

APPENDIX A: SUPPLEMENTARY MATERIAL

Patch Connectivity Metrics

We considered four connectivity variables from a previous analysis of bighorn sheep population connectivity in the Mojave Desert (Creech et al., 2014) as potential covariates in the regression of genetic diversity on NDVI. Creech et al. constructed network models of genetic connectivity (the potential for gene flow among populations) and demographic connectivity (the potential for colonization of empty habitat patches) using a genetic-based landscape resistance model (Epps et al. 2007) to estimate the strength of connections between populations in the networks. Bighorn sheep exhibit sex-biased dispersal, with males moving between patches more frequently and over greater distances than females; thus, genetic and demographic connectivity are not equivalent. Genetic connectivity is limited by the maximum effective dispersal distance (ED_{MAX}) of males, whereas demographic connectivity is limited by the shorter ED_{MAX} of females, as both sexes must disperse in order to colonize an empty habitat patch.

Two network metrics were then calculated, in each network, to characterize the degree to which each patch is connected to other network patches:

- 1) Weighted closeness (WC), which estimates how close a focal patch is to every other patch in a network and accounts for differences in the strength of connections among patches. WC reflects the long-term potential for transfer of genes or individuals to and from the focal patch because it considers all connections, including those with distant patches that would require numerous dispersal steps.
- 2) Effectively connected patches (ECP), which is simply the number of patches connected to a single focal patch along a path (single or multi-step) of effective distance $< ED_{MAX}$. ECP

describes the short-term potential for genetic or demographic connectivity between a focal patch and neighboring patches.

Thus, we used four variables to characterize patch connectivity: demographic network WC, genetic network WC, demographic network ECP, and genetic network ECP. We calculated the correlation between each of these variables and our genetic diversity indices, allelic richness (A_r) and expected heterozygosity (H_e). Demographic WC was most highly correlated with both A_r and H_e (Table A.1); therefore, we used it as our patch connectivity variable in the analysis of associations between NDVI and genetic diversity.

SUPPLEMENTARY TABLES

Table A.1. Additional information on location, size, and sampling intensity for habitat patches included in the analysis.

Habitat patch/ abbreviation	UTM coordinates¹	Patch area (km²)	# FN samples	# total genotypes	# females genotyped	# males genotyped
Cady Mountains (CAD)	558706 E, 3866694 N	280.02	0	12	2	10
Chemehuevi Mountains (CHE)	726380 E, 3833368 N	250.16	0	7	2	5
Clark Mountains/ S. Spring Range (CSS)	632064 E, 3942062	300.11	0	12	7	5
Clipper Mountains (CLI)	646173, E, 3845181 N	124.57	0	16	7	9
E. Chocolate Mountains (ECH)	714111 E, 3655250 N	283.84	0	4	2	2
Eagle Mountains (EMO)	629177 E, 3737750 N	352.14	0	31	11	20
Granite Mountains (GRA)	616799 E, 3853037 N	171.10	0	21	6	15
Iron Mountains (IRO)	665602 E, 3781324 N	97.47	0	11	4	7
Kingston Mountains/ Mesquite Range (KME)	606266 E, 3956341 N	637.53	0	5	3	2
Little San Bernardino Mountains (LSB)	559311 E, 3761688 N	357.54	0	12	6	6
Marble Mountains (MAR)	629034 E, 3835474 N	112.02	115	29	21	8
Newberry Mountains/ Ord Mountains (NOR)	527329 E, 3842314 N	406.26	0	15	12	3
Old Dad Peak/Kelso Mountains/ Marl Mountains/ Club Peak/ Indian Spring (OKM)	610459 E, 3888605 N	433.17	115	37	20	17
Old Woman Mountains (OWO)	666874 E, 3816631 N	341.60	0	16	15	11
Orocochia Mountains (ORO)	611026 E, 3715465 N	323.58	15	18	10	8
Palen Mountains/ Riverside Granite Mountains (PRG)	677337 E, 3748604 N	264.53	0	10	7	3
Piute Range/ Castle Peaks/ Castle Mountains (PCC)	674581 E, 3906940 N	306.08	0	13	10	3
Providence Mountains (PRO)	632555 E, 3866434 N	186.12	0	20	9	11

Queen Mountain (QUE)	580064 E, 3771509 N	136.43	0	11	11	0
Sheephole Mountains (SHE)	622644 E, 3785939 N	78.89	15	0	0	0
South Bristol Mountains (SBR)	614693 E, 3833663 N	96.27	15	14	7	7
Turtle Mountains (TUR)	700184 E, 3797149 N	421.80	0	14	11	3
Woods Mountains/ Hackberry Mountains (WHA)	657277 E, 3880375 N	111.27	0	23	5	18

Table A.2. Pearson's correlation coefficient (R) between connectivity metrics and genetic diversity indices.

Genetic diversity index	Correlation with			
	Demographic WC	Genetic WC	Demographic ECP	Genetic ECP
A_r	0.64	0.62	0.58	0.44
H_e	0.60	0.59	0.55	0.39

Table A.3. Pearson correlation coefficient (R) between fecal nitrogen (FN) and each of three summary statistics of the Normalized Difference Vegetation Index (NDVI) in five Mojave Desert bighorn sheep populations. The summary statistic with highest correlation for each population is shown in bold. NDVI summary statistics were log-transformed and FN was exponentiated to linearize the relationship. Median NDVI was used as the NDVI summary statistic in subsequent analyses because it had the highest correlation for the majority of individual populations and for pooled data.

