THESIS

GAP ANALYSIS OF INDIA'S WESTERN GHATS PROTECTED AREA NETWORK: INSIGHTS FROM NEW AND UNDERSTUDIED ENDEMIC SPECIES' DISTRIBUTIONS

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ABSTRACT

GAP ANALYSIS OF INDIA'S WESTERN GHATS PROTECTED AREA NETWORK: INSIGHTS FROM NEW AND UNDERSTUDIED ENDEMIC SPECIES' DISTRIBUTIONS

Protected areas are a crucial tool to meet conservation goals of the 21st century, especially in biodiverse regions threatened by land use change. This study makes use of nine years of field data collected on over 300 understudied plants and amphibians endemic to the UNESCO-recognized biodiversity hotspot of the Western Ghats of India to produce a gap analysis of its protected area network. The gap analysis updates previous analyses to reassess network coverage and to improve biodiversity distribution estimates. Software for Assisted Habitat Modeling (SAHM) queries possible species distribution models (SDMs) and predictor variables for thirty-five of these species sub-grouped by range strategies. This generates parsimonious sets of predictor variables as well as performance assessments of SDMs, which then populate batch-run distribution Maximum Entropy models (Maxent). These distributions are overlain in various ensembles to produce clade and biodiversity specific insights about high and low-occurrences areas for these species. Hotspot assessments of the region are generated using ensembled distributions and are compared to the current protected area (PA) network to identify gaps in coverage for high-occurrences of these species' distributions. Most high species co-occurrences for both amphibian and plant distributions are covered by the PA network with the exception of three regions for amphibians and six regions for plants, two of which overlap between clades. Previous studies largely or exclusively used secondary-data for their assessments while the majority of species in this study have never been modeled or included in gap analyses. This study's assessment adds new ecological information to individual species and novel contributions to conservation planning in a threatened biodiversity hotspot. This study recommends inclusion of the seven identified high-occurrences areas in

future conservation efforts for the Western Ghats and prioritization of the two areas identified as gaps in protection for both clades.

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Introduction

The conservation of nature, its diversity, and its service to human well-being is one of the most important goals of this century (IUCN 2017, UNEP 2016, Braat and de Groot 2012). Protected area (PA) demarcation is among the most frequently used tools for achieving these goals. Effective PAs have been shown to stop or reverse biodiversity and habitat loss, improve access to and consistency of ecosystem services, and improve human socio-economic conditions (Costanza et al. 1997, Butchart et al. 2010, Ferraro et al. 2011, Geldman et al. 2013). However, in many cases, standardized and systematic monitoring to evaluate the impact and effectiveness of PAs in achieving their stated goals is lacking (Bottrill et al. 2013). Case studies document PAs as achieving successes as well as being ineffective or detrimental for conservation and livelihood goals (Christie 2004, Ostrom et al. 2009, 2011). Among many possibilities, the cause of neutral or negative impacts is commonly attributed to lack of policy enforcement (e.g. paper parks: Bruner et al. 2001, Gibson et al. 2005) or the failure of PA designs to adequately protect core habitats and adapt to changing ecological needs of vulnerable species (Brandon and Kent 1992, Butchart et al. 2015).

Protected area establishment is most effective in conserving biodiversity when it targets areas with vulnerable species, defined as those of IUCN threatened-status or worse or as endemic species with restricted ranges (Das et al. 2006; Brooks et al. 2002, 2006). Biodiversity hotspot is a term that describes areas of high biological diversity and occurrence of vulnerable species (Mace and Lande 1991). Globally, thirty-six regions are defined as biodiversity hotspots, yet each site measures and qualifies its biodiversity using disparate or incomparable types of data and monitoring methods (Myers et al. 2000). Therefore biodiversity hotspots are sometimes critiqued as a metric for setting conservation priorities and should be considered as one of many possible pathways for identifying conservation policy and practice (Myers et al. 2003, Marchese et al. 2015). Despite these contentions, given limited information and resources, this study and others suggest that biodiversity hotspots are reasonable means of guiding conservation action

(Mittermeier et al. 2011). In nearly all cases, protecting these hotspots relies on *in situ* conservation interventions that prioritize areas with the highest occurrences of endemism, threatened species, species-richness, and/or intact ranges of multi-species habitat (Possingham and Wilson 2005). However, due to limitations in primary data, monitoring, variation in policies and enforcement, and/or suboptimal analytic methods, many hotspots are known only through very coarse estimations of the distributions of the biodiversity that qualifies them as hotspots (Zachos and Habel 2011, Marchese et al. 2015).

Historically, PA creation has often been based on heavily studied, large bodied or charismatic species or geophysical uniquenesses (Isaac et al. 2004, Joppa and Pfaff 2009). Including evidence-based distributions of understudied and vulnerable species in prioritization contributes to the goal-setting and goal-achieving processes in biodiversity conservation (Kullberg et al. 2015). Gap analysis is both an established scientific methodology and a practitioners' tool that assesses the current state of PA design and integrates important data into PA evaluations, policy, and management (Rodriguez et al. 2004). A gap analysis uses species distributions to identify geographic areas, or gaps, in a PA network that should be targeted for protection (Scott et al. 1993). This type of analysis has been widely used to expand and redirect management of PAs domestically and internationally (Jennings 2000, Vimal et al. 2011). Selecting which species distributions are used in the gap analysis is determined both by which species are relevant to PA conservation goals and the availability of data to estimate those distributions (Angelstam 2004, USGS Gap Analysis Program report 2013). As new data become available and species are discovered, change status of vulnerability, or are identified as important to PA goals, gap analyses must be updated to adequately reflect those changes.

The species selected to conduct a gap analysis dictate the types and degree of inferences able to be made about its results (Jennings 2000). Some groups of species can serve as ecological and conservation indicators (Dufrene and Legendre 1997). Including indicator species in a gap analysis allows results to be extrapolated to produce broader inferences about biodiversity richness and distribution or ecosystem function in the study area (Carignan and Villard 2002). For example, some literature suggests endemic plant distributions and richness correlate with overall diversity of vertebrate endemism (Kier et al. 2009). Endemic amphibian population status and distributions can also be indicators of wider trends in environmental disturbance and function (Stuart et al. 2004, Lewandowski et al. 2010). However, the diversity and conservation status of endemics plants and, in particular, endemic amphibians are shown to be in steep decline globally and yet they are comparatively understudied (Gibbons et al. 2000, Orme et al. 2005, Urbina-Cardona 2008). Despite and because they are understudied, further research on these clades represents a particularly fruitful opportunity to add to information about their conservation status and infer ecological conditions of their habitat. Their inclusion in a gap analysis would also serve the purpose of targeting vulnerable species for protection while still providing the deeper ecological insights into the health and function of the analyzed PA (Sarkar et al. 2006, Saura and Pascual-Hortal 2007).

Though including all species of conservation concern in a gap analysis is ideal, it is nearly impossible to account for all relevant, present, and transient diversity *and* its level of vulnerability on a landscape scale, even if limited to specific geographies or clades of species (Scott et al. 1993). However, accurately predicting and adding representative and ecologically demonstrative species' distributions to gap analyses begins to improve the capacity of conservation efforts to prioritize and effectively target areas in need of additional protections (Rodrigues et al. 2003). Species distribution models (SDMs) are one method for estimating those species occurrences over space and time (Elith and Leathwick 2009). SDMs use a combination of spatial and environmental predictor variables in conjunction with field data recording presences and/or absences of species to produce an estimation of habitat suitability across a defined study area (Guisan and Zimmermann 2000). Though there are many different SDMs and recognizing that it is necessary to discuss caveats and qualifications related to whichever SDM used, they are persistently shown to be useful tools in ecologic research and a valuable methodology for identifying and guiding the delineation of priority areas for species conservation (Guisan et al. 2006). Accurate and well-tested SDMs of representative species produce insightful and important data for conducting and interpreting gap analyses (Hernandez et al. 2006).

Gap analyses use multiple SDMs overlain as a single map to create heat-maps representative of the number of species occurrences per modeled spatial unit. Heat-maps and areas of high species co-occurrence (hotspots) identified therein are sometimes conflated with statistical hotspot maps. Hotspot maps represent *statistically* calculated high and low occurrences of a variable across space, such as species co-occurrence, and in ecologic sciences are often used as a representation for biodiversity richness (Myer et al. 2000, 2012). Presence of high biodiversity richness commonly serves as a metric for assessing conservation goals, often in the form of total species per area (alpha diversity) or as a percentage of distribution covered per unit area (beta and gamma diversity) (Kremen et al. 2008). Prioritization analysis builds on gap analysis models by calculating replaceability of areas given an established set of conservation goals, such as a goal to preserve 60% of habitat for 60% of total species occurring within PA boundaries. Replaceability, or the reciprocal, irreplaceability, is a measure of environmental redundancy with respect to groups of species' distributions that occur within a defined ecosystem (Rüble 1935, Brooks et al. 2006, Carawrdine et al. 2007). This method is useful for identifying areas that are critical, beneficial, or neutral to meeting conservation goals, and allows policy and practice to act in accordance with, or at least with awareness, of those trade-offs. Identify high co-occurrence areas of irreplaceable species as well as where those areas are located in relation to PA network coverage is crucial to assessing and managing current and future conservation in PAs (Prendergast et al. 1993, Myers et al. 2000).

The sub-continent of India, particularly its Western Ghats region, represents a unique opportunity for conservation planners to benefit from a gap analysis. The region faces many potential challenges to conservation such as rapid land use changes, a hyper-diverse geography, an understudied PA network, and a richness of biodiversity that continues to be discovered through newly documented species and genetic testing (UNESCO World Heritage Report 2012, Vijayakumar et al. 2014). The Western Ghats is a well-recognized biodiversity hotspot with nearly 3200 species of known vulnerable and endemic species distributed over a landscape of dynamically shifting land uses and biomes (Indian Wildlife Institute

Annual Report 2016, Table 1). Formal protections within the region have origins in the Government of India's Wildlife Protection Act (WPA) of 1972. The WPA provided an extensive legal framework for the conservation of vulnerable species and the authority to create PAs in India. In response to the WPA, the Western Ghats escarpment saw a proliferation of PA creation in an effort to preserve its high biodiversity and density of endemic and endangered species. However, studies have shown that the placement of many of those PAs was heavily influenced by convenience of location rather than evidence-based study, and in the process displaced thousands of people leading to additional unintentional land use and land cover changes (Gunawardene et al. 2007, Ormsby et al. 2011). In 2006 The Scheduled Tribes and Other Traditional Forest Dwellers Act (known as the Forest Rights Act) overrode the WPA's restricted-use mandate by allowing certain tribal ethnicities and subsistence land-users to occupy PAs and harvest natural resources therein spurning further land use changes. In 2012 UNESCO declared the region a World Heritage site referencing its extensive biological, physical, and cultural properties (UNESCO 2012). Though UNESCO's 2012 World Heritage Report advises that the current and potential future influences of land use change could negatively affect the integrity of the Western Ghats, their ecologic effects have been notably understudied in peer-reviewed literature (Sekar 2016). However, some studies have already suggested the reverse diaspora of the Forest Rights Act have had negative influences on conservation outcomes within PAs and thereby emphasize the importance of reassessing the PA networks in India and the Western Ghats (Pawar, et al. 2007, Gerlach, et al. 2013, Satish et al. 2014).

Recognizing the Western Ghats are an internationally important area rich in biodiversity, a gap analysis was conducted in 2006 (Das et al. 2006). However, this analysis retrieved or created its species distribution estimations only for species that had available secondary data. Thus its focus was primarily on mammalian and avifauna species and vegetation cover types. As noted by the authors, the estimations used to identify hotspots and gaps in PA network coverage were generated using widely varying methodologies and SDMs which may have biased the normalization of input data. In order to standardize the analysis, the authors' species estimations were retrofit to a resolution of 180km² grids cells and thus its results have been subject to scrutiny of scale and precision. In the years since this analysis, continued conservation work and scientific studies have found that there are potential weaknesses and limitations in both the conservation planning for the Western Ghats region and in the knowledge related to earlier conservation efforts and gap analyses. The objectives of this study aim to address these developments and produce a primary data-driven, refined set of estimations for species' distributions relevant to the Western Ghats' conservation goals.

The objective of the study is to produce new insights and recommendations relating to geographic protection for the species of conservation concern in this study endemic to the Western Ghats. This effort relies on estimating their distributions and high-occurrence hotspots in context of the current PA network. It achieves this goal through accomplishing the following:

- Create and assess SDMs for 69 frog and 306 plant species endemic to the Western Ghats.
- Identify areas with high co-occurrence of these species.
- Spatially assess the overlap of these areas with the existing PA network and identify gaps in protection.

The hypothesis of this study is that the PA network does not adequately cover the distributions of vulnerable amphibians and plants in the Western Ghats. This analysis builds on previous studies to assess the relationship between the geographic coverage of vulnerable species and the PA network of the Western Ghats. Key additions of this gap analysis include the use of nine years of primary data on vulnerable indicator species, a spatial resolution of 1km², and a rigorously developed and methodologically consistent set of SDMs.

