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George R Parsons, *University of Delaware*
A Brett Hauber

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A. Brett Hauber; George R. Parsons

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Nested logit has become common in estimating random utility models of recreation demand. Because welfare analysis is often the objective of estimating these models, it seems natural to ask, what effect does the choice of nesting structure have on the welfare estimates generated by these models? Therefore, we compare the results of nine nesting structures and find that the variation in welfare estimates across the models is not large. Our results are contrary to those of Kling and Thomson and Shaw and Ozog. The difference appears to originate with differences in the estimated dissimilarity coefficients in the nested models.

Key words: nested logit, nesting structure, recreation demand, recreational fishing, RUM.

Nested logit (NL) has become a common method of estimating random utility models (RUM) of recreation demand.[1] This is in large part due to the fact that NL allows the researcher to relax the well-known independence of irrelevant alternatives (IIA) restriction of the multinomial logit model. In particular, IIA imposes the restriction that the relative odds of choosing between two alternatives remains unchanged when a third alternative is introduced into the choice set; that is, the disturbances in the random utilities associated with the alternatives are independent. Researchers often find this restriction unreasonable, either because they believe a priori that certain alternatives are correlated, or because experience has shown that the data do not support it. In contrast,

A. Brett Hauber is an economist at the Research Triangle Institute. George R. Parsons is an associate professor at the University of Delaware.

[1] For a good primer on the use and properties of the NL specification of the RUM, see Morey.

NL allows the researcher to model correlations among the random utilities of subsets of alternatives by grouping these alternatives together into nests.

While there is a wide variety of nesting structures a researcher may choose in estimating such a model, there is no strict theoretical basis for choosing among them. As a result, nesting structures vary considerably across studies. Consider some examples. Hausman, Leonard, and McFadden and Parsons and Needelman nest recreation sites geographically. McConnell and Strand nest recreation sites conditional upon the choice of fishing mode and target species. Parsons and Hauber do the reverse, modeling the choice of target species as conditional upon site choice. Similarly, Hausman, Leonard, McFadden suggest modeling the choice of fishing mode as conditional upon site choice. Finally, numerous studies include a no-trip decision in the model in a nest separate from the basic site choice model (see Morey, Rowe, and Watson; Morey). While this list is not exhaustive, it demonstrates the variety of structures used. Our aim in this study, therefore, is to examine the sensitivity of the resulting welfare estimates to a researcher's choice of nesting structure.

Because welfare analysis is often the motivation for estimating random utility models of recreation demand, it seems natural to ask: what effect does the choice of nesting structure have on the welfare estimates generated by these models? To address this question, we use a data set of recreational fishing in Maine and compare the results of nine alternative nesting structures, including a non-nested specification. In all cases, we model an angler's choice among a common set of combinations of recreation sites and target species. To date, only Kling and Thomson and Shaw and Ozog have analyzed the effect of nesting structure choice on welfare estimates. They both find that different nesting structures result in substantially different welfare estimates. It is useful to know whether this is a result that will persist with other data sets, nesting structures, and types of welfare analyses.

In the next section we present the choice set used in this study, as well as the functional form of the conditional indirect utility function. We also describe the distributions of the stochastic error term used to generate the different nested models. The data are described next. Estimation results for our nine models follow, and the parameter estimates are evaluated against conditions for consistency with stochastic utility maximization. We continue by examining the resulting welfare estimates for the models and compare our findings to those of Kling and Thomson and Shaw and Ozog. We close with conclusions.

Methodology

Deterministic Utility

We assume that each angler chooses a single element from a two-dimensional choice set composed of all combinations of site and target species available in the state of Maine. Therefore, the elemental alternative chosen by an individual is a site–species combination. The full choice set consists of 2,029 fishing sites and up to four possible target species at each site (salmon, trout, bass, or other)[2]; however, not all species are present at each site.

The set of alternatives from which an individual chooses is $C = C_T - C_0 = 4,629$, where $C_T = 8,116$ is the number of conceivable alternatives (2029 × 4), and $C_0 = 3,487$ is the number of infeasible site–species combinations.[3]

In each model, an angler's conditional indirect utility function for a fishing trip to site j targeting species f is assumed to be additively separable in the unobserved errors, ε_{jf}, and takes the form

$$(1) \quad U_{jf} = \mu_{jf} + \varepsilon_{jf}$$

where $j = 1, \ldots, J$ and $f = s, t, b,$ or o (salmon, trout, bass, or other). The term μ_{jf} is the deterministic portion of utility, which is a function of explanatory variables and unknown parameters. μ_{jf} is unique to each angler. However, an individual's underlying preference ordering, captured by this deterministic portion of the indirect utility function, is the same for each of the nested models estimated in this study. μ_{jf} is assumed to be linear in the parameters and takes the form

$$(2) \quad \mu_{jf} = \alpha p_j + \beta \mathbf{x}_j + \gamma_f \mathbf{w}_{jf} + \delta \mathbf{z}_f,$$

where

$$\alpha p_j = \alpha \text{PRICE}_j,$$

$$\beta \mathbf{x}_j = \beta_1 L_j * \ln(\text{ACRES}_j)$$
$$+ \beta_2 L_j * \text{REMOTE}_j$$
$$+ \beta_3 L_j * \text{AGE} * \text{REMOTE}_j$$
$$+ \beta_4 L_j * \text{BOAT} * \text{ACCESS}_j$$
$$+ \beta_5 R_j + \beta_6 R_j * \text{MAJOR}_j$$
$$+ \beta_7 R_j * \text{TOXIC}_j,$$

and

$$\gamma_f \mathbf{w}_{jf} + \delta_{zf} = \gamma_{1f} L_j * \text{DIRT}_{jf}$$
$$+ \gamma_{2f} L_j * \text{ABUND}_{jf}$$
$$+ \delta_1 \text{FAV}_f + \delta_2 \text{BEST}_f.$$

$\alpha, \beta, \gamma_f,$ and δ are unknown parameters to be estimated and $p_j, \mathbf{x}_j, \mathbf{w}_{jf},$ and $\mathbf{z}_f$ are observed data.

Because each alternative is assumed to be a site–species combination, some alternative-specific characteristics will vary only across

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[2] The trout, bass, and other targets are aggregates of more specific targets; trout consists of brook trout, brown trout, lake trout, and other unspecified trout, bass consists of largemouth bass, smallmouth bass, and other unspecified bass, and other consists of bullhead, muskie, pickerel, white perch, and other unspecified perch.

