Original investigation

Identifying biodiversity hotspots for threatened mammal species in Iran

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ABSTRACT

Conservation biology has much more attention for biodiversity hot spots than before. In order to recognize the hotspots for Iranian terrestrial mammal species that are listed in any red list, nationally or globally, ten Species Distribution Models (SDMs) have been applied. The SDMs evaluation results based on the TSS and AUC values showed that all ten models of habitat suitability perform significantly better than the random selection for all studied species. According to the results, biodiversity hotspots for threatened mammal species are located in north, west and central of Iran, along the Zagros and Alborz mountain range. Therefore, habitats for threatened mammal species have been limited to small parts of Iran (approximately 27% of the country). These areas are severely fragmented and only 57% of them have been announced protected by the current conservation system. The suggestion is that, as the sustainability of these habitats would strongly depend on maintaining dispersal corridors to facilitate the movement of animals among the habitat fragments, conservation efforts should focus on those hotspots which are not formally protected under conservation laws.

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Introduction

For more than 60 years, global biodiversity loss have been a major international concern (Hoffmann et al., 2011; Domisch et al., 2011). Some anthropogenic factors such as introduced invasive species, land use/cover change, and climate changes threat biodiversity. The Living Planet Index (WWF and GFN, 2014) mentioned that Habitat destruction or degradation due to land use/cover change is a crucial threat in 44.8% of the vertebrate populations, when climate change could outpace land use and land cover change as the greatest threat to biodiversity in the next decades (e.g. Bellard et al., 2012). Invasive species are considerable threats for ecosystems because of their ability to extinct and eliminate wild native species (Luque et al., 2014). Obviously, losing any species, either from fauna or flora, could have drastic effects on ecosystem functions (Worm and Duffy, 2003). Therefore, preserving world's biodiversity could be accomplished by focusing on biodiversity hotspots and conservation priorities (Myers et al., 2000; Dobson et al., 2006; Schmitz et al., 2010).

In past decades, researchers considered species richness to detect biodiversity hotspots (Brummitt and Lughadha, 2003; Orme et al., 2005). However, nowadays, more debates are directed on predicting species distribution and evolutionary information. Consequently, some approaches with the combination of phylogenetic methods and geographical distribution of species have been recommended (Huang et al., 2016). Recently, the species distribution models (SDMs) have become most fundamental techniques to identify biodiversity hotspots (Platts et al., 2008; Ko et al., 2014). SDMs have been developed to predict species distribution out of presence/absence data and became important part of ecological studies (Phillips et al., 2006; Royle et al., 2012; Yackulic et al., 2013; Renner and Warton, 2013; Bosso et al., 2016; Smeraldo et al., 2017). SDMs have been ranked as one of the top five research methods in ecological sciences (Renner and Warton, 2013).

The process of protected areas selection has been mostly based on their economic value and not their on conservative importance. According to the approach, effectiveness of protected areas for the conservation of biodiversity is questionable (Rodrigues et al., 2004). Recently, the biodiversity hotspots developed using SDMs has been applied to evaluate the effectiveness of protected areas as the gap analysis (Araújo et al., 2011; Meller et al., 2014). Therefore, The objectives of this study were to (1) use species distribution models to determine the suitable habitats for threatened mammal species in Iran, (2) use an ensemble-forecasting framework to overlay the suitable habitats of threatened mammal species and assign the biodiversity hotspots, and (3) evaluate whether the current

Table 1
Threatened mammal species and results of habitat modeling (SH: suitable habitats, PSH: protected suitable habitat, suitable habitats are located in protected area, TSS: True Skill Statistic for evaluating the model, AUC: Area Under Curve).

