sustainability

Supplementary Materials

Table S1. The data set used in this study for ensemble species distribution modelling. The information includes the name of localities, geographical coordinates and origin.

No.	Name of localities	Latitude/ Longitude	Reference	No.	Name of localities	Latitude/ Longitude	* Reference
1	Ghorighale	34.9/46.5	B, C, G	30	Sardehanan	34.98/46.21	I
2	Kavat	34.88/46.51	C, F, G	31	Balebezan	35.1/46.2	I
3	Marrakhil	35.01/46.13	C, G	32	Daribar	35.16/46.36	I
4	Dourisan	35.01/46.38	B, C, G	33	Baneh	36.06/45.96	I
5	Shamshir	34.98/46.41	C, G	34	Shahoo	34.91/46.46	G
6	Pave	35.05/46.4	C, G	35	Bayangan	34.98/46.21	G
7	Najjar	35.1/46.31	C, G	36	Zali	34.98/46.46	G
8	Darian	35.13/46.31	C, G	37	Khangah	35.01/46.33	G
9	Benjun	36.55/45.51	G	38	Mirabad	35.05/46.33	C, G
10	Lashkargah	35/46.13	G	39	Selein	35.21/46.31	C, G
11	Nosme	35/46.36	G	40	Hani Garmale	35.23/46.13	G
12	Deshe	35.06/46.26	G	41	Novin	35.18/46.35	G
13	Gholani	34.9/46.45	G	42	Balkha	35.2/46.15	A, E
14	Hajij	35.16/46.35	G	43	Tawale	35.18/46.18	A, E
15	Nowsood	35.16/46.2	F	44	Siyah Guvez	35.78/45.78	E
16	Nilan	35.15/46.31	G	45	Garmik	35.71/45.76	E
17	Gola	35.78/45.83	E	46	Naav	35.16/46.35	G
18	Nowdeshe	35.18/46.23	G	47	Saqez	36.05/46.03	G
19	Biyara	35.21/46.11	E	48	Razgeh	36.05/45.51	G
20	Sargate	35.28/46.1	H	49	Shalmash	36.08/45.48	G

21	Ahmadawa	35.3/46.06	E, H	50	Baskedo	36.15/45.48	G
22	Mawat - Isawa	35.93/45.38	H	51	Basak	35.55/45.71	E
23	Halsho	36.2/45.26	H	52	Miri Sour	35.71/45.25	J
24	Hero	36.11/45.28	H	53	Penjwin	35.6/45.96	E
25	Qara and Abubakra	36.4/45.05	H	54	Zardoii	35/46.26	K
26	Jivar	35.21/46.31	C, G	55	Dizawar	35.2/46.2	K
27	Kani Bard	36.05/45.63	I	56	Khurnawa	35.06/46.31	K
28	Sonch	36.03/45.98	I	57	Daranisha	35.03/46.36	K
29	Serke	34.91/46.46	I				

* A) Nestrov 1916 [1]; B) Schmidtler and Schmidtler 1975 [2]; C) Sharifi and Assadian 2004 [3]; D) Najafimajd and Kaya 2010 [4]; E) Schneider and Schneider 2011 [5]; F) Naderi 2012 [6]; G) Afroosheh et al. 2016 [7]; H) Al-Sheikhly et al. 2013 [8]; I) Rastegar-Pouyani et al. 2015 [9]; J) Zarei et al. 2017 [10]; K) Mawloudi et al. 2019 [11].

Table S2. A brief description of the exclusionary criteria used in siting procedure.

Exclusionary criteria	
Mains roads	Various studies have shown that roads can have a significant impact on amphibian mortality [12–14]. Roads, on the other hand, lead to reduced connectivity through fragmentation of amphibian habitats and to reduced genetic diversity among populations [15–17].
Cities and high village density	Urbanization affects the distribution and abundance of amphibians [18]. It is also considered as an influential factor in reducing amphibians through the effect on habitat use relative to urbanization, movement patterns, life-history stages, breeding habitats [19,20]. Urbanization reduces genetic diversity among populations by fragmenting habitats [21,22].
Dam reservoir	The richness and abundance, as well as the survival and breeding habitat of amphibians, are affected by dams [23,24] through habitat fragmentation and ecosystem losses [24].
Unsuitable vegetation cover	The composition and structure of vegetation cover in the terrestrial environment increases the success of reproduction for amphibians and recruitment in the aquatic habitat [25–27].
Agricultural landscapes	Agricultural landscapes declined amphibians by pond loss as well as by affecting reducing population connectivity [28]. Also, fertilizers and pesticides used in agriculture have a significant effect on the survival and reproductive capacity that following by reducing the population of amphibians [29,30].
High ridge density	Mountains, especially very high altitudes, act as barriers to different populations of amphibians and impede gene flow [31,32].
Low stream density	Amphibians need the aquatic environment in the larval stage and breeding season, so droughts due to climate change, urban development, or agricultural use have a significant impact on declining amphibians [28,33,34].

Table S3. A brief description of the non-exclusionary criteria used in siting procedure.