[3] One thousand six hundred sixty-four sites do not have salmon, 458 sites do not have trout, and 1,365 sites do not have bass.

Table 1. Variable Definitions

Variables Affecting Site Choice Only (p_j, $\mathbf{x}_j$)	
$PRICE_j$	= Opportunity Cost of Time plus Travel Cost of Reaching Site j {Hourly Wage $*$ (Round Trip Travel Time in Hours) $+(0.30 *$ Round Trip Distance in Miles)}
$ACRES_j$	= Surface area of lake j in acres
$REMOTE_j$	= 1 if site j is reached only by off-road vehicle or on foot; 0 otherwise
AGE	= Age of respondent in years
BOAT	= 1 if individual fished from a boat on reported trip; 0 otherwise
$ACCESS_j$	= 1 if outboard motors are prohibited or restricted at site j; 0 otherwise
$MAJOR_j$	= 1 if river reach is on one of the major rivers in the state; 0 otherwise (Major rivers include the Allagash, Androscoggin, Aroostook, Dead, Kennebec, Mattawamkeag, Moose, Penobscot, Saco, St. John, Sandy, Presumpscot, Sebasticook, Union, Piscataquis, and St. Croix.)
$TOXIC_j$	= 1 if river reach j has elevated levels of toxics; 0 otherwise
R_j	= 1 if site j is a river or stream; 0 otherwise
L_j	= 1 if site j is a lake; 0 otherwise
Variables Affecting Both Site Choice and Species Choice ($\mathbf{w}_{jf}$)	
$DIRT_{jf}$	= 1 if site j is in nonattainment of EPA standards; 0 otherwise (bass and other are believed to be unaffected by nonpoint source pollution in lakes)
$ABUND_{jf}$	= 1 is site j has species f in abundance; 0 otherwise
Variables Affecting Species Choice Only (z_f)	
FAV_f	= 1 is species f is among the angler's three favorite species to target; 0 otherwise
$BEST_f$	= 1 if species f is the angler's favorite species to target; 0 otherwise

sites, while others may vary among species as well. The term p_j is the sum of the angler's travel and time costs of reaching site j. The vectors $\mathbf{x}_j$ and $\mathbf{w}_{jf}$ are sets of site characteristics described in equations (2). The effect of $\mathbf{x}_j$ on utility is invariant with species choice while the effect of $\mathbf{w}_{jf}$ varies with both site choice and species choice. Finally, z_f is a vector intended to capture an angler's preference for specific species. The variables used to specify deterministic utility are described in Table 1.

Distribution of the Error Term

A priori, a researcher hypothesizes the correct nesting specification based on his or her assumptions regarding substitution among alternatives in the choice set. For example, if the researcher expects that, when an angler's demand for a particular site–species combination falls because some attribute of that alternative has been degraded, he will be more likely to increase his demand for targeting another species at the same site than to increase his or her demand for the same species at a different site, the researcher

might treat each site as a unique nest and model the choice of target species as conditional on site choice. If the researcher believes that an angler is instead more likely to substitute the same target species at different sites, then a nesting specification in which site choice is conditional upon species choice might be used.[4]

Another possible method of nesting the elemental alternatives in this choice set involves dividing one dimension of the choice set into subsets. For example, the site dimension could be divided into rivers and lakes if the researcher believes that anglers are likely to consider fishing trips to two different lakes to be better substitutes than one fishing trip to a lake and another to a river. Alternatively, if the assumption is that anglers who target cold water species tend not to target warm water species and vice versa, the species dimension could be divided into cold and warm water species.

This study involves estimation of eight different nested models and one non-nested model using a common data set and the

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[4] The correct nesting structure cannot be known a priori but can be tested once the models are estimated.

common deterministic utility specification presented in equation (2).[5] The two basic nested models appear in the tree diagrams in Figures 1 and 2. Figure 1 represents a two-level nesting structure in which site choice is modeled as conditional upon species choice. In this model, all sites at which a particular species is present are grouped together. This nesting structure (two-level species–site) implies the following cumulative joint distribution for the vector of errors $\langle \varepsilon_{jf} \rangle$:[6]

$$(3) \quad F(\langle \varepsilon_{jf} \rangle)$$

$$= \exp\left\{ -\sum_{f=1}^{F} \cdot \left[\sum_{j=1}^{Jf} \exp(-\varepsilon_{jf}/\rho_f) \right]^{\rho f} \right\}$$

where ρ_f is the dissimilarity coefficient on each species nest. This dissimilarity coefficient is also commonly referred to as the inclusive value coefficient for reasons that will become apparent below.

Figure 2 provides a representation of the same choice decision except that the nesting structure has been flipped; that is, the species choice is now modeled as conditional upon the site choice. While the structure presented in Figure 1 embodies the assumption that salmon fishing at site j is a better substitute for salmon fishing at site i than is bass fishing at site i, the nesting structure in Figure 2 assumes that bass fishing at site i is a better substitute for salmon fishing at site i than is salmon fishing at site j. This second nesting structure (two-level site–species) implies the following cumulative joint distribution for the vector of errors $\langle \varepsilon_{fj} \rangle$:

$$(4) \quad F(\langle \varepsilon_{fj} \rangle)$$

$$= \exp\left\{ -\sum_{j=1}^{J} \left[\sum_{f=1}^{Fj} \exp(-\varepsilon_{fj}/\rho_j) \right]^{\rho j} \right\}$$

in which ρ_j is the dissimilarity coefficient on each site nest.