Methods

Study Area

The Western Ghats is approximately 175,000km² stretching 1,600km north-to-south and 300km east-to-west along the western escarpment of India's Deccan Plateau (UNESCO 2012, Figure 1). It contains extensive variations in physical geography with elevation ranging from sea level to 2,695 meters above sea level and averaging 1,200 meters. Its average annual temperatures are between 18 and 25 degrees Celsius, and the average annual precipitation ranges from 80cm in the northeastern reaches to over 800cm in the southwestern peninsular cloud forests (Gunawardene et al. 2007, Ramachandra et al. 2012). The region encompasses a diverse array of natural features including seven watersheds, one of the world's richest arrays of biodiversity estimated to contain hundreds to thousands of undocumented species (Bebber et al. 2007, Subramanian et al. 2015), and an array of biomes spanning montane grasslands, temperate forests and drylands, and evergreen subtropical and cloud forest ecosystems (CEPF Western Ghats Hotspot Assessment 2016, Indian Wildlife Institute Annual Report 2016). Its PA network contains thirty-nine PAs representing all six levels of IUCN management types and covering approximately 11% of the Western Ghats range (Figure 1). The study area used in SDM predictions is generated using the perimeter of the PA network with a half-degree buffer in order to fully encompass the Western Ghats extent and potential species ranges (Figure 1).

Field Data

Field data for this study consists of over 8,100 presence point locations of 69 frog and 306 plant species collected over nine years (2008 – 2017) and fourteen field seasons. The field work was done at the early onset of the monsoon (early June) or the waning weeks of the monsoon (late September) in order to maximize likelihood of successful field observations. Surveys were conducted by the biogeographical and ecology laboratory of the Centre for Ecological Research of Bangalore, India. Sampling surveys span all fourteen major massifs of the Western Ghats and represent its major biomes and the range of their associated environmental conditions. Data collection methodology utilized randomized convenience plot surveys of 20 to 100 square meters and totaled over 250 sites for frogs and 350 for plants (Figure 2). Presence-only point data were collected ranging from 6 to 207 data points per species (Appendix 1, 2). Upon collection, species were taxonomically identified to the sub-species level and biogeographically assessed for genetic relations (Vijaykumar et al. 2014; Page et al. 2016). In two cases of few presence points for allopatric sub-species, data is combined and modeled as a single SDM then manually separated into individual sub-species SDMs via GIS and expert understanding (Appendix 3). These allopatric species are known to have only recently sub-speciated and would otherwise have been modeled as a single species (Vijayakumar et al. 2014). This study would not otherwise include those allopatric species with such low presence point data.

All frog and plant species are sub-grouped by range strategies (Appendix 1, 2); three sub-groups within frogs (narrow or widely ranging and montane generalists) and two sub-groups within plants (widely or narrowly dispersing). Sub-grouping species enables a more tailored selection of predictors that reflect the unique ecologic profiles of the studied species. Criteria for how species are sub-grouped consists of life-cycle strategies, meta-data collected during field sampling such as elevation and latitudinal bands, and known biogeographical speciation patterns (Vijaykumar et al. 2016, Page and Shanker 2018).

Environmental and Spatial Predictors

Twenty-nine geospatial layers are either retrieved as prefabricated predictors or are created from remotely sensed imager for use as covariates in SDMs (Appendix 4). The Indian National Geographic data base, known as Bhuvan, provides preprocessed and mosaicked Landsat 8 imagery, a percent canopy cover layer, and forest fraction cover layer (ISRO 2018). The United Nations' Food and Agricultural Organization provides a soil type layer and a nearest-surface-water layer. The raw Landsat 8 imagery represents time periods from 2015 through 2017. Each Landsat 8 scene is from the late inter-monsoonal months in order to avoid excessive cloud cover. This time period is also typically associated with the driest time of year which, after processing, produces conservative estimations of environmental indexes for the study area. Thus, imagery of this time period is purposefully selected since, according to background literature, reaching the threshold amount of moisture and vegetative growth is the greatest limiting factor for many of the modeled species (Fu et al. 2008, Baldwin et al. 2009). The raw imagery and forest fraction layer is used to run an unsupervised classification of the land cover in the study area. This process emulates Bhuvan's methodology and was field validated by the Indian Institute Geospatial Lab (Rao et al. 2006). Defined land cover classes include three variants of forest cover (dry, wet, mixed), grassy fields, urban, rocky/barren, water surface, built-up and mixed, agricultural, and scrubland. Raw imagery is also used to derive a Normalized Difference Vegetation Index (NDVI) and Soil Adjusted Vegetation Index (SAVI) (Heute 1988). ASTER satellite imagery is used to create a digital elevation model (DEM) and subsequently derived slope and aspect predictor layers (Fischer et al. 2008). All nineteen BioClimatic II variables retrieved from the WorldClim database are also used as potential predictors. All predictor variable layers are clipped to the study area extent and standardized to a 1km^2 grid-cell resolution.

Species Distribution Models

Sub-sets of each of the sub-grouped clades are semi-randomly selected to represent a gradient of species with high and low numbers of presence points. These sub-sets, containing five to twelve species, are first modeled in Software for Assisted Habitat Modeling (SAHM). All species modeled in SAHM are subject to a covariate correlation assessment for all predictors and generates distribution estimations and a range of statistical outputs for five SDM algorithms. Results of this SAHM query are tabulated to track which predictors are most commonly selected within species subgroups and which SDM algorithms produce the highest model performance metrics (Table 2, 3). The resultant sets of parsimonious predictors are used to populate Maximum Entropy model (Maxent) SDMs for all species in this study (Table 4).

Maxent is only one of the SDM models run in the SAHM package. Others included and tested are Boosted Regression Trees (BRT), Random Forest (RF), Multivariate Adaptive Regression Splines (MARS), and Generalized Linear Model (GLM). BRT and RF are tree-based machine-learning algorithms that allow for multi-dimensional field data to be used. They use statistical modeling fitting for each data point in order to identify dominant, dynamic patterns across large data sets and large study areas (Johnson et al. 2012). The 'boosted' aspect of a BRT differentiates it from a RF in that it uses an iterative approach in its model fitting (Elith et al. 2008). The GLM model is among the first to permit presence and absence data in its estimations and allows for modeling of nonlinear geographic data in SDMs, but has been critiqued as over-fitting the data because of its tendency to throw-out predictors (McCullagh and Nelder 1989, Buckland and Elston 1993). MARS like GLM permits presence-absence, but goes a step further by splining regression between response variables and predictor data (Friedman 1991, Leathwick et al. 2006). MARS's noted strong suit is its ability to handle presence points collected in heterogeneous spatiality and resolution (Moisen and Frescino 2002). Maxent utilizes a maximum entropy Bayesian algorithm and input data-use features to predict niche-likelihood of a species rather than explicit habitat suitability (Phillips et al. 2004, Merow et al. 2007; Halvorsen et al. 2015). Maxent is designed to compute potential species distributions based on the premise of imperfect data and predictors and is well known for its predictive accuracy given limited presence points and heterogeneous study areas (Warren and Seifert 2011). Common criticisms of Maxent include that the model assumes all predictors carry equal weight and that its algorithm constrains data via limiting variance in test-trains (Fitzpatrick et al. 2013, Merow et al. 2013). Maxent is reported to be a powerful tool in its simplicity and though sometimes criticized for being an overly simple algorithm and blindly relied on by researchers, it is often found to be a useful tool for modeling small or disparate data sets to produce scientifically sound species distribution predictions (Warren and Seifert 2011, Elith et al. 2011, Philips et al. 2017).

All five SDM models are run on the predefined sub-sets of species to produce a range of statistical outputs with which model performances are compared. In cases of low presence points for species, some models, particularly BRT and RF, are not able to compute distribution estimations because their algorithms require more input data. SAHM produces evaluations of sensitivity and specificity of predictor variables, percentage of modeled area correctly classified (PCC), a true-skill statistic measuring the ratio between Cohen's kappa and PCC, as well as an receiver operation curve (ROC) plot area-under curve (AUC) value. AUC is a commonly relied upon metric that estimates the ability of a model to correctly predict its input data given a piece-wise test-split of input data (Wisz et al. 2008, West et al. 2016). These evaluation metrics are compared to elicit comparative strength of performances across SDM model algorithm per species. Models' performance is recorded to show the frequency of a model being high-performing or not within all sub-groups (Appendix 5, 6, 7). Throughout the initial SAHM query, Maxent is most frequently shown to be highest performing model and thus is chosen as the primary SDM model for this study. Using a single SDM, Maxent for instance, helps to maintain consistency of projections and data usage throughout distribution estimations. Within this initial inquiry into model performances, SAHM also allows for intra-computational selection of predictor variables by means of a covariate correlation matrix. The number of predictors selected is limited to a ratio of 1:3 and 1:12 predictors to number of presence points per species in order to prevent over fitting data to predictors (Austin 2007, Table 4). Predictors are prioritized in the following way: (1) which predictors explain the most deviance in model output, (2) which predictors correlate to other variables, and (3) which predictors are ecologically relevant to the species. No predictors are selected with 70% or higher correlation to another variable, regardless of percent deviance explained. Individual species results from SAHM's predictor and model selection inquiry are tabularized and used to populate batch-run Maxent models of the sub-grouped species.

Default Maxent parameterizations are used for all species except in cases of species with fewer than 20 presence points in which case data is jackknifed in order to avoid spatial autocorrelations by resampling data without removing data during the test-split training. In these cases the maximum number of iterations is increased from 500 to 1000 in order to permit type II errors (false-negative of species occurrence) to emerge rather than preserve the model's computational resources (Halvorsen et al. 2016). Pseudo-absences are created using randomized spatial sampling and allowed to permutate between 500 and 3000 (an average of approximately 1000 are used) depending on the number of species presence points and their spatial distribution. The threshold rule to produce a binary map of species presence is set to a 'sensitivity equal to specificity' which selects a threshold of likelihood-presence based on when type I and type II errors are balanced. This rule is commonly used within SDM literature and found to produce defensible estimations of distributions for both wide ranging and narrow ranging species (Freeman and Moisen 2008, Escalante et al. 2013). The SDMs produce both a gradient likelihood map and binary map for each species.

Ensembling and Spatial Analysis

Species' binary maps are ensembled with a cell statistic tool by sub-groupings, then by clades, then collectively across all species in the study. This yields five additive maps for each of the following sub groups: narrowly-ranging frogs, widely-ranging frogs, montane generalist frogs, narrowly-dispersing plants, and widely-dispersing plants (Figures 3, 4). Three maps of the following ensembled species groups are also created: all modeled frogs, all modeled plants, and all modeled species of frogs and plants combined (Figures 5, 6). Each cell of 1km by 1km area within each of these eight maps is thus represented by a single whole integer indicating the number of species predicted to occur in the grid cell.

These eight ensemble maps represent heatmaps of species distributions and are used to conduct an overlay analysis (Flather et al. 1997). Each map is assessed for high species co-occurrence by querying the study area for cells containing and surrounded by cells containing at least one-third of all possible species within each ensemble map. This process is conducted twice. First, it includes the entire study area and distribution data within the PA network and then a second time after removing distribution data that falls within the boundaries of the PA network (Figures 7, 8). This process reveals the high co-occurrence areas both within and outside of the PA network as well as individually either within or outside of protected areas (Figure 8). High co-occurrence points within the PA network are noted as being potential gaps in coverage. These potential gaps are then evaluated and described for ground assessment by their predictor layer metrics and classified by the land use in order to draw inference about their ecologic setting. Statistically-optimized hotspot analyses are then conducted on the all-frog and all-plant species ensemble distribution maps (PA network data included) in order to identify statistically significant areas of high or low occurrences of species. Results are overlain with heatmap-identified high co-occurrence areas in order to compare results and assess the presence of corroborative hotspot existence (Figure 9).

Results

For the majority of species, Maxent is the most consistently high-performing SDM model in SAHM (Table 2, 3). Though some more algorithmically complex models performed better in species with a higher number of presence points, Maxent is comparable to or out-performed the other models when analyzing species with fewer presence points. Specific cases of other models out-performing Maxent included results for some of the plant and frog species such as *Raorchestes akroparallagii* and *Cinnamomum keralaense*, which had both an unusually high number of presence points and were widely sampled throughout the study area. However, their presence points also tended to be clustered which gives advantage to the independent machine-learning algorithms in BRT and RF. In nearly all cases MARS and GLMs performed comparably to or less robustly than Maxent (Appendix 6). Overall, the initial SAHM inquiries appear highly effective in selecting predictors per species' subgroups and indicate the effectiveness of Maxent to conduct large-scale estimations on multivariate species and species data.

Results of the frog species models consistently used the following BioClim variables in the final selection for sub-groups: Isothermality (Bio 3), Temperature Seasonality (Bio 4), Maximum Temperature of Warmest Month (Bio 5), Annual Precipitation (Bio 12), Precipitation of Driest Month (Bio 14), and Precipitation Seasonality (Bio 15). NDVI, elevation, land cover and canopy cover are also commonly used across all frog species (Table 2). However, not all variables were used in all sub-groups. For instance, low-ranging frog species sub-group models use the Bioclim variables Precipitation of Coldest Quarter (Bio 19) and Mean Temperature of Coldest Quarter (Bio 11) rather than Temperature Seasonality (Bio 4) and Precipitation of Driest Month (Bio 14). Likewise high-ranging and montane generalist frog species used the SAVI and canopy cover variables where low-ranging species did not necessarily. AUCs across all frog models averaged 0.823 and tended to show higher AUCs for species with higher numbers of presence points (Appendix 6). The high occurrence areas identified fell largely within the previously established PAs (Figure 7). However, three areas of high co-occurrence of frogs are located outside of the network near the Munnar and Peermade hillstations and the Ooty Valley (Figure 8). The Ooty Valley is the largest geographically and highest (35 species) co-occurrence area of frogs. No high occurrence areas of frog are shown north of the state of Vasco di Gama (Latitude 15.39).

