales Bernardino Rivadavia; Instituto Patagónico de Ciencias Naturales San Martín Los Andes; Museo de La Plata, La Plata, Argentina; Natural History Museum (London) Collection Specimens; Illinois Natural History Survey Insect Collection; Naturalis Biodiversity Center; Snow Entomological Museum Collection; Bee Biology and Systematics Laboratory; ZFMK Hymenoptera collection were considered); from Salvemos Nuestro Abejorro, all images were curated by JM (Montalva et al. 2017). Citizen scientists with little or no training in bumble bee taxonomy were able to recognize *B. dahlbomii*, for example, due to its easily distinguished bright orange hairs (Falk et al. 2019; Montalva et al. 2011; Morales et al. 2022).

The existence or ability to assign accurate geographical coordinates to occurrence records is crucial for successful analysis. Therefore, an occurrence record in our preliminary dataset was retained to investigate whether the provided geographical coordinates or the locality string were sufficiently detailed to geocode a record using Google Earth. Additionally, dubious, unreliable, and duplicate occurrence records were discarded from the dataset. This process yielded 251 confident records for *B. ruderatus*, 885 for *B. terrestris*, and 321 for *B. dahlbomii* from the preliminary dataset of 5,307 records.

### Climatic data for both current and future scenarios

We obtained climatic datasets from 19 Worldclim bioclimatic variables ([www.worldclim.org](http://www.worldclim.org)) for temperature and precipitation from 1950 to 2000 (Hijmans et al. 2005), widely used in SDMs and used in other studies of bees in South America (Vivallo et al. 2019; Nascimento et al. 2022). Additionally, we used 19 bioclimatic variables available for 17 Atmosphere–Ocean Global Circulation Models (AOGCMs) from WorldClim to model the species in the future scenarios of climate change: ACCESS1-0, BCC-CSM1-1, CCSM4, CNRMCM5, GFDL-CM3, GISS-E2-R, HadGEM2-AO, HadGEM2-CC, HadGEM2-ES, INMCM4, IPSL-CM5A-LR, MIROC-ESM-CHEM, MIROC-ESM, MIROC5, MPI-ESM-LR, MRICGCM3, and NorESM1-M. from the latest IPCC report on the world’s climate (IPCC 2019).

These scenarios were also obtained on the WorldClim website to predict climate-suitable areas for species in 2070, considering the carbon representative pathway (RCP 8.5) available in the IPCC (2019) global climate report.

However, using many climatic variables can lead to overfitting models (Beaumont et al. 2005; Jiménez-Valverde et al. 2011). Therefore, in the species distribution models, we reduced the number of our variables to improve the prediction of the range of the species using principal component analysis. For this, we standardized the variables to have their mean equal to zero and variances equal to 1. Later, we ran a principal component analysis (PCA hereafter) to obtain independent principal components (PCs onwards) representing the environment variables to predict the species range. The selected PCs explained 95% of the original climatic variation. We also standardized the variables for future scenarios by setting means equal to zero and variances equal to 1. Before the PCA was run for the variables in the future scenarios, the linear coefficients obtained for the current variables were projected into each one of the future scenarios. Finally, the PCA was run for each of the future scenarios. This method was applied to obtain a dependency between the current climatic scenario and every future climatic scenario.

## Data analysis

### *Ecological niche overlap*

We applied the analysis framework of Broennimann et al. (2012) to determine the extent to which similarities existed in the environmental space occupied by the three bumble bee species. First, we created a background distribution map based on a minimum convex polygon (MCP) from the occurrence records of each species. In addition to the MCP, we added a 2-degree buffer around the occurrences as an estimate related to the species dispersal abilities and to avoid making all climatic cells, even those deemed unreachable for the species, to be used in the niche analysis. Next, the data were compiled into a matrix and analyzed using principal component analysis (PCA) to generate an environmental space [PCA-env in Broennimann et al. (2012)]. We chose to apply a PCA considering all the environmental spaces together, as this strategy reached the best

performance when comparing niches (Broennimann et al. 2012). Next, we calculated the occurrence density within each cell (4 km) of the environmental space grid for each species. The occurrence density was then modeled using a smooth kernel density function that analyzed the geographical conditions of each species (Broennimann et al. 2012). The species pairwise niche overlap was then calculated using Schoener's D metric between the modeled occurrence densities in the PCA ordination space (Broennimann et al. 2012; Schoener 1970; Warren et al. 2008).

