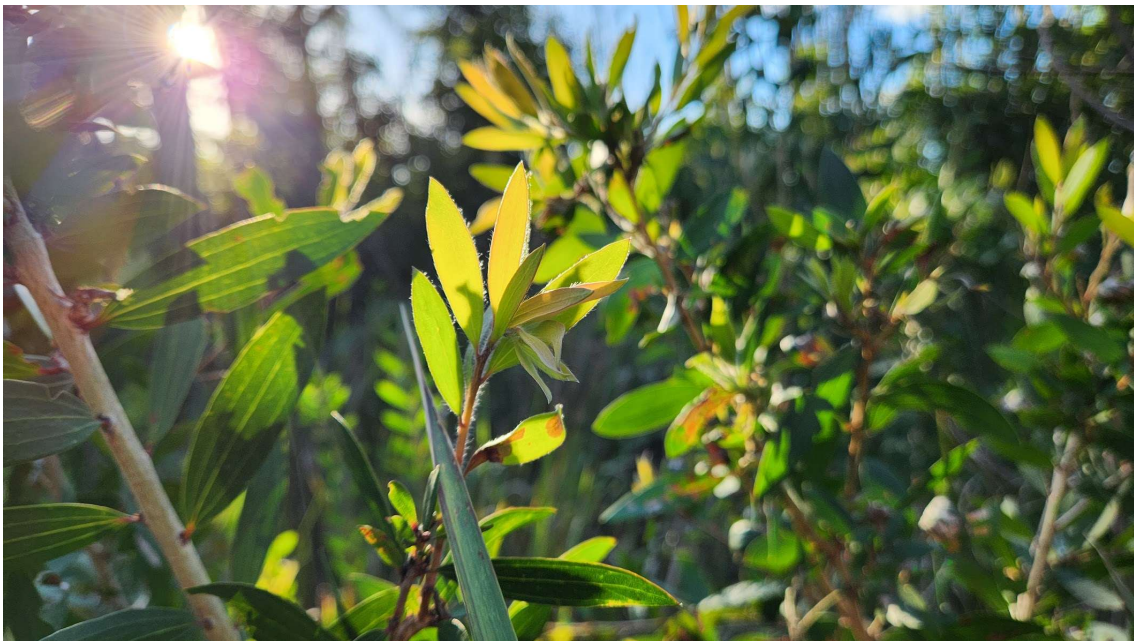


Title: Would you Mela-look-at that! The intersection of
Melaleuca quinquenervia and Myrtle rust for
restoration

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Would you Mela-look-at that! The intersection of *Melaleuca quinquenervia* and Myrtle rust for restoration

Abstract

Conservation is expensive. To maximise resources, efforts in restoration are leaning towards ‘genetic optimisation’ of planting stocks. This comes in the form of maximising the revegetation stock’s traits whether for disease resistance, drought tolerance for short-term resilience, or general genetic diversity for long-term population health. However, these traits often compromise one another. For example, the increase in a population’s average disease resistance has been demonstrated to reduce the population’s genetic diversity. This consequently raises the question – “When maximising multiple objectives, which objective should be given more weight?”. Decisions to such questions are intuitively shaped by the scenario at hand. Here, I present how the intersection of the predicted distribution from Maxent species distribution models can assist practitioners in arriving at a solution that works for them. The pathogen, Myrtle rust (*Austropuccinia psidii* (G. Winter) Beenken), and its host, *Melaleuca quinquenervia* (Cav.) S.T.Blake, is used as a case study that provide the foundation for future applications in other non-model host- pathogen dynamics.

Introduction

The broad-leaved Melaleuca, (*Melaleuca quinquenervia* (Cav.) S.T.Blake), is a widespread plant that is impacted by the disease (Pegg et al., 2018). The species is a foundational species, occupying a unique niche to form the dominant canopy of wetlands across New South Wales and Queensland (Zoete, 2001). As such, *M. quinquenervia* supports numerous ecological services from maintaining hydrological regimes (McJannet, 2008), blue carbon sink (Tran & Dargusch, 2016), nutrient sink (Bolton & Greenway, 1999; Greenway, 1994), and supporting the population of international migratory birds (Grover & Slater, 1994) and endangered bats (Benson & McDougall, 1998).

Unfortunately, *M. quinquenervia* is impacted by Myrtle rust (*Austropuccinia psidii* (G. Winter) Beenken). First seen overseas in Florida (Rayachhetry et al., 1997), Myrtle rust is now known to impact *M. quinquenervia* locally here in Australia, with only ~40% of individuals being resistant to it (Pegg et al., 2018). As a non-model species, there is a lot

unknown. For instance, there is a paucity in methods to identify resistant individuals without the limitations imposed by artificial inoculation specialised facilities. Additionally, the interaction between disease resistance in light of abiotic stressors such as drought, is also unknown and poses a concern that will be further exaggerated in upcoming climatic future. As seen in Australian Landcare bush regeneration groups, these limitations and paucity of methods have resulted in restoration stock being arbitrarily selected, without disease resistance or drought tolerance being considered. As a consequence, large losses in stock material have been experienced (S. Lubwinski, pers. comm.).

To address this loss, restoration practitioners are encouraged to tailor their planting stock to mitigating threats. This can be done through a process coined genetic optimisation. Where individuals are carefully selected to maximise desirable traits through genomic methods. This enables immediate short-term novel disease threat, such as Myrtle rust, to be targeted through disease resistance traits. Additionally, also allows us to address the necessity for long-term resilience to be integrated into restoration efforts. This long-term resilience can come in two key forms, 1) Genetic diversity for adaptive capacity, and 2) Climate resilience.

Genetic diversity is critical as traits are shaped by one or multiple genes in an individual. Genetic diversity thus creates differences between individual's traits. These differences between individuals, sourced from genetic variation, can then potentially confer resistance to novel situations not yet experienced, such as a new disease (Gibson, 2022) or new environmental stressors. As such, genetic diversity can increase adaptive capacity through increasing the diversity of traits present in a population, reducing extinction risk (Hoban et al., 2022).