Non-exclusionary criteria	
Number of newt localities	The greater the number of known habitats of the PAs appears more favourable [35].
NPAs connectivity	Populations need to disperse between different habitats to maintain their genetic diversity and prevent inbreeding [36]. Climate change, on the other hand, may lead to shifts in the range of species distribution, so that they may need the closest suitable habitat. Nearest-neighbour distance is the simplest way to measure species dispersal abilities, patch connectivity, and other scaling parameters [37].
NPAs size (Km^2)	Today, the theory of island biogeography is used to design parks and PAs [38]. According to this theory, as the size of a park or PAs increases, the number of species increases, and the probability of species extinction decreases [39–41]. In small and enclosed areas, the possibility of dispersal and establishing new species decreases due to barriers, and also, the rate of species extinction increases with the decreasing area. Therefore, larger areas have a comparative advantage in designing PAs [42–44].
NPAs shape (edge effect)	The shape of the PAs should be such that it is minimized in contact with the outside environment and the impact of external disturbances in the area (for example, human activities); [45]. By minimizing a combination of PAs boundary length and cost, we can create efficient and compact reserve systems. Because the long thin shape PAs with high edge-to-area ratios is sensitive to edge effects [46].
Climate change: NPAs future habitat suitability (2070)	Various studies confirm the negative effects of climate change on amphibians [47,48]. Climate changes shifted amphibian ranges [49,50]. Climate changes may affect dispersal capabilities [51], reproduction [52], development [52], and survival [53]. Besides, climate change can change amphibian habitats including hydrology [54], soil, and vegetation [55]. Climate change can impact competitive interactions which can alter community structure, predator-prey relationships, and food availability. Climate change dramatically influences diseases [56] and modifies pathogen-host dynamics [55,57].
Genetic diversity (Nd)	IUCN emphasizes the conservation of populations with high genetic diversity [58]. Reduction of genetic diversity is associated with inbreeding, and on the other hand, inbreeding reduces reproductive fitness [59,60].
Distance to nearest PAs (Km)	Connectivity between PAs is essential for ecological and evolutionary processes such as species range shift, migration, and gene flow [61]. These processes are vital for living populations in response to climate and landscape change [62–64]. Establishing connectivity between PAs areas is an essential priority of management and conservation programs of biodiversity [65–67].

Table S4. Habitat areas (Km²) of the Yellow-spotted mountain newt, *Neurergus derjugini*, according to different classifications and recent and future (2050 and 2070) periods under two optimistic (RCP 2.6) and pessimistic (RCP 8.5) scenarios within the MRI-CGCM3 and CCSM4 models in western Iran and northeastern Iraq.

Model	Class (%)	Recent	Future (2050)		Potential impacts	Future (2070)		Potential impacts
			(RCP 2.6)	**(RCP 8.5)**		**(RCP 2.6)**	**(RCP 8.5)**	
MRI-CGCM3	0-25	71336.80	69461.80	38003.47	-/-	72083.33	62204.86	+/-
	25-50	13888.88	13281.25	47986.11	-/-	15486.11	25659.72	+/+
	50-75	8298.61	12829.86	13211.80	+/+	10555.22	14409.72	+/+
	75-100	13333.33	11284.72	7656.25	-/-	8732.63	4583.33	-/-
CCSM4	0-25	69618.05	67968.75	60520.83	-/-	69054.13	60798.61	-/-
	25-50	8281.25	10902.77	28072.91	+/+	10329.86	27187.50	-/-
	50-75	8576.38	15329.86	15711.80	+/+	11319.44	10677.08	+/+
	75-100	20381.94	12658.25	2552.08	-/-	16163.19	8194.44	-/-

Table S5. The no-exclusionary criteria and their relative suitability obtained from 13 rating curves.

	Criterion	A pattern of rating curve	Grading values
1	Number of newt localities	Linear	1=12; 0.50=5; 0.40=4; 0.30=3; 0.20=2; 0.10=1; 0=0
2	NPAs HS (%): MRI-CGCM3: RCP85 - 2070	Categorical	1=75-100; 0.70=50-75; 0.40=25-50; 0=0-25
3	NPAs HS (%): CCSM4: RCP85 - 2070	Categorical	1=75-100; 0.70=50-75; 0.40=25-50; 0=0-25
4	NPAs shape (edge effect)	Linear	1=1.03-1.10; 0.75= 1.11-1.20; 0.50= 121-1.30; 0.25= 1.31-2.12
5	NPAs size (Km2)	Linear	0.25=0-50; 0.50=50-100; 0.75=100-200; 1=200-300
6	NPAs connectivity: nearest neighbour distance (Km)	Linear	1=56-68; 0.75=69-81; 0.50=82-94; 0.25=95-107
7	HS (%): MRI-CGCM3: RCP26 - 2070	Categorical	1=75-100; 0.70=50-75; 0.40=25-50; 0=0-25
8	HS (%): CCSM4: RCP26 - 2070	Categorical	1=75-100; 0.70=50-75; 0.40=25-50; 0=0-25
9	Genetic diversity (Nd)	Categorical	southern region= 0.60; northern region=0.40
10	Distance to other PAs (Km)	Linear	0.25=72-91; 0.50=52-71; 0.75=32-51; 1=12-31
11	Village density (Km^2)	Linear	0=0.72-1.35; 0.25=0.41-0.72; 0.50=0.20-0.41; 0.75=0.08-0.20; 1=0-0.08
12	Distance to cities	Linear	0=0-2; 0.25=2-4; 0.50=4-6; 0.75=6-8; 1=8-10-1
13	Distance to the main road	Linear	0.25=0-25; 0.50=5-10; 0.75=10-20; 1=20-30

Table S6. Weight of 13 non-exclusionary criteria result of the pair-wise comparison.

