

Environmental heterogeneity patterns plant species richness and turnover in two hyperdiverse floras

Running title: Environmental heterogeneity and plant species richness

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Abstract

Aim: To quantify the explanatory power of heterogeneity in predicting plant species richness and turnover here in the Greater Cape Floristic Region and in the Southwest Australia Floristic Region. We compare the environmental heterogeneity in each region, how species richness and turnover interact in each region to produce the observed patterns of richness, and what different forms of environmental heterogeneity better predict richness in each region. We expect the Cape to be more heterogeneous in most environmental axes, and at a finer grain, such that the consequent high levels of species turnover explain the Cape's greater species richness per unit area. We also conjecture that edaphic heterogeneity will be an important factor in predicting richness in SW Australia.

Location: The Greater Cape Floristic Region (GCFR) in southwest Africa, and the Southwest Australia Floristic Region (SWAFR)

Taxon: Vascular plants

Methods: Geospatial data, floral occurrence data → regression analyses, non-parametric

15 statistics

Results:

Main conclusions:

Keywords: biodiversity, environmental heterogeneity, fynbos, Greater Cape Floristic Region, kwongan, macroecology, species richness, species turnover, vascular plants, Southwest Australia

20 Floristic Region

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1 Introduction

Biodiversity represents the variety of living things, and the variety of ecological and evolutionary processes responsible for it (Bøhn & Amundsen, 2004). Studying the distribution of biodiversity
30 in space is a major avenue of biological research (???; Kreft & Jetz, 2007). Regional-scale geographic patterns in species richness have long been studied, particularly in biodiversity hotspots (Cook et al., 2015). The spatial distribution of species richness can be explained in terms of the physical environment. Properties of the environment have been suggested to influence species richness in three ways: (i) productivity, water, and energy to enable organismal
35 growth, and resources (i.e. niche space) to support a wider range of species (Gaston, 2000; Kreft & Jetz, 2007; Mouchet et al., 2015); (ii) stability, which enables species' persistence; and (iii) heterogeneity, which enables ecological speciation and possible barriers to gene flow, and with a wider variety of environments to facilitate species' co-existence (Thuiller et al., 2006; Mouchet et

al., 2015; Cramer & Verboom, 2016). The physical environment, then, can be used to explain
40 species richness in a local-deterministic sense, and in a historical context (Ricklefs, 1987).

The maintenance of species richness, particularly the coexistence of high numbers of species in
biodiversity hotspots, is often regarded as “paradoxical” (Hart et al., 2017), and is a central
problem in ecology (Ricklefs, 1987; Kreft & Jetz, 2007; Hart et al., 2017). Species richness is
constrained by the ability of habitats to support a variety of species—its ecological carrying
45 capacity (Mateo et al., 2017). This is exemplified in approaches to modelling species richness as a
function of environmental predictors in a correlative framework (“macro-ecological models”;
Mateo et al., 2017). Macroecological models of species richness implicitly assume that
communities are saturated, following species-area and species-energy relationships, and at
equilibrium with the environment (Mateo et al., 2017).

50 A solution to the paradox of species coexistence is environmental heterogeneity (EH): a more
heterogeneous environment has a larger environmental space, and can thus facilitate co-existence
between species at the scale of that heterogeneity. EH can also stimulate ecological speciation,
should the region be environmentally stable over evolutionary time-scales. Heterogeneity in the
physical environment is known to be positively associated with species richness (Rensburg et al.,
55 2002; Hart et al., 2017), and has been demonstrated to do so across many taxa—e.g. Canadian
butterflies (???), European vertebrates (Mouchet et al., 2015), South African birds (Rensburg et
al., 2002), in communities along marine continental margins (Levin et al., 2010), French scarab
beetles (Lobo et al., 2004), and for global terrestrial plants (Kreft & Jetz, 2007). The spatial scale
of heterogeneity, or “grain” of the environment, is important to consider (Hart et al., 2017), in the
60 same way that the spatial of absolute environmental conditions has also been considered (???;
Baudena et al., 2015; Mouchet et al., 2015). Species co-existence and biodiversity maintenance is
indeed suggested to be scale-dependent (Hart et al., 2017).

EH is often under-represented in macro-ecological models of species richness, and has recently
been found to explain up to ca. 95% of biome level species richness across South Africa (Cramer
65 & Verboom, 2016). Models that include EH yield better estimates of the richness of the Cape
flora, as they account for the role heterogeneous environments such as those in the Cape facilitate
species coexistence (Thuiller et al., 2006; Cramer & Verboom, 2016). Mediterranean-type
terrestrial biodiversity hotspots, such as the Cape flora included in the models by Cramer &

Verboom (2016), present interesting study systems in which to investigate the relationship

70 between the environment and species richness. These systems exhibit far greater species richness than predicted by their areas, productivities and latitudes (Cowling et al., 1996; Kreft & Jetz, 2007). There are five Mediterranean biodiversity hotspots on Earth: the California Floristic Province, the Mediterranean Basin, the Chilean Winter Rainfall-Valdivian Forests, the Greater Cape Floristic Region, and the Southwest Australia Floristic Region (Cowling et al., 1996; 75 Hopper & Gioia, 2004; Cook et al., 2015). These ecosystems have regular fire-cycles (Cowling et al., 1996), climatic buffering, and long term stability (Kreft & Jetz, 2007), shrubby, sclerophyllous flora (Hopper & Gioia, 2004). Together, they account for ca. 20% of global vascular plant species, yet only ca. 5% of global land surface areas (Cowling et al., 1996). Various hypotheses have been proposed to explain the high levels of plant species richness in these regions (Cook et al., 2015).

80 The species accumulation hypothesis states that the stability of these regions has allowed many species to accrue. The species co-existence hypothesis states that these hotspots may facilitate greater degrees of species co-existence in smaller spatial areas, due to fine-scale heterogeneity in their environments. Indeed, EH has evolutionary implications too, stimulating ecological speciation across sharp environmental gradients.

