THE HERPETOFAUNA OF BOQUEIRÃO DA ONÇA: AN IMPORTANT NATURAL HERITAGE SITE IN THE CAATINGA OF BRAZIL

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Table S1. Comparison of the number of species found between inventories of herpetofauna conducted in the Caatinga domain. Abbreviations for herpetofauna are A = anurans, L-A = lizards + amphisbaenians, S = snakes, Ch = chelonians, Cr = crocodilians, and Ca = caecilians. Abbreviations for Brazilian states BA = Bahia, PI = Piauí, PE = Pernambuco, RN = Rio Grande do Norte, CE = Ceará, PB = Paraíba, MA = Maranhão. N/I = Not Informed; *Specific effort not informed. Abbreviation for Methods: AES = acoustic encounter survey, CPS = compilation of previous studies, CTP = collections by third parties, ER = encounters on road, FT = funnel traps, FRP = fauna-rescue program, GT = glue trap, LC = local collectors, OE = occasional encounters, PT = pitfall traps, VES = visual encounter survey. Abbreviation for Domain: Ca = Caatinga, Ce = Cerrado, AF = Atlantic Forest, Am = Amazonia.

Locality	A	L-A	S	Ch	Cr	Ca	Total	Duration	Methods	Size (ha)	Domain	Reference
Boqueirão da Onça (BA)	24	24	27	1	0	0	76	64 d	PT, VES, AES, ER, FRP, OE	505,000	Ca	This study
Raso da Catarina (BA)	21	21	11	0	0	0	53	12 mo*	VES, AES, PT, GT	99,772	Ca	Garda et al. (2013)
Serra da Capivara (PI)	7	17	11	1	0	1	37	30 d	VES, PT, FT, GT	91,848	Ca	Cavalcanti et al. (2014)
Catimbau National Park (PE)	21	25	11	1	0	0	59	30 d	VES, PT, GT	62,000	Ca	Pedrosa et al. (2014)
Chapada Diamantina (BA)	31	19	23	2	0	0	75	30 d	VES, ER, AES, PT, GT	N/I	Ca/ Ce/ AF	Magalhães et al. (2015)
Seridó Ecological Station (RN)	19	13	8	1	0	0	41	30 d	VES, PT, GT	1,166	Ca	Caldas et al. (2016)
Ubajara National Park (CE)	25	19	23	2	0	1	67	84 d	PT, VES	6,288	Ca	de Castro et al. (2019)
João Câmara (RN)	3	10	8	0	0	0	21	55 d	FRP	1,729	Ca	Calixto and Morato (2017)
Serra das Confusões National Park (PI)	18	25	20	2	0	1	66	32 d	PT, VES	500,000	Ca/Ce	Dal Vechio et al. (2016)
Serra das Confusões National Park and Serra Vermelha (PI)	28	31	29	4	1	1	94	34, 28 d	CPS, PT, VES, GT	824,000 and N/I	Ca/Ce	Marques et al. (2023)
Betânia and Floresta (PE)	19	10	9	3	0	0	41	21 d	PT, VES	N/I	Ca	Borges-Nojosa and Santos (2005)
Serra das Almas (CE-PI)	18	20	6	0	1	0	45	24 d	PT, VES	N/I	Ca	Borges-Nojosa and Cascon (2005)

Serrita (PE)	23	16	12	2	1	0	54	11 mo*	PT, VES, CTP	3,000	Ca	Pereira et al. (2015)
Planalto da Ibiapaba (CE)	37	33	45	4	1	1	121	24 mo*	PT, VES, AES, ER, OE	536,000	Ca	Loebmann and Haddad (2010)
Nordestina (BA)	13	17	16	3	0	0	49	260 d	PT, VES	664,710	Ca	Leite et al. (2019)
Farias Brito (CE)	23	18	20	2	0	0	63	900 h/5 searches	VES	N/I	Ca	Oliveira et al. (2021)

Table S2. Taxonomic diversity results from Hill numbers of orders q=0 (Species richness), q = 1 (Shannon diversity) and q = 2 (Simpson Diversity) for each assemblage. The observed and expected (estimator) diversity were calculated summing the sampling effort (abundances) for each method applied for each assemblage. s.e. = standard error; LCL = lower confidence interval; UCL = upper confidence interval.

Assemblage	Diversity	Observed	Estimator	s.e.	LCL	UCL
Amphibians	Species richness	15.000	15.249	2.170	15.000	19.502
	Shannon Diversity	9.202	9.413	0.430	8.569	10.256
	Simpson Diversity	7.345	7.490	0.422	6.662	8.317
Lizards	Species richness	19.000	21.249	4.278	19.000	29.634
	Shannon Diversity	3.809	3.822	0.096	3.635	4.010
	Simpson Diversity	2.461	2.462	0.059	2.347	2.577
Snakes	Species richness	22.000	29.925	6.996	22.000	43.636
	Shannon Diversity	16.846	19.353	1.739	15.944	22.762
	Simpson Diversity	13.811	15.709	1.804	12.174	19.245

Table S3. Taxonomic diversity results from Hill numbers of orders q = 0 (Species richness), q = 1 (Shannon diversity) and q = 2 (Simpson diversity) for each sampled point for AES method. s.e. = standard error; LCL = lower confidence interval; UCL = upper confidence interval.