Population	N	Correlation with fecal nitrogen		
		Median NDVI	90 th percentile NDVI	Maximum NDVI
Marble Mountains	115	0.641	0.646	0.649
Old Dad Peak	115	0.675	0.644	0.641
Orocopia Mountains	15	0.129	-0.004	0.070
South Bristol Mountains	15	0.720	0.706	0.545
Sheephole Mountains	15	0.753	0.768	0.754
All populations pooled	275	0.511	0.505	0.4899

Table A.4. Models of relationship between genetic diversity and long-term NDVI for 22 bighorn sheep populations in the Mojave Desert, with Gaussian spatial correlation structure to account for spatial autocorrelation of genetic diversity among populations.

Response	Covariates	P^a	$Pseudo^b R^2$
A_r	median INDVI ^c	0.009	0.69
	(median INDVI) ²	0.018	
	log(connectivity ^d)	<0.001	
A_r	log(connectivity)	0.001	0.45
A_r	median INDVI	0.124	0.35
	(median INDVI) ²	0.307	
H_e	median INDVI	0.045	0.62
	(median INDVI) ²	0.074	
	log(connectivity)	0.003	
H_e	log(connectivity)	0.002	0.42
H_e	median INDVI	0.140	0.32
	(median INDVI) ²	0.306	

^a Significance from F -test of $\beta=0$ for given covariate

^b Efron's (1978) pseudo- R^2 , a measure of the proportion of variability explained by the model; analogous to traditional R^2 but for generalized least squares

^c Median of growing-season integrated NDVI values from 2001 through 2011

^d Demographic weighted closeness (Appendix A), a network-based measure of population connectivity

SUPPLEMENTARY FIGURES

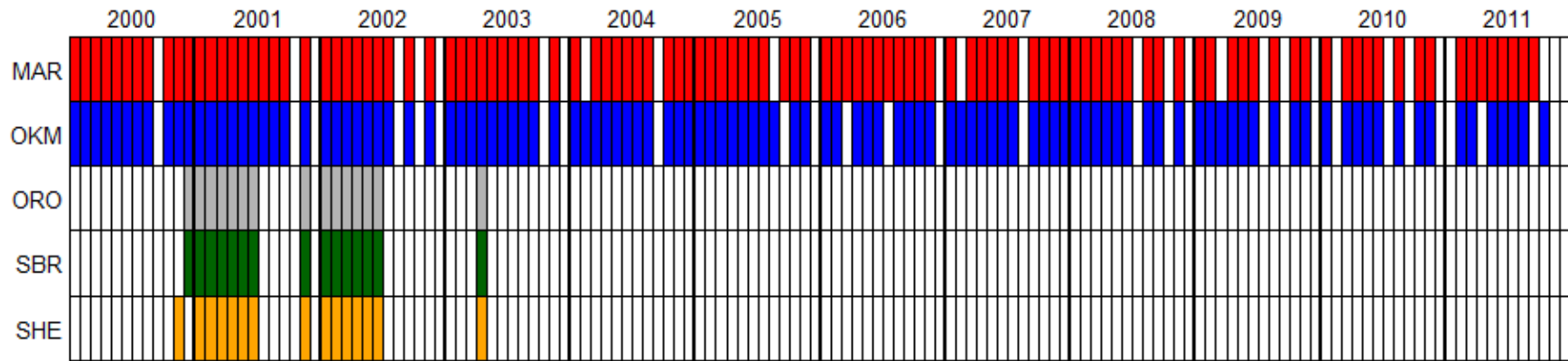


Figure A.1. Availability of fecal nitrogen data for five bighorn sheep habitat patches in the Mojave Desert: Marble Mountains (MAR), Old Dad Peak (OKM), Orocopia Mountains (ORO), South Bristol Mountains (SBR), and Sheephole Mountains (SHE). Rows represent habitat patches and columns represent chronologically ordered months between January 2000 and December 2011. Colored grid cells represent months in which fecal nitrogen was sampled for a given patch. Thicker black vertical lines separate years.

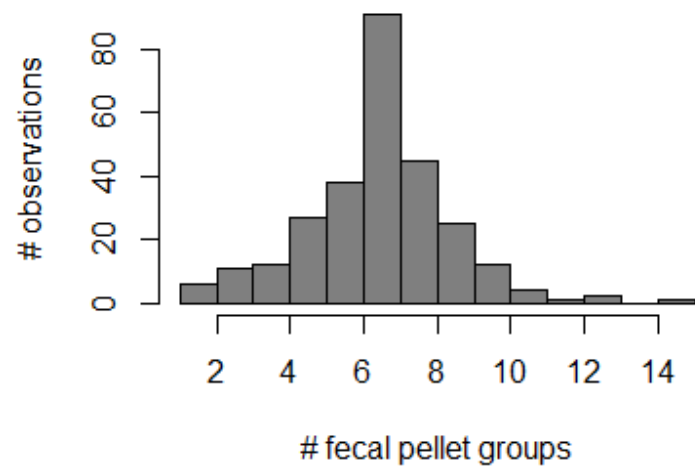


Figure A.2. Distribution of number of fecal pellet groups composited per FN observation.

