

GOLDEN AGES OR MAGIC MOMENTS?

JOHN POPE VI
Norwegian College of Fisheries
Universitetet i Tromsø
Tromsø, Norway
E-mail address: popejg@aol.com
Current address: NRC (Europe) Ltd.
The Old Rectory
Burgh St. Peter
Norfolk, UK NR34 0BT

ABSTRACT. The paper is an attempt to refute Quinn's "the Golden Age of fisheries population models has ended" hypothesis. The approach is to show it is possible to provide simple matrix based theory for use with delay difference equations applied to products of the 0th to 4th powers of length and numbers at length (Alias "proto-moments"). It compares these to models just based upon numbers and biomass. It also shows examples (of comparatively little moment) indicating how using multiple proto-moments could improve the ability of delay difference equations to handle the size dependent processes of maturity, selection, natural mortality rates and predation rates and thus improving the biological reality of these models.

KEY WORDS: Delay-difference equations, fisheries assessment, moments, Golden Ages.

Introduction: never a dull moment. Terry Quinn II's paper (Quinn [2003]), the inspiration (burr under the blanket?) for this collective edition, is a good "straight-necked" fox that gives an exciting gallop through the past of fisheries models and a "view halloo" for the future. I enjoyed the ride but my horse-sense balked at a few of the hedges.

What did I balk at? A minor balk was that I found it rather too dismissive of multispecies modeling. Predation on small/young fish is a very pertinent part of population dynamics. For example cod-sprat dynamics in the Baltic cannot be understood in isolation; cod eat sprat and sprat eat cod eggs. Ignoring multispecies effects will not do – even though it is intrinsically difficult. In fact multispecies arguments are used routinely in the management of cod-caplin stocks in the North Atlantic and implicitly taken into account elsewhere. Since

the developments of multispecies VPA form a key part of my personal Golden Age I would question its exclusion. This brings me to my major balk, firstly the concept of there having been a “Golden Age” and secondly (and not to be stomached) my working prior to it in what I guess we might regard as the “Age of Innocence”! As we all get older Terry, it’s natural to look back on our own most productive period and see it as a “Golden Age”. For us undoubtedly such times produced “Magic Moments” but I fear our seeing these as a “Golden Age” identifies us as old F**ts. It just proves we are not young Turks anymore.

So methinks the next generation of Young Turks will have their own “Magic Moments”. Certainly they will have more powerful computers. To put this into perspective, my computation course at college was on how to use hand-cranked mechanical calculators and my first pocket electronic calculator seemed a miracle. They will doubtless have new theory; for many years for me linear regression and ANOVA were high adventure. They will still have lots of problems to solve and longer time series of data to fit solutions to. What joy it would be to have 200 years worth of reliable age-based fisheries data. So far from thinking the Golden Age is over I suspect it’s still some time into the future. However, the problem will be that when it arrives neither I nor perhaps Terry (should we be spared) will understand the models produced though one could hope that John Pope IX or Terry Quinn V might!

If I really am a product of the age of innocence then it is not surprising that I like things to be so simple even I can grasp them. All too often progress must mean complication, so I felt that the best refutation of the idea of the end of the “Golden Age” is to find something simple at the heart of population dynamics that I could improve on or at least simplify. This brings me to the other “Magic Moments”¹; means, variances and other things which we learned of in statistics courses. It has been mooted that these could be used in population-dynamics (see Hilborn and Walters [1992], Quinn and Deriso [1999]) but it seems to me they seldom are, at least not in my part of the world. Nevertheless they have the potential to be magic by reducing age or length distributions down to a few variables which are descriptive of our main concerns and

¹ When I consider every thing that grows
Holds in perfection but a little moment Wm. Shakespeare, Sonnet XV

might get us off the grind of spending most of our time producing huge and expensive sets of aging data in order to provide age based fisheries assessments.

Hence in this paper I ask, is it possible to simplify our understanding of magic moments and extend the areas where they are useful? If it proves possible to extend their useful area in a simple way, for me if no one else, that would mean that the hypothesized end of my personal Golden Age is falsified. If alternatively I am only reiterating other people's ideas that I haven't read or understood properly, it just reinforces the (well-supported) Pope is an old F**t hypothesis and I can get on with pruning roses with a clear conscience.

Background: moments in time. Deriso [1980] shows how the population dynamics of age structured fish stocks may be collapsed into a delay difference equation. A number of the advantages of delay-difference equation formulations are described in Hilborn and Walters [1992] and an up-to-date summary is available in Quinn and Deriso [1999]. One way of writing these (see Quinn and Deriso [1999]) is as simultaneous recurrence relationships for both numbers and biomass. Biomass/numbers of course gives the mean weight of fish in the stock; the first moment. The idea of estimating the moments of the population size distribution is extended by Fournier and Doonan [1987] who show an approach to forming recurrence relationships for the statistical moments of the length distributions. Hence, one way of viewing delay difference equations is to see them as reducing the problem to looking at the moments of the size distribution rather than the distribution itself. This allows the expression of problems in a simpler, more analytically tractable and less parameterized form.

It is argued here, however, that for population dynamic purposes there is an advantage in keeping the state vector in terms of the sums of products of powers of length with numbers at length rather than as corrected and centered moments. These uncorrected, forms are of more biological interest than their centered standardized forms (mean, variance, skewness, kurtosis). For convenience in what follows these uncorrected forms will be called proto-moments. For example the zero'th proto-moment is the number in the total population of fishable age and the 3rd proto-moment may be converted to biomass under the assumption of isometric growth.

The column vector of all the fish population's proto-moments up to the n th may be written as

$$(1) \quad {}_n\Psi_y = |Pm_{y,m}|,$$

where $m = 0, \dots, n$. and $Pm_{y,m}$ is the m th proto-moment of a length (or length at age) distribution

$$(2) \quad Pm_{y,m} = \sum_{\text{all } L} N_{L_{a,y}} L_{a,y}^m$$

where $N_{L_{a,y}}$ is numbers at length $L_{a,y}$ at age a at the beginning of year y .