Within the plants' model results, the BioClim variables of Temperature Seasonality (Bio 4), Max Temperature of Warmest Month (Bio 5), Annual Precipitation (Bio 12), Precipitation Seasonality (Bio 15), and Precipitation of Driest Quarter (Bio 17) are consistently selected for model inclusion. Other variables including the annual minimum NDVI, elevation, canopy cover, soil type, and land cover layers are also included. Compared to widely-dispersing plants, deviance in distribution estimations of the narrowly-dispersing plants are more explained by the canopy cover variable and less so by the slope and aspect variables (Table 3). SAVI and the proximity to water variable are not generally included in SAHM's model queries nor do they show significant contributions to explained deviance in model results. The ensembled heatmaps of the plant species show more areas of high occurrence outside of PAs than the ensemble heatmaps of the frog species do. However, both have high co-occurrence points identified within and outside of the PA network. Unlike model results for the sub-grouped frog species, the widely and narrowly-dispersing plants show less distinctive ensembled ranges, likely due to the higher number of species included in the narrow versus the wide dispersing species that are modeled (212 narrow vs. 94 wide-ranging species). The average plant model AUCs are 0.791, slightly lower than that of frogs (Appendix 7). The valleys just south of the Periyar National Park and the Kollam district, Kottamala hill station region, and the Bandipur forest areas are identified as areas of high co-occurrence of plant species outside of the PA network. The Munnar hill station region and Peermade escarpment are identified as high species co-occurrence across both frog and plant clades (Figure 9).

Hotspot analysis shows that all heatmap-identified high co-occurrence areas, for both frogs and plant species, occur entirely within statistically-identified hotspots (Figure 9). The core hotspot identified for plants covers all high co-occurrence locations. However, unlike frog results, it is predicted to extend further northward along the western escarpment of the Western Ghats beyond where high species co-occurrence points are identified. The identified frog hotspots appear to be geographically narrower than those of plants and are more circumscribed to the identified high species co-occurrences locations. In the ensemble maps of both clades, hotspots and high co-occurrence areas heavily favor the southern portion of the Western Ghats study area. The hotspot for plants covers nearly all established PAs within the network whereas the hotspot for frogs does not extend to PAs north and northeast of the Ooty Valley (Figure 9).

Discussion

The value and importance of a gap analysis is to help ensure PA networks are effective in covering areas of value to the conservation of rare and endangered species. Results of this study provide that value to the Western Ghats stakeholders and support its stated hypothesis that there are gaps in PA coverage of the modeled species' distributions. It identifies areas of high co-occurrence of vulnerable and understudied frog and plant species outside of the PA network and finds both corroborating evidence for and conclusions different from previous gap analysis for the region. It also reveals large-scale geographic and ecologic patterns for the location of these high co-occurrence areas and directs attention to possible drivers of low and high species presence. This information is essential to ensuring future PA creation and other conservation interventions will target areas relevant to their biodiversity conservation directives. Results from achieving the goals and objectives of this study appear to be broadly consistent with previous literature while also offering novel insights into conservation status of the modeled clades, the dynamics of gap analyses, and a current assessment of the state of the Western Ghats' PA network.

Results from the initial SAHM assessments of individual species provide insight into overall habitat preferences for the modeled species. Annual precipitation, maximum temperature, and minimum vegetation index are shown to be the most explanative in predicting distribution of frog and plant species. This result aligns with literature on tropical species SDMs that show such species are better predicted by environmental rather than biophysical variables (Bisrat et al. 2002). Elevation and percentage canopy cover are also highly explanatory for estimations of the clades modeled in this study, which intuitively makes sense from the perspective that changes in these variables correlate to the ecological shifts that influence community make-up and thus species presence (Woodford and Williams 1987). These predictor results unite the hotspots results, leading to the conclusion that the species modeled in this study favor the tropical evergreen forests of the south rather than the more deciduous and xeric regions in the north. This perhaps suggests that endemism in the region is correspondent to or somehow supported by the narrow range of tropical environmental extremes in the southern peninsula. Across most species, the land cover predictor layer is included in the final distribution models, yet it has a lower importance in explaining deviance in the models. This suggests either that land cover is a somewhat plastic indicator of species' habitat suitability (i.e. multiple land covers can be suitable if other environmental conditions are met) or that the land cover layer variable is only a superficial or coarse indicator of distribution. The former possibility corroborates the ecological precept that habitat continuity and human-altered landscapes influence distribution of most species (Elith and Leathwick 2009, Betts et al. 2014), but is also subject to species adaptation and niche spread to other cover types. With respect to the second possibility, that land cover is unimportant, some literature suggests that this notion is more likely a modeling caveat such as having an insufficiently sophisticated land use/land cover layer or having sampling bias in field data (Dormann et al. 2007, Randin et al. 2009, Fourcade et al. 2014).

Modeled distribution estimations appear to perform well statistically and demonstrate accuracy in the context of literature and expert appraisals. Across all frog and plant SDMs, species diversity is concentrated in the southern half of the Western Ghats and even more so in the southernmost quarter. This is in alignment with previous studies estimating diversity distributions for the study area as reported in Sudhakar et al. 2015 and Vattakaven et al. 2016. The plant models tend to show wider distributions generally, a larger hotspot, and more identified co-occurrence areas than the frog models. This possibly indicates that the plants naturally occupy wider ranges or could simply be an artifact that there are more plant species modeled than frog species. Ecologically, this makes intuitive sense from the perspective of plant versus frog habitat needs. For added validation, individual frog and plant SDMs were assessed and deemed accurate by independent experts who have field, genetic, and research experience with the species' ecology and IUCN statuses (SP Vijayakumar, KS Shankar, NV Page). With support of their appraisal, this study places added confidence in its SDM predictions and its assessments of high co-occurrence areas and hotspots.

Results from the overlay analysis indicate that there are high co-occurrence areas outside of the PA network in both frog and plant clades. However, plant species show a slightly larger number and geographic range of high co-occurrence points. All high co-occurrence points across all of the studied species groupings are found to be within a statistically identified hotspot area in the Western Ghats, suggesting consistency in SDM performance and consensus across data and analyses (Vattakaven et al. 2016). The identified areas of high co-occurrence and hotspots are largely covered by the current PA network. This suggests that the past PA network was well designed even though the network was established based on data from larger bodied fauna. However, the regions of high co-occurrence identified outside of the PA network in this study should lead to the consideration of the expansion of this network. The identified areas represent gaps in protection for both individually vulnerable species and regional biodiversity, the protection of which is a conservation goal in the Western Ghats' PA network (UNESCO 2012). By identifying these areas as valuable to conservation goals and, in particular, identifying salient characteristics related to the ecology of these species, land uses within distributions, and the logistics of gazzetting these areas, this study begins to address how such gaps may be protected in the future (Rodrigues et al. 2004).

Two gaps, the Munnar and Peermade regions, are identified as hotspots and high co-occurrence areas for both frogs and plants and are known coffee and tea production regions. Three other identified areas of high co-occurrence of species are also noted as coffee and tea regions, one unique to frog distributions in the Ooty Valley and two unique to plants, one in the southern Kollam district and the northern most identified gap in protection, the Brahmagiri Valley (Figure 9). It is a notable and curious finding that such a high proportion of gaps in the PA network correlate to tea and coffee growing land uses. This leads to new questions about the relationship between the modeled species and managed plantation areas and moreover, about proper conservation management to protect these high co-occurrence areas. The pattern perhaps suggests there are other factors, such as unofficial management, ecologic symbiosis between crops and species, or cultural precepts which enable these species to occur and be conserved in high diversity in these areas. Regardless of speculation, these correlations warrant further research into the possible conservation benefits for certain types of biodiversity that may be found in traditionally managed coffee and tea plantations.

Results of this study's gap analysis show both concurrence and some divergence to the gaps in protection identified in the previous Das et al. 2006 gap analysis. For instance, Das et al. 2006 and this study identify the Badipur Forests as a gap in the PA network coverage for their respective species. However, the Das et al. study further identified three more gaps in close proximity to the Badipur Forests which this study did not identify. This suggest that these three areas plus the Badipur Forests together, considered as a larger unit, is highly important to preserving overall biodiversity richness in the region and should be further investigated. Moreover, corroborating some of the previous results from the gap analysis done by Das et al. (2006), this study identifies four of the same areas outside of formal protection. However, this analysis also finds high species diversity in areas not identified by the previous gap analysis (Das et al. 2006, Figure 10). The three areas identified in this study that are not found in the Das et al. study include two locations that are high co-occurrence areas for both frogs and plants. This suggests that depending upon which species or characteristics of clades are included, e.g. endemism or vulnerability, different results will be derived from a gap analysis. This study thereby encourages the need for a thoughtful, perhaps methodological process for selecting which species are relevant and representative to include in gap analyses to adequately address a PA network's conservation goals. Finally, the Das et al. study also identifies gaps in protection which have since been integrated into the current PA network and thus are not gaps in protection in this study. Therefore this study optimistically presents an example of how gap analysis and their resultant recommendations for protection are useful and impactful to their audience.

Limitations and Future Study

Incomplete information relevant to conservation goals and lack of sufficient or precise data for vulnerable species both limits the capacity to accurately estimate species distributions and limits the ability of gap analyses to direct and prioritize protection of biodiversity. It is therefore important to acknowledge and address the caveats of this study in order to understand how results can be interpreted and suggest future improvements. Sampling bias in the collection of data for an SDM is known to be detrimental to accurate SDM estimations of distributions (Stockwell and Paterson 2002). Though there is no indication of bias in data of this study, more can be done to bolster its input components. Additional modeled species, more presence data and inclusion of absence points could serve to increase the accuracy with which species and co-occurrence distributions are estimated. Additionally, this study utilized only one SDM, Maxent, in the final analysis largely due to its high performance in the SAHM subgrouping queries. Though use of a single SDM subjects results to persistent weakness of the algorithm, it also facilitates standardization of analysis and data-use between species distribution predictions. This study's SDMs are thereby subject to the same caveats and idiosyncrasies in their results and avoid unwieldy comparisons of variable SDMs' limitations and assumptions. There is however literature and some SAHM results within this study that indicate some species' distributions could be better estimated with other SDM model algorithms. Results from sub-groups indicate that there are predictor-specific differences in SDMs between species with differing distribution strategies, and thus it is likely that some species are modeled without their ideal set of predictors; this caveat is true all SDMs created within this study and beyond. Future studies may benefit from testing other and more refined variables or further inquiry into predictor-data matching and use of alternative SDMs or SDM ensembling methods to predict distributions. Batch-modeling SDMs may also contribute to weaknesses in model performance leading to inclusion of non-ecologically supported variables. Such models over-use easily obtained climatic or geophysical variables which would consequently yield less refined or even inaccurate SDMs (Elith et al. 2011). More complex or difficult to obtain ecological variables may out-perform or improve model performance and therefore should be used. One of the ways to address these limitations is through field validation of the SDM predictions. Field validation would serve to resolve questions related to type I and II errors in the model predictions, increase the data available for computing SDMs, and compare on-the-ground realities of a species' environment with the set of predictor variables used to explain its distribution. Unfortunately, it was beyond the scope of this study to carry out field validation. Future research should integrate field assessments to determine the degree to which endemic plant and frog species are indicators of environmental disturbance and overall endemic richness (Werner et al. 2007). This process also offers opportunity to further investigate the ecology of the species leading to better selected or new spatial and predictor variable. Furthermore, field assessments could account for predictions wherein habitat suitability is shown to be high but does not necessarily represent the true number of species occurring. For example, tea and coffee plantations show high habitat suitability but perhaps species are actually not occurring here in the numbers suggested by SDMs. Deriving and including other variables that address spatial management of land cover and land use (e.g. agriculture, permaculture, traditional harvest, etc.), land ownership and land access right (e.g. land tenure), economic valuations of ecosystem services, etc. could also be used to populate and conduct a prioritization analysis. This would results in more holistic recommendations for which areas should first be obtained for inclusion in the PA network. A prioritization analysis such as this could build on this study's findings by assessing the pragmatic conservation barriers to increasing protection for the identified gaps in the PA network (Margules and Pressey 2000). Integrating projections or time-series of variables to elicit predictive model results would also be a prudent follow-up analysis in order to assess the sustainability and adaptability of these PAs in the face of further land use change and climate change.

Conclusions and Recommendations

This study's results improve targeting and capacity of applied conservation efforts, increase scientific understanding of the Western Ghats' ecology, and create a platform to study novel permutations in an established methodology. Multiple gaps in protection for vulnerable species in the Western Ghats' PA network are identified and insights drawn about their location and environmental characteristics. These gaps as well as the individual and combined species' distributions which enabled their identification, will guide managers and policy makers in creation and design of future PAs. This will help to accommodate newly identified ranges of species and prioritize areas in order to efficiently achieve stated conservation goals regarding biodiversity. Furthermore, the individual species SDMs produced in this study and insights gleaned from their production will support new and reassessed status' for dozen of species in the IUCN species list. These new assessments and results from this study will help to target future research and surveys of the region's ecology and conservation efforts. Continued comparison of this study to previous and future gap analyses will generate new insights about assessing and prioritizing areas through spatial analysis both within the Western Ghats and in the larger body of scientific knowledge. Results of this study provide products to an array of stakeholders that can be used to further conservation goals locally and worldwide. This study provides a wealth of new information and a rich baseline for future research and immediate conservation action.