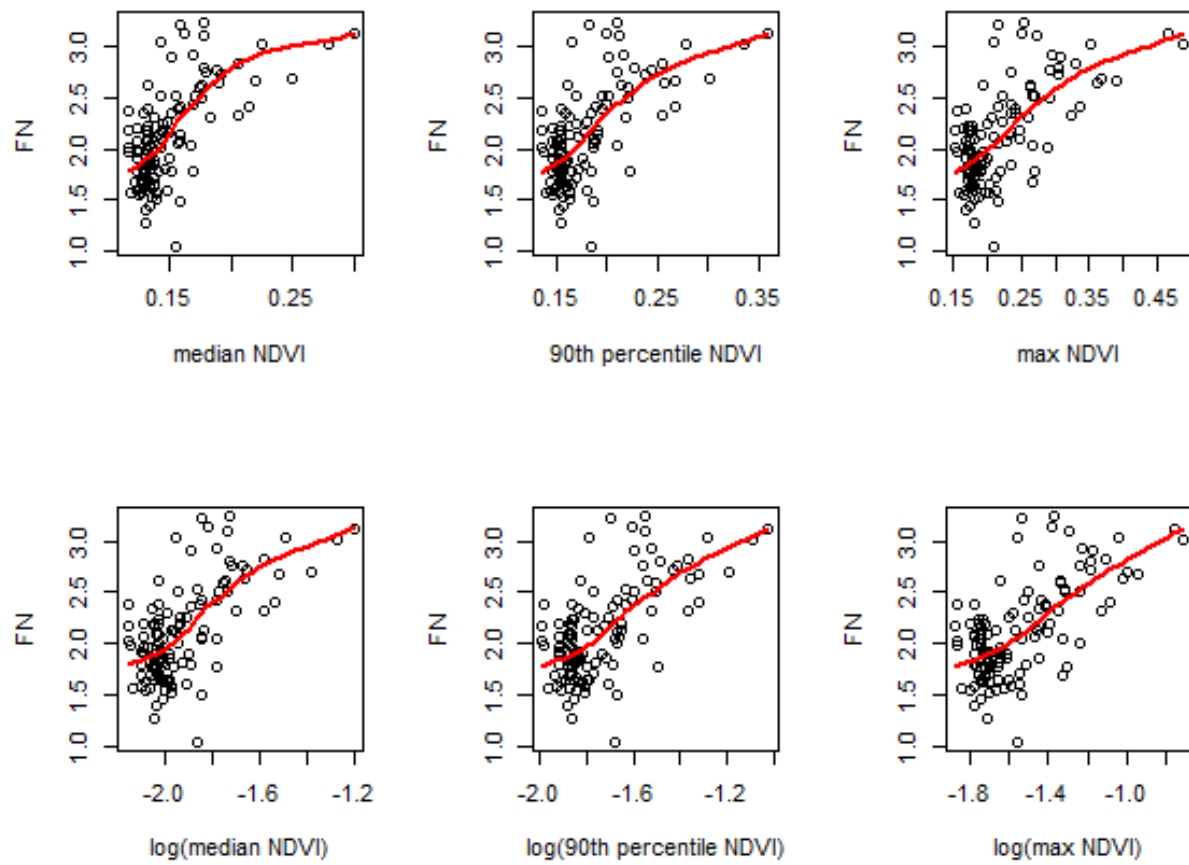


Fig. A.3. Comparison of the relationship between FN and untransformed NDVI summary statistics (top row) or log-transformed NDVI summary statistics (bottom row) for the Marble Mountains (MAR) population. Red lines are smooth curves fitted by loess.

