

**Appendix: Sensitivity Analysis**

**Table A1. Sensitivity Analysis for Ordered Dependent Variable Model – Bootstrap Estimates of Manski Bounds on Conditional Expectation of Outcome**

	<i>Exclusion Restriction: Past HCPs</i>		<i>Exclusion Restriction: No Surprises</i>	
	<i>Lower Bound</i>	<i>Upper Bound</i>	<i>Lower Bound</i>	<i>Upper Bound</i>
$E(y_0 Body\ Length)$	[0.297, 0.457]	[0.683, 0.817]	[0.257, 0.392]	[0.745, 0.851]
$E(y_1 Body\ Length)$	[0.110, 0.237]	[0.831, 0.925]	[0.000, 0.000]	[1.000, 1.000]
$E(y_0 Cum.\ Spending)$	[0.039, 0.171]	[0.901, 0.981]	[0.028, 0.157]	[0.918, 0.987]
$E(y_1 Cum.\ Spending)$	[0.025, 0.241]	[0.843, 0.982]	[0.000, 0.000]	[1.000, 1.000]
$E(y_0 Body\ Length, Cum.\ Spending)$	[0.014, 0.031]	[0.972, 0.983]	[0.013, 0.028]	[0.975, 0.983]
$E(y_1 Body\ Length, Cum.\ Spending)$	[0.001, 0.006]	[0.993, 0.998]	[0.000, 0.000]	[1.000, 1.000]

Results shown are 95% confidence intervals.

*Sensitivity Analysis: Potential Violations of the Conditional Independence Assumption*

To assess the sensitivity of our results to violations of the CIA, we use an approach developed by Ichino et al. (2008). They begin by assuming that the CIA is not satisfied given the observable covariates, but would be satisfied if one could observe one additional binary variable. They simulate this potential confounder in the data, and use it as an additional covariate in a matching estimation procedure. A comparison of estimates of the treatment effect obtained with and without matching on the simulated confounder reveals how sensitive the results are to specific sources of violation of the CIA<sup>1</sup>. This assessment is possible because the distribution of the

<sup>1</sup> These and other CIA sensitivity tests have been developed for estimates of the average treatment on the treated. Although our focus in this paper is on the average treatment effect, the test is still useful. The ATT in our model has similar magnitude to the ATE, and a sensitivity test based on the ATT provides insight about robustness to violations of the CIA.

simulated variable can be specified to reflect different hypotheses about the nature of the potential confounding factors<sup>2</sup>.

Following Ichino et al. (2008) we conduct two sensitivity tests<sup>3</sup>. The first test examines the sensitivity of treatment effect estimates to omitted unobservables that are calibrated to have a distribution similar to that of observed covariates. The results of this test are presented in table A2. The table shows the magnitude of the outcome and selection effects, as well as the treatment effect and corresponding standard error, for simulated confounders constructed to have a distribution similar to that of key observed covariates. The outcome effect ( $I$ ) measures the impact of the unobserved confounder on the relative probability of a positive outcome (recovery) when there is no treatment (no HCP). The treatment effect ( $A$ ) measures the effect of the unobserved confounder on the relative probability of being treated (having an HCP). The outcome and treatment effects of an unobserved confounder are insignificant when  $I = A = 1$  (see Ichino et al. (2008) for more details on how these effects are estimated). As a reference point, the first two rows of table A2 show the treatment effect estimated without a confounder and with a neutral confounder (which would have no outcome or selection effects). The next row shows the effect of an unobserved confounder with a distribution similar to the indicator for whether a species is a mammal. After controlling for observables, such a confounder would have a positive effect on the probability of recovery without an HCP ( $I = 3.73 > 1$ ) and a positive impact on the probability of having an HCP ( $A = 3.30 > 1$ ). Given a violation of the CIA with these characteristics, the treatment effect is close to the effect estimated without confounders,

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<sup>2</sup> An alternative sensitivity test is based on Rosenbaum bounds (Ferraro et al. 2007). This approach can be unnecessarily conservative, because there should be no bias if the unobserved confounder does not affect the outcome, even when it affects the treatment (Lee 2005). Hence, we prefer the approach presented here. However, we also estimated Rosenbaum bounds on the treatment effect, and found that our results are quite robust. The results of this sensitivity analysis are available upon request.

<sup>3</sup> We use the Stata program *sensatt* to implement these tests (see Nannicini 2007).

and remains statistically significant. The remaining rows in table A2 are interpreted in the same way. The analysis suggests that the result of a positive, significant treatment effect is robust to violations of the CIA caused by unobservables with distributions comparable to a variety of species characteristics, ESA implementation measures, and relevant characteristics of the states where species' habitat is located.

The second sensitivity test explores the characteristics of the unobserved confounding factor under which the estimate of the treatment effect becomes (statistically) zero. Ichino et al. (2008) define two parameters underlying the distribution of the confounder,  $d$  and  $s$ , so that  $d > 0$  reflects a positive impact of the confounder on the untreated outcome (an improvement in recovery without an HCP) and  $s > 0$  reflects a positive effect on the selection into treatment (whether a species has an HCP). These parameters have a non-monotonic but close relationship with  $\Gamma$  and  $\lambda$ , respectively. The analysis consists of estimating the treatment effect for increasing values of  $d$  and  $s$ , displaying the associated ranges of  $\Gamma$  and  $\lambda$ , and assessing the plausibility of the outcome and selection effects necessary to drive the treatment effect to zero. We present this analysis in table A3. The table shows that both the outcome effect and the treatment effect would have to be large before the treatment effect becomes zero. A comparison with table A2 suggests that the treatment effect remains positive and significant for values of  $\Gamma$  and  $\lambda$  considerably larger than those of confounders similar to key observed covariates. In particular, for values of the outcome effect ( $\Gamma$ ) observed in the data, the selection effect ( $\lambda$ ) would have to be implausibly large to drive the treatment effect to zero. Hence, to summarize, the results of our treatment effect models appear to be robust to reasonable failures of the CIA.