Tables and Figures

Table 1. Description of Western Ghats Hotspot qualifying characteristics, Indian Wildlife Institute 2016 Annual Report.

Characteristic of Western Ghats	Area (km^2)
Hotspot Original Extent (km^2)	189,611
Hotspot Vegetation Remaining (km^2)	43,611
Endemic Plant Species	3,049
Endemic Threatened Birds	10
Endemic Threatened Mammals	14
Endemic Threatened Amphibians	87
Extinct Species†	20
Human Population Density (people/km^2)	261
Area Protected (km^2)	26,130
Area Protected (km^2) in Categories I-IV*	21,259

Table 2. Sub-set of SAHM modeled frog species with results depicting selected covariates and highest performing model.

Frog Species	N	Covariates Selected						Best Performing Models
Pseudophilautus amboli	38	Mean of diurnal temp range	Max temp – warmest month	Landuse/land cover	Precip. Seasonality	NDVI (minnimum annual)	Canopy cover	GLM, RF
Pseudophilautus kani	42	Annual temp range	Precip. Seasonality	Precip. warmest quarter	Elevation	NDVI (minnimum annual)		RF, MAXENT
Pseudophilautus wynaadensis	105	Temp seasonality	Max temp – warmest month	Precip. Seasonality	Precip. warmest quarter	NDVI (minnimum annual)	Elevation	MAXENT, RF
Raorchestes akroparallagii	14	Temp seasonality	Max temp – warmest month	Annual Precip.	Precip. Seasonality	NDVI (minnimum annual)		RF, BRT
Raorchestes anili	85	Temp seasonality	Max temp – warmest month	Annual Precip.	Precip. Seasonality	NDVI (minnimum annual)	Canopy cover	RF, BRT
Raorchestes beddomii	78	Temp seasonality	Max temp – warmest month	Annual Precip.	Precip. coldest driest quarter	NDVI (minnimum annual)	Elevation	RF, MAXENT
Raorchestes bobingeri	40	Max temp – warmest month	Annual Precip.	NDVI (minnimum annual)	Canopy cover			MAXENT, (MARS)
Raorchestes griet	92	Isothermality	Max temp – warmest month	Precip. Seasonality	Precip. coldest driest quarter	Landuse/land cover	NDVI (minnimum annual)	MAXENT, GLM*
Raorchestes bobingeri	29	Max temp – warmest month	Precip. coldest driest quarter	Precip. warmest quarter	Precip. coldest quarter	NDVI (minnimum annual)		MAXENT, (GLM)
Raorchestes jayarami	6	Isothermality	Temp seasonality	Mean temp. coldest month	Precip. Seasonality	Precip. coldest driest quarter	Precip. coldest quarter	MAXENT
Raorchestes travancoricus	44	Max temp – warmest month	Min temp. coldest month	Precip. wettest month	Precip. coldest driest quarter	Landuse/land cover		MAXENT (GLM)
Raorchestes dubois	19	Annual temp range	Precip. wettest month	Precip. Seasonality	NDVI (minnimum annual)	Elevation		MAXENT, MARS
Raorchestes resplendens*	6	Max temp – warmest month	Precip. Seasonality	Precip. warmest quarter	Precip. coldest quarter	Elevation		MAXENT
Raorchestes primarumfii	13	Precip. driest month	NDVI (minnimum annual)	Elevation				MAXENT
Raorchestes sushili	31	Precip. Seasonality	Precip. warmest quarter	NDVI (minnimum annual)	Elevation			MAXENT

Table 3. Sub-set of SAHM modeled plant species with results depicting selected covariates and highest performing model.

Plant Species	N	Predictors Selected							Best Performing Models
Aglaia barberi	34	Max temp – warmest month	Annual Precip.	Landuse/land cover	Canopy cover	NDVI (minnimum annual)			RF, MARS
Drypetes confertiflora	20	NDVI (minnimum annual)	Canopy cover	Elevation					MAXENT, MARS
Cinnamomum malabatrum	30	Temp seasonality	Annual Precip.	NDVI (minnimum annual)	Elevation				MAXENT
Diospyros ghatensis	28	Mean of diurnal temp range	Max temp – warmest month	NDVI (minnimum annual)	Canopy cover				MAXENT, GLM
Diospyros oocarpa	19	Isothermality	Annual temp range	Annual Precip.	NDVI (minnimum annual)				MAXENT
Eugenia macrosepala	23	Temp seasonality	NDVI (minnimum annual)	Canopy cover					GLM, MAXENT
Ficus nervosa	53	Max temp – warmest month	Annual Precip.	Precip. Seasonality	Landuse/land cover	NDVI (minnimum annual)			BRT, RF, MARS
Ixora elongata	24	Temp seasonality	Annual Precip.	Precip. wettest month	Elevation				MAXENT
Microtropis wallichiana	27	Annual Precip.	Landuse/land cover	NDVI (minnimum annual)	Elevation				GLM, MARS
Psychotria nigra	87	Max temp – warmest month	Annual temp range	Precip. Seasonality	Landuse/land cover	Canopy cover	NDVI (minnimum annual)	Elevation	BRT, RF
Atuna indica	9	Temp seasonality	NDVI (minnimum annual)						MAXENT
Epiprinus mallotiformis	17	Max temp – warmest month	Canopy cover	Elevation					MAXENT, GLM
Gordonia obtusa	14	Landuse/land cover	NDVI (minnimum annual)	E					MAXENT
Humboldtia brunonis	21	Temp seasonality	Precip. warmest quarter						MAXENT, GLM
Olea dioica	46	Isothermality	Annual Precip.	Precip. coldest driest quarter	NDVI (minnimum annual)	Canopy cover	Elevation		MARS, BRT
Memecylon pseudogracile	13	Max temp – warmest month	Elevation						MAXENT
Syzygium munronii	27	Max temp – warmest month	Annual Precip.	NDVI (minnimum annual)					MAXENT, GLM
Thottea shivarajanii	11	Precip. Seasonality	Precip. coldest quarter						MAXENT
Vateria indica	47	Annual temp range	Precip. Seasonality	Precip. warmest quarter	NDVI (minnimum annual)	Canopy cover	Landuse/land cover		RF, BRT
Walsura trifolia	18	Mean of diurnal temp range	NDVI (minnimum annual)	Elevation					MAXENT

Table 4. List of SAHM determined predictor layers used in final SDM Maxent model creation by sub-groups.

Predictor Layers	Frogs (low-ranging)	Frogs (high-ranging)	Frogs (montane generalists)	Plants (low-dispersing)	Plants (high-dispersing)
BioClim 3: Isothermality	X		X		
BioClim 4: Temperature Seasonality		X	X	X	X
BioClim 5: Max Temp of Warmest Month	X	X	X	X	X
BioClim 12: Annual Precipitation	X		X	X	X
BioClim 14: Precipitation of Driest Month		X	X		
BioClim 15: Precipitation Seasonality	X		X	X	X
BioClim 17: Precipitation of Driest Quarter			X	X	X
BioClim 18: Precipitation of Warmest Quarter	X	X			
BioClim 19: Precipitation of Coldest Quarter	X				
Elevation	X	X	X	X	X
NDVI (vegetation index; annual low)	X	X	X	X	X
Soil Type				X	X
Slope				X	
Aspect					
Soil-adjusted veg index (SAVI; annual low)				X	
Percent Canopy Cover	X	X		X	X
Land use / Land cover	X		X	X	X
Total Predictors Used	10	7	10	12	10

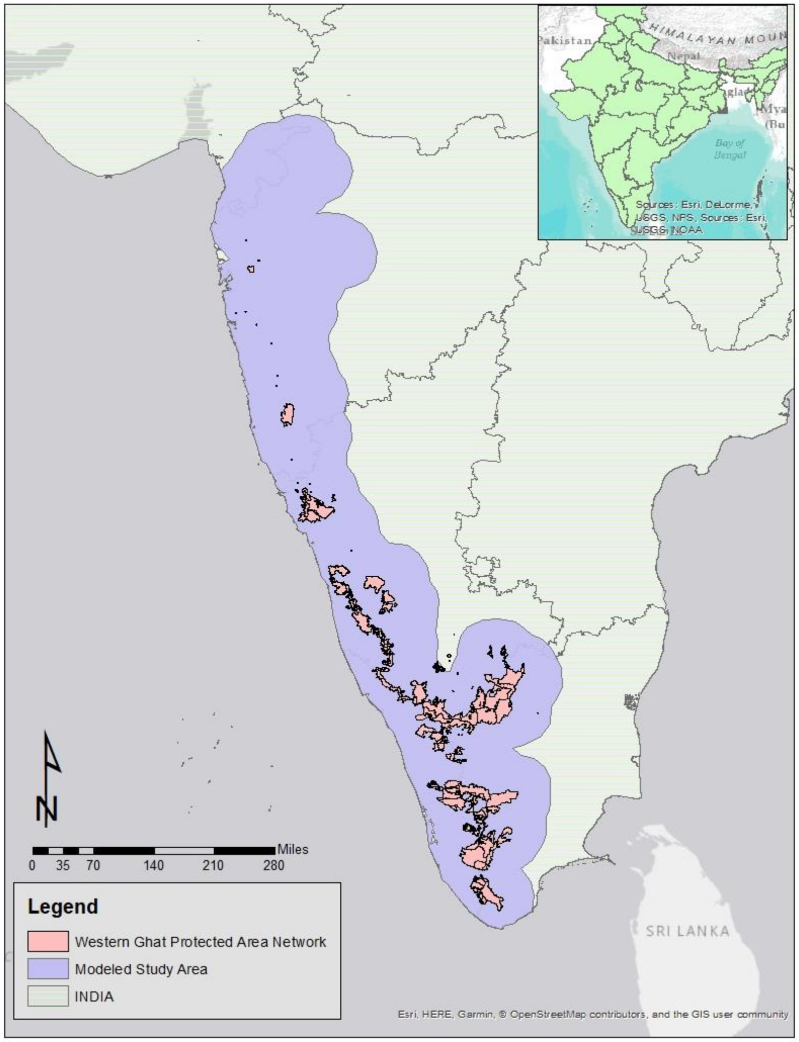

Figure 1. Map of India depicting the modeled study area for all SDMs and the Western Ghats protected area network.

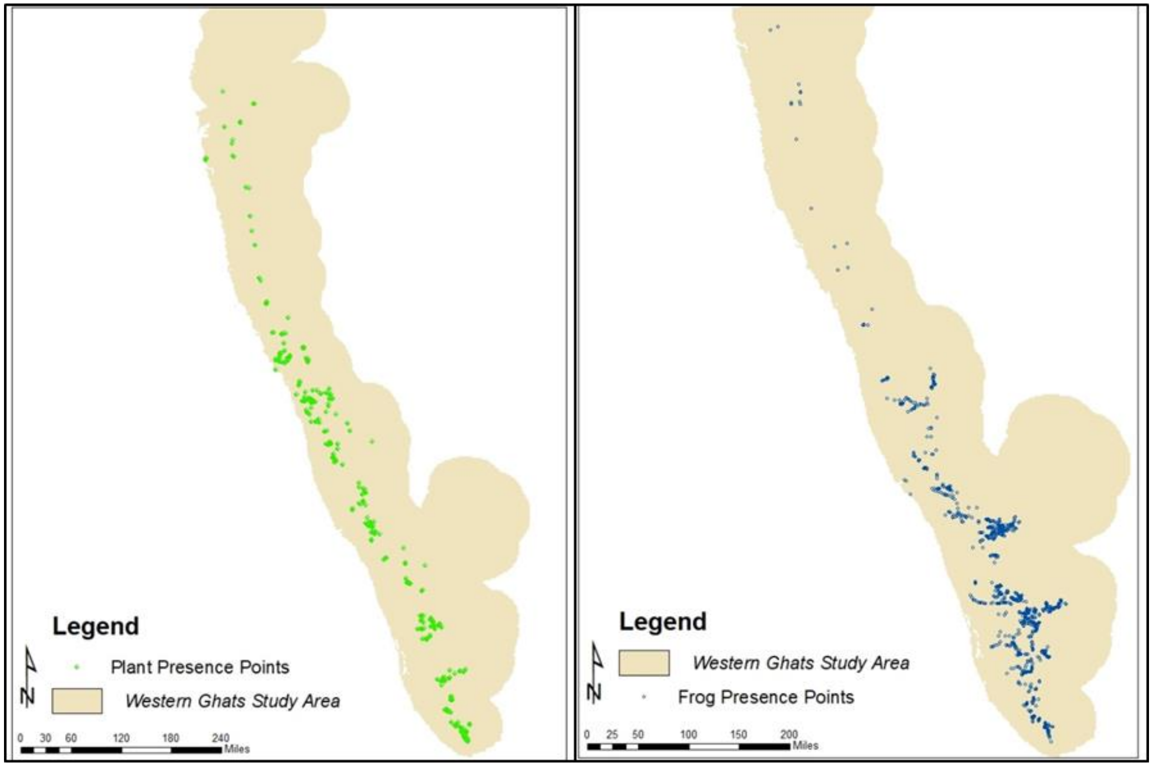

Figure 2. Left panel: map depicting where field presence data was recorded for plant species within the modeled study areas. Right panel: map depicting where field presence data was recorded for frog species within the modeled study areas. Note that all sampling occurred within the modeled area and spanned the study area.

