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Innovation and Creativity

Estimation of Size Distribution and Abundance of Zooplankton based on Measured Acoustic Backscattered Data

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Problem Description

In connection with the construction the APR, (Acoustic Plankton Recorder) at NTNU we want to investigate the use of different approaches to the estimation of size distribution and abundance of zooplankton.

To find the size distribution and abundance of zooplankton an inversion algorithm is used. The main algorithm for this purpose is the "Least Square non Negative" algorithm, but it is of interest to investigate the possibility of using other types of algorithms. It is also of interest to reduce the effect of noise in the measurements and thereby giving a more correct value for the backscattered wave from the plankton.

Based on this it was concluded that the assignment should look closer on the following technical areas.

• Investigate the possible methods suitable for noise reduction in a sonar system such as the APR.

• Look at the possibility of using the GA "Genetic Algorithm" in the inversion process.

Assignment given: 16. January 2006
Supervisor: Jens Martin Hovem, IET

ACKNOWLEDGMENTS

ABSTRACT

In the later years the scientist community has bin investigating the possibility of using zoo plankton as a commercial resource. It is therefore of interest to investigate the size distribution and abundance of zoo plankton. NTNU has for this purpose developed an Acoustical plankton recorder or APR, for determination of the size distribution and abundance of plankton. The system utilizes three frequencies namely 200 kHz, 710 kHz and 1 MHz for the task. A specific kind of plankton called Callanus finmarchicus which has primarily a size range from 1-3 mm is considered the most interesting one since it has a large population in the Norwegian Sea.

In this report the signal processing from the "raw" measured values with the APR to the calculated distribution of plankton is described. The following steps has bin carried out in the signal processing:

- First of the measured values are processed with an exact "Time Varied Gain Function" or TVG. This function will compensate for the range from the APR to the target by information about the absorption, the range, the pulse-length and the band-width of the receiver. The exact TVG function has bin used since the ordinary TVG function will give a positive bias for ranges below 10 meters
- After the TVG function the Echo Integrator equation with noise subtraction is used. This will reduce the effect of noise in the measurements and improve the linearity principle.
- At the end inversion is carried out. Two different algorithms are used in the purpose of the inversion, namely the "Least Square non Negative" and the GA algorithm. The inversion will try to find the best fit between the measured data and the mathematically modelled plankton distribution and thereby calculating the size distribution and abundance of plankton.

The echo integration with noise subtraction works by calculating the energy in the measurement over a series of samples contributing to a distance in the measurement in active mode. The samples contributing to the same distance is then used to calculate the energy in passive mode and this value is then subtracted from the energy in active mode. The accuracy of the method is dependent on the number of samples used giving better results with an increasing number of samples. Therefore the method has to be used with consideration to the resolution needed in the measurements.

The "Least Square non Negative" and the GA algorithm are compared by testing them one the same synthetic data. The result is that in some cases the "Least Square non Negative" seems to work better but in other cases the GA algorithm gives the best results. Both methods has got problems in determining the abundance of smaller plankton when large plankton or potentially air bubbles are present.

CONTENTS

1 INTRODUCTION

1.1 Organisation of the report

The report starts of with summary, introduction and definition of the assignment. The main part of the report is chapter 3 Theory/knowledge about plankton measurements. This chapter will look closer on the theory that is used in the abundance and size estimation of plankton. In chapter 4 the results are presented. The report is rounded of with discussion and conclusion in chapter 5 and 6.

1.2 Problem to be addressed

The university program Calanus is a program where several institutes at NTNU cooperate, and where the possibility of catch and utilisation of zooplankton as a commercial resource is investigated. The Acoustic groups' part of the program is to build and develop an acoustic instrument for plankton measurements. There has therefore bin given the possibility of projects in the field for students at the Acoustic division. Possible projects were participation in tests and measurements with the acoustical measuring system, data processing and representation of measured data.

The catch of zoo plankton that is situated at an early step in the food chain will provide an increase in food production and will give raw material that can be used in the feeding of animals. Fishing in both Norway and on world basis is now near the absolute limit of what is possible. It is therefore not possible to base the growth of the fish farming industry on traditional fish resources. The harvest of raw material longer down the food chain will give a viable increase in food production and animal forage.

About 90% of the energy will disappear for every step up the food chain and as a result it will be beneficiary to use zoo plankton as raw material. In the Northern-Atlantic it will be feasible to use zoo plankton as Krill, amphipods, mesopelagic fish and certain species of small squid. If we could utilize just 1% of the Norwegian Seas plankton production to salmon production we would theoretically be able to produce around 1.8 million tons of salmon every year. In comparison the production of salmon is now around 420000 tons every year. Therefore in theory, the plankton part in the food chain is a massive resource.
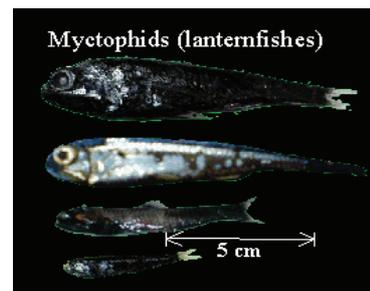
Figure 1.2.1 Mesopelagic fish.

Figure 1.2.2 Krill. Atained size: 6 cm

Figure 1.2.3 Amphipod. Size range: 2-8mm

The zooplankton that is considered the most important is a species called Calanus finmarchicus. This is because it holds an important role in the food chain and has a large population. Numbers from the Barents Sea shows that Calanus finmarchicus can stand for up to 80% of the total population of zooplankton. The sonar system developed by NTNU for size and abundance estimation is therefore constructed mainly for the purpose of estimating the abundance of Calanus finmarchicus.

Figure 1.2.4 An adult Calanus finmarchicus.
Size range: 1-3 mm.

1.3 Main idea

In the APR developed by NTNU for size and abundance estimation of plankton the main method in noise reduction is the use of averaging. However it is of interest to further reduce the effect of noise in the measurements and thereby giving a more correct measured backscattered wave from the plankton.

To find the distribution and abundance of plankton so called inversion is used. The main algorithm for this purpose is the "Least Square non Negative" algorithm but it is of interest to investigate the possibility of using other types of algorithms.

The main idea is therefore the following:

- To investigate the possibility of using Echo integration with noise subtraction to reduce the noise in the measurements.
- Look at the possibility of using the GA "Genetic Algorithm" in the inversion process and compare the results obtained by the GA to the results obtained by the "Least Square non Negative" algorithm.

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2 DEFINITION OF THE ASSIGNMENT

2.1 Requirement specification

In discussions with my main advisor on the assignment it was decided that the assignment should be mainly be angled against the investigation of methods to reduce the amount of noise in the measurements obtained by the APR developed by NTNU for abundance and size distribution of plankton.