Future climate adaptation is another factor that is to be considered for future population resilience. This can be satisfied by sourcing stock from sites that reflect the restoration site's future climate. However, it is to be noted that this method assumes local adaptation has taken place in the maternal line of the seed stock, which may not always be the case (Ramirez-Parada et al., 2024). Alternatively, genotyping stock during genomic optimisation, for known climate-adapted alleles may be a potential alternative for a more robust prediction of future climate adaptation (Capblancq et al., 2020; Fitzpatrick et al., 2021). This combination of genetic diversity and tailored adaptation of predicted adversity thus provides long-term resilience in a restoration population.

Building a population that characterises both adapted, climate and disease resilience, and adaptive, through genetic diversity, is critical to the success of a restoration project. However, it is not always straightforward as the focus on one goal often compromises on the others (Bragg et al., 2022). To address this, multi-objective optimisation algorithms can be equipped to generate solutions that find the maximal optimal of each trait. This has historically been successful in crop breeding programs (Li et al., 2022), albeit rarely for conservation (Bragg et al., 2022). Here, our study builds on the multi-objective optimisation between disease resistance, climate adapted alleles, and genetic diversity in the host-pathogen dynamic of *Melaleuca quinquenervia* and Myrtle rust.

Multi-object optimisations present different optimal solutions that restoration practitioners (also referred to as decision makers) can select from. As each solution present trade-offs, decision support systems (DSS) are used to better inform decisions. One DSS that exists for conservation scenarios are species distribution models (Pecchi et al., 2019; Sofaer et al., 2019).

Species distribution models (SDMs) use known presence-absence locations of a species of interest to create predictions of species distributions. Briefly, SDMs use algorithms such as generalised linear models (GLMs), generalized additive models (GAMs), and random forest models. These algorithms determine the relationships between the presence-absence data and climate, to map habitat suitability and thus predicted presence (Elith & Franklin, 2013).

Furthermore, future climate models can also be used to simulate potential future climatic shifts in the species' distribution under different scenarios and years. This helps illustrate to decision makers how future climatic scenarios can impact their site of concern. As such, by applying current and future SDMs, we show how decision makers can best select solutions in multi-objective optimisations in the scenario between *Melaleuca quinquenervia* and Myrtle rust.

Methods:

Melaleuca quinquenervia & Myrtle rust occurrence data and species distribution modelling

Occurrence data for model creation were collected from the recent 2023 Myrtle rust survey (<https://www.bganx.org.au/myrtle-rust-survey-2023/>, Accessed 5th August 2024) and Atlas of Living Australia (Belbin et al., 2021). Atlas of Living Australia data was filtered for human observations, survey occurrences and preserved specimens. Similarly, *Melaleuca quinquenervia* occurrence data were collected from Atlas of Living Australia data and filtered for human observations, survey occurrences and preserved specimens.

These presence data were further filtered using the R package ‘CoordinateCleaner’ (v3.0.1, Zizka et al., (2019)). These reduced datapoints to points only within Australia, non-available coordinates with the function ‘cc_val’ from the package, and the function ‘clean_coordinates’ using the tests, ‘duplicates’, ‘equal’, ‘gbif’, ‘seas’, and ‘zeros’. These tests remove datapoints that are likely false, and their details can be found in the package’s manual. In finality, Myrtle rust occurrence data was filtered to 6,216 datapoints, and *Melaleuca quinquenervia* occurrence data was filtered to 6,481 datapoints. To reduce imbalance datapoints between cells, only one occurrence datapoint was kept for each species within each raster cell of the climatic data.

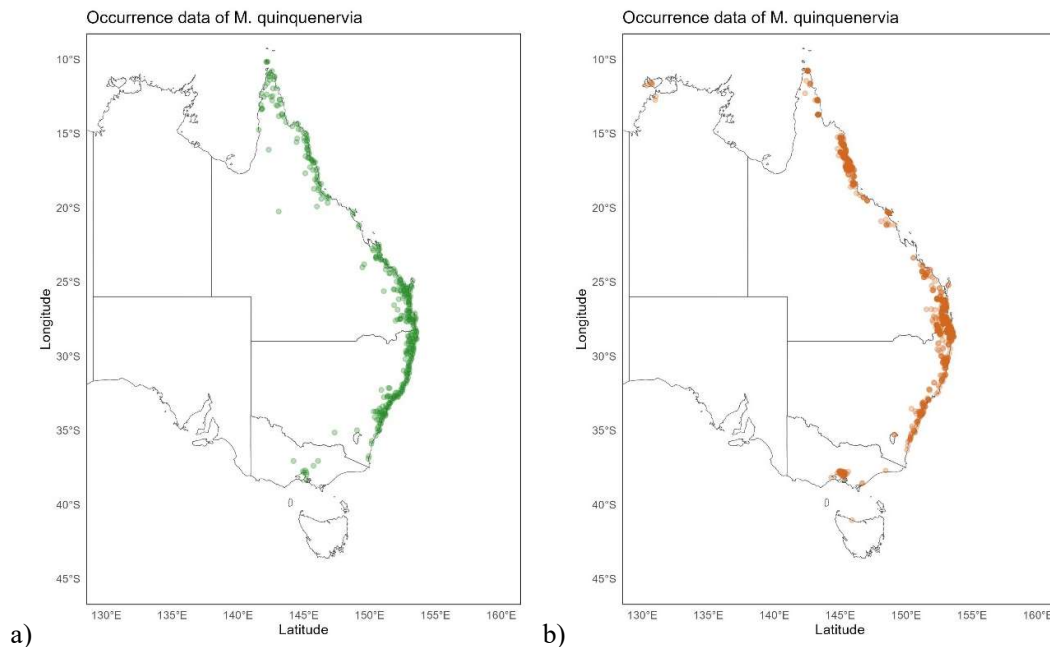


Figure 1. Presence datapoints used for a) *Melaleuca quinquenervia* and b) Myrtle rust

As presence-data only was available, absence data was generated using the function ‘randomPoints’ from the R package ‘dismo’ (v1.3-14, Hijmans et al. (2023)). Absence points were generated at a volume 10 times greater than the number of presence points for each species.

