

UNIVERSIDADE FEDERAL DE JUIZ DE FORA
INSTITUTO DE CIÊNCIAS BIOLÓGICAS
PROGRAMA DE PÓS-GRADUAÇÃO EM BIODIVERSIDADE E CONSERVAÇÃO
DA NATUREZA

Lucas Rieger de Oliveira

**Potenciais áreas de invasão de espécies exóticas de decápodes dulcícolas na América do
Sul**

Juiz de Fora

2023

Lucas Rieger de Oliveira

Potenciais áreas de invasão de espécies exóticas de decápodes dulcícolas na América do Sul

Dissertação apresentada ao Programa de Pós-graduação em Biodiversidade e Conservação da Natureza da Universidade Federal de Juiz de Fora como requisito parcial à obtenção do título de Mestre em Biodiversidade e Conservação da Natureza. Área de concentração: Processos Ecológicos e Conservação da Natureza.

Orientadora: Profª. Dra. Simone Jacqueline Cardoso

Coorientador: Prof. Dr. Pedro Manuel Silva Gentil Anastácio

Juiz de Fora

2023

Ficha catalográfica elaborada através do programa de geração automática da Biblioteca Universitária da UFJF, com os dados fornecidos pelo(a) autor(a)

de Oliveira, Lucas Rieger.

Potenciais áreas de invasão de espécies exóticas de decápodes dulcícolas na América do Sul / Lucas Rieger de Oliveira. -- 2023.
71 p.

Orientador: Simone Jaqueline Cardoso

Coorientador: Pedro Manuel Silva Gentil Anastácio

Dissertação (mestrado acadêmico) - Universidade Federal de Juiz de Fora, Instituto de Ciências Biológicas. Programa de Pós-Graduação em Biodiversidade e Conservação da Natureza, 2023.

1. Modelagem de nicho. 2. Crustáceos. 3. Adequabilidade. 4. Potencial de Invasão. I. Cardoso, Simone Jaqueline, orient. II. Anastácio, Pedro Manuel Silva Gentil, coorient. III. Título.

Lucas Rieger de Oliveira

Potenciais áreas de invasão de espécies exóticas de decápodes dulcícolas na América do Sul

Dissertação apresentada ao Programa de Pós-graduação em Biodiversidade e Conservação da Natureza da Universidade Federal de Juiz de Fora como requisito parcial à obtenção do título de Mestre em Biodiversidade e Conservação da Natureza. Área de concentração: Comportamento, Ecologia e Sistemática. Área de concentração: Processos Ecológicos e Conservação da Natureza.

Aprovada em 1 de março de 2023

BANCA EXAMINADORA

Profa. Dra. Simone Jaqueline Cardoso - Orientadora
Universidade Federal de Juiz de Fora

Prof. Dr. Pedro Manuel Silva Gentil Anastácio - Coorientador
Universidade de Évora, Portugal

Prof. Dr. André de Camargo Guaraldo
Universidade Federal do Paraná

Prof. Dr. Renato Tavares Martins
Instituto Nacional de Pesquisas da Amazônia

Juiz de Fora, 01 / 03 / 2023.



Documento assinado eletronicamente por **Renato Tavares Martins, Usuário Externo**, em 01/03/2023, às 12:28, conforme horário oficial de Brasília, com fundamento no § 3º do art. 4º do Decreto nº 10.543, de 13 de novembro de 2020.



Documento assinado eletronicamente por **Simone Jaqueline Cardoso, Professor(a)**, em 01/03/2023, às 12:28, conforme horário oficial de Brasília, com fundamento no § 3º do art. 4º do Decreto nº 10.543, de 13 de novembro de 2020.



Documento assinado eletronicamente por **André de Camargo Gualdo, Usuário Externo**, em 01/03/2023, às 12:29, conforme horário oficial de Brasília, com fundamento no § 3º do art. 4º do Decreto nº 10.543, de 13 de novembro de 2020.



Documento assinado eletronicamente por **Pedro Manuel Silva Gentil Anastácio, Usuário Externo**, em 01/03/2023, às 12:31, conforme horário oficial de Brasília, com fundamento no § 3º do art. 4º do Decreto nº 10.543, de 13 de novembro de 2020.



Documento assinado eletronicamente por **LUCAS RIEGER DE OLIVEIRA, Usuário Externo**, em 01/03/2023, às 12:38, conforme horário oficial de Brasília, com fundamento no § 3º do art. 4º do Decreto nº 10.543, de 13 de novembro de 2020.



A autenticidade deste documento pode ser conferida no Portal do SEI-Uffj (www2.uffj.br/SEI) através do ícone Conferência de Documentos, informando o código verificador **1167189** e o código CRC **FA9E4A58**.

Dedico este trabalho aos meus pais e minhas irmãs que me inspiram e me auxiliaram na realização dos meus sonhos.

AGRADECIMENTOS

Escrever dois agradecimentos em menos de um mês deve ser mais difícil que escrever toda esta dissertação. Associar graduação com pós-graduação foi um dos maiores desafios que eu enfrentei na UFJF, mas nada disso seria possível se não fosse o apoio de todos que acompanharam nessa caminhada turbulenta. Então tentarei expressar em palavras toda gratidão a todos que me fizeram chegar até aqui e não se assuste se estiver familiarizado com o texto, vocês foram importantes nas minhas duas conquistas.

Começo esses agradecimentos pautando toda minha energia a Deus, que tem sido combustível a mim em todos os momentos a que me recordo, que sempre a Ele em elevado pensamento retoma a mim a calma que preciso para prosseguir.

Não poderia iniciar esses agradecimentos por outro lugar senão a família. Minha família que como base sempre está comigo, me acalentando e me ensinando os caminhos a percorrer.

Meu agradecimento ao meu pai Francisco que sempre foi figura de persistência, com os braços sempre abertos, prontos a um abraço e a conversa sempre disposta pronta a animar e distrair. Meu pai, que sempre manteve a fé presente em nosso lar, obrigado por estar comigo.

Meu agradecimento a minha mãe Néia que inegavelmente é inconfundível, minha mãe que tem fala firme quando precisa e um coração gigante onde cabem todas as pessoas e animais. Minha mãe que cuida dos outros sempre a frente de si mesma e a quem eu espero um dia conseguir retribuir tamanha entrega. Sou grato a você.

Meu agradecimento a minha irmã Marta que é minha segunda figura materna. Sua alegria e energia movimentam todos. Marta que sempre foi a figura central dessa família. Marta que consegue reunir todos ao seu redor. Marta, minha irmã, você é fonte de segurança e conselho para mim, você que sempre esteve ao meu lado, próxima o bastante para acompanhar todas as minhas caminhadas. Muito obrigado por tudo.

Meu agradecimento a minha irmã Juliana que é emoção e calma. Ju, você completa a trindade de figuras femininas essenciais para minha vida. Sua voz é acalento e sua presença é tranquilidade. Você sempre me ouve, me aconselha, me incentiva e não me deixa duvidar da minha capacidade. Ju, obrigado por tudo.

Meu agradecimento a minha namorada Milla que está ao meu lado há 7 anos. Ela que as palavras não faltam quando preciso de consolo. Seu companheirismo e sua compreensão não me deixam nunca esquecer que não estou sozinho. Seu apoio e incentivo em todas as decisões cruciais e difíceis da vida me lembram como é bom ter alguém especial para caminhar ao meu lado. Obrigado por estar comigo sempre.

Que nunca me falte forças para ser grato por cada um de vocês em minha vida.

Agradeço a Universidade Federal de Juiz de Fora por me permitir viver uma das maiores realizações da minha vida. O sonho de me formar biólogo se tornou realidade aqui. Agradeço a Coordenação do Programa de Pós-Graduação em Biodiversidade e Conservação da Natureza que sempre esteve ao lado dos alunos, nos caminhando rumo ao sucesso, sobretudo a equipe da secretaria Priscila, Marlú, Dayane e Rosi e os coordenadores Professor Roberto Junio Pedrosa Dias e Nathan Oliveira Barros. Não poderia deixar de agradecer a professora Ximena Ovando que se dispôs contribuir com meu projeto e depositou sua confiança em mim nessa reta final.

O agradecimento a minha orientadora Simone, que antes de me orientar na Pós-graduação já estava presente na minha formação na graduação. Simone que é uma pessoa dotada de um sorriso contagiante e reconfortante, que me incentivou a seguir novos caminhos e que acolheu minhas aflições quando eu não sabia a quem recorrer. Simone você foi parte fundamental na construção da minha vida acadêmica e profissional. Obrigado por tanto.

Não poderia deixar de agradecer ao meu co-orientador professor Pedro Manuel Silva Gentil Anastácio e a Universidade de Évora em Portugal por ter me recebido tão bem e por ter tornado a experiência do intercâmbio melhor do que eu poderia esperar. Agradeço a Dra. Mafalda Gama por toda paciência comigo e com meu trabalho. Pela disposição em guiar minhas dúvidas e abraçar comigo essa experiência me faltam palavras para agradecer a vocês. Sem vocês nada disso seria possível.

Um agradecimento especial a Sonia Sosa Quezada e Érica Cardoso de Lima que foram fundamentais na tradução e revisão deste trabalho.

Meu agradecimento ao meu amigo professor Msc. Gustavo Britto da Universidade Estadual Paulista (UNESP-Assis), que além de excelente profissional é também uma pessoa comprometida e disposta a doar seus conhecimentos. Gustavo prontamente me auxiliou em todos os momentos que necessitei. Serei eternamente grato.

O agradecimento repleto de ternura vai aos meus colegas do Laboratório de Ecologia do Plâncton: Nathalia, Lécio, Paula, Karina, Gabi, Thaianne, Vitoria, Matheus, Iollanda, Jéssica, Beatriz e, em especial, ao Pedro Menini que incansavelmente amparou todos os meus questionamentos e auxiliou nos momentos mais difíceis deste trabalho. Você é parte fundamental da minha chegada até aqui.

Toda gratidão que sinto não parece caber em um papel, mas, é inegável que registrar a minha gratidão a torna eterna aos olhos de quem as leu até aqui.

Muito obrigado a todos que de alguma forma estiveram nessa caminhada, terão minha eterna gratidão.

RESUMO

As invasões biológicas representam um dos maiores desafios mais significativos no Antropoceno, impactando a biodiversidade e o funcionamento dos ecossistemas. A Modelagem de Nicho Ecológico é amplamente utilizada para mapear áreas em risco de invasões, auxiliando na prevenção da expansão de espécies invasoras e orientando esforços de conservação em ecossistemas de água doce. Os principais objetivos deste estudo foram modelar o nicho ecológico de cinco espécies de decápodes de água doce potencialmente invasoras na América do Sul: *Dilocarcinus pagei*, *Macrobrachium amazonicum*, *Macrobrachium jelskii*, *Macrobrachium rosenbergii* e *Procambarus clarkii*, e avaliar as áreas adequadas restantes para a ocorrência dessas espécies na América do Sul. Dados de ocorrência do Global Biodiversity Information Facility (GBIF) foram complementados com uma Revisão Sistemática da Literatura. As variáveis utilizadas nos modelos foram obtidas nos bancos de dados Worldclim e EarthEvi. A Modelagem de Nicho Ecológico das áreas potenciais de ocorrência foi realizada utilizando os algoritmos do pacote Biomod2 e SDM. Foi realizada a modelagem de nicho ecológico para as cinco espécies através do algoritmo MaxEnt e do ensemble com os algoritmos de melhor desempenho. Nossos resultados indicaram uma área adequada de até 11% da América do Sul. As avaliações dos modelos apresentaram valores favoráveis de TSS e AUC (>0,7 e >0,8). As áreas adequadas projetadas para a América do Sul incluíram diversas bacias hidrográficas e Áreas Protegidas. As informações geradas em nosso estudo podem ajudar a identificar áreas suscetíveis à invasão de decápodes na América do Sul e apoiar a gestão e as decisões locais.

Palavras-chave: Adequabilidade de habitat, Crustáceos, *Dilocarcinus*, Invasões biológicas, *Macrobrachium*, Modelagem de Nicho, *Procambarus*.

ABSTRACT

Biological invasions pose significant challenges in the Anthropocene, impacting ecosystem biodiversity and functioning. Ecological Niche Modeling is widely used to map areas at risk of invasions, aiding in the prevention of invasive species expansion and guiding conservation efforts in freshwater ecosystems. The main objectives of this study were to model the ecological niche of five potentially invasive species of freshwater decapods in South America: *Dilocarcinus pagei*, *Macrobrachium amazonicum*, *Macrobrachium jelskii*, *Macrobrachium rosenbergii* and *Procambarus clarkii* and evaluate remaining suitable habitats areas for the occurrence of those species in South America. Occurrence data from the Global Biodiversity Information Facility and completed with a literature review combining data. Variables used in the models were obtained from the Worldclim and EarthEvi databases. Ecological Niche Modeling of the potential areas of occurrence was performed using the Biomod2 and SDM package algorithms. Our results indicated a suitable area of up to 11% of South America. Model evaluations yielded favorable TSS and AUC values (>0.7 and >0.8). The suitable areas projected for South America included several hydrographic basins and Protected Areas. The information generated in our study can help identifying susceptible areas to decapods invasion in South America and support local management and decisions.

Keywords: habitat suitability, crustaceans, *Dilocarcinus*, biological invasions, *Macrobrachium*, niche modelling, non-native species, *Procambarus*,

LISTA DE ILUSTRAÇÕES

Figure 1 - Flowchart of the PRISMA Matrix referring to the systematic literature review process. Adapted from Moher et al. (2009, PRISMA Group). GBIF (Global biodiversity information facility); gbif.org, accessed on 2021 March. Of the 551 articles returned by the systematic review, 1367 species occurrence data (geographical coordinates) were extracted. 37

Figure 2 - Occurrence maps of species. In red: are points obtained by the systematic review. In purple: points obtained by the GBIF database, *Dilocarcinus pagei* (A) points obtained by the systematic review (n = 42). Points obtained by GBIF database (n = 20); *Macrobrachium amazonicum* (B) points obtained by the systematic review (n = 213); Points obtained by GBIF database (n = 24) and *Macrobrachium jelskii* (C) points obtained by the systematic review (n = 19); Points obtained by GBIF database (n = 116).. 39

Figure 3 - Global occurrence maps of species. In red: are points obtained by the systematic review. In purple: points obtained by the GBIF database. *Macrobrachium rosenbergii* (A) points obtained by the systematic review (n = 116). Points obtained by GBIF database (n = 20) and *Procambarus clarkii* (B) points obtained by the systematic review (n = 908). Points obtained by GBIF database (n = 5481). 40

Figure 4 - Suitability maps generated by the MaxEnt algorithm for each species A) *Dilocarcinus pagei*, B) *Macrobrachium amazonicum*, C) *Macrobrachium jelskii*, D) *Macrobrachium rosenbergii*, E) *Procambarus clarkii*..... 46

Figure 5 - Suitability maps generated by the ensemble of the GLM, GBM, GAM, and RF algorithms for each species A) *Dilocarcinus pagei*, B) *Macrobrachium amazonicum*, C) *Macrobrachium jelskii*, D) *Macrobrachium rosenbergii*, E) *Procambarus clarkii*. 47

LISTA DE TABELAS

Table 1- Average of variables' importance for the construction of the models of each species calculated by Pearson's correlation. *P. clarkii* = *Procambarus clarkii*, *D. pagei* = *Dilocarcinus pagei*, *M. rosenbergii* = *Macrobrachium rosenbergii*, *M. jelskii* = *Macrobrachium jelskii*, *M. amazonicum* = *Macrobrachium amazonicum*.....**Erro! Indicador não definido.**41

