

1 Title

2 Idea Paper: improving forecasts of community composition with lightweight biodiversity
3 monitoring across ecological and anthropogenic disturbance gradients

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31

32 Abstract

33 Accurate and up-to-date biodiversity forecasts enable robust planning for environmental
34 management and conservation of landscapes under a wide range of uses. Future predictions of
35 the species composition of ecological communities complement more frequently reported species
36 richness estimates to better characterize the different dimensions of biodiversity. The models that
37 make community composition forecasts are calibrated with data on species' geographic patterns
38 for the present, which may not be good proxies for future patterns. The future establishment of
39 novel communities represents data on species interactions unaccounted for by these models.
40 However, detecting them in a systematic way presents challenges due to the lack of monitoring
41 data for landscapes with high environmental turnover, where such communities are likely to
42 establish. Here, we propose lightweight monitoring over both ecological and anthropogenic
43 disturbance gradients using passive sensors (i.e., those that operate continuously without much
44 human input) to detect novel communities with the aim of updating models that make
45 community composition forecasts. Monitoring over these two gradients should maximize
46 detection of novel communities and improve understanding of relationships between community
47 composition and environmental change. Further, barriers regarding cost and effort are reduced by
48 using relatively few sensors requiring minimal upkeep. Ongoing updates to community
49 composition forecasts based on novel community data and better understanding of the associated
50 uncertainty should improve future decision-making for both resource management and
51 conservation efforts.

52

53 Keywords

54 community, global change, ideas for fundamental questions, species distribution modeling,
55 observation, species interactions

56

57 Research question

58 How can we improve forecasts of community composition under ongoing global change without
59 prohibitive cost or effort?

60

61 Value

62 Where species will be in the future, which will be found together, and how they will respond to
63 ongoing global change are foundational questions for ecosystem management and conservation.
64 Accurate forecasts of biodiversity enable better planning for allocation of resource use,
65 maintenance of ecosystem services, response to invasive species, and establishment of protected
66 areas (Newbold et al. 2015). Particularly, forecasts made across environmental gradients can lead
67 to more informed management for areas that are natural (e.g., set aside for conservation),
68 unnatural (e.g., under resource management), or semi-natural (e.g., socio-ecological production
69 landscapes such as *satoyama*). However, models that make biodiversity forecasts can estimate
70 inaccurate future environmental responses for species and communities if current data on
71 species' geographic patterns are not reasonable proxies for future patterns (Blois et al. 2013a).
72 Future colonizations of newly suitable areas by species, leading to the establishment of
73 communities with new species combinations (i.e., novel communities), represent heretofore
74 unknown information about community composition and species interactions. Novel
75 communities, which emerge more frequently with rapid landscape change (Finsinger et al. 2017),
76 can expand or alter existing species interactions (Williams & Jackson 2007) and lead to
77 disruptions in ecosystem services (Hobbs et al. 2006). Ongoing detection and documentation of
78 novel communities is thus of vital importance to update community composition predictions for
79 biodiversity forecasts.

80

81 Unfortunately, locating novel communities in a systematic way is a challenging exercise due in
82 large part to the lack of monitoring data across landscapes with high environmental turnover,
83 where such communities are likely to establish. Many efforts to catalog biodiversity focus on
84 flagship species or single estimates of species richness. On the other hand, biodiversity
85 monitoring systems provide high-frequency data streams and could also be harnessed to update
86 community forecasts (Bush et al. 2017). However, the high economic and labor costs can be
87 prohibitive, and existing systems often have bias in their spatial coverage and representation of

88 environmental heterogeneity (Metzger et al. 2013). Moreover, both conservation efforts (e.g.,
89 establishing protected areas; Kusumoto et al. 2017) and monitoring systems tend to prioritize
90 specific ecosystems rather than the gradients between them (Fig. 1). The resulting lack of
91 regularly updated data on novel communities can be seen as a bottleneck for prediction accuracy
92 of community composition forecasts.