85 Both the Southwest Australia Floristic Region (SWA) and the Greater Cape Floristic Region (Cape) are Mediterranean-type biodiversity hotspots, particularly in terms of plant species. Where the Cape (with an area of ca. 189,000 km²) is known to contain about 11,400 plant species (about 0.060 species per km²), SWA (area of ca. 270,000 km²) has about 3,700 species (0.014 species per km²) (???). So, the Cape has ca. 4.3 times as many species per km² as SWA. The

90 Cape and SWA are appropriately often compared, due to the similarities between their environments (e.g. oligotrophic soils, an oceanically buffered moderate climate) and their plants' ecologies (Hopper & Gioia, 2004). These two regions present unique flora out of the five Mediterranean systems, with high levels of endemism (Cowling et al., 1996), and many obligate fire-adapted species (Cowling et al., 1996). Similarities withstanding, SWA is topographically and edaphically distinct from the Cape. The former is topographically rather uniform (i.e. flat)—uniquely so among the world's five Mediterranean-climate regions (Hopper & Gioia, 2004)). SWA possesses a mesoscale chronosequence dune system (Laliberte et al., 2014; Cook et al., 2015), while the Cape is mountainous, topographically heterogeneous, and therefore associated with a large degree of spatial climatic variability, with a fine-scale mosaic of geologies

100 and soils (Cowling et al., 1996; Cramer et al., 2014; Verboom et al., 2017).

Both regions have sources of edaphic heterogeneity, but at different scales. This edaphic variability may aid in explaining the species richness in these regions (Beard et al., 2000; Verboom et al., 2017). EH can stimulate ecological speciation, should the region be stable over evolutionary time-scales, as is likely the case in both the Cape and SWA (Wardell-Johnson & Horwitz, 1996; Hopper & Gioia, 2004; Lambers et al., 2010; Cramer et al., 2014; Laliberte et al., 2014; Cook et al., 2015). For the Cape, this richness is largely known to result from long term climatic stability, and fine grain variation in geology and soils (Cramer et al., 2014). The question thus arises whether heterogeneity is a significant contributor to SWA species richness as is likely the case in the Cape. In the absence of topographic variability in SWA, it is proposed that the heterogeneity of that region is due to the juxtaposition of soil types (Laliberte et al., 2014; Cook et al., 2015), creating extreme edaphic variation.

1.1 Hypothesis-v1

Our main hypothesis is that the greater abiotic heterogeneity in the Cape, and the finer grain of that heterogeneity, compared to that of the SWA, accounts for the Cape's greater species richness per unit area. We expect the relationships between EH, species richness, and species turnover in these two regions to demonstrate this. As stated above, heterogeneous environments can (i) support diverse species assemblages, and (ii) stimulate ecological speciation. Thus, we expect species richness to covary with heterogeneity. Additionally, as one moves across a heterogeneous landscape, we expect to find greater turnover in community composition, as different environments support different species. Thus, areas of greater turnover should also be more rich, due to potential complementarity between neighbouring communities increasing total richness. Consequently, we expect that EH positively influences species richness and species turnover, and that species turnover itself positively influences species richness.

1.2 Hypothesis-v2

125 Aim: This study investigates the role EH plays in explaining vascular plant species richness in the Cape and SWA. We compare the relative importance of heterogeneity between the two regions, as

heterogeneity has the evolutionary role of facilitating speciation, and the ecological role of supporting diverse species assemblages. Spatial scale of that heterogeneity is also considered, as the heterogeneity-richness relationship can vary with habitat grain-size.

130 Our hypotheses concern the Cape and SWA’s environments and floras. Our main hypothesis is that the Cape possesses greater abiotic heterogeneity, and at finer grain, compared to SWA, such as to explain the Cape’s greater species richness per unit area, and proposed greater levels of species turnover between areas. We also conjecture that the heterogeneity that predicts species richness in SWA will be more pronounced in terms of edaphic variables. Here we attempt to assess
135 six key predictions of this hypothesis, additionally investigating a seventh prediction to test the conjectured role of edaphic heterogeneity in SWA. Dealing with the two regions’ environments, we assess (i) whether the Cape environment is more heterogeneous than that of SWA and (ii) whether the Cape environment has more pronounced heterogeneity at finer scales than that of SWA. Dealing with the distribution of species in the two regions, we assess (iii) whether the Cape
140 exhibits greater levels of species turnover between areas. Relating each regions’ environment and flora, we finally assess (iv) whether species richness and species turnover are adequately predicted by EH in both regions and whether (v) Species richness and species turnover are better predicted by different forms of EH in either region (e.g. the importance of edaphic heterogeneity in SWA).

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145 We employ classical statistical methods to analyse publicly available geospatial and species occurrence datasets.

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Species distribution models (SDMs), or environmental niche models, are sets of empirical methods that relate observed species presences (or similar data) to environmental and spatial variables,
150 often correlatively (Guisan & Thuiller, 2005). As SDMs rely chiefly on correlating observed species ranges with the conditions thereof, they provide only a model of the realised niche of a species (Raes, 2012), which can cause issues when attempting to predict responses of species to changing climate. Other assumptions of typical SDMs include that the range of species considered is in equilibrium with the environment (Altwegg et al., 2014; Guisan & Thuiller, 2005; Hannah et
155 al., 2005), thus limiting the efficacy of these models on dynamically ranged or highly vagile

species (Hannah et al., 2007). Regardless, given the dynamic nature of biotic ranges under climate change, SDMs are a valuable tool in identifying the contemporary risks posed to global and regional biodiversity.

The GCFR is a megadiverse terrestrial biogeographic region, with high levels of endemism.

160 Midgley et al. (2003) investigated the responses the now defunct Cape Floristic Region (CFR) flora to climate change. Using bioclimatic envelope models (a form of SDM), they modelled the Fynbos Biome’s distribution as a whole, and select Cape-endemic Proteaceae species’ distributions, under current and future climate (climate scenario HadCM2), and again with the impact of land use change. Their Fynbos model was an indicator of regional priority for species
165 level modelling efforts, showing a general southwards contraction of the biome. Their specific Proteaceae models yielded various results: complete extinctions for some species, range contractions for most, improbable range shifts in some, and range expansions in few. The range shifts predicted therein were acknowledged to be improbable, due to the unmodelled limitations of plant dispersal and edaphic dependence. Midgley et al. (2003) concluded that climate change is
170 likely to have severely negative for the CFR flora. However, as will be outlined below, their methods may be overpredicting losses due to climate change.