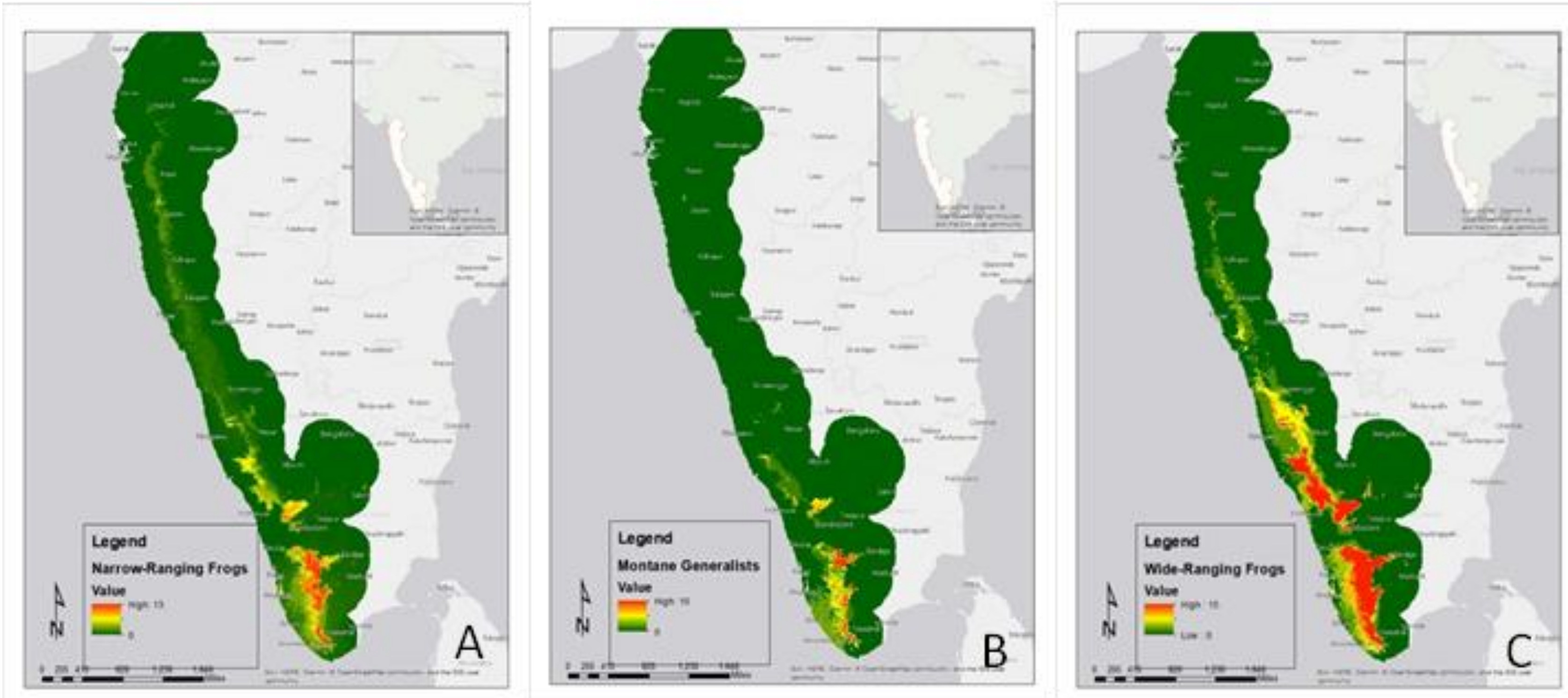

Figure 3. Ensembled maps of frog species by sub-groupings of the whole study area. Combined distributions of all narrow-ranging species (panel A), montane generalist frog species (panel B), wide-ranging frog species (panel C). Note the larger area of high-occurrence in panel C and density of species in the southern portion of the study area.

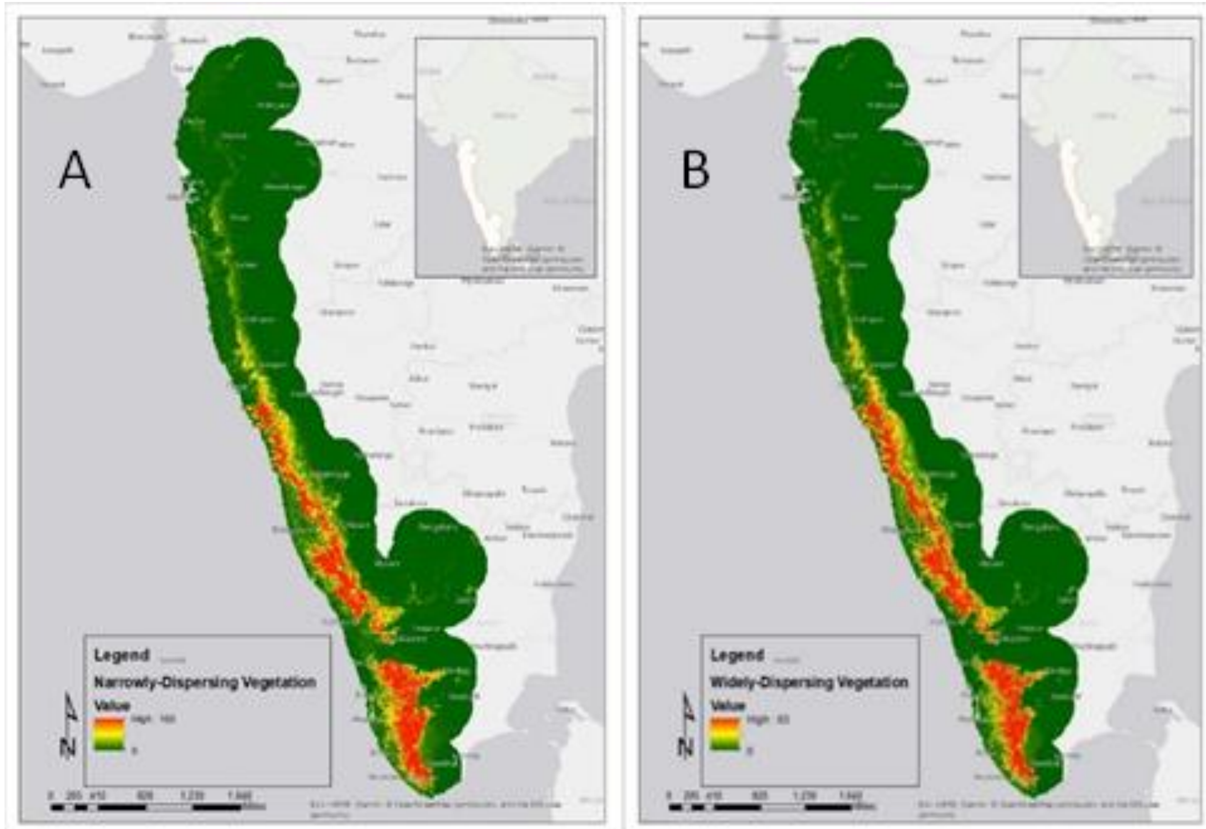

Figure 4. (panel A) Combined distributions for all narrowly-dispersing plant species. (panel B) Combined distributions for all widely-dispersing plant species. Note the similar shape of high-occurrence along the Ghats's spine, yet the widely-dispersing plants is somewhat narrower than the narrow-dispersing plants, likely an artifact of the higher number of modeled species.

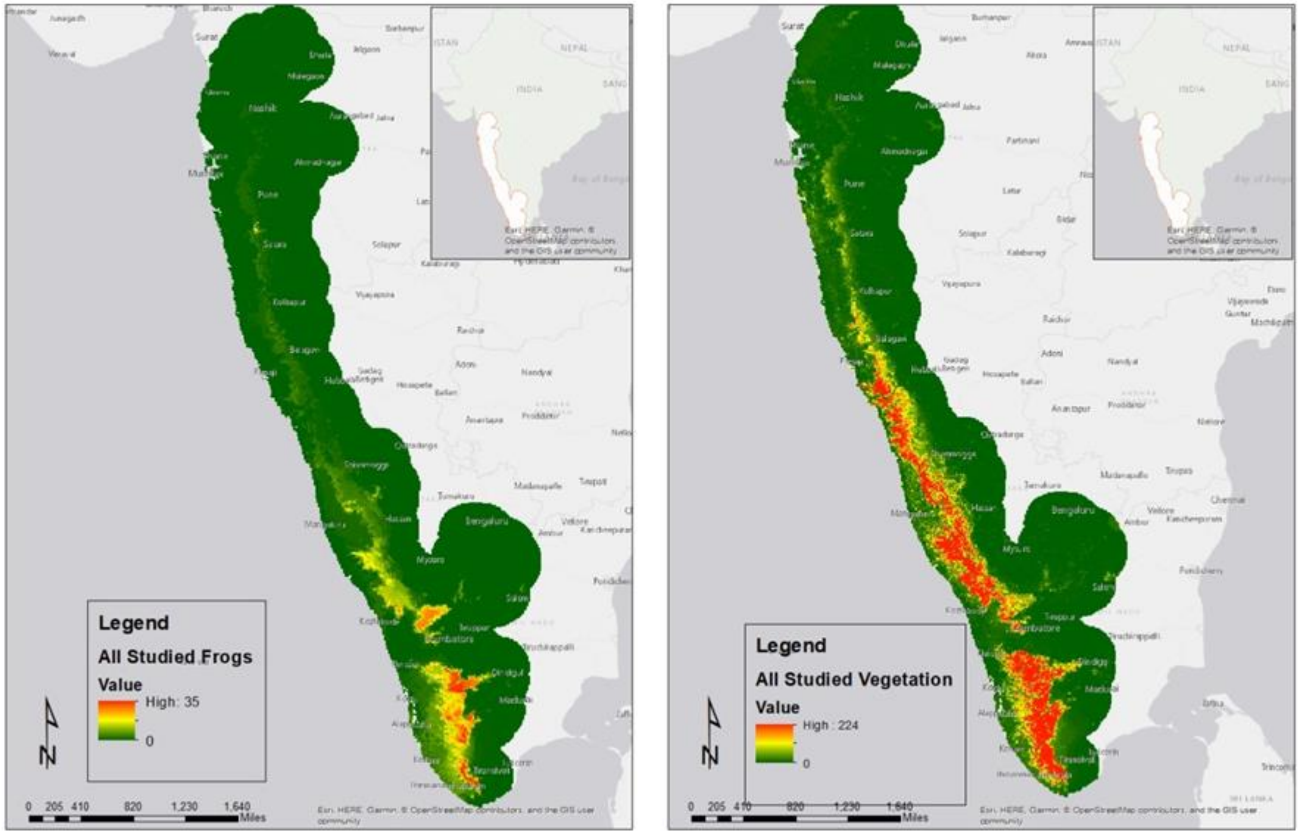

Figure 5. Left panel: Ensembled map of all modeled frog species with a high co-occurrence of thirty-five species of sixty-nine possible. Right panel: Ensembled map of all modeled plant species with a high co-occurrence of two-hundred twenty-four species of three hundred-six possible.

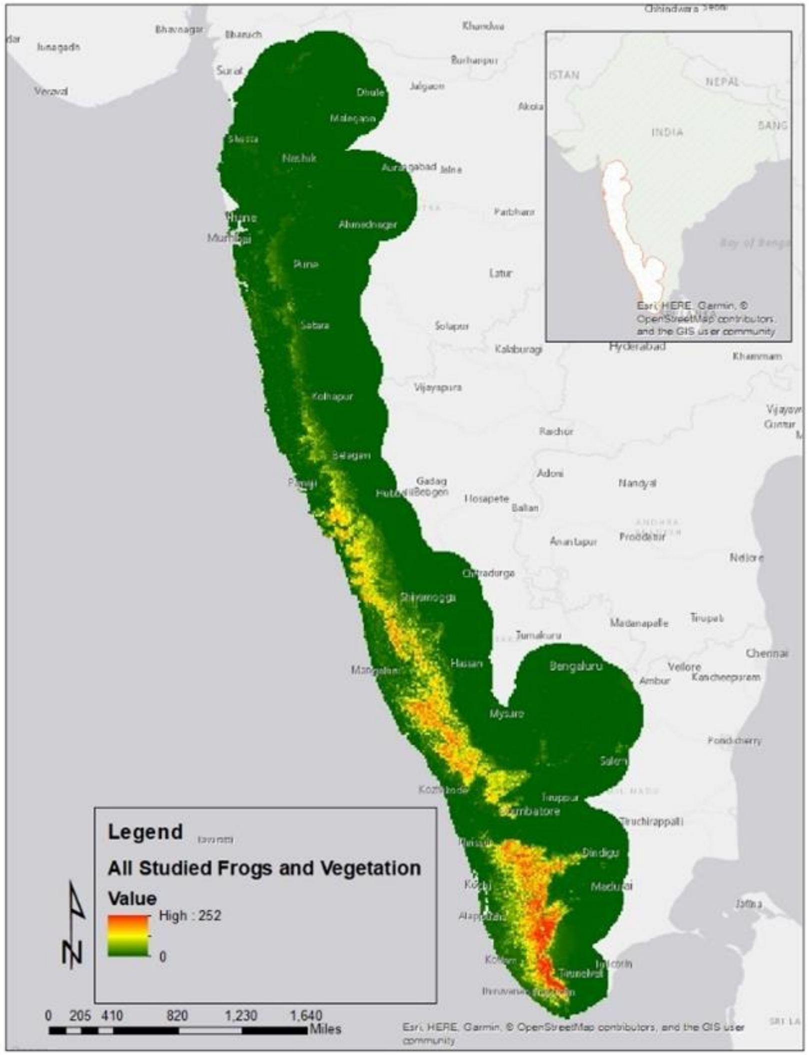

Figure 6. Ensembled map of all modeled frog and plant species' distributions with a high of two-hundred twenty-five out of three-hundred seventy-five.