Climate data was sourced from WorldClim v1.4 at a 2.5 minute degree resolution (Fick & Hijmans, 2017). This resolution was selected to ensure smoothness of the use of the application described below. 19 climatic variables from WorldClim were sourced, and later reduced to relevant variables for each species’ model. Future climate data was sourced from Coupled Model Intercomparison Project Phase 6 (CMIP6) climate data, at 2.5 minute degree resolution using the model “MPI-ESM1-2-HR” (von Storch et al., 2017). This data was sourced from WorldClim, using all available average year clusters (2021-2040, 2041-2060, 2061-2080), and scenarios (126, 245, 370, 585). These were similarly reduced to only variables that were used in present-day species distribution predictions.

As this study was interested in the intersection of the two species for decision making, the study area was restricted to a study area of the eastern coast of Australia of *M. quinquenervia*’s range. The extents of the bounding box are as follows, longitude: 137° to 159°, latitude: -42.8° to -5.62°).

Using the final presence and pseudo-absence data for each species as above, we modelled species distribution for both species using Maxent v3.3.3k for both current and future scenarios (Phillips et al., 2006). For current day scenarios 50 datapoints were kept aside for each species’ models and used to generate the reported model accuracies seen in Table 1. These accuracy measurements, along with diagnostic variable plots, personal observations, and previous studies, were used to refine the climatic variables used in the final form of the models. For *M. quinquenervia* climatic variables were reduced to bioclimatic variables 4, 5, 10, 12, 14, 15, 16. Specifically these are temperature seasonality, maximum temperature of the warmest month, mean temperature of the warmest quarter, annual precipitation, precipitation of the driest month, precipitation seasonality, and precipitation of the wettest quarter. For Myrtle rust, the climatic variables used included bioclimatic variables 1, 2, 5, 7, 8, 14. Specifically, mean annual temperature, mean diurnal range, maximum temperature of the warmest month, annual temperature range, mean temperature of the wettest quarter, and precipitation of the driest month. Once satisfied with the models, the models were

subsequently bootstrapped 10 times with 20% of occurrence datapoints set aside for robustness tests.

Using the same, climatic variables reported above, SDMs were also generated using Biomod2 v4.2-5-2 (Huang et al., 2023) using climatic data of 10 degree minutes resolution. In short, Biomod2 allows a range of different SDM algorithms to be run in succession, and ensembled to a final model. Models used included Generalised Linear Models (GLM) and Random Forest (RF) with 50 repetitions. 25% of the data provided kept for accuracy metrics. This was used to cross-validate the Maxent model to ensure quality of projections.

All scripts used to generate the models are available on the associated GitHub repository.

Practitioner accessibility

The accessibility of these model for decision-making in restoration was a key requirement for this project. To ensure this, the rasters of the output models were converted to static images and were used to create a Shiny web application v1.9.1.9000 (Chang et al. 2024). This web application uses leaflet (v 2.2.2, Graul 2016) which allows users to move through a world map and zoom in and out of locations of their choice. An alternative ‘search and fly’ button is provided, allow the user to search up specific latitude and longitudes. The different species distribution models are able to be toggled to allow users to view each separate model. Overall, this allows the decision makers to interact and search up restoration sites of interest and determine the overlay of the two species SDMs at current and future distributions.

Results:

Species Distribution Models

Both models were successfully generated, with an acceptable level of accuracy (Table 1). As seen previously, areas of high suitability for both Myrtle rust and *M. quinquenervia* were restricted to the east coast of Australia (Fig. 2-4). A high overlap was sustained in both future and current species distribution models (Fig. 2-4), with the former species increasing their range, and the latter’s range staying consistent. Bootstrapping of results of both species ensured AUC values of the model were sustained to be greater than 0.9 across all iterations (0.95 for Myrtle rust models and 0.93 for *Melaleuca quinquenervia* models).

Table 1. Maxent model accuracy for each species

Species	AUC	Pearson's R correlation
<i>Austropuccinia psidii</i>	0.973	0.478
<i>Melaleuca quinquenervia</i>	0.948	0.323

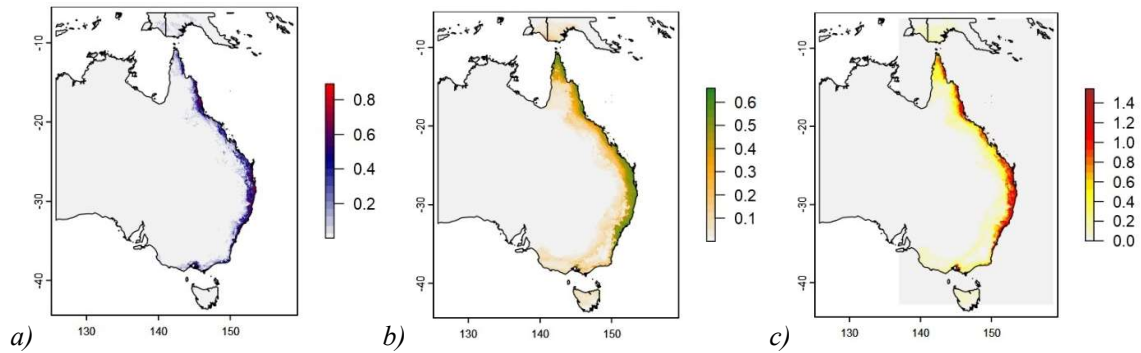


Figure 2. Predictions of area of current climate suitability using Maxent models for a) Myrtle rust, b) *Melaleuca quinquenervia*, and c) Intersection of areas of climate suitability. Where the colours indicate probability of occurrence, in accordance with colour scale to the right of each map.