	Criterion	Weights
1	Number of newt localities	0.17
2	NPAs HS (%): MRI-CGCM3: RCP85 - 2070	0.15
3	NPAs HS (%): CCSM4: RCP85 - 2070	0.12
4	NPAs shape (edge effect)	0.11
5	NPAs size (Km2)	0.09
6	NPAs connectivity: nearest neighbour distance (Km)	0.08
7	NPAs HS (%): MRI-CGCM3: RCP26 - 2070	0.07
8	NPAs HS (%): CCSM4: RCP26 - 2070	0.06
9	Genetic diversity (Nd)	0.05
10	Distance to nearest PAs (Km)	0.04
11	Village density (Km^2)	0.03
12	Distance to cities	0.02
13	Distance to the main road	0.01

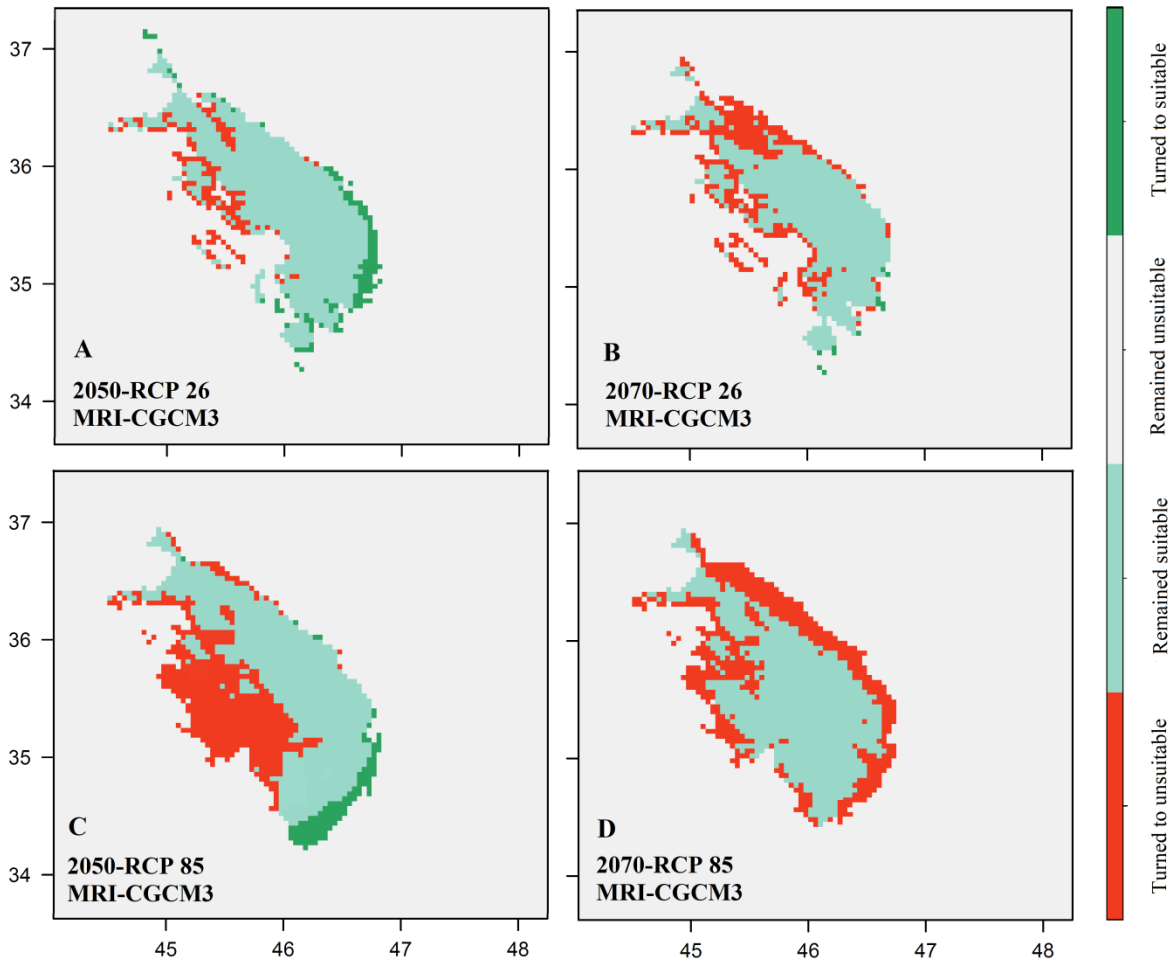

Figure S1. Species range change of *Neurergus derjugini* in currently suitable habitats (gain/loss) by 2050 and 2070 under two optimistic (RCP26) and pessimistic (RCP85) scenarios within the MRI-CGCM3 model in western Iran and northeastern Iraq.

