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What is Novometric Data Analysis?

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Novometric (Latin: *new measure*) statistical theory is introduced.

The mathematical modeling methodology which is called *o*ptimal *d*iscriminant *a*nalysis or ODA identifies nonparametric statistical models that *explicitly maximize* the (weighted) *accuracy* of predicted class assignments for the sample.[1-5]

It is crucial to understand that *accuracy* is *not* the same thing as *explained variation* or *maximum likelihood*. Neither of those centuries-old objective functions motivated development of methods which predict data very well, not even if effect sizes approach their theoretically maximum-possible values—thereby making *p*-values incomputable due to sparsity issues.[6-9]

In contrast, what one seeks using ODA is *predictive precision*. For example, imagine each individual case ("observation") in a sample is either a member of class A or class B. Further imagine a statistical model is obtained to predict whether each individual case in the sample is a member of class A or class B. ODA finds *the model* which makes the *most accurate possible predictions* into classes A *vs*. B for the sample, given the data. The most accurate solution that exists for the sample *is the optimal solution*.[1-5]

This paper briefly reviews etiology and ontogenesis of *novometric* (Latin: new measurement) statistical theory, the state-of-the-art ODA methodology.[5] Discussion first addresses crucial aspects of ODA classification models and of classification performance indices.

Classification Models and Performance

ODA is used in an effort to accurately predict a *class variable*, known as a dependent variable in legacy methods. *Attributes*, called independent variables in legacy methods, are used to predict class variables. Class variables and attributes may be ordered or (multi)categorical[10-12]; any positive number may be used as an observation-level weight (e.g., propensity score[13-15]); models may be static[16,17] or dynamic[18-26]; *a priori* hypotheses may be exploratory or confirmatory (i.e., one- or "two"-tailed); exact *p*-values and statistical power do *not* require distributional assumptions, and are easily computed[27-34]; and optimal methods are rapidly and successfully adopted by research faculty and students.[35]

Early use of maximum-accuracy predictive methods often addressed engineering objectives. Prevalent then, and still today, the tradition was to maximize the (weighted) proportion of the *total sample* correctly classified, without considering the class membership status of individual observations.[4,36-41] The associated *Percentage Accuracy in Classification* or PAC index ranges between 0% and 100% correct, however this index is *not* normed *vs*. chance.

The focus of modern research, the *Effect Strength for Sensitivity* or ESS index of classification accuracy—a function of the model mean sensitivity across classes—is adjusted by prior

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odds in order to *eliminate the effect of chance*.[4] ESS=0 is the level of classification accuracy that is expected by chance; ESS=100 is perfect (errorless) classification; and -100≤ ESS<0 indicates classification accuracy *worse* than is expected by chance.[4,42-47]

Regarding the *theoretical meaning* of ESS, the findings of original Monte Carlo investigations, in conjunction with advances made in subsequent research, motivate the continuing use of the categorical ordinal ESS descriptors as originally proposed—which have passed the test of time: ESS<25 is a relatively weak effect; ESS<50 a moderate effect; ESS<75 is a relatively strong effect; ESS<90 is a strong effect; and ESS≥90 is a very strong effect.[4] Models with a high ESS are favored in applied *translational* and *precision forecasting* applications, owing to their adaptability to the *diversity* reflected by legions of individual case profiles.

As ESS adjusts classification accuracy to compensate for the role of chance, the *distance* or D statistic adjusts ESS to compensate for the role of model complexity—operationalized formulaically in terms of number of sample strata identified by the GO model.[5] D indicates the additional number of effects (which return the mean ESS) needed to obtain a perfectly accurate model.[47-49] Models with a small D are favored in *theoretical* applications, because they retain only the empirically strongest findings.

Novometric Statistical Theory[5,50,51]

Novometric theory postulates the following set of four axioms:

Axiom 1: For a random statistical sample S_1 consisting of a class variable, one or more attributes and a weight, corresponding exact discrete 95% confidence intervals obtained for *model* and for *chance* do not overlap (i.e., a "statistically significant effect" exists).[52-56]

Axiom 2: In applications involving more than one attribute, the subset of attributes in S_1 which yields the globally optimal (GO) model having the lowest D statistic is identified via structural decomposition analysis (SDA), which involves iterative application of ODA in a manner that is conceptually analogous to principal components analysis, but that explicitly maximizes classification accuracy—instead of variance.[4,35,57-61]

Note: In my experience using ODA software, a primary utility of Axiom 2 (which required four years to authenticate) lies in the analysis of data sets having large N and many attributes bearing a weak- to moderate-strength relationship to the class variable, that degrades in LOO analysis. Analyzing such data it is not inconceivable to use CPU days in unsuccessful attempts (attributable to researcher fatigue) to identify the initial CTA model. In my personal experience, if I can obtain a descendant family (see Axiom 3) in reasonable time-on-task (an hour or less), then I often forego Axiom 2.

