Conservation macrogenetics reveals the potential hidden consequences of the 2019-2020 Black Summer fires on Australian biodiversity

Jarrod Sopniewski[1,2*], Rhiannon Schembri[3,4], Craig Moritz[4], Andrew M. Baker[5,6], Stephane Batista[5], Stephen Donnellan[7,8], Mark D. B. Eldridge[8], Emma L. Gray[5], Ian C. Gynther[6,9], Greta J. Frankham[8], Harry B. Hines[6,9], Conrad J. Hoskin[10], Michael Mahony[11], Eugene D. Mason[12], Jane Melville[13,14], Nicola J. Mitchell[1], Madeline E. F. Mutton[9], David Newell[15], Kate O'Hara[4], Paul M. Oliver[6,16], Sally Potter[3,8], Jodi J. L. Rowley[8,17], Ben C. Scheele[18], Glenn Shea[8,19], Joanna Sumner[13], Renee A. Catullo[1]

Corresponding author

[*] jarrod.sopniewski@gmail.com

Affiliations

[1] School of Biological Sciences, University of Western Australia, Crawley, WA, Australia

[2] Centre for Conservation Ecology and Genomics, University of Canberra, Bruce, ACT, Australia

[3] School of Natural Sciences, Macquarie University, Sydney, NSW, Australia

[4] Division of Ecology and Evolution, Research School of Biology and Centre for Biodiversity Analysis, The Australian National University, Acton, ACT, Australia

[5] School of Biology and Environmental Science, Queensland University of Technology, Brisbane, QLD, Australia

[6] Biodiversity and Geosciences Program, Queensland Museum, South Brisbane, QLD, Australia

[7] South Australian Museum, Adelaide, SA, Australia

[8] Australian Museum Research Institute, Australian Museum, Sydney, NSW, Australia

[9] Department of the Environment, Tourism, Science and Innovation, Moggill, QLD, Australia

[10] College of Science & Engineering, James Cook University, Townsville, QLD, Australia

[11] School of Environmental and Life Sciences, The University of Newcastle, NSW, Australia

[12] NSW Department of Climate Change, Energy, the Environment and Water, Alstonville, NSW, Australia

[13] Museums Victoria Research Institute, Melbourne, VIC, Australia

[14] School of Biological Sciences, Monash University, Clayton, VIC, Australia

[15] Faculty of Science and Engineering, Southern Cross University, Lismore, NSW, Australia

[16] Centre for Planetary Health and Food Security, Griffith University, Nathan, QLD, Australia

[17] Centre for Ecosystem Science, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, NSW, Australia

[18] Fenner School of Environment and Society, The Australian National University, Acton, ACT, Australia

[19] Sydney School of Veterinary Science, University of Sydney, Sydney, NSW, Australia

Running title

Macrogenetics reveals cryptic fire impacts

Abstract

The use of genetic analyses has become ubiquitous in conservation planning and management as biodiversity is increasingly threatened globally. Typically, such analyses are employed at the species-level, though as genetic data accrue, it is now possible to consider the genetic composition of multiple species across landscapes. Such macrogenetic perspectives can reveal the potential genetic ramifications of extreme disturbance events, such as the catastrophic Australian ‘Black Summer’ wildfires of 2019/20. This extensive event severely impacted habitats and fauna across much of eastern Australia – but whether there have been cryptic impacts upon genetically distinct populations, or significant erosion of high diversity populations across species, remains unknown. Here, we present a conservation macrogenetics framework to examine the potential genetic impacts of large-scale disturbances. Using hundreds of samples, spanning dozens of frog, mammal, and reptile species, we first demonstrate how reduced-representation sequencing can be aggregated across species to describe the distribution of genetic diversity across a landscape. We then show that, whilst variable across the study area, these unprecedented fires generally burned in areas where genetic diversity of sampled taxa was higher than areas left unburnt. Additionally, areas with high concentrations of evolutionarily distinct and short-range species were disproportionally represented in burned regions. In particular, potential cross-taxonomic adverse effects were greatest in Australia’s southeast and central eastern seaboard regions. More broadly, our work exhibits how the conservation genetics principles often applied at a species-level can be expanded to landscapes, improving our understanding of the genetic implications of large-scale disturbance events.

Keywords

conservation macrogenetics, landscape-scale, wildfire, disturbance event, conservation prioritisation, genetic diversity

1. Introduction

Biodiversity across the globe is in peril. Species from all realms of life are undergoing declines, with as many as half facing potential imminent extinction (Finn et al., 2023). The drivers of this global loss of biodiversity are primarily anthropogenic in nature, and ongoing (Ceballos et al., 2015, 2017). In particular, the multifaceted threat of climate change and its associated extreme disturbance events increasingly place pressure upon ecological communities worldwide (Dirzo et al., 2022; Habibullah et al., 2022; Kelly et al., 2020; Urban, 2015). As a result, several methods across the domains of conservation biology are employed to prevent the further erosion of biodiversity. Among these is the use of population genetics, which is becoming ubiquitous in conservation settings (Hoban et al., 2022), reflecting the premise that the maintenance of genetic diversity within species is critical to their short- and long-term persistence (DeWoody et al., 2021). As genetic data amass, the opportunity to employ these data across multiple species to describe broad, landscape scale patterns of genetic diversity has emerged. This aggregative use of data, or ‘conservation macrogenetics’, has the potential to enhance global efforts to stem biodiversity loss (Leigh et al., 2021; Schmidt, Hoban, & Jetz, 2023).

At the species-level, an understanding of genetic diversity may confer improved conservation outcomes for several reasons. Generally, higher genetic diversity in individuals and populations is a hallmark of greater evolutionary adaptive potential to environmental change (Fernandez-Fournier et al., 2021; Forester et al., 2022; Kardos et al., 2021) and elevated fitness and persistence in the face of threatening processes (Doyle et al., 2019; Reed & Frankham, 2003; Scott et al., 2020, Willoughby et al., 2017). Consequentially, the impacts of reduced genetic diversity can be substantial. Studies have found that often, across a variety of taxa, threatened species tend to have lower genetic diversity than those that are non-threatened (Canteri et al., 2021; Li et al., 2016; Willoughby et al., 2015). Exceptions to this general pattern exist; low genetic diversity does not in all cases necessitate elevated threat status (Schmidt, Hoban, Hunter, et al., 2023), and high genetic diversity is not in itself an infallible protection against population declines (Roycroft et al., 2021). However, it is fair to suggest that the retention of existing genetic diversity within wild populations is of great value to their conservation over the longer term (Frankham, 2005, 2015; Kardos et al., 2021). Indeed, for this reason, international policy targets intended to halt the further loss of biodiversity specify the retention of genetic diversity as a key aim (e.g., Target 4 of the UN’s Convention on Biological Diversity Kunming-Montreal Global Biodiversity Framework; (CBD, 2022)).

Partly in response to such targets, alongside advances in genetic sequencing and analysis methodologies, a wealth of high-quality genetic data have been generated for thousands of species (Hoban et al., 2022; Leigh et al., 2021). This provides an opportunity for comparative macrogenetics to guide the retention of biodiversity across broad spatial scales. An understanding of the distribution of genetic diversity in fine detail across landscapes provides a means to direct conservation action to areas where the cross-taxonomic benefits are greatest (Leigh et al., 2021; Nielsen et al., 2023; Paz-Vinas et al., 2015; Schmidt, Hoban, & Jetz, 2023). Several studies have already demonstrated the potential of conservation macrogenetics by describing macrogenetic trends relevant to landscape-scale conservation efforts. For example, Almeida-Rocha et al. (2020) showed that species inhabiting anthropogenically disturbed landscapes had lower genetic diversity, while Schmidt et al. (2024) revealed that the global protected area network does not adequately protect genetically diverse populations. An additional promising, though as yet unexplored, application of conservation macrogenetics is the investigation of the consequences of extreme, large-scale, stochastic disturbance events to the genetic diversity of an affected landscape. Biodiversity is increasingly threatened by such disturbances (Harris et al., 2018), and their frequency and intensity are predicted to rise further (Stott, 2016). Given the links between a species' genetic composition and its likelihood of persistence and recovery following declines (Banks et al., 2013; Kardos et al., 2021), the application of conservation macrogenetic principles to such cases could result in a deeper understanding of the potential genetic ramifications of these events, allowing for better-informed conservation efforts post-disturbance.

To examine the capacity of macrogenetics to guide conservation action in the context of environmental disturbances, we explored the genetic ramifications of the Australian 'Black Summer' wildfires of 2019 and 2020, which burned ~97,000 km^2 of vegetation across southern and eastern Australia (Ward et al., 2020). This climate change fuelled event (Abram et al., 2021) was historically unprecedented (Boer et al., 2020; Collins et al., 2021), and accordingly, the landscape-scale implications for biodiversity have been explored from multiple angles (Driscoll et al., 2024). Studies have included the estimation of the degree of species distributional overlap with fire (Ward et al., 2020), mortality estimates for multiple species (Legge et al., 2022), and potential ecological niche impacts across taxa (Sopniewski et al., 2024). However, the repercussions of these fires across the landscape, in terms of cross-taxonomic genetic composition, are unknown. The long-term consequences of this disturbance event could vary greatly depending upon the intraspecific genetic composition of species occupying impacted areas. If highly diverse regions were impacted, the ramifications of these fires could be more severe than initially thought, leaving remnant populations with a reduced ability to withstand further threatening processes and recover to their pre-fire sizes (Willoughby et al., 2015). Hence, the application of a macrogenetic approach to this case could provide a more comprehensive understanding of the genetic consequences of this disturbance across the fire-affected landscape.

Here, we provide a framework for the application of conservation macrogenetic principles at a landscape-scale following an unprecedented environmental disturbance. We first present a novel framework to calculate genetic diversity across dozens of species from three taxonomic Classes, using reduced-representation sequencing datasets in the form of single nucleotide polymorphisms (SNPs). Despite their ubiquity in conservation genetics, SNPs have thus far rarely been employed in conservation macrogenetic studies, likely due to methodological limitations regarding the comparability of genetic estimates across taxa and studies (Hemstrom et al., 2024). However, by expanding upon recent developments that have alleviated these issues (Schmidt et al., 2021; Sopniewski & Catullo, 2024), we demonstrate how SNP data can be used to generate consistent and comparable estimates of genetic diversity such that the genetic composition of a landscape, representing multiple sympatric species, can be described. We then demonstrate the utility of this framework by estimating the potential genetic impacts of the Black Summer fires across an extensive region of southern and eastern Australia, providing a novel insight into the potential consequences of this severe environmental disturbance.

2. Materials and Methods

2.1. Genomic data background

In response to the Australian 2019-2020 Black Summer fires, a project was initiated in 2020? to determine the genetic composition of potentially affected species. Coordinated by the Centre for Biodiversity Analysis at the Australian National University, with support from the National Environmental Science Program (NESP) Threatened Species Hub, BioPlatforms Australia, and tissue collections held by Australian museums, experts across a suite of vertebrate species were invited to lead genetic assessments for vertebrate species predicted to have been impacted. Species were selected that had known or suspected strong population substructure or undescribed species, and/or had sufficient tissue samples available for genetic analyses (Catullo & Moritz, 2021; Catullo et al., 2021). Group members provided genetic samples which were sufficient for study inclusion (see below) for 20 frog species, 6 mammal species, and 7 reptile species. These species were present across a study area encompassing the eastern part of South Australia (including Kangaroo Island), much of Victoria and New South Wales, and the south-eastern region of Queensland (Figure SM1), a region larger than the extent of the fires because species' distributions extend beyond burnt areas. Sequencing was performed in a similar manner for each species, and specific details for each sample can be found with their associated BioPlatforms Australia (BPA) upload (details for each in Table SM1). Briefly, DNA extractions were performed either by contributing labs using published methods or commercially available kits, or commercially by Diversity Arrays Technology Pty Ltd. (Canberra) (DArT). Extracted samples were submitted to DArT for genomic library preparation using proprietary techniques (Kilian et al., 2012). Libraries were then sequenced at the Biomolecular Resource Facility at the Australian National University.

Following sequencing, population genetic analyses were performed for each species following a standardized pipeline (Catullo et al., 2021). A formatted genetic summary was then sent to relevant species experts (coauthors, as listed in Table SM1) who prepared a species assessment based on this information (a brief example of this process is outlined in the Supplementary Material). For some species, this involved the identification of multiple species-level operational taxonomic units (OTUs) within what was considered (at the time of analysis) to be a single species in the published literature. For the purpose of this study, we considered each expert identified OTU independently. Each assessment also described populations with significant genetic divergence which should be considered conservation units (CUs) within an OTU (Palsbøll et al., 2007). These CUs formed the basis of all following analyses. Each of these species' assessments were compiled into a report for government agencies to guide conservation management, though due to the sensitivity of this data, the report is not publicly available.

