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An Example of Nonlinear UniODA

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An intuitive example of a nonlinear UniODA model is presented.

Many different types of nonlinear UniODA-based models—for example Markov processes, turnover tables, group dynamics networks, and multicategorical models—are discussed in the ODA book.[1] Recent studies of inter-rater[2] and inter-device[3] reliability of emergency medicine triage scores, and of paradoxical confounding that occurs[4] when triage data are combined for multiple pairs of raters, also involve nonlinear UniODA models. The discovery of novometric theory—the algorithm that explicitly identifies the globally optimal (maximum-accuracy) model for every unique combination of hypothesis, data geometry, and sample—suggests that under conditions of adequate statistical power it is in fact *likely* that *most* classical phenomena are *best* modeled using nonlinear UniODA models.[5-7] Nevertheless, and therefore, it is useful as well as interesting to highlight new intuitive examples of nonlinear UniODA applications as they are discovered: this is the context and motivation of the present article.

While searching for additional published examples of the Kruskal-Wallace test to compare with UniODA for expository purposes[8-10] I found McDonald's description[11] of the analytic question underlying data used herein (Table 1): "The biological question was whether protein polymorphisms (class=0) would have generally lower or higher F_{ST} values than anonymous DNA polymorphisms (class=1)".

Table 1: Data Sorted by F_{ST}

Class	F_{ST}
1	-0.006
1	-0.005
0	-0.005
0	-0.002
1	0.003
0	0.004
0	0.006
0	0.015
0	0.016
0	0.016
0	0.024
0	0.041
0	0.044
0	0.049
1	0.053
0	0.058
0	0.066
1	0.095
1	0.160
0	0.163

Comparing the classes via the Kruskal-Wallace test[11]: "For the example data, the mean rank for DNA (class 1) is 10.08 and the mean rank for protein (class 0) is 10.68, H=0.043, there is 1 degree of freedom, and the *p* value is 0.84. The null hypothesis that the F_{ST} of DNA and protein polymorphisms have the same mean ranks is not rejected."

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A complementary conclusion is obtained by conducting bivariate UniODA[1] to compare the two classes. For an application involving an *ordered* attribute, both the exploratory and the confirmatory bivariate UniODA model have the following ordinal form: if subject's score ≤ (or ≥) threshold then predict class=0; otherwise predict class=1. Exploratory UniODA identifies the specific combination of threshold and direction (≤ or ≥) that explicitly maximizes classification accuracy normed against chance, and confirmatory UniODA finds the threshold (or evaluates a specified threshold) for an *a priori* specified direction that explicitly maximizes the level of classification accuracy normed against chance.[12-14] The normed classification accuracy of a model is measured using the *e*ffect *s*trength for *s*ensitivity (ESS) statistic: for any given application ESS=0 is the level of classification accuracy expected by chance, and ESS=100 is perfect, errorless classification.[1,5,15,16] In this application the exploratory bivariate UniODA model was: if $F_{ST} \leq 0.0035$ then predict class=1; otherwise predict class=0. While this model was not statistically reliable ($p<0.55$) as a result of low statistical power, the obtained ESS of 35.7 represents a moderate effect.[1]

However, using the ODA paradigm any structural hypothesis can be tested by using an explicitly optimized (i.e., yielding maximum-accuracy for the sample) statistical classification model.[17,18] In the present study for example, the biological question can be restated as whether protein polymorphisms (class=0) generally have *either lower or higher* F_{ST} values compared to anonymous DNA polymorphisms (class=1). Parsing of the data in the context of this new analytic question is illustrated in Table 2. As seen, for this new question the threshold values are defined as the values above which (at the low end, strata C) and beneath which (at the high end, strata A) no members of class=1 are found. By definition, observations between the upper and lower thresholds (strata B) are all members of class=0.