Axiom 3: The GO model for S_1 is found in the descendant family of models that is obtained by applying the minimum denominator search algorithm (MDSA) to an initially-unrestricted enumerated classification tree analysis (CTA) model configured to predict the class variable using only the attribute(s) selected by SDA. The MDSA algorithm enables discovery of all CTA models in S_1 which vary as a function of complexity and that originate from an unadulterated (initially unrestricted) model.[5,13,18]

Note: I learned to *not* make assumptions when obtaining a descendant family. Suffice it to say, I continue to augment the minimum denominator until the software returns a message stating "no model found".

Axiom 4: Validity is assessed by using the GO model to classify an independent random S_2 (if possible), and/or for S_1 by cross-generalizability methods such as hold-out, leave-one-out (LOO) one-sample jackknife, K-of-N jackknife, split-half, multi-sample and/or bootstrap methods for

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static data[4], and using test-retest[62-67], survival (time-to-event)[21,23], little jiffy[68,69], and weighted Markov[70-74] methods with dynamic (repeated-measures) data. These types of analyses enable researchers to identify the limits of cross-generalizability of GO models when they are used to classify independent random samples.[4,5]

Discussion now considers two simple real-world examples of novometric analysis.

Gender and Cancer Incidence

Imagine evaluating if the cancer incidence rate (CIR) for all cancer types combined, assessed across numerous independent sites, differs by gender—male *vs*. female.[50]

If using a legacy methodology such as *t*-test[75-77] or logistic regression[9,78-80] to compare CIR between gender, one's conclusion would necessarily be: (a) the absence of a statistically significant effect indicates the CIR of males and females does not differ; or (b) the presence of a statistically significant effect indicates males have a (higher or lower) CIR *vs*. females.

In contrast, having only *two* options as a possible analytic solution in this example is *not* a restriction for novometric analysis.

Data were drawn from the Surveillance, Epidemiology and End Results (SEER) Program, which collects and publishes cancer incidence and survival data to assemble and report estimates of cancer incidence, survival, mortality, other measures of the cancer burden, and patterns of care, in the USA. SEER statistics routinely include information specific to race/ethnic populations and other populations defined by age, gender and geography. Herein, CIR is the number of new cancers of a specific site that occurs in a specified population in one year, expressed as the number of new cancers for every 100,000 population at risk.

Analysis involved N=608 observations. Assuming proportional reduction in sample size across successive parses: a single binary parse creates two strata each having N=304 observations; two binary parses create four strata each having N=152 observations; and three binary parses create eight strata each having N=76 observations. This sample size is more than sufficient[34] to achieve greater than 90% power to identify a moderate effect with $p<0.05$.

Table 1 summarizes findings of novometric analysis using gender to parse CIR data. The initial (6 strata) CTA model that emerged had moderate ESS: its point estimate (33.2) and the upper (41.2) and lower (25.4) bounds of the 95% CI for model-based ESS all indicate *moderate effect*. The 95% CIs for chance-based ESS lie substantially beneath corresponding 95% CIs for model-based ESS. Note that since no *two-strata* model comparing *all* males *vs*. *all* females *exists* in the descendant family, this is a statistically unmotivated, exploratory comparison.

Table 1: Parsing Cancer Incidence by Gender: All Sites Combined

Strata	MinD	ESS	Efficiency	D
6	2	33.2	5.54	12.1
		25.4-41.2	4.22-6.87	8.6-17.6
		0.33-7.57	0.06-1.26	73.3-1812
5	63	33.2	6.64	10.1
		25.3-41.2	5.05-8.23	7.1-14.8
		0.33-6.91	0.07-1.38	67.4-1510
3	80	31.9	10.6	6.4
		22.8-40.6	7.60-13.5	4.4-10.2
		0.33-7.57	0.11-2.52	36.6-906

Note: Strata is number of CTA model endpoints. MinD (for minimum denominator) is the smallest sample size for any strata. Efficiency, defined as ESS/Strata, is a normed index of relative strength of the class variable(s) used in identifying sample strata. Results for every step of MDSA analysis are tabled. For each model the first line is a point estimate; the second line gives a 95% confidence interval (CI) for the discrete distribution obtained for the model by bootstrap analysis; and the third line is a 95% CI for chance obtained using Monte Carlo analysis with 100,000 iterations. Values for model efficiency were computed by dividing ESS by the number of strata.

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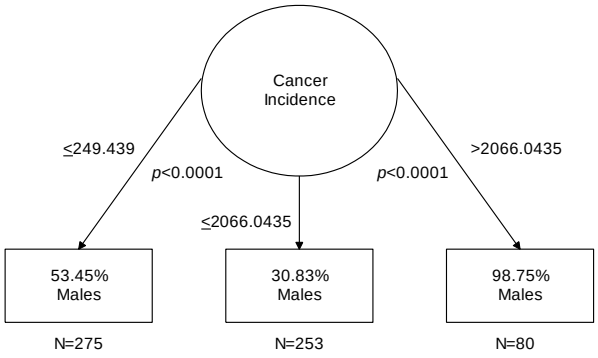
As seen in Table 1 the initial CTA model identified six strata, the smallest of which represented only two observations. The 95% CI for this endpoint (not tabled) included 0%, rendering the CTA model redundant.