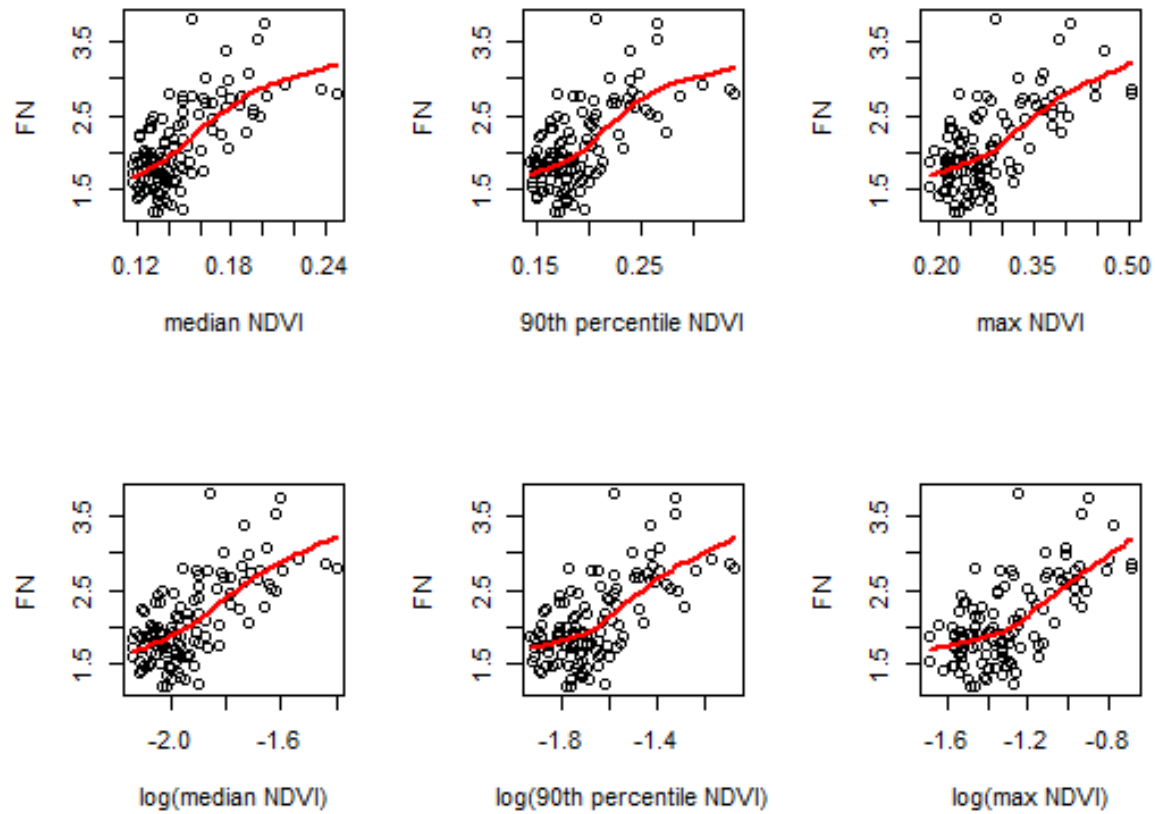


Fig. A.4. Comparison of the relationship between FN and untransformed NDVI summary statistics (top row) or log-transformed NDVI summary statistics (bottom row) for the Old Dad Peak (OKM) population. Red lines are smooth curves fitted by loess.