We tested the significance of the D metric by calculating the niche equivalency and similarity between the three pairs of species (Broennimann et al. 2012) using the ecospat package (Di Cola et al. 2017) in R, with code modifications in Silva et al. (2016). The niche equivalency test determines whether the niches of two species in two geographical ranges are equivalent (i.e., whether the niche overlap is constant when randomly reallocating the occurrences of both species among the two ranges). First, all occurrences were pooled to retain the same number of occurrences as in the original datasets and were randomly divided into two datasets. Then, niche overlap statistic D is calculated. This process was repeated 100 times (to increase the likelihood that the null hypothesis could be confidently rejected), and a histogram of the simulated values was constructed. If the observed value of D falls within the density of 95% of the simulated values, the null hypothesis of niche equivalency cannot be rejected. The niche similarity test differed from the equivalency test in determining whether the overlap between niches observed in the two ranges was distinct from those niches and whether niches were randomly chosen from the other ranges. In other words, the niche similarity test determined whether an environmental niche occupied in one range was more similar to another than predicted by chance. We shifted the observed density of occurrences in one range at random (the location of the simulated density of the center of the occurrences was chosen randomly from a pool of environments) to conduct this test. We then determined how closely the simulated niche matched the observed niche in the other range. We based the niche similarity test on 100 repetitions. If the observed overlap is greater than 95% of the simulated values, then the species occupies environments in both ranges that are more similar to each other than

expected by chance (Broennimann et al. 2012; Silva et al. 2016).

SDMs

For the SDMs, we used a spatially structured partition of the occurrences of the modeled species. Consequently, we gridded the study extent in a checkerboard fashion with an aggregation factor of two, in which the occurrences of the modeled species were allocated. Initially, we used one subset to train the models, while the second enabled us to evaluate the produced distribution range. Next, we used the occurrences from the first modeling run to train a second modeling run. Finally, we used the training occurrences to evaluate those produced in the second modeling round.

We used six different models in an ensemble approach: the Generalized Linear Model (GLM), Random Forest (RDF), Maximum Entropy (MAX), Gaussian Model (GAU), Support Vector Machines (SVM), and Maximum Likelihood (MLK). GLM and RDF are statistical methods, MAX and SVM are machine-learning methods, and GAU and MXL are Bayesian methods. The models were evaluated using the Jaccard similarity index metric (Leroy et al. 2018; Barahona-Segovia et al. 2023; Booth et al. 2013; Fern et al. 2019). This procedure measures the similarity between predictions and observations on a scale of 0 to 1. Values near 1 indicate that the model predictions perfectly match the general observations of the species, and values near 0 indicate that the models do not correspond to actual observations (Leroy et al. 2018). In addition, we used a threshold that maximizes Jaccard values concerning sensitivity and specificity. Since similarity indices do not consider pseudoabsences during model evaluation, they are less biased than other evaluation metrics. Finally, we used a weighted consensus method to produce the final species distribution considering all methods.

Results

Climatic niche overlap

The first two PCs of the PCA captured 71.39% of the variation in the climate dataset. The first PC (43.5%) corresponded to temperature variables, and the

second (27.89%) corresponded to precipitation. Additionally, the European bumble bee species exhibited niche overlap with the native species *B. dahlbomii*, with 46% (D: 0.46) overlapping with *B. ruderatus* and 61% with *B. terrestris* (D: 0.61) (Table 1; Fig. 1).