Assemblage	Diversity	Observed	Estimator	s.e.	LCL	UCL
	Species richness	4.000	4.478	1.523	4.000	7.463
AES01	Shannon diversity	2.311	2.521	0.575	1.394	3.648
	Simpson diversity	1.746	1.807	0.446	0.934	2.681
	Species richness	9.000	9.496	1.548	9.000	12.529
AES02	Shannon diversity	4.638	4.816	0.441	3.952	5.680
	Simpson diversity	3.200	3.260	0.369	2.537	3.983
	Species richness	8.000	8.000	0.684	8.000	9.341
AES03	Shannon diversity	6.604	6.943	0.473	6.015	7.871
	Simpson diversity	5.941	6.379	0.610	5.183	7.574
	Species richness	9.000	9.495	1.540	9.000	12.514
AES04	Shannon diversity	5.219	5.465	0.544	4.400	6.530
	Simpson diversity	3.700	3.805	0.470	2.883	4.726
	Species richness	3.000	3.000	0.331	3.000	3.649
AES05	Shannon diversity	2.730	2.945	0.366	2.228	3.662
	Simpson diversity	2.579	2.935	0.486	1.983	3.888

Table S4. Taxonomic diversity results from Hill numbers of orders q = 0 (Species richness), q = 1 (Shannon diversity) and q = 2 (Simpson diversity) for each sampled point for PT method. s.e. = standard error; LCL = lower confidence interval; UCL = upper confidence interval.

Assemblage	Diversity	Observed	Estimator	s.e.	LCL	UCL
	Species richness	10.000	11.994	2.618	10.000	17.125
PT01	Shannon diversity	3.435	3.500	0.235	3.040	3.961
	Simpson diversity	2.238	2.247	0.145	1.962	2.531
	Species richness	7.000	7.498	1.217	7.000	9.884
PT02	Shannon diversity	3.461	3.509	0.197	3.122	3.896
	Simpson diversity	2.681	2.699	0.174	2.358	3.040
	Species richness	10.000	11.493	3.245	10.000	17.853
PT03	Shannon diversity	2.815	2.898	0.216	2.474	3.322
	Simpson diversity	2.124	2.135	0.124	1.893	2.378
	Species richness	7.000	7.000	1.069	7.000	9.095
PT04	Shannon diversity	2.062	2.082	0.121	1.846	2.319
	Simpson diversity	1.579	1.582	0.076	1.432	1.731
	Species richness	8.000	9.989	1.908	8.000	13.730
PT05	Shannon diversity	2.823	2.898	0.230	2.447	3.350
	Simpson diversity	2.059	2.070	0.144	1.788	2.353
	Species richness	9.000	9.249	2.401	9.000	13.955
PT06	Shannon diversity	2.740	2.801	0.301	2.211	3.391
	Simpson diversity	1.860	1.868	0.160	1.555	2.181
PT07	Species richness	9.000	26.950	11.346	9.000	49.188

	Shannon diversity	2.032	2.097	0.119	1.865	2.330
	Simpson diversity	1.698	1.702	0.067	1.570	1.833
	Species richness	5.000	5.249	1.669	5.000	8.521
PT08	Shannon diversity	2.032	2.047	0.082	1.887	2.207
	Simpson diversity	1.806	1.811	0.066	1.682	1.940
	Species richness	8.000	8.664	3.325	8.000	15.182
PT09	Shannon diversity	2.486	2.529	0.127	2.280	2.778
	Simpson diversity	2.152	2.162	0.064	2.036	2.289
	Species richness	7.000	16.932	5.645	7.000	27.996
PT10	Shannon diversity	2.395	2.530	0.246	2.048	3.013
	Simpson diversity	2.142	2.159	0.085	1.993	2.325

Table S5. Taxonomic diversity results from Hill numbers of orders q = 0 (Species richness), q = 1 (Shannon diversity) and q = 2 (Simpson diversity) for each sampled point for VES method. s.e. = standard error; LCL = lower confidence interval; UCL = upper confidence interval.

Assemblage	Diversity	Observed	Estimator	s.e.	LCL	UCL
	Species richness	7.000	9.927	1.672	7.000	13.204
VES01	Shannon diversity	4.886	5.524	0.546	4.453	6.595
	Simpson diversity	4.234	4.607	0.482	3.661	5.552
	Species richness	7.000	12.714	5.848	7.000	24.176
VES02	Shannon diversity	4.829	6.548	2.003	2.623	10.473
	Simpson diversity	3.769	4.375	1.107	2.206	6.544
	Species richness	7.000	14.579	5.570	7.000	25.496
VES03	Shannon diversity	4.898	7.073	2.459	2.253	11.892
	Simpson diversity	3.882	4.622	1.589	1.507	7.736
	Species richness	4.000	4.450	1.812	4.000	8.001
VES04	Shannon diversity	3.596	4.390	1.305	1.833	6.948
	Simpson diversity	3.333	4.500	1.482	1.596	7.404
	Species richness	5.000	5.156	2.347	5.000	9.756
VES05	Shannon diversity	3.750	4.384	1.161	2.108	6.659
	Simpson diversity	2.922	3.387	1.207	1.021	5.753
	Species richness	11.000	13.626	5.007	11.000	23.439
VES06	Shannon diversity	5.975	6.668	0.897	4.910	8.425
	Simpson diversity	4.472	4.725	0.603	3.543	5.906
VES07	Species richness	6.000	6.971	0.574	6.000	8.095
	Shannon diversity	4.748	5.233	0.382	4.485	5.981