2.2. Spatial projections of conservation units

We created a spatial projection for the distribution of each CU using species distribution modelling (SDM). For each OTU, we downloaded occurrence records from the Atlas of Living Australia (all species) (ALA, 2024) and FrogID (frogs only) (Rowley & Callaghan, 2020). For OTUs that had recently undergone taxonomic revision, we used the most recent species name but ensured that we checked former species names for likely records (for example, we re-assigned *Limnodynastes dumerilii* records that were likely to be the more recently described *L. superciliaris* based on their location). We cleaned each species' dataset using broad guidelines for data filtering (Gueta & Carmel, 2016). Specifically, using R (R Core Team, 2024), we first removed records without location data. We then cropped any records from outside of an OTU's known distribution (buffered by one degree), using distributions from the Australian Frog Atlas (Cutajar et al., 2022) for frogs and IUCN distribution polygons (IUCN, 2024) for mammals and reptiles. We also removed records not recorded to at least 2 decimal places, and thinned records such that only one record was present in any 30-arcsecond grid cell (the resolution of environmental data used for subsequent modelling). All spatial data preparation was conducted using the 'terra' package in R (Hijmans et al., 2022).

We then created an SDM for each OTU. Generally, SDMs are most accurate when variables are chosen with reference to the biology of the species in question (Guisan et al., 2013), but in instances where multiple SDMs for many species are being constructed (such as here) this is often unfeasible. Hence, for each OTU, we initially employed a large suite of ecological predictors which included each of the 19 bioclimatic variables and elevation from the WorldClim 2.0 dataset (Fick & Hijmans, 2017), topographic wetness index (Gallant & Austin, 2012), mean vegetation height (Ticehurst et al., 2023), and gross primary productivity (Li & Xiao, 2019), following Sopniewski et al. (2024). Climatic layers from WorldClim were downloaded at 30 arcsecond resolution, and other layers were reprojected to match this resolution. For each OTU, we then reduced this set of ecological predictors to the largest uncorrelated set for that OTU as follows. First, using the 'terra' package, all variables were cropped to that OTU's distribution (using the species distribution polygons downloaded earlier). Second, the variance inflation factor (VIF) for each variable was calculated to determine the degree of collinearity present, and the variable with the highest VIF score was removed. This was repeated until only a set of variables for which each had a VIF score < 10 remained. Third, we used Maxent (Phillips et al., 2017), implemented via the 'dismo' package (Hijmans et al., 2017) to construct an SDM. For each species, we selected 10% of the available background cells as pseudo-absences. We note that modelling can be affected by preferential sampling bias; accordingly, prior to modelling, we created a bias layer for each taxonomic Class (frogs, mammals, and reptiles), replicating methods used in Sopniewski et al. (2022). For each OTU, this bias layer was used to weight the selection of pseudo-absences accounting for the sampling density of that OTU's Class. Finally, for each OTU, we randomly selected 20% of occurrence records to withhold for model evaluation and ran a Maxent model with the remaining 80%. Using the withheld occurrence records, we then evaluated each OTU's model using the *evaluate* function from the 'dismo' package. From this result, we were able to derive model performance statistics and environmental suitability thresholds to make binary suitable/unsuitable predictions.

Once we had created an SDM for each OTU, we aimed to make a prediction of the distribution of each individual CU within the bounds of their OTU's distribution. To do so, we employed the lineage range estimation method described by Rosauer et al. (2015) to define the likely boundaries of each CU's distribution, based on the SDMs constructed for each OTU. Briefly, for each OTU, we first loaded all locations for each genotyped sample for that OTU, as well as the associated Maxent SDM prediction, into R. We then generated a cost distance layer from sequenced locations for each CU within that OTU, with cost defined as the suitability value (as determined from the SDM) subtracted from 1 (such that cells with a low suitability had a higher cost). For each CU, a weight layer was then generated according to the inverse cube of this cost, which was then multiplied by the model likelihood such that each cell within the SDM was assigned to a particular CU. Binary presence/absence raster layers were then created: for each CU, all cells with a suitability value higher than the maximum sum of sensitivity and specificity (maxSSS) values derived from its OTU Maxent model were included in its predicted distribution. Each of these CU predictions were then assessed by relevant species experts (Table SM1), and any erroneous predictions were amended. Figures representing the final predicted distributions of each CU are presented in the Supplementary Material.

2.3. Genetic composition pipeline

Using conservation macrogenetic principles, our goal was to describe the genetic composition of the study area by amalgamating genetic data across multiple species. We described this composition in two ways. First, we calculated genetic diversity, which we measured using expected heterozygosity (H_E), observed heterozygosity (H_O), and nucleotide diversity (π). Second, we used a metric related to phylogenetic endemism, a measure of range-restricted genetic distinctiveness (Rosauer et al., 2009), which we termed 'weighted distinctiveness' (WD). We describe WD below (Section 2.3.2).

2.3.1. Population genetics statistics

We obtained the raw short read sequences for each sample described above (Section 2.1) in FASTQ format and followed Sopniewski & Catullo (2024) to prepare our data for analysis, primarily using 'Stacks' v2.0 (Catchen et al., 2013; Rochette et al., 2019). First, we trimmed the barcodes, removed uncalled bases, and discarded low quality reads using *process_radtags*. Following this, we used 'Trimmomatic' v0.39 (Bolger et al., 2014) to filter adapter sequences with the parameters "ILLUMINACLIP:TruSeq3-SE:2:20:10; LEADING:5, SLIDINGWINDOW:4:5; MINLEN:68". Loci were then constructed de novo using *ustacks*, setting "M" to 4 and using default parameters for "m"

(3) and "N" (M + 2) (Schmidt et al., 2021; Sopniewski & Catullo, 2024). Following Sopniewski & Catullo (2024), we treated each CU independently for all subsequent analyses. Continuing with the 'Stacks' pipeline, we constructed a catalogue of loci using *cstacks*, setting "n" to 4. For catalogue construction, we used either every unique sample or 20 randomly selected unique samples (whichever was smaller). All samples then had their loci matched to the catalogue using *sstacks* before being transposed, using *tsv2bam,* for population genetics statistics calculations.

For statistics calculated using 'Stacks' to be comparable, both fixed and variable sites should be used, sample sizes should be kept both low and equal, and missing data should be omitted (Schmidt et al., 2021; Sopniewski & Catullo, 2024). Accordingly, we developed a pipeline for the calculation of population genetic statistics that accounted for these requirements. For each CU, we created 'population maps' (lists of individual samples used to calculate population genetic statistics in the 'Stacks' pipeline) for groups of exactly five unique samples – a threshold chosen to minimise the effects of sample size upon diversity estimates whilst adequately representing population-wide genetic diversity (Schmidt et al., 2021; Sopniewski & Catullo, 2024). To capture any geographic variation of diversity within each CU, we spatially biased these population maps such that one population map for each individual sample was created, each time selecting four unique samples comprising of its closest geographic neighbours. We then called SNPs from the catalogue using *gstacks*, before calculating population genetic statistics using *populations*, with the call rate filter set to 1 (no missing data allowed) (Schmidt et al., 2021; Sopniewski & Catullo, 2024). Any CUs with less than five individuals could not have their genetic diversity statistics reliably calculated, thus were excluded from further analyses.

2.3.2. Weighted distinctiveness calculation

To represent range-restricted evolutionary uniqueness across the landscape, we calculated a metric we termed 'weighted distinctiveness' (WD). This metric considered the evolutionary distinctiveness of a CU, relative to its OTU, and weighted this distinctiveness by its range size. Accordingly, a CU which has been historically isolated from other CUs within its OTU, and exists in only a small area, would be allocated a high value. This measure differs from phylogenetic endemism in that it considers the evolutionary distinctiveness of a CU only in the context of its OTU, rather than the position of an OTU in a broader phylogenetic tree, i.e., we calculated the phylogenetic distinctiveness within each OTU instead of across an all-taxon phylogeny. We deemed this finer-scale approach to be more appropriate for our aims, which were to describe the distribution of genetic distinctiveness at a CU-scale across a landscape, which would be confounded by the inclusion of long ancestral branches in an all-taxon phylogeny.

First, for each OTU with more than one CU (Table SM1), we constructed a maximum likelihood phylogenetic tree in 'IQTree' (Minh et al., 2020) using the output from 'Stacks' (Supplementary Methods S1). All CUs were included in a phylogenetic tree, even if the number of samples did not permit their inclusion in genetic diversity analyses, to ensure appropriate calculation of evolutionary distinctiveness (Table SM1). Next, we converted each OTU phylogeny into an ultrametric tree using the R package 'ape' (Paradis & Schliep, 2019). We randomly selected one individual from each CU to retain and dropped all other tips, before rescaling the tree such that their branches summed to 100. This ensured that each OTU phylogeny had a maximum possible evolutionary distinctiveness (ED) value of 100, and therefore each OTU contributed an equal total ED to landscape-scale analyses. We then calculated the ED value for each CU (the proportion of the OTU's entire evolutionary history that was held within that CU) using the 'picante' package (Kembel et al., 2010). All OTUs for which only one CU existed were assigned an ED value of 100. Weighted distinctiveness (WD) values were then calculated for each CU by dividing its ED by the size of its modelled distribution (measured in square kilometres) using the 'terra' package.

2.4. Spatial aggregation of genetic composition metrics

Once we had calculated comparable genetic diversity and WD values for each CU, we stacked these together across the landscape. First, we defined genetic diversity (H_E, H_O, π) for each of our CUs. We represented these in two ways: (1) a mean value for the entire CU, calculated as the mean result of each population map repetition for that CU, and (2) a spatial projection of genetic diversity. To create the spatial projection, we first added the value of each population map result to the geographic location of the 'focal sample' upon the previously modelled CU distribution raster layer. We then interpolated these values across the CU layer using the *interpIDW* function of the 'terra' package. We repeated this process for each metric, producing three raster layers representing H_E, H_O, and π for each CU that accounted for any intra-CU variation in diversity.

For each genetic diversity metric, we then overlaid (stacked) the raster layers of all CUs and calculated the mean value for each cell in the study area using the 'terra' package in R, such that each cell across the landscape represented the mean diversity value of the CUs present in that cell. For WD, we assigned the calculated WD value of each CU to the entirety of its modelled distribution, then also calculated the mean value in the same manner. We then repeated the stacking process, for each of the three taxonomic Classes (frogs, mammals, and reptiles), and for threatened and non-threatened OTUs. Given we were interested in comparing cross-taxonomic patterns of diversity and distinctiveness, for comparative analyses, we restricted our study area further to include only cells occupied by at least 3 OTUs.

2.5. Assessing the macrogenetic impacts of the Black Summer fires

2.5.1. Describing the macrogenetic composition of the study area

First, we examined the similarity between the trends we observed for each of our genetic diversity metrics (H_E, H_O, and π) by calculating Pearson's r, using the base R 'stats' package. We also used Pearson's r to examine correlations between taxonomic Classes, for both genetic diversity and WD. When describing the genetic composition of the landscape, we used the Interim Biogeographic Regionalisation of Australia (IBRA) version 7 (DAWE, 2012) bioregions to identify areas with particularly high and low values (Figure SM1). Whenever we refer to a bioregion, we refer specifically to the cells within that bioregion that meet our threshold for inclusion in the study area (occupancy of 3 or more OTUs) – not the full extent of the bioregion.

2.5.2. Evaluating fire impact through a macrogenetic lens

The areas burned by the Black Summer fires were defined by the AUS GEEBAM Fire Severity Dataset (2019-2020) (DAWE, 2020), which details fire extent and severity over the period between 1 July 2019 and 13 February 2020. Cells within the study area were classified as either unburned, mildly burned (GEEBAM value 3) or severely burned (GEEBAM values 4 and 5) (DAWE, 2020). Our analyses considered regions 'burned' (mild and severe fire), as well as 'severely burned' (only severe fire). To explore differences between burned and unburned regions of the landscape, we generally discuss the median and range of values of areas (mean values with confidence intervals were not appropriate, given the uneven skew and non-normal distribution of our data). We described differences between burned and unburned areas across the entire study area, as well as specifically within bioregions that had substantial portions of their extent burned (>10%).

To determine where the impacts of the fires may have been most acute across the landscape, we identified burned cells that had genetic diversity or WD values within the highest quartile for each of frogs, reptiles, and mammals. We then aggregated these results to describe burned regions within the study area that were especially valuable (high genetic diversity or high WD) across each of the taxonomic groups, thereby identifying areas where the cumulative potential impacts of the fires were at their highest. Finally, we also examined any relationships at the CU-level between genetic diversity/WD and the degree to which a CU experienced fire. Specifically, we performed linear regressions for each of the metrics we had calculated and the proportion of a CU's modelled distribution that had burned. We repeated this for all CUs, each taxonomic Class, and each threat status separately.