The possibility of using the GA "Genetic Algorithm" in an inversion to determine the size distribution of plankton was also discussed.

The requirement was therefore to

- Determine which methods that would be suitable to use in the case of noise reduction.
- Determine the possibility of using the GA in the inversion and the "quality" of the results obtained by this algorithm when determining the distribution of plankton between different size groups.

2.2 Goal of the assignment

The goal of the assignment is to:
- Get insight in the theory involved in noise reduction in these kinds of systems and to find a method that will work satisfyingly.
- Learn more about the GA "Genetic Algorithm" and to use the algorithm to estimate the plankton distribution between different lengths.

3 THEORY/KNOWLEDGE ABOUT PLANKTON RECORDING

This is the main chapter of the report and it contains the theory that will be used later to calculate the abundance and size distribution of plankton.

3.1 The Acoustical Plankton Recorder APR

The instrument used to collect the data that is processed in this report is described here and a sketch of the system is shown in figure 3.1.1. The system consists of a coupling box and a computer above water, and a steel cylinder that is lower down in the water. The transducers are mounted on a plate outside of the cylinder and they are connected to the electronics inside the cylinder by three cables. The transducers are placed in a triangle to maximize the overlapping of beams. The system operates at three frequencies 200 kHz, 710 kHz and 1 MHz.
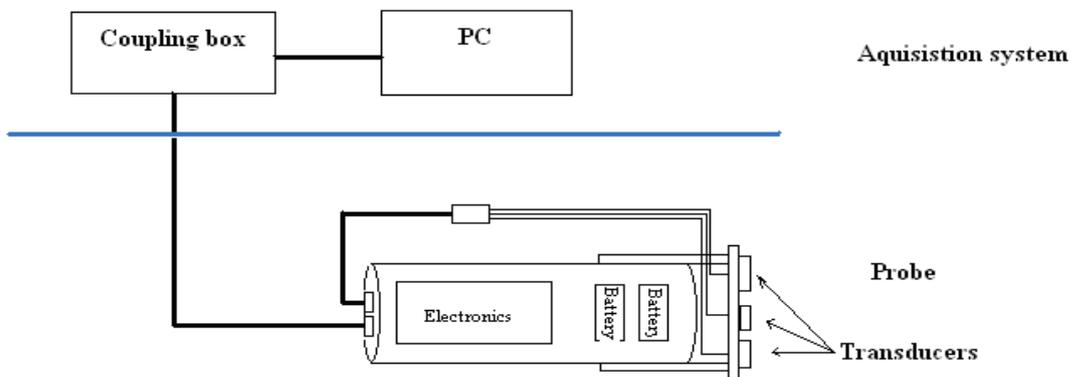

Figure 3.1.1 Sketch of the acoustical plankton recorder

The electronics consists of one control unite, three cards for reception and three cards for transmission.
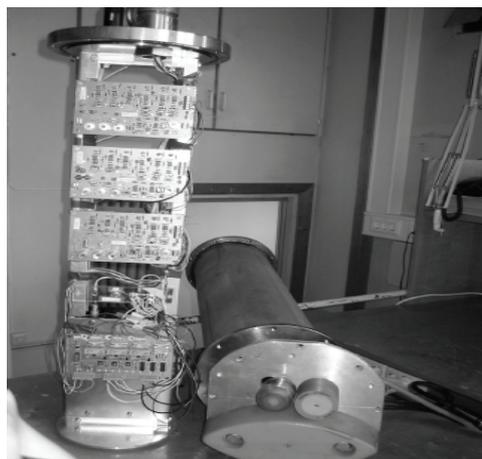
Figure 3.1.2 The demounted steel cylinder.

3.2 Echo integration

When the abundance of fish in layers or schools is large, the density becomes too high to perform individual echo counting of targets to estimate the total abundance. One alternative method is echo integration; witch has proven to be generally more applicable when estimating the quantity of fish and other scatterers in the acoustic beam.

The echo integrator is an echosounder whose output is connected to a device, which accumulates the energy in the received signal. If $v(t)$ is the voltage amplitude produced by the echosounder then the energy is the integral of the squared voltage amplitude $v(t)$ with respect to time. The echo integrator output from one transmission will then become

$$E_i = \int_{t1}^{t2} |v(t)|^2 dt \qquad (3.2.1)$$

E_i is called the echo integral. In practice the echo integrator accumulates the energy from many transmissions, and the density of scatterers is calculated from the mean echo integral and this has the symbol $\langle E \rangle$.

$$\langle E \rangle = \sum_{i=1}^{N} E_i / N \qquad (3.2.2)$$
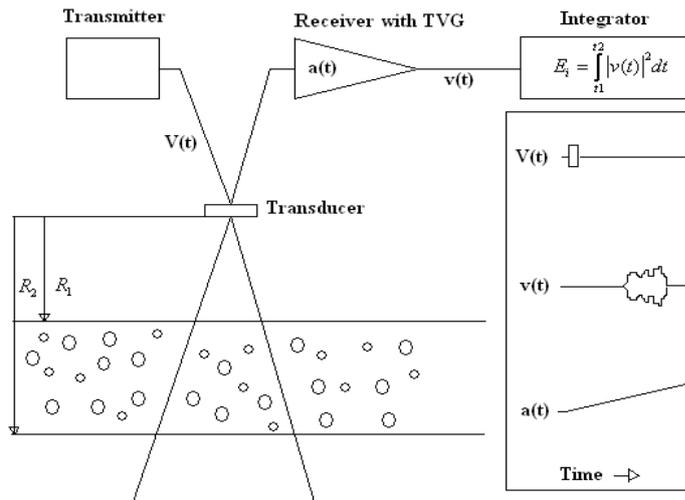
Figure 3.2.1 The figure shows a sonar system. Reflections from the targets in the range between R_1 and R_2 contribute to the integrator output E_i. The integration is performed between $t_1 = 2R_1/c$ and $t_2 = 2R_2/c$ after the beginning of the ping $V(t)$. a(t) is the range compensation witch amplifies the signal according to a mathematical model that describes the propagation losses. The time gate t_1 to t_2 is chosen to correspond to the depth channel which is to be sampled. If $t_2 - t_1$ is much longer than the pulse duration almost all the targets contributing to E_i will be in the channel bounded by $ct_1/2$ and $ct_2/2$.