The dissimilarity coefficients (inclusive value coefficients) capture the degree of correlation among alternatives within the nest such that the degree of correlation equals

$(1 - \rho^2)$. In effect, the estimated dissimilarity coefficient is an indicator of the degree of substitution among alternatives within the nest. The closer the estimated dissimilarity coefficient is to zero, the greater the substitution among alternatives within the nest. As the value of the estimated dissimilarity coefficient rises from zero within the unit interval, the degree of substitution among alternatives within the nest falls. When the dissimilarity coefficient is unity, then the well-known independence of irrelevant alternatives (IIA) condition holds and the nested model collapses to a non-nested multinomial logit model of the form

$$(5) \quad F(\langle \varepsilon_{jf} \rangle) = F(\langle \varepsilon_{fj} \rangle)$$

$$= \exp\left\{ -\sum_{f=1}^{F} \sum_{j=1}^{J} \exp(-\varepsilon_{jf}) \right\}.$$

The other models estimated in this study are developed as more general cases of those described above. First, in both the species–site and site–species models, the species dimension of the choice set is divided such that the cold water species, salmon and trout, are grouped together. This grouping is made because we believe a priori that these species are close substitutes. As a result, we have two additional models, each with three levels of nesting: three-level species–site (w/cold) and three-level site–species (w/cold).[7]

We also divide the site dimension into rivers and lakes. This gives two more three-level nested models: three-level species–site (w/river&lake) and three-level site–species (w/river&lake). Finally, we estimate two four-level models which include both the cold water nest and the river and lake nests. These are the most elaborate models estimated in our study and are referred to as the four-level species–site model and the four-level site–species model.

Choice Probabilities

Given the deterministic portion of indirect utility, μ_{jf}, and the specification of the distribution of the error term, $\langle \varepsilon_{jf} \rangle$, the probability that an individual will choose species–site combination fj can be calculated. Using

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[5] While the number of possible nesting specifications is quite large, we choose to examine only nine in this study. Each of the nesting structures we examine is derived by exploiting the multidimensional nature of the choice set as described above; however, this set of nesting specifications is far from exhaustive.

[6] Throughout this manuscript, the term "species–site model" is intended to mean a model in which site choice is conditional upon species choice, that is, a model with species at the top of the nesting structure. The elemental alternative for a species–site model is labeled "*jf*." The reverse is true for the site–species model.

[7] The cumulative joint distributions for the vector of errors associated with these and the remaining models, as well as the tree diagrams representing these models, are available from the authors upon request.
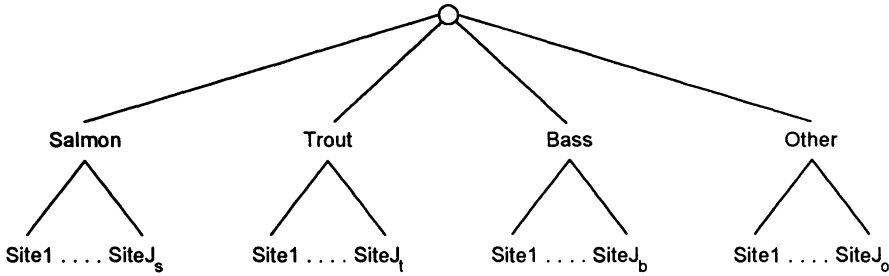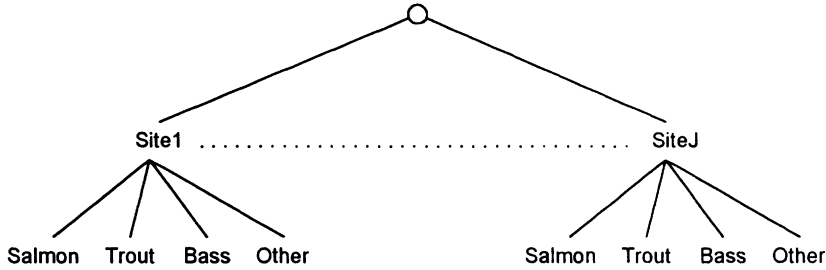
Figure 1. Two-level model (species–site)

Figure 2. Two-level model (site–species)

the two-level species–site nesting specification as an example, the probability that an angler will choose site j and target species f is

(6) $P(jf) = P(j|f) \bullet P(f).$

The probability of targeting species f at site j equals the probability of fishing at site j conditional upon the probability of targeting species f, multiplied by the probability of choosing species f. Given the distribution of the error term in equation (3) and deterministic utility specification described in equation (2), these probabilities are

$$P(j|f) = \exp((\alpha p_j + \beta \mathbf{x}_j$$
$$+ \gamma_f \mathbf{w}_{jf})/\rho_f)/I_f$$
$$P(f) = \exp(\delta z_f + \rho_f \ln(I_f))/$$
$$\left[\sum_{g=1}^{F} \exp(\delta z_g + \rho_g \ln(I_g)) \right]$$

where I_g takes the form

(7) $I_g = \sum_{i=1}^{Ng} \exp(\alpha p_i + \beta \mathbf{x}_i + \gamma_f \mathbf{w}_{ig})/\rho_g.$

I_g is the value of f for the case $f = g$ and $\sum_{i=1}^{N_g}$ sums over N_g sites in the species g nest. $\ln(I_g)$ is referred to as the "inclusive value" and is equal to the expected maximum utility of targeting species g at site i. Because ρ_g is

the unknown parameter of $\ln(I_g)$, it is often referred to as the inclusive value coefficient.

Likewise, using the two-level site–species model in equation (4) and calculating the choice probability as the probability of targeting species f, conditional on choosing site j, multiplied by the probability of choosing site j, we have

$$P(fj) = P(f|j) \bullet P(j)$$

where

$$P(f|j) = \exp((\gamma_f \mathbf{w}_{fj} + \delta z_f)/\rho_j)/Ij,$$
$$P(j) = \exp(\alpha p_j + \beta \mathbf{x}_j + \rho_j \ln(I_j))/$$
$$\left[\sum_{i=1}^{N} \exp(\alpha p_i + \beta \mathbf{x}_i + \rho_i \ln(I_i)) \right],$$

(8) $I_i = \sum_{g=1}^{F} \exp((\gamma_g \mathbf{w}_{gi} + \delta z_g)/\rho_i).$

I_j is the value of I_i for the case $i = j$ and $\sum_{g=1}^{F}$ sums over F species in the site nest.

The log likelihood function for each model takes the form

(9) $L = \sum_{n \in N} \sum_{j \in J} \sum_{f \in F} y_{njf} \ln(P_{njf})$

where $n \in N$ indexes individuals in the data set, $j \in J$ indexes sites, $f \in F$ indexes target species, y_{njf} is the number of trips taken

by individual *i* to site *j* targeting species *f*, and P_{njf} is the probability that individual *n* will target species *f* at site *j*. Essentially, we are treating each repeat trip (each repeated site and target species combination) as an independent observation. This assumption is necessary because the random utility model assumes that each choice occasion (trip) is independent; that is, the model is not capable of accounting for correlations among different trips.