3. Results

3.1. Genetic composition across the landscape

Our final dataset was comprised of 33 operational taxonomic units (OTUs), subdivided into 63 independent conservation units (CUs) (Table SM1). Of the 33 OTUs, 13 were represented by only a single CU. Frogs represented 20 of the 33 OTUs (12 of which were listed as threatened on the IUCN Red List as of 2020), 6 were mammals (3 threatened), and 7 were reptiles (none threatened). OTU richness per grid cell within the study area ranged from a single OTU to 11 (Figure SM2). For comparative analyses, we only considered cells within which our species distribution models predicted occupancy of at least 3 OTUs, which totalled to an area of 368,268 km^2.

When considering all OTUs, we found mean genetic diversity to generally follow a latitudinal gradient, with diversity being lowest in the north and highest in the south (Figure 1). This pattern was similar for each metric; both observed heterozygosity (H_O) and nucleotide diversity (π) (Figure SM3), were highly correlated with expected heterozygosity (H_E) (Pearson's r = 0.95 and 0.99, respectively), thus herein we refer only to H_E. A notable exception to the general pattern of diversity was the New England Tablelands bioregion (Figure 1b), a region to the north of the study area where diversity was higher than its surrounding bioregions. The highest diversity, found in the 'Plains' bioregions to the south of the study area (Figure 1c), appeared to be driven largely by the presence of non-threatened frogs, group which tended to have the highest diversity values (Figure SM4). Indeed, the general patterns of diversity across the study area were primarily reflective of those of frogs, the most well-represented group: H_E for frogs had a relatively high correlation with cross-taxonomic H_E (Pearson's r = 0.68), whilst mammals had a far weaker correlation (0.33), and reptiles had none (-0.03). Absolute values of genetic diversity were generally highest in frogs, followed by reptiles and mammals, and were also higher in non-threatened OTUs than threatened OTUs (Figure SM4).

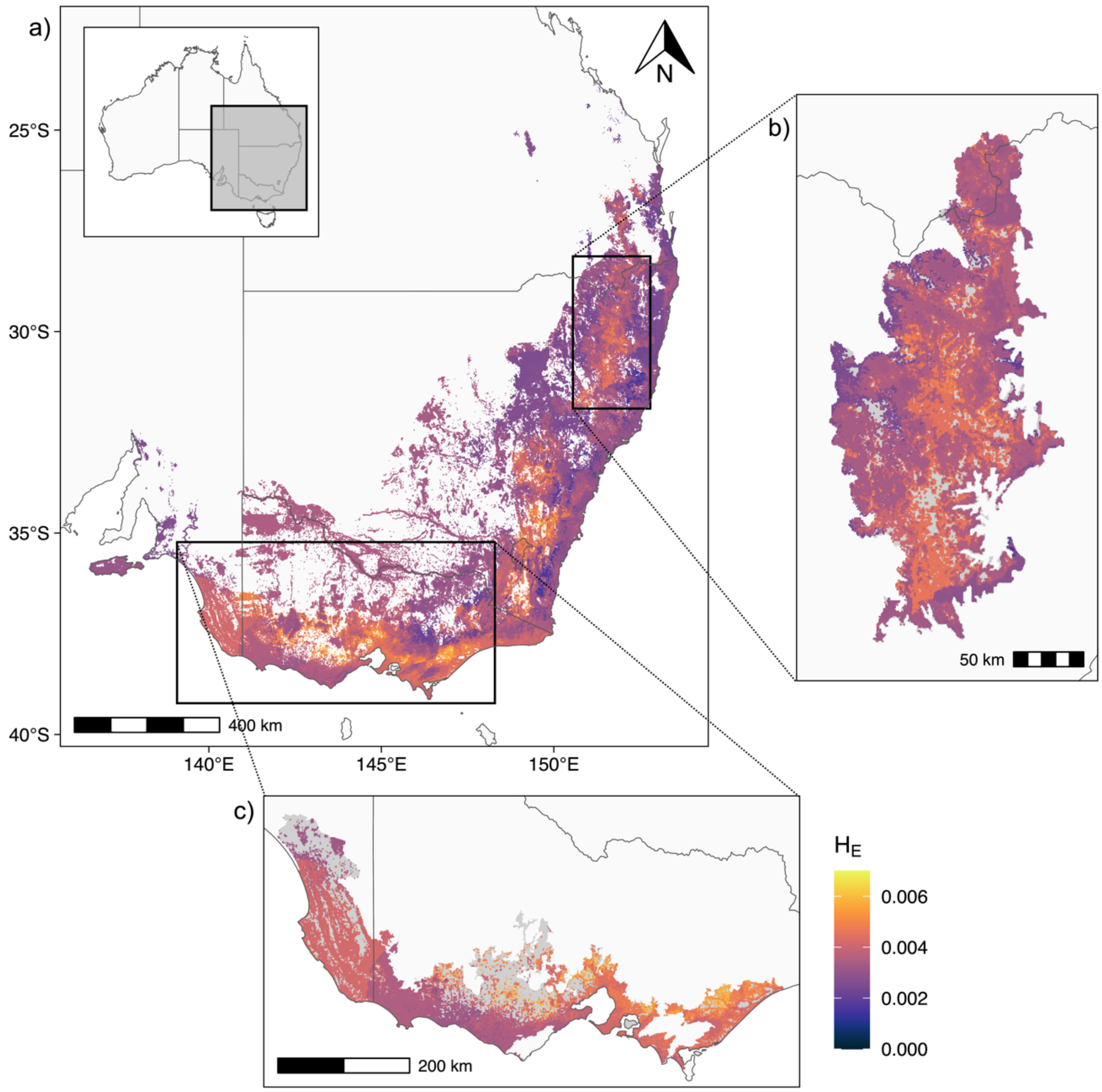

Figure 1. Expected heterozygosity (H_E) across the study area, defined by the mean H_E value of all CUs present within a cell (a). Only cells with an occupancy of 3 or more OTUs are shown. Lighter, more yellow cells are indicative of higher average H_E. A general latitudinal gradient whereby H_E increases from the north to the south can be observed, though a notable area of relatively high diversity is present in the New England Tablelands IBRA bioregion (b). H_E is highest in the southern lowland regions of the study area, specifically the South East Coastal Plain, the Naracoorte Coastal Plain, and the Southern Volcanic Plain (c). The high values in these areas are primarily driven by diverse, non-threatened frog OTUs within our dataset.

The genetic diversity patterns we described contrasted to those we observed for weighted distinctiveness (WD). The regions with evolutionarily distinct, range-restricted CUs were generally found in the peripheries of the study area. Cells within the upper decile (10%) of values were primarily observed in the Kanmantoo bioregion (which includes Kangaroo Island), the southeast coastal region, and the northern bioregions, often upon mountaintops (Figure 2). In particular, the South Eastern Queensland bioregion held multiple cells whose values were especially high. These outliers were primarily due to the presence of many short-range endemic OTUs, such as the Wollumbin Pouched Frog, *Assa wollumbin* (Figure 2), and range-restricted CUs, including CUs of the Mountain Frog, *Philoria kundagungan* (Figure 2), other *Philoria* CUs, and *Assa darlingtoni* CUs. Conversely, the lowest values for WD were observed in the inland regions west of the Great Dividing Range, where several widespread CUs reside. Intermediate weighted distinctiveness values (those inside the bounds of the 10% and 90% deciles) were far lower than the values in the northern bioregions, and patterns only became evident when these were log-transformed, which revealed a subtle pattern of decreasing WD with latitude and distance from the coast (Figure SM5). Even more so than for diversity, frog WD highly correlated with the aggregate landscape value (Pearson's r = 0.98), with weaker correlations observed for mammals (0.24), and reptiles (though far stronger than for genetic diversity: 0.47) (Figure SM6).

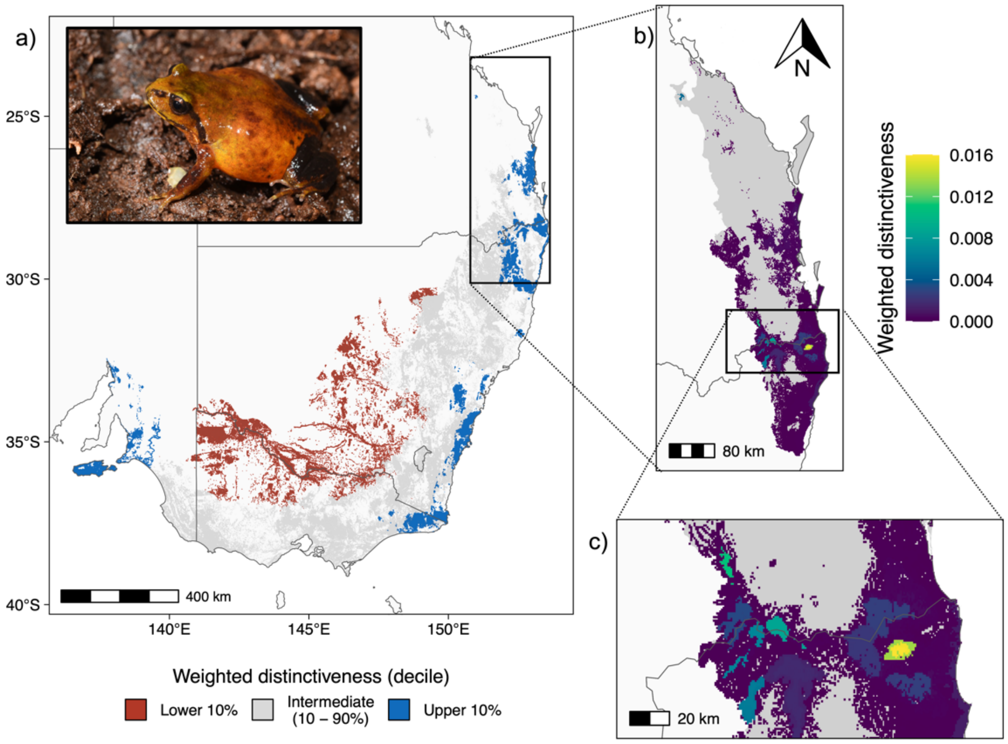

Figure 2. Mean weighted distinctiveness across the study area (all cells with three or more OTUs present). For clarity, only the upper (blue) and lower (red) deciles are shown in (a), with grey indicating cells within the study area with an intermediate value between these bounds. High values indicate that generally, the CUs present are evolutionarily distinct and have small distributions; low values denote the opposite. The highest values are found along the coastal fringes of the study area, though are especially high in the South Eastern Queensland bioregion (b). Here, the highest WD values can be observed, with some cells, generally in elevated areas, such as Wollumbin, supporting very high outlying values (c). This pattern is

primarily driven by the presence of many short-range, mountain-dwelling OTUs within this region, including the Mountain Frog, *Philoria kundagungan* (pictured). Photo credit: Jodi Rowley.

3.2. Genetic implications of the Black Summer fires

Approximately 16.4% (60,226 km^2) of our study area was burned during the Black Summer fires, and within this extent, ~44% (26,458 km^2) was burned at high severity (Figure 3). We found the potential impact of the Black Summer fires in terms of the study area's cross-OTU genetic composition to be mixed. Though fire occurred throughout the entire study area, the most genetically diverse regions (considering all taxonomic Classes) of the landscape to the south were affected to a far lesser extent than the comparatively less genetically diverse bioregions to the east and north of the study area (Figure SM7). The overlap with fire across bioregions was very unequal, ranging from negligible overlap in the South East Coastal Plain to almost two thirds overlap in the South East Corner (considering only cells within our study area). Eight bioregions had >10% overlap with fire (Figure 3), representing an area of ~201,031km^2, ~28.1% of which was burned (~12.9% severely).