Table 2- Mean AUC and TSS for each algorithm used in the niche modeling of the species *M. rosenbergii*, *P. clarkii*, *M. jelskii*, *D. pagei*, and *M. amazonicum*.**Erro! Indicador não definido.**43

Table 3 - Mean AUC and TSS for each algorithm used in the niche modeling of the species *M. rosenbergii*, *P. clarkii*, *M. jelskii*, *D. pagei*, and *M. amazonicum*. Suitability area for each species modeled in square kilometers (Km²) and the percentage relative to the territory of South America occupation. *P. clarkii* = *Procambarus clarkii*, *D. pagei* = *Dilocarcinus pagei*, *M. rosenbergii* = *Macrobrachium rosenbergii*, *M. jelskii* = *Macrobrachium jelskii*, *M. amazonicum* = *Macrobrachium amazonicum*.....48

LISTA DE ABREVIATURAS E SIGLAS

ASFA	<i>Aquatic Sciences and Fisheries Abstract</i>
AUC	<i>Area Under Curve</i> (Área sobre a curva)
GADM	<i>Global Administrative Areas Databases</i> (Banco de Dados de Áreas Administrativas Globais)
GBIF	<i>Global Biodiversity Information Facility</i>
IUCN	<i>International Union for Conservation of Nature</i> (União Internacional para a Conservação da Natureza)
MaxEnt	<i>Maximum entropy modeling</i> (Modelo de Máxima Entropia)
ROC	<i>Receiver Operating Characteristic</i>
TSS	<i>True Skill Statistics</i>
VIF	<i>Variance Inflation Factor</i> (Fator de Inflação da Variância)

LISTA DE SÍMBOLOS

± Variação máxima ou mínima de uma média (desvio padrão)

SUMÁRIO

1.	INTRODUÇÃO GERAL.....	15
	REFERENCES.....	19
2.	CAPÍTULO ÚNICO: NON-NATIVE DECAPODS IN SOUTH AMERICA: RISK ASSESSMENT AND POTENTIAL IMPACTS.....	23
	ABSTRACT.....	24
2.1.	INTRODUCTION.....	25
2.2.	METHODS.....	29
2.2.1	Study Area.....	29
2.2.2	Species selection.....	29
2.2.3	Species presence data.....	31
2.2.4	Niche modeling and variables selection.....	32
2.2.5	Modeling protocol.....	33
2.3.	RESULTS.....	36
2.3.1	Species presence data.....	36
2.3.2	Niche modeling.....	41
2.4.	DISCUSSION.....	49
2.4.1	Suitability of areas to species invasion.....	49
2.4.2	Niche modeling.....	51
3	CONCLUSION.....	54
	REFERENCES.....	55
	SUPPLEMENTARY MATERIAL 1 – Papers list resulting from the systematic review.....	67
	SUPPLEMENTARY MATERIAL 2 – Predictor variables list, extracted from WorldClim and EarthEnv databases. Highlighted with an X are the variables selected through the Variance Inflation Factor (VIF) for each species.....	68
	SUPPLEMENTARY MATERIAL 3 – a Area of suitability greater than 75% of the species <i>Dilocarcinus pagei</i>, <i>Macrobrachium amazonicum</i>, <i>Macrobrachium jelskii</i>, <i>Macrobrachium rosenbergii</i> and <i>Procambarus clarkii</i>, which overlap the hydrographic basins and Protected Areas in South America.	71

1. INTRODUÇÃO GERAL

A introdução de espécies em ambientes que não fazem parte de sua distribuição natural vem provocando danos ecológicos significativos em diversos ecossistemas ao redor do mundo, sendo a segunda maior causa de perda de biodiversidade (Williamson 1996, Strayer 2010). Na América do Sul, o número de espécies exóticas e invasoras de águas continentais tem aumentado nas últimas décadas e, associado a poluição dos ecossistemas aquáticos e as mudanças climáticas, oferece ainda mais riscos a conservação destes ambientes (Bertelsmeier et al. 2013). Estas espécies podem suportar uma gama ampla de condições ambientais devido a sua plasticidade ecológica e normalmente competem por recursos com a fauna nativa, reduzindo drasticamente estas populações, levando a perdas significativas de biodiversidade local ou até mesmo à extinção (Manfrin 2019). As águas continentais, por sua vez revelam agravantes maiores pois estão intimamente ligados à exploração dos recursos naturais, sendo muitas vezes destino final de inúmeros produtos gerados por ação antrópica (Bashir et al. 2020). Associado a isso, a proteção e a conservação destas áreas se tornam essencial para a manutenção da vida nestes ambientes.

Diversos estudos com macro e microcrustáceos demonstraram que o potencial invasor dessas espécies tem aumentado devido a uma associação de fatores que envolvem a interferência antrópica e as mudanças climáticas. (Capinha et al. 2011, Bellard et al. 2013, Mantovano et al. 2021). Dentre os crustáceos, os decápodes atraem a atenção por seu uso diverso, principalmente na culinária (Susanto 2021). Há um alto interesse econômico no investimento de criadouros de crustáceos em países em desenvolvimento como o Brasil e demais países da América do Sul, o que é um alerta para introdução destas espécies em novos ambientes. A presença de espécies invasoras pode afetar negativamente espécies nativas, causar extinções, desequilibrar a estrutura biótica de um ecossistema e afetar a economia de diversos países (Simberloff et al. 2013, Gallardo et al. 2016). A prevenção é uma das estratégias

mais eficazes para evitar o avanço de espécies invasoras, mas dependem de uma série de avaliações que determinam o potencial de invasão de uma espécie (Leung et. al 2002)

É importante destacar que espécies exóticas são espécies que ocorrem fora de sua faixa de distribuição natural. Caso essa espécie cause impactos negativos no ecossistema introduzido, ela pode ser considerada como espécie exótica invasora. Há registro de espécies exóticas e invasoras pertencentes ao grupo Decapoda em todos os continentes. Na América do Sul destacamos cinco espécies de decápodes dulcícolas que são consideradas exóticas: *Procambarus clarkii* (Girard 1852), *Macrobrachium amazonicum* (Heller 1861), *Macrobrachium jelskii* (Miers 1878), *Macrobrachium rosenbergii* (De Man 1879), e *Dilocarcinus pagei* (Stimpson 1861). Destas espécies, *P. clarkii* e *M. rosenbergii* não possuem origem na América do Sul, são nativas da América do Norte e Ásia, respectivamente, e foram introduzidas no subcontinente para fins comerciais. Já *M. amazonicum*, *M. jelskii* e *D. pagei* são nativas da Amazônia e altamente adaptadas a essa região. Por essa razão, podem ser consideradas exóticas quando introduzidas em ambientes fora de sua distribuição natural (Magalhães 2001, Magalhães et al. 2005).

Muitas espécies de decápodes possuem grande adaptação a ecossistemas de água doce, capazes de suportar altos gradientes de salinidade (McNamara & Faria 2012) e variações de temperatura (Collart & Moreira, 1993). Essa característica, garante a essas espécies uma vantagem adaptativa para colonizar novos ambientes, uma vez que, tolerar variações na temperatura e salinidade pode interferir diretamente no ciclo reprodutivo, no desenvolvimento embrionário e larval (Augusto et al. 2009, Fukuda et al. 2016, Boudour-Bouchecker et al. 2016). A tolerância a condições extremas ou atípicas são características em comum em diversas espécies invasoras, principalmente quando essas condições afetam diretamente na reprodução destas espécies.

Os trabalhos desenvolvidos na América do Sul com espécies exóticas e invasoras, pertencentes ao grupo Decapoda, em sua maioria, são limitados a estudos de carcinicultura e pouco se sabe do potencial de avanço dessas espécies em águas continentais e os seus potenciais impactos (Rocha & Barbosa 2017, David et al. 2018, Bastos et al. 2019). Esses ambientes apresentam zonas propícias para o desenvolvimento dessas espécies, tais como temperaturas mais elevadas, maior aporte de nutrientes do continente e presença de espécies nativas. Além disso, a capacidade dessas espécies em tolerar novos ambientes, sua alta capacidade reprodutiva e resistência a patógenos podem agravar ainda mais o estado de conservação dos ecossistemas aquáticos. Isso pode promover danos irreversíveis à economia e à ecologia local (Gherardi et al. 2011, Nakano & Strayer 2014).

Atualmente, o uso de softwares e da bioinformática têm funcionado como importantes ferramentas para se traçar estratégias de monitoramento e controlar o estabelecimento de espécies não nativas, bem como na tomada de decisão sobre conservação de habitats e indicação de áreas prioritárias para preservação (Kulhanek et al. 2011, Wittmann et al. 2017, Egly et al. 2019). Os Modelos de Nicho Ecológico (MNE) são ferramentas cada vez mais utilizadas em estudos de geoprocessamento, biogeografia, ecologia e no mapeamento de áreas com alto risco de invasões biológicas (Johovic et al. 2020), e têm se tornado uma tendência de pesquisa nos últimos anos (Zhao et al. 2021). A modelagem de nicho associa os conjuntos de dados biogeográficos e climáticos com a distribuição da espécie para predizer as áreas de habitat com maior adequabilidade para sua ocorrência (Elith et al. 2011, Radosavljevic & Anderson 2014). O algoritmo mais utilizado nos MNE é o MaxEnt, um método que utiliza pontos de *background* baseados no princípio de máxima entropia (Yackulic et al. 2013). Esse algoritmo tem alta popularidade devido a sua grande capacidade preditiva, em comparação a outros métodos de modelagem, e sua capacidade de reduzir alguns vieses amostrais, como

aqueles causados pelo reduzido número de presença das espécies, sendo justificado o uso em modelagens com extensa área de projeção (Phillips et al. 2006).

Trabalhos mais recentes têm utilizado algoritmos que utilizam pseudo-ausências em conjunto com dados de presença das espécies e estes têm se mostrado mais robustos e com desempenhos superiores a outros métodos (Barbet-Massin et al. 2012). Para a realização de uma modelagem de nicho, além dos dados de presença da espécie e os dados das variáveis preditoras, são necessários pontos de ausência. Porém, pontos de ausência verdadeira são quase impossíveis de serem extraídos de um fragmento natural, o que pode levar à subestimativa da verdadeira distribuição das espécies. Nesse sentido, são gerados pontos de pseudo-ausência aleatoriamente na área de projeção (Engler et al. 2004, Elith & Leathwick 2009, Barbet-Massin et al. 2012). A escolha dos algoritmos para a realização da modelagem é uma etapa muito importante, pois cada algoritmo possui vantagens e limitações (Thuiller 2003). Isso pode interferir diretamente no desempenho de cada modelo, dependendo também do número de ocorrências, pseudo-ausências e de variáveis preditoras utilizadas (Zhao et al. 2021).

Frequentemente, as invasões biológicas são tão silenciosas que os impactos só são percebidos anos mais tarde quando as ações de combate são praticamente irreversíveis (Bellard et al. 2021). Minimizar os impactos ou até mesmo erradicar espécies invasoras pode não ser uma tarefa simples, mas traçar estratégias para evitar o estabelecimento em novas zonas pode ser uma boa solução. Nesse sentido, os modelos de distribuição de espécies baseados em seu nicho têm se mostrado úteis na tomada de decisões em trabalhos ecológicos, sobretudo na indicação de áreas prioritárias para conservação, pois dispõem um papel preditivo do avanço de espécies potencialmente invasoras em regiões de habitats favoráveis (Capinha et al. 2011).

Essa dissertação teve por objetivos realizar a modelagem de nicho para cinco espécies potencialmente invasoras de decápodes dulcícolas que ocorrem no território brasileiro: *D.*

pagei, *M. amazonicum*, *M. jelskii*, *M. rosenbergii* e *P. clarkii* e indicar áreas de habitat adequadas para a distribuição destas espécies na América do Sul.

REFERENCES

- Augusto, A. et al. 2009. Evolutionary transition to freshwater by ancestral marine palaemonids: evidence from osmoregulation in a tide pool shrimp. *Aquat. Biol.*, 7 (2009), pp. 113-122.
- Barbet-Massin, M. et al. 2012. Selecting pseudo-absences for species distribution models: how, where, and how many? *Methods in ecology and evolution*, v. 3, n.2, p. 327-338.
- Bashir, I. et al. 2020. Concerns and threats of contamination on aquatic ecosystems. In *Bioremediation and Biotechnology*, Springer, Cham, p.1-26.
- Bastos, A. M. et al. 2019. Effects of environmental light colors on the larviculture of the Amazon River prawn *Macrobrachium amazonicum*. *Aquaculture International*, v. 27, n.5, p.1525-1534.
- Bellard, C. et al. 2013. Will climate change promote future invasions? *Global change biology*, v. 19, n. 12, p. 3740-3748.
- Bellard, C. et al. 2021. Looming extinctions due to invasive species: Irreversible loss of ecological strategy and evolutionary history. *Global Change Biology*, 27(20), 4967-4979.
- Bertelsmeier, C. et al. 2013. Increase in quantity and quality of suitable areas for invasive species as climate changes. *Conservation Biology*, 27(6), 1458-1467.
- Boudour-Bouchecker, N. et al. 2016. Osmoregulation in larvae and juveniles of two recently separated *Macrobrachium* species: Expression patterns of ion transporter genes. *Comparative Biochemistry and Physiology Part A: Molecular & Integrative Physiology*, 195, 39–45.
- Capinha, C. et al. 2011. Predicting worldwide invasiveness for four major problematic decapods: an evaluation of using different calibration sets. *Ecography*, v. 34, n.3, p. 448-459.
- Collart, O.O. & Moreira, L.C. 1993. Potencial pesqueiro de *Macrobrachium amazonicum* na Amazônia Central (Ilha do Careiro): variação da abundância e do comprimento. *Amazoniana*, 12:399-413.

- David, F. S. et al. 2018. Economic feasibility of intensification of *Macrobrachium rosenbergii* hatchery. *Aquaculture Research*, 49(12), 3769-3776.
- Egly, R. M. et al. 2019. Predicting the potential distribution of the non-native Red Swamp Crayfish *Procambarus clarkii* in the Laurentian Great Lakes. *Journal of Great Lakes Research*, v. 45, n. 1, p. 150-159.
- Elith, J. & Leathwick, J. R. 2009. Species distribution models: ecological explanation and prediction across space and time. *Annual Review of Ecology, Evolution and Systematics*, v.40, n.1, p. 677-697.
- Elith, J. et al. 2011. A statistical explanation of MaxEnt for ecologists. *Diversity and distributions*, v. 17, n. 1, p. 43-57.
- Engler, R. et al. 2004. An improved approach for predicting the distribution of rare and endangered species from occurrence and pseudo-absence data. *Journal of applied ecology*, v. 41, n. 2, p. 263-274.
- Fukuda, B. et al. 2016. Effect of salinity on the embryonic development of *Macrobrachium acanthurus* (Decapoda: Palaemonidae). *Invertebrate Reproduction & Development*, 61(1), 1–8.
- Gallardo, M. B. et al. 2016. Global ecological impacts of invasive species in aquatic ecosystems *Glob. Change Biol.* Pp. 151-163.
- Gherardi, F. 2006. Crayfish invading Europe: the case study of *Procambarus clarkii*. *Marine and Freshwater Behaviour and Physiology*, 39(3), 175-191.
- Gherardi, F. et al. 2011. Managing invasive crayfish: is there a hope? *Aquatic Sciences*, v.73, n.2, p.185-200.
- Johovic, I. et al. 2020. A potential threat to amphibians in the European Natura 2000 network: Forecasting the distribution of the American bullfrog *Lithobates catesbeianus*. *Biological Conservation* v. 245, p. 108551.
- Kulhanek, S. et al. 2011. Is invasion history a useful tool for predicting the impacts of the world's worst aquatic invasive species? *Ecological Applications*, v. 21, n.1, p. 189-202.
- Leung, B. et al. 2002. An ounce of prevention or a pound of cure: bioeconomic risk analysis of invasive species. *Proc. R. Soc. Lond. B. Biol. Sci.*, 269, pp. 2407-2413.