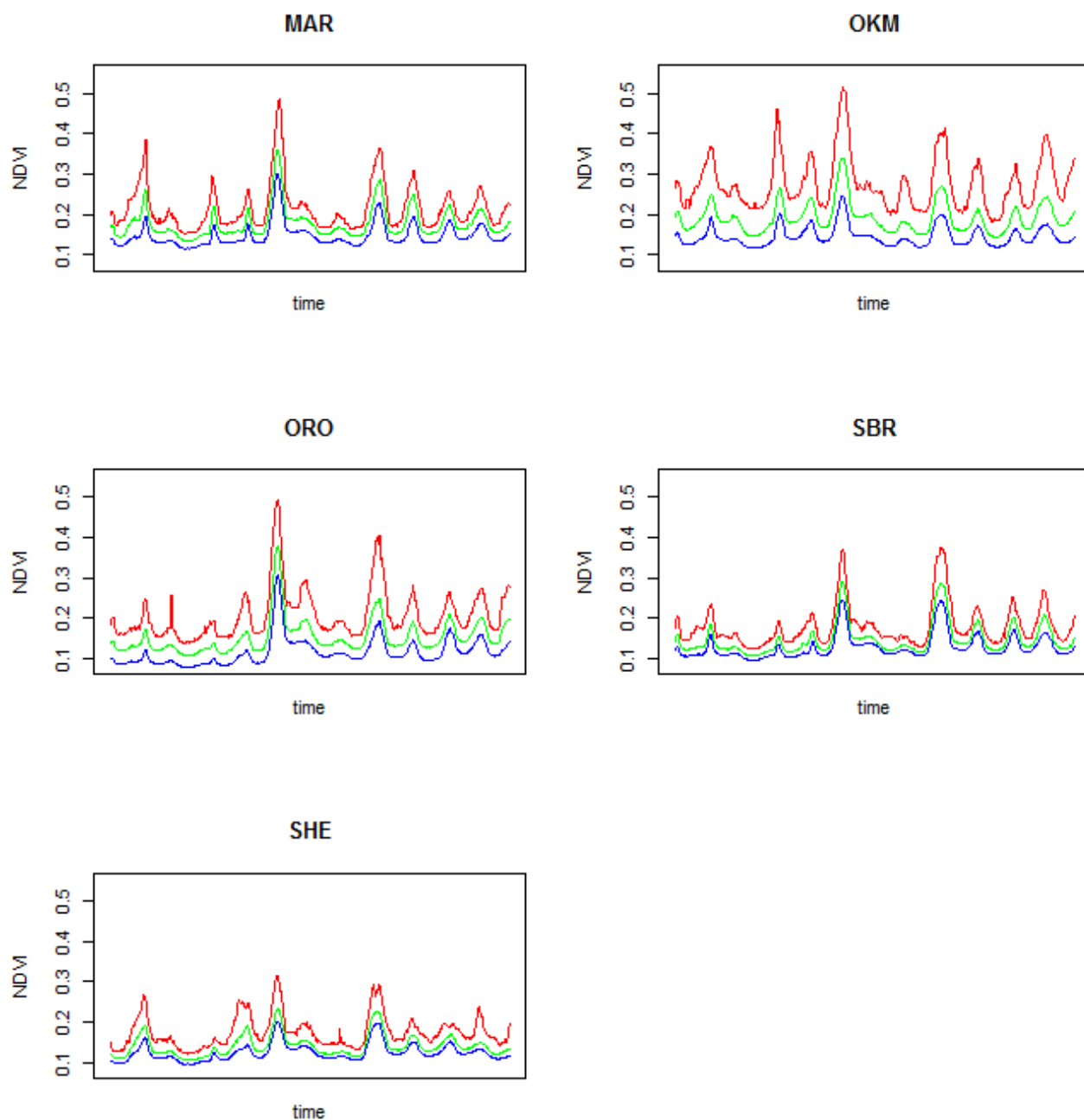


Figure A.5. Time series (2000-2011) of median NDVI (blue line), 90th percentile NDVI (green line), and maximum NDVI (red line) for five habitat patches used in FN analysis: Marble Mountains (MAR), Old Dad Peak (OKM), Orocopia Mountains (ORO), South Bristol Mountains (SBR), and Sheephole Mountains (SHE).

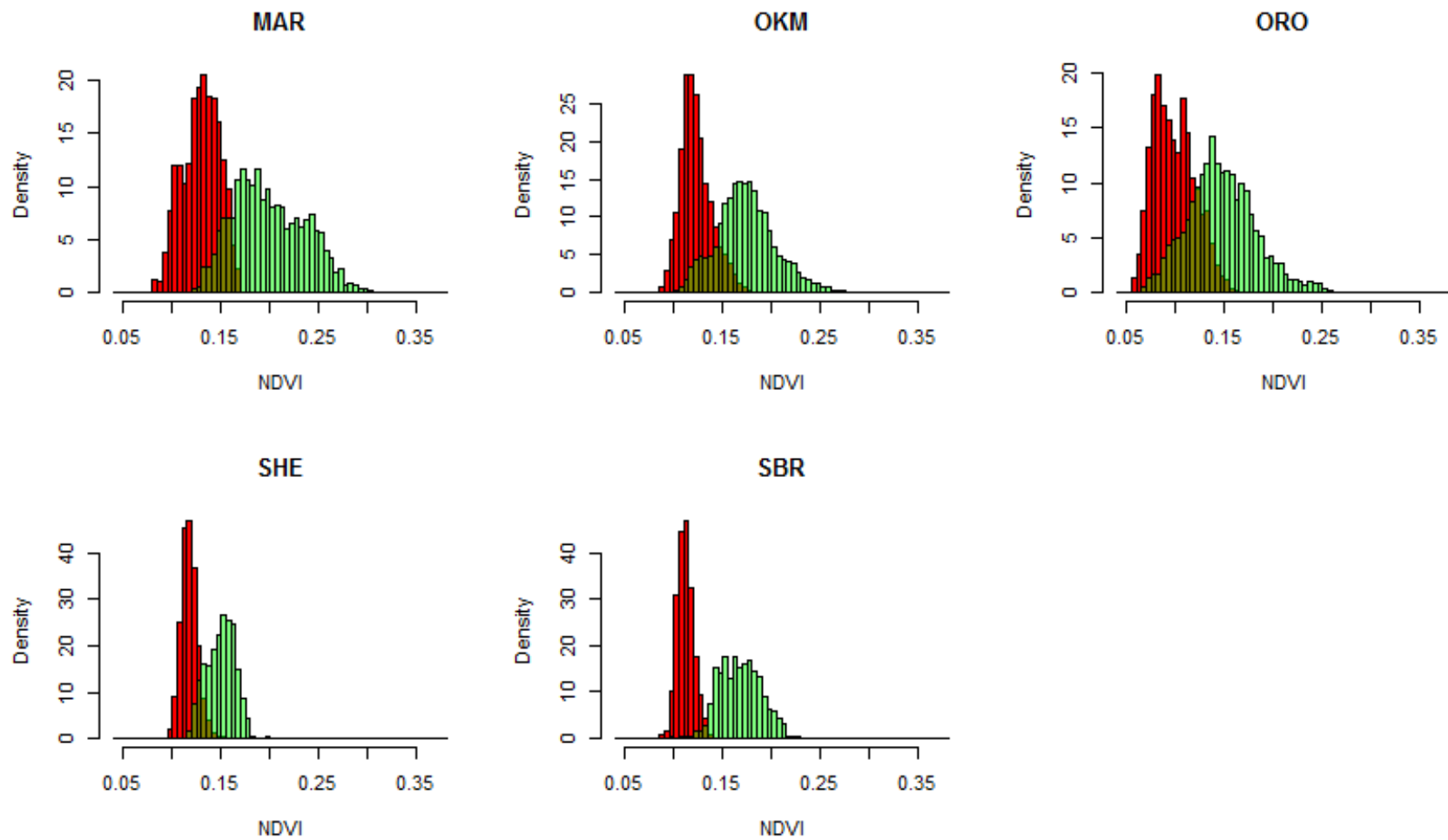


Figure A.6. Distribution of NDVI values in one growing season image (26 Feb 2009; shown in green) and one non-growing season image (29 Aug 2009; shown in red) for five habitat patches used in FN analysis: Marble Mountains (MAR), Old Dad Peak (OKM), Orocapia Mountains (ORO), South Bristol Mountains (SBR), and Sheephole Mountains (SHE).