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The last 20 years have seen much ecological research interest in and development of SDMs, using many statistical and machine-learning-based methodologies (Altwegg et al., 2014; Elith et al.,
175 2008, 2011; Guisan & Thuiller, 2005). Machine-learning-based methods in SDMs include MaxEnt (Elith et al., 2011), genetic algorithms, and adaptive neural networks (Hannah et al., 2005). The use of more advances statistics (e.g. Bayesian frameworks, ordination methods (Hannah et al., 2005)) is also seen. These two avenues of research have intersected in the development of boosted regression trees (BRTs) (originally “gradient boosting machine”; Friedman, 1999) a system of
180 recursively generated, non-linear regression trees, as outlined by Elith et al. (2008). BRTs have been used as SDMs in southern Africa before (e.g. Thuiller et al., 2006), sometimes for conservation purposes (e.g. Coetsee et al., 2009), but BRTs have yet to be used specifically to assess the responses of the regional flora to climate change. BRTs have more flexibility in their predictions than more traditional methods (e.g. GAMs), as they are non-linear and
185 machine-learning-based (Elith et al., 2008).

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2 Materials and methods

2.1 Overview

Our analyses required definitions of the boundaries of the two regions, environmental data for
190 each, and geospatially-explicit vascular plant occurrence records, all based on publicly available
data. The environmental variables chosen (Table 1) for this study were intended to cover a
reasonable spread of climatic, edaphic, and ecologically relevant environmental axes, and are not
intended to be exhaustive. We selected variables describing topography (elevation), productivity
(NDVI), soil status, and climate and climatic seasonality.

195 We carried out this investigation at four principal spatial scales: $0.05^\circ \times 0.05^\circ$ squares (the finest
common resolution among the environmental data sources used), quarter degree squares (QDS)
(Larsen et al., 2009), half degree squares (HDS) (Larsen et al., 2009) and three-quarter degree
squares (3QDS). For the Cape, most plant occurrence records are only accurate to QDS level.
Thus, any analysis involving species data was necessary limited to scales above and including
200 QDS.

Analyses were performed in R v3.5.0 (R Core Team, 2018). Version-numbers of specific R
packages used are presented in the bibliography.

2.2 Environmental data sources

Geospatially-explicit raster layers were acquired for a selection of environmental variables (Table
205 1), for the regions of interest. Here, the GCFR was treated as the areas occupied by the Succulent
Karoo and Fynbos biomes in the current delineation of South Africa's biome boundaries (Mucina
& Rutherford, 2006). The SWAFR was treated as the areas occupied by the Southwest Australia
savanna, Swan Coastal Plain Scrub and Woodlands, Jarrah-Karri forest and shrublands,
Southwest Australia woodlands, Esperance mallee, and Coolgardie woodlands in the World
210 Wildlife Fund Terrestrial Ecoregions dataset (Olson et al., 2001) in order to closely match the

currently delineated SWAFR (Gioia & Hopper, 2017, Hopper & Gioia (2004)). For the sake of readability, we shall refer to the GCFR and SWAFR simply as the Cape and SWA from hereon.

Raster data were re-projected to a common coordinate reference: WGS84 (NIMA, 2000), using the “rgdal” (???) package in R (R Core Team, 2018). All data were re-sampled to 0.05° resolution
215 using the “resample” function in the R package “raster” (???), with the “bilinear” method.

An emphasis was made on using satellite-derived environmental data in this work, in order to minimise differences in data quality and methodologies between the Cape and SWA. Additionally, satellite-derived data have been shown to benefit regional-scale species distribution models (Deblauwe et al., 2016), thus motivating their use in this regional-scale study. The environmental
220 data used in this study were derived from NASA’s SRTM digital elevation model (Farr et al., 2007), NASA’s MODIS/Terra spectroradiometric data for land surface temperature and NDVI, the Climate Hazards Group’s CHIRPS rainfall dataset (Funk et al., 2015), and the International Soil Reference and Information Centre’s SoilGrids250m edaphic dataset (Hengl et al., 2017) (Table 1). SRTM and MODIS are entirely derived from satellite measurements, whereas CHIRPS
225 is interpolated from weather station data with satellite-derived radiometric measurements.

SoilGrids250m is a machine-learning derived product, based on soil measurements as a function of many covariates, including MODIS and STRM sources (see Hengl et al., 2017), using random-forests and other classification-tree-based methods, including gradient-boosting. For the soil data considered here (Table 1), we used depth-interval weighted average values as the value
230 for a particular soil variable in a given place.

Climatic and spectral data arise from satellites monitoring properties of the Earth’s surface through time. We therefore use the mean annual values for rainfall, surface temperature, and NDVI across space in our analyses. Pronounced seasonality of rainfall is a known feature of Mediterranean systems (???). known toand timing, namely precipitation in the driest quarter
235 (PDQ) and temperature in the ... describe!->

2.3 Plant occurrence data

Geospatially-explicit records of vascular plant occurrences were downloaded from the Global Biodiversity Information Facility (GBIF, Table 1). Queries were made for tracheophyte records

from within the borders of the Cape and SWA as treated here (GBIF, 24 July 2017, GBIF (24
240 July 2017)). Only records with defined species and intra-specific ranks were kept. Intra-specific
occurrences were treated as simply being representative of their species. This resulted in FIXME
unique species names in the Cape, and FIXME in SWA.

We cleaned these data using the R package “taxise” (???, (???)) to check that these species
names had accepted-status among taxonomic databases. I queried two major taxonomic
245 databases: the Global Name Resolver (GNR), and the Taxonomic Name Resolution Service
(TNRS). Should one of either service return at least one match for a given name, then that name
was deemed accepted. Those names for which no full binomial matches were found in either
database were excluded from the final list of species. The number of species names excluded
totalled at FIXME and FIXME for the Cape and SWA respectively. Especially for SWA, these
250 numbers may be deemed appreciably high. But, the occurrence records that would be dropped, as
a consequence of these names’ removals, seemed to be distributed randomly in geographic space
in both regions. As such, any effect of the loss of these records in this analysis is uniform within
the two regions.

After the unaccepted names were removed, it was important to ensure that a species was not
255 listed under multiple synonyms. Such cases would skew the species richness data used in this
study. In light of this, the remaining names were queried in the Tropicos and Integrated
Taxonomic Information System (ITIS) databases for their known synonyms, using “taxize”. These
were collated to produce a nomenclatural “thesaurus” for the Cape and SWA species. This
consisted of a list of the accepted species names in a region, each associated with a list of known
260 synonyms. I amended species’ names in the GBIF occurrence data, in order ensure species were
listed under only one of these synonyms, as follows: For each entry in the thesaurus, for each
synonym of that entry, if that synonym appeared in the GBIF species list, I replaced all
appearances of that synonym in the species list with the original name from the thesaurus-entry
that that synonym came from.