SDMs

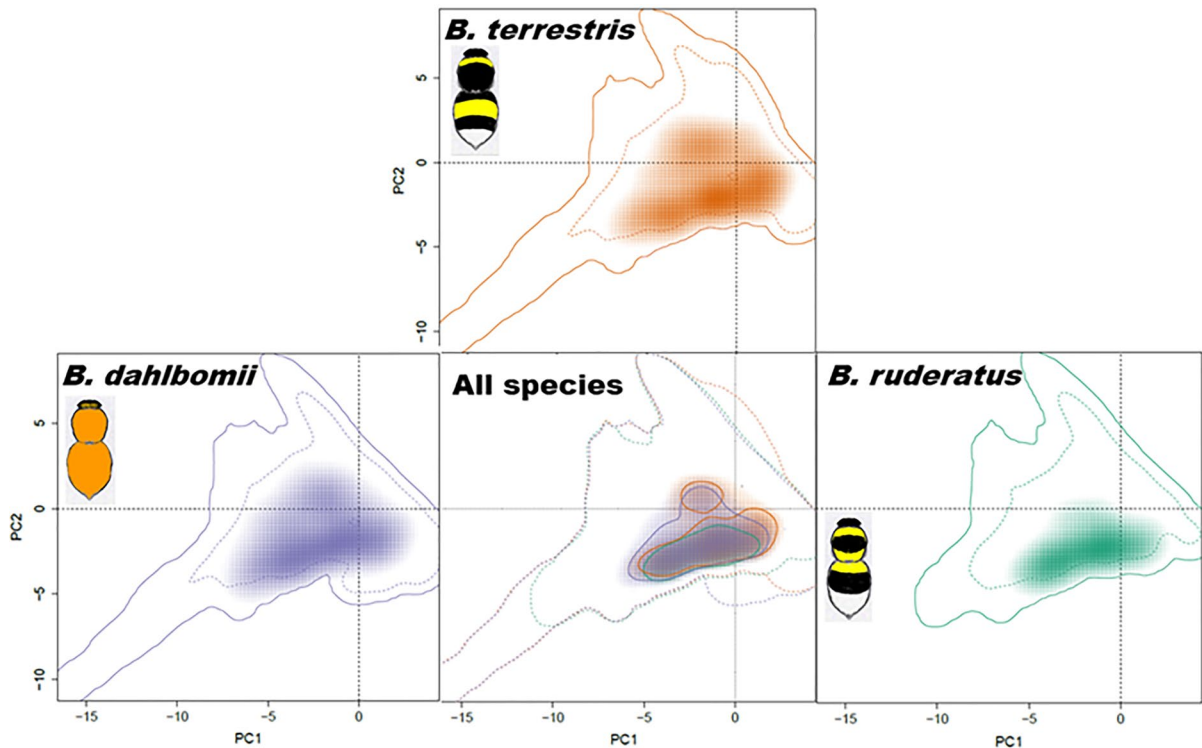
The models for *B. dahlbomii*, *B. ruderatus*, and *B. terrestris* reached mean Jaccard values of  $0.85 \pm 0.04$ ,  $0.89 \pm 0.03$ , and  $0.92 \pm 0.01$ , respectively (mean  $\pm$  standard error). For *B. dahlbomii*, GAU ( $0.94 \pm 0.01$ ), RDF ( $0.94 \pm 0.01$ ), and SVM ( $0.94 \pm 0.0$ ) had comparably high Jaccard values. For *B. ruderatus*, MAX had the highest Jaccard value ( $0.91 \pm 0.07$ ) and RDF for *B. terrestris* ( $0.90 \pm 0.01$ ; Table 2). MLK performed poorly for all three species (Table 2).