93

94 Relevant hypotheses

95 Community composition forecasts are typically made using space-for-time substitutions, which
96 employ modeled relationships between the current geographic patterns of species and
97 communities with environmental variables to predict future patterns (Blois et al. 2013b). These
98 predictions are most often made using either stacked or joint species distribution models
99 (SDMs). The stacked SDM approach involves combining the predictions of SDMs fit with
100 abiotic variables for individual species to estimate the community composition per spatial grid
101 cell, then applying a biotic filter by removing unlikely candidate species from predicted
102 communities based on knowledge of species interactions (SESAM; Guisan & Rahbek 2011). The
103 joint SDM approach models multiple species' distributions together in the same modeling
104 framework and typically measures interaction strength based on co-occurrence correlations after
105 accounting for shared environmental preferences (joint SDMs; Warton et al. 2015).

106

107 But as changes to known species interaction networks will alter community predictions for both
108 approaches, information on novel communities is crucial to improve the accuracy of long-term
109 community forecasts. Although some data exists on current novel community establishment,
110 ongoing global change will result in further shifts to present-day community structure. As
111 species turnover tends to increase with environmental heterogeneity (Buckley and Jetz 2008),
112 monitoring over gradients between different environments should be ideal for detecting existing
113 novel communities and their future emergence.

114

115 New research idea

116 We propose monitoring over environmental gradients to detect novel communities and use this
117 information to update community composition forecasts. Long-term monitoring over
118 environmental gradients at a fine temporal resolution has a high likelihood of detecting novel

119 community establishment (Fig. 1). Such detections represent information that can be used to
120 identify mismatches between observations and predictions, leading to changes in community
121 composition forecasts that rely on known relationships between species. It is important to note
122 that this approach cannot determine the causes of novel community emergence, as other casual
123 factors that correlate with environmental gradients may exist.

124

125 Our proposal includes monitoring over two main gradients driving community change:
126 ecological (e.g., forest to grassland, lowland to montane forest) and anthropogenic disturbance
127 (e.g., forest to urban, primary to logged forest). Importantly, these two gradients have different
128 temporal resolution: anthropogenic disturbance (e.g., land cover conversion) occurs on shorter
129 timescales than natural ecosystem change. Monitoring over these gradients should both
130 maximize detection of novel communities and improve understanding of community
131 relationships with environmental change. Real-time predictions of change for heterogeneous
132 landscapes using remote sensing data have exciting potential (e.g., Slingsby et al. 2020). There
133 are also examples of in situ monitoring over natural gradients to increase coverage of conditions
134 and detect species' niche shifts (Carvalho et al. 2016). However, to our knowledge this is the
135 first proposal to use in situ monitoring data from both ecological and anthropogenic disturbance
136 gradients to make real-time updates to community forecasts.

137

138 How to tackle the question through the proposed new idea

139 Here, we advocate for the implementation of lightweight, in situ monitoring systems composed
140 of transects over ecological and anthropogenic disturbance gradients in representative ecoregions
141 around the world to collect structured data on novel communities. To reduce cost and effort,
142 these transects can be composed of strategically placed passive sensors (i.e., those that operate
143 continuously without much human input) including camera traps or audio recorders (although we
144 discuss monitoring of terrestrial, relatively motile animals, the concept could be applied to other
145 systems). Large camera trap grids monitored over short time periods provide a good balance of
146 cost and accuracy for modeling species occupancy and richness, though accounting for
147 seasonality presents challenges (Kays et al. 2020). In contrast, the lightweight system we propose
148 serves only to collect detection data rather than produce datasets for modeling, utilizes different
149 sensors to improve detection and expand the taxa sampled, and addresses seasonality by

150 monitoring over annual cycles (Ross et al. 2018). Hence, fewer sensors in smaller grids or
151 transects can be sufficient. Information on novel communities can directly improve community
152 composition forecasts by updating species interaction information used to correct stacks of
153 individual-species SDMs (Fig. 2), or by updating co-occurrence patterns used by joint SDMs.
154 Additionally, these structured data can be combined with unstructured datasets (i.e.,
155 opportunistic presence data) using data integration approaches to improve the accuracy of large-
156 scale range models (Isaac et al. 2020).