Pope [2003] describes how delay difference equations may be written in terms of the proto-moments. Briefly, The Ford-Walford equation

$$(3) \quad L_{a+1,y+1} = (1 - e^{-K})L_{\infty} + e^{-K}L_{a,y}$$

describes the relationship between the length of fish at age a in year y and the length of fish in the next age and year, where L_{∞} and K are the parameters of the von Bertalanffy growth equation. Raising equation 3 to the n th power gives the recurrence relationship for $L_{a+1,y+1}^n$:

$$(4) \quad L_{a+1,y+1}^n = [(1 - e^{-K})L_{\infty} + e^{-K}L_{a,y}]^n.$$

More generally the recurrence relationship between the column vectors ${}_n\mathbf{L}_{a,y}$ {composed of the $L_{a,y}^m$ where $m = 0, 1, \dots, n$.} and ${}_n\mathbf{L}_{a+1,y+1}$ may be written as

$$(5) \quad {}_n\mathbf{L}_{a+1,y+1} = \mathbf{G}_n {}_n\mathbf{L}_{a,y}.$$

Where the growth matrix G has elements (where $i = 1 : n + 1$ and $j = 1 : n + 1$)

$$(6) \quad \begin{aligned} g_{i,j} &= 0 \quad \text{if } j > i \quad \text{else} \\ &= [(1 - e^{-K})L_{\infty}]^{(i-j)} [e^{-K}]^{(j-1)} (i-1)! / [(i-j)!(j-1)!]. \end{aligned}$$

Noting from cohort analysis (see Quinn [2003]) {where $N_{a,y}$ is the population of age a the beginning of year y , $C_{a,y}$ is the catch number

at age during the year and M is the instantaneous natural mortality rate assumed constant for all exploited ages} that:

$$(7) \quad N_{a+1,y+1} \approx N_{a,y}e^{-M} - C_{a,y}e^{-M/2},$$

and assuming growth occurs in the second half year, it is possible to generalize the approach of Deriso [1980]. Scalar multiplying the respective RHSs and LHSs of equations 5 by the respective sides of equation 7 and summing over all ages, gives

$$(8) \quad {}_n\Psi_{y+1} = \mathbf{G} \left[{}_n\Psi_y e^{-M} - {}_n\Omega_y e^{-M/2} \right] + {}_n\mathbf{L}_{c,y+1} \cdot N_{c,y+1}.$$

where c is the youngest age considered and where ${}_n\Omega_y$ is the column vector of the proto-moments of catch, i.e., the column vector of $\sum_c L_{a,y}^m C_{a,y}$, for $m = 0$ to n . In practice it may be preferable to replace $N_{c,y+1}$ by $R_{y+1-c}e^{-M'_c}$. Where R_{y+1-c} is recruitment to the $(y+1-c)$ th yearclass and M'_c is the natural mortality rate between the age at which recruitment is measured and age c .

Equation 8 provides a simple transition matrix form for updating the proto-moments of a population. Hence, given the proto-moments in year y and incoming recruitment, it is simple to make year by year forward simulations of the stock size and structure. Clearly, stock recruitment relationships may be included providing (for the moment) these may be based upon total biomass of age c and older. An advantage of using equation 8 is that it admits of size selection since there may be different harvest rates ${}_n\mathbf{H}_y$ for the various elements of ${}_n\Psi_y$. In vectors (where “ \circ ” and “ \oslash ” imply element-by-element multiplication and division of column vectors),

$$(9) \quad e^{-M/2} {}_n\mathbf{H}_y \oslash {}_n\Psi_y = {}_n\Omega_y.$$

Thus

$$(10) \quad {}_n\mathbf{H}_y / h_{y,0} = \frac{{}_n\Omega_y}{\omega_{y,0}} \oslash \frac{{}_n\Psi_y}{\psi_{y,0}}$$

where $h_{y,0}$, $\omega_{y,0}$ and $\psi_{y,0}$ represent the 0th elements of the respective vectors. Recalling equations 1 and 2, it is apparent from equation 10 that the ratio of the harvest rate on the m th proto-moment to that

of the 0th proto-moment (harvest rate of numbers) is the ratio of the average L^m of the catch to the average L^m of the population in the sea. For example the element of equation 10 corresponding to the 3rd proto-moment would indicate whether the average weight of a fish in the catch is larger or smaller than the average weight of a fish (older than age c) in the sea. This ratio is a clear indication of size selection. The ratios of the harvest rates of the other proto-moments to that of the 0th proto-moment will indicate the differences between the selection patterns of different gears (e.g. gill nets and trawls). Thus using a model with a number of proto-moments allows size selective fisheries to be modeled with considerable realism.

To illustrate the use of this approach, Figure 1 shows the results of a back of the envelope assessment of NAFO Subdivision 3Ps (Southern Newfoundland-St. Pierre Bank) cod, which includes fitting the model to the available commercial catch at age data and to trawl survey and recruitment index data available in 2001 and then making forward projections for a 15Kt TAC. Results are very similar to those of a full age based assessment of this stock based upon the same data sets (see Brattey et al. [2001]). Clearly, the simple linear nature of equation 8 would also lend itself to Kalman filter or Bayesian estimation approaches which could account for process and sampling error in, and correlation between, the variables and their predictors.

Equation 8 can also be used in the calculation of steady state yield surfaces in terms of harvest rate and of size selection. Pope [2003] shows that in the steady state an equivalent to equation 8 (given constant harvest levels H_n) can be solved for the steady state as

$$(11) \quad {}_n\Psi_{(.)}/R_{(.)} = (\mathbf{I} - \mathbf{G}\mathbf{S})^{-1} {}_n\mathbf{L}_{c,(.)}$$

where “(.)” indicates the steady state, \mathbf{I} is the identity matrix, \mathbf{S} is a diagonal matrix with elements $s_{m,m}$ of $(e^{-M} - e^{-M/2}h_m)$, where h_m is the m th elements of the vector ${}_n\mathbf{H}$. It is also shown that where R_y can be expressed as a function of $Pm_{y,3}$ and where the stock recruitment relationship has a simple functional form, an analytical solution exists for equation 11. Figure 2 taken from Pope [2003] shows the estimated yield surface for 3Ps cod assuming an appropriate Ricker stock recruitment relationship.

It is clear that delay difference equations, written in terms of a number of proto-moments, are a useful way of describing fish stock

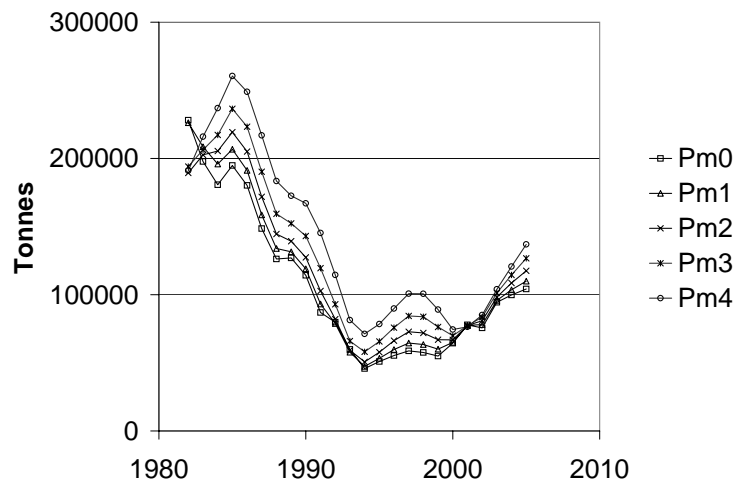


FIGURE 1. Estimated proto-moments for the NAFO subdivision 3Ps (Southern Newfoundland) cod. The 0th to 4th proto-moments are labeled Pn0-Pn4. These are based upon $(\text{weight in kg.})^{1/3}$ rather than length and numbers of fish in thousands. Pm3 is thus measured in tonnes while other proto-moments have units of fractional powers of weight.

