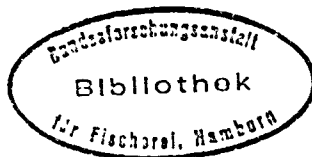


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**Effect of population structure, sampling strategy and sample size on
the estimation of length-frequency distributions and biological parameters:
a case study on brown shrimp (*Crangon crangon*)**

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Abstract

In field studies on brown shrimp (*Crangon crangon*), catches containing large numbers of animals are a common feature, and sub-sampling has become a common practice. So far, however, the cost-benefit-ratio of sampling strategies and sample sizes (in terms of workload, on the one hand, and statistical soundness of the estimated population parameters, on the other) has never been thoroughly investigated. The present study tries to solve this problem, by means of simulations on theoretical "populations" (= the combined catches of a shrimp cod-end and its cover) with known size distributions, under various conditions with respect to their size composition, and the way they are subdivided into catch fractions (cod-end cover, discards and landings).

As far as the optimal sample size is concerned, the results of the simulations showed that, in general, samples of 750 animals (all catch fractions combined), will give *sound* estimates of the mean size of the population, and *reasonable* estimates of its length-frequency distribution, provided that the original estimates of the numbers-at-length are smoothed with a moving average of order 5. For *statistically sound* estimates of the size distribution, the total number of measurements has to be increased to at least 1500.

With respect to the type of sampling strategy that is to be preferred (samples of a fixed size or proportional samples, weighted according to the relative share of each catch fraction in the population), the outcome of the simulations was much less conclusive. Because of the differences in adequacy between the two methods that were tested, the choice of the optimal sampling strategy will depend on: the kind of information one expects to obtain from the samples; the levels of precision one is aiming for; the size structure of the population in itself; and the way the population is partitioned over the various catch fractions.

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1. Introduction

In field studies on brown shrimp (*Crangon crangon*), catches containing several tens of thousands of animals are a common feature, and sub-sampling of the catches has become customary. Measuring large quantities of shrimps (say 1000 or more per sample) is a time-consuming, demanding and tedious job, particularly if the measurements have to be made by 1 or 2 mm size classes. To find an acceptable balance between workload and statistical soundness, it would be helpful to have an idea on the minimum numbers of animals that need to be measured to obtain reasonable estimates of e.g. the size composition of the catches, or the mean size of a *Crangon* population. Up to now, this question has, however, never been thoroughly addressed.

With the present study, we have tried to solve this problem, by means of computer simulations of various sampling strategies on theoretical populations with different size compositions. Initially, these investigations were started as part of another study, on the effects of population structure and sampling strategy on the estimates of the selection parameters for shrimp trawls (POLET and REDANT, 1996). This explains why the simulations were run on populations subdivided into *three* catch fractions (cover, discards and landings) instead of *two* (discards and landings), which is the kind of subdivision most shrimp biologists are used to. Later on, however, the study was extended, to also answer the questions raised by the Steering Group of RESCUE (an EC-funded research programme on the by-catches and discards in the European brown shrimp fisheries) on the optimal sampling levels for the landings and discards of *Crangon*.

A general description of the Belgian *Crangon* fishery (including an overview of the trends in landings, effort and LPUE's), and background information on the catch handling procedures onboard of the Belgian shrimp trawlers, can be found in ICES (1994 and 1996), and in POLET and REDANT (1996).

2. Methods

2.1. General background

The basic idea for the simulations was to start from a theoretical "population" with known size composition (in this case the combined catches of a shrimp trawl and its cod-end cover), which was then subdivided into three fractions, by means of equally known selection curves for the cod-end and the shrimp riddle. Next, random samples were taken from each catch fraction, under specific, user-defined conditions with respect to sampling strategy and sample size. The numbers-at-length thus obtained could then be used to recalculate the size distribution and the mean size of the population. By altering each of the elements in the system (population structure, selection parameters, sampling strategy and sample size), we hoped to be able to identify their impact on the reliability of the recalculated length frequencies and mean sizes, and to draw conclusions on the adequacy of the sampling procedures and sample sizes tested.

A similar approach has been proposed by HAMPTON and MAJKOWSKI (1987), to assess the effect of various sampling strategies on the estimates of, amongst others, growth parameters, natural and fishing mortality rates, and gear selection parameters for exploited fish stocks. Contrary to HAMPTON and MAJKOWSKI (1987), who used a complex of mathematical equations to "reconstruct" a theoretical population from a series of consecutive age cohorts, the simulations in our study were based on actual size compositions and selection curves, derived from preliminary field studies. The uncertainty on e.g. the extent of recruitment variability, the growth rates, and the natural and fishing mortality rates of *Crangon* (see ICES, 1993 and 1994, for a state of the art review on these issues), did not allow a strictly mathematical approach of the problem.

The fact that this study was based on *Crangon* populations with specific characteristics, and on specific selection curves to subdivide the populations into catch fractions, may give the impression that its outcome is applicable to this particular species and this particular fishery only. This is not necessarily the case, as will be shown in the results section. The decision to use species-specific and empirical, rather than hypothetical selection curves, mainly arose from the consideration that realistic selection curves could be expected to produce catch fractions which are similar to the ones a scientist is likely to encounter in the field. In principle, we could have used any kind of "selection" curves to subdivide the population into two or more fractions (such as e.g. a general catchability curve, or a strictly hypothetical fishermen's selection curve). Even though this would hardly have affected the conclusions from this study, their choice might have been subject to debate, and it might have cast some doubts on the veracity of the simulations, and on the overall validity of the conclusions.

2.2. Conventions on standard length

Contrary to many other commercial shrimp species (such as Penaeids and Pandalids), for which carapace length (measured from the base of the eye-socket to the posterior edge of the carapace) is the standard length measurement, there is no standardised length measurement for *Crangon*. Measuring total length is the most common practice, but depending on the author, the word "total" can have a different meaning. In this study, total length (TL) is defined as the distance between the tip of the scaphocerites and the distal margin of the fans on the stretched uropods (Figure 1). Unless stated otherwise, all size classes referred to are 1 mm TL classes, measured to the nearest mm.

2.3. The "population"

The choice of the length-frequency distribution (LFD) of the shrimps entering the cod-end of a commercial shrimp trawl (= the "population") was based on data collected during several selectivity experiments, carried out in March 1995 (POLET, unpubl. data). From these, a representative LFD was chosen, which was then used as a basis to calculate a theoretical population. Note that in this particular case, "population" stands for the combined catch of a shrimp cod-end and its cover, and not for a population in the strictly biological sense of the word.

The observed LFD (Figure 2) was first smoothed, using two consecutive runs of moving averages, to eliminate the background noise from the original numbers-at-length. The result was a typical bimodal size distribution (Figure 3), with each of the modes most likely corresponding to one age cohort (see e.g. TETARD, 1985, for details on the polymodal size structure of *Crangon* populations, and their "de-convolution" into age classes). Next, the smoothed LFD was reconstructed by means of a series of superposed normal distributions (Figure 4). Whether these do have a biological meaning or not, is of little relevance. What really matters is that the technique produced a realistic population with precisely known length frequencies, which could then be subdivided into cod-end and cover catches (Section 2.3.) and, as far as the cod-end is concerned, into discards and landings (Section 2.4.) also with precisely known LFD's.

After some preliminary simulations with this theoretical population (from now on called "Type 1" population) ⁽¹⁾, we decided to also run the simulations with two other populations, with slightly modified size compositions (Figure 5). The first one ("Type 2" population) had a much weaker first cohort, set at 1/5 of its original strength; the second one ("Type 3" population) had a much narrower first cohort (of the same numerical strength as the original one), which, in addition, was slightly moved to the right. LFD's similar to the "Type 2" population are frequently observed in certain areas and at certain times of the year, when the smallest size classes of *Crangon* are almost absent from the catches. "Type 3" is not a typical *Crangon* LFD. Nevertheless, it was included in the simulations, to obtain an indication on how the sampling strategies and sample sizes tested would perform for species that do have much narrower age cohorts (such as *Nephrops*).

2.4. Cod-end selection

The cod-end selection curves used to subdivide the populations into cod-end and cover catches were based on the results of selectivity experiments, carried out with the covered cod-end technique, under various conditions with respect to fishing ground, weather type, catch composition, etc. (POLET, unpubl. data). Two selection curves were used (Table 1 and Figure 6):

- Ogive "A": a relatively steep logit curve, with an L50 (length at 50 % retention) of 43.0 mm TL, and a selection range (the range between the lengths at 25 and 75 % retention) of 9.0 mm TL; and
- Ogive "C": a very smooth logit curve, with an L50 of 30.0 mm TL, and a selection range of 22.0 mm TL.

The steepest selection curve is typical for "clean" catches, while the other is typical for catches containing large amounts of seaweed and hydroids, which reduce the selective properties of the cod-end by clogging up the meshes (POLET, 1996).

⁽¹⁾ For reasons of consistency, the codes used to refer to populations, selection ogives and sampling strategies, are the same as in POLET and REDANT (1996).

2.5. Riddle selection

The riddle selection curve used to subdivide the cod-end fractions into discards and landings (Table 1 and Figure 6), was the same as the one used by POLET and REDANT (1996), and had an L50 of 50.0 mm TL and a selection range of 5.0 mm TL. Since riddle selection is much less sensitive to variations in catch composition than cod-end selection, we decided to run all the simulations with the same riddle selection curve.

The different combinations of theoretical population, cod-end selection curve and riddle selection curve are summarised in Table 1. From now on, each of these combinations will be referred to by the two digit code given in the first column of this table. The total numbers of shrimps in each catch fraction, for each combination of theoretical population and cod-end selection curve, are summarised in Table 2, together with their respective size ranges, and the mean size of the population as a whole. The size distributions of all populations and their catch fractions (cover, discards and landings) are shown in Figure 7.

2.6. Sampling strategies and sample sizes

Overall sample sizes (i.e. the total number of shrimps measured for all fractions combined) were arbitrarily set at 375, 750, 1500, 2250 and 3000.

In addition to various sample sizes, two different sampling strategies were investigated (Table 3):

- Sampling strategy S1: equal numbers of shrimps are taken from each catch fraction, according to the principles of simple random sampling (KREBS, 1989).
- Sampling strategy S5: the numbers of shrimps taken from each catch fraction are proportional to the relative share of that fraction in the population. Again, the samples taken are simple random samples.

Both sampling strategies are comparable to stratified random sampling (non-weighted in the case of S1; weighted in the case of S5), albeit that the boundaries between the different strata (= the catch fractions) are not as sharp as is required in stratified sampling (KREBS, 1989).

Sampling strategy S5 comes closest to taking samples from an unsorted catch (= a shrimp catch not subdivided into catch fractions). There is, however, an important difference between the two methods. In simple random samples of an unsorted catch, each draw can be chosen anywhere within the full size range of the population. Statistically spoken, this involves a potential risk of "over-" or "under-sampling" parts of the size range, especially when the number of animals measured is small. Fraction sampling does not eliminate this risk completely, but because of its similarity with stratified sampling, it can be expected to strongly reduce the extent of this problem.

Strategy S1 is straightforward and easy to use in the field, whereas S5 requires information on the numerical strength of the different catch fractions. This information can, however,

be obtained fairly easily, by raising the numbers of shrimps in the samples from each catch fraction (usually a fixed volume or weight, rather than a fixed number of animals) to total numbers caught, and by comparing the results of these calculations with the results for the other catch fractions, before starting the measurements.

2.7. The simulations

The actual simulations were run in a spreadsheet programme. Basically, they can be subdivided into five major steps:

- Step 1: simple random samples are "taken" from each catch fraction, using the spreadsheet's built-in random number generator, and the length "measurements" are stored in a length-frequency table.
- Step 2: the numbers-at-length thus obtained are raised to the level of the largest sample size tested (either 3 x 1000 for the simulations with sampling strategy S1, or 3000 proportional for those with S5), and the LFD of the population is recalculated by pooling the data for the three catch fractions.
- Step 3: the original recalculated LFD is smoothed by means of two non-weighted moving averages, viz. one of order 3 (MA3), and one of order 5 (MA5).
- Step 4: the mean size of the population is recalculated from the estimated ⁽²⁾ numbers-at-length for all catch fractions combined; the recalculated LFD's (the one with the original, non-smoothed numbers-at-length, and the two smoothed ones) are compared with the expected LFD (also raised to the equivalent of the largest sample size tested), using a Chi²-test; and the so-called "noise levels" for all size classes in the recalculated LFD's are computed from:

$$(\text{Estimated no.} - \text{Expected no.}) / (\text{Expected no.}) \times 100$$

- Step 5: the results for all runs (1000 for each combination of population structure, cod-end selection ogive, sampling strategy and sample size) are transferred to a statistical software package for further analysis.

Strictly spoken, the technique used to generate the samples was random sampling *with* replacement. In field studies, however, samples are usually taken *without* replacement. In samples with replacement, the possibility of measuring the same animal more than once cannot be excluded. This may introduce a bias in the estimates of the numbers-at-length, depending on how often the event of measuring the same animal more than once is occurring. Basically, there are two solutions to this problem. One is to "filter" the random numbers produced by the random number generator, to make sure that double draws are excluded. The other, and much simpler one, is to make the theoretical population so large

(²) Throughout the text, "recalculated" and "estimated" are used as synonyms.

that the probability of double draws is reduced to almost zero. This is the option we eventually chose for. By increasing the total number of animals in the original theoretical population (i.e. population "Type 1") to 250 000 (Table 2), the probability of a double draw was reduced to $\approx 1.5 \times 10^{-9}$ for the smallest catch fraction in the simulations (viz. the cover fraction in 2-C), and to $\approx 13.5 \times 10^{-9}$ for the largest (viz. the cover fraction in 1-A, and the discards fraction in 3-C).

At first sight, the Chi²-test is the most obvious choice to compare "observed" (read: recalculated) with "expected" length frequencies. Because of its high sensitivity (which can easily lead to excessively pessimistic conclusions on the overall degree of similarity between two data sets), it could be argued that the Chi² is not exactly the most appropriate test for this kind of investigations, where the similarity in overall shape of the size distributions is more important than the similarity between "observed" and "expected" numbers-at-length for individual size classes. From that point of view, a more rigorous test, such as Kolmogorov-Smirnov, might have been a better choice. The main reason why we decided in favour of the Chi²-test was that it can be applied to any kind of grouped data, including raised or smoothed data series with fractional numbers. The Kolmogorov-Smirnov test, on the other hand, requires a data matrix with original length measurements, which was a major bottleneck in the analysis of the type of data produced by the simulations (pooled numbers-at-length, derived from three different "samples", and raised to a common standard).