	Simpson diversity	4.391	4.877	0.479	3.938	5.817
	Species richness	6.000	8.100	4.453	6.000	16.827
VES08	Shannon diversity	4.113	5.452	2.257	1.029	9.875
	Simpson diversity	3.000	3.500	1.643	0.280	6.720
	Species richness	5.000	5.000	0.677	5.000	6.327
VES09	Shannon diversity	4.109	4.411	0.407	3.612	5.209
	Simpson diversity	3.719	4.104	0.510	3.105	5.103
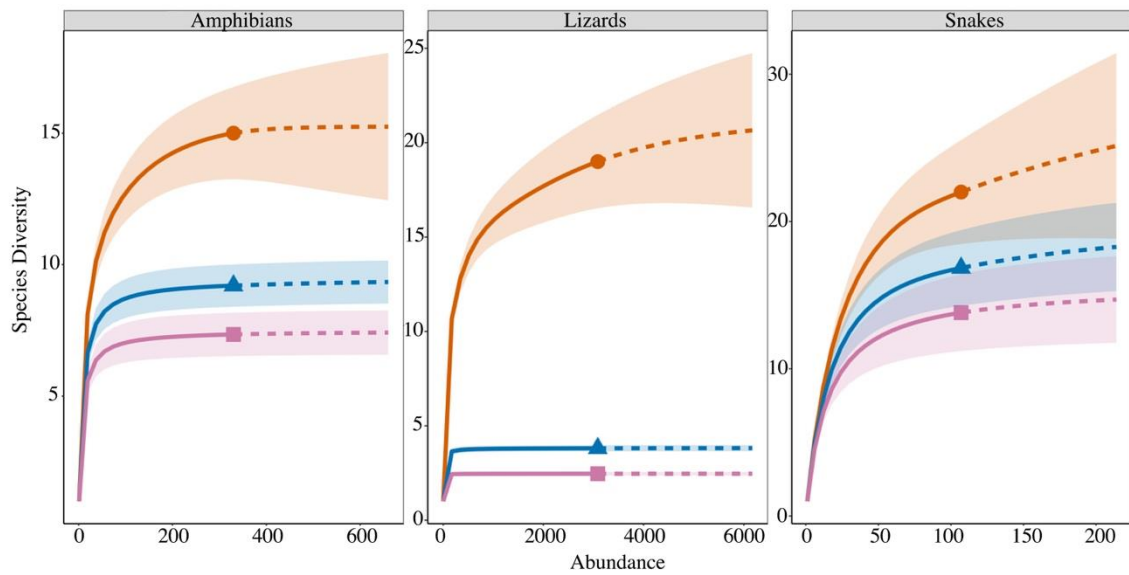
Figure S1. Hill numbers of rarefaction curves for amphibians, lizards, and snakes