All parameters are estimated by full information maximum likelihood. A unique vector of coefficient estimates is derived for each error specification. For each model, the corresponding coefficient estimates can then be used to estimate deterministic utility under different states of the world (i.e., before and after a change in site quality) and the compensating variation associated with such a change as described below. Because the number of sites is large, we estimate each of our models using a randomly drawn subset of sites. See McFadden (1978) for justification of this approach and Parsons and Kealy (1992) or Parsons and Hauber for applications. A total of thirty sites is used in estimation: the actually chosen site plus twenty-nine sites drawn from all sites in the choice set.[8] Welfare estimation is always done over the full set of sites using the parameter estimates from the random draws. Each model is estimated twenty times using different random draws (see Feather, Waters and Dietz).[9]

Data

The data set consists of 2,425 fresh-water fishing day trips taken by 143 Maine anglers during the summer and fall of 1989. These data come from a survey conducted in 1989 for the National Acid Precipitation Assessment Program (NAPAP). The details of the

survey are presented in Shankle et al. For each individual, data are available on the number of trips taken, the site visited on each trip, and the species of fish targeted on each trip. Demographic data, including income and information regarding each angler's favorite target species, are also included.

Characteristic data are available for 1,899 lakes in Maine and include information on water quality and the abundance of each species, as well as depth, elevation, and location. Lake data come from the *Maine Lake Survey* prepared by the Maine Department of Inland Fisheries and Wildlife. Approximately 98% of the lakes visited in the NAPAP survey are covered in the lake survey.

Characteristic data are also available for 130 rivers reaches in Maine. Larger rivers are divided into smaller reach segments to capture differences in location and site characteristics. The river data include information on location, the presence of salmon, and a dummy variable indicating whether the site is a reach on one of the major rivers in the state. The data set for river sites is somewhat limited because it was compiled using several Maine fishing guides.

Water quality data were obtained from the Maine 305(b) report to the U.S. Environmental Protection Agency (EPA) for 1990: *State of Maine, 1990 Water Quality Assessment*. In this report, the state identifies lakes that fail to attain certain water quality standards, primarily due to non-point source pollution. The state also identifies rivers with elevated levels of toxics.

Finally, to estimate these models, travel times and distances for each angler to all sites in the choice set are necessary. These values were determined using the software package HYWAYS/BYWAYS.

Parameter Estimates[10]

While not the primary focus of this research, the coefficient estimates are indicative of the applicability of these models to the choices of site and species made by anglers in the state of Maine. In each of our models and across all twenty draws, the results of the parameter estimation are generally consistent with expectations. The coefficient on the

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[8] In the species–site models we included the weighting term $\ln(M/J)$ in each site utility, where *M* is the full number of sites in the nest set and *J* is the number of randomly drawn sites in the nest. This adjustment accounts for randomly drawing sites. However, the differences between models using and not using this weighting term were negligible. Hence, we report parameter estimates from the randomly drawn choice set without weighting. The welfare measures are, as usual, derived over the full choice set.

[9] Although the number of random draws used in this study is somewhat arbitrary, it is greater than the number of draws used by Parsons and Kealy (1992), Feather, and Parsons and Hauber. In particular, we first estimated each model five times (as did Parsons and Hauber) and then expanded the number of draws to twenty. We found that with twenty draws, the mean and median of each estimated parameter were close, lending face validity to the use of the resulting estimates.

[10] Coefficient estimates for all 180 models (9 models * 20 random draws) are available from the authors upon request.

price term is always negative and significant, indicating that the likelihood of traveling to a particular site for the purpose of recreation is inversely related to the cost of reaching the site. Not surprisingly, the coefficients on the species preference variables are always positive and significant. The parameters on the lake-specific variables, $\ln(ACRES_j)$, $BOAT * ACCESS_j$, and $REMOTE_j$, are always positive and significant, as are those on the variables representing salmon, trout, and bass abundance, $ABUND_{jf}$, $f = s, t, b$. The coefficients on $AGE * REMOTE_j$ and $DIRT_{jf}$ are consistently negative and significant. Likewise, the parameter estimates for the river-specific variables $MAJOR_j$ and R_j are positive and significant. The coefficient on the lake-specific variable for other abundance, $ABUND_{jo}$, is always negative and significant. Since other abundance is a dummy variable equal to one for a large group of warm water species other than bass, it may be the case that anglers targeting one species in the group care little for, and perhaps even dislike, the other species included in the group.

Somewhat troublesome is the estimated coefficient on the variable $R_j * TOXIC_j$, since it is a critical element in the welfare evaluation of a river clean-up. We expected this parameter estimate to be negative since a toxic river site should yield less utility than a clean river site. However, the parameter estimate varies from positive to negative across draws and is often insignificant. This finding could be an artifact of the construction of the toxic variable. A river is labeled toxic if there is a fish consumption advisory associated with the site. It is assumed that an angler's perception of the site characteristics determines the effect a site's attributes have on his or her indirect utility. Because toxics may not be easily perceived, or if the fish consumption advisory is not widely disseminated, individual anglers may be unaware that a particular site is considered toxic. If so, it is expected that the toxic designation would have little effect on the expected utility associated with the site.

Another possible explanation for the erratic and often insignificant estimates of the toxic coefficient is that we have misspecified the deterministic portion of the indirect utility function. In particular, if fish populations are a function of toxic contamination, then the toxic characteristic of a site

may already be captured by the fish population variables ($ABUND_{jf}$). However, there are two reasons why we believe this is not driving our results. First, the variable $R_j * TOXIC_j$ is river-specific, while the population variables $ABUND_{jf}$ are lake-specific. Therefore, the indirect utility associated with fishing at a particular site is a function of only one of these variables. Second, even if the fish population and toxic variables both entered the utility function associated with a particular site, a fish consumption advisory does not necessarily indicate that fish populations will be affected. This fact is clear when one considers the EPA's ambient water quality criteria for toxic substances. Specifically, the maximum permissible levels of ambient toxics for human consumption (fish consumption advisory thresholds) are lower than the maximum permissible levels of ambient toxics for the fish species themselves, indicating that at levels above those permissible for human consumption, but below the maximum levels permissible for fish, the abundance of a fish species is not expected to be affected.