The use of raised data inevitably has an adverse effect on the results of the Chi²-tests. By raising the data, the absolute differences between "observed" and "expected" numbers-at-length are raised too, and, because of the way the Chi²-statistic for each pair of data is calculated, this results in higher Chi²-values, and hence, in lower p-values. Two arguments, however, speak for the use of raised data. First of all, raising has the advantage that it creates a common basis for the comparison and quality assessment of the results for all sample sizes tested. Secondly, it should be borne in mind that raising is a common practice in fisheries research. Most often, it is not the original but the raised data that are used e.g. in a time series analysis or in comparative studies. When the quality of these data is doubtful, the conclusions derived from them may be dubious. Therefore, the use of raised instead of non-raised data sets to run the Chi²-tests, can be considered as a prudent approach.

3. Results

3.1. Estimation of the mean size of the population

The estimates of the mean size improve with increasing sample size. Figure 8 (top) gives an example of the distributions of the recalculated mean sizes around the true mean size of the population for simulation 1-A-S1, and sample sizes of 3 x 125, 3 x 250, 3 x 500, 3 x 750 and 3 x 1000 animals each. Note that these charts do not give the actual estimates of the mean size, but their deviations from the true mean size of the population, in intervals of 0.2 mm TL each.

Figure 8 (bottom) also shows the probability-probability plots for the same data series. These clearly demonstrate that the recalculated mean sizes are normally distributed around the true mean size. With respect to these plots, it is worth mentioning that the example given is not the best available, in the sense that the results for the other simulations were at least as good, and often even better than the ones for simulation 1-A-S1.

Table 4 summarises the most important results on the estimations of the mean size. For each combination of population structure, cod-end selection ogive, sampling strategy and sample size tested (columns 1 and 2), the table gives the distribution of the deviations of the estimated mean sizes from their true value, in absolute intervals of 0.5 mm TL each (columns 3 to 6), and the parameters (mean and standard deviation, SD) of the normal distributions fitted to the deviations (columns 7 and 8).

The degree of dispersion of the recalculated mean sizes narrows down considerably when the number of shrimps measured is increased from 375 to 750, and again to 1500 (with over 95 % of the estimates at less than 0.5 mm TL above or below the true mean size, and with SD's < 0.25 mm TL) (Table 4). From then onwards, however, the gain in accuracy decreases quickly, to such a point that it becomes questionable whether it is still worth the extra investment in terms of workload, associated with the measurement of e.g. 2250 or 3000 shrimps per haul.

3.2. Estimation of the numbers-at-length for individual size classes

Effect of sample size

Figure 9 shows the box-and-whisker plots (once more for simulation 1-A-S1) of the noise levels in the non-smoothed estimates of the numbers-at-length, for all size classes with expected numbers-at-length > 1.0, and for all sample sizes tested. The boxes in these plots represent the 2.5-97.5 percentile ranges (from now on called 95 % ranges) and the whiskers the min-max ranges of the noise levels in the recalculated numbers-at-length.

Two major conclusions can be drawn from this example:

- The levels of background noise in the estimates of the numbers-at-length are inversely related to sample size. The gain in accuracy is most substantial when the number of measurements increases from 3 x 125 to 3 x 500, then gradually slows down as sample sizes increase to 3 x 750 and 3 x 1000.
- A close relationship exists between the amplitude of the noise levels and the shape of the size distribution of the population. The lowest noise levels are associated with the peaks in the LFD; the highest with the troughs and the tails, where the expected numbers-at-length are lowest (Figure 7, first page, top).

The findings for the other combinations of population structure, cod-end selection ogive and sampling strategy are very similar to the ones just described for simulation 1-A-S1. There are some differences, of course, but these are limited to the overall appearance of the box-and-whisker plots (all of which can be explained by the differences in the LFD's of the three

populations tested; see below), and to the amplitudes of the 95 % and the min-max ranges of the noise levels, particularly in the tails of the LFD's (which generally were slightly larger for sampling strategy S5 than for S1).

The relationships between the noise levels in the non-smoothed estimates of the numbers-at-length, on the one hand, and the expected numbers-at-length, on the other, are shown in Figure 10 (top). For sample sizes of 3×500 and more, these relationships are quasi-asymptotic, with a rapid decrease in the overall levels of background noise in the lower ranges of the expected numbers-at-length, and a very gentle, almost linear decrease in the upper ranges.

Similar negative asymptotic relationships between the expected numbers in a population and the levels of dispersion in their estimated values, have been reported by BECKER (1975) and JOHNSTON *et al.* (1975), in sensitivity studies on the reliability of the estimates of the numbers-at-age in commercial fish stocks, derived from length-stratified market samples.

Effect of smoothing

A representative example of the effect of smoothing on the noise levels in the estimates of the numbers-at-length is shown in Figure 11 (the example given is for simulation 1-A-S1 and a sample size of 3×500 animals). The noise reducing effect of smoothing is remarkable: from $\approx 35\%$ for the moving average of order 3, to $\approx 50\%$ for the moving average of order 5, and this for all size classes, including the ones in the tails of the size distribution.

The noise reducing effect of smoothing is also apparent from Figure 10, which shows the relationships between the noise levels in the non-smoothed (top) and the smoothed (centre and bottom) estimates of the numbers-at-length, on the one hand, and the expected numbers-at-length, on the other, for all sample sizes tested under 1-A-S1. From these graphs, it is clear that the noise levels fall off much more quickly and to much lower asymptotic values for the smoothed data than for the non-smoothed. The effect is also stronger when a moving average of order 5 is applied to the data than when a moving average of order 3 is used.

A closer look at Figure 11, however, reveals that the use of moving averages has some side effects which may force us to temper the initial enthusiasm on their noise reducing potential. For the non-smoothed estimates (Figure 11, top), the medians of the noise levels are all very close to zero, actually meaning that there is no systematic tendency towards over- or underestimating the numbers-at-length. For the smoothed data, first of order 3 (Figure 11, centre), then of order 5 (Figure 11, bottom), the medians show an increasingly strong tendency to "undulate" around the line of zero percent deviation. This phenomenon is most obvious in the lower half of the size range, i.e. in that part of the size distribution where the relatively narrow left cohort is located (Figure 7, first page).

The undulating effect is clearly demonstrated in Figure 12, which shows the medians of the noise levels in the non-smoothed (top) and in the smoothed (centre and bottom) estimates of the numbers-at-length, for all sample sizes tested under 1-A-S1 (note that the scale of

the y-axes in Figure 12 differs from the one in Figure 11). The most important conclusion that can be drawn from Figure 12 is that the undulating effect is totally independent from sample size.

The explanation of this phenomenon is fairly simple. In size distributions with narrow peaks and troughs, the use of a moving average will result in levelling off the peaks, and in filling up the troughs, by shifting fractions of the original, non-smoothed numbers-at-length down the slopes of the size distribution, on both sides of their inflexion point. The narrower the peaks and/or the troughs, and the higher the order of the moving average, the stronger this "erosive" effect will be.

Effect of sampling strategy

The effect of sampling strategy on the reliability of the recalculated numbers-at-length was examined for two combinations of population structure and cod-end selection curve, viz. 1-A and 1-C (Table 3). The performance of the two sampling strategies was tested by comparing the noise levels in the estimates of the numbers-at-length under one sampling regime (e.g. S1 and a sample size of 3×125), with the noise levels for the same size class under the other (e.g. S5 and a sample size of 375 proportional). For this purpose, the ratios between the noise levels for all size classes in the population were calculated as:

$$(95 \% \text{ range of the noise levels under S5}) / (95 \% \text{ range of the noise levels under S1})$$

If this ratio is ≈ 1 , the noise levels in the two estimates of the numbers-at-length for that particular size class are similar, and we can conclude that, on average, both sampling strategies are performing equally well (or badly). If it is > 1 , the noise levels under sampling strategy S5 are larger than those under S1, and we can conclude that, on average, S1 performs better than S5; etc.

Figure 13 shows the above mentioned ratios for the non-smoothed estimates of the numbers-at-length for 1-A (top) and 1-C (bottom). There is a marked difference between the results for the two combinations of population structure and selection ogive. In the case of 1-A, sampling strategy S5 performs much better than S1 for the size classes between 25 and 35 mm TL, whereas, in general, S1 performs slightly better for the size classes below 20 and between 35 and 60 mm TL (Figure 13, top). For 1-C, however, sampling strategy S5 performs better for the size classes between 30 and 50 mm TL, whereas, in general, S1 performs better for the size classes below 30 and above 50 mm TL (Figure 13, bottom).

The differences in performance between the two sampling strategies are closely related to the shape of the LFD's of the catch fractions (which differ from one combination of population structure and cod-end selection ogive to another), and to the way the measurements are partitioned over the different catch fractions under each sampling regime. In other words, to the relative levels of sampling intensity applied to different parts of the size distribution.

Under sampling strategy S1, all catch fractions are sampled in equal numbers. The consequence being, that the smallest fractions (in terms of numerical strength) will be "over-

sampled" and the biggest ones "under-sampled", as compared to their relative share in the population. This should not pose much of a problem, as long as all catch fractions have a fairly simple (read: unimodal) size structure. If, however, the biggest catch fraction has a bimodal size structure, the "under-sampling" will result in much higher noise levels in the estimates of the numbers-at-length in and around the trough, than would have been the case with S5, and, as a consequence, in a lower level of precision in the estimates for that part of the size range (see Section 3.2., partim *Effect of sample size*, for details on the relationship between noise levels and expected numbers-at-length).

This is clearly what happened in 1-A, where the cover fraction (which represents over 46 % of the unsorted catch; Table 2) has a bimodal size distribution with two marked peaks (Figure 7, first page, top), and where sampling strategy S1 produces less reliable estimates of the numbers-at-length for all size classes in and around the trough. To a certain extent, the same applies to 1-C, where the discards (which represent almost 44 % of the unsorted catch; Table 2) have a bimodal size distribution (Figure 7, first page, bottom), and where, once again, sampling strategy S1 was found to be less performing than S5 for the estimation of the numbers-at-length in and around the trough. In this case, however, the loss in accuracy due to the "under-sampling" of the discards, is partly compensated by the gain in accuracy resulting from the "over-sampling" of the cover fraction, which has a size range similar to that of the discards (Table 2 and Figure 7, first page, bottom).

The same elements also explain why sampling strategy S1 scores better than S5 for estimating the numbers-at-length in the lower ranges of the size distribution in simulation 1-C, and in the upper ranges of the size distribution in simulations 1-A and 1-C. In all cases, the explanation must be sought in the relative degree of "over-sampling" of the catch fractions containing the size classes in question (landings in the case of 1-A; cover and landings in 1-C).

With respect to this problem, it is worth mentioning that the use of a moving average has little or no effect on the differences in performance between the two sampling strategies. In absolute terms, the differences in noise level between the two estimates of the numbers-at-length decrease (as a result of the overall noise reducing effect of the moving average), but their ratios do not.

3.3. Estimation of the numbers in selected groupings of size classes

In species for which the application of analytical assessment techniques poses problems, alternative approaches are often used to evaluate the state of exploitation of the stocks. These include a variety of indices, such as mean sizes of catches and landings, seasonal and annual landings-per-unit-effort of the largest size classes in the population, etc. (see e.g. ICES, 1995, for an overview of the indices used for *Nephrops*). Similar approaches have also been proposed for the evaluation of *Crangon* stocks (unpubl. minutes of the 1994 and 1996 meetings of the ICES Study Group on Life History, Population Biology and Assessment of *Crangon* Stocks). It should be clear, however, that the usefulness of such indices for assessment and management purposes strongly depends on their statistical soundness, and that unreliable estimates of e.g. the relative abundance of the oldest

animals in a population may lead to erroneous conclusions on the state of exploitation of the stock in question.

In view of the considerable levels of background noise in the estimates of the numbers-at-length of, amongst others, the largest animals in the theoretical populations (Section 3.2., partim *Effect of sample size*), we decided to "re-run" simulations 1-A-S1 and 1-A-S5, with the specific aim to investigate the reliability of the estimates of the numbers of shrimps in selected groupings of size classes (viz. all shrimps ≥ 50 mm, ≥ 60 mm and ≥ 70 mm TL). The procedure followed to run these simulations was similar to the one used to estimate the numbers-at-length for individual size classes (Section 2.7.).

The results of these simulations (noise levels in the recalculated numbers for each grouping of size classes and each sample size tested) are summarised in Figure 14. The estimates for the size group ≥ 50 mm TL are generally good to excellent, with 95 % of the noise levels below 10 %, even for the smallest sample sizes. Those for the size group ≥ 60 mm TL are generally acceptable to good, with 95 % of the noise levels below 25 % for the smallest sample sizes, and below 15 % for combined sample sizes of 1500 animals and more. And those for the size group ≥ 70 mm TL are generally poor, with considerable proportions of the noise levels exceeding 25 %, except for the very largest sample sizes tested.

The accuracy of the estimates is clearly related to the relative abundance of the different size groups in the population. Shrimps ≥ 50 mm TL represent ≈ 34 % of the population, those ≥ 60 mm TL ≈ 11 %, and those ≥ 70 mm TL only ≈ 2 % (Figure 7, first page). In view of these differences in abundance, the differences in accuracy between the estimated numbers should not come as a complete surprise. Striking, however, are the relatively high levels of dispersion in the estimates for the size group ≥ 60 mm TL, which, after all, represents about 1/10 of the population. This puts another light on the general belief that grouping is a powerful means to minimise the background noise in the estimates of numbers-at-length. If the samples are small (say, less than 250 animals per catch fraction), the noise reducing effect of grouping will be small too, even for size groups which are not exactly what might be called "poorly represented" in the catches.

With respect to the general outcome of these simulations, it is also worth mentioning that the differences between the two sampling strategies (S1; Figure 14, top; and S5; Figure 14, bottom) were largely insignificant.

3.4. Similarity between recalculated and "true" size distributions

The results of the Chi²-tests on the overall degrees of similarity between the recalculated and the true size distributions, for each combination of population structure, cod-end selection ogive and sampling strategy, are summarised in Figure 15. The plots in Figure 15 show the percentages of runs giving p-values above several critical threshold values (viz. ≥ 0.50 , ≥ 0.75 and ≥ 0.90), under various conditions with respect to sample size and smoothing technique.