sampled at the Boqueirão da Onça, state of Bahia, northeastern Brazil. Orange lines represent the species richness (q = 0), blue lines represent the Shannon diversity (q = 1), and the purple lines represent the Simpson diversity (q = 2). Continuous line is the observed diversity, and the dashed line represents the expected diversity. Shaded areas are the confidence intervals.
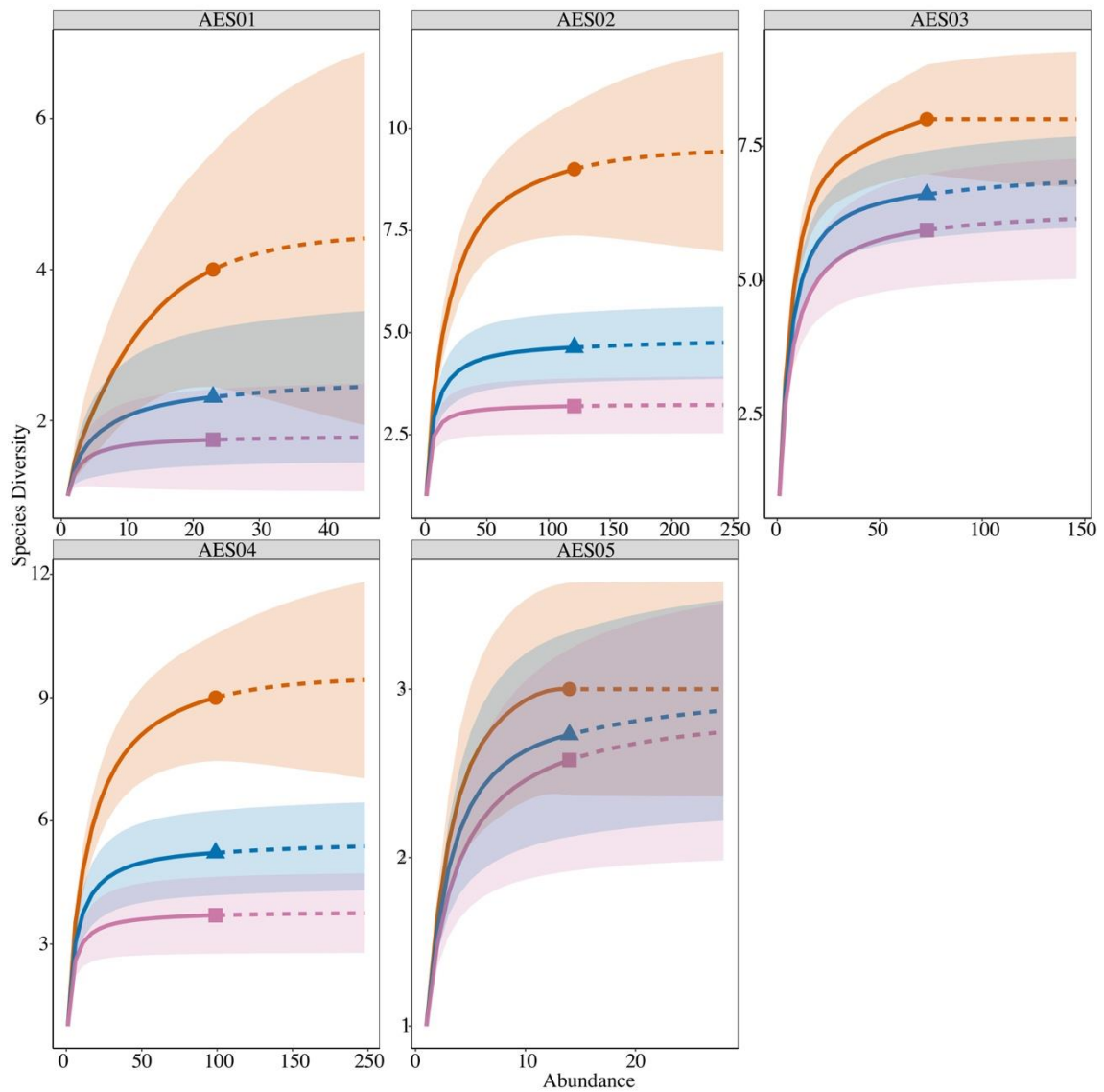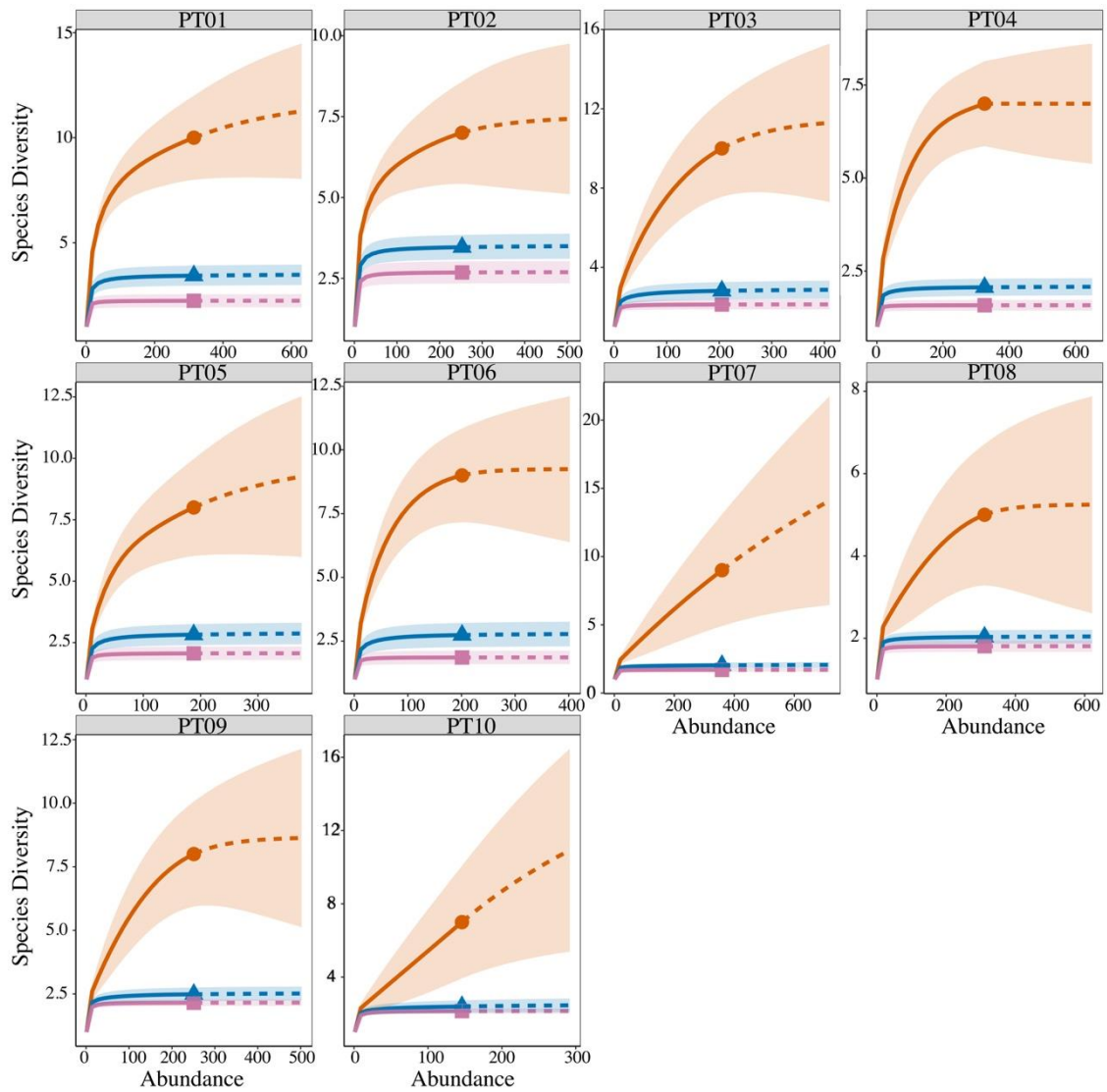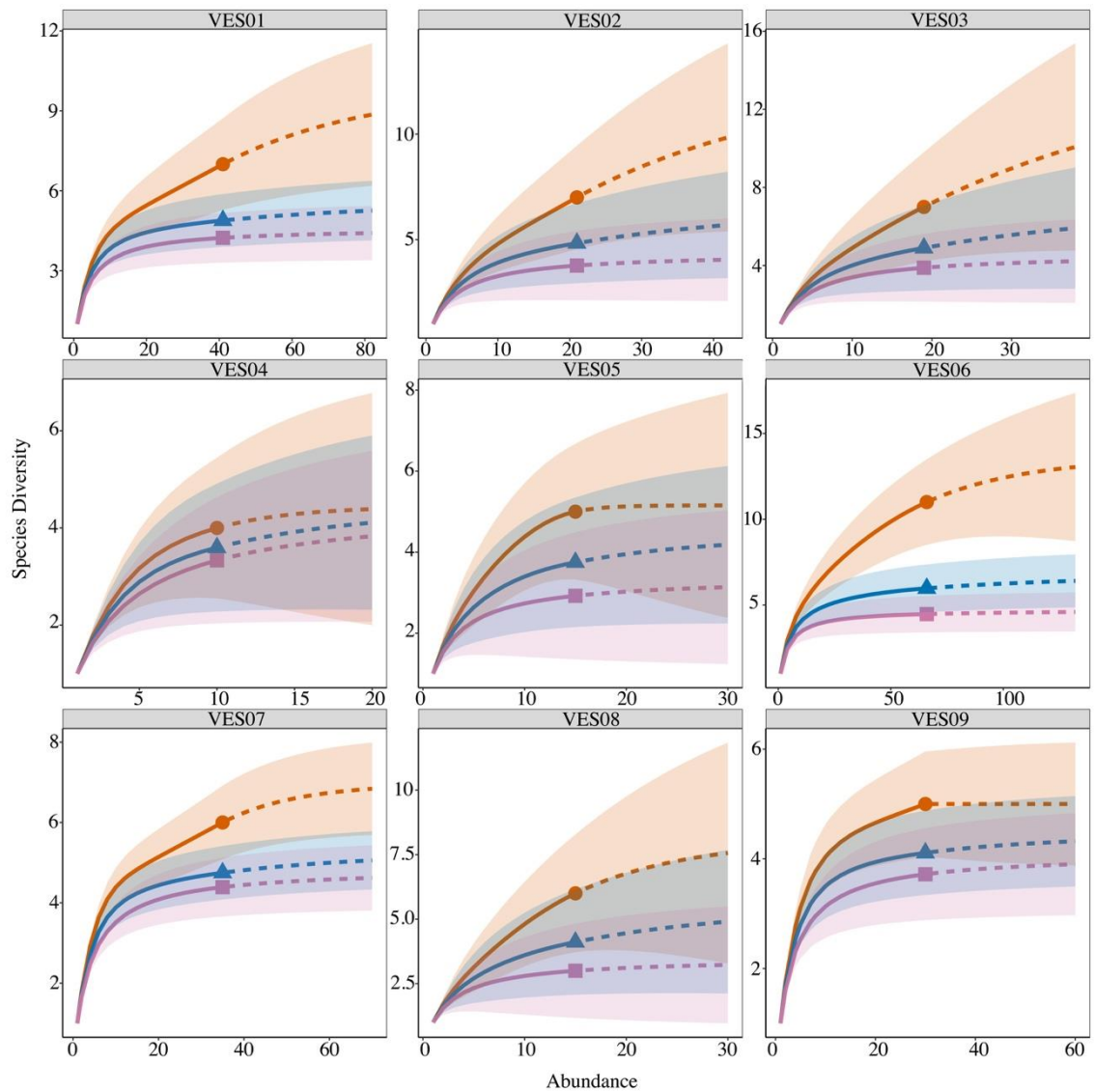
Figure S2. Hill numbers of rarefaction curves for sampled areas by AES method at the Boqueirão da Onça, state of Bahia, northeastern Brazil. Orange lines represent the species richness (q = 0), blue lines represent the Shannon diversity (q = 1), and the purple lines represent the Simpson diversity (q = 2). Continuous line is the observed diversity, and the dashed line represents the expected diversity. Shaded areas are the confidence intervals.