In the current climate scenario, the native species *B. dahlbomii* occurred throughout the southern portion of South America, comprised of the

**Table 1** Main results of the multivariate analyses, considering Schoener's D metric and the *p* values obtained using the similarity test (I), niche unfilling (U), niche expansion (E), and niche stability (S) of the climatic niche of the species

	<i>B. ruderatus</i>	<i>B. terrestris</i>	<i>B. dahlbomii</i>
Schoener's D metric			
<i>B. ruderatus</i>	–	–	–
<i>B. terrestris</i>	0.67	–	–
<i>B. dahlbomii</i>	0.46	0.61	–
Niche similarity			
<i>B. ruderatus</i>	–	<b>0.01</b>	0.05
<i>B. terrestris</i>	<b>0.01</b>	–	<b>0.02</b>
<i>B. dahlbomii</i>	0.05	<b>0.02</b>	–
Niche unfilling			
<i>B. ruderatus</i>	–	0.006	0.005
<i>B. terrestris</i>	0.162	–	0.005
<i>B. dahlbomii</i>	0.166	0.026	–
Niche expansion			
<i>B. ruderatus</i>	–	0.162	0.166
<i>B. terrestris</i>	0.006	–	0.026
<i>B. dahlbomii</i>	0.005	0.005	–
Niche stability			
<i>B. ruderatus</i>	–	0.838	0.834
<i>B. terrestris</i>	0.994	–	0.974
<i>B. dahlbomii</i>	0.995	0.995	–

Bold values were statistically significant.



**Fig. 1** Climatic conditions suitable for *B. dahlbomii* (left panel), *B. terrestris* (upper panel), *B. ruderatus* (right panel), and the overlap of all three bumble bee species (middle panel). Results obtained from the environmental niche analysis. The

solid and dashed lines illustrate 100% and 50% of the available (background) climate for each bumble bee species in their South American ranges. PC: principal components

**Table 2** Summary of the SDMs obtained for the GAU, GLM, MLK, MAX, RDF, and SVM algorithms based on Jaccard values ( $\pm 1$  SE)

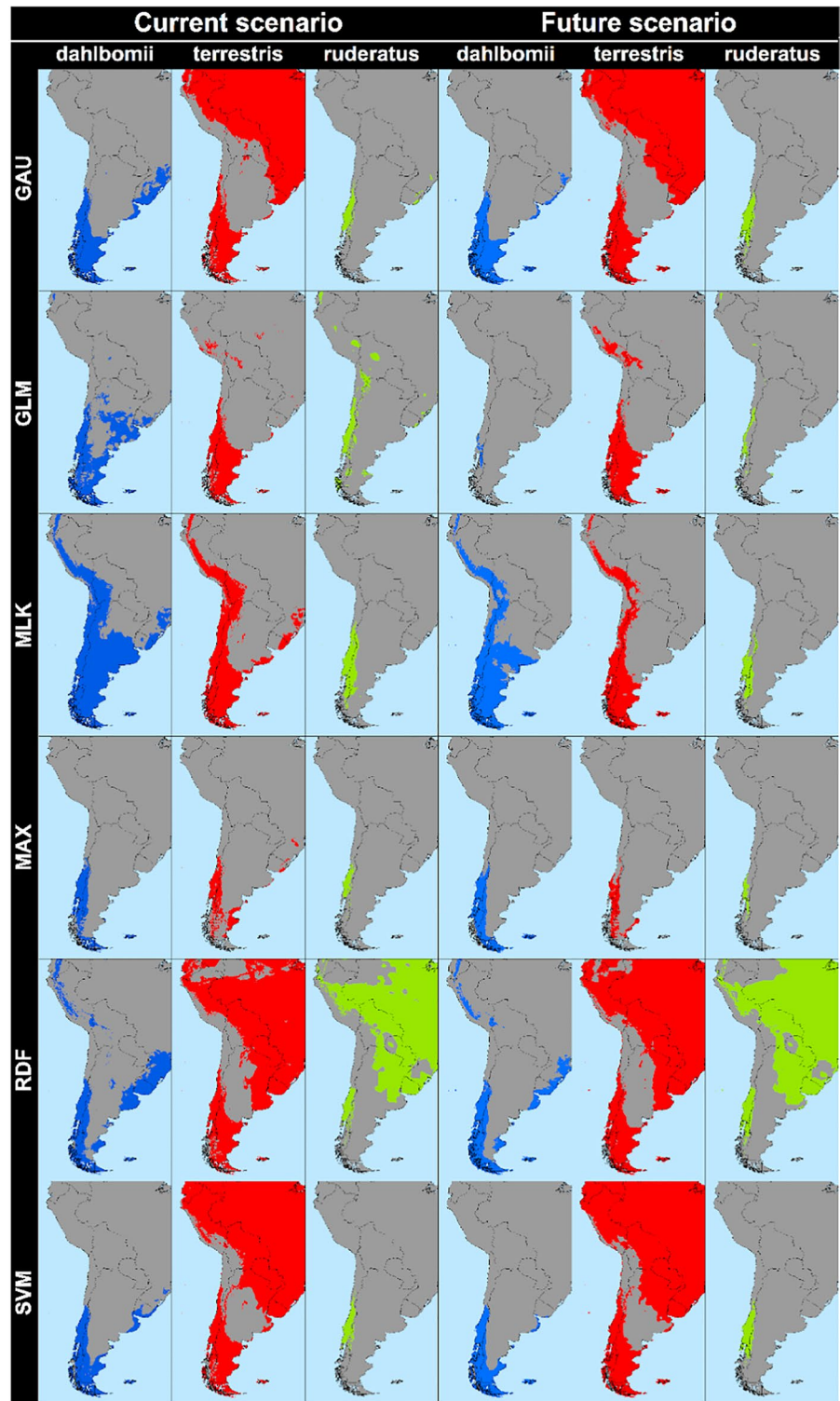
Modeling method	<i>B. ruderatus</i>	<i>B. terrestris</i>	<i>B. dahlbomii</i>
GAU	0.81 $\pm$ 0.07	0.88 $\pm$ 0.01	0.94 $\pm$ 0.01
GLM	0.73 $\pm$ 0.02	0.78 $\pm$ 0.12	0.77 $\pm$ 0.04
MLK	0.50 $\pm$ 0.00	0.50 $\pm$ 0.00	0.50 $\pm$ 0.00
MAX	0.91 $\pm$ 0.07	0.88 $\pm$ 0.01	0.91 $\pm$ 0.03
RDF	0.85 $\pm$ 0.07	0.90 $\pm$ 0.01	0.94 $\pm$ 0.01
SVM	0.85 $\pm$ 0.07	0.86 $\pm$ 0.01	0.93 $\pm$ 0.01