Effect of sample size

Except for simulation 2-A-S1, which shows a slightly different picture (see below), the overall appearance of the graphs in Figure 15 is very similar. If we take the results for simulation 1-A-S1 (Figure 15, first page, top left corner) as an example, we see that:

- The similarity between the non-smoothed recalculated LFD's and the true LFD of the population is generally poor, even for the largest sample sizes (with only ≈ 20 % of the runs giving a p-value ≥ 0.90 for a sample size of 3×750 , and only ≈ 65 % giving a p-value ≥ 0.90 for a sample size of 3×1000).
- The similarity between recalculated and true LFD's increases considerably when a moving average is applied to the data. This effect is stronger in the case of the moving average of order 5 than in that of order 3.
- With a sample size of 3×250 , almost 80 % of the runs gives a p-value ≥ 0.90 , provided that a moving average of order 5 is applied to the data. With a sample size of 3×500 , however, over 90 % of the runs gives a p-value ≥ 0.90 , provided that a moving average of order 3 is used.
- For sample sizes of 3×750 and more, close to 100 % of the runs gives a p-value ≥ 0.90 , whichever smoothing technique is used.

These findings are of particular importance when it comes to deciding which combination of sample size and smoothing technique provides the best "cost-benefit ratio" between workload and statistical soundness of the recalculated LFD's.

Effect of sampling strategy

At first sight, the results concerning the effect of sampling strategy on the accuracy of the recalculated LFD's are far from being consistent. In the case of 1-A, sampling strategy S5 performs slightly better than S1 (Figure 15, first page, top row) but for 1-C, it is exactly the opposite (Figure 15, first page, bottom row).

The differences in overall performance between the two sampling strategies are associated with their differences in performance with regard to the estimation of the numbers-at-length in particular parts of the size range. In 1-A, sampling strategy S1 scored worse than S5 for the estimation of the numbers-at-length in and around the trough between the two cohorts (Section 3.2., partim *Effect of sampling strategy*), i.e. in a critical part of the size distribution where the expected numbers-at-length are low, and where even relatively small differences between "observed" and "expected" numbers will result in higher Chi²-statistics (i.e. higher than in the case of S5), and hence in lower p-values. Conversely, in 1-C, sampling strategy S5 scored worse than S1, especially in the upper and lower ranges of the size distribution (Section 3.2., partim *Effect of sampling strategy*). Again, these are the parts of the size range where the expected numbers-at-length are low, and where relatively small deviations will result in higher Chi²-statistics (i.e. higher than in the case of S1), and hence in lower p-values.

It is important to notice that the differences in adequacy between the two sampling strategies gradually disappear with increasing sample size, provided that a moving average is applied to the data. For combined sample sizes of 1500 and more, the differences are almost negligible (Figure 15, first page).

Effect of population structure

The results for the other simulations (except for 2-A-S1) are very similar to those described earlier in this section for 1-A-S1 (Figure 15). This is an important finding, because it proves that, within certain limits (see below), the size structure of the population in itself hardly affects the reliability of the recalculated length-frequency distributions.

As already mentioned, there is one exception to this rule, viz. simulation 2-A-S1. It should be emphasised, however, that in this simulation, the cover fraction had a very peculiar size composition, with a marked peak at the right, and a low "shoulder" at the left (Figure 7, second page, top). When sample sizes are small, there is a considerable degree of scattering in the estimates of the numbers-at-length for the size classes in the "shoulder". This results in high Chi²-statistics and, as a consequence, in low p-values. The adverse effect of the scattering on the p-values largely disappears when the size of the samples is increased, and when, as a result of a better coverage, the estimates of the numbers-at-length in that part of the size distribution improve.

Theoretically, something similar could be expected for simulation 2-C-S1, which starts from the same population, and the same initial size structure, as simulation 2-A-S1. In this case, however, the weak left cohort is partitioned over two catch fractions, viz. cover and discards (Figure 7, second page, bottom). For the discard fraction, the precision of the estimates of the numbers-at-length in the "shoulder" can be expected to be poor, for the same reasons given in the previous paragraph. In the case of 2-C-S1, however, this is largely compensated by the much higher levels of precision in the corresponding estimates of the numbers-at-length derived from the cover fraction, which, under sampling regime S1, is heavily "over-sampled" as compared to the other catch fractions.

4. General discussion

Similar investigations, to which the results of this study could be compared, are extremely scarce in the scientific literature. Most papers on the adequacy of sampling strategies or sample sizes to estimate population compositions either deal with the subject from a mostly mathematical point of view (see e.g. FOURNIER, 1983; SOLANA-SANSORES and ARREGUIN-SANCHEZ, 1990 and 1991), or they pertain to the estimation of age distributions (see e.g. BECKER, 1975; JOHNSTON *et al.*, 1975), where the number of classes to be estimated is much smaller than in size distributions, and where the overall shape of the distributions usually is much simpler. Both the shape of the distribution and the number of classes to be estimated, however, are important elements in the discussion on optimal sampling strategies and sample sizes (Sections 3.2., 3.3. and 3.4.). The more complex the shape of the distribution, and the larger the number of classes for which estimates of the

numbers-at-age or length are needed, the larger the samples that will be required to achieve a certain level of precision in the estimates.

Next to the actual findings of this study, a number of additional considerations should be taken into account, when it comes to applying the results of this simulation exercise to field studies on *Crangon*, or on other (shrimp) species.

In this, mostly theoretical simulation study, the samples taken from the different catch fractions were *simple random samples*. This means that each draw was independent from the others, and that all animals in a catch fraction had an equal chance of being chosen. In sea or port sampling programmes, however, "batch sampling" is the most common technique. Batch sampling is a typical example of non-probability sampling, where the consecutive draws are not fully independent from one another. Under the right conditions, non-probability sampling may give the same results as simple random sampling (KREBS, 1989). In sea sampling programmes, these conditions *may* be met, provided that the animals in each catch fraction are randomly distributed. Therefore, it is of crucial importance to make sure that the shrimps in each fraction are thoroughly mixed before the samples are collected, and that the sampling devices are not size-selective.

With respect to the comment, made in Section 2.6., that sampling strategy S5 comes closest to taking samples of an unsorted catch, it is important to emphasise that by "unsorted" catch we mean an *unsorted catch of shrimps* (= not subdivided into e.g. discards and landings), and not the unsorted catch as it appears when the cod-end of a shrimp trawl is emptied. Preliminary experiments on the adequacy of various sampling techniques for the fish by-catches of shrimp trawlers (REDANT, unpubl. data), revealed that the quantities of shrimp contained in a single box of unsorted catch, can easily vary by up to 100 %, depending on the amount and the composition of the by-catches, in the broadest sense of the word (fish, invertebrates, lumps of peat and sand, litter, etc.). Whether this has an impact on the size composition of the shrimp samples, remains to be investigated but, if not properly remedied, it will definitely have an impact on the estimates of abundance indices, such as CPUE's, LPUE's, or the numbers of shrimp caught per unit area swept.

This study focused on the estimation of mean sizes and size distributions of the shrimp catches from a *single haul*. In most sampling programmes, however, it is common practice to pool the data from a series of hauls, to obtain an estimate of the average size composition of the shrimp population in a wider area or over a longer period of time. Replicate samples of the same population (i.e. with exactly the same size distribution) are likely to result in different estimates of the numbers-at-length for each size class. Their medians, however, can be expected to give a fair approximation of the true numbers-at-length in the population (Section 3.2., partim *Effect of smoothing*). When pooling data from various locations, we are dealing with a different scale of variability. Unless further information is available on the amplitude of the geographic and temporal variations in the size composition of *Crangon* populations, and on the processes that determine variability, the effect of pooling data from various areas or over longer time periods on the error levels in the averaged estimates is difficult to predict.

So far, no attempts have been made to also include the human factor in the simulations. Preliminary inter-calibration exercises, carried out at the Fisheries Research Station, showed that this factor can be extremely important, particularly in extensive sampling programmes, where several people are involved in measuring the samples. Intuitively, one is inclined to assume that the errors due to misreading follow a random distribution. The results of the inter-calibration exercises made it perfectly clear that this is not the case. Here too, the use of a smoothing technique, such as a moving average, can be helpful to reduce the (extra) noise in the estimated numbers-at-length caused by misreading. It is important to remember, however, that, despite its considerable noise reducing potential, a moving average is not some sort of "magic wand", capable of turning even the most crummy data set into a reliable length-frequency distribution.

5. Conclusions

As in most other simulation studies on the adequacy of sampling programmes, the conclusions from this study can be subdivided into "good" and "bad" news.

- The good news is that, *in most cases*, combined samples of 750 animals (i.e. either 250 per catch fraction, or 750 proportional) will give *sound* estimates of the mean size of a population, and *reasonable* estimates of its length-frequency distribution, provided that, for the latter, the observed numbers-at-length are smoothed by means of a non-weighted moving average of order 5. With respect to using a moving average of this order it should, however, be stressed that there is a serious risk of underestimating the numbers-at-length in the peaks, and of overestimating the numbers-at-length in the troughs of the size distribution.
- The bad news is that, for *statistically sound* estimates of the size distribution, the total number of animals to be measured has to be at least 1500 (i.e. either 500 per catch fraction, or 1500 proportional). Again, provided that a moving average is applied to the original estimates of the numbers-at-length. In this case, however, a non-weighted moving average of order 3 can suffice.

This is not the kind of conclusions one might have hoped for, but at least, it has the advantage that we know now with much more certainty what the "cost" of statistical soundness really is.

The results of this study are much less conclusive as to the type of sampling strategy (equal or proportional sample sizes) that is to be preferred. Because of the differences in adequacy between the two methods, under various conditions with respect to the size structure of the population, the optimal sampling strategy will depend on: the kind of information one expects to obtain from the samples; the levels of precision one is aiming for; the size structure of the population in itself; and the way the population is partitioned over the different catch fractions. For combined sample sizes of 1500 animals and more, however, the differences in adequacy between the two sampling strategies are almost negligible. This fact, and the strictly logistic argument that samples of a set size are much

easier to collect than proportional samples, make sampling strategy S1 the better choice for *general* studies on the size composition of *Crangon* populations.

For studies requiring statistically sound estimates on *particular parts of the population*, however, neither of the sampling strategies that were tested may give satisfactory results. In that case, one may have to consider the possibility of "over-sampling" critical parts of the size range, in an attempt to improve the overall quality of the estimates.

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Table 1 - General features of the simulations.			
Code (*)	Theoretical population	Cod-end selection curve (**)	Riddle selection curve (**)
1-A	"Type 1" : standard See Figure 5	Ogive "A" : steep a = - 10.75 ; b = 0.25 See Figure 6	Standard a = - 22.70 ; b = 0.45 See Figure 6
1-C	"Type 1" : standard As in 1-A	Ogive "C" : smooth a = - 3.00 ; b = 0.10 See Figure 6	Standard As in 1-A
2-A	"Type 2" : first cohort reduced to 1/5 of its original strength See Figure 5	Ogive "A" : steep As in 1-A	Standard As in 1-A
2-C	"Type 2" : first cohort reduced to 1/5 of its original strength As in 2-A	Ogive "C" : smooth As in 1-C	Standard As in 1-A
3-A	"Type 3" : narrow first cohort, slightly moved to the right See Figure 5	Ogive "A" : steep As in 1-A	Standard As in 1-A
3-C	"Type 3" : narrow first cohort, slightly moved to the right As in 3-A	Ogive "C" : smooth As in 1-C	Standard As in 1-A
(*)	Codes refer to the combinations of population type (first digit) and cod-end selection curve (second digit), used in the simulations		
(**)	a and b refer to parameters a and b in the logit curve : $RR = 1 / (1 + \exp(-(a + b \cdot TL)))$ in which RR = retention rate, and TL = total length		

Table 2 - Numbers (N, in 1000) and size ranges of Crangon (mm TL) in each catch fraction (as generated from the theoretical populations), and mean size of the theoretical populations used in the simulations.								
Code (*)	Cover		Discards		Landings		Total	Mean size population (mm TL)
	N	Size range (**)	N	Size range (**)	N	Size range (**)	Sum of N's	
1-A	115.4	13-57	60.0	33-58	74.6	43-78	250.0	43.56
1-C	66.5	13-62	109.2	16-58	74.3	42-78	250.0	43.56
2-A	72.3	16-58	59.4	32-58	74.6	43-79	206.4	47.70
2-C	38.6	16-63	93.5	19-58	74.3	42-79	206.4	47.70
3-A	113.9	20-57	61.5	28-58	74.6	43-78	250.0	44.65
3-C	60.2	20-62	115.5	21-58	74.3	42-78	250.0	44.65

(*) Codes refer to the combinations of population type (first digit) and cod-end selection curve (second digit), used in the simulations

(**) Size ranges refer to those size classes, for which the expected numbers-at-length in the largest sample sizes tested were > 1.0

Table 3 - Sampling strategies and sample sizes tested.										
Code (*)	Sampling strategy S1					Sampling strategy S5				
	Equal sample sizes (3 x Ns), with sample sizes (Ns) set at :					Proportional sample sizes, with total no. of shrimp measured (Nt) set at :				
	125	250	500	750	1000	375	750	1500	2250	3000
1-A	x	x	x	x	x	x	x	x	x	x
1-C	x	x	x	x	x	x	x	x	x	x
2-A	x	x	x	x	x					
2-C	x	x	x	x	x					
3-A	x	x	x	x	x					
3-C	x	x	x	x	x					

(*) Codes refer to the combinations of population type (first digit) and cod-end selection curve (second digit), used in the simulations

Table 4 - Percentual distribution of the deviations of the recalculated mean sizes from their "true" values, and parameters of the normal distributions fitted to the actual deviations, for different combinations of population structure, cod-end selection curve, sampling strategy and sample size.															
Simulation & sampling strategy	No. of shrimps measured	Deviation (+ or -) from "true" mean size (mm)				Parameters of normal fit (mm)		Simulation & sampling strategy	No. of shrimps measured	Deviation (+ or -) from "true" mean size (mm)				Parameters of normal fit (mm)	
		≤ 0.5	0.6-1.0	1.1-1.5	> 1.5	Mean	SD			≤ 0.5	0.6-1.0	1.1-1.5	> 1.5	Mean	SD
1-A-S1	375	73.0	24.0	2.9	0.1	0.03	0.45	2-A-S1	375	83.7	15.5	0.8	---	0.02	0.36
	750	88.1	11.6	0.3	---	0.01	0.33		750	95.2	4.8	---	---	-0.01	0.26
	1500	97.3	2.7	---	---	0.00	0.23		1500	99.7	0.3	---	---	0.01	0.18
	2250	98.8	1.2	---	---	0.01	0.20		2250	99.7	0.3	---	---	0.00	0.15
	3000	99.9	0.1	---	---	0.00	0.17		3000	100.0	---	---	---	0.00	0.12
1-A-S5	375	76.4	21.7	1.8	0.1	0.00	0.43	2-C-S1	375	80.5	18.8	0.7	---	0.01	0.39
	750	91.2	8.7	0.1	---	-0.01	0.30		750	94.5	5.5	---	---	-0.01	0.27
	1500	98.5	1.5	---	---	0.00	0.21		1500	98.8	1.2	---	---	0.00	0.20
	2250	99.5	0.5	---	---	0.00	0.17		2250	99.9	0.1	---	---	0.00	0.15
	3000	99.7	0.3	---	---	0.00	0.15		3000	100.0	---	---	---	0.00	0.14
1-C-S1	375	72.0	22.9	4.9	0.2	-0.01	0.49	3-A-S1	375	82.7	16.7	0.6	---	0.02	0.38
	750	88.2	11.6	0.2	---	0.00	0.33		750	94.3	5.7	---	---	0.02	0.25
	1500	96.6	3.4	---	---	-0.01	0.24		1500	99.3	0.7	---	---	0.01	0.19
	2250	99.2	0.8	---	---	0.00	0.19		2250	99.9	0.1	---	---	0.00	0.16
	3000	99.9	0.1	---	---	0.00	0.18		3000	100.0	---	---	---	-0.01	0.14
1-C-S5	375	70.3	26.1	3.6	---	0.01	0.48	3-C-S1	375	75.4	23.1	1.5	---	0.01	0.43
	750	87.4	12.2	0.4	---	0.01	0.34		750	90.8	9.1	0.1	---	0.01	0.30
	1500	97.8	2.2	---	---	0.00	0.23		1500	98.3	1.7	---	---	0.00	0.21
	2250	99.3	0.7	---	---	0.00	0.19		2250	99.8	0.2	---	---	0.00	0.17
	3000	99.8	0.2	---	---	0.00	0.18		3000	100.0	---	---	---	0.01	0.15