The parameters of primary interest in this study are the dissimilarity (inclusive value) coefficients. As mentioned above, these parameters capture the degree of correlation among alternatives within a nest. McFadden (1981) has shown that $0 < \rho \leq 1$ is a necessary and sufficient condition for the nested model to be consistent with utility maximization. Borsch-Supan, however, identifies local sufficiency conditions permitting $\rho > 1$. Kling and Herriges and Herriges and Kling (1996) extend the work of Borsch-Supan by developing and implementing empirical tests for these locally sufficient conditions. The result of these efforts has been to expand the bounds of acceptable values of ρ, but only slightly. In particular, Herriges and Kling (1996) find that $1 < \rho < 2$ will more often than not fail to meet the Borsch-Supan conditions.[11]

Atherton et al. and Hausman, Leonard, and McFadden provide an alternative interpretation of $\rho > 1$. From a purely statistical perspective, if $\rho > 1$ then there is greater correlation among the utilities of elements of different nests than among the utilities of elements within the same nest. For example, in the two-level model with site at the top, an estimated dissimilarity coefficient on a site

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[11] We conducted the Kling and Herriges tests on a number of our two-level models and found no instance in which the result changed the conclusions presented later in this section.

nest, ρ_j, greater than one would indicate that a given species at site i is a better substitute for the same species at site j than is another species at site j. While estimates of $\rho > 1$ may not be wholly consistent with stochastic utility maximization per se, models in which dissimilarity coefficients exceed one still capture the nature of substitutability among alternatives and may thereby represent individual choice behavior.

The estimates of the dissimilarity coefficients in this study are consistently positive and statistically significantly greater than zero at a 1% level of confidence. However, what is important is that these estimates lie within the unit interval. Table 2 summarizes the dissimilarity coefficient estimates relative to the condition that $0 < \rho \leq 1$. Columns (3)–(5) display the minimum, median, and maximum values of the dissimilarity coefficient estimates for each model across the twenty draws. Columns (6)–(8) show the number of times in twenty draws that an estimate is statistically significantly greater than one, thereby violating McFadden's condition for consistency with utility theory.

The results in column (6) reveal that in the models in which site choice is conditional upon species choice (species–site), the dissimilarity coefficients on the bass and other species nests, ρ_{bass} and ρ_{other}, lie within the unit interval in a large majority of the draws. In addition, the median estimates for these two dissimilarity coefficients are less than one in all four species–site models. In contrast, the dissimilarity coefficients on the salmon and trout nests in the species–site models are often statistically significantly greater than one. In particular, these two dissimilarity coefficients lie outside the unit interval more often than not in both the two-level and three-level (w/cold) species–site models. However, in the three-level species–site (w/river&lake) and the four-level species–site models, the dissimilarity coefficients on the salmon and trout nests lie within the unit interval more often than not.

The dissimilarity coefficient estimates on the higher order nests provide additional information as to the consistency of the nesting structures with utility maximization. As shown in column (7), in a large number cases in the species–site models, the dissimilarity coefficient on the cold water nest, ρ_{cold}, exceeds one with statistical significance. This result suggests that bass and ρ_{other} are closer substitutes for salmon and trout than we had

expected and that the cold water nest may be inappropriate.

We were unable to estimate separate dissimilarity coefficients for each of the river and lake nests in either the three-level species–site (w/river&lake) or four-level species–site models. Specifically, when we attempted to estimate these models with unrestricted river and lake dissimilarity coefficients, the maximum likelihood estimates would not converge. This is most likely due to the small number of river or lake sites in the salmon nest. Inclusion of the river–lake partition, however, provides encouraging results. The dissimilarity coefficient on the river and lake nests, $\rho_{river/lake}$, in the species–site models is usually positive and less than one [see column (8)], indicating that there is greater substitution among rivers or among lakes than between the two.

Using consistency with utility theory as a guide then, we find that among the species–site models, the preferred nesting structure is the three-level species–site model that includes the river and lake nests. Among all the models, this is the only one that consistently resulted in dissimilarity coefficient estimates within the acceptable range.

Turning to the site–species models, we must first note that, because of the large number of sites, we were unable to estimate a unique dissimilarity coefficient for each site. Therefore, following Parsons and Hauber, we estimated one dissimilarity coefficient for lake sites, $\rho_{site(lake)}$, and another for river sites, $\rho_{site(river)}$. The results presented in column (6) of Table 2 reveal that the dissimilarity coefficient on the lake sites is often statistically significantly greater than one and the median estimates of the dissimilarity coefficient on the river sites is often greater than one (although these estimates are usually not statistically significantly greater than one). We can conclude from these results that there is most likely more substitution occurring between sites than within a particular site. In addition, more substitution appears to be occurring between river and lake sites than is occurring just among lake sites or just among river sites. Therefore, treating each site as a separate nest is probably not consistent with utility theory.

Following our treatment of the site-specific nests above, we estimate two unique dissimilarity coefficients for the cold nests in the site–species models: one for river sites

Table 2. Estimates of the Dissimilarity Coefficients

(1) Model	(2) Dissimilarity Coefficient	(3) Minimum	(4) Median	(5) Maximum	(6) Number of Times in 20 Draws $\rho > 1$ [a]
2-Lvl Species–Site	ρ_{salmon}	0.634	1.082	2.317	10
	ρ_{trout}	0.636	1.010	2.237	9
	ρ_{bass}	0.576	0.783	1.593	3
	ρ_{other}	0.371	0.535	0.983	0
3-Lvl Species–Site (cold water nest)	ρ_{salmon}	0.684	1.085	2.338	10
	ρ_{trout}	0.644	1.102	2.414	12
	ρ_{bass}	0.610	0.853	1.608	3
	ρ_{other}	0.384	0.575	1.005	0
	ρ_{cold}	0.895	1.101	1.270	12
3-Lvl Species–Site (river & lake nests)	ρ_{salmon}	0.448	0.963	3.274	8
	ρ_{trout}	0.422	0.915	0.801	8
	ρ_{bass}	0.396	0.655	1.404	3
	ρ_{other}	0.202	0.403	1.599	1
	$\rho_{river/lake}$	0.560	0.843	1.528	3
4-Lvl Species–Site	ρ_{salmon}	0.474	0.982	3.264	8
	ρ_{trout}	0.421	0.941	3.192	8
	ρ_{bass}	0.393	0.674	1.385	5
	ρ_{other}	0.201	0.413	1.986	1
	ρ_{cold}	0.862	1.069	1.293	10
	$\rho_{river/lake}$	0.560	0.877	1.505	5
2-Lvl Site–Species	$\rho_{site(lake)}$	0.489	1.221	1.910	13
	$\rho_{site(river)}$	0.447	1.023	1.733	7
3-Lvl Site–Species (cold water nest)	$\rho_{site(lake)}$	0.274	1.297	1.958	13
	$\rho_{site(river)}$	0.235	0.966	1.561	7
	$\rho_{cold(lake)}$	0.203	0.841	1.278	5
	$\rho_{cold(river)}$	0.563	1.701	3.446	17
3-Lvl Site–Species (river & lake nests)	$\rho_{site(lake)}$	0.658	1.333	2.729	14
	$\rho_{site(river)}$	0.541	1.074	2.052	10
	$\rho_{river/lake}$	0.648	1.166	1.682	13
4-Lvl Site–Species	$\rho_{site(lake)}$	0.345	1.430	2.670	14
	$\rho_{site(river)}$	0.302	1.051	2.055	9
	$\rho_{cold(lake)}$	0.265	0.945	1.969	8
	$\rho_{cold(river)}$	0.710	1.704	4.181	17
	$\rho_{river/lake}$	0.660	1.179	1.758	12