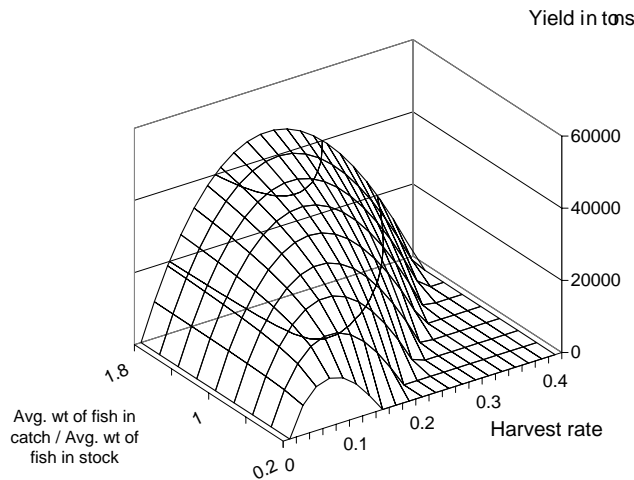


FIGURE 2. Yield isopleth surface for the NAFO Subdivision 3Ps cod stock at average levels of temperature. Yield is plotted against the biomass harvest rate and selection (ratio of average weight of a fish in the catch to average weight of a fish, older than age c , in the stock).

dynamics. What follows is an attempt to show why the burden of carrying additional proto-moments is worthwhile and to show ways in which the basic model set out in equation 8 can be adapted to provide additional realism in the formulation.

How many population proto-moments should be retained; Just a few moments? Statistical theory (Yule and Kendall [1947]) indicates that higher moments are difficult to estimate with any accuracy and it seems likely that the first few proto-moments will carry most information about the number and size structure of the population. The 0th proto-moment of the size structure (numbers) and the 3rd proto-moment (convertible to biomass) are of obvious interest to population dynamics. However, in order to deal with factors such as biomass (based upon the 3rd proto-moment) equation 8 indicates it is necessary to also carry the 1st and 2nd proto-moments. By analogy with biomass, these might be regarded as the biolength (how long the stock would be if deployed in “line astern” and related to the bioarea of the stock (how much surface area the stock has). At first glance these appear to be nuisance variables and it is reasonable to ask if carrying these extra terms is worthwhile.

Quinn and Deriso [1999] appear to prefer to write delay-difference models for numbers and biomass. For a one-year prediction that starts from known population sizes, this more parsimonious model seems perfectly adequate but it appears to be biased for longer term predictions. Kimura et al. [1996] also found it to be biased when process error was added. Bias would not be surprising since (at least with von Bertalanffy growth) it is length rather than weight that is linearly related between ages in a cohort.

To illustrate the bias with the parsimonious (numbers and biomass only) model, a simulation was set up for a stock with 3Ps cod-like growth with ages from 3 to 20 ages. It was simulated using uniformly random annual recruitment and varying annual fishing mortality rate (annual rates were drawn uniformly at random between zero and a maximum rate) and produced exact catch and population sizes. These were used to provide estimates of the 5 proto-moments of catch. The biomass could thus be projected using the age based approach, using the numbers and biomass approach or using the 0th to 4th proto-moment approach outlined above (note that in this test only the 0th to

3rd proto-moments are needed for the estimation of biomass and the 4th proto-moment is a free loader).

Simulations were made using all three methods started from the same initial population and drew on the same catch and recruitment data. These simulate biomass for a 100 year period. This was repeated 100 times at each of 4 levels of maximum fishing mortality rate. The 0th to 4th proto-moment approach provided estimates which were always very highly correlated with the age based biomass estimates. Correlation (all made through the origin) was slightly lower on low maximum fishing mortality rate {0.92 when maximum fishing mortality was 0.1, perhaps due to the lack of a plus group in the age based model} but virtually perfectly correlated when maximum fishing mortality rate was 0.4 or higher (see Table 1). By contrast the numbers and biomass model diverged quite rapidly from the age based model and provided a biased estimate of biomass, particularly at higher fishing mortality rates. Thus, for long term simulation and steady state calculations the 0th to 4th proto-moment model has performed better for this stock. For fitting past data there might be similar advantages in using the unbiased model, but for year-to-year predictions there is probably rather little benefit.

TABLE 1. The average r^2 values and slopes of regressions of the age based biomass on the biomass estimates from delay difference equations with a numbers and biomass formulation and with a 0th to 4th proto-moment formulation. The results are averaged over 100 runs of forward simulations of 100 years each.

	Number and Biomass		0th to 4th Proto-moments	
Max F	r^2	slope	r^2	slope
0.1	0.92	0.75	0.92	0.91
0.2	0.94	0.74	0.97	0.94
0.4	0.91	0.68	1.00	0.99
0.8	0.83	0.57	1.00	1.03

Further study of the simulation model revealed that the population at each age was strongly correlated with multiple regressions made using the 0th to 4th proto-moments as independent variables. At a maximum

fishing-mortality rate of 0.4, multiple regressions using the 0th to 4th proto-moment explained on average about 60% of the variation of the numbers at each age from 3 to 20. Making equivalent regressions with the first m proto-moments from the 0th to the m th indicated an almost linear increase in the variation explained (up to $m = 4$). Thus, the correspondence to the underlying age based population increases with the number of proto-moments considered.

There are strong suggestions in recent studies of effective egg production (Marshall et al. [1998], Marteinsdottir and Steinarsson [1998]) that larger fish may be more effective egg producers than smaller spawners. It is thus possible that effective egg production is related to a higher power of length than L^3 . Hence, for biological reasons it may well be worthwhile to model stocks in terms of the 0th to the 4th proto-moment of the population to assist with the estimation of effective egg production. It is also worth noting that if both catch and any estimates of population abundance are sampled for length, then there are no extra data collection costs associated with the use of five rather than two proto-moments. Hence, there seems little reason not to use all five.

How might carrying extra proto-moments help in describing the population dynamics of a system? A benefit of carrying a number of proto-moments is that they may be used to better approximate the proto-moments of a size distribution formed as the product of an initial population at length distribution multiplied by some function of size. Such sums of products are repeatedly required in population dynamics (for example to describe the egg production or to form the catch-rate by a selective gear). Hence to be able to convert between the proto-moments of the basic population length distribution and those of a product distribution is useful.