Figure S3. Hill numbers of rarefaction curves for sampled areas by PT method at the Boqueirão da Onça, state of Bahia, northeastern Brazil. Orange lines represent the species richness (q = 0), blue lines represent the Shannon diversity (q = 1), and the purple lines represent the Simpson diversity (q = 2). Continuous line is the observed diversity, and the dashed line represents the expected diversity. Shaded areas are the confidence intervals.

Figure S4. Hill numbers of rarefaction curves for sampled areas by VES method at the Boqueirão da Onça, state of Bahia, northeastern Brazil. Orange lines represent the species richness (q = 0), blue lines represent the Shannon diversity (q = 1), and the purple lines represent the Simpson diversity (q = 2). Continuous line is the observed diversity, and the dashed line represents the expected diversity. Shaded areas are the confidence intervals.
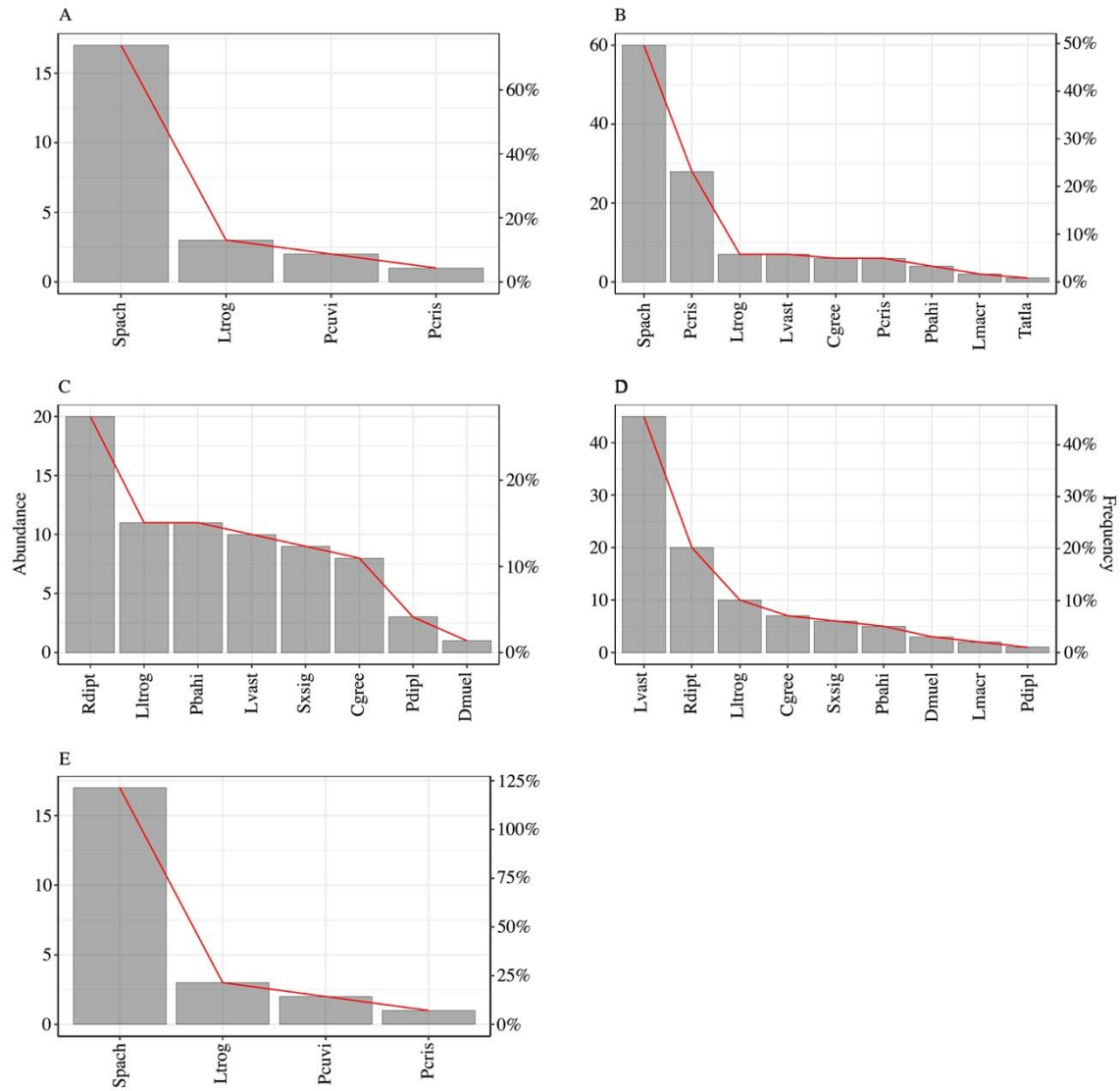
Figure S5. Amphibians' abundance for each sampled area by AES method at the Boqueirão da Onça, state of Bahia, northeastern Brazil. (A) AES01, (B) AES02, (C) AES03, (D) AES04 and (E) AES05. Grey bars represent the total abundance (primary Y axis), and the red lines represent the relative abundance (secondary Y axis) of amphibian species. *Corythomantis greeningi* (Cgree), *Dermatonotus muelleri* (Dmuel), *Leptodactylus macrosternum* (Lmacr), *Leptodactylus troglodytes* (Ltrog), *Leptodactylus vastus* (Lvast), *Phyllomedusa bahiana* (Pbahi), *Physalaemus cicada* (Pcica), *Physalaemus cuvieri* (Pcuvi), *Pleurodema diplolister* (Pdipl), *Proceratophrys cristiceps*