265 Lastly, I removed any species from both regions that are invasive aliens or non-indigenous. Alien
species lists for plants in South Africa and Australia were acquired from the IUCN’s Global
Invasive Species Database (<http://www.iucngisd.org/gisd/>).

The final total plant species richness in each region was FIXME and FIXME for the Cape and

SWA respectively. These final collections of species occurrence records were converted to

270 raster-layers, wherein pixel-values represented the species, genus and family richness of vascular plants within that pixel. These rasters were produced at QDS, HDS, and 3QDS resolutions.

2.4 Analyses

2.4.1 Quantifying environmental heterogeneity

First, in order to assess predictions (i) and (ii), we needed to describe the EH in both regions.

275 Using the R package “raster” (???), we used a modified version of the “roughness” index in the “terrain” function: for a three by three neighbourhood of cells, our index of roughness is the average square-root of the squared difference between each of the n neighbour cells’ values x_i and the central focal cell’s value x_{focal} :

$$Roughness = \frac{1}{n} \sqrt{\sum_{i=1}^n (x_{focal} - x_i)^2} \quad (1)$$

This value, notionally the standard deviation of values relative to the focal value, is ascribed to

280 the focal cell. Note, in order to use as much data from within regions’ borders as possible, roughness was computed if a focal cell had at least one neighbour cell—that is, roughness is defined where $n_{x_{focal}} \geq 1$. Using this index of heterogeneity, we produced raster layers of each of our nine environmental variable’s heterogeneity. We compared the distributions of roughness values in each variable in each region with non-parametric Mann-Whitney U -tests, as almost all
285 variables could not be normalised by log-transformations. We also compare the effect size of the Cape vs SWA using the “common language effect size” ($CLES$), using the R package “canprot”. The $CLES$ is the proportion of all pairwise comparisons between two sample groups’ observations where one group’s value is greater than the other. In our case, of all pairwise comparisons of a variable’s roughness values between the Cape and SWA, we calculated the $CLES$ as the
290 proportion of pairs where Cape roughness values were greater than that of SWA. This allowed us to assess prediction (i). To compare the spatial scales of heterogeneity (prediction (ii)) between each region, we repeated this analysis at all four spatial scales. Once again, this entailed recalculating the roughness layer for each variable after the original layer (0.05 degrees resolution)

had been rescaled to each of the coarser resolutions.

295 2.4.2 Quantifying species turnover

Regarding prediction (iii), we wished to compare the general degree of species turnover in each region. To compare the extent of species turnover between the Cape and SWA, we determined two metrics of species turnover. The first, computes the mean species turnover as Jaccard distance (???) between each pair of QDS within each HDS (\bar{J}_{QDS} , based on HDS with $2 \leq n \leq 4$ QDS) in both regions. The second is defined in terms of Whittaker's additive definition of β -diversity (???), where

$$\gamma = \alpha + \beta \quad (2)$$

Here, we treat species richness at the HDS-scale (S_{HDS}) as γ and at the QDS-scale as α . Intuitively, the species richness of an area is the result of the richness of sites within that area and the difference in species complements between those sites. Thus, we use here an additively defined residual turnover (T_{HDS} ; i.e. $\beta = \alpha - \gamma$) as the proportion of S_{HDS} unexplained by the mean species richness of HDS' constituent QDS (\bar{S}_{QDS}). We compare the distributions of \bar{J}_{QDS} and T_{HDS} using non-parametric Mann-Whitney U -tests, in order to guard against non-normality.

2.4.3 Predicting richness and turnover with environmental heterogeneity

Regarding prediction (iii), we wished to compare the general degree of species turnover in each region. For (iv) and (v) we modelled species richness (S) and turnover as a function of various combinations of environmental and environmental heterogeneity variables in both regions.

2.4.3.1 From BIO3013F Protea-SDMs project methods

To explore which axes of environmental heterogeneity have most influence on vascular plant species richness, and differences in the importance of difference axes between the Cape and SWA, we employed boosted regression tree (BRT) modelling techniques. BRTs provide a machine learning-based model of response variables and do so without involving normal null-hypothesis

significance testing. Here, two sets of BRT models were developed from the Protea Atlas occurrence records: BRTs for each of the 203 species of Proteaceae (i.e. SDMs) for which the results thereof were averaged by genus, and BRTs for each of the 13 genera directly, wherein
320 occurrence data was used to create genus-level models. The latter can be thought of as genus distribution models, or GDMs hereafter.

BRT model construction was performed, as detailed by Elith et al. (2008) in R (v3.2.4; R Development Core Team, 2014) using the package gbm (v. 2.1.1; Ridgeway, 2007). Following iterative parameter optimisation for learning rate and tree complexity, Gaussian BRT models
325 were constructed with tree complexity = 5 (number of nodes of each tree, i.e. the maximum interaction depth the model is permitted to fit), learning rate = 0.005 (shrinkage factor controlling the contribution of each tree to the final model), bagging fraction = 0.7 (proportion of training data randomly chosen to generate each tree) and cross-fold validation = 10 (i.e. use 10 different randomly selected training data sets). The total explained deviance was calculated as
330 the difference between total and cross-validated deviance divided by the total deviance. The models were developed with all variables (those retained, above) and then simplified using the protocol suggested by Elith et al. (2008) to retain the minimum number of variables contributing to the models of each species or genus.

2.4.3.2 From Hons thesis methods

335 Boosted regression trees are a flexible machine-learning modelling technique (Elith et al., 2008), that allow testing for relationships between a response and a set of predictors without the use of null-hypothesis significance testing (Elith et al., 2008). BRTs have been employed previously to model species richness (Thuiller et al., 2006; see Mouchet et al., 2015; Cramer & Verboom, 2016) as macro-ecological models. BRTs were implemented here to predict vascular plant species
340 richness in each cell, as a function of environmental variables roughness-values in those cells, as a Gaussian response. BRT-models were developed for the GCFR, SWAFR, and for a merged dataset of both regions' data. This combined model included a discrete term for the region. These three regional-scopes were modelled with datasets at the QDS, HDS, and 3QDS resolutions derived from the original environmental data using bilinear resampling (???). The
345 $\log(x + 1)$ -transform of species richness was used, in order to satisfy the assumptions of a Gaussian response. Note, this is not strictly because BRTs have any parametric assumptions

concerning the distribution of the response variable, but rather to aid in applying the Gaussian-family of BRT algorithms to the richness data available.