3.3 Compensation for range with TVG function

To compensate for range when echo integration is used we have to use a 20 log R TVG function. When the range is much larger than the pulse length the approximate TVG function is expressed in decibels as $A(t)$ and as $a_0(t)$ in linear scale.

$$A(t) = 20\log(R) + 2\alpha R \qquad\qquad (3.3.2)$$

$$a_0(t) = (ct)\exp(\beta ct/2) \qquad\qquad (3.3.2)$$

Here β is the acoustic absorption coefficient in nepers per meter, α is the absorption coefficient in decibel per meter and $ct/2=R$. This function only provides exact compensation in the case of an infinitely short sounding pulse or at infinite range. It is good enough for ranges of most fish targets, but for targets close to the transducer we have to use the exact function, and particularly when calibrating the equipment with a standard target. This is because the pulse lasts for a certain period of time, and therefore the compensation should be made rather on echo waveform basis than on sample basis. MacLennan (1987) has shown that the following function is a good enough representation for all practical purposes.

$$a_0(t) = c(t - t_0)\exp(\beta ct/2) \qquad\qquad (3.3.3)$$

Here t_0 is the optimal start time of the TVG function and it depends upon the pulse length and the bandwidth of the receiver. t_0 is always more than half the pulse duration. A more exact approach for calculation of the exact TVG function involves using the shape of the echo envelope. The pulse shape can be modelled as the pulse from a target with flat frequency response acquired by a receiver with a simple LCR bandpass filter.

$$V(t) = \begin{cases} 1 - e^{-\pi Bt} & , t < T \\ (e^{\pi Bt} - 1)e^{-\pi Bt} & , t >= T \end{cases} \qquad\qquad (3.3.4)$$

Here B is the receiver bandwidth and T is the transmitted pulse length.

This function is used to calculate the following expression for the moments I_m (normalized to pulse length T) for the signal $|V(t)|^2$.

$$I_m = \frac{\int\limits_{-\infty}^{\infty} t^m e^{\beta ct} |V(t)|^2 dt}{T^m \int\limits_{-\infty}^{\infty} e^{\beta ct} |V(t)|^2 dt} \tag{3.3.5}$$

When using so called "40logR" TVG function, which applies for single target detection the following expression is used to calculate the exact TVG function.

$$g_{40\log R}(t) = (ct)^2 e^{\beta ct/2} \sqrt{1 + a_1(T/t) + a_2(T/t)^2 + a_3(T/t)^3 + a_4(T/t)^4} \tag{3.3.6}$$

With $a_1 = -4I_1$, $a_2 = -6I_2 + 12I_1^2$, $a_3 = -4I_3 + 24I_1I_2 - 24I_1^3$, $a_4 = -I_4 + 8I_1I_3 + 6I_2^2 - 36I_1^2I_3 + 24I_1^4$

The "20logR" TVG function which applies for distributed or multiple targets (e.g. fish schools and plankton) has an exact function given by:

$$g_{20\log R}(t) = (ct)e^{\beta ct/2} \sqrt{1 + b_1(T/t) + b_2(T/t)^2} \tag{3.3.7}$$

With $b_1 = -2I_1$, $b_2 = 2I_1^2 - I_2$.

In the APR developed by NTNU for abundance and size estimation of plankton the following values are given for the three frequencies used in the system.

Table 3.3.1 The Band-width of the receiver at each frequency used in the APR

Frequency	200kHz	710kHz	1MHz
-3dB band-width	19kHz	18kHz	11kHz

The pulse length at all frequencies is 1.2 ms. The values given in Table 3.3.1 will give the results in fig. 3.3.1, fig. 3.3.2 and fig. 3.3.3 for the modelled echo pulse at the three frequencies.

Fig 3.3.1 Model of the echo pulse at 200 kHz from a target with flat frequency response acquired with a simple LCR bandpass filter at the three frequencies used in the APR developed by NTNU.

Fig 3.3.2 Model of the echo pulse at 710 kHz from a target with flat frequency response acquired with a simple LCR bandpass filter at the three frequencies used in the APR developed by NTNU.
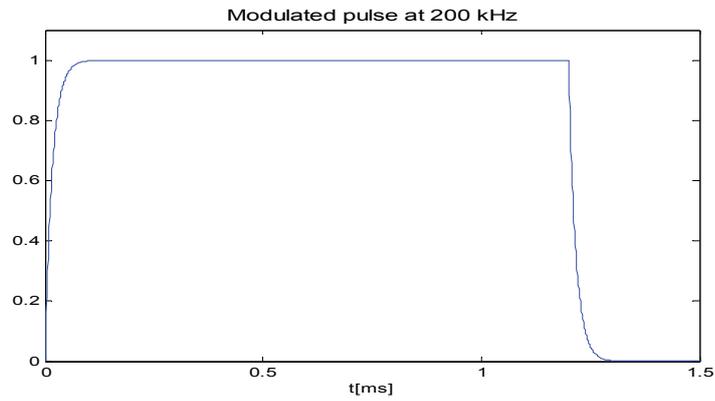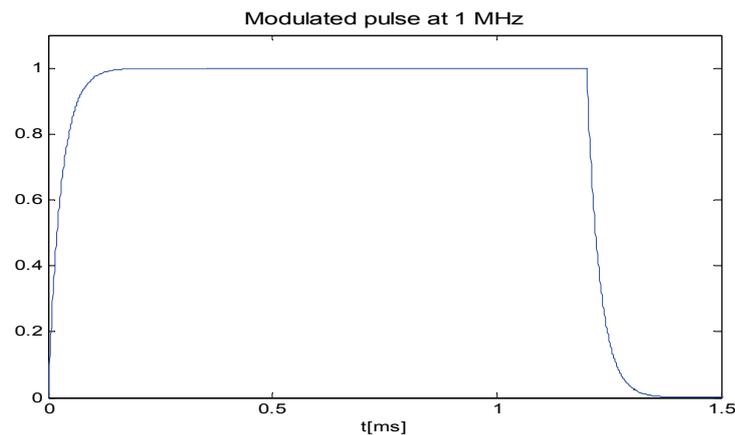

Fig 3.3.3 Model of the echo pulse at 200 kHz from a target with flat frequency response acquired with a simple LCR bandpass filter at the three frequencies used in the APR developed by NTNU.
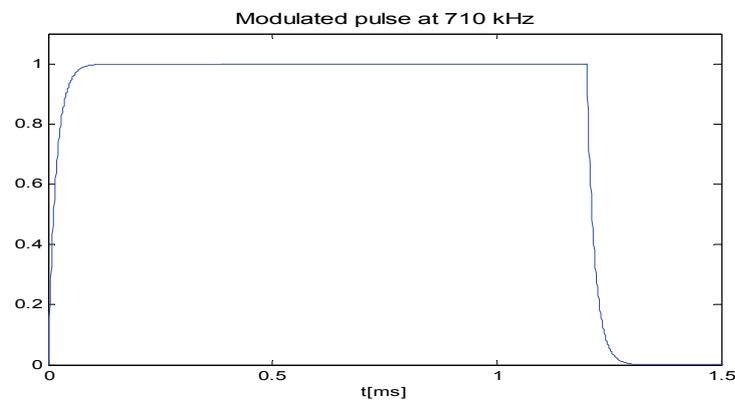
The modulated pulses will not exactly correspond to the real echo from a standard target sphere in the sonar system but it will give a good approximation. To take account for the frequency response of a real target, a target detection algorithm has to precede the TVG correction phase. This procedure involves additional computational coast and will not be mentioned further in this text.