- Magalhães, C. 2001. Diversity, distribution, and habitats of the macro-invertebrate fauna of the Río Paraguay and Río Apa, Paraguay, with emphasis on Decapod Crustaceans. A Biological Assessment of the Aquatic Ecosystems of the Río Paraguay Basin, Alto Paraguay, Paraguay. Conservation International. RAP Bulletin of Biological Assessment, Washington, 19, 68-72.
- Magalhães, C. et al. 2005. Exotic species of freshwater decapod crustaceans in the state of São Paulo, Brazil: records and possible causes of their introduction. Biodiversity & Conservation, v. 148, p. 1929-1945.
- Manfrin, C. et al. 2019. Detection and control of invasive freshwater crayfish: from traditional to innovative methods. Diversity, v.11, n.1.
- Mantovano, T. et al. 2021. A global analysis of the susceptibility of river basins to invasion of a freshwater zooplankton (*Daphnia lumholzi*). Freshwater Biology, v. 66, n. 4, p. 683-698.
- McNamara JC & Faria SC, 2012. Evolution of osmoregulatory patterns and gill ion transport mechanisms in the decapod Crustacea: a review. J Comp Physiol B 8, 997-1014.
- Nakano, D. & Strayer, D. L. 2014. Biofouling animals in fresh water: biology, impacts, and ecosystem engineering. Frontiers in Ecology and the Environment, v .12, n.3, p. 167-175.
- Phillips, S. J. et al. 2006. Maximum entropy modeling of species geographic distributions. Ecological modelling, v. 190, n. 3-4, p. 231-259.
- Radosavljevic, A., & Anderson, R. P. 2014. Making better MaxEnt models of species distributions: complexity, overfitting and evaluation. Journal of biogeography, v. 41, n. 4, p. 629-643.
- Rocha, S. S. D., & Barbosa, R. D. J. 2017. Population biology of *Macrobrachium jelskii* (Miers, 1877) (Decapoda, Palaemonidae) from an artificial pond in Bahia, Brazil. Nauplius, v.25.
- Simberloff, J. D. Et al. 2013. Impacts of biological invasions: what's what and the way forward Trends Ecol. Evol., 28 (2013), pp. 58-66
- Strayer, D. L. 2010. Alien species in fresh waters: ecological effects, interactions with other stressors, and prospects for the future. Freshwater biology, v. 55, p. 152-174.

- Susanto, G. N. 2021. Crustacea: The Increasing Economic Importance of Crustaceans to Humans. In *Arthropods-Are They Beneficial for Mankind?* IntechOpen. V.232.
- Williamson, M. 1996. *Biological invasions*. Springer Science & Business Media.
- Wittmann, M. E. et al. 2017. Refining species distribution model outputs using landscape-scale habitat data: forecasting grass carp and *Hydrilla* establishment in the Great Lakes region. *Journal of Great Lakes Research*, v. 43, n.2, p.298-307.
- Yackulic, C. B. et al. 2013. Presence-only modelling using MaxEnt: when can we trust the inferences?. *Methods in Ecology and Evolution*, 4(3), 236-243.
- Zhao, G. et al. 2021. Analysis of the distribution pattern of Chinese *Ziziphus jujuba* under climate change based on optimized biomod2 and MaxEnt models. *Ecological Indicators* v. 132, p. 108256.

2. CAPÍTULO ÚNICO: NON-NATIVE DECAPODS IN SOUTH AMERICA: RISK ASSESSMENT AND POTENTIAL IMPACTS

(Under review in the journal Water)

Lucas Rieger de Oliveira^{1*}, Gustavo Britto^{2,5}, Mafalda Gama³, Ximena Maria Constanza

Ovando¹, Pedro Anastácio³, Simone Jaqueline Cardoso^{1,4}

¹ Graduate Program in Biodiversity and Nature Conservation, Institute of Biology, Federal University of Juiz de Fora, Rua José Lourenço Kelmer, São Pedro, Juiz de Fora, MG, 36036-900, Brazil.

² Graduate Program in Biosciences, Applied Statistics Laboratory (LEA), São Paulo State University, Avenida Dom Antônio 2100, Assis, São Paulo, BR, 19806-900, Brazil.

³ MARE – Marine and Environmental Sciences Centre / ARNET – Aquatic Research Network, Institute for Research and Advanced Training (IIFA), Portugal / Department of Landscape, Environment and Planning, University of Évora, 7002-554, Évora, Portugal.

⁴ Department of Zoology, Institute of Biology, Federal University of Juiz de Fora, Rua José Lourenço Kelmer, São Pedro, Juiz de Fora, MG, 36036-900, Brazil.

⁵Department of Biology, São Paulo State University, Avenida Dom Antônio 2100, Assis, São Paulo, BR, 19806-900, Brazil.

***Corresponding author:**

E-mail: lucas.rieger2014@gmail.com

Number phone: +55 32 988853252.

ABSTRACT

Biological invasions are among the major challenges of the Anthropocene, affecting multiple dimensions of ecosystem's biodiversity and functioning. In freshwater, non-native species are among the main drivers of biodiversity loss, requiring substantial management actions. Ecological Niche Modeling is widely used for mapping areas with potential risk of biological invasions, helping to prevent the possible expansion of invasive species and providing a basis for conservation plans. The main objectives of this study were: i) model the ecological niche of five potentially invasive species of freshwater decapods in South America: *Dilocarcinus pagei*, *Macrobrachium amazonicum*, *Macrobrachium jelskii*, *Macrobrachium rosenbergii* and *Procambarus clarkii*; ii) evaluate remaining suitable habitats for the occurrence of these species in South America. Occurrence data for the selected species were obtained in the *Global Biodiversity Information Facility* (GBIF) and completed with a literature review combining data until 2021. Variables used in the models to predict niche suitability were related to climate, topography and hydrology and were obtained from the Worldclim and EarthEvi databases. Species Distribution Modeling of the potential areas of occurrence was performed using the Biomod2 and SDM package algorithms. Our results indicated a suitable area of up to 11% of South America. Model evaluations were considered excellent (TSS > 0.7 and AUC > 0.8). The suitable areas projected for South America included several hydrographic basins and environmental protection areas. The information generated in our study can help identifying susceptible areas to decapods invasion in South America and support local management and decisions.

Keywords: habitat suitability, crustaceans, *Dilocarcinus*, biological invasions, *Macrobrachium*, niche modelling, non-native species, *Procambarus*,

2.1 INTRODUCTION

Introductions of species into environments outside their natural distribution have caused significant ecological damage in several ecosystems, representing the second leading cause of biodiversity loss worldwide (Williamson 1996, Strayer 2010). The presence of non-native species negatively affects native counterparts, causes extinctions, and disrupts the biotic structure of the ecosystem, also affecting the economies of several countries (Simberloff et al. 2013, Gallardo et al. 2016).

In South America, the number of non-native and invasive freshwater species has increased in the last decade, mainly due to the climate change, degradation of aquatic ecosystems such as predatory fishing and urbanization (Capinha et al. 2011, Bellard et al. 2013, Mantovano et al. 2021, Bertelsmeier et al. 2013). Non-native species can tolerate a wide range of environmental conditions due to their ecological plasticity, having advantages in resource competition with native fauna, drastically reducing local populations, and leading to significant biodiversity loss and extinction (Manfrin 2019).

In freshwater ecosystems, macro and microcrustaceans are among the species with the highest invasive potential and are often related to exploitation of natural resources and anthropogenic impacts (Bashir et al. 2020). Among non-native crustaceans, decapods are the most frequent and often linked to aquaculture, which has significantly increased in developing countries such as Brazil and other countries in South America as a food resource alternative (Susanto 2021). Many decapod species are highly adapted to freshwater ecosystems but can tolerate different salinities (McNamara & Faria 2012) and temperature variations (Collart & Moreira, 1993). This feature provides these species with an adaptive advantage to colonize new environments, as temperature and salinity variations can directly affect their reproductive cycle

and embryonic and larval development (Augusto et al. 2009, Fukuda et al. 2016, Boudour-Bouchecker et al. 2016). Reproductive cycle tolerance to extreme or atypical conditions is also a common characteristic in several non-native species.

The introduction of non-native species and the possibility of biological invasions are constant threats to South America's biodiversity. The South American subcontinent covers more than 17 million km² and approximately 23% of all freshwater bodies in the world, making it one of the world's most biodiverse region (Junk 2013). Due to its large territorial extension and latitudinal amplitude, South America has different climates, ranging from intense humidity in the Amazon Forest to strong aridity in the Atacama Desert and the Caatinga. It also presents an extensive combination of terrains that interfere with terrestrial and aquatic ecosystems. Thus, the selection of climate, topographic and hydrological variables is important to evaluate the possible impacts of non-native decapod species on South American aquatic ecosystems (Cantonati et al. 2020; Torremorrel et al. 2021).

In South America, *Procambarus clarkii* (Girard 1852), *Macrobrachium amazonicum* (Heller 1861), *Macrobrachium jelskii* (Miers 1878), *Macrobrachium rosenbergii* (De Man 1879), and *Dilocarcinus pagei* (Stimpson 1861) are five important freshwater decapods with a strong invasive potential: among these, *P. clarkii* and *M. rosenbergii* are native from North America and Asia, respectively, and were introduced in South America for commercial purposes, while *M. amazonicum*, *M. jelskii* and *D. pagei* are native from the Amazon region but are likely to invade other regions of the South America.

Currently, *P. clarkii* and *M. rosenbergii* species are globally distributed and their impacts are widely known (Souty-Grosset et al. 2016; Oliveira & Santos 2021). The occurrence of these non-native species in areas of environmental protection can negatively impact the community of native species in the long term, as reported by (New et al. 2000), which reinforces the care with the sustainability of the cultivation of *M. rosenbergii*. *P. clarkii*, for

example, is a non-native species considered one of the most invasive crustacean species in the world and has managed to escape from all cultivation systems in which it has been cultivated to date. Most records of *P. clarkii* introduction outside the natural environment had commercial purposes in aquaculture. However, the possible cause of introduction in South America was probably due to commercialization as a pet, since the species was never cultivated for commercial interests in the continent (Magalhães et al. 2005, Loureiro et al. 2015). There are many records of introductions when owners of these animals or traders discarded or abandoned their crayfish in the natural environment, without worrying about the impacts that could be provoked (Loureiro et al. 2015, Souty-Grosset et al. 2016).

Procambarus clarkii causes impacts on various sectors of the economy, such as rice fields, compromising crop drainage and damaging fishing nets (Anastácio & Marques 1997, Wakasugi 2013, Ramalho & Anastácio 2015). Likewise, several studies recorded the negative impact of *P. clarkii* on amphibian communities, as juveniles are part of their diet, and on the diversity of aquatic plants (Cruz et al. 2008, Holdich 2017). It is important to point out that *P. clarkii* is omnivorous, which can lead to significant destruction of macrophyte diversity, in addition to preying heavily on insects and mollusks, reducing the resources available to native species. An even more serious aggravating factor is that the species can be a vector of diseases by carrying several species of helminths and has been an important transmitter of the crayfish plague, caused by the fungus *Aphanomyces astaci* (Aquiloni et al. 2011). Although *P. clarkii* is highly resistant to this pest, this fact is of great concern to the native crayfish community (Lodge et al. 2012).

The other species, *M. Amazonicum*, *M. jelskii*, and *D. pagei* are native to the Amazon region (Magalhães et al. 2005, Garcia et al. 2021). The species *M. jelskii* and *M. amazonicum* were introduced to serve as food for some species of fish previously introduced in culture tanks and reservoirs in the region (Santos & Coelho 2021). While *D. pagei* believed that its

introduction in other regions has been accidental, through the transport of fish and macrophytes (Magalhães et al. 2005), and there are records of these species in some basins in the Southeast region of Brazil and close to the Pantanal. Most of the research carried out in South America on non-native decapods is limited to studies on shrimp farming, and little is known about the potential of farmed species to invade inland waters and cause negative impacts (Rocha & Barbosa 2017, David et al. 2018, Bastos et al. 2019).

Currently, the use of Ecological Niche Modeling (ENM) tools is providing important knowledge for monitoring and controlling the establishment of non-native species, as well as supporting decision-making on habitat conservation and the identification of priority areas for preservation (Kulhanek et al. 2011, Wittmann et al. 2017, Egly et al. 2019). ENMs are increasingly used in geoprocessing and biogeography projects for mapping areas with a high risk of biological invasions (Johovic et al. 2020, Zhao et al. 2021), by identifying high suitability areas for the modelled species. ENM associates biogeographic and climate data with species distribution to predict suitable areas for species occurrence (Elith et al. 2011, Radosavljevic & Anderson 2014).

In ENM, MaxEnt is the most widely used algorithm due to its high predictive capacity and ability to reduce sample biases. It uses background points based on the principle of maximum entropy to make predictions from incomplete or insufficient information, justifying its use in modeling with a large projection area (Yackulic et al. 2013). Recent studies have used MaxEnt to review species pseudo-absences and found it to be more robust and effective than other methods (Phillips et al. 2006, Barbet-Massin et al. 2012). Species distribution models based on ecological niche determination have proven to be helpful in environmental research and decision-making, especially in identifying priority areas for conservation (Capinha et al. 2011). Therefore, the aims of this study were: i) model the ecological niche of five non-native species of freshwater decapods in South America: *D. pagei*, *M. amazonicum*, *M. jelskii*, *M.*

rosenbergii and *P. clarkia*; ii) determine the extent of suitable habitats areas for the occurrence of those species in South America.

2.3. METHODS

2.2.1. Study Area

South America subcontinent has a roughly triangular shape, being widest towards the north where it extends over 5,000 km from east to west just south of the Equator, and tapering southward (Orme, 2007). Three-quarters of South America are located within tropical latitudes and under the influence of the Intertropical Convergence Zone and related circulation systems, creating diverse patterns of weather, climate, and climatic variability. Further north, there is no such barrier and moist surface winds from the equatorial Atlantic attracted by deep seasonal convection over Amazonia, penetrate far inland toward the Andes, bringing much cloud and rain to the foothills of the Eastern Cordillera (Orme, 2007). Three large freshwater basins dominate the South American continent: Amazon, Orinoco and Paraná-Paraguay (also known as La Plata), and four structural elements are relevant to the form and behavior of these three large basins: (1) the Andes; (2) foreland basins in the east of the Andes to southward from the mouth of the Orinoco to the Chaco-Paraná basin and (3) the Guiana and Brazilian shields reflecting Precambrian cratons and orogenic belts of metamorphic rocks; (4) the Central Amazon Basin, a large cratonic downward with some graben structures dating back to early Paleozoic era, connecting the foreland basins to the west with a graben that localizes the Amazon estuary at the Atlantic coast (Dunne & Mertes, 2007).