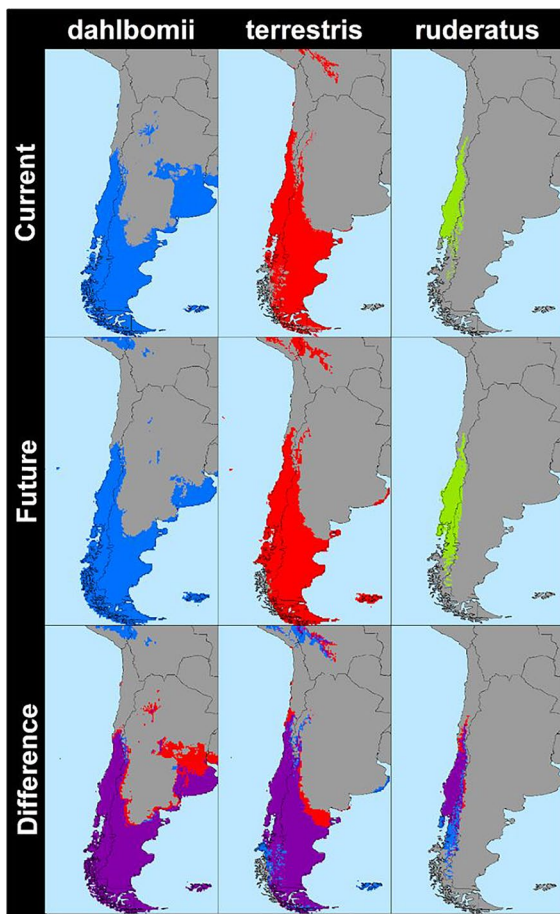
Mediterranean regions of Chile, the Andes Mountains range (from the latitude 30° to south), the Patagonia of Argentina/Chile, the Malvinas/Falkland Islands, and the Atlantic region of Argentina/Uruguay near Mar del Plata (Figs. 2 and 3). *Bombus ruderatus* distribution is associated with the Mediterranean zone of Chile, reaching the temperate rainforest (Valdivian