The sum of the product of population numbers at length N_L and a function $\rho(L)$ that may be expressed as a power series in L

$$(12) \quad \rho(L) = a_0 + a_1L + a_2L^2 \dots a_qL^q \dots$$

will have (using equation 2) a n th proto-moment D_n given by

$$(13) \quad D_n = \{a_0Pm_n + a_1Pm_{n+1} + a_2Pm_{n+2} \dots a_qPm_{n+q} \dots$$

Clearly if all proto-moments of the population size distribution were available, it would be possible to generate proto-moments of the prod-

uct distribution. However, since proto-moments are essentially summaries of the length distribution, it is clearly desirable to have considerably fewer of them than there are length or age groups. Hence, the question must be, can a distribution be reasonably approximated using a relatively small subset of low order proto-moments, for example the 0th to 4th? This would mean writing,

$$(14) \quad Dn \approx b_{0-n}NL^0 + b_{1-n}NL^1 + b_{2-n}NL^2 + b_{3-n}NL^3 + b_{4-n}NL^4.$$

This is equivalent to asking if $\rho(L)$ can adequately be approximated by

$$(15) \quad \rho(L) \sim b_{0-n}L^{0-n} + b_{1-n}L^{1-n} + b_{2-n}L^{2-n} + b_{3-n}L^{3-n} + b_{4-n}L^{4-n}.$$

Unless $n = 0$ this will mean using negative powers of L in the approximation but, as will be shown in the following subsections, this formulation can often be effective.

More realistic spawning biomass. An apparent limitation in using delay difference equations is the need to regard the stock biomass as proportional to the spawning stock biomass. However, as indicated above it should be possible to express the proto-moments of the product of some size weighting function and the population size distribution in terms of the proto-moments of the population size distribution. Consider a maturity ogive at length L $\{\text{Mat}(L)\}$ given by

$$(16) \quad \text{Mat}(L) = 1/[1 + e^{\{0.1*(50.0-L)\}}].$$

Using a simple unweighted regression of $\text{Mat}(L)$ on L^{-3} , L^{-2} , L^{-1} and L , an approximation can be developed. An example is

$$(17) \quad \begin{aligned} \text{Mat}(L) \sim & -59410.1*L^{-3} + 7638.0*L^{-2} - 338.61*L^{-1} \\ & + 5.7125 - 0.020114*L. \end{aligned}$$

Figure 3 shows this approximation with the true ogive over the fitted range. It is clear that they are in close agreement over this range. Note, however, that the fit of the approximation is markedly less good if it is extrapolated outside the fitted range (for example it is negative at 10cm and is about 0.91 at 130cm). Clearly it is important to fit the approximation over an appropriate range.

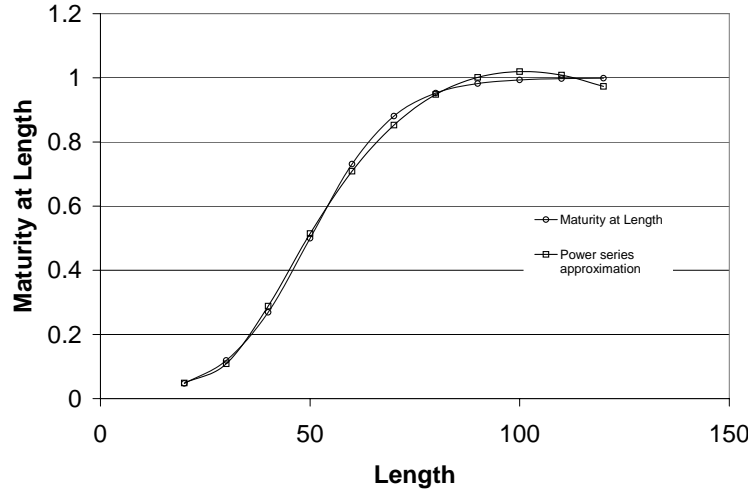


FIGURE 3. Comparison of a maturity at age curve and an approximation based upon powers (-3 to +1) of Length.

In this approximation the variables L^{-3} , L^{-2} , L^{-1} , L^0 , L were chosen so that a spawning stock biomass (SSB) could be estimated from the proto-moments of the population distribution, i.e.

(18)

$$\begin{aligned}
 \text{SSB}_y &= \sum_{\text{all } L} \text{cf.Mat}(L).L^3.N_L \\
 &\cong \text{cf.}[-59410.1 + 7638.0.L - 338.61.L^2 + 5.7125.L^3 \\
 &\quad - 0.020114.L^4].N_L \\
 &\cong \text{cf.}[-59410.1, 7638.0, -338.61, 5.7125, -0.020114] \cdot \Psi_y
 \end{aligned}$$

where cf is the condition factor. A simple example indicates that this can provide a good approximation to spawning stock biomass. Consider a population that has an initial population of 1000 at length 20cm for which a proportion of fish (s) survive growth through every 10cm group length up to 120 cm. Suppose further that it has maturity at age given by equation 16. The true estimate of SSB and the approximate estimate of SSB, based on equation 18, varied by no more than 0.3% to -0.1% for s , ranging from 0.9 to 0.2. For all practical purposes the

approximations to SSB were nearly the same as the true level. There are however two cautions to note:

1. More abrupt maturity curves would be more difficult to approximate adequately.
2. The approximation balances large positive and negative multiples of the proto-moments which might multiply errors unless these are correlated.

Using this approach to estimating a more realistic spawning stock biomass based upon ${}_n\Psi_y$ still allows equation 11 to be solved for steady states when the hypothesized stock recruitment is of a simple form such as the Ricker or Beverton and Holt equations.

Selective sampling. It is straightforward to estimate the observable proto-moments D_m ($m = 0 - 4$) from a size selective fishing survey or commercial catch per unit effort data series. Clearly for data fitting purposes it is important to link these observable proto-moments D_m (with the column vector of their 0-4th proto-moments symbolised by ${}_4\Delta_y$) to the unobserved ${}_4\Psi_y$ of the population. Again low order polynomial approximations (with some negative powered length terms) to the selection ogives seem a reasonable approach. These approximations might be based upon simple regressions on the form of the adopted selection curve. Alternatively they might be obtained from the results of an extended age based simulacrum of the stock formed with broadly realistic growth, and mortality and random recruitment. Such a simulated population could then be sampled with selection patterns that were appropriate for particular gears (e.g., with logistic ogives for trawls or normal distributions for gillnets) and proto-moments of the sampled distributions be easily estimated. The best fits of these to the proto-moments of the simulated population then provide conversion coefficients to use with the real populations equations.