Figure 1 - Standard lengths of brown shrimp (*Crangon crangon*).
 TL = total length ; CL = carapace length

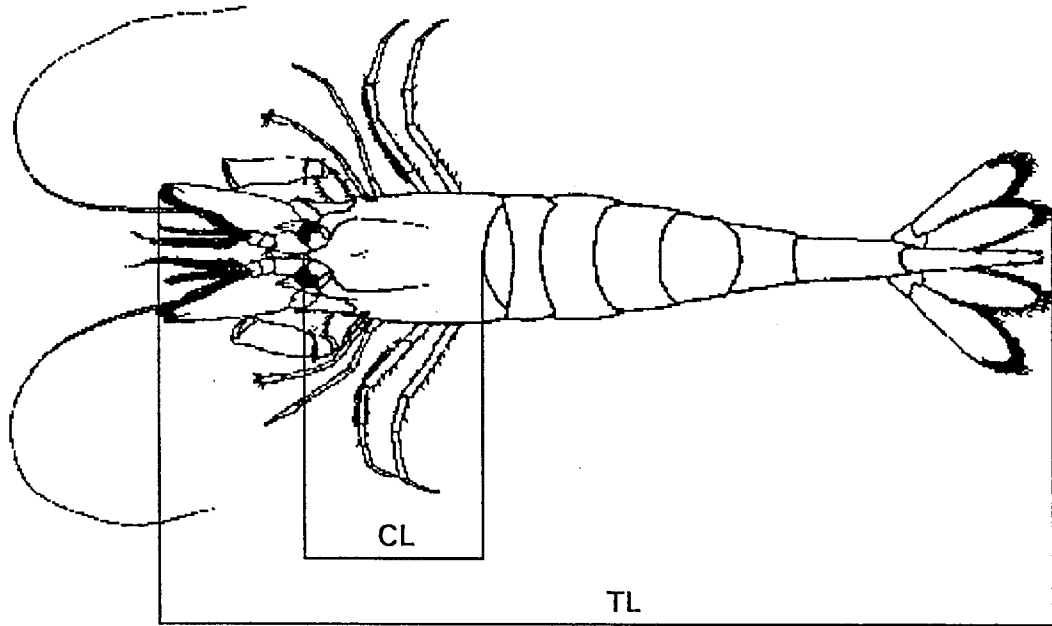


Figure 2 - Original size distribution of the shrimp catches,
 used as a basis to calculate the theoretical populations.
 Based on data collected in March 1995.

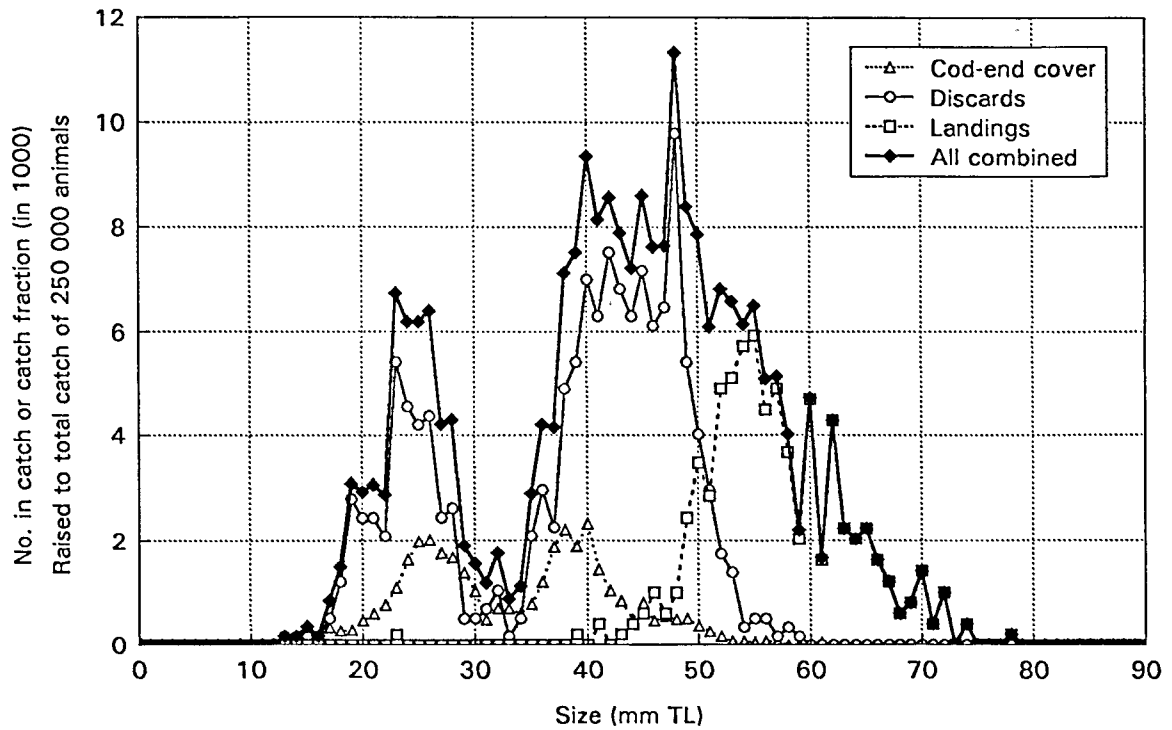


Figure 3 - Smoothed size distribution of the shrimp catches, used as a basis to calculate the theoretical populations.

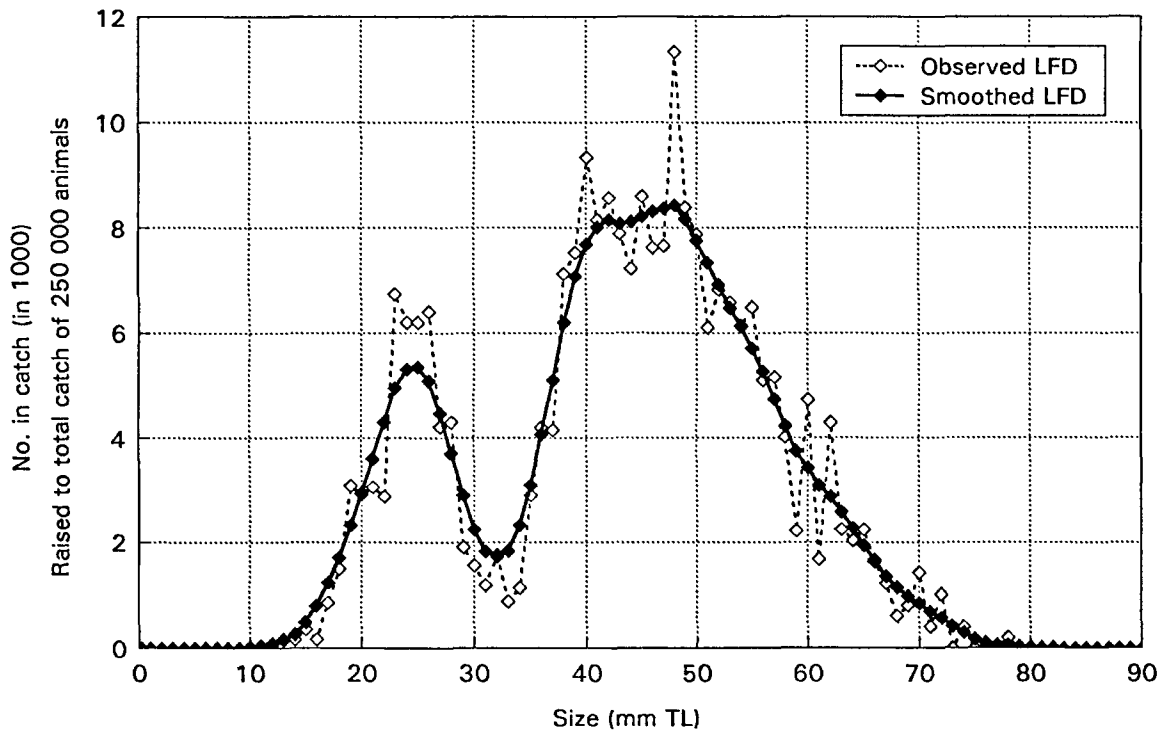


Figure 4 - "Reconstructed" size distribution of the shrimp catches, calculated by means of a series of superposed normal distributions.

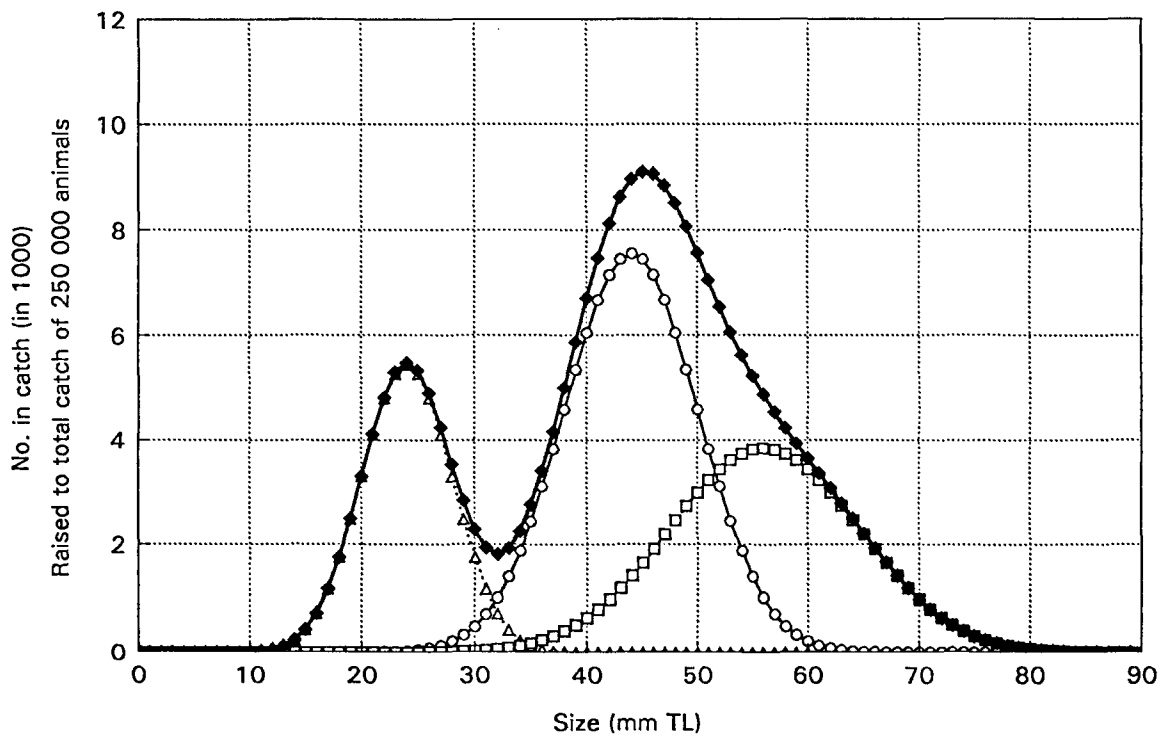


Figure 5 - Theoretical populations, used in the simulations.

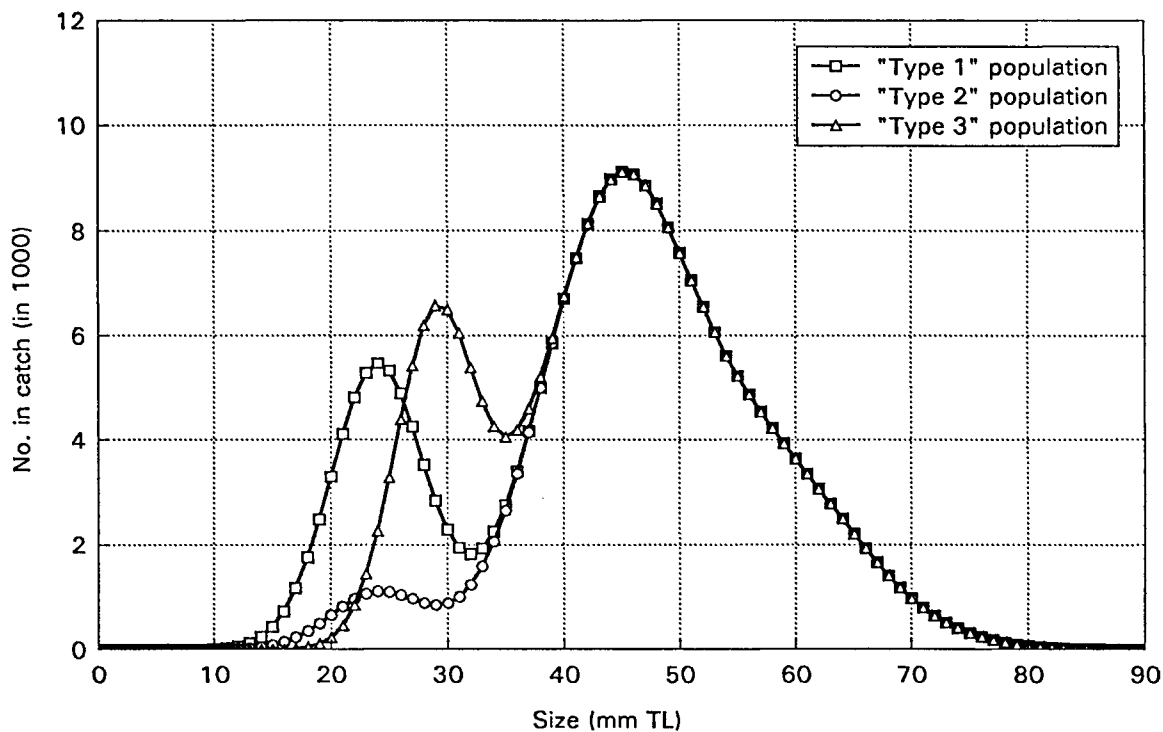


Figure 6 - Cod-end and shrimp riddle selection ogives, used to subdivide the theoretical populations into catch fractions.