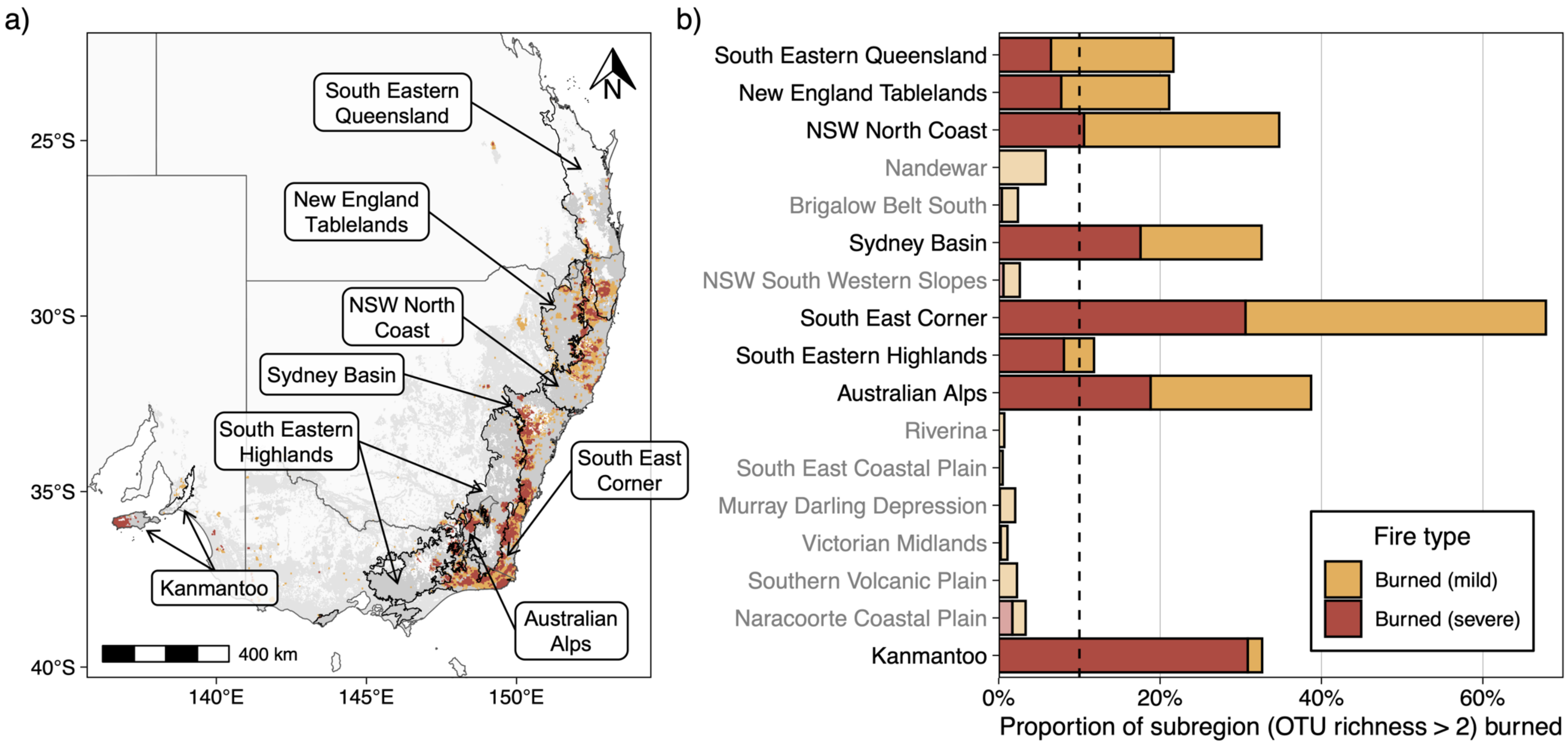

Figure 3. Regions burned during the Black Summer fires by mild (yellow) and severe (red) fires within the study area (a), and the proportion of cells with an OTU richness > 2 within each bioregion that were fire affected (b). Bioregions where >10% of OTU-sufficient cells were burned are indicated in both panels, with the dashed line in (b) highlighting this threshold.

We found that across the study area, when considering diversity across all OTUs, fires generally burned in regions where H_E was lower (Figure 4a, Table SM2). However, this was not the case when taxonomic Classes were considered independently. In fact, for frogs and reptiles, the median H_E values for burned cells were higher than for unburned cells, suggesting that fires burned in slightly more diverse regions of the landscape. For mammals, however, we observed minimal differences in the diversity of burned and unburned regions. For WD, we found that fires burned generally in regions with higher values (Figure 4b, Figure SM8). For this metric, this pattern was evident when all OTUs were considered in aggregate, and for each individual taxonomic Class, where the median value of WD in burned areas, relative to unburned areas, was highest for reptiles, followed by frogs and then mammals.

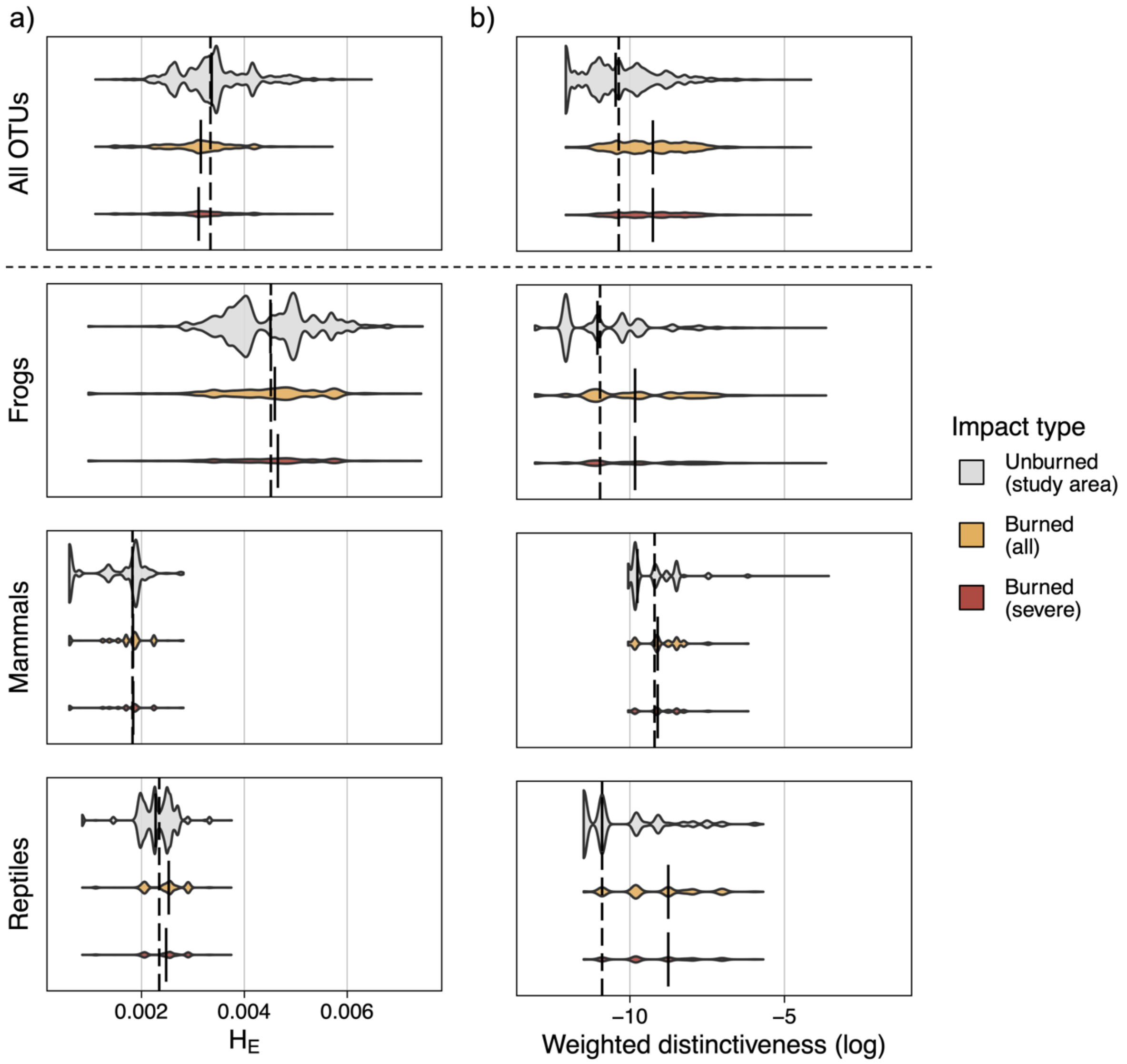

Figure 4. The spread of values for expected heterozygosity (a) and weighted distinctiveness (log transformed) (b) in unburned regions (grey), all burned regions (yellow), and severely burned regions (red) of the study area. Shown are values for all OTUs considered in aggregate, as well as for each taxonomic Class. The width of each 'burned' violin plot is proportional to the amount of the study area that was

burned for each severity category within the relevant group. In each panel, the dashed line indicates the median value across all burned and unburned cells in the study area for that group, with the smaller solid lines reflecting the median values for each impact type (unburned, burned, severely burned). Where these solid bars appear to the right of the dashed line in each panel, this indicates that the median value for cells within the relevant impact type (e.g., severely burned), is higher than the median value across all cells in the study area (for that group).

3.3. Variable potential genetic impacts across the landscape

Given that patterns of diversity across the landscape in taxonomic Classes did not reflect those derived from all OTUs considered together, we further explored potential fire impacts separately within each Class. We found that the likelihood for burned regions generally to be more genetically diverse and have higher WD values than unburned regions was not equally represented across the landscape (Figure 5, Table SM3). Further, the regions where impacts were potentially at their highest (in the context of genetic diversity and WD) were not necessarily equivalent for each taxonomic Class; for example, whilst the fires burned highly valuable (considering WD) regions for reptiles in the NSW North Coast bioregion, for frogs and mammals, the fires generally burned less important areas of this bioregion. However, we did observe consistent, cross-taxonomic trends in some bioregions. Considering both H_E and WD in the New England Tablelands bioregion, for instance, the fires appeared to have predominately burned in important regions for all taxa.

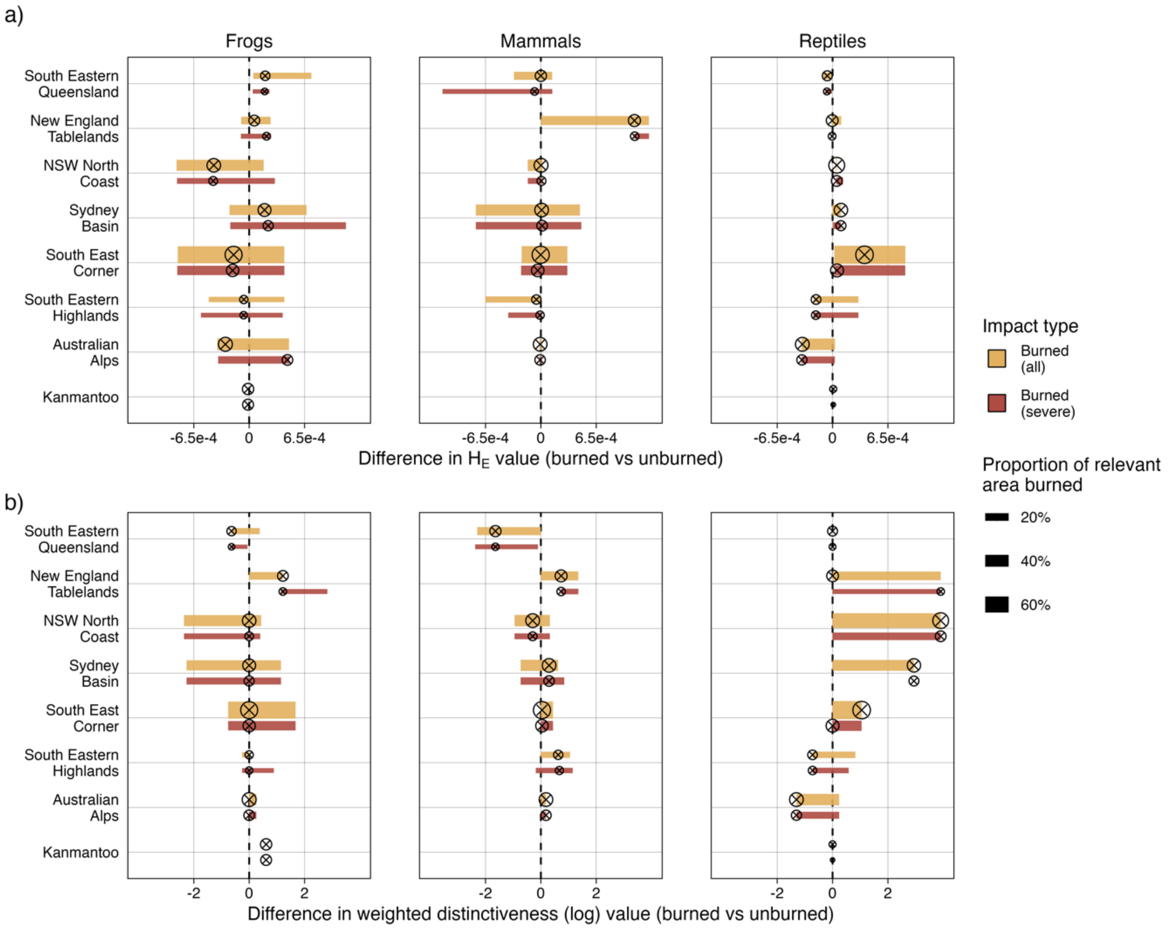

Figure 5. The relative difference of values in burned areas compared to unburned areas for H_E (a) and weighted distinctiveness (b), grouped by IBRA bioregion and taxonomic Class. In each panel, the dashed line represents the median value for the unburned area of the relevant bioregion. The points indicate the difference in median values for the burned regions relative to the unburned regions: negative differences (left of the dashed line) show that the median value for the burned region was lower than that for the unburned region (i.e., the fires burned predominately in areas of the bioregion where the relevant value was lower). Given the uneven skew of data, bars are included to represent the interquartile range for these values and are presented for both (yellow) all fires and (red) severe fires (points coincide with these bars). Both bars and points are sized according to the area within each bioregion (where the relevant taxonomic Class is present) that was burned, with larger sizes indicating that a greater proportion of that bioregion was fire-affected. Note that within our dataset, no mammals were present in the Kanmantoo bioregion.