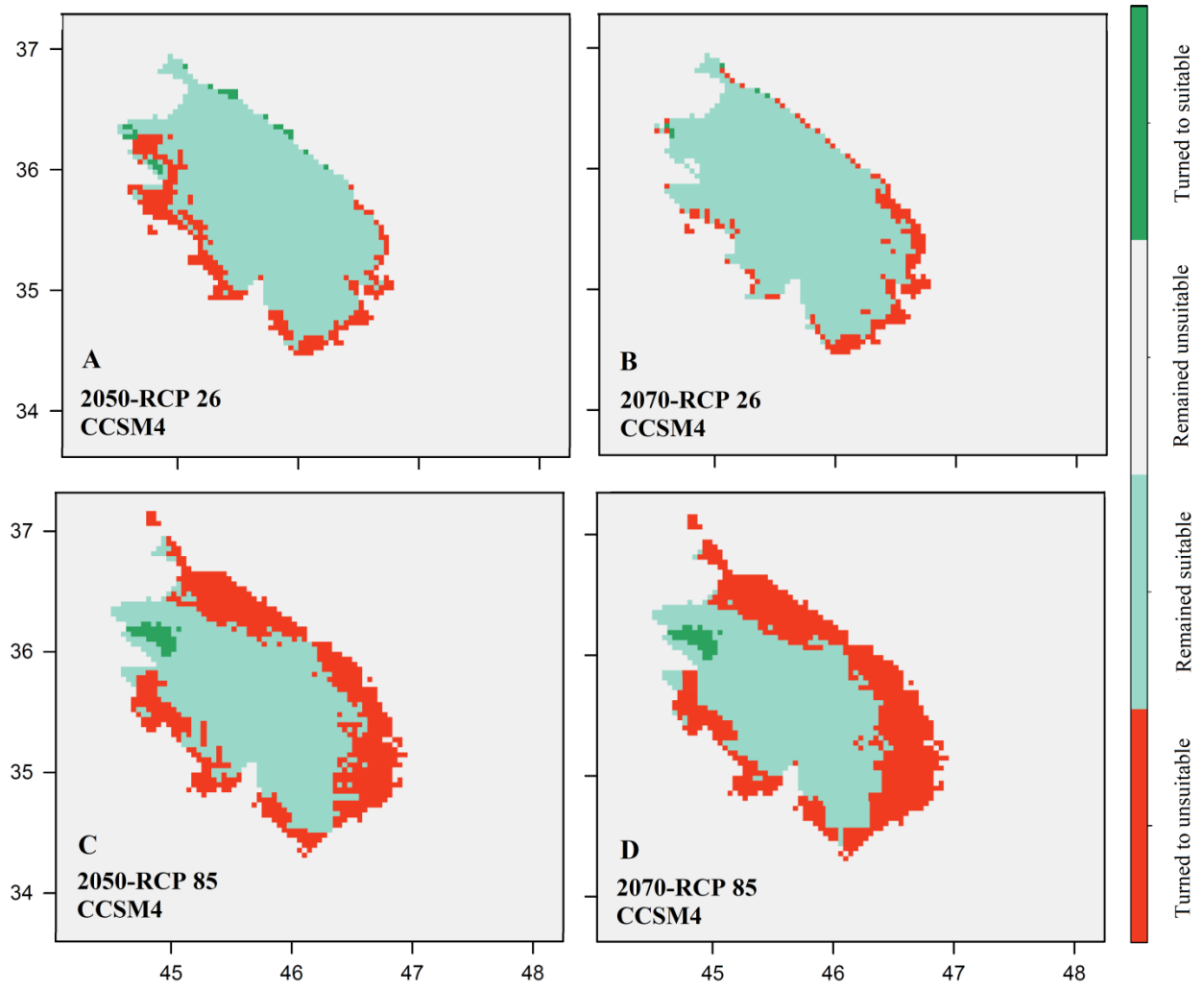

Figure S2. Species range change of *Neurergus derjugini* in currently suitable habitats (gain/loss) by 2050 and 2070 under two optimistic (RCP26) and pessimistic (RCP85) scenarios within the CCSM4 model in western Iran and northeastern Iraq.