Tab 3.2.1 The normalized moments calculated for the three frequencies used in the sonar system developed by NTNU. The values used for the calculation of the absorption coefficient are: Salinity=35, depth=0, temperature=10 and pH=8. The pulse length used is 1.2ms.

Normalized moments	200kHz (BW=19kHz)	710kHz (BW=18kHz)	1MHz (BW=11kHz)
I_1	0.5148	0.5180	0.5297
I_2	0.3462	0.3494	0.3603
I_3	0.2616	0.2646	0.2747
I_4	0.2109	0.2136	0.2231

The calculated exact TVG functions are compared with the ordinary 20logR functions for the three frequencies using the values given for the APR developed by NTNU and the normalized moments given in table 3.2.1. The functions are given in decibels from -15 to 30dB and are plotted in the area from 0.5 meters to 10 meters.
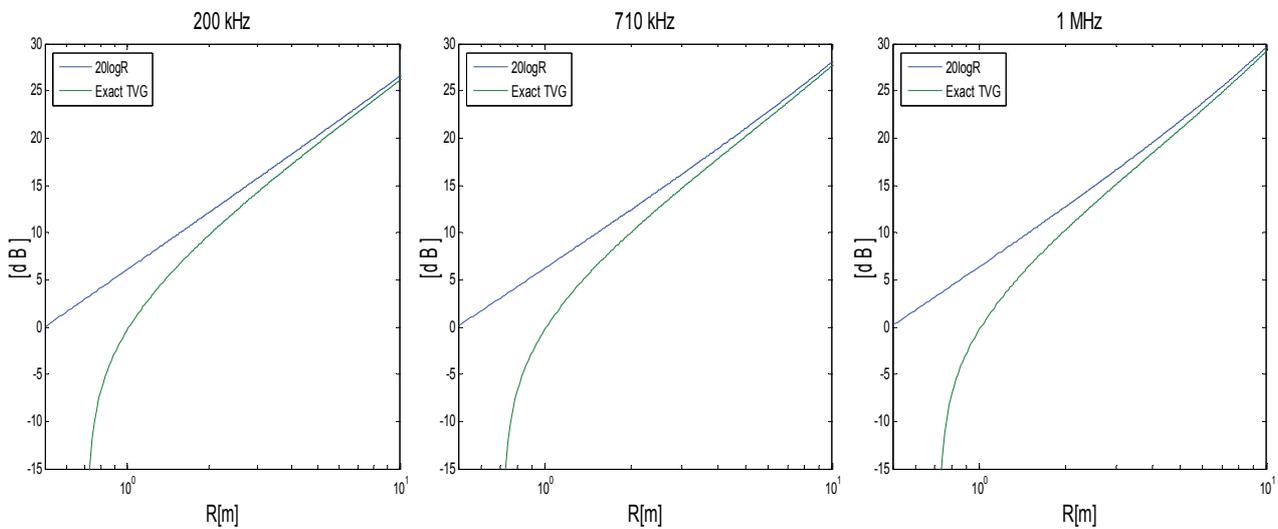
Fig 3.3.4 Exact TVG function $g_{20logR}(t)$ compared with the 20logR function at the three frequencies used in the APR developed by NTNU.

When calculating the difference between the exact TVG function and the 20logR function shown in fig 3.3.5 for APR developed by NTNU. it is evident that continuous time varied gain can not be used in the ranges below 10 meters. The reason for this is that in the 20 logR case the end of the echo will be artificially amplified causing a larger value to be predicted than really encountered

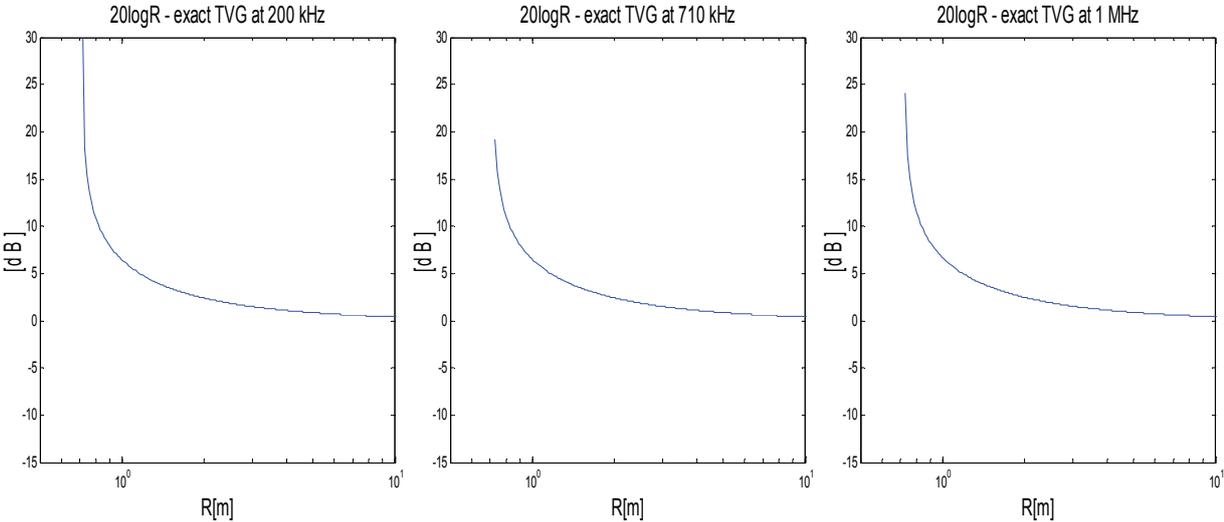**Fig 3.3.5** The difference between the exact function and the 20logR function at the three frequencies used in the APR developed by NTNU.

3.4 The echo integrator equation

The integration is performed between times t_1 and t_2 witch corresponds to the depth channel R_1 to R_2, and E is the average integrator output over many transmissions. When the integration is progressing the transducer may be on a moving ship and at the same time the fish is also mobile, and therefore many different fish will contribute to E. If the number of fish is large and they are randomly positioned in the beam, then E will be proportional to the density ρ which is the number of fish per unit area in the chosen depth range.