To infer where the potential impacts from the Black Summer fires may have been most acute, we identified burned areas within the upper quartile of H_E and WD (amongst all burned areas). Across the landscape, we found that the most affected areas generally differed between taxonomic Classes; however, burned areas to the south tended to be in areas of higher genetic diversity than to the north, and conversely, WD values tended to be higher in the north than to the south (Figure 6a). Within Classes, high-diversity areas rarely coincided with high-WD areas: for frogs and reptiles, only ~1% of areas burned were in the upper quartile of each measure (for mammals, this was <0.1%). When we considered the valuable regions for all Classes together, regions where the fires may have had their largest cumulative effect became clear (Figure 6b). Specifically, within the South East Corner bioregion, 32% of all burned areas were highly valuable for frogs, reptiles, and mammals (considering both H_E and WD), with a further 36% of these being valuable for at least 2 Classes. The Australian Alps (14% 3 Classes, 28% 2 Classes) and the NSW North Coast (8% 3 Classes, 18% 2 Classes) were also noteworthy.

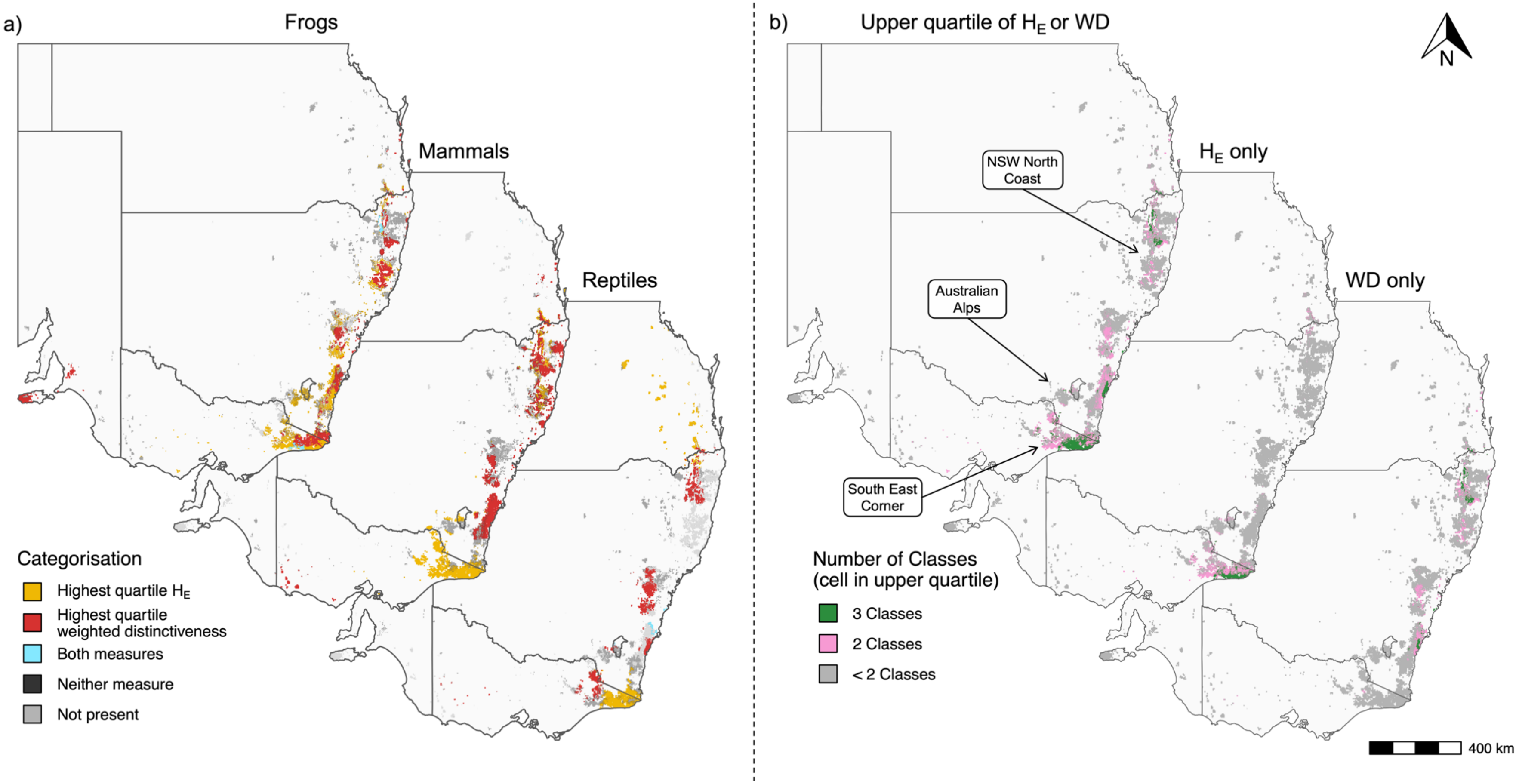

Figure 6. Categorisation of areas burned in the Black Summer fires for each taxonomic Class (a), and the number of Classes for which burned areas were considered valuable (b). In (a), yellow shows burned areas that had values in the upper quartile of all burned areas for H_E; red, the same, though for weighted distinctiveness (WD); blue, areas that were in both of these categories; dark grey, areas that were in neither; and light grey, where fires burned, but no OTUs within the relevant Class were present. In (b), green shows areas that were in the upper quartile for each of the taxonomic Classes, for both metrics together and for each metric independently; pink, areas that were valuable for any two taxonomic Classes; and grey, areas that were valuable for either one or no Classes. Three IBRA bioregions where fires disproportionately burned in areas valuable for many Classes are indicated in (b).

Finally, we compared the landscape-scale trends we observed to those obtained from considering independent CUs (Figure 7, Figure SM9). Using linear regressions across all CUs, as well as within each group (taxonomic Class and threat status), we found no significant trends between measures of genetic diversity or WD and the proportion of a CU's distribution that was burned, apart from observed heterozygosity in frogs, which was lower in CUs that had a greater proportion of their distribution burned (β = -0.002, p = 0.013) (Table SM4).

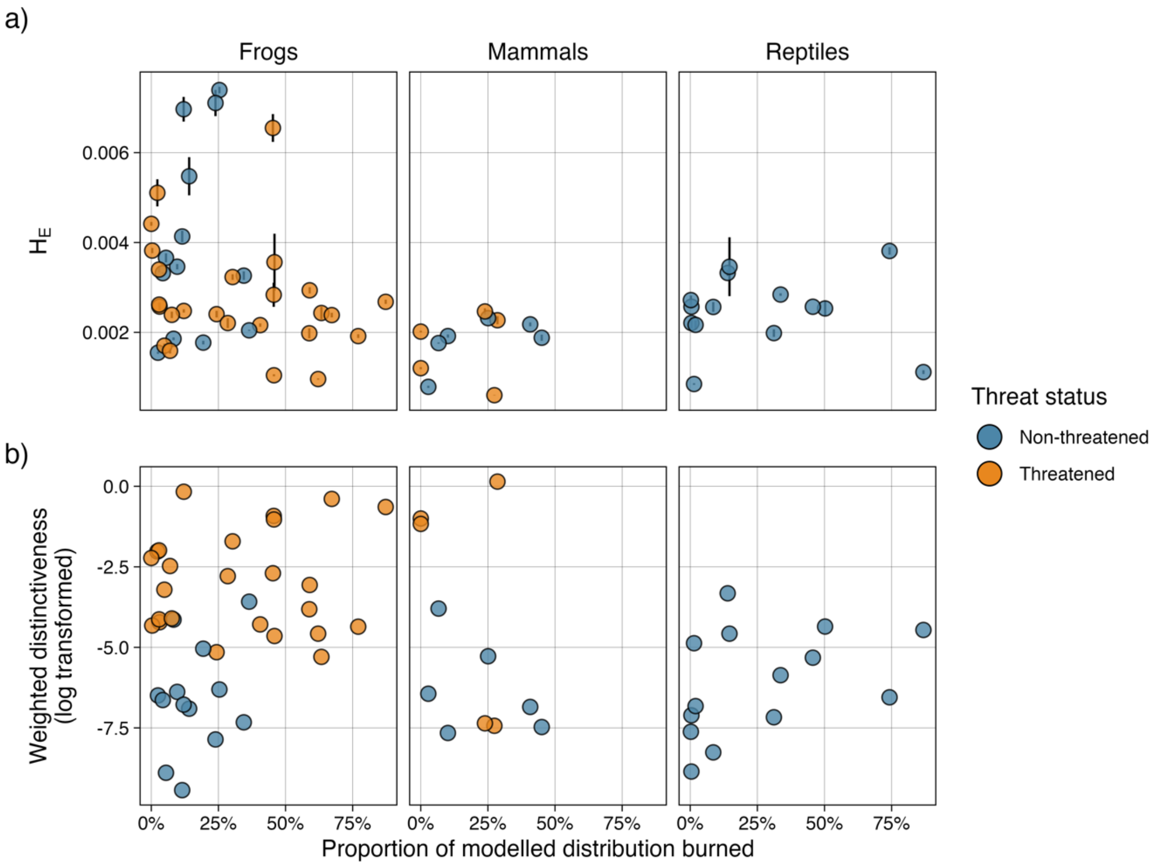

Figure 7. Expected heterozygosity (a) and the weighted distinctiveness (log transformed) (b) for each CU considered in the study compared to the proportion of its modelled distribution that was burned. Error bars in (a) give the 95% confidence intervals for H_E estimates for each CU. Points are coloured according to their threat status, with blue indicating non-threatened OTUs, and yellow threatened OTUs.

4. Discussion

4.1. The genomic impact of Australia's Black Summer fires

Australia's Black Summer fires impacted hundreds of native species. Whilst species responses to these fires were variable (e.g., Driscoll et al., 2024; Legge et al. 2022; Ensbey et al. 2023), several studies have demonstrated adverse effects, both for specific taxa (including frogs, Beranek et al., 2023; Heard et al., 2023; mammals, Woinarski et al., 2023; and reptiles, Letnic et al., 2023) and whole landscapes (Sopniewski et al., 2024; Ward et al., 2020). Our results extend this body of work. We show that Australia's Black Summer fires generally burned in areas characterised by high genetic diversity and evolutionarily distinct, short-range CUs for a subset of frogs, mammals, and reptiles. We also demonstrate that the potential consequences of these fires were uneven across the landscape – within the fire footprint, genetic diversity was highest in the southeast, and weighted distinctiveness highest in the northeast of the study area. Collectively, these results enhance our understanding of the potential impacts to biodiversity from this globally significant disturbance event.

Within taxonomic Classes, we found that fires generally occurred in regions with higher genetic diversity (Figure 4, Table SM2). This is concerning given that these areas are key to the recovery and persistence of affected species. Relative to other populations with lower genetic diversity, the local populations that contribute to higher aggregate diversity within burned areas are more likely to have greater fitness and viability (DeWoody et al., 2021; Kardos et al., 2021), and be subject to lower levels of inbreeding, thus reducing the cumulative load of deleterious alleles within their populations (Keller & Waller, 2002; Robinson et al., 2019). Both in the presence or absence of any threatening process, including these fires, it is these high-diversity populations that are the most valuable for ensuring the long-term viability of the species, both *in situ* (DeWoody et al., 2021; Fernandez-Fournier et al., 2021; Harrisson et al., 2014) or by acting as a source of genetic diversity for conservation translocations or captive breeding (Ralls et al., 2020; Whiteley et al., 2015). Further, in several bioregions, we found that genetic diversity was higher in severely burned regions than those only mildly burned (Figure 5, Table SM3). For species that were negatively impacted by the fires, other studies have found or predicted that the consequences were often more pronounced in severely burned areas (Driscoll et al., 2024; Legge et al., 2022; Letnic et al., 2023), thus in these areas (for example, frogs and mammals in the New England Tablelands bioregion), the long-term ramifications of these fires could be especially bleak.

It should also be considered that where fires burned in more genetically diverse areas of the landscape, the populations most exposed were perhaps those best placed to face this disturbance. As mentioned previously, it is these populations that likely have higher abundance, fitness, and general capacity to rebound following a demographic reduction (Doyle et al., 2019; Reed & Frankham, 2003;

Scott et al., 2020, Willoughby et al., 2017). In instances where fires did burn in more diverse areas, less diverse populations that may have a lower capacity to rebound following the disturbance were more often spared. However, the consequences for a species collectively may be greater if mortality is higher in more genetically diverse populations, as the cumulative loss of diversity through a genetic bottleneck will likely be more pronounced (Banks et al., 2013; Kardos et al., 2021). Resultingly, the total breadth of genetic diversity present within a species, and its capacity to persist through subsequent threatening events, could be reduced.