Scripts S1. The scripts used in the biomod2 settings.

```
## setup environment ----
setwd('workdir')
## install the latest release of biomod2
devtools::install_github('biomodhub/biomod2')
## load the required packages
library(biomod2)
library(ggplot2)
library(gridExtra)
library(raster)
library(rasterVis)
## read data ----
derjugini_occ <- read.csv('../data/derjugini_occ.csv')
summary(derjugini_occ)
bioclim_ND_sub <-
 raster::stack(
  c(
   bio_1  = '../data/worldclim_ND/worldclim_ND_bio_1.asc',
   bio_2  = '../data/worldclim_ND/worldclim_ND_bio_2.asc',
   bio_4  = '../data/worldclim_ND/worldclim_ND_bio_4.asc',
   bio_12 = '../data/worldclim_ND/worldclim_ND_bio_12.asc',
   bio_13 = '../data/worldclim_ND/worldclim_ND_bio_13.asc',
   bio_14 = '../data/worldclim_ND/worldclim_ND_bio_18.asc'
  )
 )

bioclim_ND_sub

## format the data ----
derjugini_data <-
 BIOMOD_FormatingData(
  resp.var = derjugini_occ['neurergus.derjugini'],
  resp.xy = derjugini_occ[, c('long', 'lat')],
  expl.var = bioclim_ND_sub,
  resp.name = "neurergus.derjugini",
  PA.nb.rep = 10,
  PA.nb.absences = 57,
  PA.strategy = '  random '
 )

## formatted object summary
derjugini_data

## plot of selected pseudo-absences
plot(derjugini_data)

## define individual models options ----
derjugini_opt <-
 BIOMOD_ModelingOptions(
  GLM = list(type = 'quadratic', interaction.level = 1),
  GBM = list(n.trees = 1000),
  CTA = list(CV.tree = 50),
  ANN = list(CV.ann = 5),
  SRE = list(quant=0.025)
 )

## run the individual models ----
derjugini_models <-
```

```
 BIOMOD_Modeling(
   data = derjugini_data,
   models = c("GLM", "GBM", "RF", "CTA", "ANN", "SRE", "FDA", "MARS"),
   models.options = derjugini_opt,
   NbRunEval = 10,
   DataSplit = 80,
   VarImport = 3,
   modeling.id = "demo1"
 )

## asses individual models quality ----

## get models evaluation scores
derjugini_models_scores <- get_evaluations(derjugini_models)

## derjugini_models_scores is a 5 dimension array containing the scores of the models
dim(derjugini_models_scores)
dimnames(derjugini_models_scores)

## plot models evaluation scores
models_scores_graph(
  derjugini_models,
  by = "models",
  metrics = c("ROC","TSS","KAPPA"),
  xlim = c(0.5,1),
  ylim = c(0.5,1)
)

models_scores_graph(
  derjugini_models,
  by = "cv_run" ,
  metrics = c("ROC","TSS","KAPPA"),
  xlim = c(0.5,1),
  ylim = c(0.5,1)
)

models_scores_graph(
  derjugini_models,
  by = "data_set",
  metrics = c("ROC","TSS","KAPPA"),
  xlim = c(0.5,1),
  ylim = c(0.5,1)
)

## check variable importance
(derjugini_models_var_import <- get_variables_importance(derjugini_models))

## make the mean of variable importance by algorithm
apply(derjugini_models_var_import, c(1,2), mean)

## individual models response plots
derjugini_glm <- BIOMOD_LoadModels(derjugini_models, models='GLM')
derjugini_gbm <- BIOMOD_LoadModels(derjugini_models, models='GBM')
derjugini_ randomForest <- BIOMOD_LoadModels(derjugini_models, models='RF')
derjugini_rpart <- BIOMOD_LoadModels(derjugini_models, models='CTA')
derjugini_nnet <- BIOMOD_LoadModels(derjugini_models, models='ANN')
derjugini_sre <- BIOMOD_LoadModels(derjugini_models, models='SRE')
derjugini_fda <- BIOMOD_LoadModels(derjugini_models, models='FDA')
derjugini_earth <- BIOMOD_LoadModels(derjugini_models, models='MARS')
```

```
glm_eval_strip <-
  biomod2::response.plot2(
    models  = derjugini_glm,
    Data = get_formal_data(derjugini_models,'expl.var'),
    show.variables= get_formal_data(derjugini_models,'expl.var.names'),
    do.bivariate = FALSE,
    fixed.var.metric = 'median',
    legend = FALSE,
    display_title = FALSE,
    data_species = get_formal_data(derjugini_models,'resp.var')
  )

gbm_eval_strip <-
  biomod2::response.plot2(
    models  = derjugini_gbm,
    Data = get_formal_data(derjugini_models,'expl.var'),
    show.variables= get_formal_data(derjugini_models,'expl.var.names'),
    do.bivariate = FALSE,
    fixed.var.metric = 'median',
    legend = FALSE,
    display_title = FALSE,
    data_species = get_formal_data(derjugini_models,'resp.var')
  )

rf_eval_strip <-
  biomod2::response.plot2(
    models  = derjugini_rf,
    Data = get_formal_data(derjugini_models,'expl.var'),
    show.variables= get_formal_data(derjugini_models,'expl.var.names'),
    do.bivariate = FALSE,
    fixed.var.metric = 'median',
    legend = FALSE,
    display_title = FALSE,
    data_species = get_formal_data(derjugini_models,'resp.var')
  )

cta_eval_strip <-
  biomod2::response.plot2(
  models  = derjugini_rpart,
  Data = get_formal_data(derjugini_models,'expl.var'),
  show.variables= get_formal_data(derjugini_models,'expl.var.names'),
  do.bivariate = FALSE,
  fixed.var.metric = 'median',
  legend = FALSE,
  display_title = FALSE,
  data_species = get_formal_data(derjugini_models,'resp.var')
)