2.3.1. Species selection

The study focuses on five freshwater decapod species that have high potential for invasion in South America, including the already invasive *Procambarus clarkii* and *M. jelskii*,

which cause negative impacts such as predation and competition with native species (Magalhães et al. 2005, Anastácio et al. 2009, Capinha et al. 2011, Palaoro et al. 2013, Vera-Silva et al. 2016), and *D. pagei*, *M. rosenbergii* and *M. amazonicum*, classified as non-native species but with great potential for invasion (Taddei & Herrera 2010, Anger 2013, Iketani et al. 2016).

Dilocarcinus pagei is a freshwater crab with a high osmoregulation capacity and resistance to different environments, potentiating the possibility of it becoming an invasive species (Augusto et al. 2007). Although native to the Amazon region, as well as *M. jelskii* and *M. amazonicum*, there are no records of this species being cultivated for economic and commercial purposes. The apparent lack of commercial interest may decrease the likelihood of deliberate introductions in new regions. However, accidental introductions through the transport of fish or macrophytes could explain the presence of this species in the Paraná River basins, Pantanal, and other regions in South America (Magalhães et al. 2005, Taddei & Herrera 2010).

Macrobrachium amazonicum is a species native to the Amazon region, with its natural distribution in the hydrographic basin of the Amazon and Orinoco River (Holthuis, 1952, Rodriguez 1982). This species is notable among the genus *Macrobrachium* because it can inhabit inland areas, not being limited to coastal and estuarine regions (Anger 2013). It is considered the shrimp species with the greatest potential for commercial cultivation in the region, which increases the possibility of it being introduced outside of its native area (Kutty et al. 2000).

Macrobrachium jelskii has habitat and morphological characteristics very similar to those of *M. amazonicum*. However, its distribution is more restricted to coastal areas from Venezuela to Bahia and Espírito Santo states in Brazil. It does not adapt as easily to inland waters as *M. amazonicum*, although there are occasional records of this species in the interior

of the subcontinent, such as in Brazil (Minas Gerais and São Paulo States) and Bolivia (Melo 2003, Magalhães et al. 2005).

Macrobrachium rosenbergii is a freshwater shrimp native to inland waters of the Indo-Pacific region and widely distributed in India, Vietnam, and Indonesia (New 2000). It was introduced in South America in the mid-1980s in the Amazon region, and in recent years, concerns have been raised about its potential impacts (Instituto Chico Mendes de Conservação da Biodiversidade – ICMBIO 2019, FAO-DIAS, 2022). There are occasional records of this species in northeastern Brazil (Gurupi and Parnaíba Rivers) and the Paraná River basin near Argentina’s border (Loebmann et al. 2010, Silva-Oliveira et al. 2011, Silva et al. 2020).

Procambarus clarkii is a crayfish native to North America, widely distributed in northern Mexico and the south-central of the United States (Huner 1988). While there are few records of this species in South America, its presence in Colombia and in São Paulo State (Brazil) may signal its invasive potential (Silva & Bueno 2005, Camacho-Portocarrero et al. 2021).

2.3.1. Species presence data

For the systematic review in order to compile data of the presence of five species, four article databases were used – *Web of Science* (www.webofscience.com 2021), *Scopus* (www.scopus.com 2021) *Scielo* (<https://www.scielo.br> 2021), and *Aquatic Science and Fisheries Abstract* (ASFA, proquest.libguides.com/asfa 2021). The same search term was used across all databases: “(*Procambarus* OR *Macrobrachium* OR *Dilocarcinus*) AND (31stuary* OR wetland* OR mangrove* OR freshwater OR “aquatic environment” OR “aquatic ecosystem*” OR lake* OR river* OR pond* OR reservoir* OR “drainage basin*” OR lagoon* OR “river basin*” OR stream* OR waterfall* OR watercourse* OR brook* OR creek*)”. All peer-reviewed articles published in any language from 1945 to January 29th, 2021, were used in this review. The year 1945 was chosen as the earliest possible date on the platforms, and

January 29th, 2021, was the date of the search. All articles found in the four databases search were exported to a .RIS file, classified, and duplicates were removed using EndNote Program (version x9.3.2) (The EndNote Team, 2022). Articles without duplicates were exported to Microsoft Excel (Microsoft Corporation 2018) for application of the inclusion and exclusion criteria, i.e., articles with species occurrence records including geographic coordinates are included. Articles without geographic coordinates but with location descriptions were separated and later georeferenced using the Google Earth website (earth.google.com/, 2022). Experimental studies with captive animals, laboratory or aquaculture tanks, reports, scientific notes (except new species records), pre-prints, and book chapters were not included in the screening. The remaining occurrences were collected from the records published in the *Global Biodiversity Information Facility* (GBIF 2022) database. All articles selected in the data screening are listed in supplementary material 1 (SM1). A PRISMA matrix (Moher et al. 2009) was generated to provide a better visualization of the results and to detail the occurrence data collection. The main records were those found through the systematic review of the literature, while additional records were obtained from GBIF occurrences.

2.2.4. Niche modeling and variables selection

The occurrence data of selected species were statistically combined with biogeographical predictor variables extracted from *WorldClim* (worldclim.org 2022) and *EarthEnv* (earthenvi.org 2022) databases to predict the species' suitable niche based on the selected environment (Elith & Leathwick 2009). As *EarthEnv* variables are only available at a resolution of 30 arc-second resolution (1 km) and *Worldclim* variables at a resolution of 2.5 arc-minute resolution (4,5 km), we used the “raster package” (Hijmans 2022) on R-program (4.1.2 version) (R Core Team 2022) and the QGIS program (3.16.16 version) (QGIS Development Team 2022) to standardize all predictor variables to approximately 5 km². The

variables for South America were cropped using the “tidyverse” (Wickham et al. 2018) and “rnatuarearth” (South 2017) packages of the R program.

The EarthEnv data is available in high resolution for rivers and lakes and shows monthly average values over each water body (Domisch et al. 2015, Egly et al. 2021). However, for large lakes where conditions can be highly variable, the raster presents a single value that does not adequately cover the range of environmental conditions and habitats available for freshwater environments. To address this issue, the 19 Worldclim bioclimatic variables were also added in the modeling. This approach has been previously used in modeling studies for various non-native or invasive species (Gama et al. 2016, Johovich et al. 2020, Low et al. 2021).

The EarthEnv variables were selected based on the species’ biology, therefore hydroclimate, topography, flow, and precipitation were used. All variable layers were extracted from netCDF-4 files available on the EarthEnv platform and were clipped to the same extension and resolution as the Bioclimatic variables. Once standardized, the variables were included in the same dataset, totaling 60 predictor variables from both databases (SM2). After including these layers into a single dataset, multicollinearity between the variables was assessed using the Variance Inflation Factor (VIF) in the “USDMM” package (Naimi et al. 2014) of the R-program. Finally, highly correlated variables were excluded from the niche modeling, with the default cutoff set at greater than or equal to 10 to avoid collinearity in statistical models (Naimi et al. 2014).

2.2.5. Modeling protocol

All occurrence records of the selected species were filtered to ensure unique coordinates and exclude problematic points, such as those in oceans, biased towards large institutions, capitals, centroids, redundant data, and duplicates. To further remove any sampling

and spatial biases that could negatively impact model construction, the “spThin” package was used (Aiello-Lammens et al. 2019). To perform niche modeling for the five decapods species, predictive variables for the entire globe were selected in the same way as the occurrence records. The South American subcontinent was then selected by performing a cut.

The niche modelling for all species was carried out based on their respective native regions and projected onto the area of interest. For example, to perform niche modeling of *P. clarkii*, the model was built using North America and projected onto South America. Likewise, the niche modelling for *M. rosenbergii* was performed for the entire Asian continent and projected onto South America. This approach aims to minimize spatial sampling bias and avoid overfitting of the models, which can occur when using species records from the entire globe. In this sense, a more reliable and realistic model is expected.

Models were evaluated using the area under the ROC (*receiver operating characteristic*) curve (AUC) and the *true skill statistics* (TSS). AUC values range from 0 to 1, with values of 0.9-1 considered excellent and 0.8-0.9 considered good. TSS values are threshold-dependent and can range from -1 to +1, with positive values ranging from 0.2 to 0.5 considered poor, from 0.6 to 0.8 considered useful, and values greater than 0.8 considered excellent (Coetzee et al. 2009, Peterson & Soberón 2012).

Random selection of pseudo-absence points was used (Thuiller et al. 2021) as it was observed that these algorithms tend to perform better because they manage to reduce the spatial bias and select points where the species have low suitability for occurrence (Barbet-Massin et al. 2012). In this sense, the number of pseudo-absences was standardized for each species to reduce this bias further, since an insufficient or excessive number of pseudo-absences can generate over-prediction models, which produce maps with either very high suitability for the species or with no biological sense. Thus, the models were run using 10 replicates of each randomly generated pseudo-absences set with the default number of 1000 pseudo-absences for

all species. Records were entered using a 2.5 arc-minutes resolution for South America and randomly divided into test and training, using 20% and 80% of the data, respectively, according to Thuiller's proposal (Thuiller et al. 2009).

The nine algorithms selected from the Biomod2 package were: *generalized linear models* (GLM) (Guisan et al. 2002), *generalized boosted models* (GBM) (Elith et al. 2008), *generalized additive models* (GAM) (Guisan et al. 2002), *classification tree analysis* (CTA) (Vayssières et al. 2000), *artificial neural networks* (ANN) (Lek & Guégan 1999), *surface range envelope* (SRE) (Nix & Busby 1986), *flexible discriminant analysis* (FDA) (Hastie et al. 1994), *multivariate adaptive regression spline* (MARS), (Friedman 1991) and *random forest* (RF) (Breiman 2001). These algorithms generated predictions using the default settings of the Biomod2 model (Deka & Morshed 2018). Individual predictions were then averaged to create an ensemble approach, with the four algorithms showing the best performance selected based on the average TSS and AUC values for all species. The four highest means of the TSS individual algorithm, with a cutoff value of 0.7, and the four highest means of the AUC individual algorithm, were selected to produce the final ensemble approach (Marmion et al. 2009).

According to Sillero & Barbosa (2021), it is not recommended to create an ensemble model by combining different modeling techniques. In this sense, we created a parallel model to MaxEnt that uses background data as absence data. This model was created using the "SDM" package (Naimi & Araújo 2016) and default settings of 10000 background points (Phillips et al. 2006). The modeling was performed at a resolution of 2.5 arc minutes and divided randomly into test and training subsets, with 20% and 80%, respectively, similar to the Biomod2 package. We identified the contribution of each variable to the model for each species using the default settings of the Biomod2 package and SDM, which selects variables using Pearson's Correlation. We generated suitability maps by combining the means of each generated model

using the four best-performing algorithms according to the TSS value for the ensemble (Marmion et al. 2009). AUC values were also considered for algorithm selection, and only algorithms with AUC greater than 0.8 were selected for the ensemble. The models used were classified as good or excellent (Dakhil et al. 2019, Freitas et al. 2019). The dataset of the models was grouped into a single map through the “raster” and “terra” packages (Hijmans et al. 2022) in R. For each species, we calculated the total suitability area using the field calculator and the *GRASS GIS r.class* tools (Westervelt & Shapiro 2022) in QGIS, with a cut-off point above 0.75. Finally, priority areas with a high risk of invasion were defined by superimposing the suitability areas of each species on the Protected Areas (Pas) and Watersheds shapefile layers, available in the databases of the International Union for Conservation of Nature (IUCN 2021).

2.3. RESULTS

2.3.1. Species presence data

The systematic review of the literature resulted in 10,850 articles from the four databases, obeying all inclusion criteria and search terms. After removing the duplicates using Endnote, 9,597 unique articles that were exported to Microsoft Excel. Further screening excluded 8,592 articles that did not meet the inclusion criteria, leaving 1,005 articles that contained species locations. After the final screening step, which removed duplicate coordinates and papers with identical locations, there were 551 articles remaining. The systematic review data is presented in the PRISMA flow diagram (figure 1).

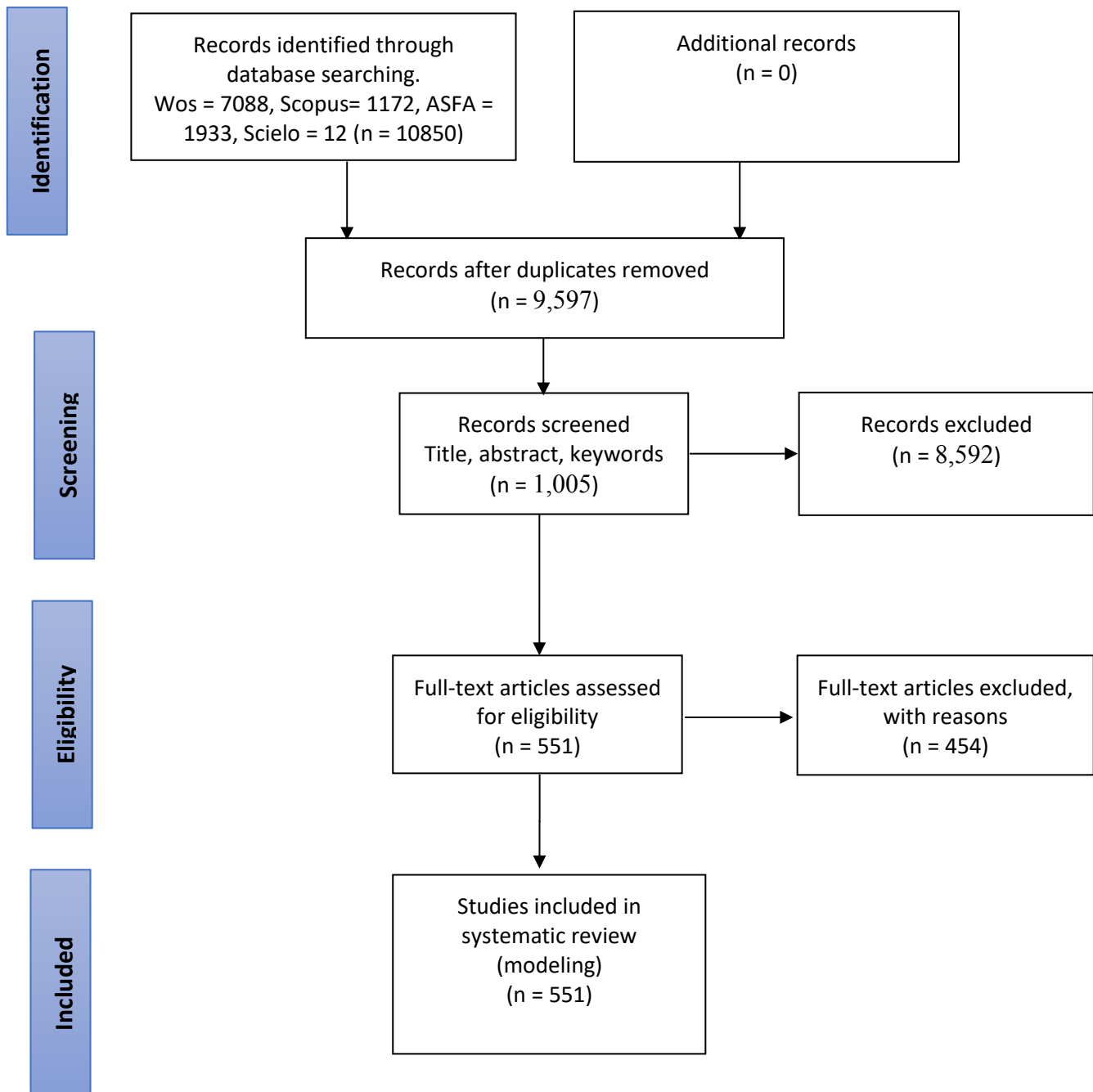


Figure 1: Flowchart of the PRISMA Matrix referring to the systematic literature review process. Adapted from Moher et al. (2009, PRISMA Group). GBIF (Global biodiversity information facility); gbif.org, accessed on 2021 March. Of the 551 articles returned by the systematic review, 1367 species occurrence data (geographical coordinates) were extracted.