rainforest) and some parts of the Argentinean Patagonia (Figs. 2 and 3). For *B. terrestris*, the models reached a pattern similar to that of *B. dahlbomii*. The models also predicted suitable regions for *B. terrestris* in the northern parts of Chile, including areas of the Atacama Desert and regions of the southern Andes Mountains of Peru and Bolivia (Figs. 2 and 3). According to the models, the predicted current distribution for *B. ruderatus* was more restricted.

Considering the predicted future distribution of the three species (Fig. 3), the native bumble bee species, *B. dahlbomii*, showed a slight retraction in the northern part of its geographic range (Chilean Mediterranean region). However, the models predicted a suitable area in southern Peru (Fig. 3). The most prominent retraction in the predicted distributions under the pessimistic scenario was near the Río de la Plata region of Argentina/Uruguay. Under the pessimistic scenario, the European bumble bee *B. terrestris* predicted distribution retracted, mainly in Argentinean Patagonia. However,

**Fig. 2** Results of SDMs depicting current and future scenarios for the three bumblebee species based on GAU, GLM, MLK, MAX, RDF, and SVM algorithms





**Fig. 3** Summary of SDM results showing the current, future, and differences between scenarios. For the current scenario panels, each color (e.g., blue, red, and green) represents the predicted distribution for each *Bombus* species (blue for *B. dahlbomii*, red for *B. terrestris*, and green for *B. ruderatus*). For future panels, each color represents the predicted distributions for each *Bombus* species (blue for *B. dahlbomii*, red for *B. terrestris*, and green for *B. ruderatus*). For the difference panels, red represents the area predicted to be lost, blue represents the area predicted to be gained, and purple represents the climatically stable areas that do not change from current to future model predictions for the three species

similar to *B. dahlbomii*, a suitable area was predicted in southern Peru (Fig. 3). In the case of *B. ruderatus*, the species moved toward southern Chile and Argentina (Fig. 3).

## Discussion

Hortal et al. (2015) identified seven data shortfalls that challenge the progress of ecological and biogeographic research fields. This research addresses two shortfalls considering the cases of the native *B. ruderatus* and invasive *B. terrestris* and *B. ruderatus* in South America. More specifically, our study addresses the Wallacean shortfall, i.e., the lack of data for the geographic distribution of a species or taxon (Whittaker et al. 2005). Depending upon the extent of missing data, the impacts of either species conservation or the detection of invasive species can affect the outcome of analyses and decision making (Lomolino and Heaney 2004; Whittaker et al. 2005). Our study also addresses the Eltonian shortfall, i.e., “the lack of knowledge about interactions among species or among groups of species” (Hortal et al. 2015).

Citizen science and SDMs were effective tools for tracking and predicting the distribution patterns of the endangered *B. dahlbomii* and the introduced species *B. ruderatus* and *B. terrestris*. However, despite the widespread use of SDMs, this method may present concerns when considering the nature of interactions between species on macroecological scales and across large areas, as biotic and abiotic variables interact in complex ways (Silva et al. 2018). While recognizing these limitations, we demonstrated that modeling could help address the knowledge gaps that arise following the invasion of a new species.

Here, we showed the potential distribution of three bumble bee species, two invasive species (*B. ruderatus* and *B. terrestris*) and one native species (*B. dahlbomii*). Specifically, we evaluated the spatial and multivariate overlap of introduced and native bumble bee species using SDMs and multivariate analyses. We show a high niche climatic overlap between *B. ruderatus* and *B. terrestris* (D: 0.67, Fig. 1; Table 1). Additionally, there is an overlap in the niche between these species and *B. dahlbomii* (Fig. 1; Table 1). These values indicate possible competition for resources or a high risk of disease spillover between these species with *B. dahlbomii*, with *B. terrestris* being the most likely threat (Arbetman et al. 2013; Arismendi et al. 2016; Madjidian et al. 2008; Morales et al. 2013; Schmid-Hempel et al. 2014). Furthermore, in some areas where species distributions are sympatric, *B. dahlbomii* populations sharply declined (Morales et al. 2013, 2016). For this reason, a high niche



overlap signals an increased threat to the persistence of *B. dahlbomii* (Morales et al. 2016).