ann_eval_strip <-
  biomod2::response.plot2(
  models  = derjugini_nnet,
  Data = get_formal_data(derjugini_models,'expl.var'),
  show.variables= get_formal_data(derjugini_models,'expl.var.names'),
  do.bivariate = FALSE,
  fixed.var.metric = 'median',
  legend = FALSE,
  display_title = FALSE,
  data_species = get_formal_data(derjugini_models,'resp.var')
)
```

```
sre_eval_strip <-
  biomod2::response.plot2(
  models  = derjugini_sre,
  Data = get_formal_data(derjugini_models,'expl.var'),
  show.variables= get_formal_data(derjugini_models,'expl.var.names'),
  do.bivariate = FALSE,
  fixed.var.metric = 'median',
  legend = FALSE,
  display_title = FALSE,
  data_species = get_formal_data(derjugini_models,'resp.var')
)

fda_eval_strip <-
  biomod2::response.plot2(
  models  = derjugini_fda,
  Data = get_formal_data(derjugini_models,'expl.var'),
  show.variables= get_formal_data(derjugini_models,'expl.var.names'),
  do.bivariate = FALSE,
  fixed.var.metric = 'median',
  legend = FALSE,
  display_title = FALSE,
  data_species = get_formal_data(derjugini_models,'resp.var')
)

mars_eval_strip <-
  biomod2::response.plot2(
  models  = derjugini_earth,
  Data = get_formal_data(derjugini_models,'expl.var'),
  show.variables= get_formal_data(derjugini_models,'expl.var.names'),
  do.bivariate = FALSE,
  fixed.var.metric = 'median',
  legend = FALSE,
  display_title = FALSE,
  data_species = get_formal_data(derjugini_models,'resp.var')
)

## run the ensemble models ----
derjugini_ensemble_models <-
  BIOMOD_EnsembleModeling(
    modeling.output = derjugini_models,
    em.by = 'all',
    eval.metric = 'TSS',
    eval.metric.quality.threshold = 0.8,
    models.eval.meth = c('TSS','ROC','KAPPA'),
    prob.mean = FALSE,
    prob.cv = TRUE,
    committee.averaging = TRUE,
    prob.mean.weight = TRUE,
    VarImport = 0
  )

## asses ensemble models quality ----
(derjugini_ensemble_models_scores <- get_evaluations(derjugini_ensemble_models))

## do models projections ----

## current projections
derjugini_models_proj_current <-
  BIOMOD_Projection(
    modeling.output = derjugini_models,
```

```
  new.env = bioclim_ND_sub,
  proj.name = "current",
  binary.meth = "TSS",
  output.format = ".img",
  do.stack = FALSE
 )

derjugini_ensemble_models_proj_current <-
 BIOMOD_EnsembleForecasting(
  EM.output = derjugini_ensemble_models,
  projection.output = derjugini_models_proj_current,
  binary.meth = "TSS",
  output.format = ".img",
  do.stack = FALSE
 )


## future projections

## load 2050_BC26 bioclim variables
bioclim_ND_2050_BC26 <-
 stack(
  c(
   bio_1  = '../data/worldclim_ND/worldclim_ND_2050_BC26_bio_1.asc',
   bio_2  = '../data/worldclim_ND/worldclim_ND_2050_BC26_bio_2.asc',
   bio_4  = '../data/worldclim_ND/worldclim_ND_2050_BC26_bio_4.asc',
   bio_12 = '../data/worldclim_ND/worldclim_ND_2050_BC26_bio_12.asc',
   bio_13 = '../data/worldclim_ND/worldclim_ND_2050_BC26_bio_13.asc',
   bio_14 = '../data/worldclim_ND/worldclim_ND_2050_BC26_bio_14.asc'
  )
 )

derjugini_models_proj_2050_BC26 <-
 BIOMOD_Projection(
  modeling.output = derjugini_models,
  new.env = bioclim_ND_2050_BC26,
  proj.name = "2050_BC26",
  binary.meth = "TSS",
  output.format = ".img",
  do.stack = FALSE
 )

derjugini_ensemble_models_proj_2050_BC26 <-
 BIOMOD_EnsembleForecasting(
  EM.output = derjugini_ensemble_models,
  projection.output = derjugini_models_proj_2050_BC26,
  binary.meth = "TSS",
  output.format = ".img",
  do.stack = FALSE
 )


 ## load 2050_BC85 bioclim variables
 bioclim_ND_2050_BC85 <-
  stack(
   c(
    bio_1  = '../data/worldclim_ND/worldclim_ND_2050_BC85_bio_1.asc',
    bio_2  = '../data/worldclim_ND/worldclim_ND_2050_BC85_bio_2.asc',
    bio_4  = '../data/worldclim_ND/worldclim_ND_2050_BC85_bio_4.asc',
    bio_12 = '../data/worldclim_ND/worldclim_ND_2050_BC85_bio_12.asc',
```

```
    bio_13 = '../data/worldclim_ND/worldclim_ND_2050_BC85_bio_13.asc',
    bio_14 = '../data/worldclim_ND/worldclim_ND_2050_BC85_bio_14.asc'
   )
  )

 derjugini_models_proj_2050_BC85 <-
  BIOMOD_Projection(
   modeling.output = derjugini_models,
   new.env = bioclim_ND_2050_BC85,
   proj.name = "2050_BC85",
   binary.meth = "TSS",
   output.format = ".img",
   do.stack = FALSE
  )

 derjugini_ensemble_models_proj_2050_BC85 <-
  BIOMOD_EnsembleForecasting(
   EM.output = derjugini_ensemble_models,
   projection.output = derjugini_models_proj_2050_BC85,
   binary.meth = "TSS",
   output.format = ".img",
   do.stack = FALSE
 )

## load 2070_BC26 bioclim variables
bioclim_ND_2070_BC26 <-
 stack(
  c(
   bio_1  = '../data/worldclim_ND/worldclim_ND_2070_BC26_bio_1.asc',
   bio_2  = '../data/worldclim_ND/worldclim_ND_2070_BC26_bio_2.asc',
   bio_4  = '../data/worldclim_ND/worldclim_ND_2070_BC26_bio_4.asc',
   bio_12 = '../data/worldclim_ND/worldclim_ND_2070_BC26_bio_12.asc',