In the APR developed by NTNU the sampling frequency is 50000 Hz. This means that it samples the input voltage every 20 μs, equal to 0.015 m increments for c=1490 m/s. The voltage above a threshold given by the user is converted by an ADC to a bit word. When using echo integration the echo voltages are squared and summed over the 0.0015 m range increments.

The range that we want to investigate can be divided into a number of smaller areas where integration is performed for each smaller area. This will make it possible to determine the density of scatterers for different ranges. It is also possible to measure the density in each range interval over time. This is done by calculating the sum of squares values for each depth interval after a final specified number of transmissions. The echo integrator equation can be derived from the sonar equations with the use of the expression for the volume reverberation.

$$RL = SL - 2TL + Sv + 10\log(v) \tag{3.4.1}$$

The reverberation volume V is given by

$$V = \frac{c\Delta T}{2}R^2\Omega \tag{3.4.2}$$

Here Ω is the effective beam width. The two way transmission loss is given as

$$2TL = 40\log(R) + 2\alpha R \tag{3.4.3}$$

This in combination with the range dependent volume V leads to a transmission loss of

$$2TL = 20\log(R) + 2\alpha R \tag{3.4.4}$$

When an exactly correct TVG is used the term in eq.3.4.4 is fully compensated and does not appear in the equation. The pressure waves that make up **RL** act on the transducer which in combination with the cable and echo-sounder system gain produces a voltage at the output **VR** whose amplitude at any instant of time is equal to **RL**+ G_x. (G_x is the transducer, cable, echo-sounder system gain in dB/ V. $(\mu \text{ Pa})^{-1}.1\text{m}^{-1}$. This can be written as

$$VR = SL + G_x + Sv + 10\log(c\Delta T/2) + 10\log(\Omega) \qquad (3.4.4)$$

The echo integration for the discrete case for each range interval is given as

$$E_x = \sum_{n1}^{n2} v(n)^2 \qquad (3.4.5)$$

Here **n1** and **n2** is the samples that specify the range interval we want to integrate over. When we want to find a final value for each depth interval over a number of transmissions we have to use the following expression for each range interval.

$$E_{xf} = \sum_{trn=1}^{P} E_x \qquad (3.4.6)$$

P is the number of transmissions in a sequence. To get this equation to coincide with the equation for **VR** we have to divide the expression for E_{xf} on the total number of samples that we have integrated over in each depth interval. The result is expressed in dB.

$$10\log(\frac{E_{xf}}{NxP}) = SL + G_x + Sv + 10\log(c\Delta T/2) + 10\log(\Omega) \qquad (3.4.7)$$

The source level **SL** is defined as the sound level at a distance of 1m in dB relative to 1 µPa. So In other words the source level is given as 20 $\log(p_0)$ where p_0 is the sound pressure at a distance of 1 m. The gain G_x is given as 20 $\log(g_x)$, where g_x is given as the difference between the voltage at the output of the sonar system and the sound pressure at the transducer. The S_v part of the equation is equal to 10 $\log(\rho^*\sigma_{bs})$. The expression can now be written as

$$\frac{E_{xf}}{N_xP} = P_0^2 g_x^2 \rho_{xf}\sigma_{bs}\Omega c\Delta T/2 \qquad (3.4.8)$$

This expression can also be written as

$$\rho_{xf} = \frac{E_{xf}\, \bar{g}_x}{[P_0\, g_x]^2 [N_x P][\Omega c \Delta T / 2]\sigma_{bs}}$$

(3.4.9)

The term $\bar{g}_x$ is the **TVG** correction factor for each interval x.

Table 3.4.1 The parameters in the echo integrator equation

Parameter	Description
$\bar{g}_x$	constant for TVG correction in (x) interval
ρ_{xf}	density of scatterers for the (x) interval in scatterers/m^3
P	number of transmissions per sequence
N_x	number of 0.015m increments per (x) interval
ΔT	pulse duration
σ_{bs}	average backscattering cross-section
g_x	Transducer, cable, echo-sounder system gain in V.µPa^{-1}.1m^{-1}
c	speed of acoustic waves

3.5 The TVG correction factor

The TVG correction factor $\bar{g}_x$ is calculated from the TVG error. The TVG error is calculated by measuring the difference *A(t)* between the voltage at the input and output of the receiver with time. These measurements should be made with electronic instruments that respond fast enough to record the change of gain over the operating difference of the echosounder. We can then see how the ratio *A(t)/(exact_TVG(t))* changes with time, and this is the TVG correction factor. In the case where the TVG function is made by the analogue technique, where non-linear components are used in the feedback loop around the amplifier, the TVG error varies smoothly with time and the maximum error is large. In the case where a digital TVG function is used the TVG error varies rapidly around 0 dB, and the maximum error is small. The rapid changes are caused by the digital quantisation, because the digital circuits adjust the gain in fixed increments. The quantisation error is not considered important at the range of most fish targets, but it is relevant to the echo from the standard target during calibration. The error is normalized by supposing that the gain is correct at the range of the standard target. The TVG correction factor is then calculated as an average of the error over the time corresponding to the depth channel of the echo integration. For more details see Fisheries acoustics, appendix D (chapter 5). In this report calibration of the equipment won't be mentioned further and it is believed that the echo sounder is calibrated correctly. The TVG correction is therefore simply set to unity and it disappears from the echo integrator equation.

3.6 Linearity principle

In the foregoing project (*calanus - akustisk mengdemåling av plankton)* the inversion of the sonar-data was a linear process. In other words the output amplitude of the sonar-system is proportional to the quantity of targets having similar acoustical properties.

The linearity principle may be stated as follows. We are considering an aggregation of targets witch are insonified over a period of time by N transmissions (pings) that are generated by an echosounder. At any instant of time the received signal will consist of overlapping echoes from targets within the sampling volume. Linearity requires that the mean sampled energy from all the targets is equal to the sum of the echo energies if they were insonified separately. There are two main assumptions that are required for linearity.

1. The targets are randomly distributed in the insonified space, ensuring that the phases of each target are randomly distributed relative to each other.
2. The targets move between each transmission so that a new random set of phases is generated.

The echo energy from a single ping is E_i. All the E_i will be different because the targets will move with time and cause the phase to vary. An alternative method would be to sample different sampling volumes on the same ping, or for the transducer to move and sample a different volume and in this way sample a set of n randomly distributed targets. When we have a large number of observations the ensemble average $\langle E \rangle$ tends to the true mean. Note that we can sample a number of different realizations and derive the ensemble average and not just by sampling the same realisation many times or by a single observation of a large number of targets.