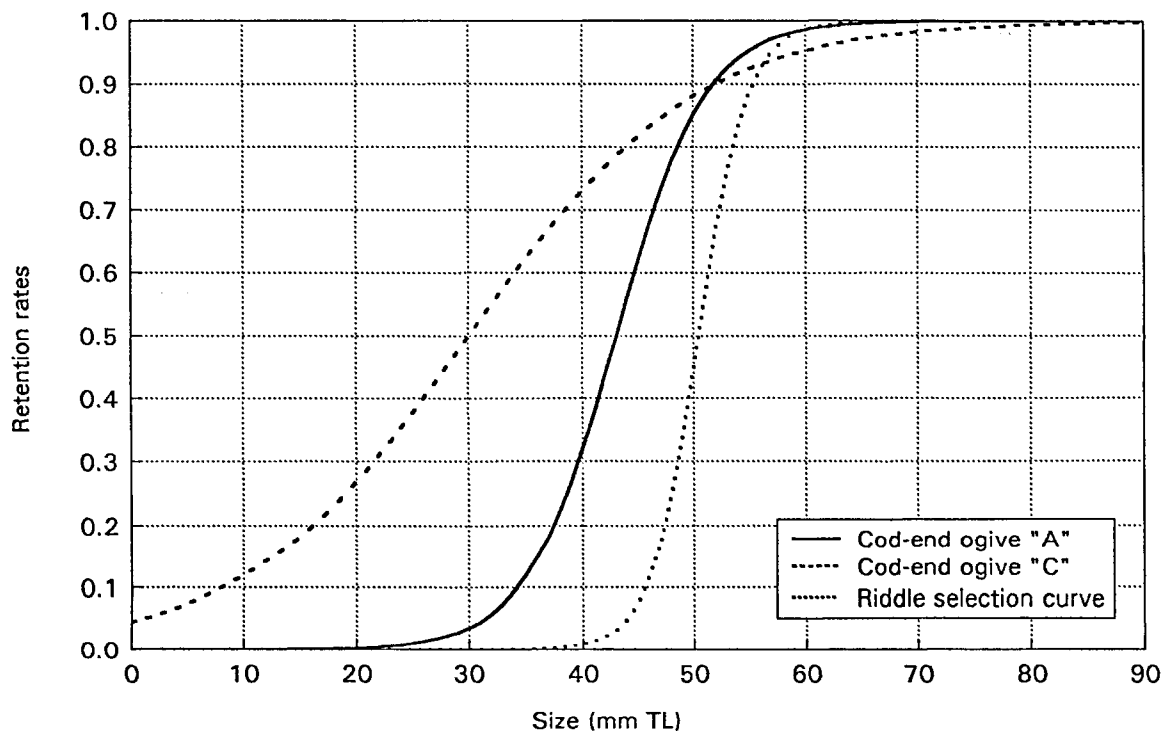


Figure 7 - Size distributions of the theoretical populations, and their subdivision into catch fractions.

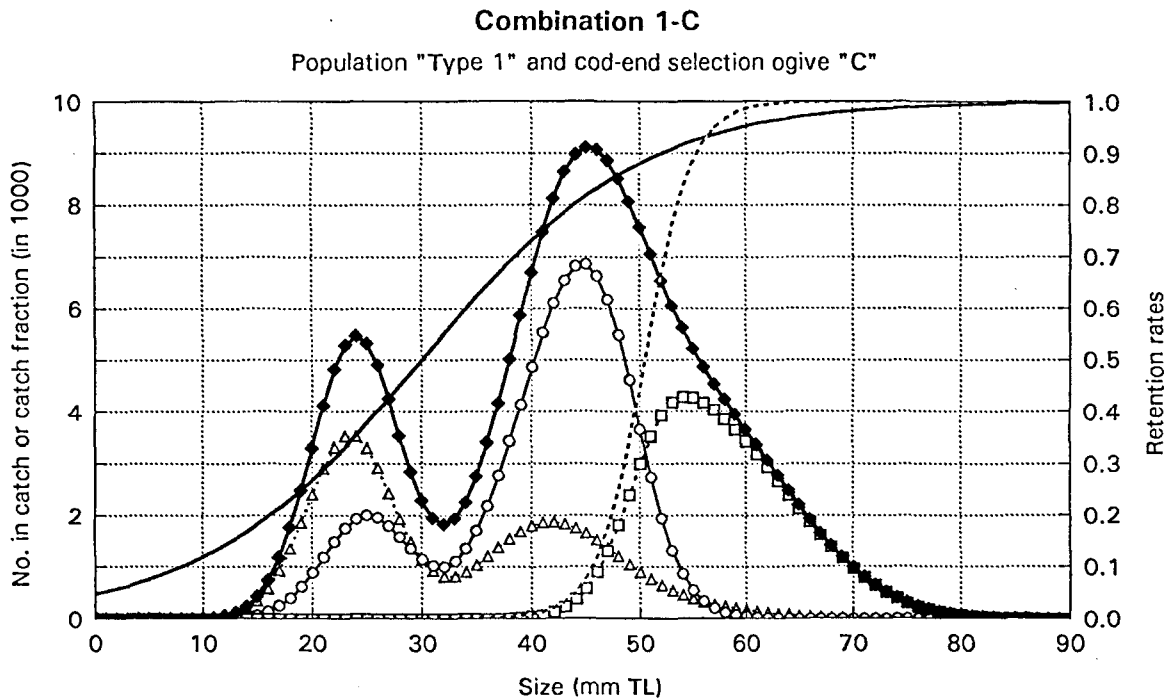
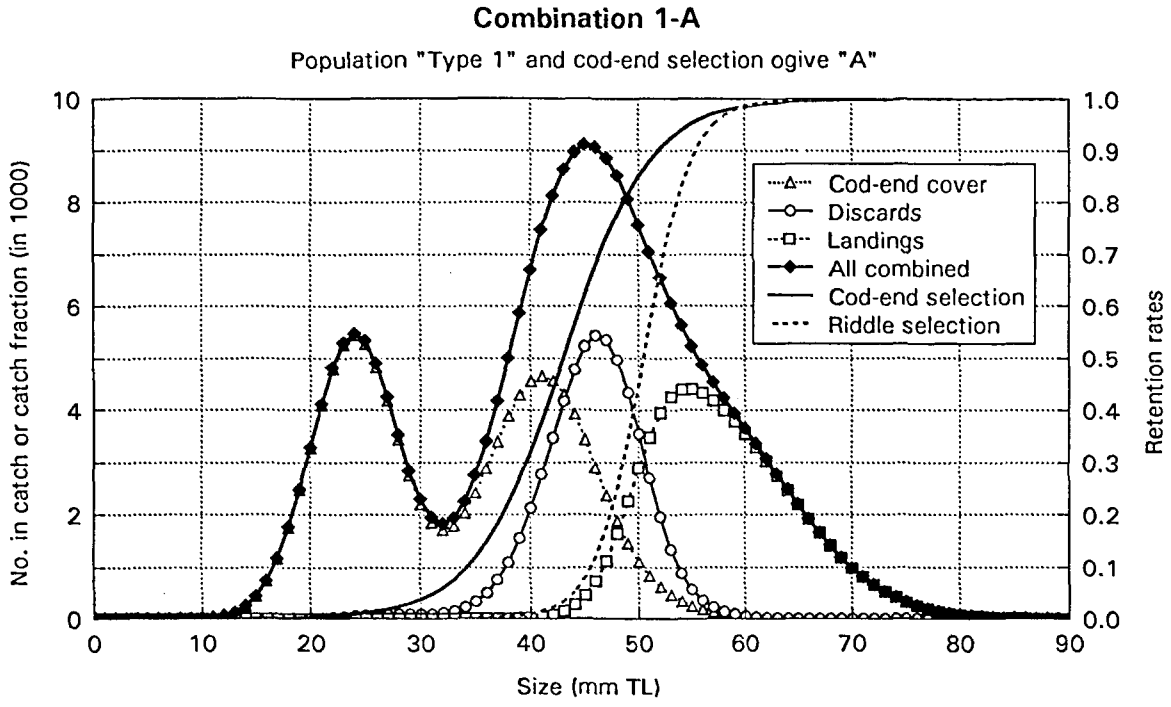


Figure 7 (continued) - Size distributions of the theoretical populations, and their subdivision into catch fractions.

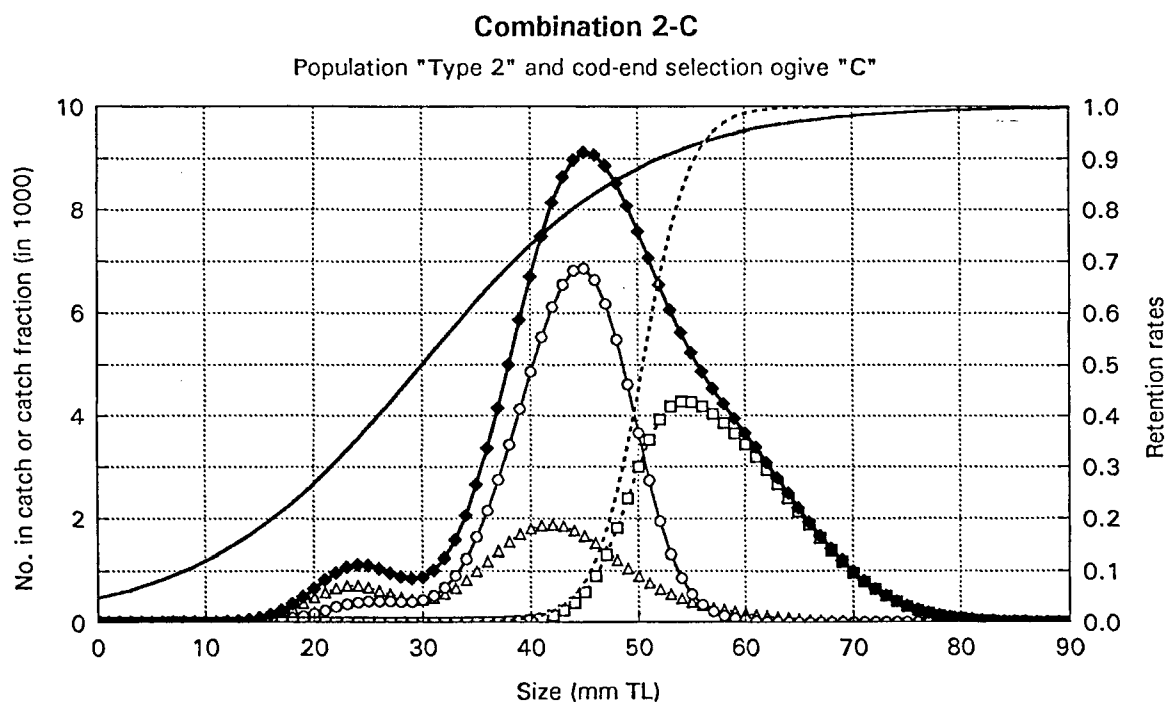
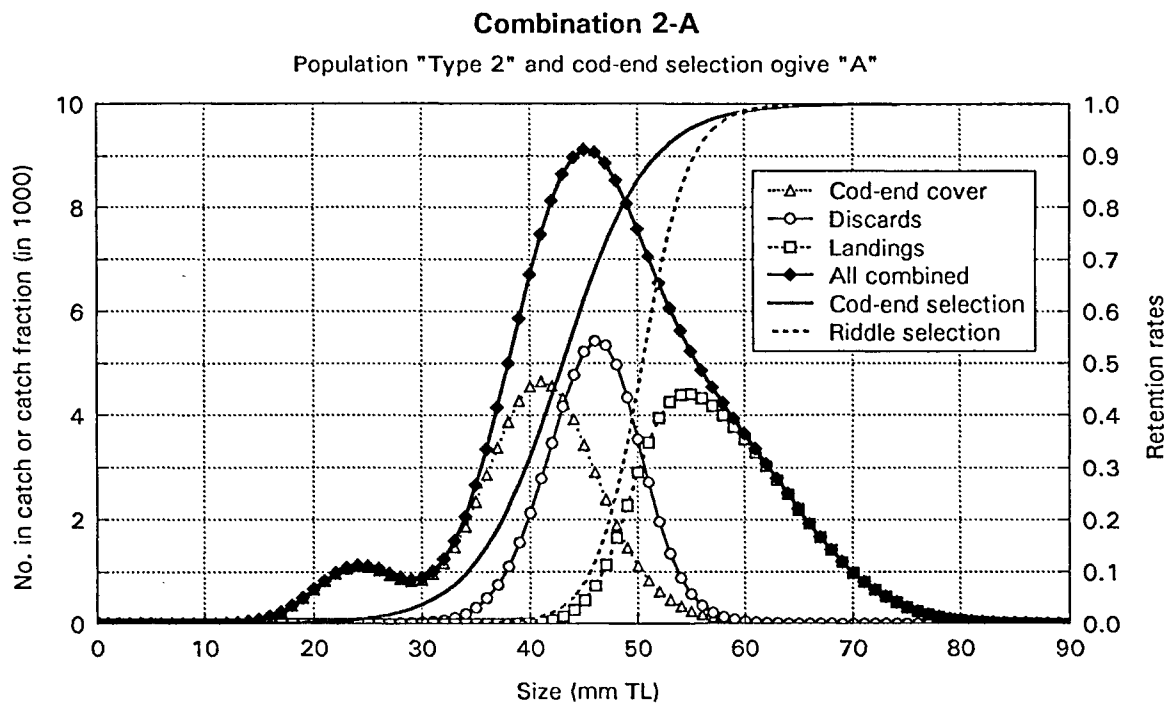


Figure 7 (continued) - Size distributions of the theoretical populations, and their subdivision into catch fractions.