   bio_13 = '../data/worldclim_ND/worldclim_ND_2070_BC26_bio_13.asc',
   bio_14 = '../data/worldclim_ND/worldclim_ND_2070_BC26_bio_14.asc'
  )
 )

derjugini_models_proj_2070_BC26 <-
 BIOMOD_Projection(
  modeling.output = derjugini_models,
  new.env = bioclim_ND_2070_BC26,
  proj.name = "2070_BC26",
  binary.meth = "TSS",
  output.format = ".img",
  do.stack = FALSE
 )

derjugini_ensemble_models_proj_2070_BC26 <-
 BIOMOD_EnsembleForecasting(
  EM.output = derjugini_ensemble_models,
  projection.output = derjugini_models_proj_2070_BC26,
  binary.meth = "TSS",
  output.format = ".img",
  do.stack = FALSE
 )


 ## load 2070_BC85 bioclim variables
 bioclim_ND_2070_BC85 <-
  stack(
```

```
    c(
      bio_1  = '../data/worldclim_ND/worldclim_ND_2070_BC85_bio_1.asc',
      bio_2  = '../data/worldclim_ND/worldclim_ND_2070_BC85_bio_2.asc',
      bio_4  = '../data/worldclim_ND/worldclim_ND_2070_BC85_bio_4.asc',
      bio_12 = '../data/worldclim_ND/worldclim_ND_2070_BC85_bio_12.asc',
      bio_13 = '../data/worldclim_ND/worldclim_ND_2070_BC85_bio_13.asc',
      bio_14 = '../data/worldclim_ND/worldclim_ND_2070_BC85_bio_14.asc'
    )
  )

 derjugini_models_proj_2070_BC85 <-
  BIOMOD_Projection(
    modeling.output = derjugini_models,
    new.env = bioclim_ND_2070_BC85,
    proj.name = "2070_BC85",
    binary.meth = "TSS",
    output.format = ".img",
    do.stack = FALSE
  )

 derjugini_ensemble_models_proj_2070_BC85 <-
  BIOMOD_EnsembleForecasting(
    EM.output = derjugini_ensemble_models,
    projection.output = derjugini_models_proj_2070_BC85,
    binary.meth = "TSS",
    output.format = ".img",
    do.stack = FALSE
 )

## check how projections looks like
plot(derjugini_ensemble_models_proj_2050_BC26, str.grep = "EMca|EMwmean")
plot(derjugini_ensemble_models_proj_2050_BC85, str.grep = "EMca|EMwmean")
plot(derjugini_ensemble_models_proj_2070_BC26, str.grep = "EMca|EMwmean")
plot(derjugini_ensemble_models_proj_2070_BC85, str.grep = "EMca|EMwmean")

## compute Species Range Change (SRC) ----
## load binary projections
derjugini_bin_proj_current <-
 stack(
   c(
     ca = "neuregus.derjugini/proj_current/individual_projections/neuregus.derjugini_EMcaByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img",
     wm                                                                                                                                  =
"neuregus.derjugini/proj_current/individual_projections/neuregus.derjugini_EMwmeanByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img"
   )
 )

derjugini_bin_proj_2050_BC26 <-
 stack(
   c(
     ca = "neuregus.derjugini/proj_2050_BC26/individual_projections/neuregus.derjugini_EMcaByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img",
     wm                                                                                                                                  =
"neuregus.derjugini/proj_2050_BC26/individual_projections/neuregus.derjugini_EMwmeanByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img"
   )
 )


 derjugini_bin_proj_2050_BC85 <-
   stack(
     c(
       ca = "neuregus.derjugini/proj_2050_BC85/individual_projections/neuregus.derjugini_EMcaByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img",
```

```
      wm                                                                                                    =
"neuregus.derjugini/proj_2050_BC85/individual_projections/neuregus.derjugini_EMwmeanByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img"
    )
 )

derjugini_bin_proj_2070_BC26 <-
 stack(
   c(
     ca = "neuregus.derjugini/proj_2070_BC26/individual_projections/neuregus.derjugini_EMcaByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img",
     wm                                                                                                    =
"neuregus.derjugini/proj_2070_BC26/individual_projections/neuregus.derjugini_EMwmeanByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img"
   )
 )


 derjugini_bin_proj_2070_BC85 <-
   stack(
     c(
       ca = "neuregus.derjugini/proj_2070_BC85/individual_projections/neuregus.derjugini_EMcaByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img",
       wm                                                                                                    =
"neuregus.derjugini/proj_2070_BC85/individual_projections/neuregus.derjugini_EMwmeanByTSS_mergedAlgo_mergedRun_mergedData_TSSbin.img"
     )
 )

## SRC current -> 2050
SRC_current_2050_BC26 <-
 BIOMOD_RangeSize(
   derjugini_bin_proj_current,
   derjugini_bin_proj_2050_BC26
 )

SRC_current_2050_BC26$Compt.By.Models


## SRC current -> 2050
SRC_current_2050_BC85 <-
 BIOMOD_RangeSize(
   derjugini_bin_proj_current,
   derjugini_bin_proj_2050_BC85
 )

SRC_current_2050_BC85$Compt.By.Models