Through the literature review, we found approximately 20% more occurrence records compared to those obtained through GBIF (n = 6,801). In total, we recorded a total of 1,367 occurrences which were included in the occurrence records spreadsheet. Out of these records, there were 42 unique coordinates for *D. pagei*, 213 for *M. amazonicum*, 116 for *M. jelskii*, 105 for *M. rosenbergii*, and 908 for *P. clarkii*. The considerable increase in records of occurrences, obtained through the systematic review of the literature, can be observed in the maps of Figure 2 and 3, resulting in better performance of the models as the number of occurrences increased.

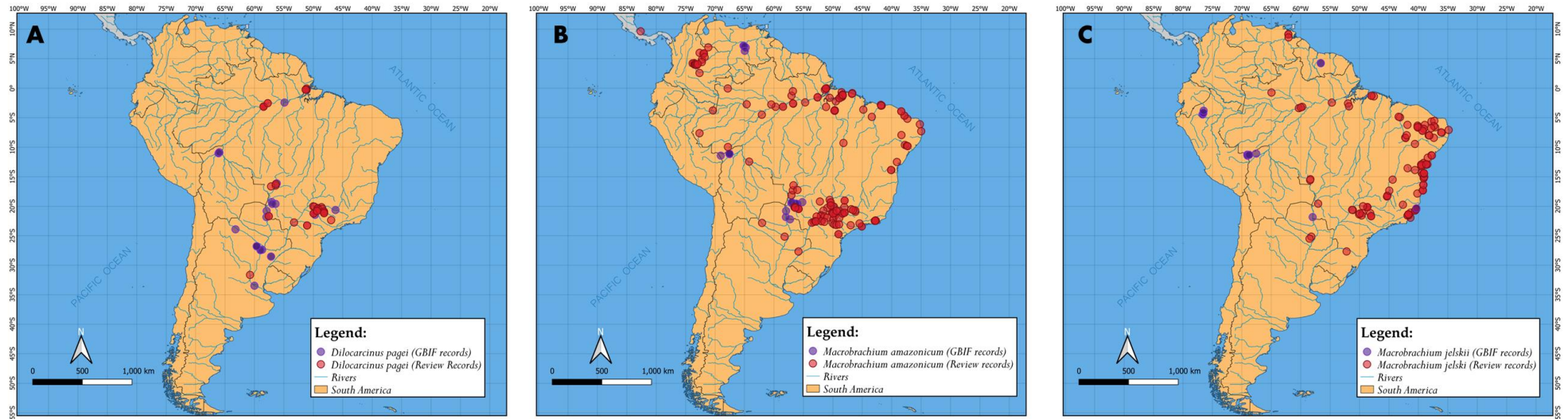


Figure 2: Occurrence maps of species. In red: are points obtained by the systematic review. In purple: points obtained by the Global Biodiversity Information Facility database, *Dilocarcinus pagei* (A) points obtained by the systematic review (n = 42). Points obtained by GBIF database (n = 20); *Macrobrachium amazonicum* (B) points obtained by the systematic review (n = 213); Points obtained by GBIF database (n = 24) and *Macrobrachium jelskii* (C) points obtained by the systematic review (n = 19); Points obtained by GBIF database (n = 116).

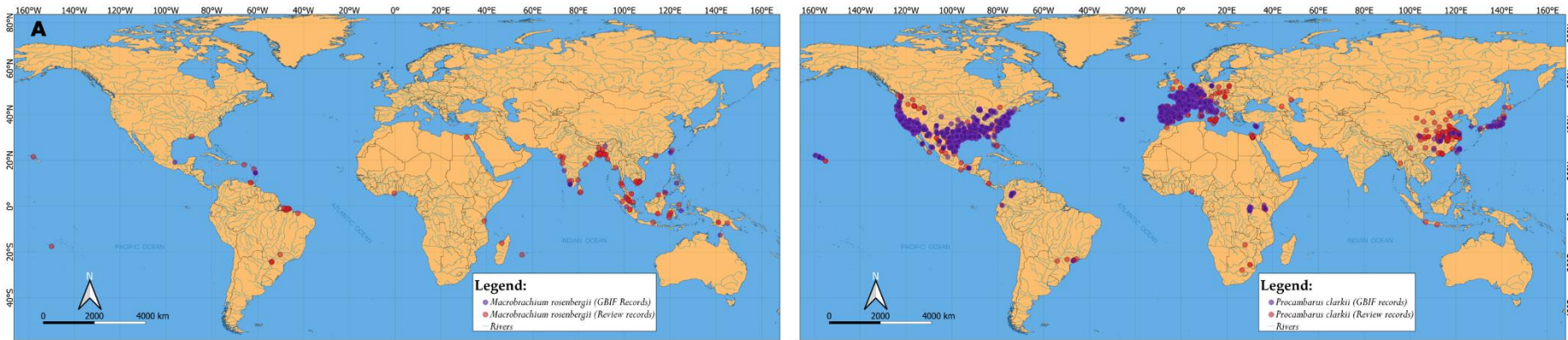


Figure 3: Global occurrence maps of species. In red: are points obtained by the systematic review. In purple: points obtained by the GBIF database. *Macrobrachium rosenbergii* (A) points obtained by the systematic review (n = 116). Points obtained by GBIF database (n = 20) and *Procambarus clarkii* (B) points obtained by the systematic review (n = 908). Points obtained by GBIF database (n = 5481).

2.3.2. Niche modeling

All the variables selected (bioclimatic, hydrological, topographic, flow, and precipitation) by VIF to create the ENM for each species are listed in the table provided in Supplementary Material 2 (SM2). Despite the exclusion of many predictor variables, the only common variable among all five species after VIF selection was the sum of monthly precipitation in November (prec11). The other variables that were present in at least four of the five species were minimum elevation (Elev1), precipitation of warmest quarter (BIO18), and the average diurnal interval for hydrological variables (hydro2) (Table 1).

The temperature and precipitation variables had a significant influence on the most important predictor variables for constructing the models for each species (Table 1), with the terrestrial variables of *WorldClim* being important for all species. Additionally, precipitation, elevation, and hydrology were important for at least one species. We also note the November precipitation variable (prec11) which was selected by VIF for all species in the present study (SM2) but was not considered as the three most important variables (Table 1).

Table 1: Average of variables' importance for the construction of the models of each species calculated by Pearson's correlation. *P. clarkii* = *Procambarus clarkii*, *D. pagei* = *Dilocarcinus pagei*, *M. rosenbergii* = *Macrobrachium rosenbergii*, *M. jelskii* = *Macrobrachium jelskii*, *M. amazonicum* = *Macrobrachium amazonicum*.

bio1 = Annual Mean Temperature, **bio4** = Temperature Seasonality, **bio8** = Mean Temperature of Wettest Quarter, **bio9** = Mean Temperature of Driest Quarter, **bio13** = Precipitation of Wettest Month, **bio14** = Precipitation of Driest Month, **bio18** = Precipitation of Warmest Quarter, **prec2** = Sum of monthly precipitation February, **prec5** = Sum of monthly precipitation May, **prec7** = Sum of monthly precipitation July, **hydro2** = Mean Diurnal Range, **hydro9** = Mean Temperature of Driest Quarter, **hydro14** = Precipitation of Driest Month.

Species	Variable importance		
<i>M. amazonicum</i>	hydro14 (0.26)	bio4 (0.25)	hydro2 (0.18)
<i>D. pagei</i>	bio14 (0.41)	bio8 (0.39)	bio18 (0.27)
<i>M. jelskii</i>	prec5 (0.55)	hydro2 (0.49)	bio9 (0.45)
<i>P. clarkii</i>	bio1 (0.49)	prec7 (0.12)	prec2 (0.07)
<i>M. rosenbergii</i>	bio13 (0.31)	hydro9 (0.24)	bio8 (0.2)

Table 2 display the mean TSS and AUC values for each algorithm used in the modeling performed with the “Biomod2” (Thuiller et al. 2021) and “sdm” (Naimi & Araújo 2016) packages. The algorithms with the highest mean TSS and AUC values were RF (0.86) and (0.96), GBM (0.82) and (0.95), GAM (0.77) and (0.92), and GLM (0.76) and (0.90), respectively. The other algorithms (SRE, CTA, MARS, FDA, and ANN) that were considered less predictive by the model evaluation were not included in the ensemble.

Table 2: Mean AUC and TSS for each algorithm used in the niche modeling of the species *M. rosenbergii*, *P. clarkii*, *M. jelskii*, *D. pagei*, and *M. amazonicum*. With asterisk (*) the final mean only with the algorithms selected for the ensemble. The algorithms that were selected for the ensemble are highlighted in bold. (**) The MaxEnt algorithm was generated separately and was not part of the ensemble. GLM = *generalized linear models*, GBM = *Generalized Boosted Models*, GAM = *generalized additive models*, CTA = *classification tree analysis*, ANN = *artificial neural networks*, SER = *surface range envelope*, FDA = *flexible discriminant analysis*, MARS = *multivariate adaptive regression spline*, RF = *random forest*. *P. clarkii* = *Procambarus clarkii*, *D. pagei* = *Dilocarcinus pagei*, *M. rosenbergii* = *Macrobrachium rosenbergii*, *M. jelskii* = *Macrobrachium jelskii*, *M. amazonicum* = *Macrobrachium amazonicum*.

Algorithm	<i>D. pagei</i>		<i>M. amazonicum</i>		<i>M. jelskii</i>		<i>M. rosenbergii</i>		<i>P. clarkii</i>	
	TSS	ROC	TSS	ROC	TSS	ROC	TSS	ROC	TSS	ROC
SRE	0.52	0.76	0.42	0.71	0.27	0.64	0.44	0.72	0.51	0.76
CTA	0.60	0.78	0.60	0.71	0.65	0.84	0.80	0.91	0.83	0.94
RF	0.85	0.94	0.82	0.95	0.83	0.95	0.89	0.97	0.89	0.98
MARS	0.76	0.90	0.73	0.92	0.71	0.90	0.81	0.94	0.80	0.96
FDA	0.64	0.84	0.68	0.89	0.69	0.89	0.81	0.92	0.80	0.96
GLM	0.76	0.84	0.71	0.91	0.76	0.85	0.79	0.93	0.81	0.95
GBM	0.83	0.95	0.79	0.94	0.78	0.93	0.87	0.97	0.85	0.97
GAM	0.71	0.90	0.77	0.92	0.77	0.90	0.77	0.89	0.84	0.97

	<i>D. pagei</i>		<i>M. amazonicum</i>		<i>M. jelskii</i>		<i>M. rosenbergii</i>		<i>P. clarkii</i>	
Algorithm	TSS	ROC	TSS	ROC	TSS	ROC	TSS	ROC	TSS	ROC
ANN	0.72	0.88	0.53	0.80	0.54	0.79	0.70	0.86	0.74	0.89
MaxEnt**	0.73	0.84	0.82	0.94	0.72	0.94	0.77	0.93	0.75	0.94
Mean*	0.80	0.90	0.77	0.93	0.79	0.91	0.82	0.93	0.85	0.97

The suitability maps for all species created by MaxEnt are displayed in figure 4. All models generated by MaxEnt had good performances, as indicated by their AUC and TSS values, with values above 0.9 and 0.7, respectively, except for *D. pagei*, which presented an AUC value of 0.84. Nevertheless, this still represents a useful predictive model (table 2). The ensemble maps created by Biomod2 also presented excellent performance, based on the averages AUC and TSS values, as shown in Figure 5. All species had AUC values greater than 0.9, with *D. pagei* having slightly lower values in some algorithms, but still with an excellent average of 0.9. The algorithms presented varied TSS values, but all had an average above 0.7.

The ensemble result maps with niche suitability areas are shown in Figure 5 (A-E). *Dilocarcinus pagei* (figure 5A), and *M. amazonicum* (Figure 5B) suitability maps were very similar, overlapping in almost the same hydrographic basins in the central region of South America. The areas of greatest suitability are in the La Plata basin, in Brazilian territory and the middle portion of the Uruguay-Brazil basin and the Amazon River basin. The *M. jelskii* suitability map (Figure 5C) showed its greatest suitability zones close to the Brazilian coast that correspond to East Brazil, South Atlantic Coast and Uruguay-Brazil, South Atlantic Coast River basins. Finally, the niche models for *M. rosenbergii* (Figure 5D) and *P. clarkii* (figure 5E) showed excellent performance with the largest areas of suitability among all species. The areas of greatest suitability are in mainly in the Southern South America (La Plata River basin). More than 1.9 million Km² of South American territory have a suitability greater than 0.75 for *P. clarkii*, while 953,640 Km² of South American territory is suitable for *M. rosenbergii* (Table 3).

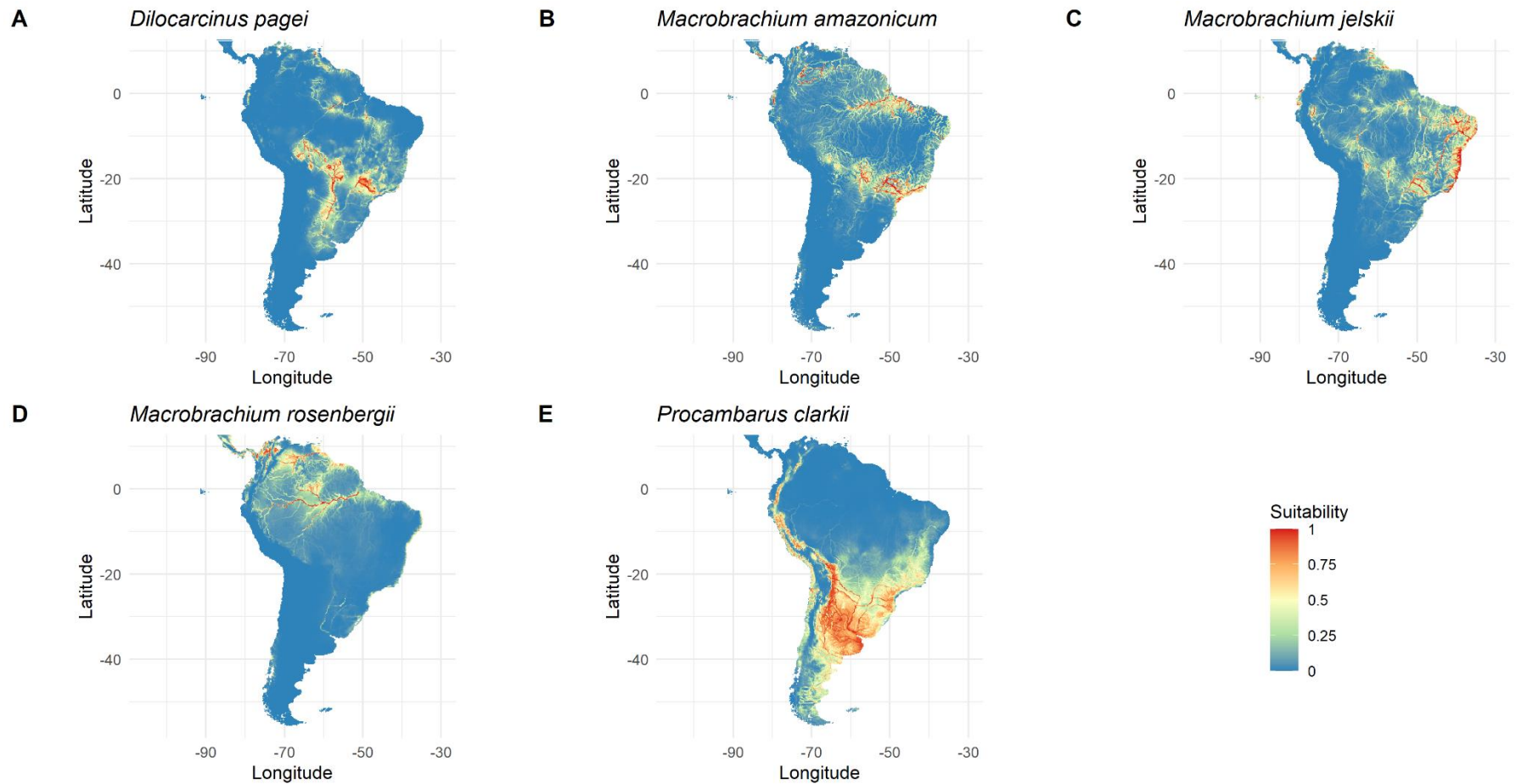


Figure 4: Suitability maps generated by the MaxEnt algorithm for each species A) *Dilocarcinus pagei*, B) *Macrobrachium amazonicum*, C) *Macrobrachium jelskii*, D) *Macrobrachium rosenbergii*, E) *Procambarus clarkii*.