In the current scenario, the distribution maps implied that both introduced species could potentially migrate to and occupy an extensive area in South America (Figs. 2 and 3). Although *B. ruderatus* was more restricted to Patagonia, the non-native distribution of *B. terrestris* extended north into Peru and Bolivia. Should this scenario unfold, *B. terrestris* could put more strain on *B. funebris* populations and could potentially affect the populations of other native pollinators with adverse outcomes (Morales et al. 2013; Vanbergen et al. 2018; Nascimento et al. 2022). The models indicated areas suitable in the Mediterranean region of Chile for *B. terrestris* (Fig. 3), which Acosta et al. (2016) reported as having low suitability. In addition, our models present a wider distribution for *B. terrestris* compared to the results of Fontúrbel et al. (2021).

The future scenario shows a decrease in the area occupied by the bumble bee species (Fig. 3), especially *B. ruderatus* and *B. dahlbomii*. The models indicated that *B. ruderatus* would probably move toward southern Patagonia, while *B. dahlbomii* would likely disappear near the northern Mediterranean region of South America, confirming the trends shown in a previous study (Morales et al. 2022). This is analogous to the trend of European and North American bumble bee species that have experienced northward or high-elevation shifts in distribution (Kerr et al. 2015). Furthermore, in South America, *B. bellicosus* has shown declines in distribution due to climatic conditions (Martins and Melo 2010; Martins et al. 2015). These movements could affect the abundance of these bumble bee species and cause pollination mismatches (Miller-Struttman et al. 2015; Valdivia et al. 2016).

Invasive exotic bees can negatively impact native ecosystems (Goulson 2003; Iwasaki and Hogendoorn 2022). Notably, they can compete with native pollinators for floral and local nesting resources and transmit parasites and pathogens (Arbetman et al. 2013; Schmid-Hempel et al. 2014; Arismendi et al. 2016, 2021; Morales et al. 2016; Smith-Ramírez et al. 2018; Aizen et al. 2019). Although the pervasive examples of invasive species are numerous, some exotic bees may cause positive effects on their invaded ranges, for instance, in insular environments (Silva et al. 2017). When there is overlap in the species niches, these

impacts may be exacerbated according to the classical competitive exclusion principle (Hardin 1960). For example, in a recent study, *B. terrestris* was defined as an ecological niche constructor, where its foraging behavior over the native plant *Fuchsia magellanica* Lam. (Onagraceae) harms *B. dahlbomii* (Rosenberger et al. 2022). We found substantial evidence of climatic niche overlap between exotic species (*B. ruderatus* and *B. terrestris*) and native species (*B. dahlbomii*) in current and future climatic scenarios.

Moreover, the niche of the native species *B. dahlbomii* fitted almost entirely inside the niche of the European bumblebee *B. terrestris*. Therefore, under future CC projections, native species continue to share most of their niche with exotic species. We urge conservation efforts toward prohibiting the importation of this and other exotic species that have become invasive in this region to safeguard the well-being of native bumblebees and prevent potential harm to similar species in neighboring countries. (Aizen et al. 2019).

In summary, we expect that the ongoing population decrease of *B. dahlbomii* will continue in the near future. This is likely to occur either because both *B. terrestris* and *B. ruderatus* are relentless competitors for resources at local scales or because of their significant niche and potential distribution overlaps. Considering existing population data and modeled predictions, the existence of *B. dahlbomii* in South America relies on active decisions related to the effective control of commercial hives of *B. terrestris* and *B. ruderatus* and the management of natural environments to increase population recruitment of *B. dahlbomii*. Nonetheless, even with such active actions taking place, the future of the southernmost bumble bee worldwide remains uncertain.

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