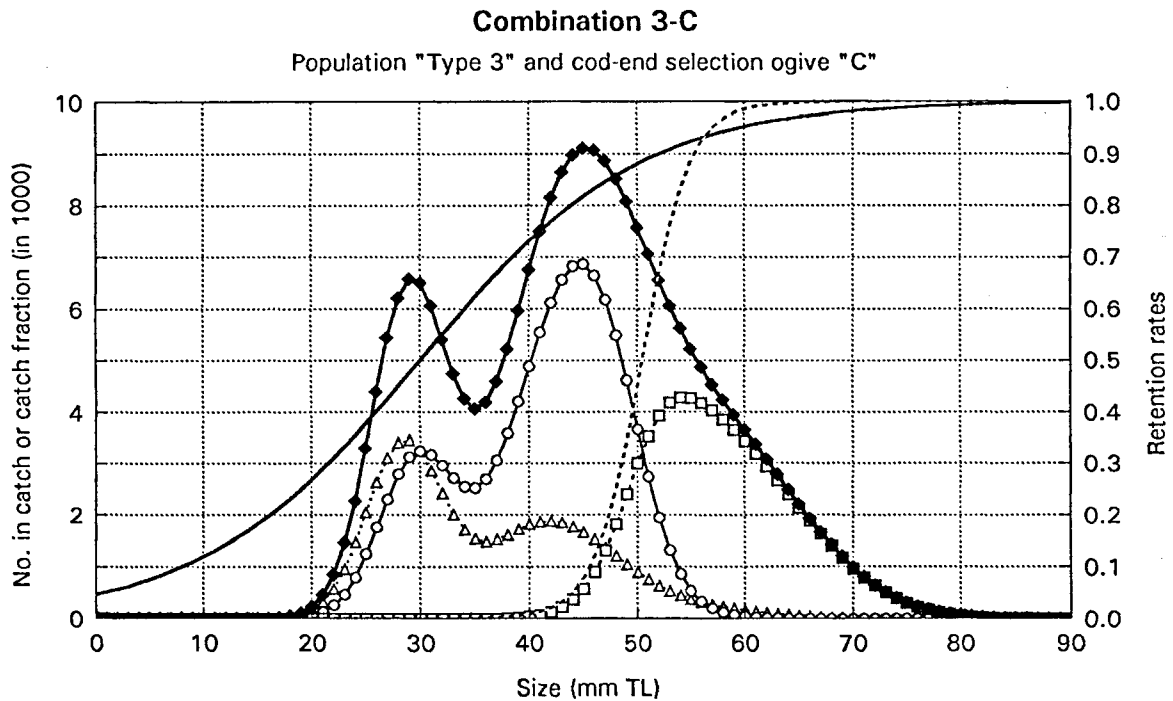
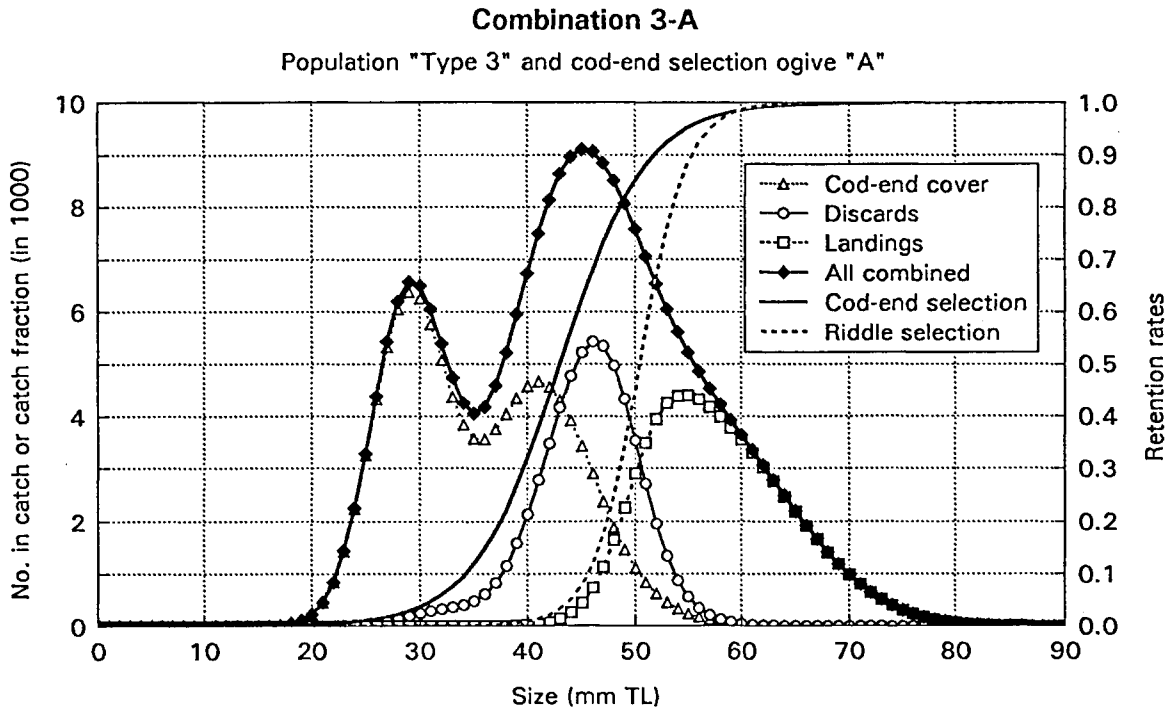


Figure 8 - Effect of sample size (N) on the estimates of the mean size of the population (top), and corresponding probability-probability plots for the recalculated mean sizes (bottom). The example given is for simulation 1-A-S1.

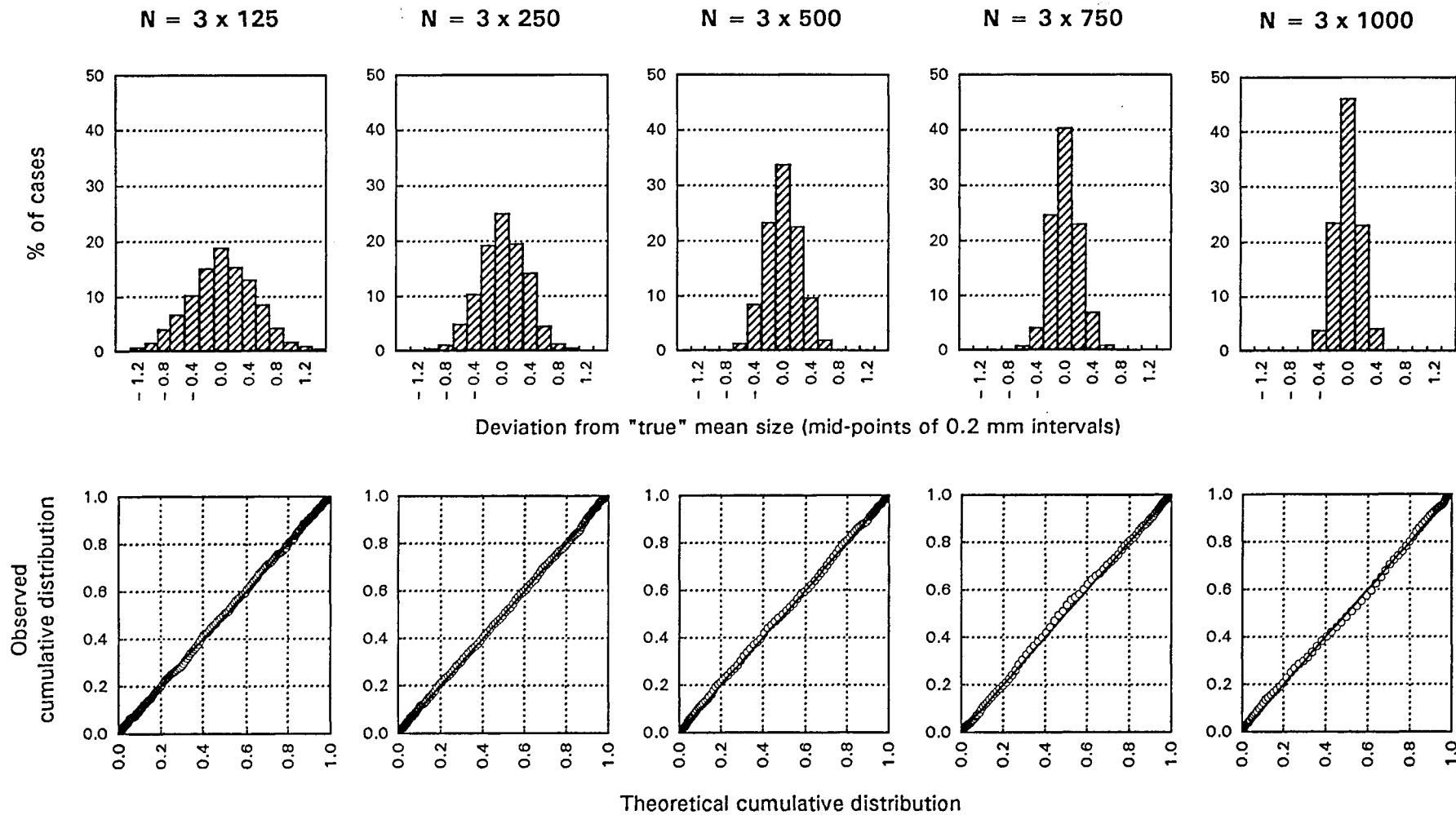


Figure 9 - Effect of sample size (N) on the estimates of the numbers-at-length.

The example given is for simulation 1-A-S1.

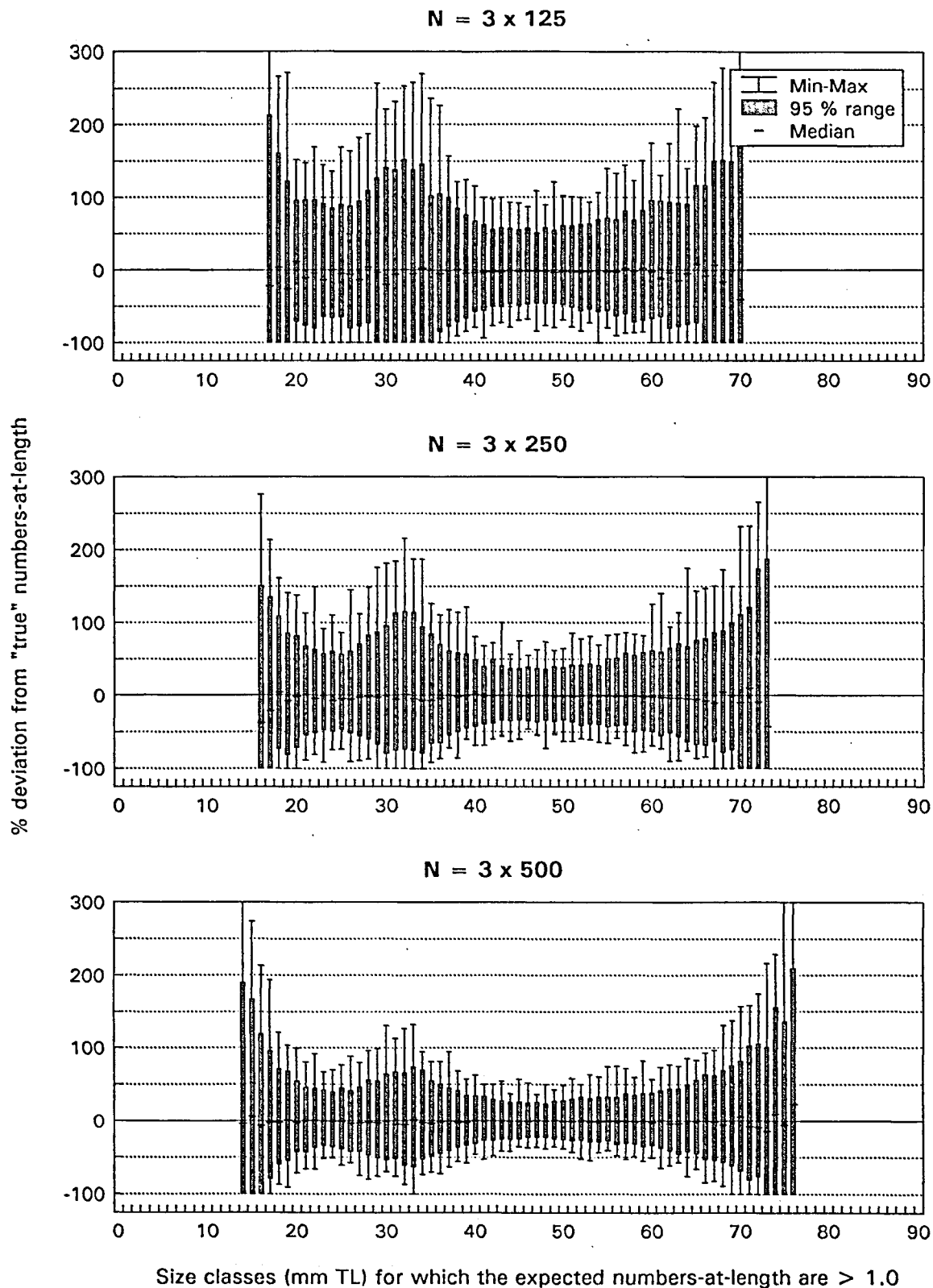


Figure 9 (continued) - Effect of sample size (N) on the estimates of the numbers-at-length.

The example given is for simulation 1-A-S1.