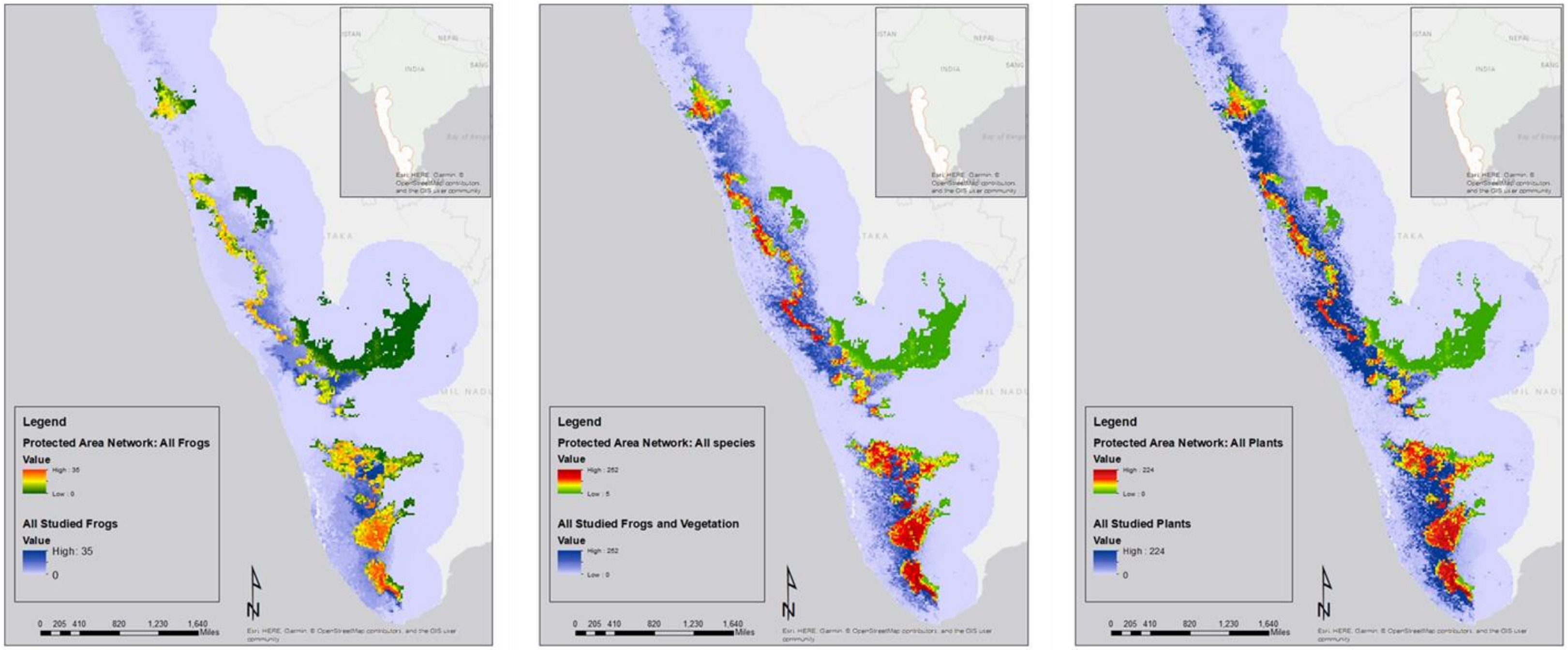

Figure 7. Ensembled maps depicting species co-occurrences within and outside of the protected area network. Green to red indicate low to high species co-occurrence within the network. Light to dark blue represents low to high species co-occurrence outside of the network.

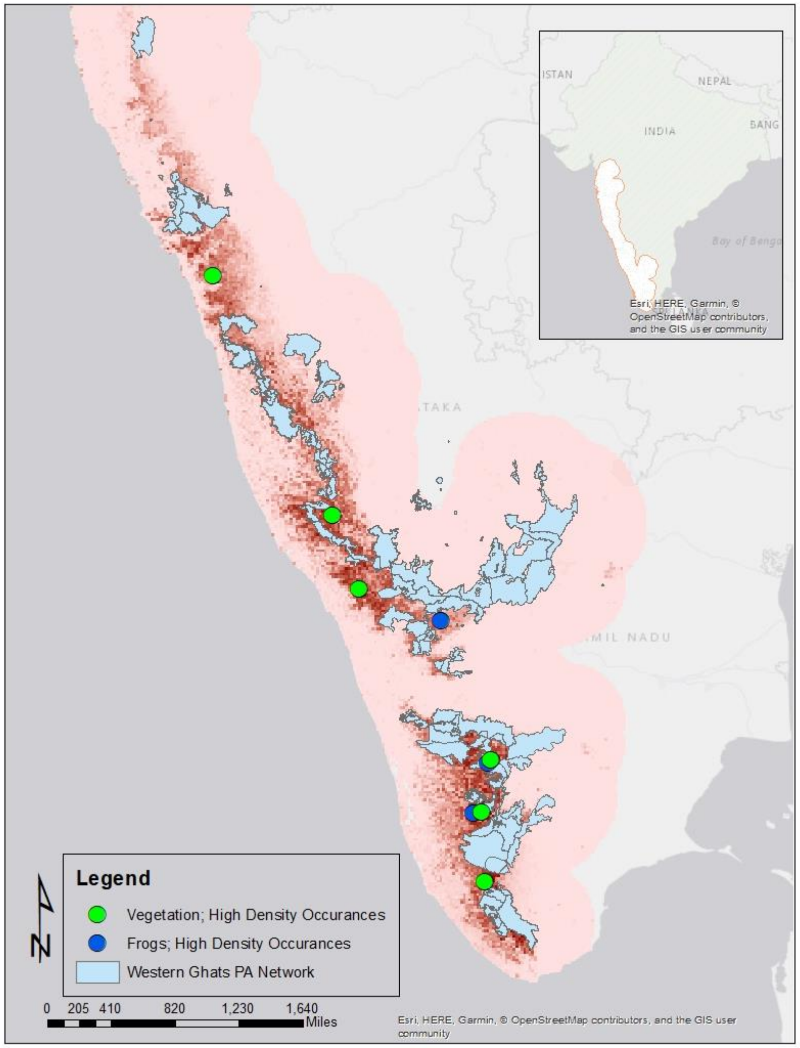

Figure 8. Heatmap with frog and plant species ensembled and the protected area network overlain. Green and blue circles indicate high species co-occurrence of plants and frogs respectively, identified outside of the protected area network.

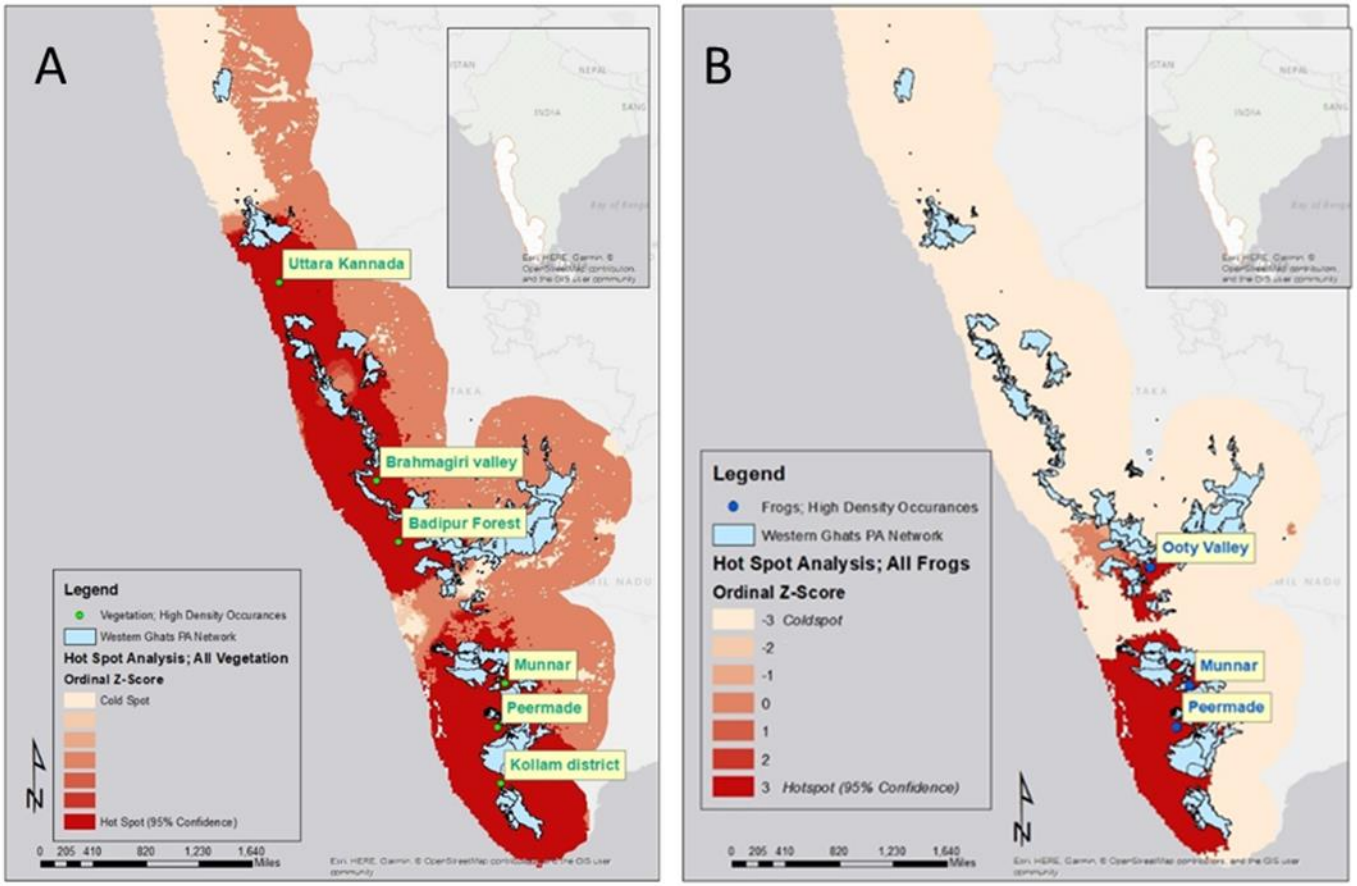

Figure 9. (Panel A) Statistical hotspot analysis of all plants with heatmap identified high species co-occurrence locations. (Panel B) Hotspot analysis of all modeled frogs with locations of heatmap identified high species co-occurrence areas. Note the hotspot extent's coverage of the protected area network as well as the heatmap identified high species co-occurrence areas.

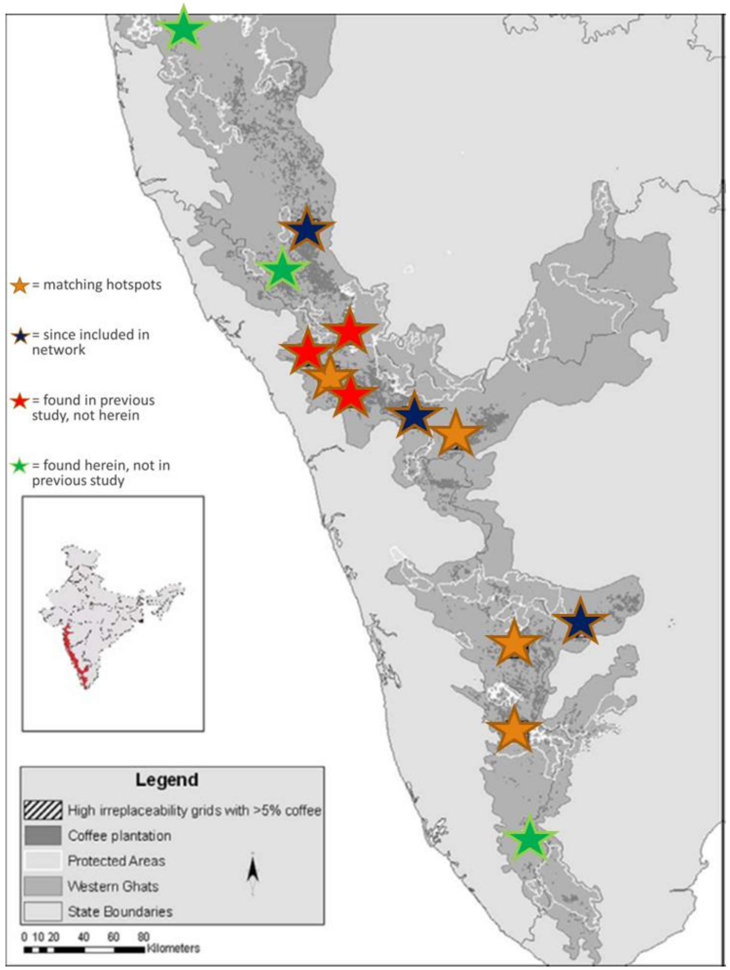

Figure 10. Map of priority conservation areas identified by a previous gap analysis (Das et al. 2006). Different color stars overlay all previous study and this study's identified high species co-occurrence areas. Note the newly identified and matching areas indicating high likelihood of conservation value.