The linearity principle states that the sum of the energy from the individual targets that is in the insonified area will be the expected value for $\langle E \rangle$. This means that the following mathematical condition must hold for any number of targets n.

$$\underset{N \to \infty}{Lim}\left[\langle E \rangle\right] = n\bar{e} \tag{3.6.1}$$

This states that when the number of observations N is very large the ensemble average will be equal to the sum of the individual targets.

The value $\bar{e}$ is the average result from the individual targets e_j

$$\bar{e} = \sum_j e_j / n \tag{3.6.2}$$

When measuring the abundance of fish N should be 20 or more to achieve a reasonably accurate asymptotic result for $\langle E \rangle$. In the APR developed by NTNU the standard value for N is 16.

The main hypothesis of the linearity principle is that the targets are randomly positioned causing the phases in the reflections from the individual targets to be incoherent to one another. When two signals are incoherent to one another it means that the phases of the two signals are completely unrelated. The differences in phase are said to be equally probable. The phases are said to be coherent when the phases are constant over a series of ping.
As an example of this we can consider two signals received together having a phase difference η and an angular frequency ω.

$$v(t) = A_1 \sin(\omega t) + A_2 \sin(\omega t + \eta) \tag{3.6.3}$$

Here A_1 and A_2 are the amplitudes of the two signals and t is the time.
The squared result of the sum will then be a *sin* wave with amplitude of

$$A_T^2 = A_1^2 + A_2^2 + 2 A_1 A_2 \cos\eta \tag{3.6.4}$$

If we have many observations of pairs of echoes with random phases then the $\cos\eta$ term will cancel out and the mean squared amplitude is

$$\bar{A}_T^2 = A_1^2 + A_2^2 \tag{3.6.5}$$

If we assume that the amplitude of the two signals have the same value the result can be written as

$$A_T^2 = 2 \times A^2 \tag{3.6.6}$$

For any number of signals we can write the result as

$$A_T^2 = n \times A^2 \tag{3.6.7}$$

Where n is the number of targets. This proves the linearity principle because the squared amplitude is proportional to the energy of the signal.

The proportionality between the energy and the squared amplitude comes from the fact that the energy of the signal is obtained by integrating the intensity with respect to time. The intensity is given by

$$I = p^2 / \rho c \qquad (3.6.8)$$

The sound pressure is proportional to the amplitude of the voltage in the echosounder output. The intensity is proportional to the squared pressure if we ignore the variation in the acoustic impedance $\mathbf{Z} = \rho c$. The variation of the acoustic impedance is typically just a few percent in the sound path under normal oceanic and freshwater conditions and this is the reason why the variation can be ignored. As a consequence of this relation the echo integrator works by first squaring the voltage of the echosounder output before the integration is performed. Since the energy is proportional to backscattering cross section we can use the following relationship

$$\sigma_{bs,T} = n \times \overline{\sigma}_{bs} \qquad (3.6.9)$$

This means that total backscattering cross section will be the sum of the backscattering from all the individual targets.

If the targets are not randomly positioned we can get some special conditions where coherent scattering can occur. For example if the fish in a school where placed regularly in layers with a distance between them of a half wavelength, then the echo back to the sonar would be the sum of the echoes from the individual targets.

$$v(t) = A_1 \sin(\omega t) + A_2 \sin(\omega t + 2\pi) \qquad (3.6.10)$$

Let the amplitude from the individual targets be the same and sum the result we get

$$v(t) = 2 \times A \sin(\omega t) \qquad (3.6.11)$$

The squared amplitude from any number of targets will then become

$$A_T^2 = n^2 \times A^2 \qquad (3.6.12)$$

The total scattered pressure from the school will therefore be the sum of the scattered pressure from the individual targets, but the energy will increase with the squared value of the number of targets in the school.

3.7 Non – linear effects

At very high densities of fish the linearity principle fails because of effects caused by scattering between the individual targets in the school, and shadowing effects where the targets in the front attenuates the wave so the targets in the back will have lower incident intensity then expected. The two effects will cause the reflected pressure back to the echo sounder to increase at a slower rate then expected as the density of the fish school increases.

The most important non-linear effect is believed to bee the shadowing effect. The amount of signal reduction when the sound wave propagates through a fish school is determined by the area-density of the intervening fish and the extinction cross-section σ_e, which is the measure of removal of energy by each fish from the sound wave.
It has bin found that first order scattering theory, with an addition of an attenuation term to account for shadowing is adequate to explain constant fish densities in the wild.
The linearity principle is modified to become

$$\lim_{N \to \infty} \left[\langle E \rangle \right] = n \bar{e} \left[1 - \exp(-2h\rho'\sigma_e) \right] / (2h\rho'\sigma_e) \qquad (3.7.1)$$

In this equation ρ' is the number of fish per unit volume averaged over the thickness h of the aggregation. We can see from the equation that when $h\rho'\sigma_e$ is very small the equation will be almost identical to the equation for the linearity principle, and shadowing will in this case not be important.

The acoustic field at a given target is given by the incident wave produced by the echo sounder and the reflections from all the other targets. When the scattering field dominates the total field, then high order multiple scattering is important. This effect would cause a school of fish to retain the acoustic energy inside the school by the scattering between the individual fish. The energy will slowly escape, and therefore the echo back to the transducer will last longer than expected. The lengthened echo will show as a diffuse ragged tail after a more solid mark from the first order scattering from the fish school. The tail can be made by a few fish situated at a distance grater then the fish school, but this is in most cases unlikely. When measuring plankton it is believed that we can discard the non-linear processes. This is because the extinction cross section σ_e of the individual plankton is very small.

3.8 Noise

Noise is any signal other than the reverberation and it's caused by independent effects. The noise is present in the receiver even when the transmitter is switched off. There are many different sources of noise in the sea and they can be classified into three groups' namely physical, biological and artificial noise. Some examples of the different kinds of noise are listed below

Table 3.8.1 Different kinds of noise divided in physical, biological and artificial noise

Type of noise in the sea	Example of noise
Physical	Wind, breaking waves, turbulence, thermal noise
Biological	Animal sound and movement
Artificial	Shipboard machinery, propeller, water around the hull