BRTs are developed through the iterative generation of non-linear regression trees. BRTs are an ensemble-approach, in which a prediction is based on the weighted-sum of the predictions of progressively less important trees, as opposed to the predictions of one tree (Elith et al., 2008). This is representable as follows, with response \bar{Y}_i , weights w_j , and regression-trees $T(X)_j$ (as functions of some matrix of predictor variables X), for $i \rightarrow nt$ number of trees:

$$\bar{Y}_i = \sum_{j=1}^{nt} w_j T(X)_j \quad (3)$$

As recommended by Elith et al. (2008), BRT models were trained on a set of non-collinear predictor variables, across a range of *tc* and *lr* settings, using `gbm.step` in the `dismo` (???).

Collinear predictor variables can skew the interpretation of results, as the relatively influence of mutually collinear variables is reduced. Collinearity among the 9 environmental predictor variables and their respective 9 roughness-equivalents was assessed using `removeCollinearity` in the R package `virtualspecies` v1.4-2 (???), such that variables were no more than 75% collinear (Pearson's $r \geq 0.75$). When faced with a cluster of collinear variables, one variable was chosen manually therefrom (with the exception of NDVI and MLST, which were collinear, but it was considered desirable to include both, as NDVI was found to be an important predictor of species richness previously (Cramer & Verboom, 2016)). Where possible, the roughness-equivalent of an environmental variable was included if its absolute-equivalent could also be included. For the sake of comparison between regions' models, the same set of non-collinear predictor variables was used for training all models (Figure ??). The final predictor set consisted of (i) elevation, rough-elevation, NDVI, and rough-NDVI; (ii) the climatic variables MAP, rough-MAP, PDQ, rough-PDQ, PCV, rough-PCV, MLST, rough-MLST, TCQ, and rough-TCQ; and (iii) the edaphic variables CECSOL, rough-CECSOL, rough-OCDENS, BLDFIE, rough-BLDFIE, CRFVOL, rough-CRFVOL, CLYPPT, rough-CLYPPT, SLTPPT, and SNDPPT. When interpreting the results of BRTs, it is important to consider the effects of the variables included as representative of the effect of the excluded variables with which it is collinear—e.g. any interpretation of the effect of SNDPPT on species richness would then be also considered to be descriptive of the effect of soil pH on species richness (Figure ??).

375 BRTs have three important parameters that users have control over: the learning rate (lr) (i.e. the rate at which iterative trees reduce predictive deviance during model-training), tree complexity (tc) (i.e. the interaction depth), and the number of trees (nt). In order to select ideal lr , tc and nt , 25 candidate BRT-models (for each regional-scope, for each spatial scale) were trained on the final predictor set for a range of tc values (1 to 5), and for each of those over a range of lr values
380 (0.001, 5×10^{-4} , 1×10^{-4} , 5×10^{-5} , and 1×10^{-5}). The function `gbm.step` optimises nt using cross-validation during model training (Elith et al., 2008) by halting iteration when predictions begin to overfit. For all models, I used 10 cross-validation folds, a tolerance-threshold of 5×10^{-4} , a bagging-fraction of 0.75 (the default in `dismo`), and trained models starting with 1 tree, with each iterative step adding 1 tree, up to a maximum of 10,000 trees.

$$pseudo\ R^2 = 1 - \frac{model\ deviance}{null\ deviance} \quad (4)$$

385 The optimum configuration of lr and tc for the final model is a trade-off between model fit (pseudo- R^2 ; Equation 3) and complexity (nt) (Figure ??). As the effect of nt on pseudo- R^2 and nt is negligibly small (Figure ??A), or non-significant (Figure ??B), a tc of 5 was chosen for the final model. This follows the recommendations of Elith et al. (2008), where lr and tc are advised to be adjusted inversely. This was chosen in order to account for the complex interactions
390 determining species richness. To avoid overfitting, an intermediate lr of 0.001 was chosen (Figure ??A). Thus, these configured models ($tc = 5, lr = 0.001$), for each regional-scope, for each spatial scale, were simplified further (using `gbm.simplify` in `dismo`), in order to remove predictor variables that contribute little, specific to each model. These simplified predictor sets produced by `gbm.simplify` were then used to re-train the models configured with $tc = 5, lr = 0.001$. These
395 final 9 models (i.e. 3 regional-scopes across 3 spatial scales) are interpreted in this study.

3 Results

3.1 Describing environmental heterogeneity across scales

Across all variables considered, the Cape is more environmentally heterogeneous in the majority of pairwise comparisons of grid-cells ($CLES > 0.50$, Mann-Whitney U -test: $P < 0.05$, Figure 1).

400 The Cape is thus more environmentally heterogeneous than SWA overall, but the degree to which it is more heterogeneous varies between environmental variables. These effects also vary somewhat with the spatial scale concerned. In some variables, the differentiation between Cape and SWA heterogeneity lessens at coarser scales (Figure 1b). Indeed, when comparing the overall ranking and medians of Cape vs SWA roughness values for each variable, we only find non-significant
405 differences at the coarser 3QDS scale (Mann-Whitney U tests, $P > 0.05$, Figure 1b).

Most obviously, and as expected, topographic heterogeneity is greatest in the Cape (Figure 1). Though SWA has a slightly wider distribution of elevational roughness values at coarse scales (e.g. 3QDS) compared to fine scales (0.05°), so does the Cape. As such, the relative difference between the two regions seems invariant with spatial scale ($CLES \approx 0.95$, Figure 1b). This
410 concurs with our expectations, as the Cape is mountainous and known to have steep elevational gradients (??), while SWA is much more topographically uniform.

Climatic heterogeneity presents less differentiation between the Cape and SWA than elevational roughness (Figure 1a), though still the Cape predominates (Figure ??b). Notably, the difference between Cape and SWA mean annual rainfall and land surface temperature heterogeneity lessens
415 when considered at coarse spatial scales (3QDS scale, Figure ??b). Rainfall seasonality (PDQ), however, is similarly more heterogeneous in the Cape across all spatial scales considered.

Biological productivity, as measured by NDVI, varies spatially to a similar extent in the Cape and SWA (i.e. is more similarly heterogeneous, $CLES < 0.60$, Figure 1).

Concerning edaphic variables, the Cape and SWA are similarly heterogeneous at coarser scales,
420 particularly in terms of CEC and Soil C (Figure 1b).

3.2 Comparing species turnover in the two regions

Following calculations of \bar{J}_{QDS} and T_{HDS} for each HDS-cell in each region, we used non-parametric Mann-Whitney U -tests to compare the distributions of values in the Cape and SWA. The Cape possesses generally greater floristic turnover than SWA, no matter how turnover
425 is defined (Figure 2).