		Acinonyx jubatus (Schreber, 1775)	Capra aegagrus (Erxleben, 1777)	Gazella Subgutturosa (Güldenstädt, 1780)	Hyaena hyaena (Linnaeus, 1758)	Lutra lutra (Linnaeus, 1758)	Otocolobus manul (Pallas, 1776)	Ovis orientalis (Gmelin, 1774)	Ovis Vignei (Blyth, 1841)	Panthera Pardus (Linnaeus, 1758)	Ursus thibetanus (Swinhoe, 1864)	Vormela peregusna (Güldenstädt, 1770)	Biodiversity hotspot
Status	National	CR	VU	VU	NT	NT	NT	VU	VU	EN	CR	VU	–
	Global	VU	VU	CR	NT	NT	NT	VU	VU	VU	VU	VU	–
Presence records		38	260	44	57	102	24	64	61	137	71	27	
SH/PSH	PSH (%)	28.44	58.76	35.33	65.61	7.29	28.86	41.51	27.03	53.09	3.07	2.47	56.65
	PSH (ha)	4823556.41	9965706.40	5992682.66	11127032.08	1235877.06	4894646.74	7040000.29	4584985.54	9003380.41	521069.92	418410.56	9607899.22
	SH (%)	4.74	31.31	15.34	27.46	5.95	15.31	19.93	16.07	28.03	4.85	12.70	26.61
	SH (ha)	7678256.03	50721138.16	24841817.61	44480721.62	9645126.23	24808351.77	32284571.52	26028256.29	45405976.21	7849507.81	20571639.61	43112370.06
TSS	SRE	0.75	0.85	0.76	0.75	0.76	0.81	0.87	0.81	0.75	0.91	0.89	–
	RF	0.82	0.89	0.73	0.75	0.76	0.86	0.87	0.87	0.821	0.81	0.91	-
	MARS	0.81	0.86	0.81	0.92	0.82	0.83	0.82	0.84	0.86	**0.94**	0.88	–
	MaxEnt	**0.89**	**0.93**	**0.92**	**0.93**	**0.95**	**0.93**	**0.92**	**0.92**	**0.96**	0.84	0.8	–
	GLM	0.88	0.74	0.75	0.76	0.77	0.86	0.72	0.74	0.75	0.83	0.82	–
	GAM	0.80	0.80	0.81	0.81	0.86	0.85	0.70	0.82	0.81	0.86	0.75	–
	FDA	0.84	0.73	0.84	0.85	0.82	0.87	0.86	0.88	0.88	0.85	0.65	–
	CART	0.77	0.83	0.86	0.8	0.92	0.90	0.72	0.78	0.90	0.85	0.89	–
	BRT	0.82	0.73	0.72	0.76	0.70	0.82	0.84	0.89	0.88	0.80	0.70	–
	ANN	0.82	0.78	0.83	0.91	0.79	0.73	0.80	0.83	0.81	0.81	0.60	–
AUC	SRE	0.72	0.85	0.76	0.75	0.76	0.81	0.80	0.80	0.705	0.91	0.80	–
	RF	0.82	0.89	0.79	0.75	0.76	0.86	0.87	0.878	0.821	0.81	**0.91**	-
	MARS	0.81	0.86	**0.91**	0.92	0.82	0.85	0.84	0.83	0.89	0.80	–
	MaxEnt	**0.92**	**0.92**	0.82	**0.93**	**0.96**	**0.92**	**0.91**	**0.91**	0.81	**0.94**	0.80	–
	GLM	0.88	0.74	0.75	0.76	0.77	0.83	0.72	0.74	0.75	0.83	0.82	–
	GAM	0.80	0.80	0.81	0.86	0.85	0.80	0.82	0.81	0.82	0.86	0.85	–
	FDA	0.86	0.73	0.84	0.85	0.86	0.87	0.86	0.87	0.82	0.82	0.69	–
	CART	0.89	0.87	0.85	0.89	0.95	0.90	0.75	0.73	**0.92**	0.82	0.81	–
	BRT	0.88	0.74	0.78	0.73	0.72	0.88	0.87	0.86	0.86	0.81	0.82	–
	ANN	0.88	0.77	0.81	0.90	0.74	0.74	0.81	0.82	0.87	0.85	0.84	–

The best model with highest TSS and AUC value is in bold.