The table contains just a few examples and is not intended to be a complete list. In addition to the noise in the sea there will also be an electrical noise in the receiver witch adds to the acoustic noise. In fishery sonar's the acoustic noise is likely to be the dominating factor. The noise is usually illustrated in terms of its frequency composition. The noise spectrum level is the noise power per unit frequency interval, and can be seen as the power of the noise after it has bin passed through an ideal filter with a bandwidth of 1 Hz. The noise most often systematically varies with frequency but individual sources such as a propeller can cause peaks in the noise spectrum. Fig. 3.8.1 illustrates the ambient noise in the sea. In the frequency region from 0.5- 25 kHz wind induced waves are the main source of noise and the level of noise depends upon the sea state. The noise in this region decreases with frequency. At high frequencies the noise level increases because of thermal noise and above 300 kHz it will be the dominating factor. In addition to the sources that has bin mentioned here and is shown in fig. 3.81 we will have additional noise caused by shipping and turbulence. At frequencies below 20 Hz the noise is mostly caused by large scale oceanic turbulence. Shipping can cause peaks in the spectrum which are most often present in the area around 100 Hz.
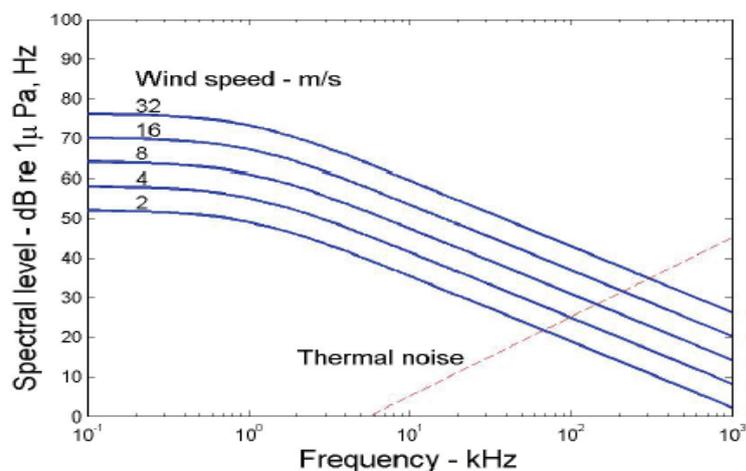

Figure 3.8.1 The figure illustrates the ambient noise in the sea.

3.9 The threshold bias

When a signal threshold is applied to eliminate the noise in an echosounder, any echo smaller than the threshold is also ignored. The observed density of targets is therefore biased because some proportion of the population of targets has not bin detected. The bias depends upon the signal and noise amplitudes (SNR). If the echo probability distribution function (PDF) of the target species is known then a correction may be applied to the estimated abundance. Unfortunately the real PDF is rarely known well enough for this purpose, and therefore it should be avoided if possible. Nunnallee (1990) has proposed an alternative to the signal threshold when dealing with noise in echo integration. He measures the noise level at the echosounder output with the transmitter switched off. Subsequently the noise contribution is subtracted from the echo integrals with no threshold applied. The procedure does not allow for reverberation, but it has the advantage that the threshold bias is completely eliminated. In the case of measuring plankton the reverberation is the main interest and therefore the method should work fine in this case.

3.10 Averaging

Signal averaging is often used to suppress noise in a repetitive measurement signal affected by random noise, and the process can even be used when the r.m.s. value is much less than the value of the noise. Suppose that a signal consisting of *p* repetitive cycles with noise, each having a duration *T* are fed into an averager. From each cycle *p* there are taken *N* samples that are stored. The samples are exactly synchronized. This means that the *i*th sample is taken at exactly the same time in each cycle. The first sampled values from each of the *p* sections are added together and divided by *p*. The average value of the i*th* sample becomes

$$y_i^{av} = \frac{1}{p}(y_{i1} + y_{i2} + ... + y_{ip}), \quad i = 1, ..., N \tag{3.10.1}$$

Each of these N sample values are then displayed at the appropriate time to give the averaged signal. The sampled values of the signal are approximately equal so the averaged signal will therefore be approximately equal to the real signal. The noise component on the other hand varies between each sample, and therefore some of the noise signals will cancel each other out and therefore the averaged noise component will be reduced in magnitude.

The improvement in signal – to – noise ratio can be readily calculated for random noise with a Gaussian probability density function. Suppose that an ensemble of Gaussian signals y_1 to y_2 with a standard deviation σ_1 to σ_p is averaged. The standard deviation of the averaged signal will then become

$$\sigma_{AV} = \sqrt{(\frac{\sigma_1^2}{p^2} + \frac{\sigma_2^2}{p^2} + ... + \frac{\sigma_p^2}{p^2})} \tag{3.10.2}$$

And If $\sigma_1 = \sigma_2 = \sigma$ then

$$\sigma_{AV} = \sqrt{(\frac{p\sigma^2}{p^2})} = \frac{\sigma}{\sqrt{p}} \tag{3.10.3}$$

When averaging over 16 signals: $\sigma_{AV} = \sigma / \sqrt{16} = \sigma / 4$ i.e. we will have a reduction in standard deviation by a factor of 4. As a consequence of this the r. m. s. value of the noise will also be reduced by a factor of 4. This will give an increase of signal – to - noise ratio of 12dB.

3.11 Attenuation

The mysterious large attenuation of sound around 20 kHz was first explained in laboratory experiments performed by R.W. Leonard (1949) and his students O. B. Wilson (1954) and D. Bies (1955). It was found that relatively small amounts of magnesium sulphate salts were causing a molecular relaxation phenomenon. In the 1970s, Fisher and Simmons (1977) and Mellen and Browning (1977) found through laboratory experiments a second relaxation phenomena due to boric acid in the sea water that is moderated by the pH level in the sea water. Francouis and Garrison (1982) have developed an empirical formula that is given by the sum of the two relaxation terms and the viscosity component:

$$\alpha = \frac{A_1 P_1 f_1 f^2}{f^2 + f_1^2} + \frac{A_2 P_2 f_2 f^2}{f^2 + f_2^2} + A_3 P_3 f^2 \quad dB\!\!\Big/\!\!_{km} \tag{3.11.1}$$

The alternative coefficient β in nepers per kilometre is equal to α divided by 8.69. The formula is claimed to predict α to an accuracy of 5 % for temperatures from -1.8 to 30 degrees, salinity from 30 to 35 ppt, and frequencies from 400 to 1 MHz. The pH value in sea water is usually in the range from 7.8 – 8.2. If the precise value is not known it is a reasonable assumption that pH=8 when calculating α.
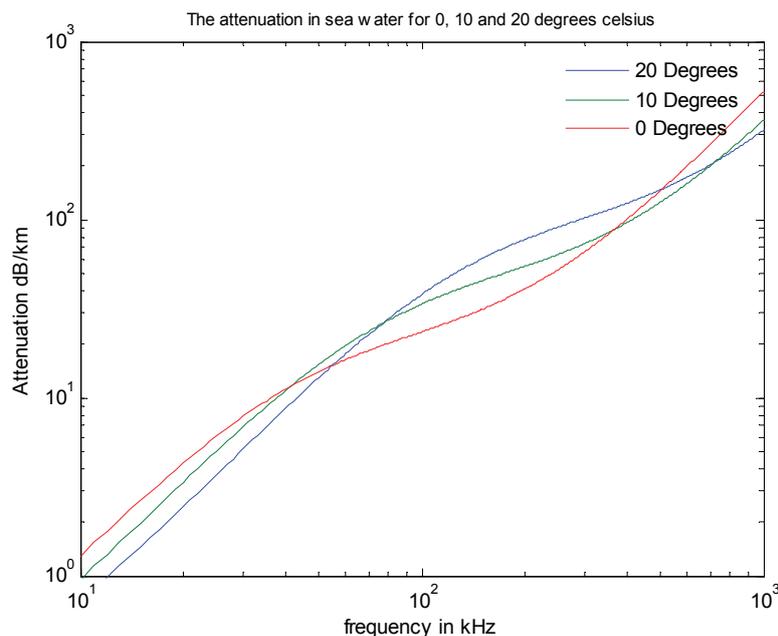