In step two of the minimum denominator selection algorithm, a LOO-stable five-strata CTA model was obtained yielding moderate ESS equivalent to that of the initial six-strata model, as assessed by point estimate and by 95% CI overlap. The five-strata model had 6.64/5.54 or 19.9% greater efficiency as assessed by point estimate, however this difference wasn't statistically significant because the five- and six-strata 95% CIs for efficiency overlapped. The smallest strata for this model had N=63 patients.

In step three the final LOO-stable model in the descendant family identified three patient strata. Based on point estimates the final model achieved 31.9/33.2 or 96% of overall accuracy (ESS) *vs*. the other models. And, examining 95% CIs for model-based ESS reveals that all models had comparable ESS (the three-strata model had greater efficiency *vs*. the six-strata model). However, because the lower-bound of ESS of the three-attribute model was 22.8 (or relatively weak), the ESS for the three-strata model indicates a *weak-moderate* effect.

Having achieved comparable strength, and greater parsimony and efficiency *vs*. other models in the descendant family, the three-strata model is selected as being the GO model of the relationship between gender and all-site cancer incidence. Illustrated in Figure 1, circles (model nodes) represent attributes (cancer incidence); arrows indicate model branches; rectangles are model end-points and represent sample strata; numbers adjacent to arrows are the value of the *cutpoint* for the node; numbers beneath nodes are the exact per-comparison Type I error rate for the parse; the number of observations classified in each endpoint is indicated beneath the endpoint; and the percentage of male observations is given inside the endpoint.

Figure 1: Three-Strata CTA Model Predicting Cancer Incidence by Gender, All Cancer Sites



As seen, the sample strata having *lowest* cancer incidence (≤0.25%) was approximately equally represented by males and females, and it comprised 275/608 or 45% of the total sample. In contrast, the sample strata with *highest* cancer incidence (>2.06%) was dominated (98.8%) by males, and comprised 13% of the sample. And, the sample strata having an *intermediate* cancer incidence (0.26%-2.065%) was 69.2% female and comprised 42% of the total sample.

Fear, Specific Recommendation, and Inoculation Shot-Taking Behavior

Classic research tested the *a priori* hypothesis that fear and specificity of recommendation synergistically influence a person's decision to have a tetanus inoculation.[81] Data analysis by χ^2 missed the hypothesized interaction: "…specific plans for action influence behavior while level of fear does not" (p. 27).

For these data, CTA with shot taking (yes *vs*. no) used as class variable, and fear and specific recommendation as attributes, found a relatively strong, cross-generalizable two-strata model (Figure 2) supporting the *a priori* hypothesis that fear and specific recommendations synergistically predict shot-taking behavior.[82] The confusion matrix for this three-strata model is presented in Table 2.

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Figure 2: Fear and Specific Recommendation Predict Shot-Taking Behavior

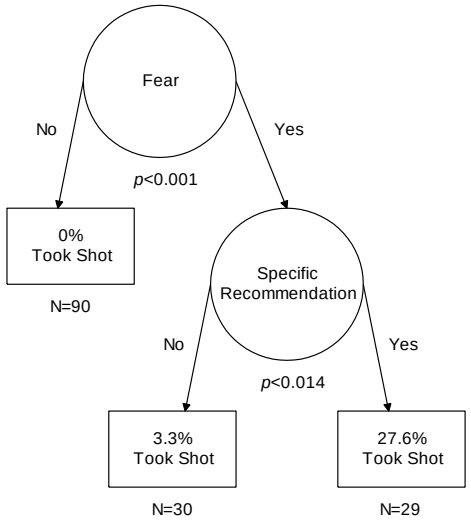

Table 2: Confusion Matrix for CTA Model, Factorial Design, Fear and Specific Recommendation

		Predicted Behavior		
		No Shot	Shot	
Actual	No Shot	119	21	85.0%
Behavior	Shot	1	8	88.9%

A statistically reliable, reproducible, and strong effect (ESS=73.9) emerged: as seen, 7 in 8 of the people refusing the shot, and 8 in 9 of the people accepting the shot, were correctly predicted by the model. Consistent with the original hypothesis, fear and specific recommendation interact to affect shot-taking behavior. As the root variable, fear plays the dominant role. When there is no fear, 0% of 90 people took the shot. When there is fear, but no specific recommendation is given, 3.3% of 30 people took the shot. However when there is fear and specific recommendation, 27.6% of 29 people took the shot.

Coda

In the event that this brief introduction leaves one wanting to know more, I recommend a few papers discussing modeling ordered class variables[83-85], matrix display of findings[86,87], and generating novometric confidence intervals using R software.[88] In addition, articles are available which contrast novometric analysis with legacy methods such as ANOVA[89-93], Friedman test[94], log-linear analysis[95-99], logit analysis[100], logistic regression[101], Markov analysis[102,103], regression/correlation[104-109], polychoric correlation[110,111], Probit analysis[112], recursive causal analysis[113], sign test[114], stepwise analysis[115], temporal analysis[116-119], and Yule's Q.[120]

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Author Notes

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