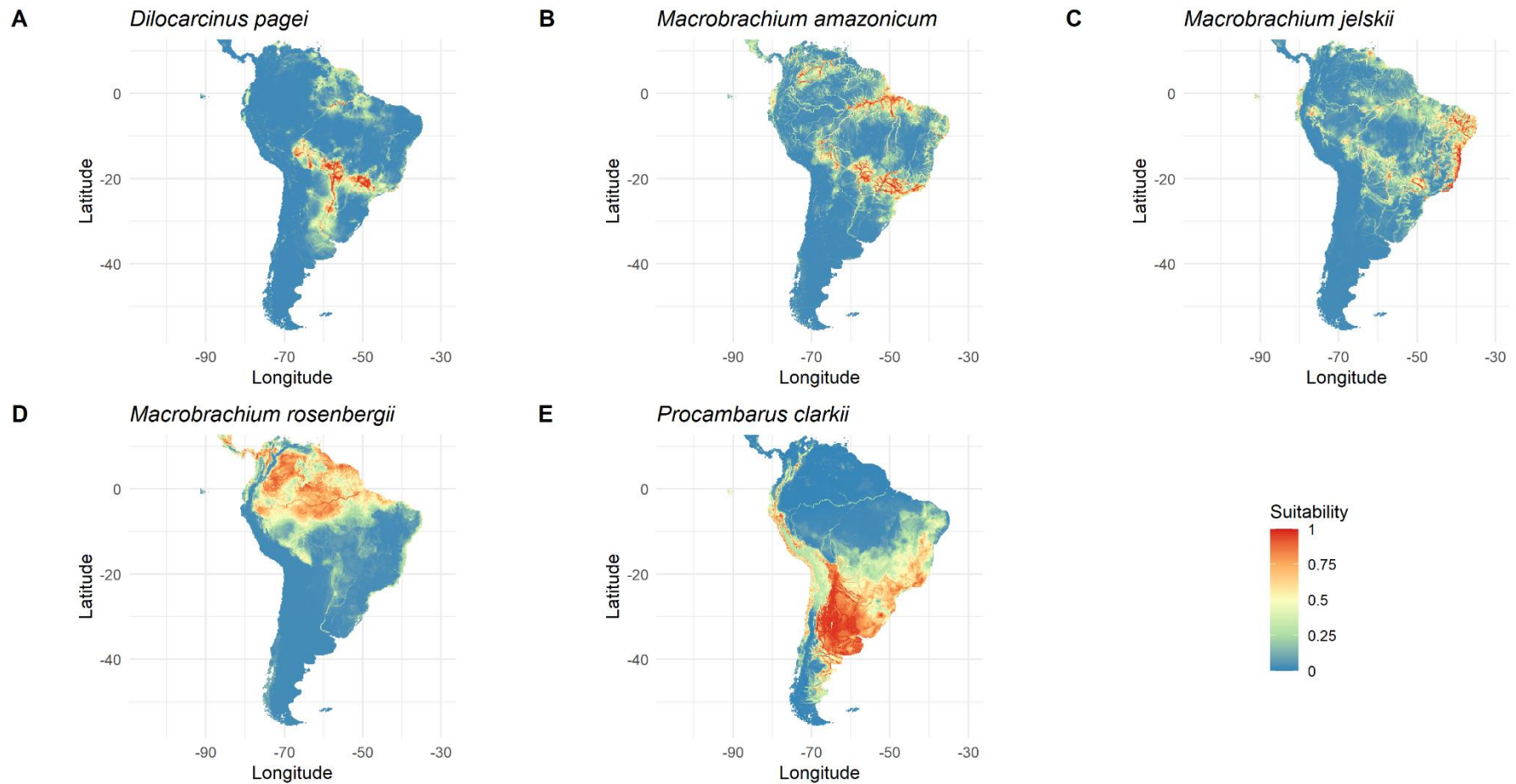


Figure 5: Suitability maps generated by the ensemble of the GLM, GBM, GAM, and RF algorithms for each species A) *Dilocarcinus pagei*, B) *Macrobrachium amazonicum*, C) *Macrobrachium jelskii*, D) *Macrobrachium rosenbergii*, E) *Procambarus clarkii*.

Table 3: Suitability area for each species modeled in square kilometers (Km²) and the percentage relative to the territory of South America occupation. *P. clarkii* = *Procambarus clarkii*, *D. pagei* = *Dilocarcinus pagei*, *M. rosenbergii* = *Macrobrachium rosenbergii*, *M. jelskii* = *Macrobrachium jelskii*, *M. amazonicum* = *Macrobrachium amazonicum*

Species	Ensemble		MaxEnt	
	Suitability area (Km ²)	Suitability area (%)	Suitability area	Suitability area (%)
<i>D. pagei</i>	315,772.00	1.78	219,116.00	1.24
<i>M. amazonicum</i>	528,434.00	2.99	282,224.00	1.59
<i>M. jelskii</i>	313,870.00	1.77	280,939.00	1.59
<i>M. rosenbergii</i>	953,640.00	5.39	171,715.00	0.97
<i>P. clarkii</i>	1,962,112.00	11.09	846,132.00	4.78

Thus, we highlight all the PAs and the main watersheds, susceptible to invasion, as priority areas for conservation and is shown on Supplemental Material 3 (SM3). This areas were defined which were defined by overlapping the IUCN layers of PAs and hydrographic basins for South America with the areas of suitability greater than 75%, extracted from the maps of fitness of the five species modeled for this study.

2.4. DISCUSSION

2.4.1. Suitability of areas to species invasion

The species that attracted the most attention in terms of high potential for invasion was *M. amazonicum*, out of the three species that occur naturally in South America. This species is the most commercially exploited among the *Macrobrachium* species (Kutty et al. 2000), and the results of the study highlight the urgent need for management strategies. Our results indicate that a large area ($\pm 3\%$ of the entire territory of South America) is suitable for the occurrence of *M. amazonicum*. This area overlaps with several watersheds in the Southeast Region of Brazil and areas close to the Mato Grosso Pantanal, which also includes regions of Paraguay and Argentina (Pettovello 1996), as well as areas of environmental protection.

The species that showed the greatest suitability area were *P. clarkii* and *M. rosenbergii*, with $\sim 11\%$ and 6% of the total South American territory being suitable for these species, respectively. *Procambarus clarkii* is a well-studied species that is ecologically and economically important. As a result, numerous modeling studies have been conducted to predict its invasive potential in both present and future scenarios, with global or regional projections. These studies have results similar to those presented in our study (Capinha et al. 2011, Palaoro et al. 2013, Zhang et al. 2020a). In addition, a study in Mexico has demonstrated that *P. clarkii* can overlap habitats with native freshwater shrimp belonging to the genus *Macrobrachium*, resulting in significant impacts on the community of these species

(Hernández et al. 2008). However, no affected organisms or impacts resulting from the presence of *P. clarkii* in South America have yet been described. Nevertheless, due to its great invasive potential, the presence of this species in aquatic ecosystems is a cause for concern (Moraes-Valenti & Valenti. 2007; Maciel & Valenti, 2009).

For *M. rosenbergii*, little is known about the effects of introducing this species in South America, although evidence of invasions and impacts on native species on almost all continents (Iketani et al. 2016). The Amazon region requires particular attention and containment strategies due to the Amazon Forest domain and nearly the entire Amazon River and Orinoco basin. Several native species occur in this region, including the native range of three of the five species studied in this study, as well as others with great ecological importance for the Amazon freshwater ecosystems. The primary cause of escape and establishment of *M. rosenbergii* in non-native environments is the lack of monitoring and maintenance of culture tanks (Iketani 2011), and all impacts discussed in the literature have only described on other continents. This serves as a warning for a possible long-term biological invasion of *M. rosenbergii* in South America. Additionally, native species are at risk of competition for food and resources since *M. rosenbergii* can tolerate diverse environmental conditions (Silva-Oliveira et al. 2011).

The suitable areas modelled for *M. jelskii* were limited to regions near the Brazilian coast, which may prevent the species from colonizing limiting factor for possible colonization within the continent, being a natural impediment to the advancement of the species. However, the species has been found in interior regions, indicating that its ecological plasticity may allow for successful colonization in new areas. Anthropogenic actions, may be the main cause of the introduction of this species outside the Amazon region, as is the case for *M. amazonicum* and *D. pagei*. However, little is known about the biology and ecology of these species and it is imprecise to calculate the impacts caused outside its natural distribution (Latini et al. 2016).

The presence of this species in coastal and estuarine regions within the Atlantic Forest domain, which includes several biological reserves, PAs, RPPN and Integral Protection Areas, raises concerns about its spread in South America. Although some authors consider *M. jelskii* an invasive species, the lack of studies demonstrating impacts makes this statement questionable (Magalhães et al. 2005, Latini et al. 2016, da Silva et al. 2018).

2.4.2. Niche modeling

The MaxEnt algorithm was used to generate models of the ecological niche for different species, with AUC values above 0.9 indicating good suitability areas, which were compared to models generated by other algorithms (Peterson & Soberón 2012). However, TSS values were lower for some species, with only *M. amazonicum* having TSS values above 0.8. The ensemble of the best models generated by the different algorithms was used to select the best models for each species, resulting in AUC means above 0.9 for all species. *P. clarkii* had the highest TSS and AUC values due to a higher number of presence records. Sampling biases and noise were minimized with systematic reviews, which contributed to the species occurrence data by increasing the sample universe and reducing spatial bias (Sillero & Barbosa 2021). Terrestrial variables, especially bioclimatic and topographic variables, were used to build the models. The lack of more accurate data for freshwater ecosystems makes the use of terrestrial variables advisable. However, for large extensions such as a country or continent, predictors with high enough resolution and global scale are needed (Domisch et al. 2015, Friedrichs-Manthey et al. 2020).

The use of MaxEnt and Biomod2 algorithms brought relevant information to the present work because even using two different modeling tools, the results were similar, both in the suitability maps and in the model evaluation, both with excellent results according to the literature. However, the differences observed in the models of suitability generated by the

MaxEnt algorithm and by the ensemble are due to the difference in sensitivity and performance of the algorithms, which does not influence the quality of the model (Saupe et al. 2012, Zhang et al. 2015). While the study provides new information on the potential niche of exotic and invasive species, further research is needed to better understand their distribution in Brazil. Future work should focus on collections and fieldwork in high-risk areas to verify whether they are already colonized, as well as projecting future results in conjunction with climate change data to gain more accurate information about species expansion.

Few studies used the overlapping of terrestrial and aquatic predictor variables simultaneously, especially when referring to crustaceans (Egly et al. 2018, Zhang et al. 2020b). In this sense, by concomitantly associating terrestrial variables and aquatic variables as a single set of predictive variables, we managed to build a more robust model capable of mitigating the inherent deficits of each database, being the first work that modeled crustacean species associating the WorldClim terrestrial bioclimatic variables and EarthEnv aquatic variables.

Another point that corroborates our results was that the training models, using only WorldClim data, presented results that were overfitted or without biological meaning and, when designed for the interest region, presented a low performance. Something similar occurred in Low et al. (2021) who also obtained low predictive capacity. However, when associating the WorldClim variables with the IPCC predictive variables, which allowed contrasting the biases of the two variables, they exhibited greater environmental similarity between the training areas and testing, resulting in predictions with better performance. Some studies managed to predict the invasive capacity of some species, including *P. clarkii*, by associating the Worldclim predictor variables with the aquatic variables available in the United States Great Lakes database (Egly et al. 2019, Kovalenko et al. 2018). While (Lodge et al. 2016) showed that new SDM tools, including EarthEnv's unique freshwater variables, are estimating invasion probability with increasing accuracy, especially when combining local

habitat data. However, it is almost unanimous that the characterizations of freshwater conditions available in the databases are still primitive and with many limitations that need improvement until more accurate data appear to make the ENM even more robust. This condition still makes the aquatic species ENM dependent on terrestrial variables (Domish et al. 2015, Jetz et al. 2019).

The contribution of precipitation variables to the model construction was significant for all species, as it aligns with the reproductive cycle and favorable environments for larval development. The rainy season, particularly from November to March, is correlated with the reproductive peak for some species like *M. jelskii* (Barros-Alves et al. 2012, Mussolin et al. 2013). High precipitation leads to a decrease in salinity, favoring embryonic development and larval growth, while dry seasons result in higher salinity and, in turn, favoring reproduction in some species. The importance of precipitation variables in the models was further supported by studies showing the positive relationship between rain volume, nutrient input and decreases the salinity. (Lal et al. 2012, Boudour-Bouchecker et al. 2013, Guimaraes, 2014, Soeiro et al. 2016). In contrast, in the dry season, salinity is higher, favoring reproduction in these periods, resulting in high production of eggs throughout the year in most species (Fukuda et al. 2016). This factor corroborates the precipitation variables of the driest month (bio14 and hydro14) that were the most important for the *D. pagei* and *M. amazonicum* models, respectively.

The reproductive physiology of decapods is directly affected by air and water temperature, as they promote the growth of gonadal tissues (Adiyodi & Adiyodi 1970, Wear, 1974, Gamba 1997). In addition, the average diurnal interval (Hydro2), which analyzes the fluctuation of the maximum and minimum water temperature throughout the year, was important in the construction of the models of *M. jelskii* and *M. amazonicum*. Studies with *M. amazonicum* and other species of the *Macrobrachium* reinforce that this temperature fluctuation can directly influence the number of individuals (Collart & Moreira 1993,

Mantelatto & Barbosa 2005). Finally, the average temperature of the warmest quarter (bio8) was important for the construction of the models of *M. rosenbergii* and *D. pagei*. Thus, the period of the year with the highest temperatures and, consecutively, the highest precipitation rates, allows the decapod species to have more reproductive success, and these variables are important for their ecological niche definition.