This latter approach has the virtue that it weights the approximation to fit best to the more sensitive parts of the size distribution. For example, clearly the 0th moment D_0 is likely to be more influenced by the goodness of fit to the more numerous smaller sizes while the 4th proto-moment may be better fitted by an approximation that has better fit to the larger sizes. Using this approach on a simulacrum of 3Ps cod provides a conversion matrix \mathbf{B} such that ${}_4\Delta_y = \mathbf{B}^* {}_4\Psi_y$ for

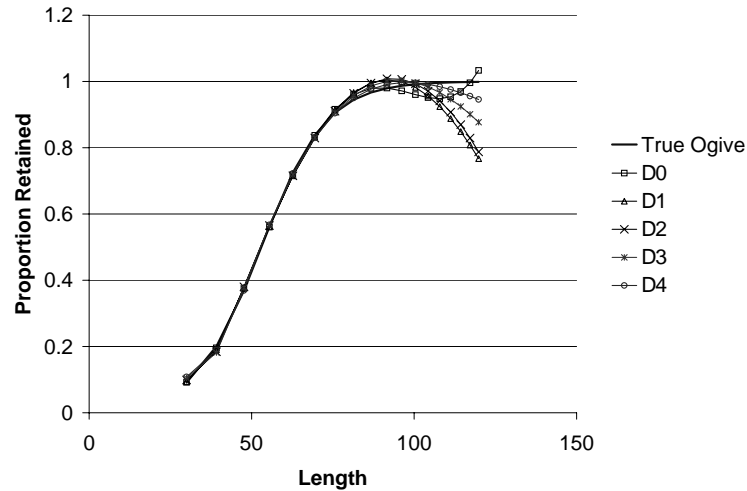


FIGURE 4. Comparison of the true selection ogive for a trawl and estimated ogives obtained from regression of the 0th to 4th “trawl” sampled proto-moments on the population proto-moments given by a simulacrum of 3Ps cod.

the sampled proto-moments ${}_4\Delta_y$ of a trawl with a 50% retention length of 50cm.

The rows of the matrix **B** can be used to estimate the approximate selection curves (Figure 4) that the matrix implies are used for the conversions. Notice that the conversion curve for D_0 flips up at high length because numbers of fish here are few and the fit to low length is more important.

Figure 5 provides results from an equivalent matrix for a gill net with a maximum retention at 60cm. This is far rougher and less impressive than the trawl result, particularly on the largest sizes, but it still explains 80-90% of the variation of the D_m seen in the simulacrum stock. It is important to recall that the purpose of the approximation is to estimate the sample proto-moments rather than fit selection curves. For the sample proto-moments the negative error (Figure 5) in the curve for moment 0 seen from 80cm–100cm may well be largely balanced by the positive error on fish over 100cm. Moreover, for the lower order sample proto-moments the fit may be better with a larger error for big fish but a better fit to the smaller more numerous fish.

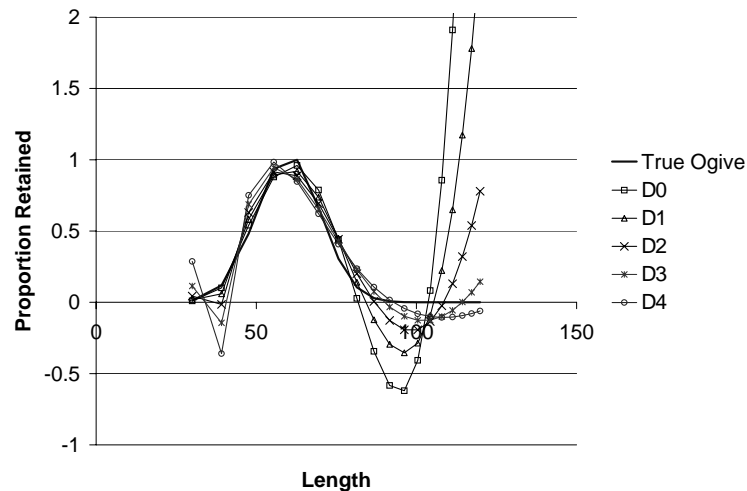


FIGURE 5. Comparison of the true selection ogive for a gill net and estimated ogives obtained from regression of the 0th to 4th “gill net” sampled proto-moments on the population proto-moments given by a simulacrum of 3Ps cod.

While these conversion matrices were calculated relative to one simulacrum of the stock they appear robust to widely varying assumptions about mortality rate and indeed to reductions in L_{∞} . Hence, it should be possible to build up libraries of conversion matrices suited to various sampling gears.

It would clearly be desirable to be able to relate the elements of \mathbf{B} to the parameters of a selection curve, but so far it has not proven possible to find an adequate equation in these terms. A brief study of the conversion coefficients for the 0th moment of the trawl showed the coefficient to vary with the 50% retention size in a sinusoidal fashion. Figure 6 shows the relationship between the estimated (0,0) element (i.e., the value in the first row and column of matrix \mathbf{B}) and the 50% retention length. Although this one coefficient can be fitted closely using an approximation formula (see Figure 6), collectively the approximate estimates for these coefficients do not lead to a believable ogive. Clearly, more work is needed here by an eager young Turk!

Natural mortality rates that vary by size. For some stocks the simple relationship of equation 8 cannot be applied because natural

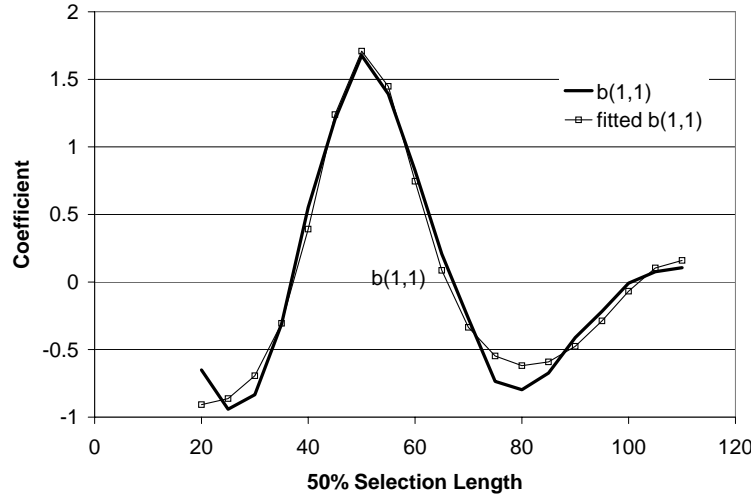


FIGURE 6. The value of $b(1,1)$ in matrix \mathbf{B} plotted as a function of 50% selection length. The graph also shows an approximation function fitted to this curve.

mortality rate is thought to vary by size. Thus, the constants of equation 7 vary by size and apparently this prevents the products of equation 5 and 7 being summed over ages to give equation 8. However, this ability can be restored if the natural survival rate e^{-M} and half-year survival rate $e^{-M/2}$ are written as appropriate polynomials in L or $1/L$. As an example, assessments of southern bluefin tuna use one of a range of postulated age specific natural mortality vectors (one set is given in Table 2). This table also shows the values of e^{-M} and of $e^{-M/2}$ and the results of linear approximations suited to correcting population numbers and catch numbers for this varying natural mortality rate.