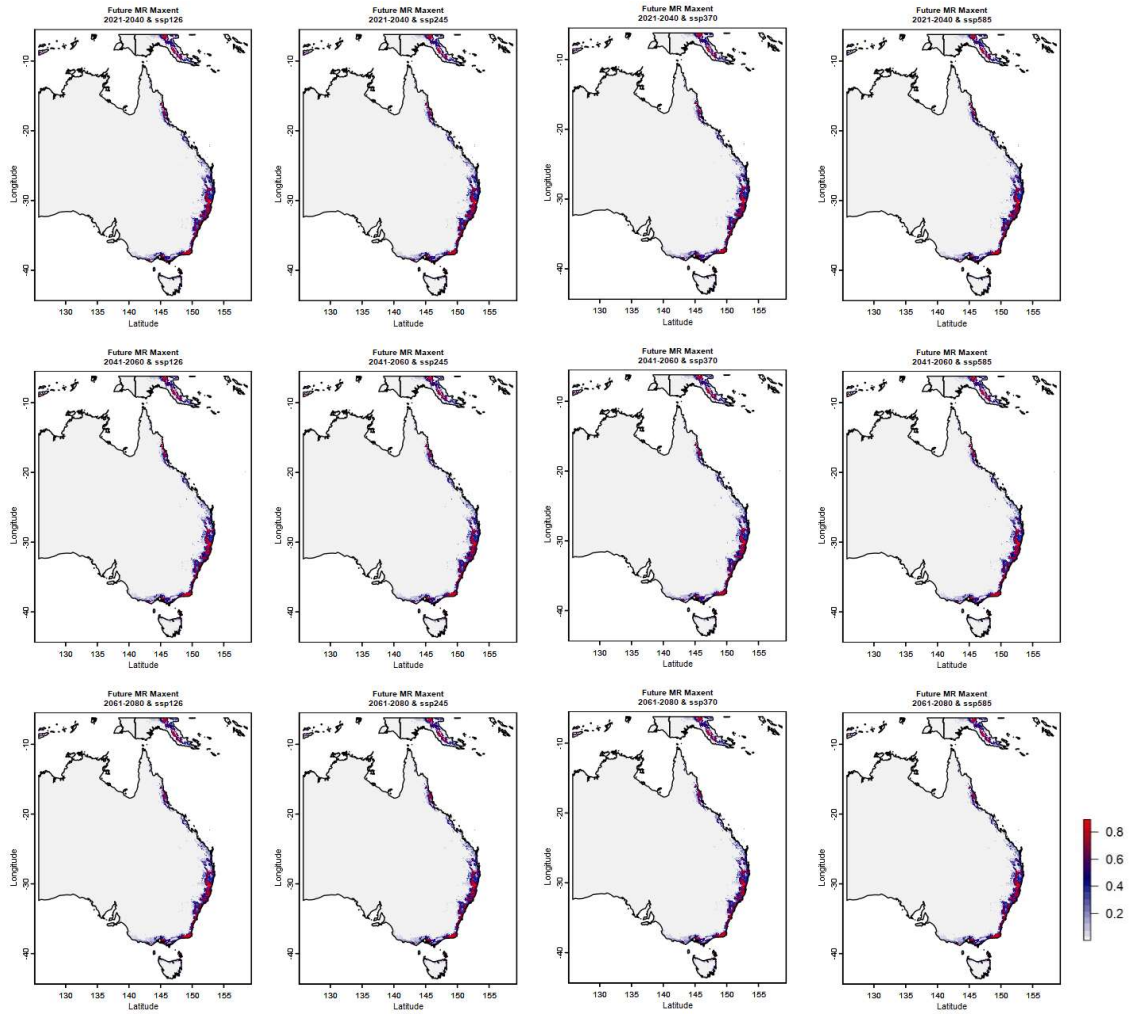


Figure 3. Area of future climate suitability of the intersection of Myrtle rust under different average year clusters and future climate scenarios. Where the colours indicate probability of occurrence, in accordance with colour scale to the right of the figure.