3. CONCLUSION

Our results demonstrated that the Southeast Region of Brazil and the Pantanal are particularly vulnerable to invasion by freshwater decapods species. In addition, our study underscores the importance of conservation and preservation of vulnerable habitats, particularly those located within Biological Reserves and Protected Areas, to prevent colonization by invasive species. However, we believe that our findings can inform efforts to protect aquatic and terrestrial biodiversity and guide the development of conservation and management measures to mitigate the risks of invasion and promote sustainable development.

REFERENCES

- Adiyodi, K. G. & Adiyodi, R. G. 1970. Endocrine control of reproduction in decapod crustacea. *Biological Review* 45:121-165.
- Aiello-Lammens, M.E., et al. 2019. spThin: Functions for Spatial Thinning of Species Occurrence Records for Use in Ecological Models. - <<https://cran.r-project.org/web/packages/spThin/index.html>>.
- Anastácio, P. M., & Marques, J. C. 1997. Crayfish, *Procambarus clarkii*, effects on initial stages of rice growth in the lower Mondego River valley (Portugal). *Freshwater crayfish*, v.11, p. 608-617.
- Anastácio, P. M. et al. 2009. Population dynamics of the invasive crayfish (*Procambarus clarkii*, Girard, 1852) at two marshes with differing hydroperiods. In: *Annales de Limnologie-International Journal of Limnology*. EDP Sciences, p. 247-256.
- Anger, K. 2013. Neotropical *Macrobrachium* (Caridea: Palaemonidae): on the biology, origin, and radiation of freshwater-invading shrimp. *Journal of Crustacean Biology*, v. 33, n. 2, p. 151-183.
- Aquiloni, L. et al. 2011. The North American crayfish *Procambarus clarkii* is the carrier of the oomycete *Aphanomyces astaci* in Italy. *Biological Invasions*, 13(2), 359-367.
- ASFA. 2022. Aquatic Sciences and Fisheries Abstracts. ProQuest – Clarivate LibGuides - <<https://proquest.libguides.com/asfa>>- accessed August 2022.
- Augusto, A. et al. 2007. Adaptive shifts in osmoregulatory strategy and the invasion of freshwater by brachyuran crabs: evidence from *Dilocarcinus pagei* (Trichodactylidae). *Journal of Experimental Zoology Part A: Ecological Genetics and Physiology*, v. 307, n.12, p.688-698.
- Augusto, A. et al. 2009. Evolutionary transition to freshwater by ancestral marine palaemonids: evidence from osmoregulation in a tide pool shrimp. *Aquatic Biology*., 7 (2009), pp. 113-122.
- Barbet-Massin, M. et al. 2012. Selecting pseudo-absences for species distribution models: how, where, and how many? *Methods in ecology and evolution*, v. 3, n.2, p. 327-338.

- Barros-Alves, S. P. et al. 2012. Population biology of shrimp *Macrobrachium jelskii* (Miers, 1778) (Decapoda, Palaemonoidea) at the Grande River the northwest of the state of Minas Gerais, Brazil. *Acta Limnologica Brasiliensia*, 24(3):266-275.
- Bashir, I. et al. 2020. Concerns and threats of contamination on aquatic ecosystems. In *Bioremediation and Biotechnology*, Springer, Cham, p.1-26.
- Bastos, A. M. et al. 2019. Effects of environmental light colors on the larviculture of the Amazon River prawn *Macrobrachium amazonicum*. *Aquaculture International*, v. 27, n.5, p.1525-1534.
- Bellard, C. et al. 2013. Will climate change promote future invasions? *Global change biology*, v. 19, n. 12, p. 3740-3748.
- Bertelsmeier, C. et al. 2013. Increase in quantity and quality of suitable areas for invasive species as climate changes. *Conservation Biology*, 27(6), 1458-1467.
- Boudour-Bouchecker, N. et al. 2013. Adaptation to freshwater in the palaemonid shrimp *Macrobrachium amazonicum*: comparative ontogeny of osmoregulatory organs. *Cell and Tissue Research*, 353 (2013), pp. 87-98
- Boudour-Bouchecker, N. et al. 2016. Osmoregulation in larvae and juveniles of two recently separated *Macrobrachium* species: Expression patterns of ion transporter genes. *Comparative Biochemistry and Physiology Part A: Molecular & Integrative Physiology*, 195, 39–45.
- Breiman, L. 2001. Random forests. *Machine learning*, v .45, n. 1, p. 5-32.
- Camacho-Portocarrero, R. F. et al. 2021. Areas at risk of invasion by *Procambarus clarkii* (Decapoda: Cambaridae) a crayfish introduced in Colombia. *Revista de Biología Tropical*, v.69, n.1, p. 77-89.
- Cantonati, Marco, et al. "Characteristics, main impacts, and stewardship of natural and artificial freshwater environments: consequences for biodiversity conservation." *Water* 12.1 (2020): 260.
- Capinha, C. et al. 2011. Predicting worldwide invasiveness for four major problematic decapods: an evaluation of using different calibration sets. *Ecography*, v. 34, n.3, p. 448-459.

- Coetzee, B. W. et al. 2009. Ensemble models predict Important Bird Areas in southern Africa will become less effective for conserving endemic birds under climate change. *Global Ecology and Biogeography*, v. 18, n.6, p. 701-710.
- Collart, O.O. & Moreira, L.C. 1993. Potencial pesqueiro de *Macrobrachium amazonicum* na Amazônia Central (Ilha do Careiro): variação da abundância e do comprimento. *Amazoniana*, 12:399-413.
- Cruz, M. J. et al. 2008. Collapse of the amphibian community of the Paul do Boquilobo Natural Reserve (central Portugal) after the arrival of the exotic American crayfish *Procambarus clarkii*. *The Herpetological Journal*, v.18, n.4, p. 197-204.
- da Silva, T. E. et al. 2018. Morphometric differences between two exotic invasive freshwater caridean species (genus *Macrobrachium*). *Invertebrate Reproduction & Development*, v. 62, n. 4, p. 221-228.
- Dakhil, M. A. et al. 2019. Past and future climatic indicators for distribution patterns and conservation planning of temperate coniferous forests in southwestern China. *Ecological Indicators*, v. 107, p.105559.
- David, F. S. et al. 2018. Economic feasibility of intensification of *Macrobrachium rosenbergii* hatchery. *Aquaculture Research*, 49(12), 3769-3776.
- Deka, M. A., & Morshed, N. 2018. Mapping disease transmission risk of Nipah virus in South and Southeast Asia. *Tropical Medicine and Infectious Disease*, v.3, n. 2, p. 57.
- Domisch, S. et al. 2015. Near-global freshwater-specific environmental variables for biodiversity analyses in 1 km resolution. *Scientific data*, v. 2, n.1, p. 1-13.
- Dunne T, Mertes LAK. Rivers. In: Veblen TT, Young KR, Orme AR. *The physical geography of South America*. New York: Oxford University Press; 2007. pp. 76-90.
- EarthEnv. 2022. Global, remote-sensing supported environmental layers for assessing status and trends in biodiversity, ecosystems, and climate. -<<https://www.earthenv.org/>>- accessed August 2022.
- Egly, R. M. 2018. Applying new aquatic habitat data to manage invasive and imperiled crayfishes in North America. - Master's thesis, University of Illinois, United States.
- Egly, R. M. et al. 2019. Predicting the potential distribution of the non-native Red Swamp Crayfish *Procambarus clarkii* in the Laurentian Great Lakes. *Journal of Great Lakes Research*, v. 45, n. 1, p. 150-159.

- Egly, R. M. et al. 2021. Updated occurrence data and species distribution modeling of the invasive amphipod *Apocorophium lacustre* in North America. *Freshwater Science*, v. 40, n. 1, p. 162-174.
- Elith, J. et al. 2008. A working guide to boosted regression trees. *Journal of animal ecology*, v. 77, n. 4, p. 802-813.
- Elith, J. & Leathwick, J. R. 2009. Species distribution models: ecological explanation and prediction across space and time. *Annual Review of Ecology, Evolution and Systematics*, v.40, n.1, p. 677-697.
- Elith, J. et al. 2011. A statistical explanation of MaxEnt for ecologists. *Diversity and distributions*, v. 17, n. 1, p. 43-57.
- FAO-DIAS. 2022. *Macrobrachium rosenbergii*. Fisheries and Aquaculture Division [online]. - <<https://www.fao.org/fishery/en/introsp/3105/en>>, accessed August 2022.
- Freitas, G. et al. 2019. Spatial ecology and conservation of the microendemic ovenbird Cipo Cinclodes (*Cinclodes espinhacensis*) from the Brazilian highlands. *Journal of Field Ornithology*, v. 90, n. 2, p. 128-142.
- Friedman, J. H. 1991. Estimating functions of mixed ordinal and categorical variables using adaptive splines. Stanford University CA Lab for Computational Statistics.
- Friedrichs-Manthey, M. et al. 2020. From topography to hydrology—The modifiable area unit problem impacts freshwater species distribution models. *Ecology and evolution*, v. 10, n. 6, p. 2956-2968.
- Fukuda, B. et al. 2016. Effect of salinity on the embryonic development of *Macrobrachium acanthurus* (Decapoda: Palaemonidae). *Invertebrate Reproduction & Development*, 61(1), 1–8.
- Gallardo, M. B. et al. 2016. Global ecological impacts of invasive species in aquatic ecosystems. *Global Change Biology* Pp. 151-163
- Gama, M. et al. 2016. Predicting global habitat suitability for *Corbicula fluminea* using species distribution models: The importance of different environmental datasets. *Ecological Modelling*, 319, 163-169.
- Gamba, A.L. 1997. Biología reproductiva de *Macrobrachium jelskii* (Miers, 1877) y *Macrobrachium amazonicum* (Heller, 1862) en Venezuela (Crustacea, Decapoda, Palaemonidae). *Acta Científica Venezolana* 48:19-26.

- Garcia, D. A. Z. 2021. Live bait trade as a pathway for the introduction of non-native species: the first record of *Dilocarcinus pagei* in the Paranapanema river basin. *Oecologia Australis*, 25(3), 775-785.
- GBIF – Global Biodiversity Information Facility. 2022. GBIF Home Page. - <https://www.gbif.org>, accessed August 2022.
- Guisan, A. et al. 2002. Generalized linear and generalized additive models in studies of species distributions: setting the scene. *Ecological Modelling*, v. 157, n. 2-3, p. 89-100.
- Guimaraes, R. H. E. 2014. Influência da sazonalidade sobre as águas estuarinas dos furos da ilha de Colares (baía do Marajó). Dissertação Universidade Federal do Pará, Instituto de Geociências, Programa de Pós-Graduação em Geologia e Geoquímica.
- Hastie, T. et al. 1994. Flexible discriminant analysis by optimal scoring. *Journal of the American statistical association*, v. 89, n. 428, p. 1255-1270.
- Hernández, L. et al. 2008. Geographic expansion of the invasive red crayfish *Procambarus clarkii* (Girard, 1852) (Crustacea: Decapoda) in Mexico. *Biological Invasions*, v.10, n. 7, p. 977-984.
- Hijmans, R. J. et al. 2022. Raster: Geographic Data Analysis and Modeling. -<https://cran.r-project.org/web/packages/raster/index.html>-
- Holdich, D. M. 2017. The negative effects of established crayfish introductions. In *Crayfish in Europe as alien species*. Routledge, p. 31-47.
- Holthuis, L. B. 1952. A general revision of the Palaemonidae (Crustacea Decapod Natantia) of the Americas. II. The subfamily Palaemonidae.
- Huner, J. V. 1988. *Procambarus* in North America and elsewhere. *Freshwater crayfish: biology, management and exploitation.*, 239-261.
- Instituto Chico Mendes de Conservação da Biodiversidade – ICMBIO. 2018. Guia de orientação para o manejo de espécies exóticas invasoras em unidades de conservação federais. Ministério do Meio Ambiente, p.65.
- Iketani, G. et al. 2011. The history of the introduction of the giant river prawn, *Macrobrachium rosenbergii* (Decapoda, Palaemonidae), in Brazil: New insights from molecular data. *Genetics and Molecular Biology*, v.34, p.142-151.

- Iketani, G. et al. 2016. Successful invasion of the Amazon Coast by the giant river prawn, *Macrobrachium rosenbergii*: evidence of a reproductively viable population. *Aquatic Invasions*, v.11, n.3.
- Jetz, W. et al. 2019. Essential biodiversity variables for mapping and monitoring species populations. *Nature ecology & evolution*, v.3, n.4, p. 539-551.
- Johovic, I. et al. 2020. A potential threat to amphibians in the European Natura 2000 network: Forecasting the distribution of the American bullfrog *Lithobates catesbeianus*. *Biological Conservation* v. 245, p. 108551.
- Junk, W. J. 2007. Freshwater fishes of South America: Their biodiversity, fisheries, and habitats—a synthesis. *Aquatic Ecosystem Health & Management*, 10(2), 228-242.
- Kovalenko, K. E. et al. 2018. Great Lakes coastal fish habitat classification and assessment. *Journal of Great Lakes Research*, 44(5), 1100-1109.
- Kulhanek, S. et al. 2011. Is invasion history a useful tool for predicting the impacts of the world's worst aquatic invasive species? *Ecological Applications*, v. 21, n.1, p. 189-202.
- Kutty, M. N. et al. 2000. Culture of other prawn species. *Freshwater prawn culture: the farming of *Macrobrachium rosenbergii**, p. 393-410.
- Lal M. M. et al. 2012. Salinity and temperature requirements for larviculture of the Monkey River prawn *Macrobrachium lar* (Fabricius, 1798) (Decapoda: Caridea: Palaemonidae). *Aquaculture*. 366:1–8.
- Latini A. O. et al. 2016. Espécies exóticas invasoras de águas continentais no Brasil. Ministério do Meio Ambiente, Brasília.
- Lek, S. & Guégan, J. F. 1999. Artificial neural networks as a tool in ecological modeling, an introduction. *Ecological Modelling*, v. 120, n. 2-3, p. 65-73.
- Lodge, D. M. et al. 2012. Global introductions of crayfishes: evaluating the impact of species invasions on ecosystem services. *Annual Review of Ecology, Evolution and Systematics*, v.43, n. 449, p. 2012.
- Lodge, D. M. et al. 2016. Risk analysis and bioeconomics of invasive species to inform policy and management. *Annual Review of Environment and Resources*, 41, 453-488.

- Loebmann, D. et al. 2010. The invasion of five alien species in the Delta do Parnaíba Environmental Protection Area, Northeastern Brazil. *Revista de Biologia Tropical*, v.58, n.3, p. 909-923.
- Loureiro, T. G. et al. 2015. Distribution, introduction pathway, and invasion risk analysis of the North American crayfish *Procambarus clarkii* (Decapoda: Cambaridae) in Southeast Brazil. *Journal of Crustacean Biology*, v. 35, n. 1, p.88-96.
- Low, B. W. et al. 2021. Predictor complexity and feature selection affect MaxEnt model transferability: Evidence from global freshwater invasive species. *Diversity and Distributions*, v. 27, n. 3, p. 497-511.
- Maciel, C. R., & Valenti, W. C. 2009. Biology, fisheries, and aquaculture of the Amazon River prawn *Macrobrachium amazonicum*: a review. *Nauplius*, 17(2), 61-79.
- Magalhães, C. et al. 2005. Exotic species of freshwater decapod crustaceans in the state of São Paulo, Brazil: records and possible causes of their introduction. *Biodiversity & Conservation*, v. 148, p. 1929-1945.
- Manfrin, C. et al. 2019. Detection and control of invasive freshwater crayfish: from traditional to innovative methods. *Diversity*, v.11, n.1.
- Mantelatto, F. L. M., & Barbosa, L. R. 2005. Population structure and relative growth of freshwater prawn *Macrobrachium brasiliense* (Decapoda, Palaemonidae) from São Paulo State, Brazil. *Acta Limnologica Brasiliensia*, 17(3), 245-255.
- Mantovano, T. et al. 2021. A global analysis of the susceptibility of river basins to invasion of a freshwater zooplankton (*Daphnia lumholtzi*). *Freshwater Biology*, v. 66, n. 4, p. 683-698.
- Marmion, M. et al. 2009. Evaluation of consensus methods in predictive species distribution modeling. *Diversity and distributions*, v. 15, n. 1, p. 59-69.
- McNamara JC, Faria SC, 2012. Evolution of osmoregulatory patterns and gill ion transport mechanisms in the decapod Crustacea: a review. *Journal of Comparative Physiology B* 8, 997-1014.
- Melo, G. A. S. 2003. Manual de identificação dos Crustacea Decapoda de água doce do Brasil. Edições Loyola.
- Microsoft Corporation. 2018. Microsoft Excel. URL <https://office.microsoft.com/excel>.