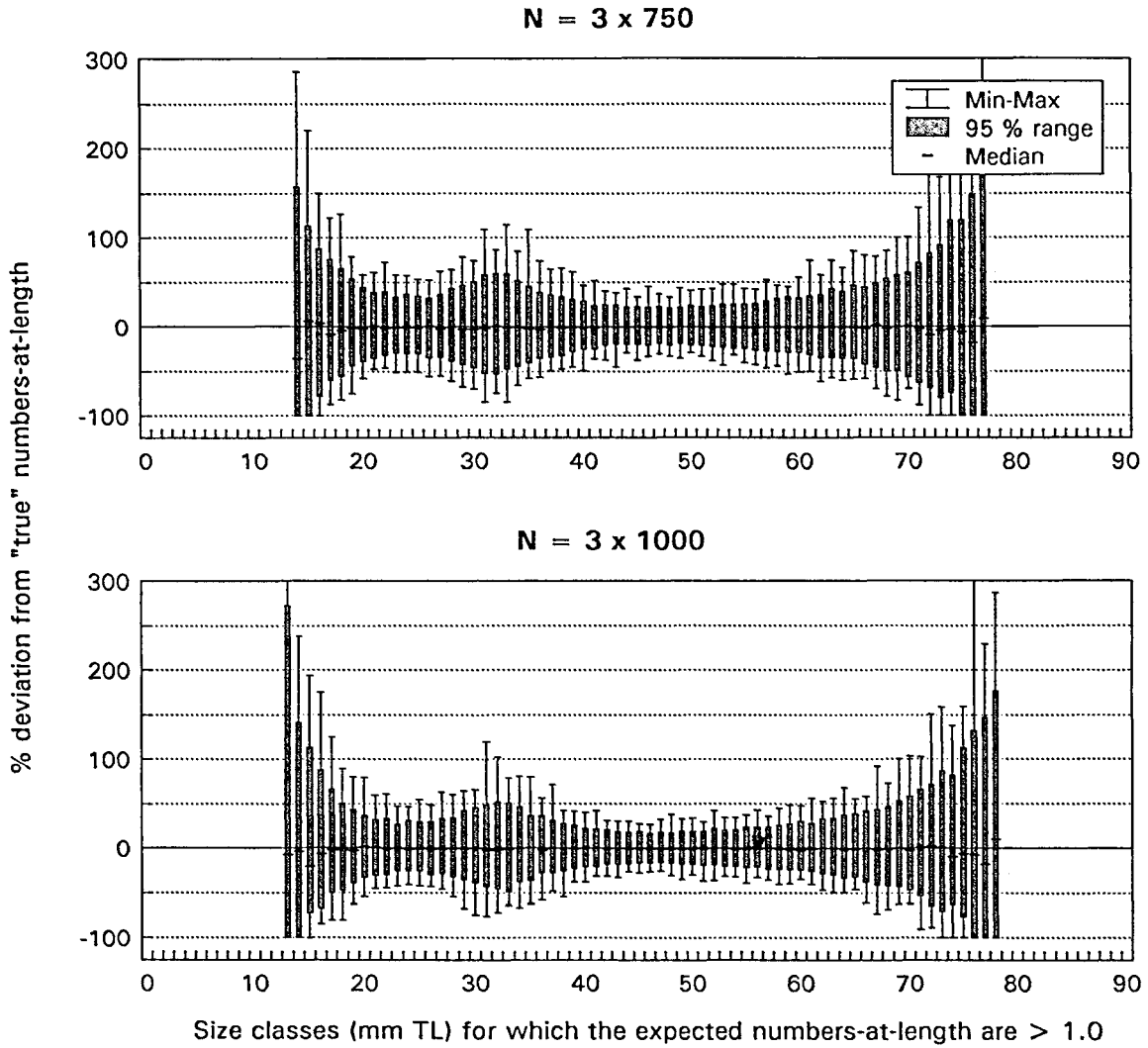


Figure 10 - Relationships between the 95 % ranges of the noise levels in the estimated numbers-at-length and the expected numbers-at-length, for different sample sizes (N) and smoothing regimes.

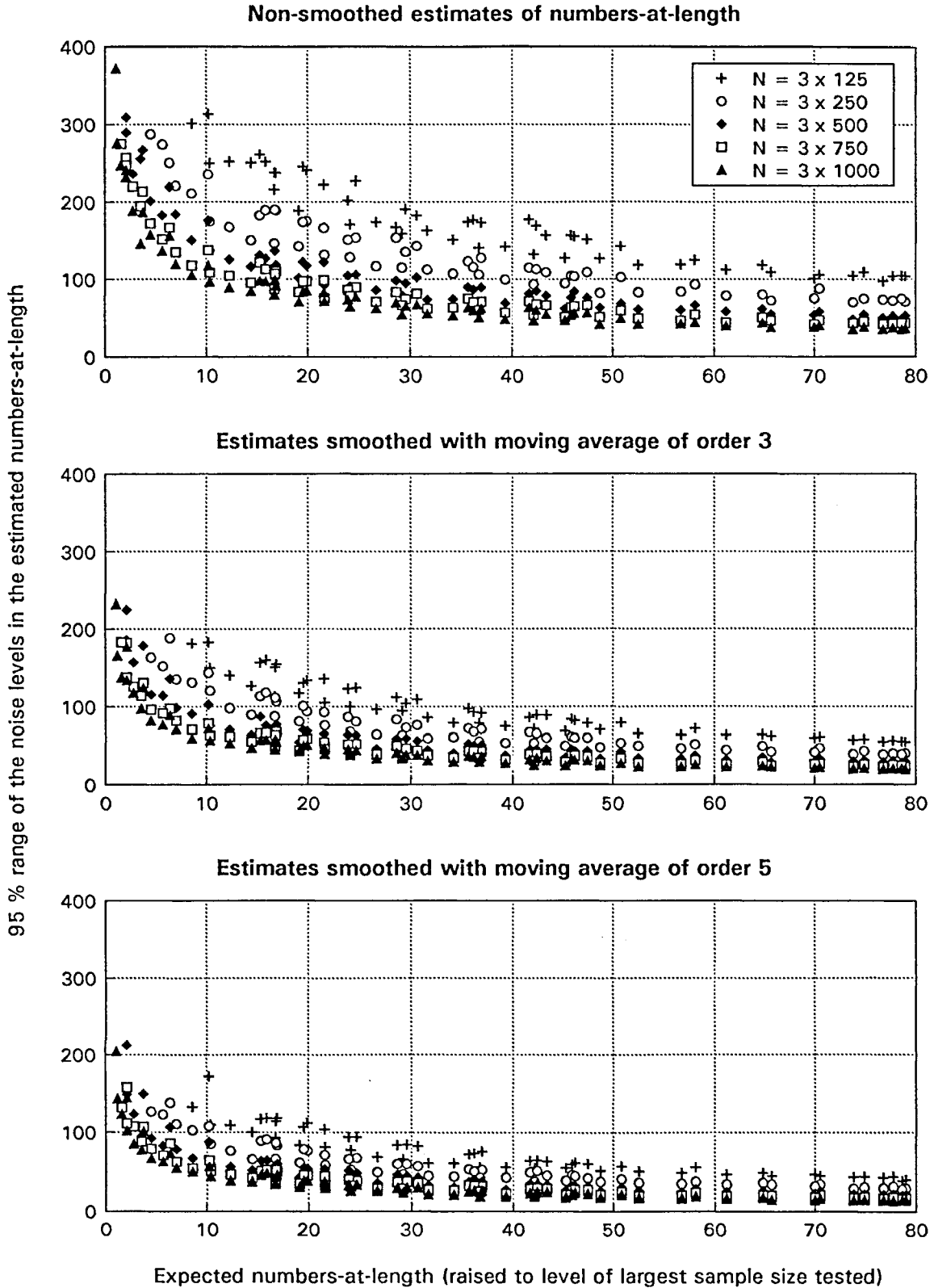


Figure 11 - Effect of smoothing on the estimates of the numbers-at-length.

The example given is for simulation 1-A-S1.

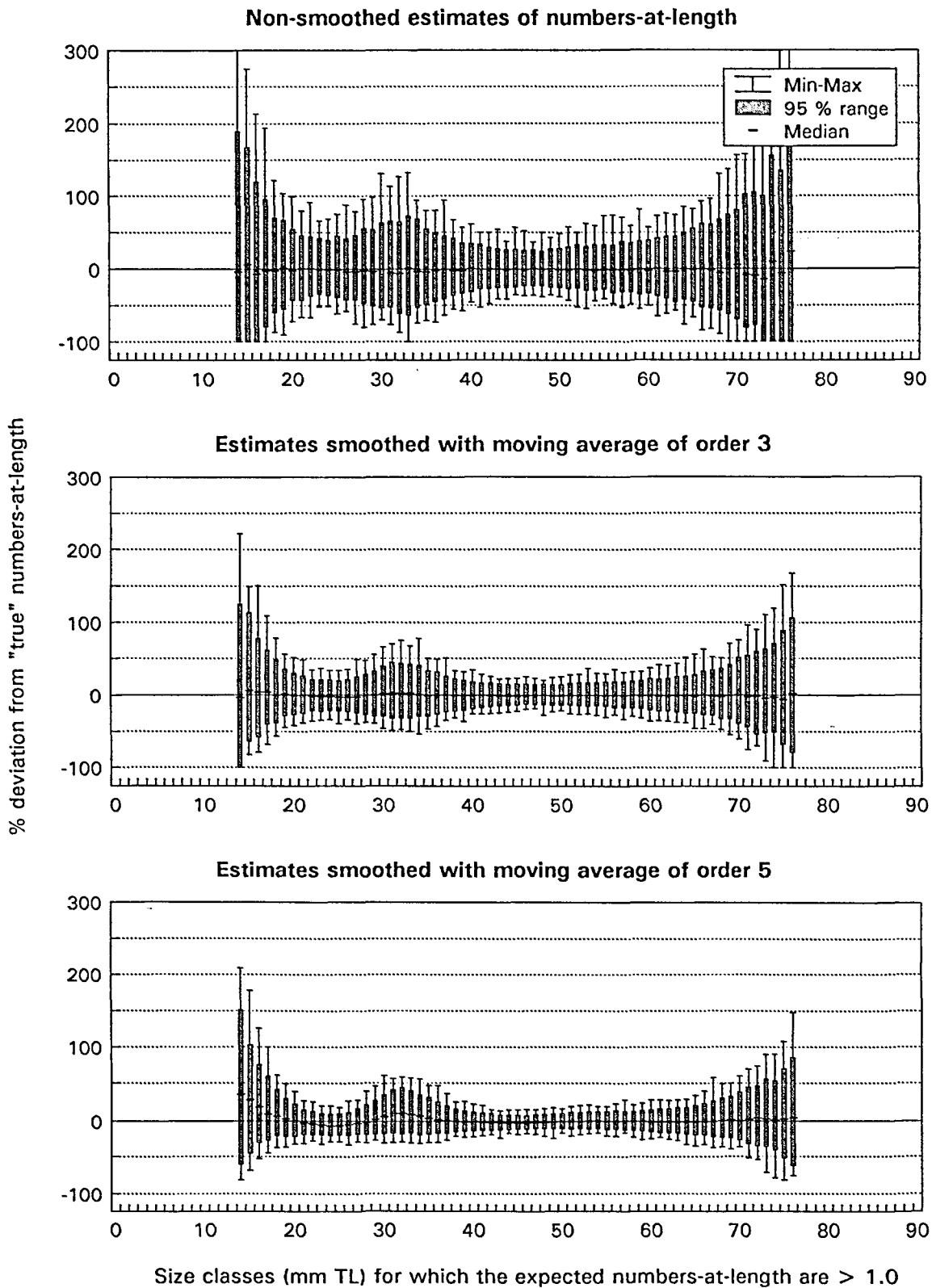


Figure 12 - Effect of smoothing on the medians of the noise levels in the estimated numbers-at-length, for different sample sizes (N). The example given is for simulation 1-A-S1.

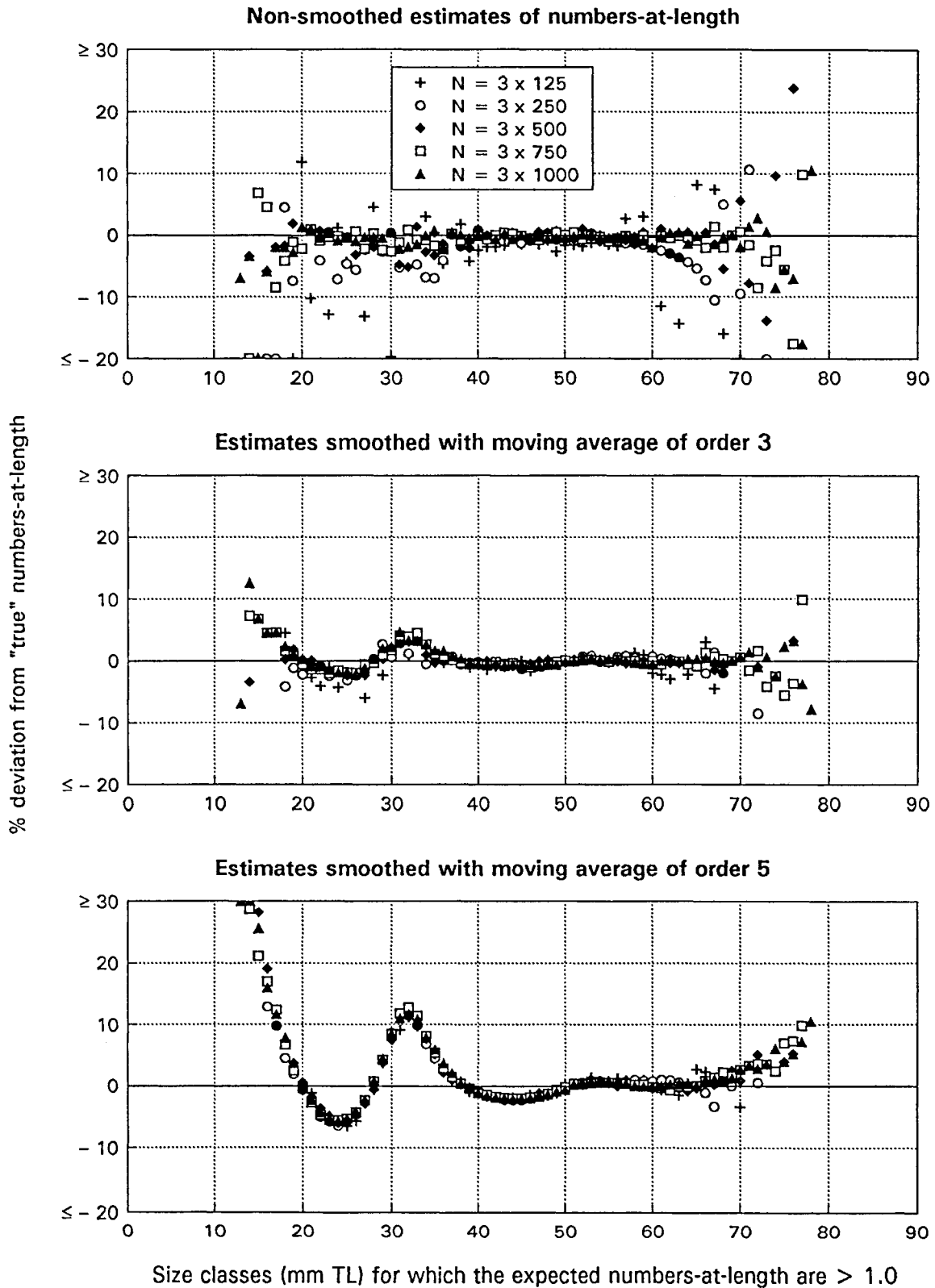


Figure 13 - Ratios between the 95 % ranges of the noise levels under sampling strategies S5 and S1, for different sample sizes (N).