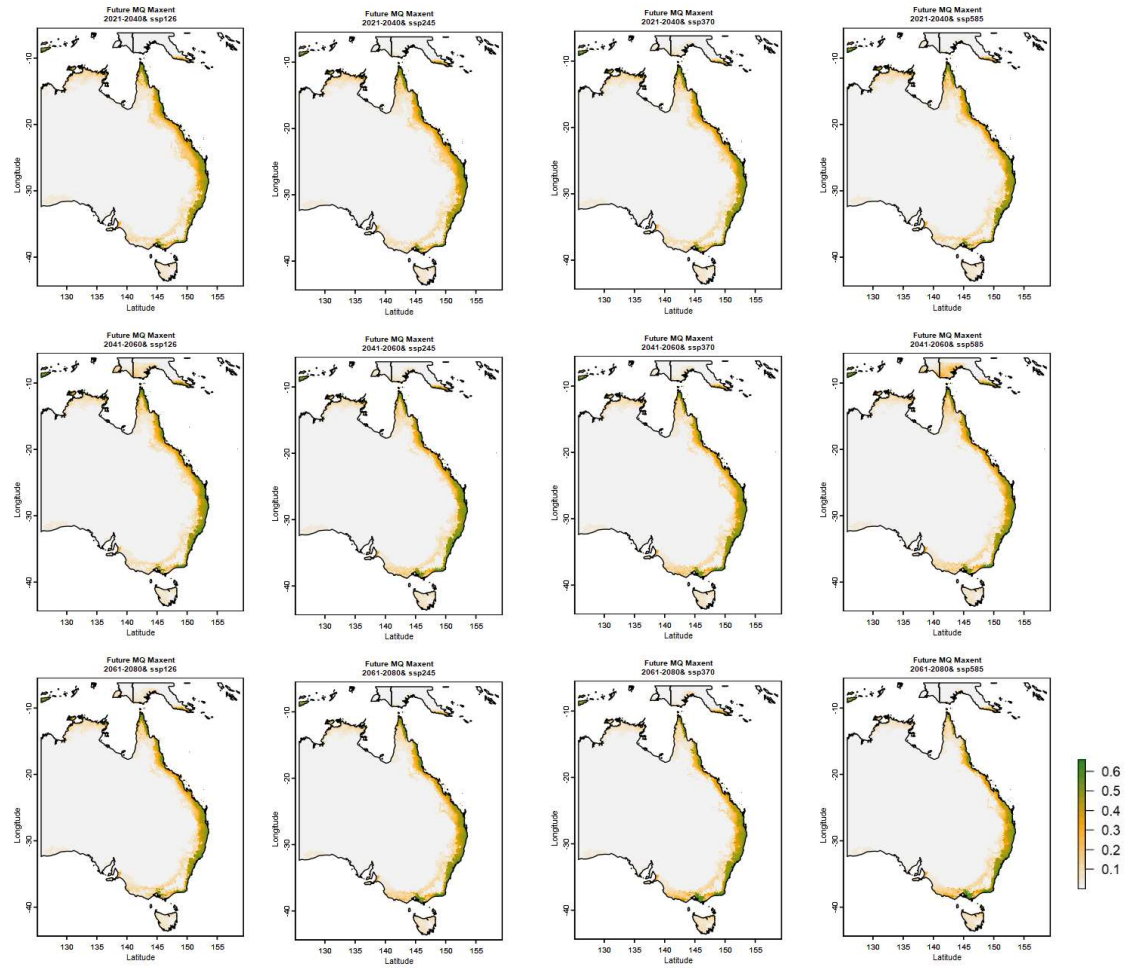


Figure 4. Area of future climate suitability of the intersection of *Melaleuca quinquenervia* under different average year clusters and future climate scenarios. Where the colours indicate probability of occurrence, in accordance with colour scale to the right of the figure.

BIOMOD2 was also used to create SDMs using the same environmental variables as that of Maxent for present-day distribution. Model predictions of the distribution is illustrated in Figure 5, corresponding accuracies in Table 2 and variable explanatory power in Supplementary Table 3 & 4. Where, sensitivity is the proportion of ground truth presences were correctly predicted, and specificity is the ground truth pseudo-absences correctly predicted.

Table 2. BIOMOD2 ensemble model accuracy for each species

Species	Sensitivity	Specificity	Calibration
<i>Austropuccinia psidii</i>	95.941	91.472	0.874
<i>Melaleuca quinquenervia</i>	94.737	94.359	0.891

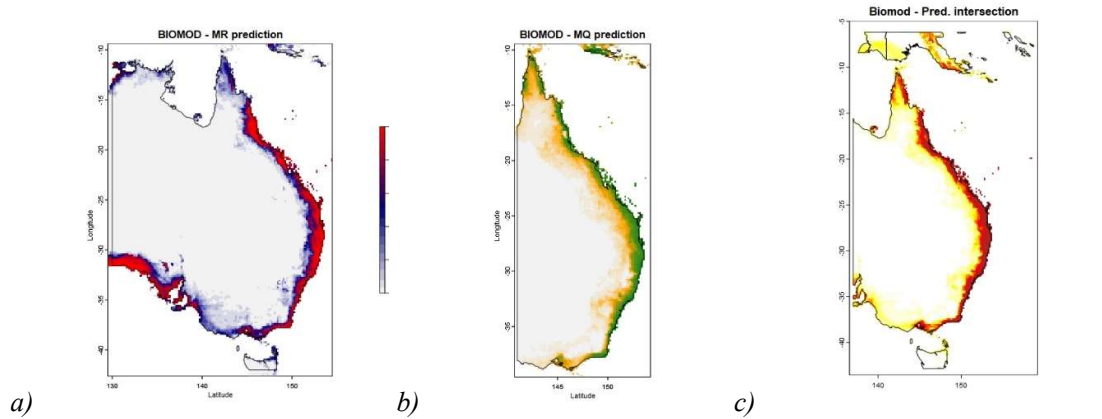


Figure 5. Predictions of area of current climate suitability using BIOMOD2 ensemble models for a) Myrtle rust, b) *Melaleuca quinquenervia*, and c) Intersection of areas of climate suitability. Where the colours indicate probability of occurrence, in accordance with colour scale to the right of each map.