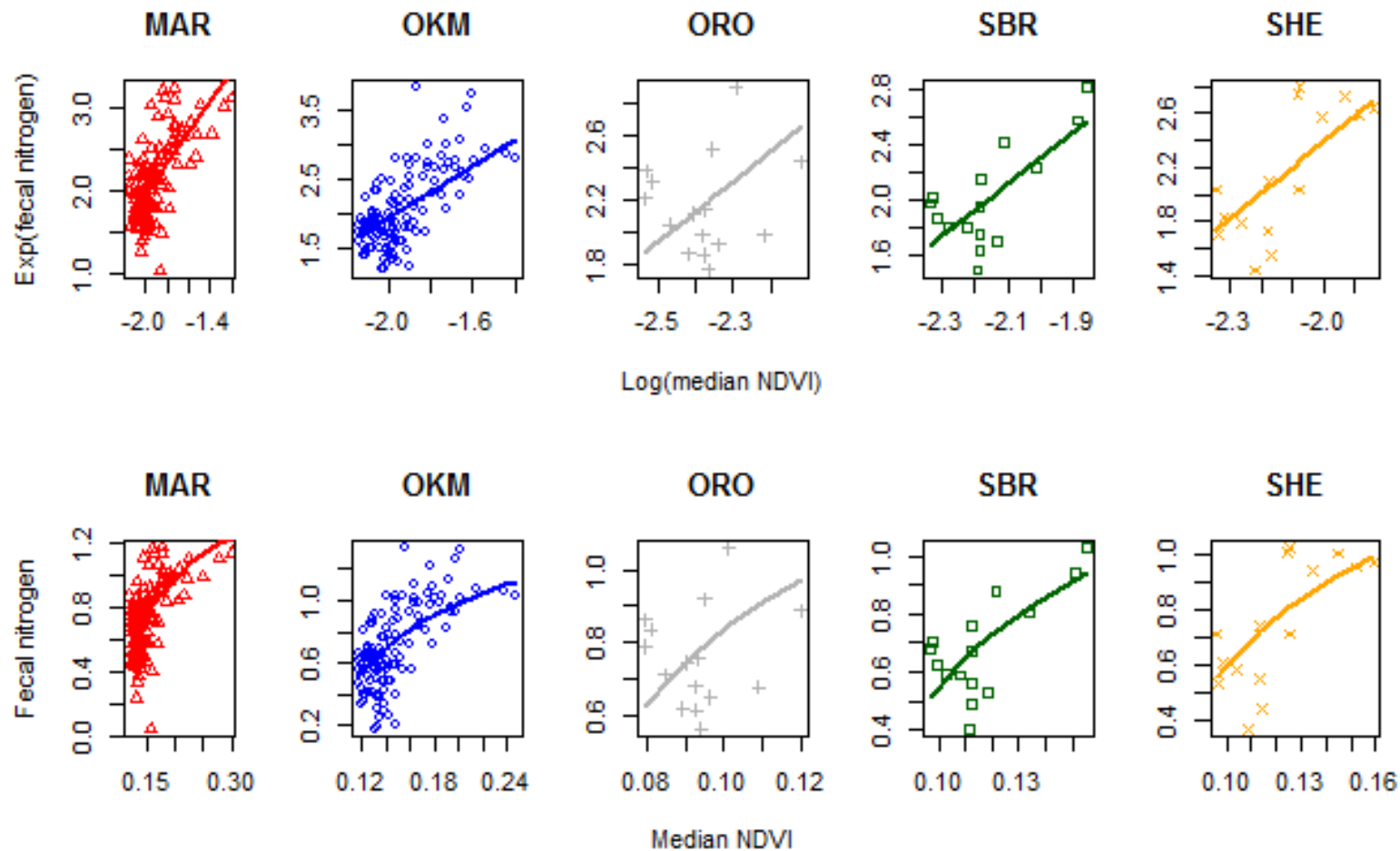


Figure A.7. Relationship between fecal nitrogen and Normalized Difference Vegetation Index (NDVI) at the sample level for five populations: Marble Mountains (MAR), Old Dad Peak (OKM), Orocopia Mountains (ORO), South Bristol Mountains (SBR), and Sheephole Mountains (SHE) bighorn sheep populations from 2000 through 2011. Regression lines are from the best-fitting model with equal slopes but different intercepts for the patches. Top row of plots shows relationship modeled in linear regression analysis: log-transformed NDVI, FN back-transformed to original scale via exponentiation. Bottom row of plots shows relationship that is most biologically interpretable: NDVI on original scale, FN log-transformed to be linearly related to apparent digestibility.