157

158 As uncertainty remains an issue for community composition forecasts made over space and time,
159 it must be recognized that model predictions need validation and should be interpreted with
160 caution. Although the modeling approaches discussed above can serve as diagnostic tools to help
161 generate hypotheses about community assembly processes, both have existing methodological
162 limitations (Zurell et al. 2020). Further, presence of species in new areas could reflect itinerant
163 dispersal or short-lived sink populations rather than self-sustaining populations, and models of
164 global climate and anthropogenic change used to make community forecasts have inherently
165 high uncertainty. Thus, field validation (i.e., community inventories to evaluate model
166 performance) and consideration of ancillary data (i.e., population studies to confirm novel
167 community establishment) are advisable before any management or policy decisions are made. It
168 is important to note that uncertainty in community forecasts can also be harnessed to estimate
169 different scenarios of community dynamics across a landscape.

170

171 The importance of updated forecasts of (novel) ecological communities and how best to apply
172 them to improve future decision-making is crucial to demonstrate to managers and conservation
173 practitioners. For example, we expect forecasts to show how ecological gradients themselves
174 should be considered high priority areas for monitoring and conservation actions due to their
175 ability to maintain processes that foster evolutionary potential and ecological resilience to change
176 (Blair et al. 2013).

177

178 Motivation

179 The ideas we propose here originate from discussions between the authors about how to improve
180 community composition forecasts using new biodiversity monitoring strategies, and we wanted

181 to share these ideas with the field to spark new ways forward for predicting community change.
182 We intend to use the ideas in this paper as a foundation for future grant proposals.

183

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190

191 Conflict of Interest

192 The authors have no conflicts of interest to report regarding this paper.

193

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259 Figure 1. Comparison of different passive data collection approaches in terms of cost (financial
260 and labor) and detecting novel communities, designated on a scale of “low” (yellow), “medium”
261 (orange), and “high” (red). Opportunistic occurrence data is low-cost to acquire, but represents
262 an amalgam of various sampling areas, times, and methodologies, making it difficult to detect
263 the confirmed establishment of novel communities. Grid arrays ($n \times n$) of passive sensors for a
264 single ecosystem collect structured data that can more reliably detect community occupancy yet
265 are high-cost. Alternatively, a linear array ($n \times 1$) of passive sensors collects structured data
266 along a gradient and samples areas with greater environmental heterogeneity, which should
267 result in higher detectability of novel communities with a lower cost.

268

269 Figure 2. A conceptual example of how novel community detection can change landscape-level
270 community composition forecasts on short timescales (no significant climate change, but
271 possible ecological or anthropogenic change). This example was created using range estimates of
272 virtual species in R and real data on climatic variables and Japanese ecoregions (Supplemental
273 Information 1, 2). Two linear arrays of passive sensors monitor surrounding areas (black circles)
274 across the gradient between two ecoregions (west: dark gray, east: light gray) delineated by a
275 white dotted line. Species A occurs across both the east and west ecoregions, while species C
276 occurs only in the east due to abiotic constraints. In time 1 (Panel (a)), species B occurs only in
277 the west due to biotic constraints. Thus, although the fundamental niche of species B includes
278 areas in the east ecoregion, it is not included in the eastern community predictions. In time 2
279 (Panel (b)), the biotic constraint is released and species B can colonize parts of the east
280 ecoregion, resulting in the establishment of novel communities BC and ABC. This information is
281 used to extend the range prediction of species B into the east ecoregion, resulting in an updated
282 community composition forecast.

Novel
community
detection

Low

Medium

High

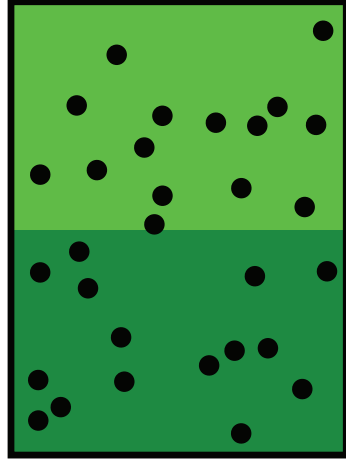
Cost
(financial, labor)