[a] Number of times in twenty draws that the dissimilarity coefficient listed in column 2 is statistically significantly greater than 1 at a 99% confidence level.

and one for lake sites. In both the unrestricted three-level site–species (w/cold) and four-level site–species models, the cold dissimilarity coefficients on the lake sites are consistently less than one. In contrast, in these models, the cold dissimilarity coefficients on the river sites are consistently greater than one. These results indicate that there is likely to be more substitution among salmon and trout at lake sites and less substitution among the cold water species at river sites.

Similar to our experience with the species–site models, we were unable to estimate unique parameters on the river or lake nests in the three-level site–species (w/river&lake) and four-level site–species models. Again, the parameter estimates would not converge. This is most likely a result of the small number of river sites relative to lake sites in any one angler's choice set. In contrast to our

findings in the species–site models, however, the common dissimilarity coefficient on the river and lake nests in the site–species models is more often than not statistically significantly greater than one, indicating that more substitution occurs between rivers and lakes than among rivers or among lakes. This result is most likely capturing some of the substitution across sites for the same species as indicated by the relatively large dissimilarity coefficients for lake and river sites in the site–species models and the relatively small dissimilarity coefficients for the species nests in the four-level species–site model.

The results in Table 2 also reveal that, even though there are many cases in this study in which the median estimated dissimilarity coefficients across the twenty draws are greater than one, these estimates are usually close to one. For example, the highest median estimate of a dissimilarity coefficient across all eight nested models is 1.70. This result differs significantly from that of Kling and Thomson, who find that the dissimilarity coefficients often exceed two and are sometimes greater than four. The implications of this result will be discussed in the next section.

Welfare Estimates

The welfare effect of a change in site quality can be represented as the difference between the maximum expected utility of a trip, with and without the change, divided by the estimated coefficient on the travel cost variable (Small and Rosen, Hanemann, Morey). If we assume that income effects are zero, the closed-form expression for compensating variation (CV) associated with a change in the quality of one or more alternatives, or the elimination of an alternative, takes the form

$$(10) \quad \text{CV} = EV = [EU^1 - EU^0]/-\alpha$$

where α is the coefficient on the travel cost term (see Table 1) and can be interpreted, in absolute value, as the marginal utility of income. The zero income effects assumption, though widely used, has its limitations. Under this assumption, the value per unit of characteristic, as well as the value of access, is assumed to be independent of income. Neither may be realistic.

EU^0 and EU^1 represent the maximum expected utility of a trip without and with

the change, respectively. In a simple two-level model in which site choice is conditional upon species choice, EU^a takes the form

$$(11) \quad EU^a = \ln\left[\sum_{f=1}^{F} \exp(\delta z_f + \rho_f \ln(I_f))\right] + 0.57$$

where $I_f = \sum_{i=1}^{Nf} \exp((\alpha p_i + \beta \mathbf{x}_i + \gamma_f \mathbf{w}_{if})/\rho_f)$ is the inclusive value for species nest f, a is equal to zero or one, and ρ_f is the dissimilarity coefficient on species nest f, capturing the degree of substitution among sites within each species nest.

For each of our models, we estimate welfare effects for three policy scenarios. These policy scenarios include the clean up of all lakes that do not meet EPA quality standards, the clean up of all toxic river sites, and the elimination of salmon as a possible target species. The first two scenarios each provide an estimate of the benefits of a hypothetical pollution clean-up or abatement program, while the third provides an estimate of the overall value of salmon fishing day trips. In the lake clean-up scenario, all polluted lakes are assumed to be cleaned. Because cold water species (salmon and trout) are often greatly affected by non-point source pollution while other species such as bass and other remain unaffected, the lake clean-up has the added effect of making both salmon and trout abundant in the formerly dirty lakes even if neither of these species was present before the clean-up. In the river clean-up, all rivers are assumed to be free of toxins, thereby removing all fish consumption advisories. Salmon elimination is accomplished by removing salmon from all sites at which it was formerly present. The median per trip values across the twenty random draws for our nine models for all three welfare scenarios are presented in Table 3. In Table 3, estimates of the per-trip value for cleaning polluted lakes range from $3.60 per person in the two-level species–site model to $1.89 in the non-nested model. The per-trip value for removing all fish consumption advisories on rivers ranges from $1.32 in the three-level site–species (w/cold) model to $1.11 in the three-level species–site (w/river&lake) model. Eliminating salmon as a target species results in per-trip losses ranging from $3.67 per person for the three-level species–site (w/cold) model to $2.74 for the non-nested model.

Table 3. Median Per-Trip Welfare Estimates

Model	Scenario 1	Scenario 2	Scenario 3
Non-nested	$1.89	$1.14	$2.74
Two species–site	$3.60	$1.24	$3.50
Three species–site (cold)	$3.58	$1.23	$3.67
Three species–site (R/L)	$2.52	$1.11	$3.51
Four species–site	$2.52	$1.16	$3.71
Two site–species	$2.91	$1.23	$3.19
Three site–species (cold)	$2.82	$1.32	$3.21
Three site–species (R/L)	$3.08	$1.15	$3.43
Four site–species	$2.89	$1.29	$3.29

Notes: For each model we have twenty estimates corresponding to our twenty random draws. We calculated the average per trip value across all individuals in the sample for each model and here we report the median value across the twenty models.
Scenario 1: Clean up all dirty lakes and restore salmon and trout to abundance.
Scenario 2: Clean up all toxic rivers having fish consumption advisories.
Scenario 3: Eliminate salmon fishing at all sites.