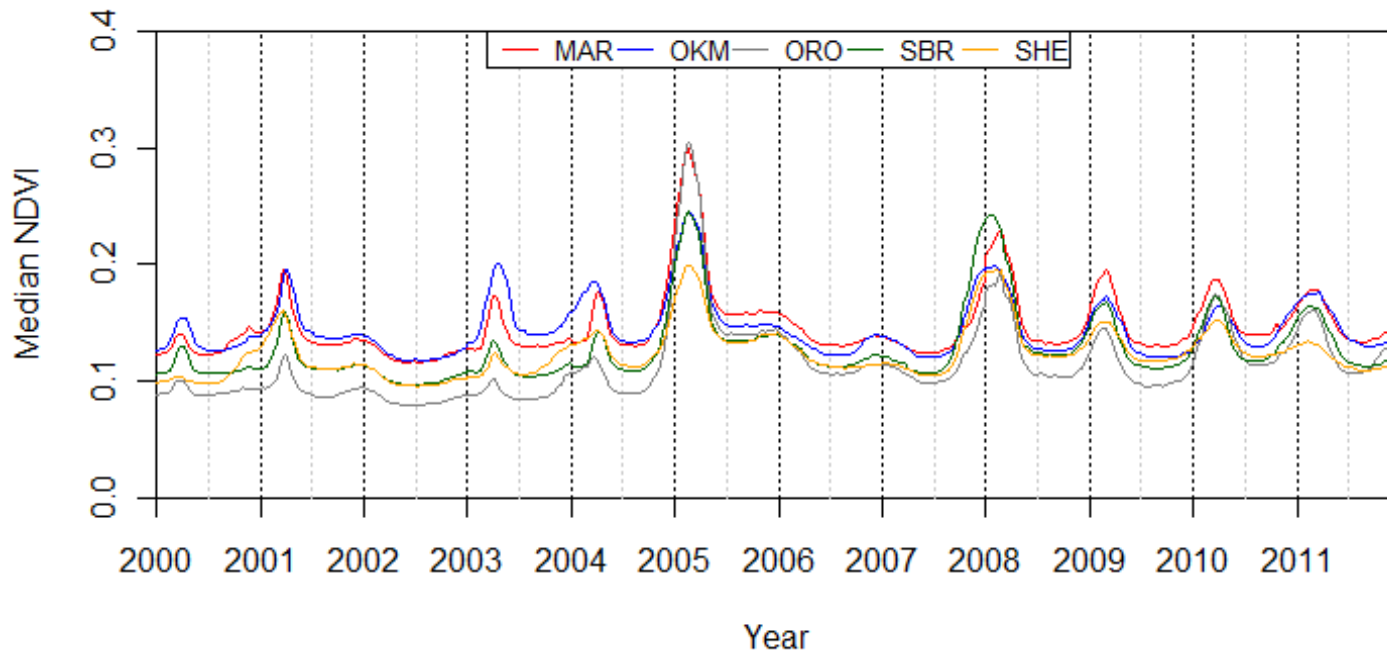


Figure A.8. Time series of the median Normalized Difference Vegetation Index (NDVI) from 2000 through 2011 for five patches of bighorn sheep habitat in the Mojave Desert that were included in fecal nitrogen analysis: Marble Mountains (MAR), Old Dad Peak (OKM), Orocopia Mountains (ORO), South Bristol Mountains (SBR), and Sheephole Mountains (SHE). Dotted black and gray vertical lines represent January 1 and July 1, respectively, of each year.