**Table A2. Sensitivity Analysis for Treatment Evaluation Models: Effects of Calibrated Confounders**

	<i>Outcome Effect <math>\Gamma</math></i>	<i>Selection Effect <math>\Lambda</math></i>	<i>Treatment Effect</i>	<i>Std. Error</i>
No Confounder	-	-	0.452***	0.176
Neutral Confounder	1.00	1.00	0.410**	0.195
<i>Confounder-like</i>				
Mammal	3.732	3.302	0.410**	0.194
Body Length	1.264	4.114	0.407**	0.195
Distinct	1.471	1.123	0.405**	0.194
Nonmigratory	2.652	1.954	0.411**	0.192
Carnivore	3.336	13.088	0.387*	0.205
Conflict	0.677	8.148	0.407**	0.200
Final Plan	2.416	0.147	0.386*	0.217
Cumulative Spending	0.673	6.176	0.415**	0.196
Population Growth	1.007	4.242	0.407**	0.195
Land Values	1.734	1.015	0.421**	0.191

Note: \*, \*\*, \*\*\* indicate parameter significance at  $\alpha = 10\%$ ,  $5\%$ , and  $1\%$  respectively.

**Table A3. Sensitivity Analysis for Treatment Evaluation Models: Characterizing Confounders That Reduce the Treatment Effect**

	$s = 0.05$	$s = 0.10$	$s = 0.15$	$s = 0.20$	$s = 0.25$	$s = 0.30$
	$\Lambda \in$	$\Lambda \in$	$\Lambda \in$	$\Lambda \in$	$\Lambda \in$	$\Lambda \in$
	[2.19,3.59]	[3.08,10.27]	[5.58,12.44]	[11.60,144.94]	[361.00,2708.97]	[2911.4,5244.8]
$d = 0.05$	0.414**	0.402**	0.391*	0.385*	0.367*	0.367*
$\Gamma \in [1.42, 1.60]$	(0.194)	(0.197)	(0.202)	(0.206)	(0.214)	(0.214)
$d = 0.10$	0.410**	0.394**	0.381*	0.364*	0.346	0.346
$\Gamma \in [2.01, 2.25]$	(0.194)	(0.199)	(0.203)	(0.206)	(0.213)	(0.213)
$d = 0.15$	0.405**	0.398**	0.384*	0.364*	0.344	0.344
$\Gamma \in [2.69, 3.10]$	(0.197)	(0.197)	(0.203)	(0.205)	(0.219)	(0.219)
$d = 0.20$	0.400**	0.382*	0.363*	0.348	0.327	0.327
$\Gamma \in [3.81, 4.25]$	(0.199)	(0.202)	(0.208)	(0.213)	(0.219)	(0.219)
$d = 0.25$	0.400**	0.379*	0.361*	0.338	0.315	0.315
$\Gamma \in [4.97, 5.91]$	(0.198)	(0.204)	(0.206)	(0.210)	(0.219)	(0.219)
$d = 0.30$	0.395**	0.370*	0.346*	0.326	0.300	0.277
$\Gamma \in [7.75, 11.26]$	(0.197)	(0.203)	(0.208)	(0.214)	(0.215)	(0.222)

Results presented are treatment effects, with standard errors in parentheses.

Note: \*, \*\*, \*\*\* indicate parameter significance at  $\alpha = 10\%$ ,  $5\%$ , and  $1\%$  respectively.

**Table A4. Sensitivity Analysis: Alternative Recovery Measure - 2004 Red List Score**

Estimator	Effects on Recovery
<i>IV Ordered Probit</i>	
	<i>Marginal Effects</i>
Prob (Red List Status = Extinct)	- 0.105 (0.089)
Prob (Red List Status = Critically Endangered)	- 1.584 <sup>***</sup> (0.491)
Prob (Red List Status = Endangered)	- 1.045 <sup>***</sup> (0.400)
Prob (Red List Status = Vulnerable)	0.152 (0.333)
Prob (Red List Status = Near Threatened)	0.490 <sup>**</sup> (0.238)
Prob (Red List Status = Least Concern)	2.093 <sup>***</sup> (0.593)
<i>Treatment Evaluation Models</i>	
	<i>Average Treatment Effects</i>
<i>OLS on covariates</i>	1.030 <sup>*</sup> (0.573)
<i>OLS on propensity score</i>	1.072 <sup>***</sup> (0.414)
<i>Nearest-neighbor covariate matching (inverse variance)</i>	1.246 <sup>***</sup> (0.336)
<i>Nearest-neighbor covariate matching (Mahalanobis)</i>	1.467 <sup>***</sup> (0.361)
<i>Nearest-neighbor propensity score matching</i>	1.054 <sup>***</sup> (0.390)
<i>Kernel propensity score matching (Gaussian)</i>	1.011 <sup>**</sup> (0.398)
Observations	96

Note: \*, \*\*, \*\*\* indicate parameter significance at  $\alpha = 10\%$ ,  $5\%$ , and  $1\%$  respectively. Standard errors in parentheses.

## References

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