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Appendix

Appendix 1. Table of sub-grouped frog species with number of presence points.

Endemic Frog Species Supgroups					
Narrow Ranging Species	**Presence Points (N)**	**Wide Ranging Species**	**Presence Points (N)**	**Montane-generalist Species**	**Presence Points (N)**
Pseudophilautus amboli	38	Raorchestes anili	85	Raorchestes bobingeri	6
Pseudophilautus kani	42	Raorchestes archeos	7	Raorchestes aureus	12
Pseudophilautus wynaadensis	193	Raorchestes archeos(sis)	12	Raorchestes chotta	6
Raorchestes agasthyaensis	24	Raorchestes autochrynchos	8	Raorchestes chromoasynchysi	15
Raorchestes akroparallagii	6	Raorchestes beddomii	85	Raorchestes chromokudre	15
Raorchestes blandus	21	Raorchestes bell thigh	7	Raorchestes chromomuthi	3
Raorchestes charius	19	Raorchestes blandus(sis)	4	Raorchestes chromomuthi (sis)	18
Raorchestes coonoor	18	Raorchestes bombayensis	12	Raorchestes dubois	119
Raorchestes coonoor (sis)	70	Raorchestes chalazodes	19	Raorchestes kadalarensis	29
Raorchestes emeralidi	7	Raorchestes chalazodes (sis)	8	Raorchestes kaikatti	6
Raorchestes flaviocularis	10	Raorchestes chlorosomma	12	Raorchestes kaikatti (sis)	7
Raorchestes graminirupes	34	Raorchestes crustai	15	Raorchestes malampandaram	6
Raorchestes hassanensis	14	Raorchestes echinatus	6	Raorchestes manohari	13
Raorchestes luteolus	42	Raorchestes ghatei	92	Raorchestes nerostagona	58
Raorchestes manohari	13	Raorchestes glandulosus	37	Raorchestes primar	7
Raorchestes marki	65	Raorchestes greit	14	Raorchestes primar (sis)	17
Raorchestes munnarensis	43	Raorchestes griet (sis)	6	Raorchestes primarumfii	24
Raorchestes ochlandrae	21	Raorchestes jayarami	68	Raorchestes sushili	19
Raorchestes ponmudi	77	Raorchestes johnceei	18		
Raorchestes pothigai	7	Raorchestes travancoricus	44		
Raorchestes primar	13				
Raorchestes primarumfii	13				
Raorchestes ravii	16				
Raorchestes resplendes	72				
Raorchestes signatus	8				
Raorchestes theuerkaufi	47				
Raorchestes tinniens	14				
Raorchestes tuberohumerus	72				
Raorchestes uthamani	8				

Appendix 2. Table of sub-grouped plant species with number of presence points.

Endemic Vegetation Species Subgroups			
Narrow-dispersing Sepceis	**Presence Points (N)**	**Widely-dispersing Species**	Presence Points (N)
Actinodaphne angustifolia	24	Aglaia austroindica	7
Actinodaphne bourdillonii	25	Aglaia barberi	34
Actinodaphne campanulata	8	Aglaia bourdillonii	9
Actinodaphne hookerii	7	Cinnamomum keralaense	6
Actinodaphne lawsonii	8	Cinnamomum macrocarpum	6
Actinodaphne malabarica	26	Cinnamomum malabatrum	30
Actinodaphne salicina	9	Cinnamomum sulphuratum	7
Agasthamalaia pauciflora	18	Diospyros angustifolia	12
Glycosmis arborea	6	Diospyros assimilis	21
Aglaia lawii	15	Diospyros barberi	6
Aglaia malabarica	36	Diospyros bourdillonii	21
Aglaia perviridis	9	Diospyros candolleana	70
Aglaia simplicifolia	15	Diospyros foliolosa	8
Aidia densiflora	6	Diospyros ghatensis	28
Anacolosa densiflora	7	Diospyros hirsuta	6
Apollonias arnottii	6	Diospyros humilis	11
Aporusa bourdillonii	21	Diospyros neilgherrensis	6
Ardisia missionis	10	Diospyros nilagirica	8
Ardisia pauciflora	7	Diospyros oocarpa	19
Ardisia rhomboidea	14	Diospyros paniculata	51
Ardisia stonei	61	Diospyros pruriens	6
Arenga wightii	33	Diospyros pyrocarpoides	6
Artocarpus hirsutus	9	Diospyros saldanhae	41
Atalantia wightii	9	Diospyros sylvatica	55
Atuna indica	57	Dipterocarpus bourdilloni	8
Atuna travancorica	8	Dipterocarpus indicus	56
Baccaurea courtallensis	15	Drypetes confertiflora	20
Beilschmiedia dalzelii	8	Drypetes elata	53
Beilschmiedia wightii	12	Drypetes gardnerii	6
Bentickia condapanna	8	Drypetes malabarica	10
Blachia denudata	10	Drypetes oblongifolia	25
Blachia umbellata	20	Drypetes wightii	13
Blepharistemma serratum	7	Dysoxylum beddomei	6
Calophyllum apetalum	18	Dysoxylum binectariferum	18
Calophyllum austroindicum	8	Dysoxylum malabaricum	57
Calophyllum polyanthum	10	Eugenia argentia	6
Canthium travancoricum	8	Eugenia floccosa	6
Capparis rheedii	33	Eugenia galibidu	9
Casearia rubescens	7	Eugenia macrosepala	23
Casearia wynadensis	9	Eugenia rottleriana	6
Chionanthus courtallensis	21	Eugenia singampattiana	6
Chionanthus linocieroides	22	Eugenia thwaitesii	26
Chionanthus mala-elengi	9	Ficus beddomei	10
Chrysophyllum roxburghii	9	Ficus nervosa	53
Cleistanthus malabaricus	41	Flacourtia montana	83
Cleistanthus travancorensis	13	Garcinia gummi-gutta	49
Croton malabaricus	28	Garcinia indica	30
Cryptocarya anamalayana	10	Garcinia pictorius	7
Cryptocarya beddomei	103	Garcinia rubro-echinata	6
Cryptocarya neilgherrensis	48	Garcinia talbotii	49
Cryptocarya wightiana	16	Glochidion ellipticum	66
Cullenia exarillata	6	Glochidion malabaricum	7
Cyathocalyx zeylanicus	6	Gluta travancorica	14
Cynometra bourdillonii	6	Ixora brachiata	94
Cynometra travancorica	21	Ixora elongata	24
Daphniphyllum neilgherrense	16	Ixora lanceolaria	6
Dendrocnide sinuata	23	Microtropis latifolia	7

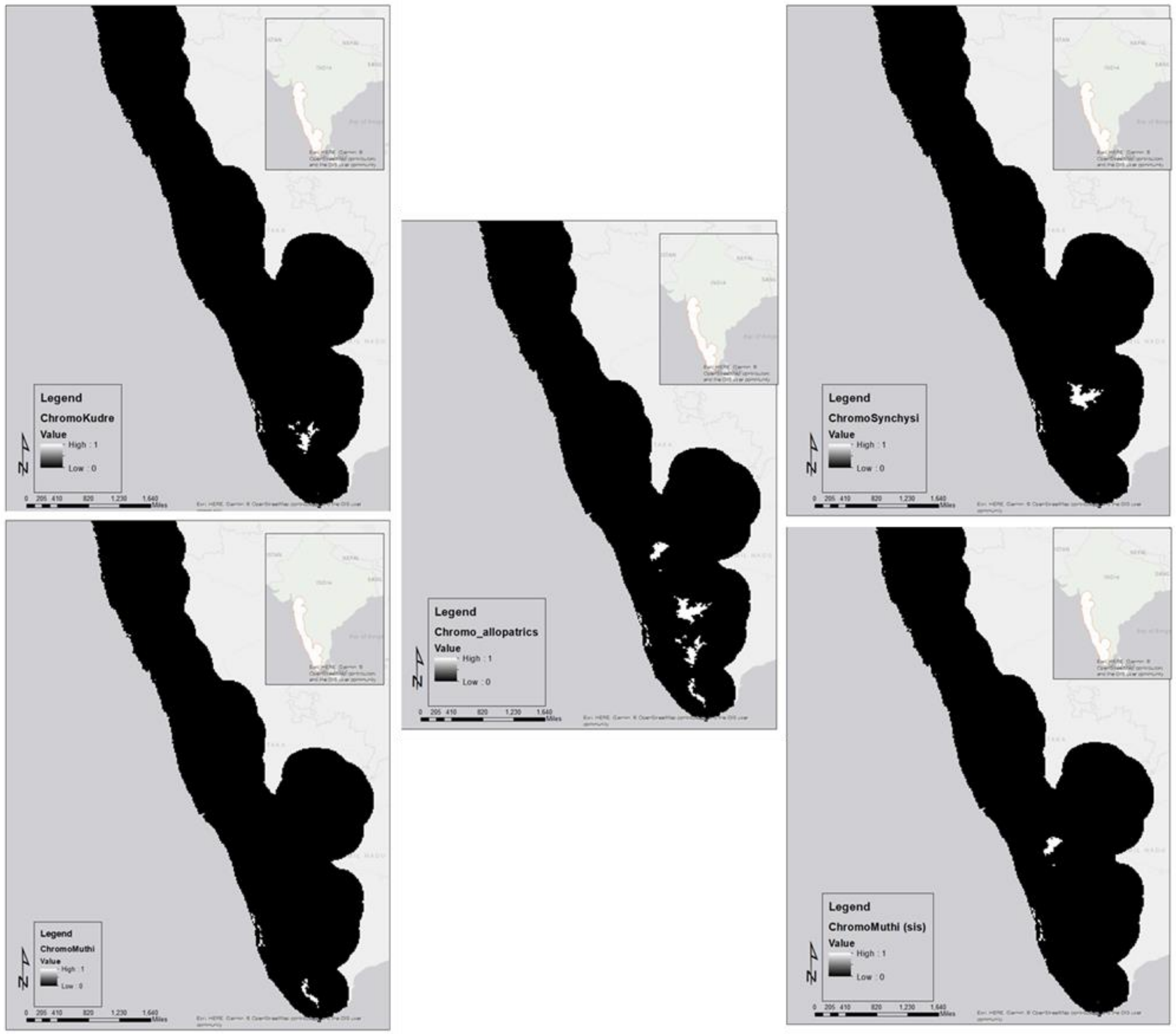
Dillenia bracteata	14
Dimorphocalyx beddomei	8
Dimorphocalyx lawianus	7
Ehretia canarensis	6
Elaeocarpus munronii	17
Elaeocarpus venustus	9
Epiprinus mallotiformis	9
Erythroxylum moonii	6
Erythroxylum obtusifolium	6
Euonymus angulatus	25
Euonymus dichotomus	9
Euonymus indicus	8
Euonymus paniculatus	27
Exoecaria oppositifolia	20
Glycosmis macrocarpa	9
Glyptopetalum grandiflorum	23
Gomphandra coriacea	16
Goniothalamus cardiopetalus	7
Goniothalamus rhynchantherus	6
Goniothalamus wightii	7
Goniothalamus wynaadensis	14
Gordonia obtusa	8
Gymnacranthera farquhariana	6
Helicia nilagirica	24
Heritiera papilio	74
Holigarna arnottiana	9
Holigarna beddomei	7
Holigarna ferruginea	82
Holigarna grahamii	39
Holigarna nigra	17
Homalium zeylanicum	14
Hopea canarensis	6
Hopea erosa	6
Hopea glabra	36
Hopea parviflora	43
Hopea ponga	9
Hopea racophloea	9
Hopea utilis	21
Humboldtia brunonis	6
Humboldtia decurrens	9
Humboldtia vahliana	10
Hunteria zeylanica	22
Hydnocarpus alpina	9
Hydnocarpus macrocarpa	80
Hydnocarpus pentandra	37
Isonandra lanceolata	7
Isonandra perrottetiana	19
Kingiodendron pinnatum	145
Knema attenuata	12
Lasianthus jackianus	19
Lepisanthes deficiens	8
Leptonychia caudata	6
Ligustrum perrottetii	15
Litsea bourdillonii	62
Litsea floribunda	6
Litsea ghatica	8
Litsea keralana	61
Litsea laevigata	7
Litsea ligustrina	33
Litsea mysorensis	43
Litsea oleoides	19
Litsea stocksii	6
Litsea travancorica	7