## SRC current -> 2070
SRC_current_2070_BC26 <-
 BIOMOD_RangeSize(
   derjugini_bin_proj_current,
   derjugini_bin_proj_2070_BC26
 )

SRC_current_2070_BC26$Compt.By.Models


## SRC current -> 2070
SRC_current_2070_BC85 <-
 BIOMOD_RangeSize(
   derjugini_bin_proj_current,
   derjugini_bin_proj_2070_BC85
 )
```

```
SRC_current_2070_BC85$Compt.By.Models

derjugini_src_map <-
 stack(
  SRC_current_2050_BC26$Diff.By.Pixel,
  SRC_current_2050_BC85$Diff.By.Pixel
  SRC_current_2070_BC26$Diff.By.Pixel,
  SRC_current_2070_BC85$Diff.By.Pixel
 )
names(derjugini_src_map) <- c("ca cur-2050_BC26", "wm cur-2050_BC26","ca cur-2050_BC85", "wm cur-2050_BC85", "ca cur-2070_BC26", "wm cur-2070_BC26","ca cur-2070_BC85", "wm cur-2070_BC85")

my.at <- seq(-2.5, 1.5, 1)
myColorkey <-
 list(
  at = my.at, ## where the colors change
  labels =
   list(
    labels = c("lost", "pres", "abs","gain"), ## labels
    at = my.at[-1] - 0.5 ## where to print labels
   )
 )

rasterVis::levelplot(
 derjugini_src_map,
 main = "neuregus derjugini range change",
 colorkey = myColorkey,
 col.regions=c('#f03b20', '#99d8c9', '#f0f0f0', '#2ca25f'),
 layout = c(2,2)
)

## compute the stratified density of probabilities on SRC ----
## the reference projetion
ref <- subset(derjugini_bin_proj_current, "ca")

## define the facets we want to study
mods <- c("GLM", "GBM", "RF", "CTA", "ANN", "SRE", "FDA", "MARS")
data_set <- c("PA1", "PA2","PA3", "PA4","PA5", "PA6","PA7", "PA8","PA9", "PA10")
cv_run <- c("RUN1", "RUN2", "RUN3", "RUN4","RUN5", "RUN6","RUN7", "RUN8","RUN9", "RUN10","Full")

## construct combination of all facets
groups <-
 as.matrix(
  expaderjugini.grid(
   models = mods,
   data_set = data_set,
   cv_run = cv_run,
   stringsAsFactors = FALSE)
 )

## load all projections we have produced
all_bin_proj_files <-
 list.files(
  path = "neuregus.derjugini",
  pattern = "_TSSbin.img$",
  full.names = TRUE,
  recursive = TRUE
 )
```

```
## current versus 2050_BC26 (removed the projections for current, 2050_BC86, 2070_BC26, 2070_BC85)
current_aderjugini_2050_BC26_proj_files <- grep(all_bin_proj_files, pattern="2050_BC26", value=T)

## current versus 2050_BC85 (removed the projections for current, 2050_BC26, 2050_BC26, 2070_BC85)
current_aderjugini_2050_BC85_proj_files <- grep(all_bin_proj_files, pattern="2050_BC85", value=T)

## current versus 2070_BC26 (removed the projections for current, 2070_BC86, 2070_BC26, 2070_BC85)
current_aderjugini_2070_BC26_proj_files <- grep(all_bin_proj_files, pattern="2070_BC26", value=T)

## current versus 2070_BC85 (removed the projections for current, 2070_BC26, 2070_BC26, 2070_BC85)
current_aderjugini_2070_BC85_proj_files <- grep(all_bin_proj_files, pattern="2070_BC85", value=T)

 ## keep only projections that match with our selected facets groups
 selected_bin_proj_files <-
  apply(
  groups, 1,
   function(x){
    proj_file <- NA
    match_tab <- sapply(x, grepl, current_aderjugini_2050_BC26_proj_files)
    match_id <- which(apply(match_tab, 1, all))
    if(length(match_id)) proj_file <- current_aderjugini_2050_BC26_proj_files[match_id]
    proj_file
   }
 )


  ## keep only projections that match with our selected facets groups
  selected_bin_proj_files <-
   apply(
   groups, 1,
    function(x){
     proj_file <- NA
     match_tab <- sapply(x, grepl, current_aderjugini_2050_BC85_proj_files)
     match_id <- which(apply(match_tab, 1, all))
     if(length(match_id)) proj_file <- current_aderjugini_2050_BC85_proj_files[match_id]
     proj_file
    }
 )

 ## keep only projections that match with our selected facets groups
 selected_bin_proj_files <-
  apply(
  groups, 1,
   function(x){
    proj_file <- NA
    match_tab <- sapply(x, grepl, current_aderjugini_2070_BC26_proj_files)
    match_id <- which(apply(match_tab, 1, all))
    if(length(match_id)) proj_file <- current_aderjugini_2070_BC26_proj_files[match_id]
    proj_file
   }
 )


  ## keep only projections that match with our selected facets groups
  selected_bin_proj_files <-
   apply(
   groups, 1,
    function(x){
     proj_file <- NA
```

```
    match_tab <- sapply(x, grepl, current_aderjugini_2070_BC85_proj_files)
    match_id <- which(apply(match_tab, 1, all))
    if(length(match_id)) proj_file <- current_aderjugini_2070_BC85_proj_files[match_id]
    proj_file
   }
 )

## remove no-matching groups
to_remove <- which(is.na(selected_bin_proj_files))
if(length(to_remove)){
 groups <- groups[-to_remove,]
 selected_bin_proj_files <- selected_bin_proj_files[-to_remove]
}

## build stack of selected projections
proj_groups <- stack(selected_bin_proj_files)

ProbDensFunc(
 initial = as.vector(ref),
 projections = raster::as.matrix(proj_groups),
 groups = t(groups),
 plothist = TRUE,
 resolution = 300,
 cvsn = FALSE
)
```

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