3.3 Predicting richness and turnover with environmental heterogeneity

Species richness and turnover data were related to BRT-models ...

4 Discussion

Conclusion: The Cape is more generally environmentally heterogeneous than the SWA, as

430 expected (see prediction (i)). Though, there are cases where the SWA is arguably
at-least-as-heterogeneous as the Cape, and we can observe here extreme regions of high edaphic
heterogeneity, at fine scales, in SWA. These surpass the edaphic heterogeneity of the Cape,
supporting our seventh prediction/conjecture.

We also have support for prediction (ii), as seen in Fig. ??.

435 I have provided support for the hypothesis that the difference in plant species richness between
the GCFR and SWAFR is accounted for by the fact that the GCFR is more abiotically
heterogeneous than the SWAFR. As expected, the GCFR is shown to possess (i) a quantifiably
more heterogeneous environment, and (ii) is heterogeneous at a finer spatial scale than the
SWAFR. I have shown that vascular plant species richness (iii) can be explained in terms of
440 environmental conditions, including environmental heterogeneity, in both the GCFR and
SWAFR. Also, I have shown that (iv) the set of environmental axes that explain plant species
richness, both absolute and as heterogeneity, differs between the GCFR and SWAFR. These
findings contribute towards an understanding of the ecological conditions that facilitate species
coexistence (and likely stimulate ecological speciation) in these two regions.

445 These two regions present differentiable environmental spaces, each with heterogeneity varying
across spatial scales. The clear separation of the regions' topographic features is as expected
(Figures ??A, ??). Indeed, topography seems to be the most striking distinction between the
regions. The Cape region has been found previously to have the second highest median
topographic heterogeneity of the five Mediterranean-climate regions (Bradshaw & Cowling, 2014).

450 The GCFR has a much wider range of scales exhibited in the heterogeneity across its
environmental axes. Notably, each region has finer scale heterogeneity in some variables, and
coarser scale in others—neither region is necessarily more fine or coarse than the other, as it

depends on the variable concerned. BRT-models of species richness in both regions reveal species richness to depend on those environmental axes that differentiate the two regions (Figures ??),
455 ??). The importance of variables is also shown to vary with spatial scale (Figure ??), as previously suggested may be the case when modelling geographic patterns of biodiversity (Baudena et al., 2015). Indeed, as Cowling et al. (1996) describes differing patterns of species richness across spatial scales, so do the predictors of those patterns vary with scale (Hart et al., 2017).

The fact that a combination of absolute and roughness variables is also as predicted by the
460 hypothesis in this study. In the models developed by Cramer & Verboom (2016) for South Africa, roughness in topography was largely superseded as an important predictor of species richness by other roughness variables. My models, however, did not show this. Similar to the study by Rensburg et al. (2002), my models revealed roughness in topography and other variables to be important. Although, Rensburg et al. (2002) considered differences within pixels, as opposed to
465 this study, which considered differences between pixels. My models, those of Cramer & Verboom (2016), and those of Rensburg et al. (2002), do not all concur as to the role of roughness in elevation vs. more biologically meaningful variables in explaining species richness. The source of these discrepancies is unclear, though no doubt complex. The complements of environmental variables and methodologies used in these studies do differ, limiting extensive comparison between
470 these analyses.

The determinants of vascular plant species are shown to be region specific (Figures ??, ??, ??). The importance of MAP and roughness in rainfall seasonality (PCV) in predicting richness in the SWAFR (Figure ??I, ??J), aligns with the steep climatic gradients observed there (Cook et al., 2015). The soil variables that determine plant species richness in the model for the SWAFR
475 (Figures ??K, ??L) differ to those that determine richness in the GCFR (Figures ??G, ??H), further highlighting the edaphic differences between these two regions. Although both are nutrient leached systems, the SWAFR is flat, with soil-chronosequences (Laliberte et al., 2014; Cook et al., 2015), while the GCFR is mountainous (Cowling et al., 1996; Cramer et al., 2014; Verboom et al., 2017). The importance of roughness in soil density, and absolute texture, in the
480 SWAFR (Figures ??K, ??L) highlights the changes in soil that are associable with age of the substrate (e.g. particle size) as being biologically relevant to species richness. The positive effect of soil clay content on species richness in the SWAFR aligns with the findings of Laliberte et al. (2014) that richness in the SWAFR increases with soil age.

NDVI is more heterogeneous across the GCFR than the SWAFR (Figures ??A). The fact that thermal variables tend to be more rough in the GCFR (Figure ??A) is likely due to possible covariance of the MODIS/Terra products with topography, as MODIS data used here describes land surface temperature. As the GCFR is topographically rugged, the roughness of NDVI may arise from this. Despite this, NDVI is an integrating variable, which captures information about productivity, light availability, and soil nutrients (Power et al., 2017). The fact that absolute NDVI contributes to predicting species richness in the GCFR, especially at finer spatial scales (Figure ??E) demonstrates the role of ecological productivity in facilitating the coexistence of diverse species assemblages. Environmental heterogeneity, then, is integral to explaining patterns of species richness, but must be considered along with resource- and energy-availability axes. In so much as a diverse environmental space supports more species, the materials and productivity required for biota to thrive are also needed to support species (???; Gaston, 2000; Bøhn & Amundsen, 2004; Kreft & Jetz, 2007). As such, my findings, along with those of previous studies (Rensburg et al., 2002; Thuiller et al., 2006; Kreft & Jetz, 2007; Cramer & Verboom, 2016), suggest that there is ecological and evolutionary consequence to resource availability *and* environmental heterogeneity, in that they tend to be positively associated with species richness.

The combined BRT-model of species richness for both regions reveals soil clay content as an important predictor, at coarse spatial scales, despite this variable not being particularly important within each region separately (Figure ??). Though this model does not strictly consider the regions as separate, this finding may indicate that the relationship between clay content and species richness differs between the regions. So far as clay content can be used to predict species richness, it matters more to those predictions when applied to large sections (i.e. coarse scales) of each regions.