(Pcris), *Rhinella diptycha* (Rdipt), *Rhinella granulosa* (Rgran), *Scinax sp.* (Spach),

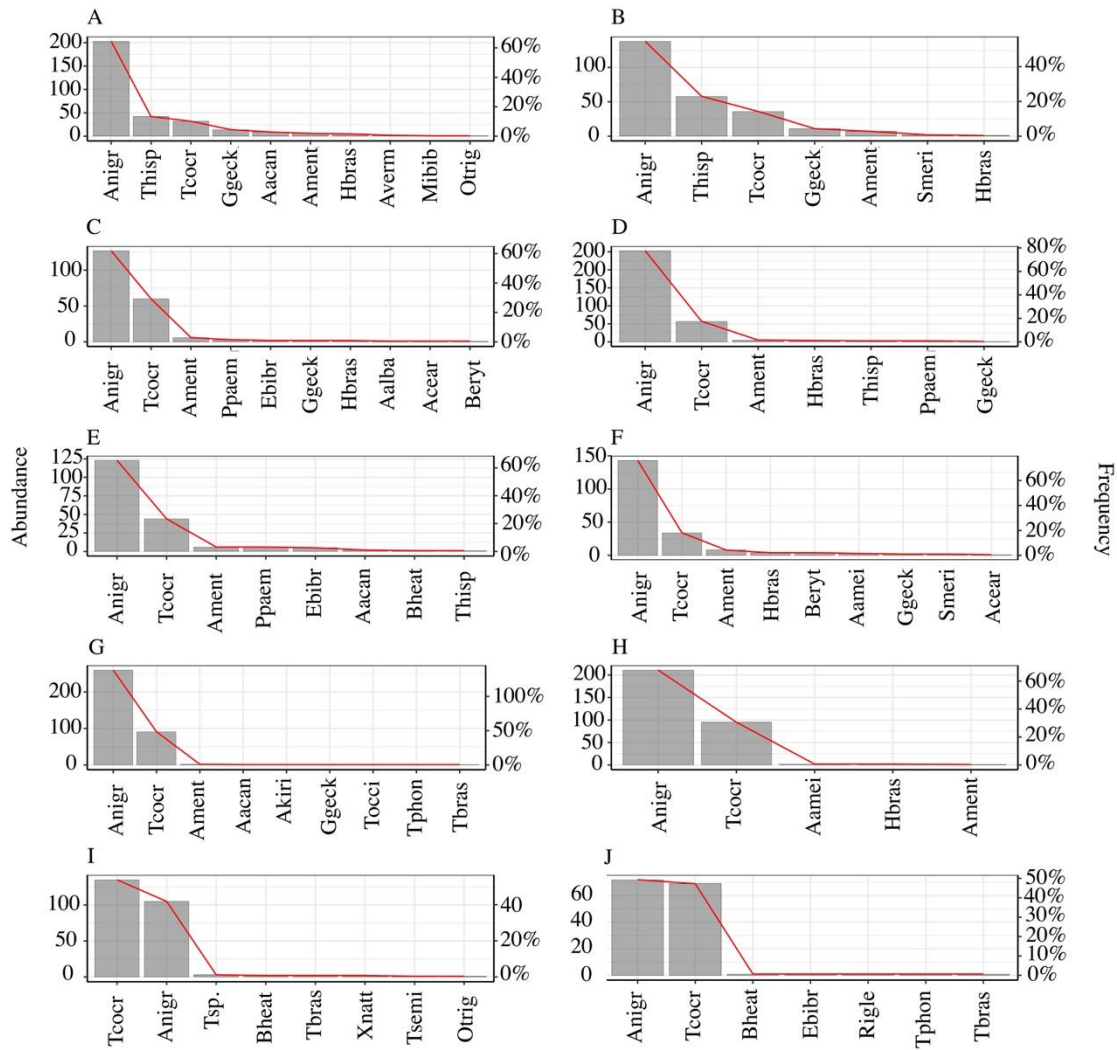*Scinax x-signatus* (Sxsig), *Trachycephalus atlas* (Tatla).

Figure S6. Reptiles' abundance for each sampled area by PT method at the Boqueirão da Onça, state of Bahia, northeastern Brazil. (A) PT01, (B) PT02, (C) PT03, (D) PT04, (E) PT05, (F) PT06, (G) PT07, (H) PT08, (I) PT09 and (J) PT10. Grey bars represent the total abundance (primary Y axis), and the red lines represent the relative abundance (secondary Y axis) of reptile's species. *Acratosaura mentalis* (Ament), *Ameiva ameiva* (Aamei), *Ameivula nigrigula* (Anigr), *Amphisbaena acangaoba* (Aacan), *Amphisbaena alba* (Aalba), *Amphisbaena kiriri* (Akiri), *Amphisbaena vermicularis* (Averm), *Apostolepis cearensis* (Acear), *Boiruna sertaneja* (Bsert), *Bothrops erythromelas* (Beryt), *Brasiliscincus heathi* (Bheat), *Enyalius bibronii* (Ebibr), *Epicrates assisi* (Eassi), *Gymnodactylus geckoides* (Ggeck), *Hemidactylus brasilianus* (Hbras),

Leptodeira annulata (Lannu), *Micrurus ibiboboca* (Mibib), *Oxybelis aeneus* (Oaene),

Oxyrhopus trigeminus (Otrig), *Phyllopezus pollicaris* (Ppoll), *Pseudoboa nigra* (Pnigr),

Psilops paeminosus (Ppaem), *Rodriguesophis iglesiasi* (Rigle), *Salvator merianae*

(Smeri), *Taeniophallus occipitalis* (Tocci), *Tantilla boipiranga* (Tsp.), *Thamnodynastes*

phoenix (Tphoe), *Trilepida brasiliensis* (Tbras), *Tropidurus cocorobensis* (Tcoco),