The formulae used respectively for these approximations are

$$(19) \quad e^{-M} = 0.589 + 0.00234L - 4.80E^{-6}L^2,$$

$$(20) \quad e^{-M/2} = 0.778 + 0.00129L - 2.66E^{-6}L^2.$$

Multiplying equation 19 by numbers at age and summing over all ages thus leads to the update of stock numbers in the absence of catch

$$(21) \quad \sum_L e^{-M} N_{L,y} = \{0.589, 0.00234, -4.8 \times 10^{-6}, 0.0, 0.0\}_n \Psi_y.$$

TABLE 2. An age based natural mortality rate vector used for southern bluefin tuna together with length based polynomial approximations to the e^{-M} and $e^{-M/2}$ vectors.

Age	4	5	6	7	8	9	10	11
Length	98	112	124	134	140	146	150	158
M	0.26	0.25	0.24	0.2	0.2	0.18	0.16	0.15
e^{-M}	0.77	0.78	0.79	0.82	0.82	0.84	0.85	0.86
Approx.	0.73	0.78	0.81	0.83	0.84	0.84	0.84	0.84
$e^{-M/2}$	0.88	0.88	0.89	0.90	0.90	0.91	0.92	0.93
Approx.	0.88	0.89	0.90	0.90	0.91	0.91	0.91	0.92

More generally equations such as 21 could be written as matrix operations and hence the ${}_n\Psi_y e^{-M} - {}_n\Omega_y e^{-M/2}$ in equation 8 could be replaced by a matrix vector operation:

$$(22) \quad \mathbf{M}_{\text{full}} {}_n\Psi_y - \mathbf{M}_{\text{half}} {}_n\Omega_y.$$

For the southern bluefin tuna example, possible cell values of M_{full} are given in Table 3.

TABLE 3. A possible form for \mathbf{M}_{full} for updating population proto-moments of the southern bluefin tuna subject to a size varying natural mortality rate.

0.589	0.00234	-4.80-06	0.0	0.0
-30.4	1.12	-0.000526	0.0	0.0
0	-30.4	1.12	-0.000526	0.0
0	0	-30.4	1.12	-0.000526
0	0	-0.177	-14.0	0.921

Multispecies predation considerations. The introduction makes it clear that multispecies (particularly predation) effects are potentially important to realistic population dynamics. As a simple example, Nielsen et al. [1994] found that recruitment to the Northeast Arctic cod was affected by three factors. These were environment (as manifested

by temperature on the Kola meridian), predation by juvenile cod (ages 3 and 4) on incoming young of the year and the spawning stock biomass. The importance of those effects on the variation of recruitment to the fishery were in that order. More recent work (Marshall et al. [1998]) would also indicate the need to include capelin biomass, which is in turn affected by the abundance of juvenile herring and by the abundance of cod. Thus, for some stocks, including predation or other multispecies effects is important. Hence, if a proto-moment based approach is to be generally useful it may need to be able to include predation effects. What follows is a brief exploration of this possibility.

One approach to estimating predation mortality is to use the multispecies virtual population analysis (MSVPA), (ICES [1984]). The central equation of this approach is that the number eaten $d_{p,a,P,A,y}$ of prey species p of age a by a predator species P of age A in year y is,

(23)

$$d_{p,a,P,A,y} = \frac{\bar{N}_{P,A,y} \text{Ration}_{P,A} \bar{N}_{p,a,y} \text{suit}_{p,a,P,A}}{\sum_{r=\text{all prey species}} \sum_{s=\text{all prey ages}} \bar{N}_{r,s,y} \text{suit}_{r,s,P,A} wt_{r,s}},$$

where wt is mean weight at age, $\bar{N}...$ are the average populations of predator and prey species at age, Ration is the weight the predator eats during a period and suitability (suit) is a constant with respect to year that partitions the predators' ration between the available prey biomasses. Traditionally the suitability terms were estimated by fitting each term to stomach content data. However, it was found that these could be approximated by the form

(24)

$$\text{suit}_{p,a,P,A} = \alpha_{p,P} e^{-0.5 * ((\ln(wt_{P,A}/wt_{p,a}) - \mu)/\sigma)^2}$$

where $\alpha_{p,P}$ is a constant. This form explained about half of the variation of suit in terms of a species-to-species term and a Gaussian function of the natural logarithm of the ratio of the weight of the predator to the weight of the prey.

Clearly it would seem difficult to include full predation effects in a proto-moment assessment since these depend both upon the size of the predator and the size and availability of all potential prey species (r, s) as well as that of the prey in question. Despite these problems Horbowy [1996] has been able to propose a production model approach to forming

multispecies models. Earlier attempts were also made based on simple (Schaefer-like) multispecies production model approaches. This latter approach was surprisingly effective at predicting the results of long term age based forecasts based on the full results of MSVPA for the North Sea (ICES [1989, section 8.1]). This suggests that predation could be largely predicted in terms of predator stock biomass and thus a proto-moment approach to multispecies modeling might be possible.

Dividing equation 23 by $\bar{N}_{p,a,y}$ gives the predation mortality rate $M2_{p,a,P,A,y}$ which clearly will still be influenced by the biomass of the other prey items as well as by the specific predator and prey. However, one simplification which might help in initiating a proto-moment approach to multispecies modeling is to omit other prey species from the model of M2. The Model of Nilssen et al. [1994] uses a simplified model of predation mortality rate which treats predator biomass as similar in its effect to fishing effort. Thus, mortality resulting from predation by species P of age A will be in proportion to that predators' biomass and a specific predator and prey species and ages "catchability constant" called "unit M2" (UM2):

$$(25) \quad M2_{p,a,P,A,y} = \text{UM2}_{p,a,P,A} B_{P,A,y}.$$

This equation omits other potential prey from consideration. It had early been found (ICES [1986, section 6.6]) that $\text{UM2}_{p,a,P,A}$ could be adequately approximated by an equation with a similar functional form to equation 24,

$$(26) \quad \text{UM2}_{p,a,P,A} = \text{um2}_{p,P} e^{-0.5 * ((\ln(wt_{P,A}/wt_{p,a}) - \mu)/\sigma)^2}$$

where $\text{um2}_{p,P}$ is a constant. Pope et al. [2001] used this approach to model an extended data set for the Northeast Arctic cod, using the Nilssen et al. [1994] values of $\text{um2}_{p,P} = 2.7 \times 10^{-7}$ per t for cod eating cod, with $\mu = 4.688$ and $\sigma = 1.699$.

From equation 25 it is possible to approximate how much of the m th proto-moment of the prey is eaten by all ages of the predator as

$$(27) \quad d_{m,p,P,y} \equiv \sum_{\text{all } a} \sum_{\text{all } A} \bar{N}_{p,a,y} L_{p,a}^m \text{UM2}_{p,a,P,A,m} N_{P,A,y} L_{P,A}^3$$

where $d_{m,p,P,y}$ is the consumption of the m th proto-moment of the prey population by the predator population in year y . Note that (as

was seen for harvest rates in equation 9) a different aggregate M2 might well apply to each level of m . For example, predators might eat mostly small fish removing a large proportion of the numbers of fish (0th proto-moment) but a small proportion of the fish biomass (3rd proto-moment). Moreover, for formulation reasons approximations used for UM2 have to vary with m and thus UM2 is given an m suffix.