Low

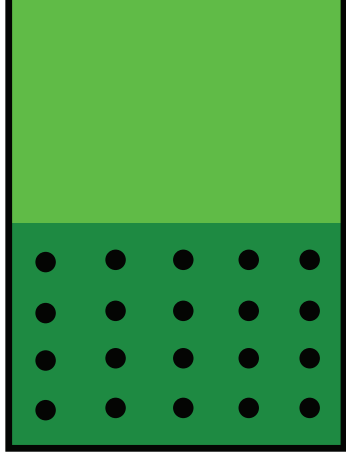
High

Medium

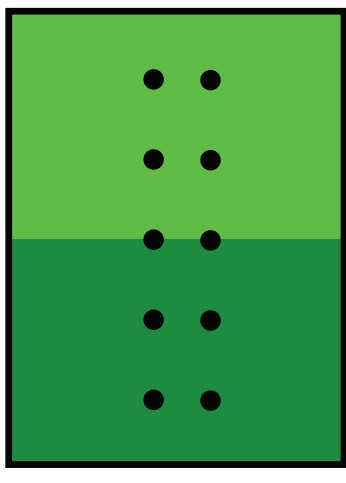
Strategy



Opportunistic
occurrence data

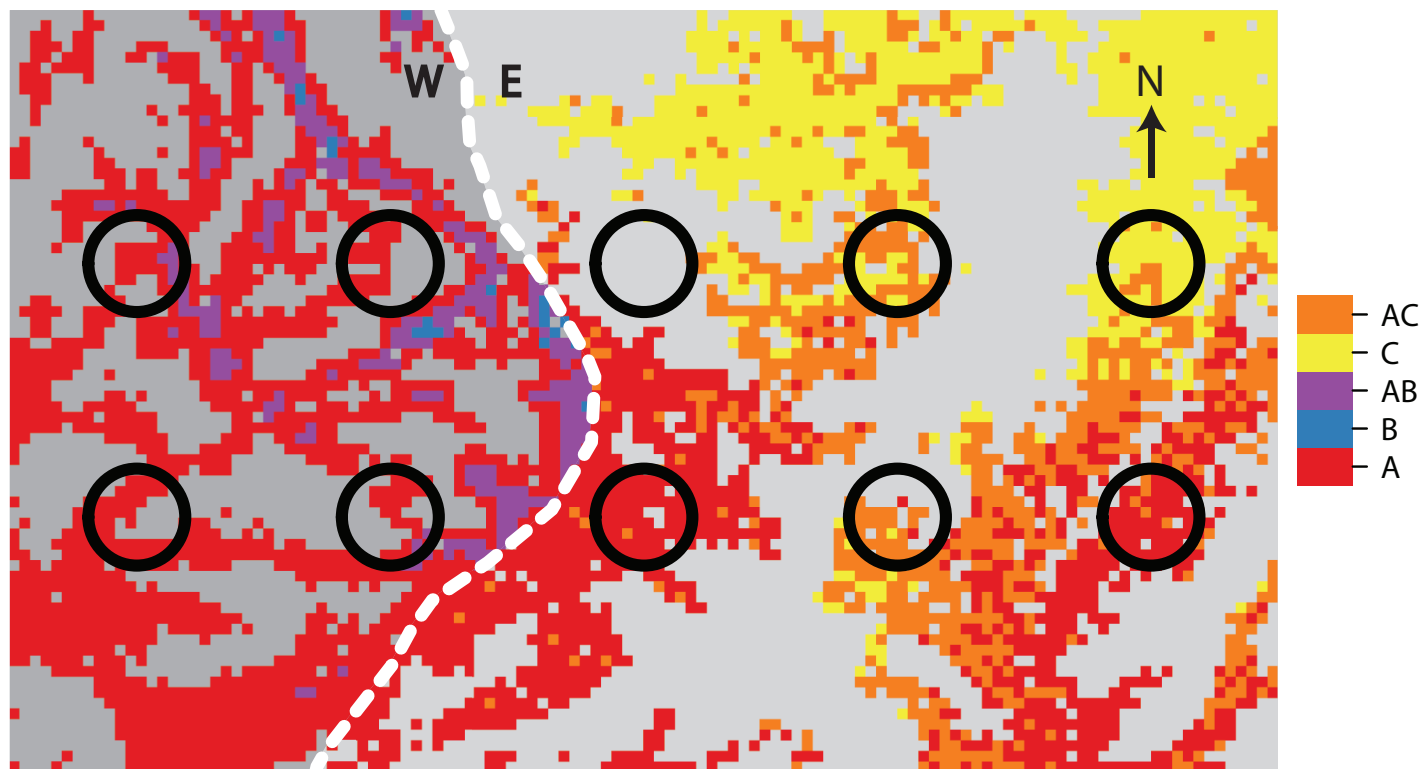


Passive sensor
grid array
(ecosystem-focused)