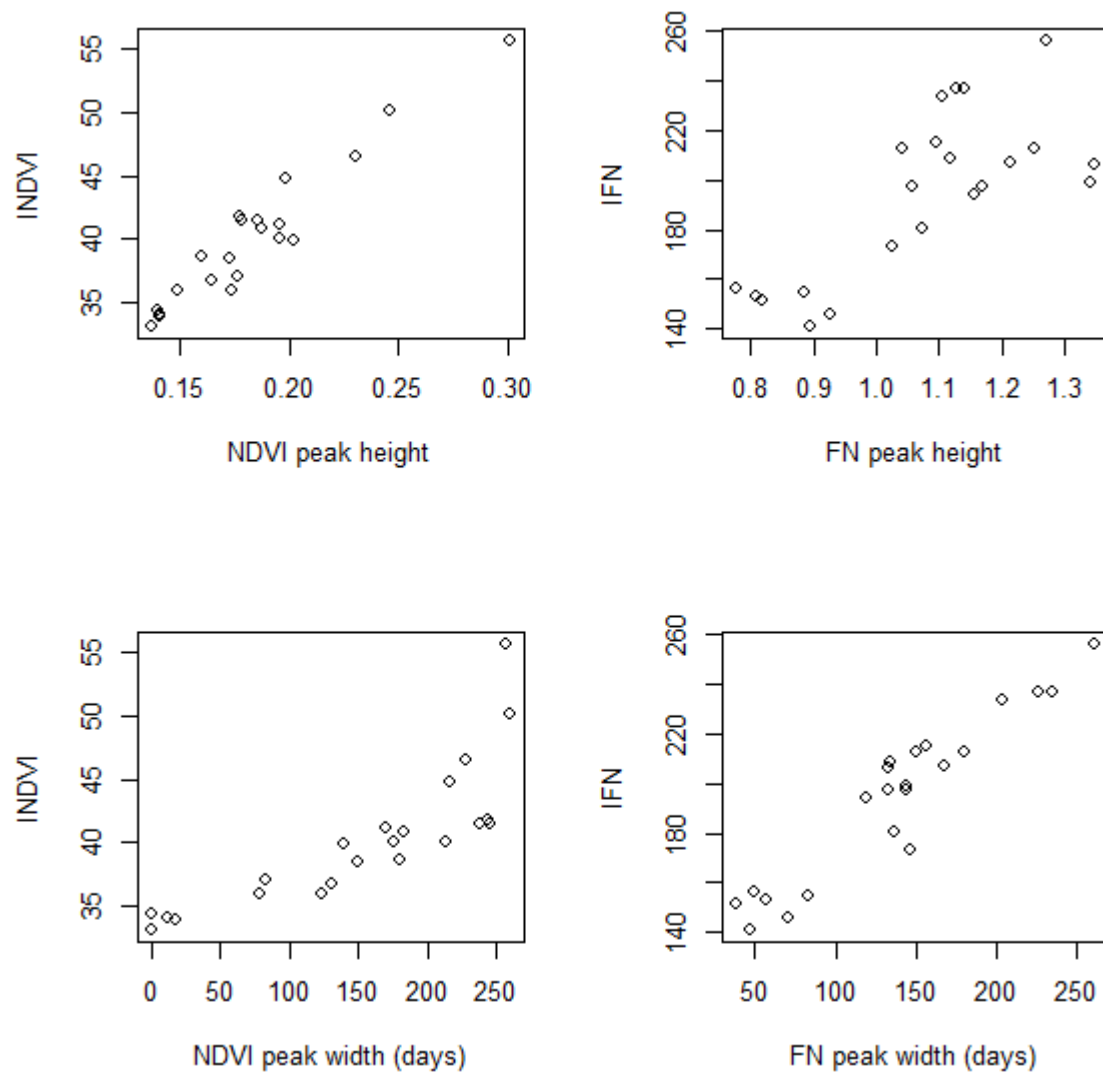


Figure A.9. Relationships between IFN or INDVI and peak height or peak width during the 2001 through 2011 growing seasons in the Marble Mountains and Old Dad Peak patches (n=22).

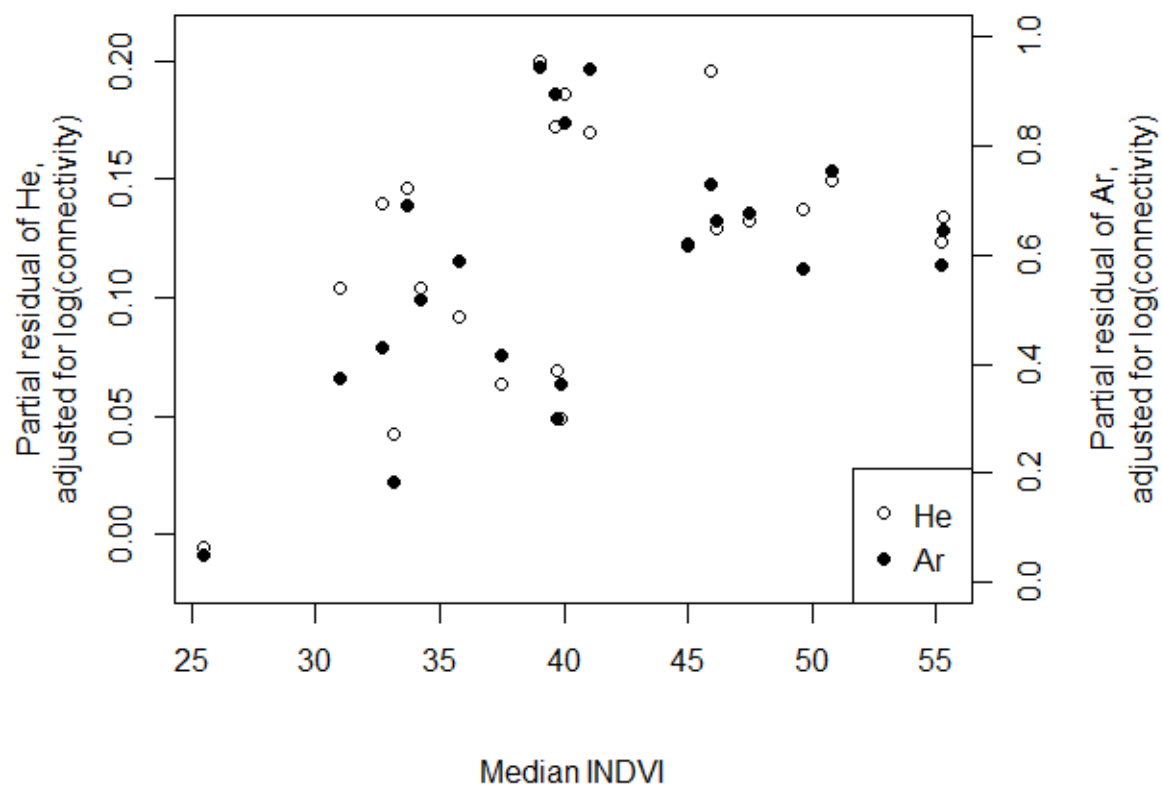


Figure A.10. Relationship between genetic diversity (expected heterozygosity [H_e] and allelic richness [A_r]) and Normalized Difference Vegetation Index (NDVI) for 22 Mojave Desert populations, after accounting for population connectivity. NDVI is calculated as the median of growing-season integrated NDVI from 2001 through 2011. Plot shows partial residuals from linear model of H_e or A_r as a function of median INDVI and log(connectivity).