Even more consistently than for genetic diversity, we found weighted distinctiveness to be higher in burned than unburned regions (Figure 4). The consequences of negative fire impacts to areas with high WD are less nuanced than for genetic diversity. Our WD metric measures the distinct evolutionary history of a CU relative to its OTU, thus capturing adaptations and genetic variability unique to that CU; for these reasons, as well as the fact that once lost, they cannot be recovered, evolutionarily distinct CUs are of especially high conservation priority (Cadotte & Davies, 2010; Dufresnes et al., 2023; Moritz, 1994, 2002). Further, WD prioritises CUs with small, restricted distributions. Not only are these CUs more susceptible to any future local habitat or environmental changes (Manes et al., 2021), but by virtue of existing in more restricted areas (and thus likely in lower numbers), they are intrinsically at a greater extinction risk prior to a fire event (Newsome et al., 2019), amplifying any potential consequences resulting from these fires. Burned areas with high WD are therefore likely some of the most adversely affected. Generally, we found these to be to the north of the study area, in the New England Tablelands and South East Queensland bioregions. Notably, several CUs with particularly high WD had relatively low overlap with fire (Figure 7), highlighting that by nature of having short ranges, areas of high impact related to WD will be localised. As climate change continues and disturbance events such as these increase in frequency, the likelihood of these high WD CUs being adversely affected will coincidingly escalate, however.

4.2. The opportunities and challenges of macrogenetic approaches for conservation following disturbance events

Here, we have shown how the aggregation of population genetics statistics across landscapes can uncover macrogenetic spatial patterns that are not apparent when considering species in isolation. In the context of the Black Summer fires, we should perhaps expect to observe a relationship between fire and the genetic composition metrics considered here. These fires burned predominately in native forests (Davey & Sarre, 2020), and natural environments generally harbour greater genetic diversity than disturbed or modified areas (Miraldo et al., 2016; Schmidt et al., 2020). Further, extensive areas of Australia's Gondwanan rainforests, a region noted for its high concentrations of short-range endemic species with distinct evolutionary histories (Kooyman et al., 2020), were substantially affected. Hence our results, which show that the fires tended to burn in areas of the landscape with higher genetic diversity and WD for frogs, mammals, and reptiles, are perhaps to be expected. The fact that we mainly observed no relationships between CU-level genetic composition metrics and the proportion of their distributions burned (Figure 7, Table SM4) further demonstrates the utility of our macrogenetic approach. Although trends between diversity or uniqueness and areas impacted by fire were mostly (apart from H_O in frogs) not observable at a CU-scale, our finding that areas of high and low diversity across species clustered in regions across the landscape allowed us to identify regions where cumulative impacts may be higher. For example, we showed that across taxonomic Classes, the fires in the South East Corner and NSW North Coast bioregions (and surrounds, including parts of the New England Tablelands) impacted the most diverse and distinct CUs in our dataset, highlighting these areas as important candidates for focused conservation actions (for example, postfire weed management and feral animal control).

The ability to estimate where in the landscape the genetic impacts of an event such as the Black Summer fires are most acute is beneficial. However, a macrogenetic approach employed in isolation is likely insufficient. Indeed, a frequent criticism of such methods is a potential disconnect between landscape patterns and *in situ* realities (Santini et al., 2021). An example of this disparity is apparent in our own results. The pouched frog, *Assa darlingtoni*, had an estimated 22% of its distribution (Ward et al., 2020) and 36% of its environmental niche (Sopniewski et al., 2024) burned in the 2019-2020 fires. However, the high-value, genetically diverse populations of *A. darlingtoni* we identified experienced fire to a far lesser degree, with the greatest fire overlap occurring in the least diverse CU (Table SM1, Supplementary OTU Figures). Whilst not a positive outcome for this low-diversity CU, for the species in its entirety, it is likely that a greater proportion of the species' total genetic diversity has been unaffected by the fires. This differs to our landscape-scale findings and is a fortunate result, given that Beranek et al. (2023) found *A. darlingtoni* occupancy to be particularly adversely affected by the Black Summer fires. Whilst the benefits of macrogenetic approaches to informing conservation actions after major disturbances such as megafires should be appreciated, they are best used in tandem with on-the-ground, species-specific actions (Zizka et al., 2021).

A key finding of our study, with major implications for conservation macrogenetic studies, was the differences in the overall levels and spatial patterns of genetic diversity we observed between taxonomic Classes. Whilst the methods we employed allow for direct comparison of genetic diversity estimates across species (Schmidt et al., 2021; Sopniewski & Catullo, 2024), these must be considered in context; i.e., the raw value of H_E for one CU (such as a mammal) may not hold the same significance as it would for another, evolutionarily distant CU (such as a frog). Genetic diversity across taxa is influenced by life history, ecological strategy, and relative population size, thus the differences we observed are to be expected (Ellegren & Galtier, 2016; Romiguier et al., 2014). This is an important consideration for future macrogenetic studies that utilise our stacking approach – whilst heterozygosity estimates may be comparable when the appropriate methods are followed (Schmidt et al., 2021; Sopniewski & Catullo, 2024), only biologically comparable OTUs should be considered together. Importantly, our stacking of diversity metrics within Classes allowed us to observe variable spatial patterns of genetic diversity among groups, resulting in the areas we estimated to have experienced the most severe potential impacts varying across the landscape for each taxonomic Class. We were able to utilise this information and infer regions of the study area where the impacts of the fires may have been greatest across taxonomic Classes, namely by identifying regions important to all three (Figure 6). However, these contextual differences in patterns of genetic diversity remain an important factor to consider in macrogenetic analyses and any resultant conservation actions.

The variable taxonomic patterns we observed across the landscape also highlight a caveat with our study that is emblematic of perhaps the biggest obstacle to the wider incorporation of conservation macrogenetic studies: a lack of data (Hoban et al., 2022). Despite a rapid increase in the accessibility of genetic data for conservation research (Hoban et al., 2022; Hohenlohe et al., 2021), it remains challenging to amass data that is sufficiently representative of the diversity of species present in any given landscape. Our study is large in the context of conservation genomics, particularly considering the use of SNP data: our final dataset included samples from 1,205 unique individuals, representing over 30 OTUs. However, this pales in comparison to the true diversity of the study area, where hundreds of species from the three vertebrate Classes we examined overlapped with the Black Summer fires (Ward et al., 2020), not to mention the thousands of bird, freshwater fish, invertebrate, and plant species present in the landscape (Dricsoll et al., 2024). Currently, conservation macrogenetic studies such as ours are largely limited by the availability of samples. To enhance future studies, ongoing collection of genetic samples remains key and should be a priority, particularly for museums (Catullo et al., 2021); it is also critical that such institutions are adequately funded to support this continual data collection.

We observed non-random patterns of diversity and uniqueness across the landscape, and it is likely these patterns may be shared more broadly. Drivers of intra- and interspecific differences in genetic diversity – both natural (Figuerola-Ferrando et al., 2023; Paz-Vinas et al., 2015) and anthropogenic (Almeida-Rocha et al., 2020; De Kort et al., 2021; Schmidt et al., 2020) – can act similarly upon sympatric species across landscapes, resulting in non-random spatial patterns of cross-taxonomic diversity across a landscape. Our findings here could thus, in theory, be used to infer potential impacts for related sympatric species that we were unable to include in our study. However, in our case, this must be done cautiously, as we described these patterns from relatively few overlapping OTUs. We can be confident in our findings for the OTUs we considered, though to confirm these patterns more broadly, more genomic data are critical. Given that genetic analyses in conservation assessment are increasingly utilised (Willi et al., 2022), and that it is commonplace to upload genetic sequences to the public domain accompanying publication (Crandall et al., 2023), more extensive analyses to confirm these patterns will likely soon be feasible.

Though Australia's Black Summer fires were historically unprecedented, similar events have since occurred elsewhere in the world and are predicted to increase in frequency (Cunningham et al, 2024; Kelly et al., 2020). Alongside numerous other threatening processes the natural world faces (Dirzo et al., 2022; Habibullah et al., 2022; Urban, 2015), biodiversity is in peril. To direct conservation actions to where they will be most effective, new tools are needed to understand biodiversity at scale, both in response to, and in preparation for, sudden disturbance events and other processes that can trigger population declines and extinctions. Conservation macrogenetics is a promising avenue to do so (Leigh et al., 2021; Schmidt, Hoban, & Jetz, 2023), and here we have demonstrated how it can be comprehensively deployed in response to a major disturbance event. We advocate for the continued collection of genetic data, and for greater funding of institutions such as museums and herbaria that hold and curate these resources for the research community. If we can ensure that genetic information continues to accumulate, then our framework can be engaged in numerous contexts to support multilateral efforts to halt the global reduction of biodiversity.

References

Abram, N. J., Henley, B. J., Sen Gupta, A., Lippmann, T. J. R., Clarke, H., Dowdy, A. J., Sharples, J. J., Nolan, R. H., Zhang, T., Wooster, M. J., Wurtzel, J. B., Meissner, K. J., Pitman, A. J., Ukkola, A. M., Murphy, B. P., Tapper, N. J., & Boer, M. M. (2021). Connections of climate change and variability to large and extreme forest fires in southeast Australia. *Communications Earth & Environment, 2*(1), 8. https://doi.org/10.1038/s43247-020-00065-8

Almeida-Rocha, J. M., Soares, L. A. S. S., Andrade, E. R., Gaiotto, F. A., & Cazetta, E. (2020). The impact of anthropogenic disturbances on the genetic diversity of terrestrial species: A global meta-analysis. *Molecular Ecology, 29*(24), 4812–4822. https://doi.org/10.1111/mec.15688

ALA (2024). Atlas of Living Australia occurrence download at https://doi.org/10.26197/ala.05992084-8c86-47e4-b58d-4ae2a9b8f780. Accessed on 10 May 2024.

Banks, S. C., Cary, G. J., Smith, A. L., Davies, I. D., Driscoll, D. A., Gill, A. M., ... & Peakall, R. (2013). How does ecological disturbance influence genetic diversity? *Trends in ecology & evolution*, *28*(11), 670-679. https://doi.org/10.1016/j.tree.2013.08.005

Beranek, C. T., Hamer, A. J., Mahony, S. V., Stauber, A., Ryan, S. A., Gould, J., ... & Mahony, M. (2023). Severe wildfires promoted by climate change negatively impact forest amphibian metacommunities. *Diversity and Distributions*, *29*(6), 785-800. https://doi.org/10.1111/ddi.13700

Boer, M. M., Resco de Dios, V., & Bradstock, R. A. (2020). Unprecedented burn area of Australian mega forest fires. *Nature Climate Change, 10*(3), 171–172. https://doi.org/10.1038/s41558-020-0716-1

Bolger, A. M., Lohse, M., & Usadel, B. (2014). Trimmomatic: A flexible trimmer for Illumina sequence data. *Bioinformatics, 30*(15), 2114–2120. https://doi.org/10.1093/bioinformatics/btu170

Cadotte, M. W., & Jonathan Davies, T. (2010). Rarest of the rare: advances in combining evolutionary distinctiveness and scarcity to inform conservation at biogeographical scales. *Diversity and Distributions*, *16*(3), 376-385. https://doi.org/10.1111/j.1472-4642.2010.00650.x

Canteri, E., Fordham, D. A., Li, S., Hosner, P. A., Rahbek, C., & Nogués-Bravo, D. (2021). IUCN Red List protects avian genetic diversity. *Ecography, 44*(12), 1808–1811. https://doi.org/10.1111/ecog.05895

Catchen, J., Hohenlohe, P. A., Bassham, S., Amores, A., & Cresko, W. A. (2013). Stacks: an analysis tool set for population genomics. *Molecular Ecology, 22*(11), 3124–3140. https://doi.org/10.1111/mec.12354

Catullo, R. A., Schembri, R., Tedeschi, L. G., Eldridge, M. D., Joseph, L., & Moritz, C. C. (2021). Benchmarking taxonomic and genetic diversity after the fact: Lessons learned from the catastrophic 2019–2020 Australian bushfires. *Frontiers in Ecology and Evolution*, *9*, 645820. https://doi.org/10.3389/fevo.2021.645820

Catullo, R., & Moritz, C. (2021). Genetic assessment of bushfire-impacted vertebrate species. NESP Threatened Species Recovery Hub Project 8.3.3 Final report, Brisbane.