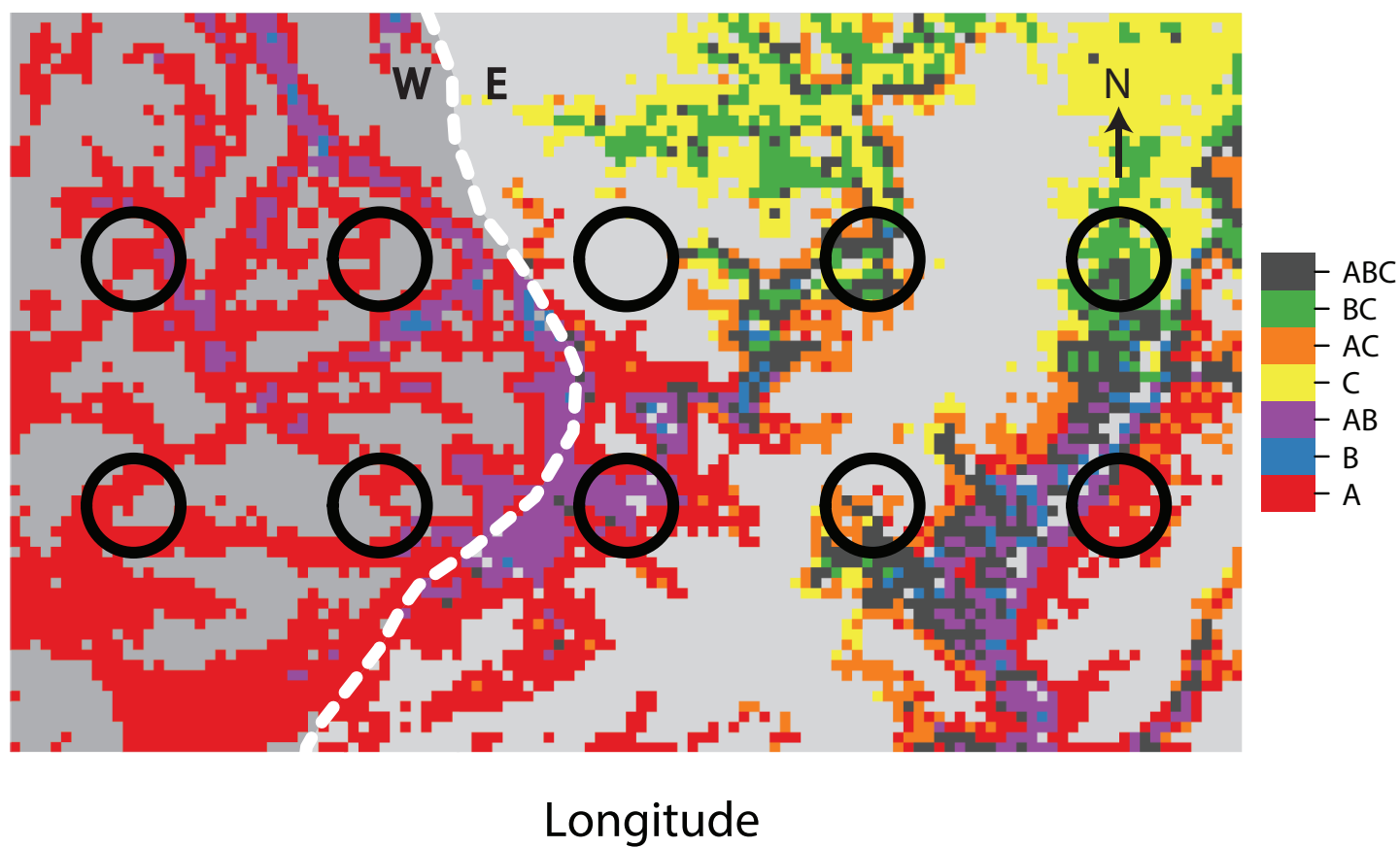


Passive sensor
linear array
(gradient-focused)