The variation in welfare estimates across the models is not large. Among the nested models only, the difference between the highest and lowest median estimates is 35.3% in the lake clean-up scenario, 17.3% in the river clean-up scenario, and 15.1% in the salmon elimination scenario.

These findings run counter to Kling and Thomson (see their Table 4) who find that welfare estimates can vary widely across alternative nested models by up to 174%.[12] The difference between our results and those of Kling and Thomson appears to originate with the estimates of the dissimilarity coefficients. As noted above, we find that the dissimilarity coefficients are often close to one, and that there is not a great deal of variation across the models. Kling and Thomson find much more variation in the dissimilarity coefficients across their models. In particular, their parameters that exceed one are often much greater that one. In a few cases the parameters are greater than four.

Shaw and Ozog (see their Table 2) also find that welfare estimates are sensitive to the choice of nesting structure. In fact, under one of the two nesting specifications considered in their study, welfare estimates could not be meaningfully calculated. The authors referred to their estimates as "nonsensical." Like Kling and Thomson, their dissimilarity coefficients varied widely between the two models. In one case, a dissimilarity coefficient

[12] Note that we could have used the Krinsky–Robb technique to simulate standard errors for the welfare estimates (see Krinsky and Robb, Kling and Thomson, Parsons and Kealy 1994) but we cannot compare the differences between welfare estimates in formal statistical tests because they are not independent random variables. Kling and Thomson attempted no such formal test either.

was estimated to be greater than ten. Unlike Kling and Thomson and our model, Shaw and Ozog also allow for nonlinear income effects. That more general specification may contribute to some of the sensitivity as well. Our interpretation of the difference in these findings is as follows:

When nesting structures are specified correctly, utility theoretic substitution patterns are revealed through dissimilarity coefficient estimates lying within the unit interval. The closer the dissimilarity coefficient is to zero, the greater the degree of substitution (or similarity) among alternatives within the nest. When nesting structures are specified incorrectly (inconsistent with utility theory), the *same* substitution patterns are revealed through dissimilarity coefficients greater than one. The high dissimilarity coefficient estimates in the incorrect model signal that there are poor substitutes within each nest, and reveal that there is a great deal of cross-nest substitution (or cross-nest similarity) present in the data. The greater the size of the dissimilarity coefficient, the greater is the degree of cross-nest substitution.

It stands to reason that data sets having strong correlation patterns among the random utilities will tend to have highly variable dissimilarity coefficient estimates as the nesting structures are altered. These estimates will be low (less than one) when the nests are specified accurately and high (much greater than one) when specified inaccurately. This point is confirmed by Herriges and Kling (1997) in a rather novel Monte Carlo study. They used fabricated data for which they know the parameters of site utility, the correct nesting structure, and size of the dissimilarity

coefficients in the nests. When a model is estimated using the fabricated data but an incorrect nesting structure, the dissimilarity coefficient is larger than one, signaling cross-nest substitution which we know is true. The lower the known dissimilarity coefficient is set in the true model, the higher the estimated dissimilarity coefficient is in the misspecified model.

It appears as though the Kling and Thomson and Shaw and Ozog data sets have some strong correlation patterns along the lines they are considering for nesting. This creates the wide variability in their dissimilarity coefficient estimates as the nesting structures are altered. The large variation in the dissimilarity coefficient estimates translates into large variation in the welfare estimates across the models. When correlation patterns in the data are strong, accurately accounting for them is important for welfare estimation. Again, this result is confirmed by Herriges and Kling (1997) in their Monte Carlo study. When their true models had low dissimilarity coefficients, their misspecified models not only had large dissimilarity coefficients, but also reported welfare estimates that deviated widely from the true values. In our analysis, in contrast with Kling and Thomson and Shaw and Ozog, the dissimilarity coefficients tend to be closer to one. The actual correlation patterns in our data set appear to be less important. Hence, when we misspecify our model the dissimilarity coefficients are larger than one, but not to the extent observed in these other studies. Since correlation is less important in our data set (at least along the lines we a considering), accounting for it accurately is less important for the welfare estimates. Indeed, there is little loss in accuracy across our nested models.[13]

It is important to note that correlation among alternatives within a nest may result from measurement inaccuracies as well. If the researcher simply lacks good information on rivers, for example, it is more likely that rivers will have shared unobserved characteristics leading to dissimilarity coefficient estimates that will be sensitive to the position of rivers in the nesting structure. Hence, large variation in dissimilarity coefficient estimates and, in turn, welfare estimates is likely to be more common in models with simple specifications

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[13] It is possible that other nesting structures using our data would have generated dissimilarity coefficients which deviated further from one. For example, if we had considered nesting by geographic regions or fishing modes, we may have found dissimilarity coefficients much closer to zero or significantly larger than one.

that do not account for those attributes that matter to individuals.

It is also worth noting that the welfare estimates from the nested logit models in our analyses are larger than the estimates from the non-nested models. This appears to be due to the welfare scenarios we are considering. All three cases consider large changes within specific nests that generate substitution across nests. Since the nested models are accounting for substitution within the nests, this cross-nest substitution generates larger values in the nested models. Small changes at one or two sites within a nest would have produced the opposite effect. Again, the differences here are not dramatic.

Kling and Thomson present a series of likelihood ratio tests comparing their different nesting structures. They use a likelihood dominance test suggested by Pollock and Wales. They find that the models which are least consistent with utility theory dominate (in a statistical sense) the models which are consistent with utility theory. That is, the models with largest dissimilarity coefficients greater than one tended to have the highest likelihood values. This finding is consistent with that of Ben-Akiva and Lerman (pp. 317–19). We find the same in our models. In our case, the species–site models are "most" consistent with utility theory, but the site–species models tend to dominate in statistical tests. However, we are skeptical of these tests. They assume that the likelihood values from each model are based on the underlying probabilities generated from a well-behaved multivariate pdf. All of the models with dissimilarity coefficients falling outside the unit interval do not, by definition, have well-behaved distributions since they permit probabilities that are negative or greater than one. This being the case, we cannot be certain that the likelihood ratios have a χ-squared distribution nor that they are valid for use in statistical tests.