CBD, (2022). Final text of Kunming-Montréal Global Biodiversity Framework. https://www.cbd.int/article/cop15-final-text-kunming-montreal-gbf-221222

Ceballos, G., Ehrlich, P. R., Barnosky, A. D., García, A., Pringle, R. M., & Palmer, T. M. (2015). Accelerated modern human-induced species losses: Entering the sixth mass extinction. *Science Advances, 1*(5), e1400253. https://doi.org/10.1126/sciadv.1400253

Ceballos, G., Ehrlich, P. R., & Dirzo, R. (2017). Biological annihilation via the ongoing sixth mass extinction signaled by vertebrate population losses and declines. *Proceedings of the National Academy of Sciences of the United States of America, 114*(30), E6089–E6096. https://doi.org/10.1073/pnas.1704949114

Collins, L., Bradstock, R. A., Clarke, H., Clarke, M. F., Nolan, R. H., & Penman, T. D. (2021). The 2019/2020 mega-fires exposed Australian ecosystems to an unprecedented extent of high-severity fire. *Environmental Research Letters*, *16*(4), 044029. https://doi.org/10.1088/1748-9326/abeb9e

Crandall, E. D., Toczydlowski, R. H., Liggins, L., Holmes, A. E., Ghoojaei, M., Gaither, M. R., Wham, B. E., Pritt, A. L., Noble, C., Anderson, T. J., Barton, R. L., Berg, J. T., Beskid, S. G., Delgado, A., Farrell, E., Himmelsbach, N., Queeno, S. R., Trinh, T., Weyand, C., … Toonen, R. J. (2023). Importance of timely metadata curation to the global surveillance of genetic diversity. *Conservation Biology, 37*(4), e14061. https://doi.org/10.1111/cobi.14061

Cunningham, C. X., Williamson, G. J., & Bowman, D. M. (2024). Increasing frequency and intensity of the most extreme wildfires on Earth. *Nature ecology & evolution*, *8*(8), 1420-1425. https://doi.org/10.1038/s41559-024-02452-2

Cutajar, T. P., Portway, C. D., Gillard, G. L., & Rowley, J. J. (2022). Australian Frog Atlas: species' distribution maps informed by the FrogID dataset. *Technical Reports of the Australian Museum*, *36*, 1-48.

Davey, S. M., & Sarre, A. (2020). The 2019/20 Black Summer bushfires. *Australian Forestry*, *83*(2), 47-51. https://doi.org/10.1080/00049158.2020.1769899

Department of Agriculture, Water, and Environment (DAWE). (2020). AUS GEEBAM Fire Severity Dataset (2019-2020).

Department of Agriculture, Water and the Environment (DAWE) (2012). Interim Biogeographic Regionalisation for Australia v.7 (IBRA).

DeWoody, J. A., Harder, A. M., Mathur, S., & Willoughby, J. R. (2021). The long-standing significance of genetic diversity in conservation. *Molecular Ecology, 30*(17), 4147–4154. https://doi.org/10.1111/mec.16051

De Kort, H., Prunier, J. G., Ducatez, S., Honnay, O., Baguette, M., Stevens, V. M., & Blanchet, S. (2021). Life history, climate and biogeography interactively affect worldwide genetic diversity of plant and animal populations. *Nature Communications, 12*(1), 516. https://doi.org/10.1038/s41467-021-20958-2

Dirzo, R., Ceballos, G., & Ehrlich, P. R. (2022). Circling the drain: the extinction crisis and the future of humanity. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences, 377*(1857), 20210378. https://doi.org/10.1098/rstb.2021.0378

Doyle, J. M., Willoughby, J. R., Bell, D. A., Bloom, P. H., Bragin, E. A., Fernandez, N. B., Katzner, T. E., Leonard, K., & DeWoody, J. A. (2019). Elevated heterozygosity in adults relative to juveniles provides evidence of viability selection on eagles and falcons. *The Journal of Heredity, 110*(6), 696–706. https://doi.org/10.1093/jhered/esz048

Driscoll, D. A., Macdonald, K. J., Gibson, R. K., Doherty, T. S., Nimmo, D. G., Nolan, R. H., ... & Phillips, R. D. (2024). Biodiversity impacts of the 2019–2020 Australian megafires. *Nature*, 1-8. https://doi.org/10.1038/s41586-024-08174-6

Dufresnes, C., Poyarkov, N., & Jablonski, D. (2023). Acknowledging more biodiversity without more species. *Proceedings of the national Academy of Sciences*, *120*(40), e2302424120. https://doi.org/10.1073/pnas.2302424120

Ellegren, H., & Galtier, N. (2016). Determinants of genetic diversity. *Nature Reviews Genetics, 17*(7), 422–433. https://doi.org/10.1038/nrg.2016.58

Ensbey, M., Legge, S., Jolly, C. J., Garnett, S. T., Gallagher, R. V., Lintermans, M., ... & Zukowski, S. (2023). Animal population decline and recovery after severe fire: Relating ecological and life history traits with expert estimates of population impacts from the Australian 2019-20 megafires. *Biological conservation*, *283*, 110021. https://doi.org/10.1016/j.biocon.2023.110021

Fernandez-Fournier, P., Lewthwaite, J. M. M., & Mooers, A. Ø. (2021). Do we need to identify adaptive genetic variation when prioritizing populations for conservation? *Conservation Genetics, 22*(2), 205–216. https://doi.org/10.1007/s10592-020-01327-w

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.

Figuerola-Ferrando, L., Barreiro, A., Montero-Serra, I., Pagès-Escolà, M., Garrabou, J., Linares, C., & Ledoux, J. (2023). Global patterns and drivers of genetic diversity among marine habitat-forming species. *Global Ecology and Biogeography, 32*(7), 1218–1229. https://doi.org/10.1111/geb.13685

Finn, C., Grattarola, F., & Pincheira-Donoso, D. (2023). More losers than winners: investigating Anthropocene defaunation through the diversity of population trends. Biological Reviews of the Cambridge Philosophical Society, 98(5), 1732–1748. https://doi.org/10.1111/brv.12974

Forester, B. R., Beever, E. A., Darst, C., Szymanski, J., & Funk, W. C. (2022). Linking evolutionary potential to extinction risk: applications and future directions. *Frontiers in Ecology and the Environment, 20*(9), 507-515. https://doi.org/10.1002/fee.2552

Frankham, R. (2005). Genetics and extinction. *Biological conservation*, *126*(2), 131-140. https://doi.org/10.1016/j.biocon.2005.05.002

Frankham, R. (2015). Genetic rescue of small inbred populations: meta-analysis reveals large and consistent benefits of gene flow. *Molecular Ecology, 24*(11), 2610–2618. https://doi.org/10.1111/mec.13139

Gallant, J., & Austin, J. (2012). Topographic Wetness Index derived from 1" SRTM DEM-H. v2. CSIRO. https://doi.org/10.4225/08/57590B59A4A08

Garner, B. A., Hand, B. K., Amish, S. J., Bernatchez, L., Foster, J. T., Miller, K. M., Morin, P. A., Narum, S. R., O'Brien, S. J., Roffler, G., Templin, W. D., Sunnucks, P., Strait, J., Warheit, K. I., Seamons, T. R., Wenburg, J., Olsen, J., & Luikart, G. (2016). Genomics in

Conservation: Case Studies and Bridging the Gap between Data and Application. *Trends in Ecology & Evolution, 31*(2), 81–83. https://doi.org/10.1016/j.tree.2015.10.009

Gueta, T., & Carmel, Y. (2016). Quantifying the value of user-level data cleaning for big data: A case study using mammal distribution models. *Ecological Informatics*, *34*, 139-145. https://doi.org/10.1016/j.ecoinf.2016.06.001

Guisan, A., Tingley, R., Baumgartner, J. B., Naujokaitis-Lewis, I., Sutcliffe, P. R., Tulloch, A. I., ... & Buckley, Y. M. (2013). Predicting species distributions for conservation decisions. *Ecology Letters*, *16*(12), 1424-1435.

Habibullah, M. S., Din, B. H., Tan, S.-H., & Zahid, H. (2022). Impact of climate change on biodiversity loss: global evidence. *Environmental Science and Pollution Research International, 29*(1), 1073–1086. https://doi.org/10.1007/s11356-021-15702-8

Harrisson, K. A., Pavlova, A., Telonis-Scott, M., & Sunnucks, P. (2014). Using genomics to characterize evolutionary potential for conservation of wild populations. *Evolutionary Applications, 7*(9), 1008–1025. https://doi.org/10.1111/eva.12149

Harris, R. M. B., Beaumont, L. J., Vance, T. R., Tozer, C. R., Remenyi, T. A., Perkins-Kirkpatrick, S. E., Mitchell, P. J., Nicotra, A. B., McGregor, S., Andrew, N. R., Letnic, M., Kearney, M. R., Wernberg, T., Hutley, L. B., Chambers, L. E., Fletcher, M. S., Keatley, M. R., Woodward, C. A., Williamson, G., … Bowman, D. M. J. S. (2018). Biological responses to the press and pulse of climate trends and extreme events. *Nature Climate Change, 8*(7), 579–587. https://doi.org/10.1038/s41558-018-0187-9

Heard, G. W., Bolitho, L. J., Newell, D., Hines, H. B., Norman, P., Willacy, R. J., & Scheele, B. C. (2023). Drought, fire, and rainforest endemics: A case study of two threatened frogs impacted by Australia's "Black Summer". *Ecology and Evolution, 13*(5), e10069. https://doi.org/10.1002/ece3.10069

Hemstrom, W., Grummer, J. A., Luikart, G., & Christie, M. R. (2024). Next-generation data filtering in the genomics era. *Nature Reviews Genetics*. https://doi.org/10.1038/s41576-024-00738-6

Hijmans, R. J., Bivand, R., Forner, K., Ooms, J., Pebesma, E., & Sumner, M. D. (2022). Package 'terra'.

Hijmans, R. J., Phillips, S., Leathwick, J., & Elith, J. (2017). Package 'dismo'. *Circles*, *9*(1), 1-68.

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 of the Cambridge Philosophical Society, 97*(4), 1511–1538. https://doi.org/10.1111/brv.12852

Hohenlohe, P. A., Funk, W. C., & Rajora, O. P. (2021). Population genomics for wildlife conservation and management. *Molecular Ecology, 30*(1), 62–82. https://doi.org/10.1111/mec.15720

IUCN. 2024. The IUCN Red List of Threatened Species. Version 2024-1. https://www.iucnredlist.org. Accessed on 10 May 2024.

Kardos, M., Armstrong, E. E., Fitzpatrick, S. W., Hauser, S., Hedrick, P. W., Miller, J. M., Tallmon, D. A., & Funk, W. C. (2021). The crucial role of genome-wide genetic variation in conservation. *Proceedings of the National Academy of Sciences of the United States of America, 118*(48). https://doi.org/10.1073/pnas.2104642118

Keller, L., & Waller, D. M. (2002). Inbreeding effects in wild populations. *Trends in Ecology & Evolution, 17*(5), 230–241. https://doi.org/10.1016/S0169-5347(02)02489-8

Kelly, L. T., Giljohann, K. M., Duane, A., Aquilué, N., Archibald, S., Batllori, E., ... & Brotons, L. (2020). Fire and biodiversity in the Anthropocene. *Science*, *370*(6519), eabb0355. https://doi.org/10.1126/science.abb0355

Kembel, S. W., Cowan, P. D., Helmus, M. R., Cornwell, W. K., Morlon, H., Ackerly, D. D., Blomberg, S. P., & Webb, C. O. (2010). Picante: R tools for integrating phylogenies and ecology. *Bioinformatics, 26*(11), 1463–1464. https://doi.org/10.1093/bioinformatics/btq166

Kilian, A., Wenzl, P., Huttner, E., Carling, J., Xia, L., Blois, H., Caig, V., Heller-Uszynska, K., Jaccoud, D., & Hopper, C. (2012). Data production and analysis in population genomics. *Methods in Molecular Biology*, 67–89.