Tropidurus hispidus (Thisp), *Tropidurus semitaeniatus* (Tsemi), *Xenodon nattereri*
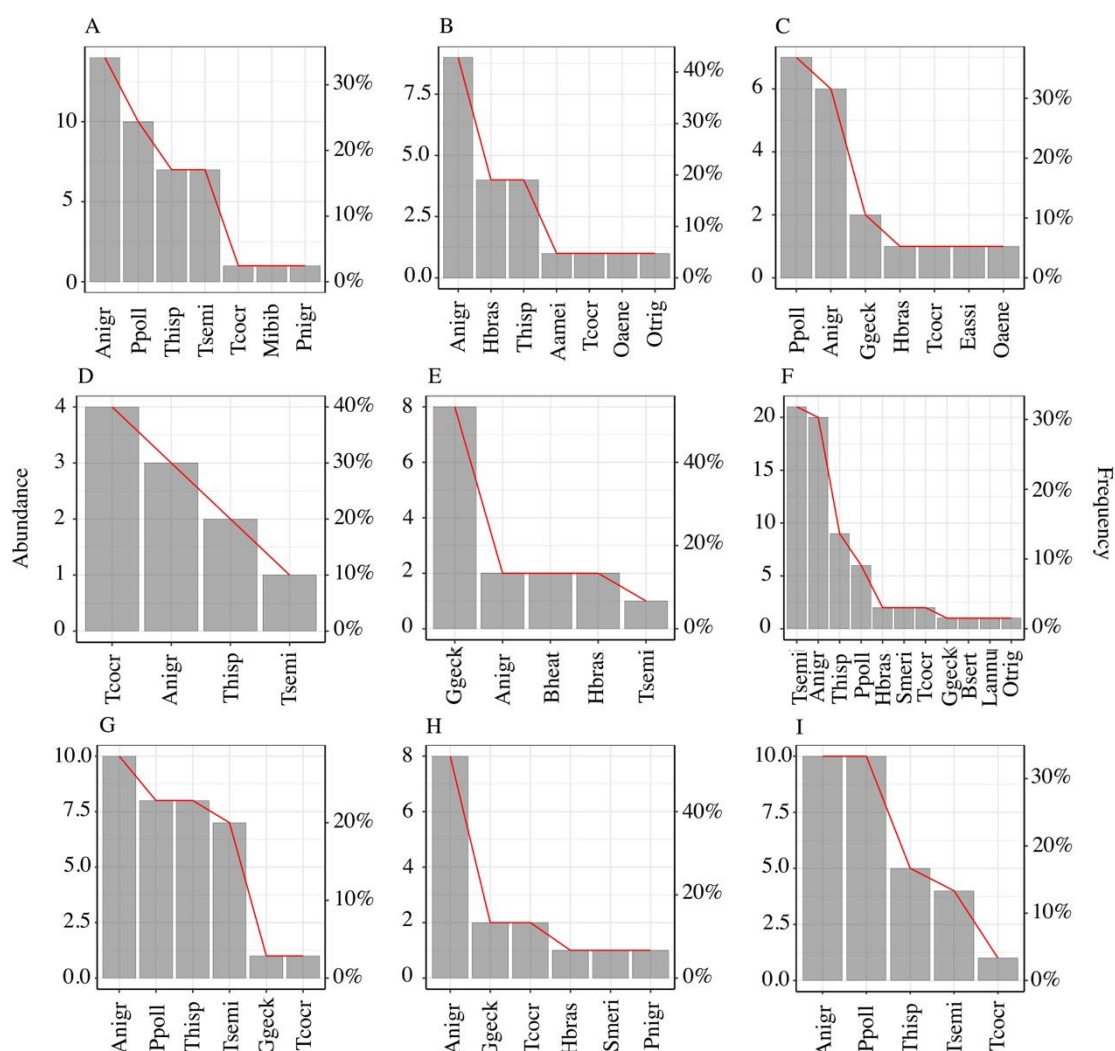
(Xnatt).

Figure S7. Reptiles' abundance for each sampled area by VES method at the Boqueirão

da Onça, state of Bahia, northeastern Brazil. (A) VES01, (B) VES02, (C) VES03, (D)

VES04, (E) VES05, (F) VES06, (G) VES07, (H) VES08, (J) VES09. Grey bars represent the total abundance (primary Y axis), and the red lines represent the relative abundance (secondary Y axis) of reptile's species. *Acratosaura mentalis* (Ament), *Ameiva ameiva* (Aamei), *Ameivula nigrigula* (Anigr), *Amphisbaena acangaoba* (Aacan), *Amphisbaena alba* (Aalba), *Amphisbaena kiriri* (Akiri), *Amphisbaena vermicularis* (Averm), *Apostolepis cearensis* (Acear), *Boiruna sertaneja* (Bsert), *Bothrops erythromelas* (Beryt), *Brasiliscincus heathi* (Bheat), *Enyalius bibronii* (Ebibr), *Epicrates assisi* (Eassi), *Gymnodactylus geckoides* (Ggeck), *Hemidactylus brasilianus* (Hbras), *Leptodeira annulata* (Lannu), *Micrurus ibiboboca* (Mibib), *Oxybelis aeneus* (Oaene), *Oxyrhopus trigeminus* (Otrig), *Phyllopezus pollicaris* (Ppoll), *Pseudoboa nigra* (Pnigr), *Psilops paeminosus* (Ppaem), *Rodriguesophis iglesiasi* (Rigle), *Salvator merianae* (Smeri), *Taeniophallus occipitalis* (Tocci), *Tantilla boipiranga* (Tsp.), *Thamnodynastes phoenix* (Tphoe), *Trilepida brasiliensis* (Tbras), *Tropidurus cocorobensis* (Tcoco), *Tropidurus hispidus* (Thisp), *Tropidurus semitaeniatus* (Tsemi), *Xenodon nattereri* (Xnatt).