Kreft & Jetz (2007) modelled global terrestrial vascular plant species richness, which focussed on primarily absolute environmental values, underestimated the richness of the Cape flora. Though Kreft & Jetz (2007) did include topographic heterogeneity in their predictor set, topography is often a proxy for more biologically meaningful variables (Cramer & Verboom, 2016). This explains why the inclusion of these variables (e.g. roughness in mean annual precipitation) yields more accurate predictions of species richness. Indeed, Thuiller et al. (2006) also included topographic heterogeneity. Cramer & Verboom (2016) described 68% of species richness at the QDS scale across South Africa. Regarding the GCFR, depending on whether one consults

515 pseudo- R^2 (Table 3), the ratio of mean predicted to observed richness per grid-cell (Table 5), or
the distributions of predicted vs. observed richness values per grid-cell (Figure ??), I have
achieved a similarly suitable level of predictive accuracy. There is, though, still unexplained
species richness in light of my models. As Cramer & Verboom (2016), Rensburg et al. (2002),
Thuiller et al. (2006), and Mouchet et al. (2015) have done, these macro-ecological models are
520 a-historical. Evolutionary considerations of species richness in geographic space are worthwhile,
especially in regions with environments stable over evolutionary time.

The findings here are correlative. There are, however, many proposed mechanisms to explain the
correlative signals demonstrated here. My findings support the hypothesis that Mediterranean
systems' plant species richness is a function of spatial variability in environmental conditions.
525 This can stimulate diversification, and maintain that diversity by providing a range of habitats for
species co-existence. Oligotrophic soils can stimulate an increase in functional diversity, through
the evolution of diverse nutrient acquisition strategies (Lambers et al., 2010; Verboom et al.,
2017) (e.g. sclerophylly (Cramer et al., 2014; Cook et al., 2015)). An aspect of the environment I
have neglected to consider is fire, shown to also contribute to predictions here in the GCFR
530 (Cramer & Verboom, 2016). Cardillo (2012) have shown the structuring forces behind species
co-occurrence patterns, and thus likely species richness, differ between species-pairs with different
post-fire responses and those with similar post-fire responses.

Though the GCFR was correctly predicted to have, on average, more species per grid-cell at HDS
and 3QDS scales than the SWAFR, this was not the case for QDS grid-cells (Table 5). This
535 demonstrates that the GCFR is indeed overall more rich in plant species than the SWAFR, but a
given HDS in the SWAFR contains fewer species than a given GCFR HDS. Thus, the greater
richness in the GCFR is a product of greater turnover in species at spatial scales no more coarse
than the HDS. Species turnover is an interesting aspect to species richness studies, as it species
turnover is implicit to species-area and co-existence-area relationships (Hart et al., 2017). One
540 could expect patterns of endemism and species turnover to concur with patterns in environmental
heterogeneity to some degree.

Following from the understanding that functionally diverse assemblages, which are more likely to
be more species rich, are likely to arise and/or occur in areas with diverse ecological pressures
(Molina-Venegas et al., 2015), one would expect, then, heterogeneous habitats such as those in

545 Mediterranean-type biodiversity hotspots to exhibit high levels functional beta diversity along steep environmental gradients (Molina-Venegas et al., 2015). If the niches concerning these functions are phylogenetically conserved among those biota, then one would also expect high levels of species and phylogenetic beta diversity along these gradients (Molina-Venegas et al., 2015). This concurs with the notion put forward by Power et al. (2017), wherein megadiverse
550 systems such as these represent the results of “phylogenetic niche conservatism on a heterogeneous landscape”. Thus, species and phylogenetic turnover should covary with environmental heterogeneity in some way. Indeed, endemism, at certain scales, could also follow this pattern. Thuiller et al. (2006) demonstrated that there is phylogenetic and biome related determinants of species richness. This makes sense, in light of the difficulty of crossing biome
555 boundaries in Mediterranean systems (Power et al., 2017). NDVI and light availability, and the heterogeneity therein, are associated with high levels of floristic turnover (Power et al., 2017). This may be indicative of ecological specialisation precluding species from crossing these boundaries, thus increasing the level of endemism within a region, while also increasing the level of turnover, and thus likely species richness, along environmental gradients. Although, this may
560 be debated. Beard et al. (2000) state that the high levels of endemism in SWAFR are function of habitat specialisation to soil mosaics. Cf. Laliberte et al. (2014), who say that this endemism is likely due to environmental filtering along these soil turnover sequences, as opposed to the juxtaposition of specialised species along soil gradients.

I have demonstrated support for the idea that environmental heterogeneity is positively
565 associated with species richness, particularly Mediterranean systems. In the SWAFR and the GCFR, high levels of endemism and biodiversity are also likely the results of long-term landscape and climatic stability (Hopper, 1979). Thus, the roles of environmental variability through space, and stability through time, are the two main ways in which the environment relates to biodiversity in these regions.

570 **Table captions**

Captions are also repeated alongside their respective tables for readability.

Table 1: Georeferenced vascular plant species occurrence and environmental data sources used in

this study. The temporal extent of data used is described where applicable. Abbreviations are as follows: MAP, mean annual precipitation; PDQ, precipitation in the driest quarter; CEC, cation
 575 exchange capacity.

Figure captions

Captions are also repeated alongside their respective figures for readability.

Figure 1: Types of environmental heterogeneity, compared between the the Cape and
 SWA—namely for (a) elevation, (b) climatic variables, (c) NDVI and (d) soil variables—in each
 580 panel consisting of three sub-panels per variable type. The upper row of panels shows example
 distributions of roughness values (Equation (1)), showing the different extremes in environmental
 heterogeneity observed in each region when compared at fine (0.05°) and coarse (3QDS) scales.
 Each distribution has under it area 1. Histograms were constructed using 20 breaks. In the lower
 row of panels, these distributions of roughness values were compared between the Cape and SWA
 585 at each of the four spatial scales, not just 0.05° and 3QDS, using non-parametric Mann-Whitney
 U -tests to test for differences. The “common language effect size” (*CLES*, see text) describes
 these differences (b). U -tests for almost all environmental variables yielded significant differences
 ($P < 0.05$) between Cape and SWA values (NS, non-significant differences). *CLES* for 0.05° res. is
 for 5000 random cells in each region, as the Mann-Whitney U -test cannot handle more than a few
 590 thousand values per sample when comparing.

Figure 2: Species turnover, described in two forms ((a) mean Jaccard distance between QDS in
 each HDS (\bar{J}_{QDS}), (b) additively defined turnover (T_{HDS} , see Equation (2)) as a proportion of
 HDS richness (S_{HDS})), compared between the Cape and SWA. Mann-Whitney U -tests between
 the Cape and SWA distributions of \bar{J}_{QDS} and T_{HDS} yielded significant differences.

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Biosketches

700 **Ruan van Mazijk** is a Masters student broadly interested in comparative biology and ...