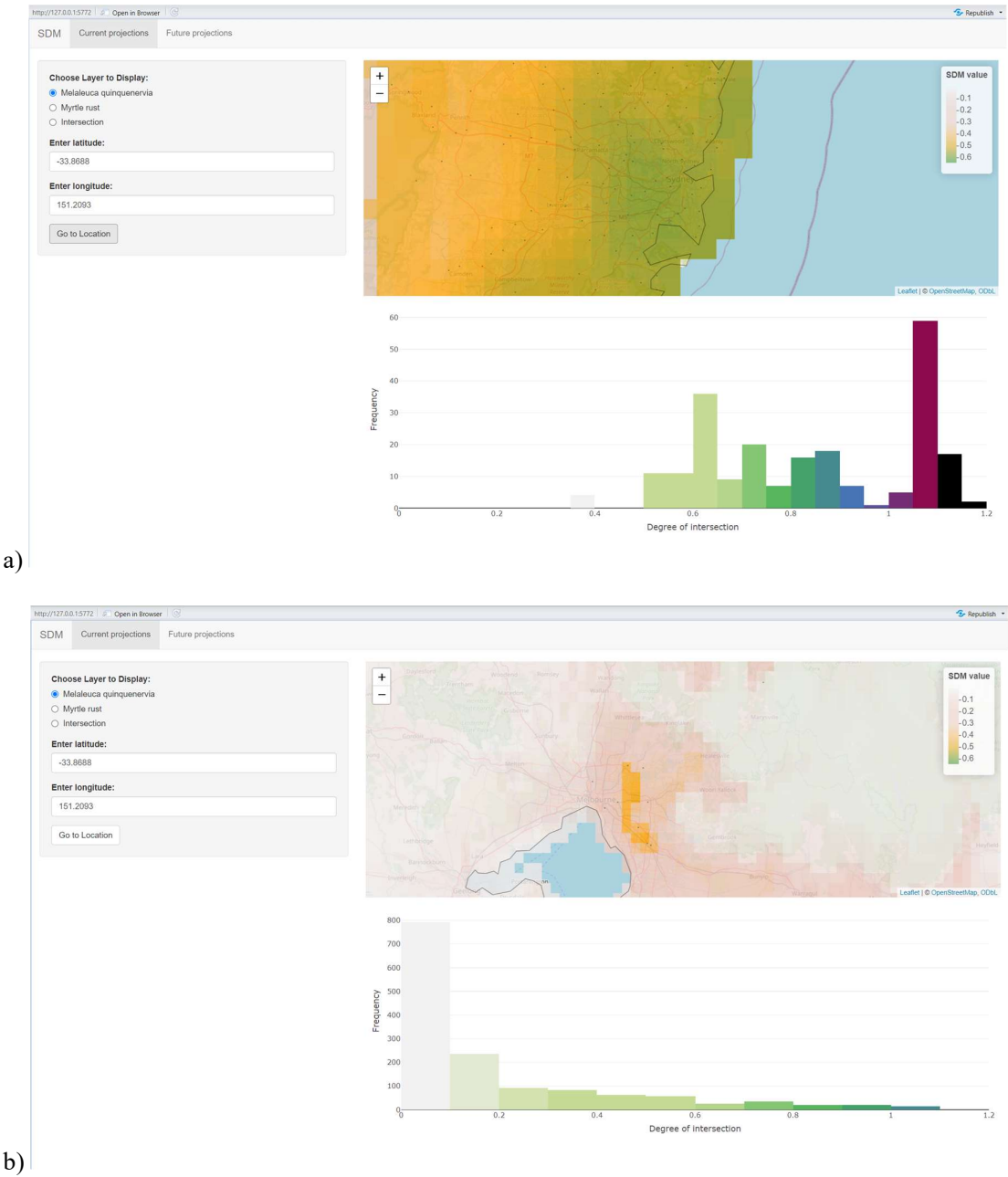
Application Deployment

An interactive application was created successfully using rasters of the predictions generated by the Maxent models. It functions as intended allowing, users to interact with the SDMs for comparisons between different species, and future climate scenarios and their years.

In the first tab of the application, users are able to zoom and pan across different locations of the study area. As the map changes, the bounding box of the map shifts. This bounding box is used to calculate a corresponding frequency histogram of the degree of intersection between both species' distribution probability – where a higher intersection of probable distribution results in higher frequency values (Fig. 6a), and vice versa (Fig 6b).

The second tab focuses on future distributions. Similarly, users are able to explore the map and different layers of different species, average year cluster (2021-2040, 2041-2060, 2061-

2080) and climate scenarios (SSP126, SSP245, SSP370, SSP585). A calculated difference between present and future distributions are also available (Fig 7).



bounding box is also outputted. a) High intersection site at Sydney, NSW, Australia. b) Low intersection site example at Melbourne, VIC, Australia.

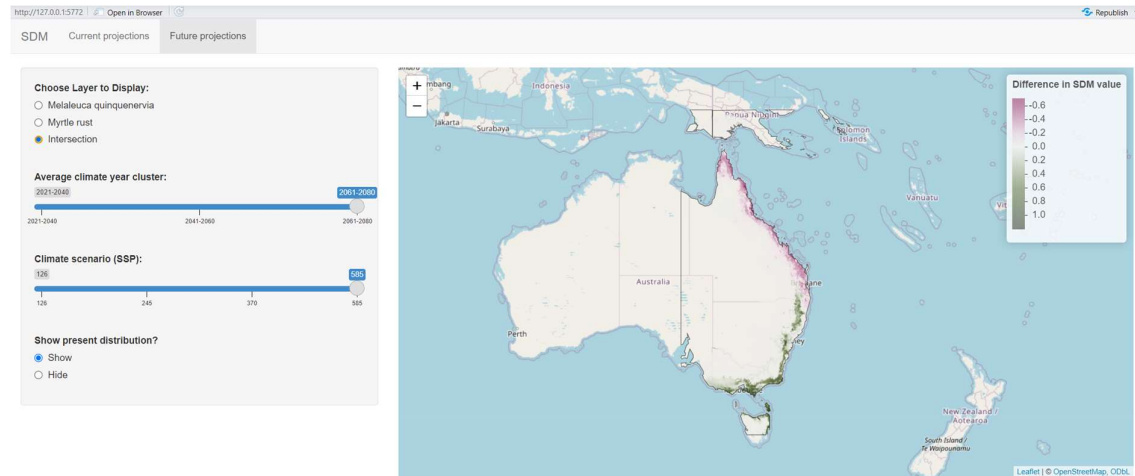


Figure 7. Second application tab. Future distributions of *Melaleuca quinquenervia*, *Austropuccinia psidii* and their intersection projected onto a leaflet world map. Different layers are able to be triggered to show the different future distributions.

Discussion

This study provides restoration practitioners with an additional decision support tool in response to the growing trend of genetic optimisation in conservation. As multi-objective optimisation techniques result in multiple options that practitioners can proceed with, DSS can assist in proceeding with the selection of a solution best suited for a specific scenario. Here, this study presents a DSS that utilises species distribution models of a restoration species, *Melaleuca quinquenervia*, and the biotic threat Myrtle rust (*Austropuccinia psidii*).

The SDMs created for these two species, were of sufficient accuracy to illustrate a framework that can be improved upon. When in comparison to the multi-model ensemble modelling attempt using BIOMOD2, Maxent showed a more conservative predicted species distribution, which better matches ground-truth data observed in-field. It is suggested that greater systematic ground-truthing actions of predicted presence and absence to be conducted. Alternatively, future presence observations for each species can be used to cross-validate

each model. These observations are also recommended to be used to update models periodically to better match ground-truth species ranges as datasets grow. With novel biotic diseases such as Myrtle rust, updating models with greater sample sizes would be particularly beneficial as they lack public awareness and historical research foundations (Carroll & Pearson, 1998; Mitchell et al., 2017; Wisz et al., 2008).