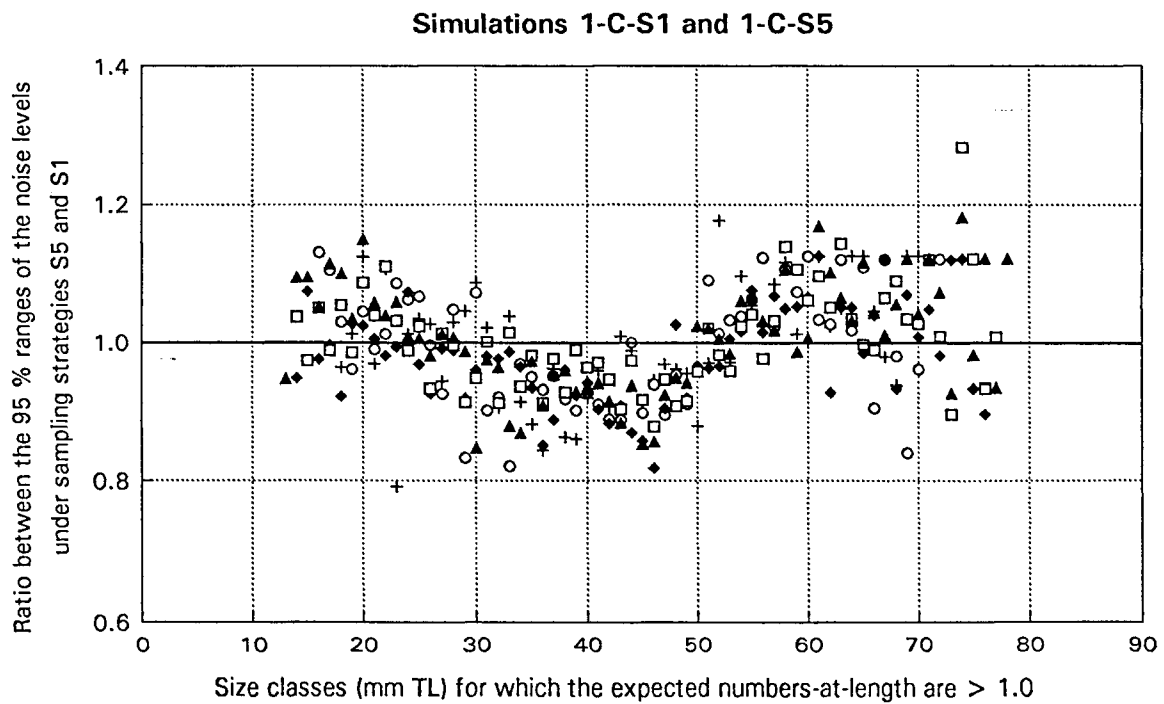
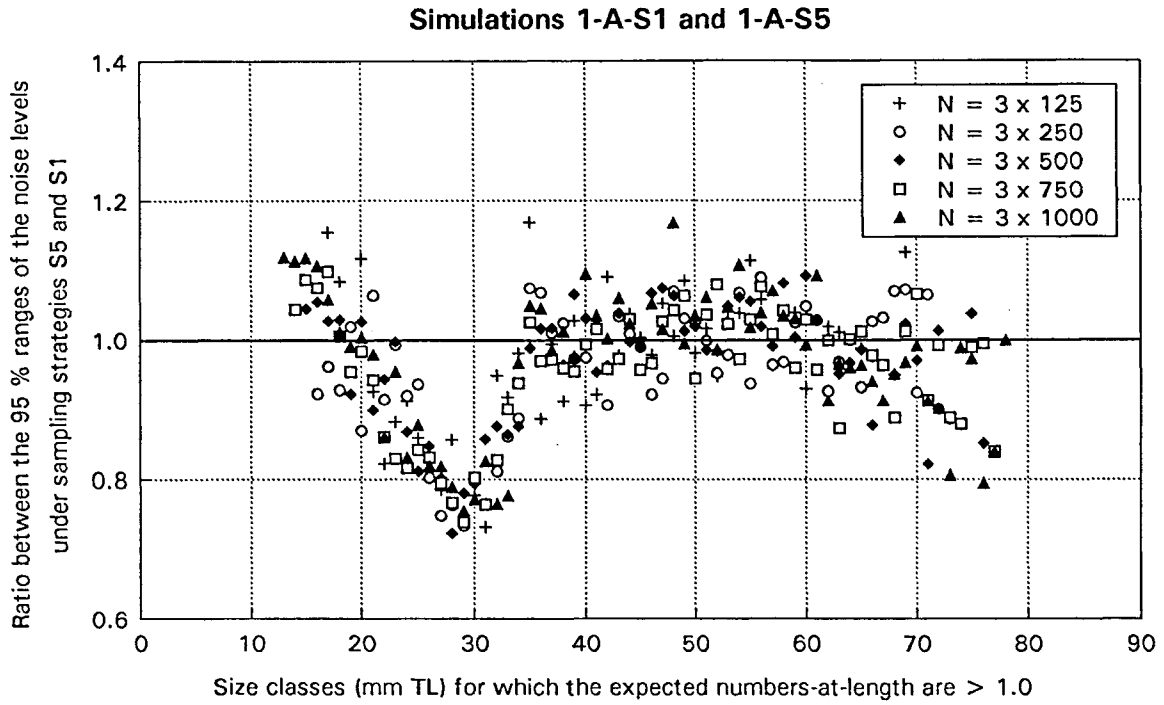


Figure 14 - Effect of sampling strategy and sample size on the estimates of the numbers of shrimps in selected groupings of size classes.

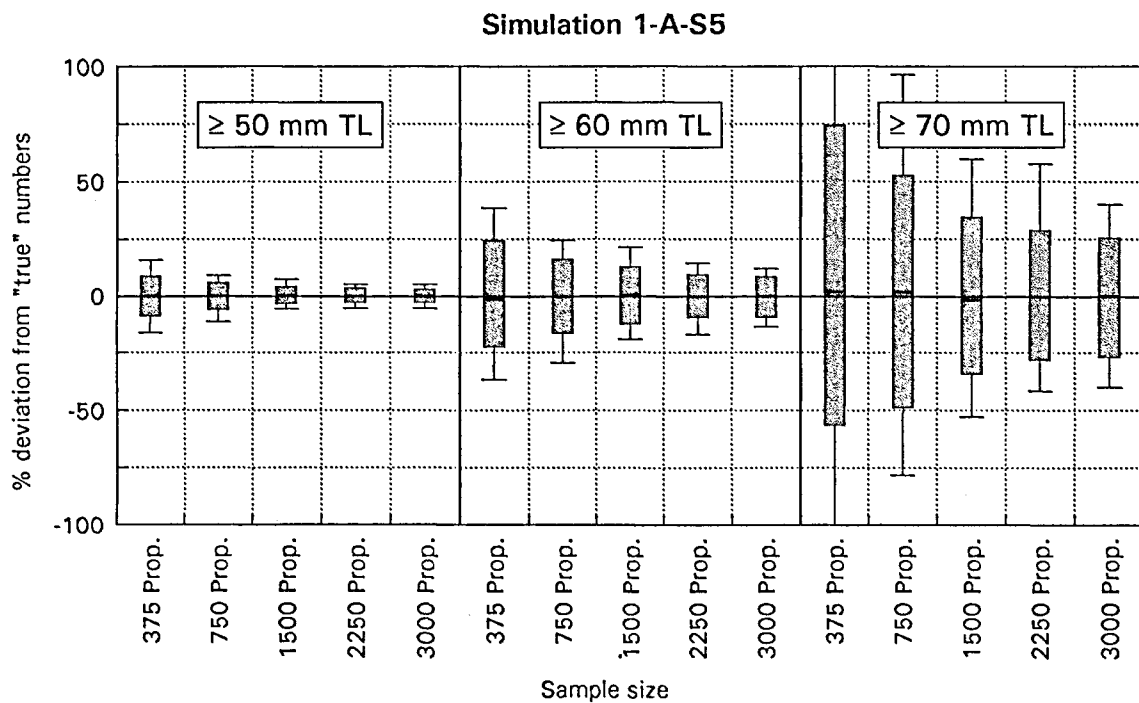
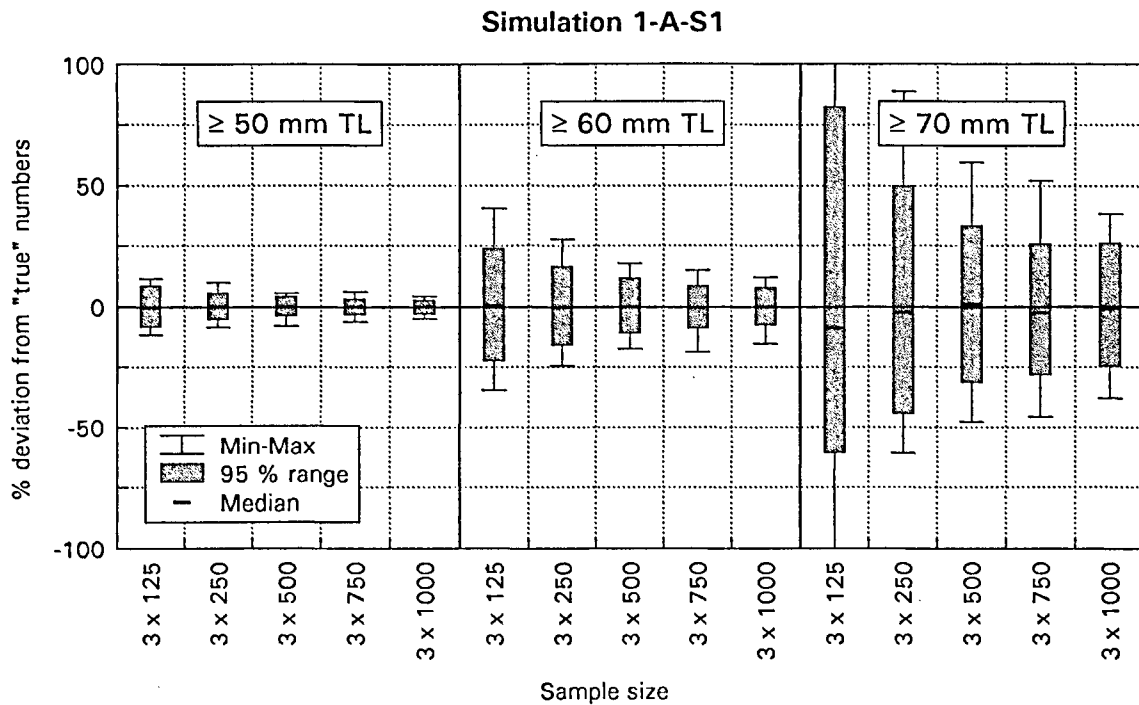


Figure 15 - Percentages of runs giving Chi² p-values ≥ 0.50 , ≥ 0.75 and ≥ 0.90 , under various conditions with respect to size structure of the population, sampling strategy, sample size and smoothing regime.

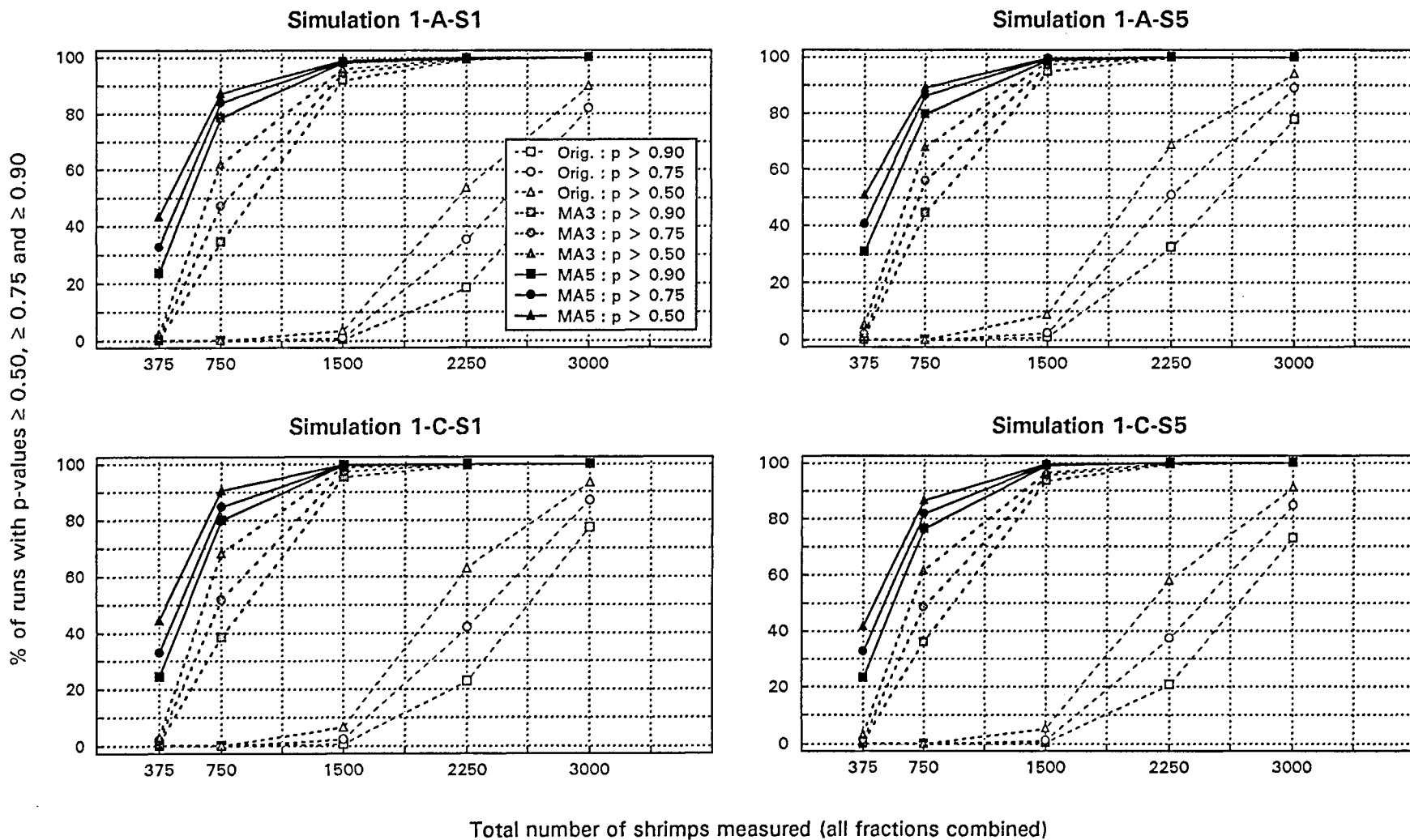


Figure 15 (continued) - Percentages of runs giving Chi² p-values ≥ 0.50 , ≥ 0.75 and ≥ 0.90 , under various conditions with respect to size structure of the population, sampling strategy, sample size and smoothing regime.