Michael D. Cramer

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Author contributions

MDC and GAV conceived the study question, which RVM investigated under their supervision for
705 his BSc Hons project. The analyses and programming work were largely devised by RVM, with
input from the other authors, and was carried out by RVM. RVM wrote the first draft of the
manuscript and all authors contributed equally thereafter.

Tables

Table 1: Georeferenced vascular plant species occurrence and environmental data sources used in this study. The temporal extent of data used is described where applicable. Abbreviations are as follows: MAP, mean annual precipitation; PDQ, precipitation in the driest quarter; CEC, cation exchange capacity.

Variable	Source	Temporal extent	Citation
Plant species occurrences	GBIF	TODO	??, ??
Elevation	SRTM v2.0		??
NDVI	MODIS (MOD13C2)	Feb. 2000 to Apr. 2017	??
Climatic variables			
Surface temperature	MODIS (MOD11C3)	Feb. 2000 to Apr. 2017	??
MAP	CHIRPS v2.0	Jan. 1981 to Feb. 2017	??
PDQ	CHIRPS v2.0	Jan. 1981 to Feb. 2017	??
Soil variables			
CEC	SoilGrids250m (CECSOL M 250m)	TODO	??"
Clay	SoilGrids250m (CLYPPT M 250m)		
Soil C	SoilGrids250m (OCDENS M 250m)		
pH	SoilGrids250m (PHIKCL M 250m)		

Figures

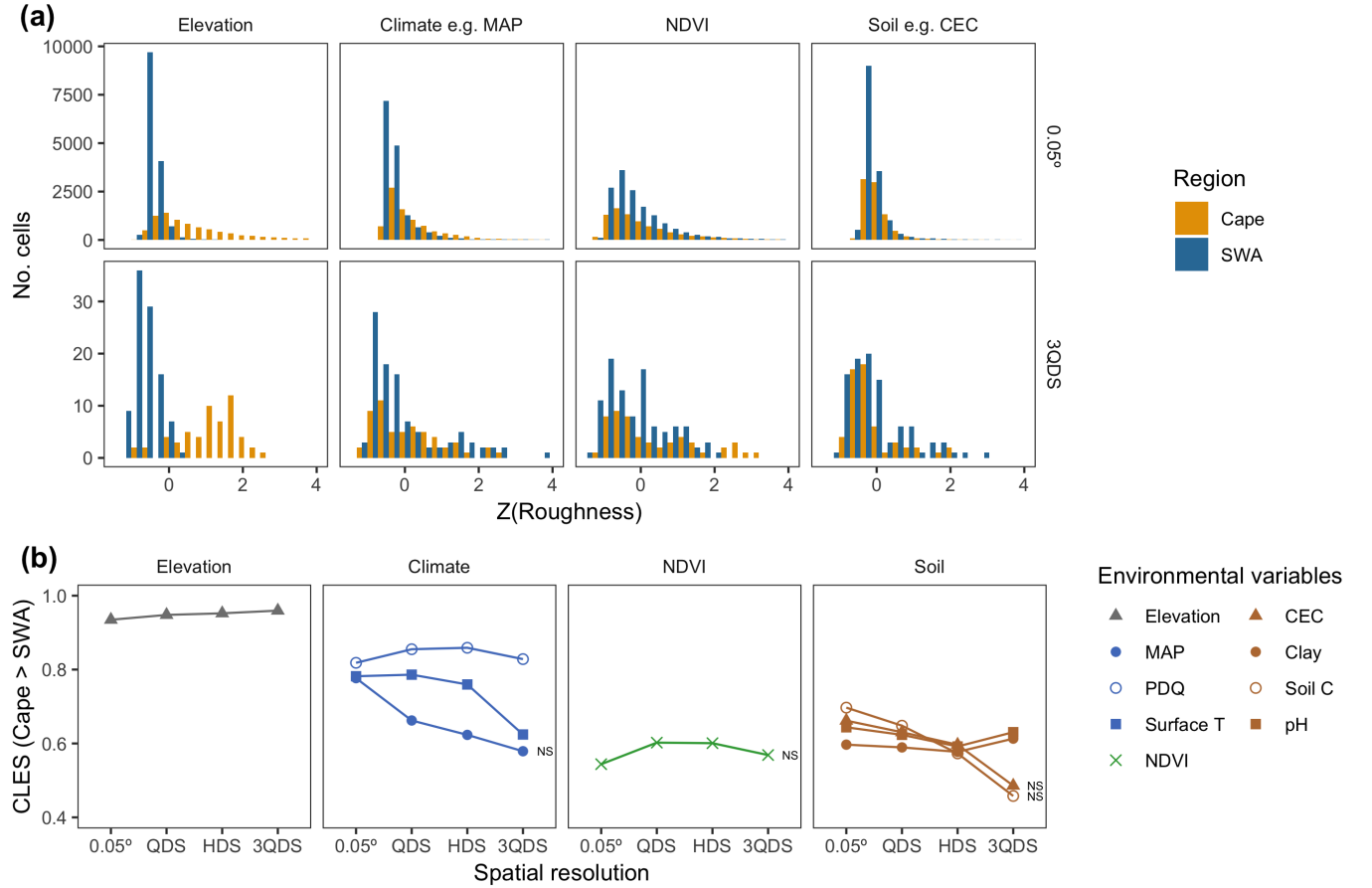


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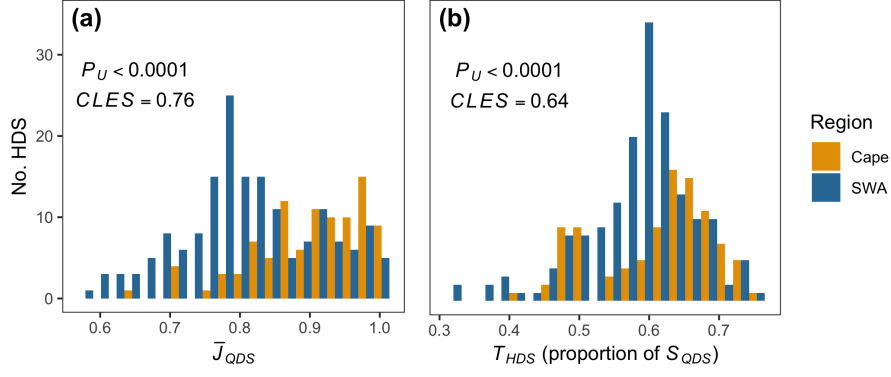


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