Kooyman, R. M., Watson, J., & Wilf, P. (2020). Protect Australia's gondwana rainforests. *Science*, *367*(6482), 1083-1083. https://doi.org/10.1126/science.abb2046

Legge, S., Rumpff, L., Woinarski, J. C. Z., Whiterod, N. S., Ward, M., Southwell, D. G., Scheele, B. C., Nimmo, D. G., Lintermans, M., Geyle, H. M., Garnett, S. T., Hayward-Brown, B., Ensbey, M., Ehmke, G., Ahyong, S. T., Blackmore, C. J., Bower, D. S., Brizuela-Torres, D., Burbidge, A. H., … Zukowski, S. (2022). The conservation impacts of ecological disturbance: Time-bound estimates of population loss and recovery for fauna affected by the 2019–2020 Australian megafires. *Global Ecology and Biogeography, 31*(10), 2085–2104. https://doi.org/10.1111/geb.13473

Leigh, D. M., van Rees, C. B., Millette, K. L., Breed, M. F., Schmidt, C., Bertola, L. D., Hand, B. K., Hunter, M. E., Jensen, E. L., Kershaw, F., Liggins, L., Luikart, G., Manel, S., Mergeay, J., Miller, J. M., Segelbacher, G., Hoban, S., & Paz-Vinas, I. (2021). Opportunities and challenges of macrogenetic studies. *Nature Reviews Genetics, 22*(12), 791–807. https://doi.org/10.1038/s41576-021-00394-0

Letnic, M., Roberts, B., Hodgson, M., Ross, A. K., Cuartas, S., Lapwong, Y., Price, O., Sentinella, N., & Webb, J. K. (2023). Fire severity influences the post-fire habitat structure and abundance of a cool climate lizard. *Austral Ecology, 48*(7), 1440–1453. https://doi.org/10.1111/aec.13410

Li, H., Xiang-Yu, J., Dai, G., Gu, Z., Ming, C., Yang, Z., Ryder, O. A., Li, W.-H., Fu, Y.-X., & Zhang, Y.-P. (2016). Large numbers of vertebrates began rapid population decline in the late 19th century. *Proceedings of the National Academy of Sciences of the United States of America, 113*(49), 14079–14084. https://doi.org/10.1073/pnas.1616804113

Li, X., & Xiao, J. (2019). Mapping photosynthesis solely from solar-induced chlorophyll fluorescence: A global, fine-resolution dataset of gross primary production derived from OCO-2. *Remote Sensing*, 11(21), 2563. https://doi.org/10.3390/rs11212563

Manes, S., Costello, M. J., Beckett, H., Debnath, A., Devenish-Nelson, E., Grey, K.-A., Jenkins, R., Khan, T. M., Kiessling, W., Krause, C., Maharaj, S. S., Midgley, G. F., Price, J., Talukdar, G., & Vale, M. M. (2021). Endemism increases species' climate change risk in areas of global biodiversity importance. *Biological Conservation*, 109070. https://doi.org/10.1016/j.biocon.2021.109070

Minh, B. Q., Schmidt, H. A., Chernomor, O., Schrempf, D., Woodhams, M. D., von Haeseler, A., & Lanfear, R. (2020). IQ-TREE 2: New models and efficient methods for phylogenetic inference in the genomic era. *Molecular Biology and Evolution*, *37*(5), 1530–1534. https://doi.org/10.1093/molbev/msaa015

Miraldo, A., Li, S., Borregaard, M. K., Flórez-Rodríguez, A., Gopalakrishnan, S., Rizvanovic, M., Wang, Z., Rahbek, C., Marske, K. A., & Nogués-Bravo, D. (2016). An Anthropocene map of genetic diversity. *Science, 353*(6307), 1532–1535. https://doi.org/10.1126/science.aaf4381

Moritz, C. (1994). Defining "Evolutionarily Significant Units" for conservation. *Trends in Ecology & Evolution, 9*(10), 373–375. https://doi.org/10.1016/0169-5347(94)90057-4

Moritz, C. (2002). Strategies to protect biological diversity and the evolutionary processes that sustain it. *Systematic biology*, *51*(2), 238-254. https://doi.org/10.1080/10635150252899752

Newsome, T. M., Wolf, C., Nimmo, D. G., Kopf, R. K., Ritchie, E. G., Smith, F. A., & Ripple, W. J. (2019). Constraints on vertebrate range size predict extinction risk. *Global Ecology and Biogeography, 29*(1), 76-78. https://doi.org/10.1111/geb.13009

Nielsen, E. S., Hanson, J. O., Carvalho, S. B., Beger, M., Henriques, R., Kershaw, F., & von der Heyden, S. (2023). Molecular ecology meets systematic conservation planning. *Trends in Ecology & Evolution, 38*(2), 143–155. https://doi.org/10.1016/j.tree.2022.09.006

Palsbøll, P. J., Bérubé, M., & Allendorf, F. W. (2007). Identification of management units using population genetic data. *Trends in Ecology & Evolution, 22*(1), 11–16. https://doi.org/10.1016/j.tree.2006.09.003

Paradis, E., & Schliep, K. (2019). ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. *Bioinformatics, 35*(3), 526–528. https://doi.org/10.1093/bioinformatics/bty633

Paz-Vinas, I., Loot, G., Stevens, V. M., & Blanchet, S. (2015). Evolutionary processes driving spatial patterns of intraspecific genetic diversity in river ecosystems. *Molecular Ecology, 24*(18), 4586–4604. https://doi.org/10.1111/mec.13345

Phillips, S. J., Anderson, R. P., Dudík, M., Schapire, R. E., & Blair, M. E. (2017). Opening the black box: An open-source release of Maxent. *Ecography*, *40*(7), 887-893.

Ralls, K., Sunnucks, P., Lacy, R. C., & Frankham, R. (2020). Genetic rescue: A critique of the evidence supports maximizing genetic diversity rather than minimizing the introduction of putatively harmful genetic variation. *Biological Conservation*, *251*, 108784. https://doi.org/10.1016/j.biocon.2020.108784

Reed, D. H., & Frankham, R. (2003). Correlation between Fitness and Genetic Diversity. *Conservation Biology, 17*(1), 230–237. https://doi.org/10.1046/j.1523-1739.2003.01236.x

R Core Team. (2023). R: A Language and Environment for Statistical Computing (4.3.0). R Foundation for Statistical Computing, Vienna, Austria.

Robinson, J. A., Räikkönen, J., Vucetich, L. M., Vucetich, J. A., Peterson, R. O., Lohmueller, K. E., & Wayne, R. K. (2019). Genomic signatures of extensive inbreeding in Isle Royale wolves, a population on the threshold of extinction. *Science Advances, 5*(5), eaau0757. https://doi.org/10.1126/sciadv.aau0757

Rochette, N. C., Rivera-Colón, A. G., & Catchen, J. M. (2019). Stacks 2: Analytical methods for paired-end sequencing improve RADseq-based population genomics. *Molecular Ecology, 28*(21), 4737–4754. https://doi.org/10.1111/mec.15253

Romiguier, J., Gayral, P., Ballenghien, M., Bernard, A., Cahais, V., Chenuil, A., ... & Galtier, N. (2014). Comparative population genomics in animals uncovers the determinants of genetic diversity. *Nature*, *515*(7526), 261-263. https://doi.org/10.1038/nature13685

Rosauer, D. F., Catullo, R. A., VanDerWal, J., Moussalli, A., & Moritz, C. (2015). Lineage range estimation method reveals fine-scale endemism linked to Pleistocene stability in Australian rainforest herpetofauna. *PLoS One*, *10*(5), e0126274. https://doi.org/10.1371/journal.pone.0169726

Rosauer, D., Laffan, S. W., Crisp, M. D., Donnellan, S. C., & Cook, L. G. (2009). Phylogenetic endemism: a new approach for identifying geographical concentrations of evolutionary history. *Molecular Ecology, 18*(19), 4061–4072. https://doi.org/10.1111/j.1365-294X.2009.04311.x

Rowley, J. J., & Callaghan, C. T. (2020). The FrogID dataset: expert-validated occurrence records of Australia’s frogs collected by citizen scientists. *ZooKeys*, *912*, 139.

Roycroft, E., MacDonald, A. J., Moritz, C., Moussalli, A., Portela Miguez, R., & Rowe, K. C. (2021). Museum genomics reveals the rapid decline and extinction of Australian rodents since European settlement. *Proceedings of the National Academy of Sciences of the United States of America, 118*(27). https://doi.org/10.1073/pnas.2021390118

Santini, L., Antão, L. H., Jung, M., Benítez-López, A., Rapacciuolo, G., Di Marco, M., Jones, F. A. M., Haghkerdar, J. M., & González-Suárez, M. (2021). The interface between Macroecology and Conservation: existing links and untapped opportunities. *Frontiers of Biogeography, 13*(4). https://doi.org/10.21425/F5FBG53025

Schmidt, C., Domaratzki, M., Kinnunen, R. P., Bowman, J., & Garroway, C. J. (2020). Continent-wide effects of urbanization on bird and mammal genetic diversity. *Proceedings of the Royal Society B*, *287*(1920), 20192497. https://doi.org/10.1098/rspb.2019.2497

Schmidt, C., Hoban, S., Hunter, M., Paz-Vinas, I., & Garroway, C. J. (2023). Genetic diversity and IUCN Red List status. *Conservation Biology, 37*(4), e14064. https://doi.org/10.1111/cobi.14064

Schmidt, C., Hoban, S., & Jetz, W. (2023). Conservation macrogenetics: harnessing genetic data to meet conservation commitments. *Trends in Genetics, 39*(11), 816–829. https://doi.org/10.1016/j.tig.2023.08.002

Schmidt, C., Karachaliou, E., Vandergast, A., Crandall, E., Falgout, J., Hunter, M., Kershaw, F., Leigh, D., O’Brien, D., Paz-Vinas, I., Segelbacher, G., & Garroway, C. (2024). The global protected area network does not harbor genetically diverse populations. EcoEvoRxiv. https://doi.org/10.32942/X26G7Z

Schmidt, T. L., Jasper, M., Weeks, A. R., & Hoffmann, A. A. (2021). Unbiased population heterozygosity estimates from genome-wide sequence data. *Methods in Ecology and Evolution, 12*(10), 1888-1898. https://doi.org/10.1111/2041-210X.13659

Scott, P. A., Allison, L. J., Field, K. J., Averill-Murray, R. C., & Shaffer, H. B. (2020). Individual heterozygosity predicts translocation success in threatened desert tortoises. *Science, 370*(6520), 1086–1089. https://doi.org/10.1126/science.abb0421

Sopniewski, J., Catullo, R., Ward, M., Mitchell, N., & Scheele, B. C. (2024). Niche-based approach to explore the impacts of environmental disturbances on biodiversity. *Conservation Biology*, e14277. https://doi.org/10.1111/cobi.14277

Sopniewski, J., & Catullo, R. A. (2024). Estimates of heterozygosity from single nucleotide polymorphism markers are context-dependent and often wrong. *Molecular Ecology Resources, 24*(4), e13947. https://doi.org/10.1111/1755-0998.13947

Sopniewski, J., Scheele, B. C., & Cardillo, M. (2022). Predicting the distribution of Australian frogs and their overlap with Batrachochytrium dendrobatidis under climate change. *Diversity and Distributions*, *28*(6), 1255-1268. https://doi.org/10.1111/ddi.13533

Stott, P. (2016). How climate change affects extreme weather events. *Science, 352*(6293), 1517–1518. https://doi.org/10.1126/science.aaf7271

Ticehurst, C., Newnham, G., & Mokany, K. (2023). Annual vegetation height images for Australia from GEDI and Landsat data. v1. CSIRO. https://doi.org/10.25919/5z99-h749

Urban, M. C. (2015). Accelerating extinction risk from climate change. *Science, 348*(6234), 571–573. https://doi.org/10.1126/science.aaa4984

Ward, M., Tulloch, A. I. T., Radford, J. Q., Williams, B. A., Reside, A. E., Macdonald, S. L., Mayfield, H. J., Maron, M., Possingham, H. P., Vine, S. J., O'Connor, J. L., Massingham, E. J., Greenville, A. C., Woinarski, J. C. Z., Garnett, S. T., Lintermans, M., Scheele, B. C., Carwardine, J., Nimmo, D. G., … Watson, J. E. M. (2020). Impact of 2019-2020 mega-fires on Australian fauna habitat. *Nature Ecology & Evolution, 4*(10), 1321–1326. https://doi.org/10.1038/s41559-020-1251-1

Whiteley, A. R., Fitzpatrick, S. W., Funk, W. C., & Tallmon, D. A. (2015). Genetic rescue to the rescue. *Trends in Ecology & Evolution, 30*(1), 42–49. https://doi.org/10.1016/j.tree.2014.10.009

Willi, Y., Kristensen, T. N., Sgrò, C. M., Weeks, A. R., Ørsted, M., & Hoffmann, A. A. (2022). Conservation genetics as a management tool: The five best-supported paradigms to assist the management of threatened species. *Proceedings of the National Academy of Sciences of the United States of America, 119*(1). https://doi.org/10.1073/pnas.2105076119

Willoughby, J. R., Ivy, J. A., Lacy, R. C., Doyle, J. M., & DeWoody, J. A. (2017). Inbreeding and selection shape genomic diversity in captive populations: Implications for the conservation of endangered species. *PLoS One*, *12*(4), e0175996. https://doi.org/10.1371/journal.pone.0175996

Willoughby, J. R., Sundaram, M., Wijayawardena, B. K., Kimble, S. J. A., Ji, Y., Fernandez, N. B., Antonides, J. D., Lamb, M. C., Marra, N. J., & DeWoody, J. A. (2015). The reduction of genetic diversity in threatened vertebrates and new recommendations regarding IUCN conservation rankings. *Biological Conservation, 191*, 495–503. https://doi.org/10.1016/j.biocon.2015.07.025

Woinarski, J. C. Z., Cripps, J., Durkin, L., Law, B., Legge, S. M., Macak, P. V., Nelson, J., & Rumpff, L. (2023). Impacts of the 2019–20 wildfires on native mammals. In L. Rumpff, S. M. Legge, S. van Leeuwen, B. A. Wintle, & J. C. Z. Woinarski (Eds.), *Australia's Megafires: Biodiversity Impacts and Lessions from 2019-2020* (pp. 211-226). CSIRO Publishing.

Zizka, A., Barratt, C. D., Ritter, C. D., Joerger-Hickfang, T., & Zizka, V. M. A. (2021). Existing approaches and future directions to link macroecology, macroevolution and conservation prioritization. *Ecography, 2022*(6). https://doi.org/10.1111/ecog.05557