The host-pathogen pair used in this study provides a framework that can be extended to incorporate other species. However, by doing so individual models would have to be created independently for each species, each with a tailored suite of climatic variables. Multi-model ensemble modelling have been observed to be potentially more accurate than single model attempts (Huang et al., 2023). The extra cost for time is a point to be considered and balanced against the potential increase in accuracy, especially in scenarios where a large number of species require processing.

Predicting species distribution for conservation purposes have been used historically in a wide range cases, including conservation (Qazi et al., 2022). Despite this, the adoption of these tools in conservation decision making are limited by the ease of interpretation of the models created (Sofaer et al., 2019). As such our integration of the SDM's output into an interactive software enables users to better interpret results for their scenario. We encourage others to further develop this to integrate other tools useful for conservation management decisions. For instance, this may include genetic provenancing, as done in Restore and Renew (Rossetto et al., 2019), for insight on where to source material for restoration. This will enable a streamlined process of different tools and techniques that together synthesise to support the success of conservation action plans.

Data Accessibility

All scripts used are available at: https://github.com/KarinaGuo/MQ_SDM/

References

- Belbin, L., Wallis, E., Hobern, D., & Zerger, A. (2021). The Atlas of Living Australia: History, current state and future directions. *Biodiversity Data Journal*, 9, e65023. <https://doi.org/10.3897/BDJ.9.e65023>
- Benson, D., & McDougall, L. (1998). Ecology of Sydney plant species. Part 6. Dicotyledon family Myrtaceae. *Cunninghamia*, 5, 808–987.
- Bolton, K. G. E., & Greenway, M. (1999). Pollutant removal capability of a constructed wetland receiving primary settled sewage. *Water Science and Technology*, 39(6). [https://doi.org/10.1016/S0273-1223\(99\)00140-7](https://doi.org/10.1016/S0273-1223(99)00140-7)
- Bragg, J. G., Van Der Merwe, M., Yap, J. S., Borevitz, J., & Rossetto, M. (2022). Plant collections for conservation and restoration: Can they be adapted and adaptable? *Molecular Ecology Resources*, 22(6), 2171–2182. <https://doi.org/10.1111/1755-0998.13605>
- Capblancq, T., Fitzpatrick, M. C., Bay, R. A., Exposito-Alonso, M., & Keller, S. R. (2020). Genomic Prediction of (Mal)Adaptation Across Current and Future Climatic Landscapes. *Annual Review of Ecology, Evolution, and Systematics*, 51(1), 245–269. <https://doi.org/10.1146/annurev-ecolsys-020720-042553>
- Carroll, S. S., & Pearson, D. L. (1998). The effects of scale and sample size on the accuracy of spatial predictions of tiger beetle (Cicindelidae) species richness. *Ecography*, 21(4), 401–414. <https://doi.org/10.1111/j.1600-0587.1998.tb00405.x>
- Elith, J., & Franklin, J. (2013). Species Distribution Modeling. In *Encyclopedia of Biodiversity* (pp. 692–705). Elsevier. <https://doi.org/10.1016/B978-0-12-384719-5.00318-X>
- Fick, S. E., & Hijmans, R. J. (2017). WorldClim 2: New 1-km spatial resolution climate surfaces for global land areas. *International Journal of Climatology*, 37(12), 4302–4315. <https://doi.org/10.1002/joc.5086>
- Fitzpatrick, M. C., Chhatre, V. E., Soolanayakanahally, R. Y., & Keller, S. R. (2021). Experimental support for genomic prediction of climate maladaptation using the machine learning approach Gradient Forests. *Molecular Ecology Resources*, 21(8), 2749–2765. <https://doi.org/10.1111/1755-0998.13374>
- Gibson, A. K. (2022). Genetic diversity and disease: The past, present, and future of an old idea. *Evolution*, 76(S1), 20–36. <https://doi.org/10.1111/evo.14395>

Greenway, M. (1994). Litter accession and accumulation in a *Melaleuca quinquenervia* (Cav.) S.T. Blake wetland in south-eastern Queensland. *Marine and Freshwater Research*, 45(8), 1509. <https://doi.org/10.1071/MF9941509>

Grover, D. R., & Slater, P. J. (1994). Conservation value to birds of remnants of *Melaleuca* forest in suburban Brisbane. *Wildlife Research*, 21(4), 433–444.

Hoban, S., Archer, F. I., Bertola, L. D., Bragg, J. G., Breed, M. F., Bruford, M. W., Coleman, M. A., Ekblom, R., Funk, W. C., Grueber, C. E., Hand, B. K., Jaffé, R., Jensen, E., Johnson, J. S., Kershaw, F., Liggins, L., MacDonald, A. J., Mergeay, J., Miller, J. M., ... Hunter, M. E. (2022). Global genetic diversity status and trends: Towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. *Biological Reviews*, 97(4), 1511–1538. <https://doi.org/10.1111/brv.12852>

Huang, D., An, Q., Huang, S., Tan, G., Quan, H., Chen, Y., Zhou, J., & Liao, H. (2023). Biomod2 modeling for predicting the potential ecological distribution of three *Fritillaria* species under climate change. *Scientific Reports*, 13(1), 18801. <https://doi.org/10.1038/s41598-023-45887-6>

Li, Y., Kaur, S., Pembleton, L. W., Valipour-Kahrood, H., Rosewarne, G. M., & Daetwyler, H. D. (2022). Strategies of preserving genetic diversity while maximizing genetic response from implementing genomic selection in pulse breeding programs. *Theoretical and Applied Genetics*, 135(6), 1813–1828. <https://doi.org/10.1007/s00122-022-04071-6>

McJannet, D. (2008). Water table and transpiration dynamics in a seasonally inundated *Melaleuca quinquenervia* forest, north Queensland, Australia. *Hydrological Processes*, 22(16), 3079–3090. <https://doi.org/10.1002/hyp.6894>