Equation 26 has a RHS which is a function of prey and predator size. It might thus be amenable to approximation by a polynomial expansion in terms of appropriate positive and negative powers of prey and predator weight or length. A suitable approximation of $UM2_{p,a,P,A,m}$ might be the polynomial form:

$$(28) \quad UM2_{p,a,P,A,m} \equiv {}_4LPREY_m^* \Phi_m^* {}_4LPRED$$

where ${}_4LPRED$ is the column vector of $L(P,A)^{i-3}$ for the predator {where $i = 0, 1, 2, 3, 4$ } and where ${}_4LPRED_m$ is the row vector of $L(p,a)^{j-m}$ of the prey species $\{j = 0, 1, 2, 3, 4\}$ and where Φ_m is a 5 by 5 matrix of constants. Note that the RHS of equation 28 is a scalar and also note that separate 5 by 5 matrices have to be estimated for each value of m .

The apparently peculiar powers of length used in ${}_4LPRED$ and ${}_4LPREY_m$ are chosen so that

$$(29) \quad {}_4\Psi_{y,P} = \sum_{\text{all } A} {}_4LPRED_A \cdot L_{P,A}^3 \cdot N_{P,A,y}$$

and

$$(30) \quad {}_4\Psi'_{y,p} = \sum_{\text{all } a} {}_4LPREY_{m,a} \cdot L_{p,a}^m \cdot N_{p,a,y}.$$

Hence, substituting equations 28, 29 and 30 into equation 27 gives:

$$(31) \quad d_{m,p,P,y} \equiv {}_4\Psi'_{y,p} \Phi_m {}_4\Psi_{y,P}.$$

Initial attempts to approximate $UM2_{p,a,P,A,m}$ in the form of equation 28 were reasonably successful. Figure 7 shows the value of $UM2_{p,a,P,A,m}$ obtained from the equation 26 function (True) plotted over an array of L_P and L_p (for $\mu = 4.688$ and $\sigma = 1.699$), together with equivalent

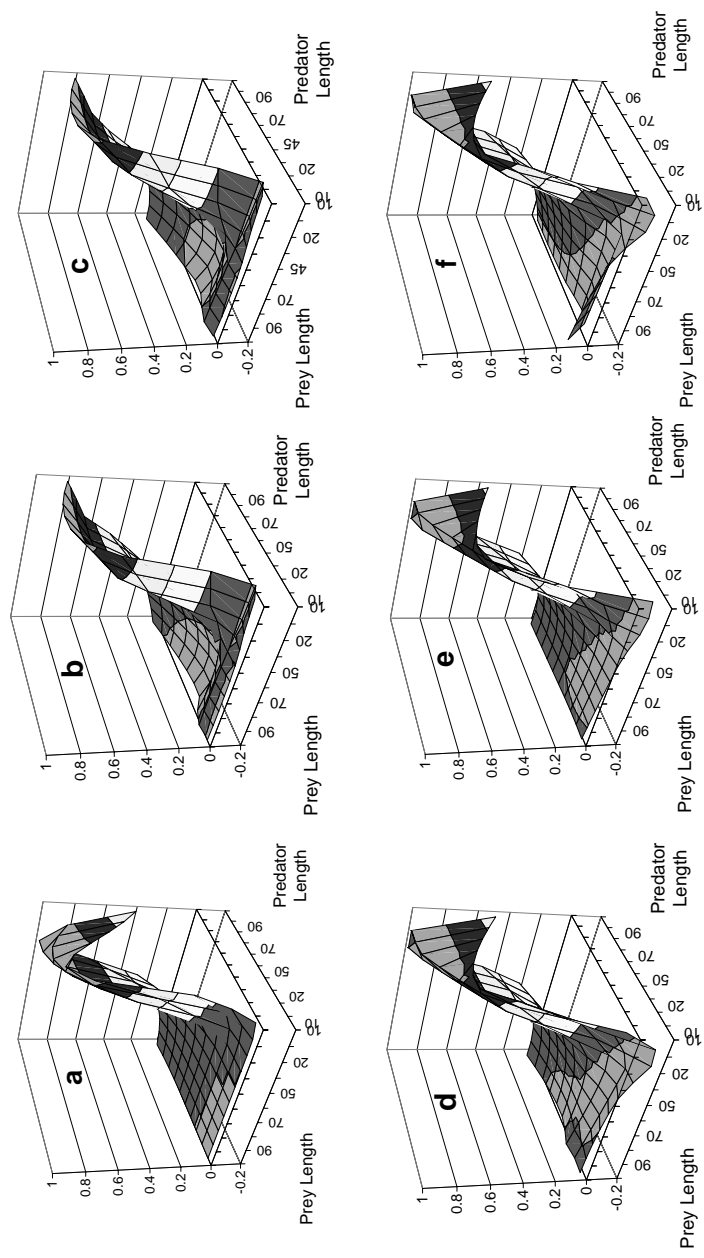


FIGURE 7. The Gaussian function of $3\text{Ln}\{L(\text{Pred})/L(\text{Prey})\}$ with mean 4.688 and SD 1.699 used as the model of proportionate predation mortality rate by length of predator and prey. The figures show a) its true form, and b) – f), the quadratic form approximations best suited to estimating the predation loss of each of the proto-moments from 0–4.