- Moher D. et al. 2009. The PRISMA Group. Preferred Reporting Items for Systematic Reviews and Meta-Analyses: The PRISMA Statement. PLoS Med, 6(7).
- Moraes-Valenti, P. M. & Valenti, W. C. (2007). Effect of intensification on grow out of the Amazon River prawn, *Macrobrachium amazonicum*. Journal of the World Aquaculture Society, 38(4), 516-526.
- Mossolin, E. C et al. 2013. Population and reproductive features of the freshwater shrimp *Macrobrachium jelskii* (Miers, 1877) from São Paulo state, Brazil. Acta Scientiarum, Biological Sciences. 35(3):429-436.
- Naimi, B. et al. 2014. usdm: Uncertainty Analysis for Species Distribution Models. -<<https://cran.r-project.org/web/packages/usdm/index.html>>-
- Naimi, B. & Araujo, M.B. 2016. “sdm”: a reproducible and extensible R platform for species distribution modeling.” Ecography, v. 39, p. 368-375.
- Nix, H. A., & Busby, J. 1986. BIOCLIM, a bioclimatic analysis, and prediction system. Division of Water and Land Resources: Canberra.
- New, M. B. 2000. History and global status of freshwater prawn farming. Freshwater prawn culture: the farming of *Macrobrachium rosenbergii*, 1-11.
- New, M. B. et al. 2000. Sustainability of freshwater prawn culture. Freshwater prawn culture: the farming of *Macrobrachium rosenbergii*, 429-434.
- Oliveira, C. D. L. D., & Santos, L. V. R. (2021). Distribution of the giant river prawn *Macrobrachium rosenbergii* (De Man, 1879) in Brazil: 43 years after its introduction. Nauplius, 29.
- Orme, A. R. The Physical Geography of South America. In: The tectonic framework of South America. Veblen TT, Young KR, Orme AR, editors. Oxford University Press; 2007. pp. 3-22.
- Palaoro, A. et al. 2013. Niche conservatism and the potential for the crayfish *Procambarus clarkii* to invade South America. Freshwater Biology, v. 58, n.7, p. 1379-1391.
- Peterson, A. T., & Soberón, J. 2012. Species distribution modeling and ecological niche modeling: Getting the concepts right. Natureza & Conservação, v .10, n.2, p .102–107.

- Pettovello, A. D. 1996. First Record of *Macrobrachium amazonicum* (Decapoda, Palaemonidae) in Argentina. *Crustaceana*, v, 69 n.1, p.113-114.
- Phillips, S. J. et al. 2006. Maximum entropy modeling of species geographic distributions. *Ecological modelling*, v. 190, n. 3-4, p. 231-259.
- QGIS Development Team. 2022. QGIS Geographic Information System. Open-Source Geospatial Foundation Project. URL <http://qgis.osgeo.org>.
- R Core Team. 2020. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.
- Radosavljevic, A., & Anderson, R. P. 2014. Making better MaxEnt models of species distributions: complexity, overfitting, and evaluation. *Journal of Biogeography*, v. 41, n. 4, p. 629-643.
- Ramalho, R. O., & Anastácio, P. M. 2015. Factors inducing overland movement of invasive crayfish (*Procambarus clarkii*) in a ricefield habitat. *Hydrobiologia*, v. 746, n.1, p.135-146.
- Rocha, S. S. D., & Barbosa, R. D. J. 2017. Population biology of *Macrobrachium jelskii* (Miers, 1877) (Decapoda, Palaemonidae) from an artificial pond in Bahia, Brazil. *Nauplius*, v.25.
- Rodriguez, G. 1982. Fresh-water shrimps (Crustacea, Decapoda, Natantia) of the Orinoco basin and the Venezuelan Guyana. *Journal of Crustacean Biology*. 2: 378-391.
- Santos, L. V. R., & Coelho Filho, P. A. 2021. An update of the amazon prawn (*Macrobrachium amazonicum*) distribution in the low course of the São Francisco River (northeast Brazil). *Neotropical Biology and Conservation*, 16(1), 105-114.
- Saupe, E. et al. 2012. Variation in niche and distribution model performance: the need for a priori assessment of key causal factors. *Ecological Modelling*, 237, 11-22.
- Scopus. 2022. Elsevier. -<https://www.scopus.com/>- accessed August 2022.
- Sillero, N., & Barbosa, A. M. 2021. Common mistakes in ecological niche models. *International Journal of Geographical Information Science*, v.35, n.2, p.213-226.
- Silva, H. L. M. D., & Bueno, S. L. D. S. 2005. Population size estimation of the exotic crayfish *Procambarus clarkii* (Girard) (Crustacea, Decapoda, Cambaridae) in the Alfredo Volpi City Park, São Paulo, Brazil. *Revista Brasileira de Zoologia*, v. 22, p. 93-98.

- Silva, T. A. D. et al. 2020. First records of non-native species Malaysian prawn *Macrobrachium rosenbergii* (Decapoda: Palaemonidae) in an important South American hydrographic system. *Acta Limnologica Brasiliensia*, 32.
- Silva-Oliveira, G. C. et al. 2011. The invasive status of *Macrobrachium rosenbergii* (De Man, 1879) in Northern Brazil, with an estimation of areas at risk globally. *Aquatic Invasions*, v. 6, n. 3, p. 319-328.
- Simberloff, J. D. et al. 2013. Impacts of biological invasions: what's what and the way forward *Trends Ecol. Evol.*, 28 (2013), pp. 58-66
- Soeiro, R. K. S. et al. 2016. Relationship between the coastal origin of the freshwater prawn *Macrobrachium amazonicum* and salinity levels in the hatchery. *B. Inst. Pesca*, 691-703.
- South, A. 2017. rnaturalearth: World Map Data from Natural Earth. -<https://cran.r-project.org/web/packages/rnaturalearth/index.html>>-
- Souty-Grosset, C. et al. 2016. The red swamp crayfish *Procambarus clarkii* in Europe: impacts on aquatic ecosystems and human well-being. *Limnologica*, 58, 78-93.
- Strayer, D. L. 2010. Alien species in fresh waters: ecological effects, interactions with other stressors, and prospects for the future. *Freshwater Biology*, v. 55, p. 152-174.
- Susanto, G. N. 2021. Crustacea: The Increasing Economic Importance of Crustaceans to Humans. In *Arthropods-Are They Beneficial for Mankind?* IntechOpen. v.232.
- Taddei, F. G., & Herrera, D. R. 2010. Growth of the crab *Dilocarcinus pagei* Stimpson, 1861 (Crustacea, Brachyura, Trichodactylidae) in the Barra Mansa dam, Mendonca, SP. *Boletim do Instituto de Pesca São Paulo*, v. 36, n. 2, p. 99-110.
- The EndNote Team. 2013. Endnote. Clarivate. Philadelphia, PA. URL <https://endnote.com/>.
- Thuiller, W. et al. 2009. BIOMOD—a platform for ensemble forecasting of species distributions. *Ecography*, v.32, n.3, p.369-373.
- Thuiller, W. et al. 2021. biomod2: Ensemble Platform for Species Distribution Modeling. -<https://cran.r-project.org/web/packages/biomod2/index.html>>-
- Torremorell, A., Hegoburu, C., Brandimarte, A. L., Rodrigues, E. H. C., Pompêo, M., da Silva, S. C., ... & Navarro, E. (2021). Current and future threats for ecological quality management of South American freshwater ecosystems. *Inland Waters*, 11(2), 125-140.

- Vayssières, M. P. et al. 2000. Classification trees: An alternative non-parametric approach for predicting species distributions. *Journal of vegetation science*, v. 11, n. 5, p. 679-694.
- Vera-Silva, A. L. et al. 2016. Distribution and genetic differentiation of *Macrobrachium jelskii* (Natantia: Palaemonidae) in Brazil reveal evidence of non-natural introduction and cryptic allopatric speciation. *Journal of Crustacean Biology*, v. 36, n.3, 373-383.
- Wakasugi, K. 2013. Actual situation and measures of paddy field leakage by *Procambarus clarkii*. *Agric Hortic*, v. 88, p.795 - 806.
- Wear, R. G. 1974. Incubation in British decapod Crustacea, and the effects of the temperature on the rate and success of embryonic development. *Journal of the Marine Biological Association of the United Kingdom* 54:745-762.
- Web of Science. 2022. Clarivate Analytics. -<<https://www.webofscience.com/>>- accessed August 2022.
- Westervelt, J. & Shapiro, M. 2022. GRASS GIS Manual. U.S. Army Construction Engineering Research Laboratory. -<<https://grass.osgeo.org/grass78/manuals/r.class.html>>-
- Wickham, H. 2018. tidyverse: Easily Install and Load the 'Tidyverse'. -<<https://cran.r-project.org/web/packages/tidyverse/index.html>>-
- Williamson, M. 1996. *Biological Invasions*. Springer Science & Business Media.
- Wittmann, M. E. et al. 2017. Refining species distribution model outputs using landscape-scale habitat data: forecasting grass carp and *Hydrilla* establishment in the Great Lakes region. *Journal of Great Lakes Research*, v. 43, n.2, p.298-307.
- WorldClim. 2022. Global climate and weather data. -<<https://worldclim.org/>>- accessed August 2022.
- Yackulic, C. B. et al. 2013. Presence-only modelling using MaxEnt: when can we trust the inferences? *Methods in Ecology and Evolution*, 4(3), 236-243.
- Zhao, G. et al. 2021. Analysis of the distribution pattern of Chinese *Ziziphus jujuba* under climate change based on optimized biomod2 and MaxEnt models. *Ecological Indicators* v. 132, p. 108256.
- Zhang, L. et al. 2015. Consensus forecasting of species distributions: The effects of niche model performance and niche properties. *PloS one*, 10(3), e0120056.

Zhang, Z. et al. 2020a. Impacts of climate change on the global potential distribution of two notorious invasive crayfishes. *Freshwater Biology*, 65(3), 353-365.

Zhang, Z. et al. 2020b Future climate change will severely reduce habitat suitability of the Critically Endangered Chinese giant salamander. *Freshwater Biology*, 65(5), 971-980.

SM1: Papers list resulting from the systematic review

File in attachment

SM2: Predictor variables list, extracted from WorldClim and EarthEnv databases. Highlighted with an X are the variables selected through the Variance Inflation Factor (VIF) for each species. *P. clarkii* = *Procambarus clarkii*, *D. pagei* = *Dilocarcinus pagei*, *M. rosenbergii* = *Macrobrachium rosenbergii*, *M. jelskii* = *Macrobrachium jelskii*, *M. amazonicum* = *Macrobrachium amazonicum*.

Variable	Description	<i>M. rosenbergii</i>	<i>M. jelskii</i>	<i>M. amazonicum</i>	<i>P. clarkii</i>	<i>D. pagei</i>
<i>Worldclim</i>						
Bio1	Annual Mean Temperature					
Bio2	Mean Diurnal Range				X	
Bio3	Isothermality		X			
Bio4	Temperature Seasonality			X		X
Bio5	Max Temperature of Warmest Month	X			X	
Bio6	Min Temperature of Coldest Month					
Bio7	Temperature Annual Range					
Bio8	Mean Temperature of Wettest Quarter				X	X
Bio9	Mean Temperature of Driest Quarter	X	X		X	
Bio10	Mean Temperature of Warmest Quarter					
Bio11	Mean Temperature of Coldest Quarter					
Bio12	Annual Precipitation					
Bio13	Precipitation of Wettest Month	X	X		X	
Bio14	Precipitation of Driest Month	X	X	X		
Bio15	Precipitation Seasonality			X		X
Bio16	Precipitation of Wettest Quarter					
Bio17	Precipitation of Driest Quarter					
Bio18	Precipitation of Warmest Quarter	X	X	X		X
Bio19	Precipitation of Coldest Quarter	X				

Variable	Description	<i>M. rosenbergii</i>	<i>M. jelskii</i>	<i>M. amazonicum</i>	<i>P. clarkii</i>	<i>D. pagei</i>
<i>EarthEnvi</i>						
Prec1	Sum of monthly precipitation January	X				
Prec2	Sum of monthly precipitation February			X	X	
Prec3	Sum of monthly precipitation March		X			
Prec4	Sum of monthly precipitation April	X			X	
Prec5	Sum of monthly precipitation May	X	X			
Prec6	Sum of monthly precipitation June					
Prec7	Sum of monthly precipitation July				X	
Prec8	Sum of monthly precipitation August					
Prec9	Sum of monthly precipitation September	X		X		X
Prec10	Sum of monthly precipitation October					X
Prec11	Sum of monthly precipitation November	X	X	X	X	X
Prec12	Sum of monthly precipitation December					
Hydro1	Annual Mean Temperature					
Hydro2	Mean Diurnal Range	X	X	X	X	
Hydro3	Isothermality					
Hydro4	Temperature Seasonality					
Hydro5	Max Temperature of Warmest Month					
Hydro6	Min Temperature of Coldest Month				X	
Hydro7	Temperature Annual Range					
Hydro8	Mean Temperature of Wettest Quarter		X	X		
Hydro9	Mean Temperature of Driest Quarter					
Hydro10	Mean Temperature of Warmest Quarter					
Hydro11	Mean Temperature of Coldest Quarter					
Hydro12	Annual Precipitation					
Hydro13	Precipitation of Wettest Month		X			
Hydro14	Precipitation of Driest Month	X	X	X		

Variable	Description	<i>M. rosenbergii</i>	<i>M. jelskii</i>	<i>M. amazonicum</i>	<i>P. clarkii</i>	<i>D. pagei</i>
Hydro15	Precipitation Seasonality					
Hydro16	Precipitation of Wettest Quarter					
Hydro17	Precipitation of Driest Quarter					
Hydro18	Precipitation of Warmest Quarter	X				
Hydro19	Precipitation of Coldest Quarter				X	
Elev1	Minimum elevation	X	X	X	X	
Elev2	Maximum elevation					
Elev3	Elevation range		X	X	X	
Elev4	Average Elevation					
Slope1	Minimum slope	X		X	X	X
Slope2	Maximum slope					
Slope3	Slope range	X				X
Slope4	Average slope	X			X	X
Flow1	Number of upstream stream grid cells					
Flow2	Number of upstream catchment grid cells					

SM3: Area of suitability greater than 75% of the species *Dilocarcinus pagei*, *Macrobrachium amazonicum*, *Macrobrachium jelskii*, *Macrobrachium rosenbergii* and *Procambarus clarkii*, which overlap the hydrographic basins and Protected Areas in South America.

File in attachment