Microtropis stocksii	7
Microtropis wallichiana	27
Psychotria anamallayana	9
Psychotria dalzellii	27
Psychotria flavida	9
Psychotria nigra	87
Psychotria truncata	13
Pterospermum reticulatum	20
Pterospermum rubiginosum	6
Saprosma corymbosum	6
Saprosma indica	16
Schefflera capitata	9
Schefflera racemosa	7
Schefflera rostrata	9
Semecarpus auriculata	15
Semecarpus travancorica	6
Sercandra chloranthoides	17
Spondias indica	7
Syzygium benthamianum	6
Syzygium calophyllifolium	7
Syzygium codyensis	6
Syzygium densiflorum	11
Syzygium gardneri	116
Syzygium hemisphericum	48
Syzygium laetum	94
Syzygium lanceolatum	8
Syzygium liniare	8
Syzygium mundagam	25
Syzygium munronii	27
Syzygium palghatense	9
Syzygium phillyraeoides	11
Syzygium rubicundum	9
Syzygium stocksii	9
Syzygium tamilnadensis	9
Syzygium travancoricum	8
Syzygium zeylanicum	9
Total N:	**2050**

Litsea UM	6
Litsea venulosa	7
Litsea wightiana	19
Lophopetalum wightianum	9
Macaranga indica	37
Macaranga peltata	6
Madhuca bourdillonii	6
Madhuca neriifolia	12
Mallotus aureo-punctatus	11
Mallotus beddomei	9
Mallotus distans	6
Mallotus rhamnifolius	11
Mallotus stenanthus	10
Mammea suriga	54
Mangifera indica	49
Mastixia arborea	13
Maytenus rothiana	52
Meiogyne pannosa	44
Meiogyne ramarowii	26
Melicope lunu-ankenda	7
Memecylon gracile	24
Memecylon heyneanum	10
Memecylon malabaricum	13
Memecylon pseudogracile	10
Memecylon randeriana	34
Memecylon talbotianum	6
Memecylon terminale	27
Memecylon umbellatum	23
Memecylon wightii	9
Meteoromyrtus wynaadensis	6
Michelia nilagirica	7
Miliusa gokhalaei	7
Miliusa nilagirica	27
Miliusa sp	9
Miliusa wightiana	7
Miliusa wynadica	7
Mitragyna tubulosa	9
Mitrephora grandiflora	7
Myristica dactyloides	9
Myristica fatua	8
Myristica malabarica	128
Nageia wallichiana	9
Nathopodytes nimmoniana	51
Neolitsea fischeri	8
Nothopegia aureo-fulva	22
Nothopegia beddomei	7
Nothopegia heyneana	6
Nothopegia racemosa	89
Nothopegia travancorica	9
Octotropis travancorica	43
Olea dioica	26
Ormosia travancorica	7
Orophea erythrocarpa	64
Orophea shivarajanii	10
Orophea thomsoni	9
Orophea zeylanica	7
Otonephelium stipulaceum	18
Palaquium bourdillonii	9
Palaquium ellipticum	50
Paracroton pendulus	6
Persea macrantha	108
Phaeanthus malabaricus	48
Pinanga dicksonii	103

Pittosporum dasycaulon	14
Poeciloneuron indicum	20
Polyalthia coffeoides	7
Polyalthia fragrans	37
Polyalthia shendurunii	21
Popowia beddomeana	68
Prismatomeris tetrandra	7
Pterygota alata	7
Reinwardtiodendron anamalaiense	6
Sageraea grandiflora	19
Stereospermum colais	82
Symplocos macrocarpa	18
Symplocos rosea	10
Tabernaemontana gamblei	9
Tabernaemontana heyneana	13
Tarenna nilagirica	9
Terminalia travancorensis	37
Thottea dinghoui	6
Thottea shivarajanii	10
Thottea siliquosa	7
Tricalysia apiocarpa	11
Tricalysia sphaerocarpa	6
Turpinia malabarica	7
Vateria indica	16
Vepris bilocularis	17
Vernonia travancorica	47
Walsura trifolia	47
Xanthophyllum arnottianum	8
Xylopia parvifolia	46
Total N:	**4446**

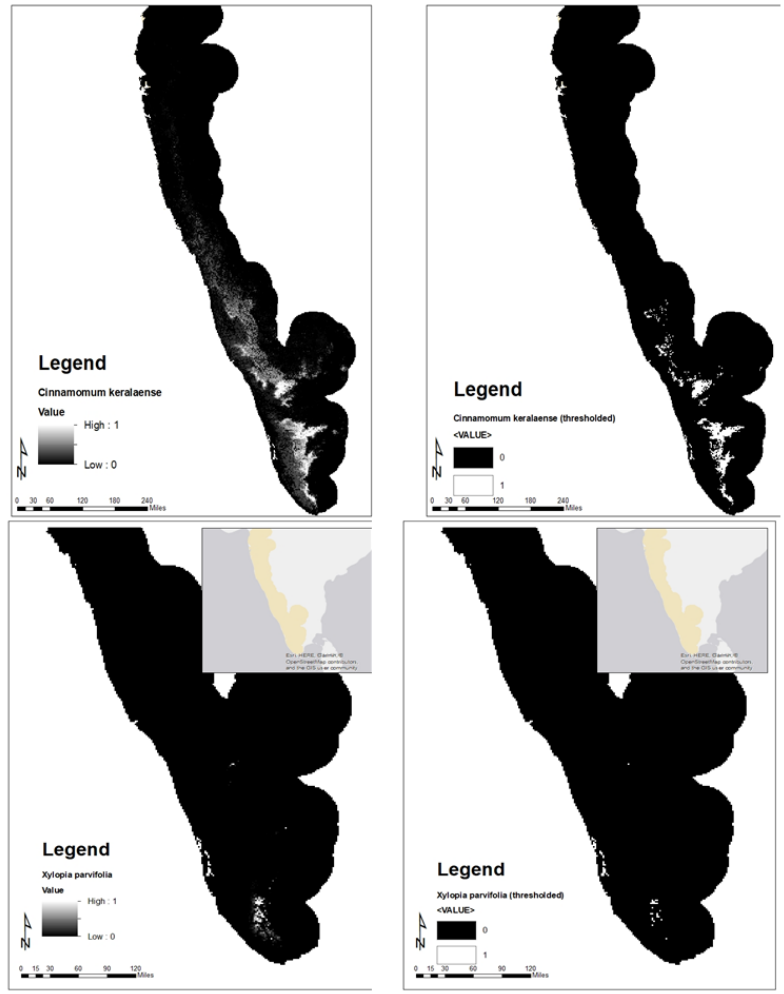
Appendix 3. Center map: SDM created from combined data from four sub-species: Chromo – kudre, synchysi, muthi, and muthi (sis). The four accompanying panels depict the manual separation of the center panel into ranges of sub-species.



Appendix 4. List of predictor variables used in SAHM inquiries. Note that not all predictors are used in final model creation – see table 4.

Predictor Layers	Source	Date Captured/Calculated	Notes
BioClim 1: Annual Mean Temperature	WorldClim	Monthly (September 2017)	Retreived
BioClim 2: Mean Diurnal Range	WorldClim	Monthly (September 2017)	Retreived
BioClim 3: Isothermality	WorldClim	Monthly (September 2017)	Retreived
BioClim 4: Temperature Seasonality	WorldClim	Monthly (September 2017)	Retreived
BioClim 5: Max Temp of Warmest Month	WorldClim	Monthly (September 2017)	Retreived
BioClim 6: Min Temp of Coldest Month	WorldClim	Monthly (September 2017)	Retreived
BioClim 7: Temperature Annual Range	WorldClim	Monthly (September 2017)	Retreived
BioClim 8: Mean Temperature of Wettest Quarter	WorldClim	Monthly (September 2017)	Retreived
BioClim 9: Mean Temp of Driest Quarter	WorldClim	Monthly (September 2017)	Retreived
BioClim 10: Mean Temp of Warmest Quarter	WorldClim	Monthly (September 2017)	Retreived
BioClim 11: Mean Temp of Coldest Quarter	WorldClim	Monthly (September 2017)	Retreived
BioClim 12: Annual Precipitation	WorldClim	Monthly (September 2017)	Retreived
BioClim 13: Precipitation of Wettest Month	WorldClim	Monthly (September 2017)	Retreived
BioClim 14: Precipitation of Driest Month	WorldClim	Monthly (September 2017)	Retreived
BioClim 15: Precipitation Seasonality	WorldClim	Monthly (September 2017)	Retreived
BioClim 16: Precipitation of Wettest Quarter	WorldClim	Monthly (September 2017)	Retreived
BioClim 17: Precipitation of Driest Quarter	WorldClim	Monthly (September 2017)	Retreived
BioClim 18: Precipitation of Warmest Quarter	WorldClim	Monthly (September 2017)	Retreived
BioClim 19: Precipitation of Coldest Quarter	WorldClim	Monthly (September 2017)	Retreived
Elevation	ASTER imagery	April 2017	Remotely Sensed
NDVI (vegetation index; annual low)	Landsat 8 (NASA, USGS)	May 2017	Remotely Sensed
Soil-adjusted veg index (SAVI; annual low)	Landsat 8 (NASA, USGS)	May 2017	Remotely Sensed
Soil Type	UN Food and Agricultural Organization	N/A	Retreived
Nearness to Surface Water	UN Food and Agricultural Organization	N/A	Retreived
Slope	DEM (ASTER)	April 2017	Remotely Sensed
Aspect	DEM (ASTER)	April 2017	Remotely Sensed
Percent Canopy Cover	Bhuvan (ISRO)	January -May 2017	Retreived
Percent Canopy Cover	Bhuvan (ISRO)	January -May 2017	Retreived
Land use / Land cover	Bhuvan, Landsat 8 (ISRO, NASA, USGS)	March 2016 - May 2017	Raw imagery retrieved, classification analysis

Appendix 5. Top panels: SAHM outputs depicting a gradient (left) and binary (right) distribution estimation of a wide-ranging species. Lower panels: SAHM outputs depicting a gradient (left) and binary (right) distribution estimation of a low-ranging species.



Appendix 6. Statistical model outputs from initial SAHM runs of a sub-set of frog species. Red-filled boxes are wide-ranging, blue-filled boxes are narrow-ranging, and green-filled boxes are montane generalist species.

Frog Species	N	Percent Correctly Classified	AUC	True-Skill Statistic	Cohen's Kappa	Best Performing Model Reported
Pseudophilautus amboli	38	0.876	0.901	0.762	0.876	GLM
Pseudophilautus kani	42	0.711	0.834	0.787	0.923	MAXENT
Pseudophilautus wynaadensis	105	0.746	0.829	0.823	0.534	RF
Raorchestes akroparallagii	14	0.651	0.952	0.454	0.786	MAXENT
Raorchestes anili	85	0.164	0.777	0.830	0.565	BRT
Raorchestes beddomii	78	0.502	0.778	0.543	0.572	RF
Raorchestes bobingeri	40	0.569	0.678	0.615	0.121	MAXENT
Raorchestes griet	92	0.666	0.792	0.326	0.205	MARS
Raorchestes bobingeri	29	0.274	0.777	0.293	0.495	MAXENT
Raorchestes jayarami	6	0.271	0.705	0.600	0.300	MAXENT
Raorchestes travancoricus	44	0.809	0.848	0.100	0.373	MAXENT
Raorchestes dubois	19	1.062	0.857	0.824	0.368	MAXENT
Raorchestes resplendens*	6	1.083	0.910	-0.017	0.807	MAXENT
Raorchestes primarumfii	13	0.256	0.863	0.415	0.488	MAXENT
Raorchestes sushili	31	0.740	0.774	0.651	0.393	MAXENT

Appendix 7. Statistical model outputs from initial SAHM runs of a sub-set of plant species. Yellow-filled boxes are wide-ranging and green-filled boxes are narrow-ranging species.

Plant Species	N	Percent Correctly Classified	AUC	True-Skill Statistic	Cohen's Kappa	Best Performing Model Reported
Aglaia barberi	34	0.669	0.816	0.585	0.379	MARS
Drypetes confertiflora	20	0.609	0.848	0.276	0.906	MAXENT
Cinnamomum malabatrum	30	0.764	0.855	0.729	0.563	MAXENT
Diospyros ghatensis	28	0.831	0.793	0.479	0.818	GLM
Diospyros oocarpa	19	0.769	0.780	0.212	0.958	MAXENT
Eugenia macrosepala	23	0.500	0.906	0.654	0.720	GLM
Ficus nervosa	53	0.684	0.693	0.792	0.698	BRT
Ixora elongata	24	0.604	0.963	0.305	0.382	MAXENT
Microtropis wallichiana	27	0.692	0.575	0.600	0.636	MARS
Psychotria nigra	87	0.708	0.718	-0.061	0.873	RF
Atuna indica	9	0.581	0.856	0.730	0.436	MAXENT
Epiprinus mallotiformis	17	0.548	0.637	0.556	0.523	MAXENT
Gordonia obtusa	14	0.812	0.726	0.274	0.624	MAXENT
Humboldtia brunonis	21	0.576	0.967	0.922	0.504	MAXENT
Olea dioica	46	0.771	0.779	0.339	0.458	MARS, BRT
Memecylon pseudogracile	13	0.791	0.820	0.253	0.363	MAXENT
Syzygium munronii	27	0.831	0.897	0.242	0.457	MAXENT, GLM
Thottea shivarajanii	11	0.824	0.835	0.570	0.418	MAXENT
Vateria indica	47	0.638	0.838	-0.394	0.554	RF
Walsura trifolia	18	0.565	0.775	0.298	0.459	MAXENT