Mitchell, P. J., Monk, J., & Laurenson, L. (2017). Sensitivity of fine-scale species distribution models to locational uncertainty in occurrence data across multiple sample sizes. *Methods in Ecology and Evolution*, 8(1), 12–21. <https://doi.org/10.1111/2041-210X.12645>

Pecchi, M., Marchi, M., Burton, V., Giannetti, F., Moriondo, M., Bernetti, I., Bindi, M., & Chirici, G. (2019). Species distribution modelling to support forest management. A literature review. *Ecological Modelling*, 411, 108817. <https://doi.org/10.1016/j.ecolmodel.2019.108817>

- Pegg, G., Lee, D. J., & Carnegie, A. J. (2018). Predicting impact of *Austropuccinia psidii* on populations of broad leaved *Melaleuca* species in Australia. *Australasian Plant Pathology*, 47(4), 421–430. <https://doi.org/10.1007/s13313-018-0574-8>
- Phillips, S. J., Anderson, R. P., & Schapire, R. E. (2006). Maximum entropy modeling of species geographic distributions. *Ecological Modelling*, 190(3–4), 231–259. <https://doi.org/10.1016/j.ecolmodel.2005.03.026>
- Qazi, A. W., Saqib, Z., & Zaman-ul-Haq, M. (2022). Trends in species distribution modelling in context of rare and endemic plants: A systematic review. *Ecological Processes*, 11(1), 40. <https://doi.org/10.1186/s13717-022-00384-y>
- Ramirez-Parada, T. H., Park, I. W., Record, S., Davis, C. C., Ellison, A. M., & Mazer, S. J. (2024). Plasticity and not adaptation is the primary source of temperature-mediated variation in flowering phenology in North America. *Nature Ecology & Evolution*, 8(3), 467–476. <https://doi.org/10.1038/s41559-023-02304-5>
- Rayachhetry, M. B., Elliott, M. L., & Van, T. K. (1997). Natural Epiphytotic of the Rust *Puccinia psidii* on *Melaleuca quin-quenervia* in Florida. *Plant Disease*, 81(7), 831–831. <https://doi.org/10.1094/PDIS.1997.81.7.831A>
- Rossetto, M., Bragg, J., Kilian, A., McPherson, H., Van Der Merwe, M., & Wilson, P. D. (2019). Restore and Renew: A genomics-era framework for species provenance delimitation. *Restoration Ecology*, 27(3), 538–548. <https://doi.org/10.1111/rec.12898>
- Sofaer, H. R., Jarnevich, C. S., Pearse, I. S., Smyth, R. L., Auer, S., Cook, G. L., Edwards, T. C., Guala, G. F., Howard, T. G., Morissette, J. T., & Hamilton, H. (2019). Development and Delivery of Species Distribution Models to Inform Decision-Making. *BioScience*, 69(7), 544–557. <https://doi.org/10.1093/biosci/biz045>
- Tran, D. B., & Dargusch, P. (2016). *Melaleuca* forests in Australia have globally significant carbon stocks. *Forest Ecology and Management*, 375, 230–237. <https://doi.org/10.1016/j.foreco.2016.05.028>
- von Storch, J.-S., Putrasahan, D., Lohmann, K., Gutjahr, O., Jungclaus, J., Bittner, M., Haak, H., Wieners, K.-H., Giorgetta, M., Reick, C., Esch, M., Gayler, V., de Vrese, P., Raddatz, T., Mauritsen, T., Behrens, J., Brovkin, V., Claussen, M., Crueger, T., ... Roeckner, E. (2017). *MPI-M MPIESM1.2-HR model output prepared for CMIP6 HighResMIP* (Version 20230720)

[Application/x-netcdf]. Earth System Grid Federation.

<https://doi.org/10.22033/ESGF/CMIP6.762>

Wisn, M. S., Hijmans, R. J., Li, J., Peterson, A. T., Graham, C. H., Guisan, A., & NCEAS Predicting Species Distributions Working Group. (2008). Effects of sample size on the performance of species distribution models. *Diversity and Distributions*, 14(5), 763–773.
<https://doi.org/10.1111/j.1472-4642.2008.00482.x>

Zizka, A., Silvestro, D., Andermann, T., Azevedo, J., Duarte Ritter, C., Edler, D., Farooq, H., Herdean, A., Ariza, M., Scharn, R., Svantesson, S., Wengström, N., Zizka, V., & Antonelli, A. (2019). CoordinateCleaner: Standardized cleaning of occurrence records from biological collection databases. *Methods in Ecology and Evolution*, 10(5), 744–751.
<https://doi.org/10.1111/2041-210X.13152>

Zoete, T. (2001). Variation in the vegetation of Melaleuca quiquenervia dominated forested wetlands of the Moreton region. *Plant Ecology*, 152(1), 29–57.
<https://doi.org/10.1023/A:1011431911988>

Supplementary Information

Supplementary Table 1. Variable contribution for Maxent modelling of *Austropuccinia psidii*

Bioclimatic variable (Fick & Hijmans, 2017)	Contribution
5	0.359
7	0.225
6	0.18
2	0.111
8	0.061
18	0.04
14	0.016
1	0.009

Supplementary Table 2. Variable contribution for Maxent modelling of *Melaleuca quinquenervia*

Bioclimatic variable (Fick & Hijmans, 2017)	Contribution
12	0.489
5	0.238
4	0.177
10	0.086
14	0.006
15	0.003
16	0.001

Supplementary Table 3. Variable contribution for Biomod Ensemble modelling of *Austropuccinia psidii*

Bioclimatic variable (Fick & Hijmans, 2017)	Contribution
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7	1.000000
6	0.873
1	0.733
5	0.672
8	0.617
14	0.124
2	0.062
18	0.045

Supplementary Table 4. Variable contribution for Biomod Ensemble modelling of *Melaleuca quinquenervia*

Bioclimatic variable (Fick & Hijmans, 2017)	Contribution
12	0.641
10	0.243
5	0.256
16	0.187
4	0.180
15	0.045
14	0.018