(a) Time 1



(b) Time 2



Supplemental Information 1

We used virtual species with predefined climatic preferences to demonstrate how detection of a novel community can update landscape-level predictions of community composition (see Supplemental Information 2 for code). We focused on a transition area in central Honshu island, Japan ($x_{\min} = 137$, $x_{\max} = 138$, $y_{\min} = 35.3$, $y_{\max} = 35.9$) between the Taiheiyō evergreen forests (west) and Taiheiyō montane deciduous forests (east) WWF ecoregions (Olson et al. 2001) and defined virtual species' niches based on long-term average temperature and precipitation values (bio1 and bio12) from the CHELSA dataset (Karger et al. 2017, Karger et al. 2018). We simulated 3 species' niches (A, B, and C) with Gaussian responses to reflect different climatic preferences and used them to construct suitability rasters, which we then converted to presence-absence maps using a logistic function (Leroy et al. 2016). Species A has higher suitability in the west ecoregion, species C in the east ecoregion, and species B has high suitability throughout. In time step 1, to simulate species restricted to particular ecoregions, we masked the east ecoregion from the range of species B and the west ecoregion from that of species C. Thus, time step 1 does not have any grid-cell community predictions that include all species. In time step 2, we allowed the range of species B to extend to the east, demonstrating an update to a community forecast after discoveries of novel communities BC and ABC (see Fig. 2). All analyses were performed in R (R Core Team 2021); vector data operations were conducted with package *sf* (Pebesma 2018), gridded data operations with the package *raster* (Hijmans 2021), and plotting with the package *rasterVis* (Perpiñán Lamigueiro & Hijmans 2021).

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# Supplemental Information 2 for Kass et al. Ecological Research Idea
Paper 2021
# This code reproduces the analysis for Figure 2 described in
Supplemental Information 1

# load packages
# NOTE: make sure to update all packages
# rasterVis may need to be updated with
remotes::install_github('oscarperpinan/rasterVis')
# to plot the categorical raster legends correctly
library(virtualspecies)
library(sf)
library(dismo)
library(RColorBrewer)
library(rasterVis)
library(latticeExtra)
library(dplyr)

# define local directory where data lives and where files should be saved
# NOTE: data used in this analysis are publicly available from:
# CHELSA bioclimatic variables (bio1 and bio12; file names may differ):
# https://chelsa-climate.org/bioclim/
# WWF: https://www.worldwildlife.org/publications/terrestrial-ecoregions-
of-the-world
d <- ""

# load CHELSA bioclimatic data and rename variables
f.ras <- file.path(d, "CHELSA_bioclim")
envs <- stack(file.path(f.ras, "CHELSA_bio10_01.tif"),
              file.path(f.ras, "CHELSA_bio10_12.tif"))
names(envs) <- c("bio1", "bio12")
# define analysis extent
e <- extent(c(xmin=137, xmax=138, ymin=35.3, ymax=35.9))
# crop CHELSA data to extent
envs <- crop(envs, e)

# load WWF ecoregions polygon shapefile (free to download)
ecoreg <- read_sf(file.path(d, "wwf_ecoregions/wwf_terr_ecos.shp"))
# filter out the ecoregions of interest
ecoreg <- ecoreg %>% filter(grepl(c("Nihonkai|Taiheiyu|Honshu"),
ECO_NAME))

# make a mask of the climate rasters for each ecoregion
reg1 <- mask(envs, ecoreg %>%
              filter(ECO_NAME == "Taiheiyu evergreen forests"))
reg2 <- mask(envs, ecoreg %>%
              filter(ECO_NAME == "Taiheiyu montane deciduous forests"))

# define climatic responses for virtual species, chosen to make species A
# have higher suitability in the Taiheiyu evergreen forests, species C
# to have higher suitability in the Taiheiyu montane deciduous forests,
# and species B to have areas of high suitability throughout
spA.resp <- formatFunctions(bio1 = c(fun = 'dnorm', mean = 140, sd = 60),
                           bio12 = c(fun = 'dnorm', mean = 1500, sd =
400))
spB.resp <- formatFunctions(bio1 = c(fun = 'dnorm', mean = 120, sd = 40),
                           bio12 = c(fun = 'dnorm', mean = 1300, sd =
200))

```

```

spC.resp <- formatFunctions(bio1 = c(fun = 'dnorm', mean = 100, sd = 40),
                           bio12 = c(fun = 'dnorm', mean = 1200, sd =
600))