Conclusions

In Kling and Thomson's closing comments they remark that,

> "Many of the results in this data set may not be generalizable to other recreation demand applications. To this end, it would be useful to examine the sensitivity of welfare measures for other data sets to the same of set

of specification issues here. Only by examining the magnitudes of specification differences across a variety of data sets can any generalizations be fruitfully made" (p. 113).

While they consider a number of different specification issues with nested logit models, we focus most of our analysis on the sensitivity of welfare estimates to changes in nesting structure. Our results suggest that welfare estimates may or may *not* be highly sensitive to the choice of nesting structure. It depends on the data set and the nest structures chosen by the analyst. In our application, the results are not particularly sensitive to the change in structure.

We have argued that the variation in the welfare estimates in recreation demand studies largely tracks the variation in the dissimilarity coefficient estimates across nested models. Kling and Thomson and Shaw and Ozog found wide variation in their dissimilarity coefficient estimates and we found relatively little variation. We argue that the greater the degree of actual correlation among random utilities, the greater is the likelihood of observing wide variation in dissimilarity coefficient estimates and, in turn, wide variation in welfare estimates across different nesting structures.

It is important to keep in mind that we have assumed linear income effects throughout this analysis. That restriction may have contributed to our finding of "insensitivity." We leave that question open for further research.

References

Atherton, T., M. Ben-Akiva, D. McFadden, and K. Train. "Micro-Simulation of Local Residential Telephone Demand Under Alternative Service Options and Rate Structures." *Telecommunications Demand Modelling: An Integrated View.* A. Fontenay et al., eds., pp. 137–63. New York: North-Holland, 1990.

Borsch-Supan, A. "On the Comparability of Nested Logit Models With Utility Maximization." *J. Econometrics* 43(March 1990):373–88.

Ben-Akiva, M., and S.R. Lerman. *Discrete Choice Analysis: Theory and Application to Travel Demand.* Cambridge MA: MIT Press. 1985.

Feather, P.M. "Sampling and Aggregation Issues in Random Utility Model Estimation." *Amer. J. Agr. Econ.* 76(November 1994):772–79.

Hanemann, W.M. "Applied Welfare Analysis with Qualitative Response Models." California Agr. Exp. Sta., 1982.

Hausman, J.A., G.K. Leonard, and D. McFadden. "A Utility Consistent, Combined Discrete-Choice and Count Data Model Assessing Recreational Use Losses Due to Natural Resource Damage." *J. Public Econ.* 56(January 1995):1–30.

Herriges, J.A., and C.L. Kling. "The Performance of Nested Logit Models When Welfare Estimation is the Goal." *Amer. J. Agr. Econ.* 79(August 1997):792–802.

——. "Testing the Consistency of Nested Logit Models with Utility Maximization." *Econ. Lett.* 50(January 1996):33–39.

Kling, C.L., and J.A. Herriges. "An Empirical Investigation of the Consistency of Nested Logit Models with Utility Maximization." *Amer. J. Agr. Econ.* 77(November 1995):875–84.

Kling, C.L., and C.J. Thomson. "The Implications of Model Specification for Welfare Estimation in Nested Logit Models." *Amer. J. Agri. Econ.* 78(February 1996):103–14.

Krinsky, I., and A. Robb. "On Approximating the Statistical Properties of Elasticities." *Rev. Econ. and Statist.* 68(November 1986):715–19 (correction, *Rev. Econ. and Statist.* 72(February 1990):189–90).

McConnell, K.E., and I.E. Strand. *"The Economic Value of Mid and South Atlantic Sportfishing, Volume II."* Report on EPA Cooperative Agreement, University of Maryland, 1994.

McFadden, D. "Econometric Models of Probabilistic Choice." *Structural Analysis of Discrete Data.* C.F. Manski and D. McFadden, eds., pp. 198–272. Cambridge MA: MIT Press, 1981.

——. "Modelling the Choice of Residential Location." *Spatial Interactioin Theory and Planning Models.* A. Karquist et al., eds., pp. 75–96. Amsterdam: North-Holland, 1978.

Morey, E.R. "Two RUMs UnCLOAKED: Nested-Logit Models of Site Choice and Nested-Logit Models of Participation and Site Choice." *Valuing Recreation and the Environment.* C. Kling and J. Herriges, eds., pp. 65–120. Northampton, MA: Edward Alger, 1999.

Morey, E.R., R.D. Rowe, and M. Watson. "A Repeated Nested-Logit Model of Atlantic Salmon Fishing." *Amer. J. Agr. Econ.*

75(August 1993):578–92.

Parsons, G.R., and A.B. Hauber. "Spatial Boundaries and Choice Set Definition in Random Utility Models of Recreation Demand." *Land Econ.* 74(February 1998):32–48.

Parsons, G.R., and M.J. Kealy. "Benefits Transfer in a Random Utility Model of Recreation." *Water Resour. Res.* 30(August 1994):2477–84.

——. "Randomly Drawn Opportunity Sets in a Random Utility Model of Lake Recreation." *Land Econ.* 68(February 1992):93–106.

Parsons, G.R., and M.S. Needelman. "Site Aggregation in a Random Utility Model of Recreation." *Land Econ.* 68(November 1992):413–33.

Pollack, R., and T. Wales. "The Likelihood Dominance Criterion." *J. Econometrics* 47(February 1991):227–42.

Shankle, S.A., J.E. Englin, W.H. Monroe, D.M. Beck, M.F. Casinelli, H. Saunders, and S.E. Grover. *Freshwater-Based Recreation in the Upper Northeast: Data Collection and Documentation.* Pacific Northwest Laboratory, Batelle Memorial Institute, 1990.

Shaw, W.D., and M.T. Ozog. "Modeling Overnight Recreation Trip Choice: Application of a Repeated Nested Multinomial Logit Model." *Environ. and Resour. Econ.* 13(June 1999):397–414.

Small, K.A., and H.S. Rosen. "Applied Welfare Economics with Discrete Choice Models." *Econometrica* 49(1981):105–30.

Waters, S.M., and K.J. Dietz. "Measuring the Stability of Choice Set Randomization in Discrete Choice Models." Unpublished, Triangle Economic Research, 1995.