Table 2: Parsed Data Sorted by F_{ST}

Class		F_{ST}
1		-0.006
1		-0.005
0	A	-0.005
0		-0.002
1		0.003
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0		0.004
0		0.006
0		0.015
0	B	0.016
0		0.016
0		0.024
0		0.041
0		0.044
0		0.049
---	---	---
1		0.053
0		0.058
0	C	0.066
1		0.095
1		0.160
0		0.163

Manual identification and evaluation of these thresholds via UniODA is straightforward. First, test the directional hypothesis that class=1 observations have lower F_{ST} values than class=0 observations: this identifies the threshold value [(0.003 + 0.004) / 2] = 0.0035, that separates strata A from strata B and C. Second, test the directional hypothesis that class=1 observations have greater F_{ST} values than class=0 observations: this identifies the threshold [(0.049 + 0.053) / 2] = 0.051 that separates strata C from strata A and B. However, attributable to less-than-perfect classification accuracy in combination with the small sample and associated inadequate statistical power, these analyses were unrevealing: exact *p*'s<0.29 and 0.44, ESS's=35.7 and 28.6, respectively. Given identical results for a sample three times as large, the following globally optimal model[5,16] would emerge:

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Figure 1A: Globally Optimal Model Addressing the Restated Biological Question

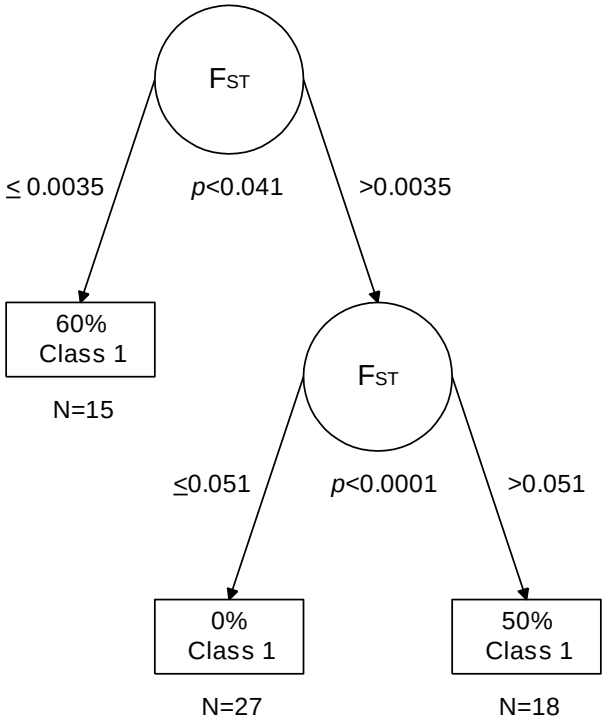
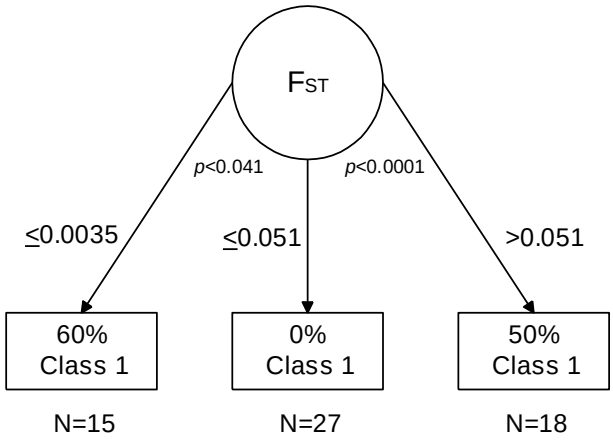


Figure 1B: Simplified Representation of the Globally Optimal Model



Note that the nonlinear UniODA model (Figure 1B) identified the thresholds described earlier. For this model ESS=64.3, a relatively strong effect.[1]

Alas, nevertheless, the sample is what it is, so what can be done regarding the paucity of statistical power? Cross-classification findings obtained by applying the nonlinear UniODA model depicted in Table 2 (if Strata=A or C then predict class=1; if Strata=B then predict class= 0) to classify the sample are reported in Table 3.

Table 3: Cross-Classification Table for the Nonlinear UniODA Model Depicted in Table 2 Applied to Classify the Sample

		Predicted Class 0	1
Actual Class	0	9	0
	1	5	6

UniODA applied to this result[1] indicates a relatively strong (ESS= 54.6) and statistically reliable (exact directional $p<0.0120$, non-directional $p<0.0141$) effect. ESS for this approach is lower than that (64.3) yielded by the model in Figure 1B, because the latter separates subjects with extreme F_{ST} values into two groups, rather than combining them into a single group as in Table 3. Combining different groups can induce Simpson's paradox: the effect here is to reduce estimated effect.[19-21] The importance of replication in such research can't be understated.[22]

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Author Notes

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