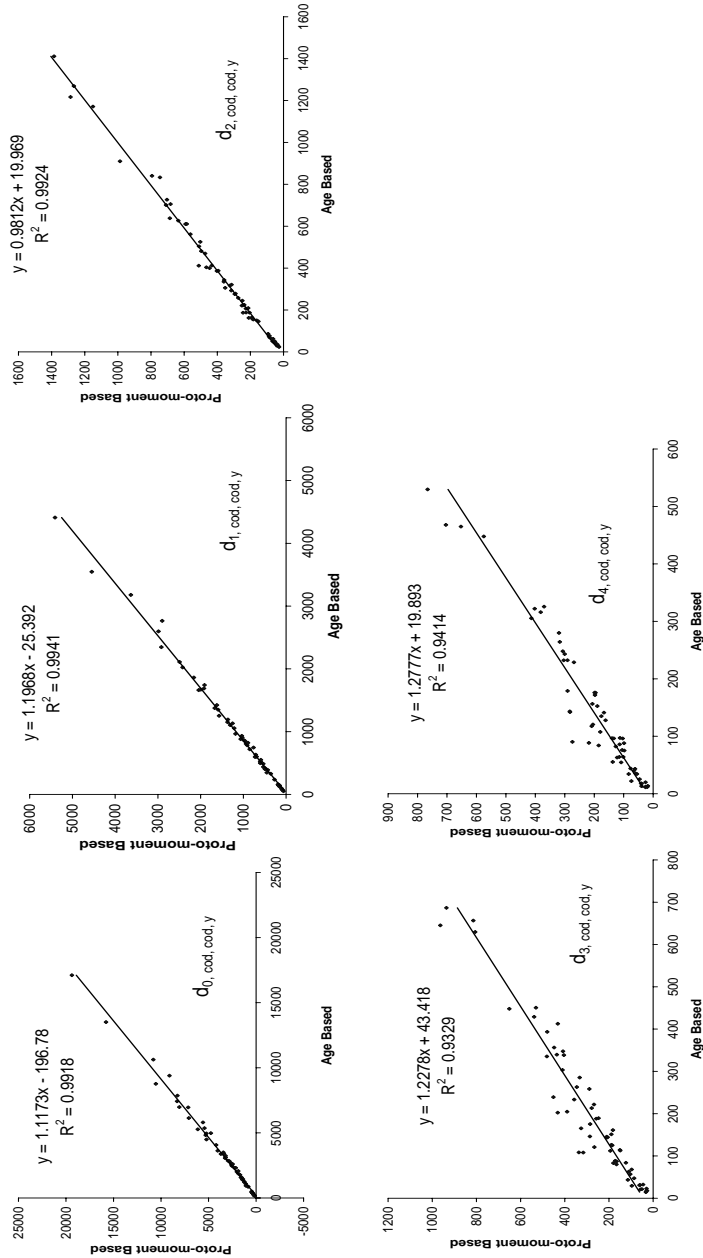


FIGURE 8. Comparison of proto-moment based estimates against age based estimates of predation loss of each population proto-moment for Northeast Arctic cod eating cod.

fits made using the equation 28 (polynomial form) approximations for each $m = 0 - 4$. The higher values of m appear to provide better fits of this function. Equivalent approximations made using the cube root of fish weight rather than length had similar fits.

To test how well these approximations would estimate consumption losses to the proto-moments of a fish stock, the data and model of Pope et al. [2001] were used to estimate age based values of $d_{m,p,P,y}$ and these were compared to the proto-moments based estimates. Figure 8 shows the plot of the proto-moment based $d_{m,p,P,y}$ on the equivalent age based estimate. The linear regression results shows that the proto-moment estimates of consumption are close to those calculated by an age based model. In this case of cod cannibalism, equation 31 reduces to the quadratic form

$$(32) \quad d_{m,\text{cod},\text{cod},y} \equiv {}_4\Psi'_{y,\text{cod}} \cdot \Phi_m \cdot {}_4\Psi_{y,\text{cod}}$$

and hence, from standard linear algebra results, Φ_m can be reduced to either a symmetric or to an upper triangular matrix. This reduces the number of constants to be estimated from 25 to 15 for each Φ_m .

In the current example the terms of Φ_m were chosen to best fit the $\text{UM2}_{p,a,P,A}$ function shown in equation 26 for a range of p,a and P,A but in practice Φ_m could probably be better estimated by making a simulacrum of the age based model to estimate long time series of $d_{m,p,P,y}$ and ${}_4\Psi_{y,\text{cod}}$ and then choosing the elements of the Φ_m which gave the best fit to the $d_{m,p,P,y}$ (equation 32). This approach should give near optimal weighting to the fit of equation 32.

The age range used in this Northeast Arctic cod cannibalism example is from 6 months up to a 15 year old plus group; most of the stock numbers come from the first 3 or 4 ages on which high M2's apply. Conversely, the biomass is largely composed of older ages. Thus the regions of the UM2_m surfaces (shown in Figure 7) that are most important to fit well will vary with the proto-moment whose consumption is being estimated.

Conclusions: The moment of truth. This paper was conceived as a short outline of how the use of delay difference models, using the 0th to 4th proto-moments of the size distribution of a fish stock as a state vector, could be extended to describe more complex fishery population

dynamics. Chapter 5 of Quinn and Deriso [1999] provides a sound background to delay difference models but appears to advocate a more parsimonious sub-sample of the proto-moments, for example numbers and biomass. However, using the 5 (0th to 4th) proto-moments has distinct advantages. Amongst these are

1. The ability to work in a simple matrix framework for updates.
2. The availability of proto-moment terms for all normal stock assessment needs; numbers, biomass and possibly NL^4 for egg production together with L , NL^1 and NL^2 (biolength and bioarea), though these from a population dynamic point of view are perhaps nuisance variables.
3. Sufficient terms to express subtle variations in size based harvest (for example, a trawl and a gill net would harvest the various proto-moments at different harvest levels).
4. Sufficient terms to provide adequate polynomial approximation functions for many size-based processes such as maturity, gear selection, natural mortality rate and consumption.
5. This approach shares with the more parsimonious models a reduced need for data and has the ability to track the main population processes of concern to fisheries management without having to include addition parameterizations (i.e. L_∞ , K and M remain the essential parameters).
6. It also shares a simple linear structure of updates through time and can have simple linear approximations to link data to the state vector. It would thus be well suited to Kalman filter or other state vector approaches to estimation.
7. The approach should fit in well with a management procedures approach to management based on CPUE measures.
8. It seems at least possible that the approach could be extended to consider simple multispecies processes.

Thus, with Hazlitt we might say, “It is great to shake off the trammels of the world and of public opinion ... and become the creature of the (*proto*-)moment”. Or just feel that the “Golden Age” might have at least a year or two to run.

To incorporate realism into models of fish populations based on proto-moments this paper makes extensive use of approximations to

mimic curvilinear length based processes. It is suggested that size based functions which link the proto-moments to observables (such as survey or commercial catch rates) or to estimates (such as the spawning stock biomass) may be well approximated by polynomials of appropriate positive and negative powers of length. Thus a key question is how to best estimate the coefficients of these polynomial approximations. Since these polynomial functions serve to convert the 5 proto-moments state vector to provide estimates of other factors, the best approximations will be those that best make this conversion, rather than those that provide the best overall fit to the function describing the length based process. This is because the conversion of particular proto-moments will be more affected by the fit of the function at some sizes than at others. Thus, fits based upon the regression of observables or estimates on the proto-moments obtained from reasonable simulacra of the stock in question seem likely to be more satisfactory² than least squared fits of the polynomials in length to the true functions.

Finally, one word, Terry, with respect to Golden Ages (or rather two) “Rodney Jones”. Rodney Jones of the Marine Laboratory of Aberdeen, Scotland, should be numbered right in there with the great and good of our science. Many of us who have had a bright idea have been chagrined to find that Rodney thought of it 40 years ago but only published it as an ICES mimeograph.

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² “Art comes to you proposing frankly to give nothing but the highest quality to your moments as they pass, and simply for those moments’ sake.” W. Pater

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