# generate suitability rasters for virtual species
spA <- generateSpFromFun(raster.stack = envs[[c("bio1", "bio12")]],
                        parameters = spA.resp, plot = TRUE)
plot(st_geometry(ecoreg), add=TRUE)
spB <- generateSpFromFun(raster.stack = envs[[c("bio1", "bio12")]],
                        parameters = spB.resp, plot = TRUE)
plot(st_geometry(ecoreg), add=TRUE)
spC <- generateSpFromFun(raster.stack = envs[[c("bio1", "bio12")]],
                        parameters = spC.resp, plot = TRUE)
plot(st_geometry(ecoreg), add=TRUE)

# use logistic function to convert suitability rasters to
# binary presence-absence rasters (i.e., range estimates)
# NOTE: seeds are set to ensure reproducibility of original analysis
set.seed(462)
spA.pa <- convertToPA(spA, beta = 0.75)
set.seed(462)
spB.pa <- convertToPA(spB, beta = 0.75)
set.seed(462)
spC.pa <- convertToPA(spC, beta = 0.75)

# make a mask of the PA map for species B for Taiheiyu evergreen forests
# and a mask for species C for Taiheiyu montane deciduous forests
# NOTE: this limits their distributions to these ecoregions
spB.pa.reg1 <- mask(spB.pa$pa.raster, reg1$bio1)
spB.pa.reg1[is.na(spB.pa.reg1)] <- 0
spC.pa.reg2 <- mask(spC.pa$pa.raster, reg2$bio1)
spC.pa.reg2[is.na(spC.pa.reg2)] <- 0

# overlay the PA maps for all species to get community composition for
two times,
# where time 1 has species B restricted to region 1 and species C to
region 2, and
# time 2 has species B allowed to extend to both regions
# NOTE: this is done by multiplying species B and C by different powers
of 10
# to create a community "code"
# NOTE: the levels set are different because time 2 has more different
communities
# than time 1
envs.cc.t1 <- overlay(spA.pa$pa.raster, spB.pa.reg1, spC.pa.reg2,
                    fun = function(x,y,z) x + 10*y + 100*z)
envs.cc.t1[envs.cc.t1==0] <- NA
envs.cc.t1 <- as.factor(envs.cc.t1)
levels(envs.cc.t1)[[1]]$community <- c("A","B","AB","C","AC")
envs.cc.t2 <- overlay(spA.pa$pa.raster, spB.pa$pa.raster, spC.pa.reg2,
                    fun = function(x,y,z) x + 10*y + 100*z)
envs.cc.t2[envs.cc.t2==0] <- NA
envs.cc.t2 <- as.factor(envs.cc.t2)
levels(envs.cc.t2)[[1]]$community <- c("A","B","BC","AB","AC","C","ABC")

# define colors for plotting different communities
cols <- c(brewer.pal(9, "Set1")[1:6], "#4d4d4d")
names(cols) <- c("A","B","BC","AB","AC","C","ABC")

```



```
theme1 <- rasterTheme(cols[levels(envs.cc.t1)[[1]][,2]])
theme2 <- rasterTheme(cols[levels(envs.cc.t2)[[1]][,2]])

# define points to depict passive sensors for biodiversity monitoring
pts <- matrix(c(rep(seq(137.1, 137.9, 0.2), 2), rep(35.7, 5), rep(35.5,
5)), ncol=2) %>% SpatialPoints()

# plot maps for time 1 and time 2
# NOTE: colors and lines in Figure 2 were further edited in Adobe
Illustrator
pdf(file.path(d, "fig2.pdf"), onefile = TRUE)
print(levelplot(envs.cc.t1, par.settings = theme1, main = "Time 1") +
  layer(sp.polygons(as(ecoreg, "Spatial"), lwd = 3, lty = 3)) +
  layer(sp.points(pts, col="black", lwd=5, pch=21, cex=5)))
print(levelplot(envs.cc.t2, par.settings = theme2, main = "Time 2") +
  layer(sp.polygons(as(ecoreg, "Spatial"), lwd = 3, lty = 3)) +
  layer(sp.points(pts, col="black", lwd=5, pch=21, cex=5)))
dev.off()
```