Figure 3.11.1 Sound pressure attenuation rate given in dB/km for sea water at temperatures 0, 10 and 20 degrees Celsius. The calculations are made from the empirical formula made by Francouis and Garrison (1982). Parameters are pH=8; S=35 ppt; and depth, z = 0.

From fig. 3.11.1 it can be seen that the attenuation varies with a large amount according to the temperature, and the difference between the attenuation at the different temperatures can be ass much as 100dB/km at high frequencies. This illustrates the importance of having as right temperature as possible when calculating the attenuation in a sonar system.

Boric Acid Component in Sea Water

$$A_1 = \frac{8.68}{c} 10^{(0.78 \text{pH} - 5)} \text{ dB km}^{-1}\text{kHz}^{-1}$$

$$P_1 = 1$$

$$f_1 = 2.8 \left(\frac{S}{35}\right)^{0.5} 10^{[4 - 1245/(273 + T)]} \text{ kHz} \tag{3.11.2}$$

$$c = 1412 + 3.21T + 1.19S + 0.0167z \quad \text{m/s}$$

Magnesium Sulphate Component in Sea Water

$$A_2 = 21.44 \frac{S}{c}(1 + 0.025T) \text{ dB km}^{-1}\text{kHz}^{-1}$$

$$P_2 = 1 - 1.37 \times 10^{-4} z + 6.2 \times 10^{-9} z^2 \tag{3.11.3}$$

$$f_2 = \frac{8.17 \times 10^{[8 - 1990/(273 + T)]}}{1 + 0.0018(S - 35)} \text{ kHz}$$

Pure water (viscosities) component for $T <= 20°C$

$$A_3 = 4.937 \times 10^{-4} - 2.59 \times 10^{-5} T + 9.11 \times 10^{-7} T^2 - 1.5 \times 10^{-8} T^3 \text{ dB km}^{-1}\text{kHz}^{-2} \quad (3.11.4)$$

Pure water (viscosities) component for $T > 20°C$

$$A_3 = 4.964 \times 10^{-4} - 1.46 \times 10^{-5} T + 1.45 \times 10^{-7} T^2 - 6.5 \times 10^{-10} T^3 \text{ dB km}^{-1}\text{kHz}^{-2} \quad (3.11.5)$$

$$P_3 = 1 - 3.83 \times 10^{-5} z + 4.9 \times 10^{-10} z^2 \tag{3.11.6}$$

3.12 Model for acoustical backscattering from Calanus

Calanus can be modelled mathematically by assuming that it has a scattered acoustic field like a fluid filled sphere. Anderson (1950) solved this problem with a mathematical model of this type of body, and it will be used in this report with some adjustments. The orientation of the scatterers has no importance in this model since a sphere is geometrically the same from all directions. The hypothesis is that even though the plankton has a different scattered field for different directions, the total scattered field for all directions will be the same as for a fluid filled sphere. Two fluid filled models are usually used: The full modal solution proposed by Anderson (1950) and a truncated model version that is only dependent on the two vibration modes. The last model has got experimental support by studies performed by *Costello et al.* (1989) and this is the model that has bin used in this report. The mathematical equations that are utilized here are collected from the book *Fundamentals of Acoustical Oceanography*. We make use of the "acoustical scattering length" for plankton given in the equation below:

$$L \equiv \frac{ia}{ka} \sum_{m=0}^{M-1} (-1)^m P_m(\mu) \frac{(2m+1)}{1+iCm} \qquad (3.12.1)$$

where

$$Cm \equiv \frac{j'_m(k_1 a) n_m(ka) - ghj_m(k_1 a) n'_m(ka)}{j'_m(k_1 a) j_m(ka) - ghj_m(k_1 a) j'_m(ka)} \qquad (3.12.2)$$

and

$$g \equiv \frac{\rho_1}{\rho_0} \qquad h \equiv \frac{c_1}{c_0} \qquad (3.12.3)$$

Here g is the relative ratio between the density in the plankton and the density of the media and h is given as the relative ratio between the velocity of the sound wave in the plankton and the velocity of the sound wave in the media. M is the number of modes used in the solution and as mentioned earlier the first two modes will be used here. If we should have made use of a full modal solution studies has shown that it sufficient to use $M \geq ka + 1$ modes. This will give a result that is approximately equal to an infinite number of modes. The solution is often given as the "back scattering cross section" or as the target strength TS given I dB.

The backscattering cross section is given as

$$\sigma_{bs} = |L_{bs}|^2 \qquad (3.12.4)$$

The backscattering cross section is often shown relative to the real cross section to the sphere.

$$\sigma_{bs} / (\pi a^2) \qquad (3.12.5)$$

The target strength is given as

$$TS(f) = 10\log(\sigma_{bs}(f)) \qquad (3.12.6)$$

In the literature there are measured values for Calanus that connects the length of the plankton to the radius of a fluid filled sphere. This means that calanus with a given length can be approximated by a fluid filled sphere with radius given by:

$$a_{es} = \gamma L^\delta \qquad (3.12.7)$$

It has bin found that Calanus finmarchicus has the values $\gamma = 0,21$ and $\delta = 1,02$. This equation together with equation for scattered field from the plankton gives the information that is needed to describe the target strength TS from the plankton. The mathematical model for Calanus finmarchicus is described by the relative velocity, the relative density, the wave number in the media and the length of the plankton. The model therefore describes the scattered field from the plankton with four parameters. The Institute of Marine Research in Bergen has done measurements on the mass density of Calanus and has found that when it is situated in stage CIV of its lifecycle it will have a density of around 1.038 g/m³. For the relative velocity little research has bin done on Calanus finmarchicus. However on Calanus plumchrus research has shown a relative velocity of 1.02. It is these values that has bin used in the plot in figure 3.12.1 and is later used in the inversion.
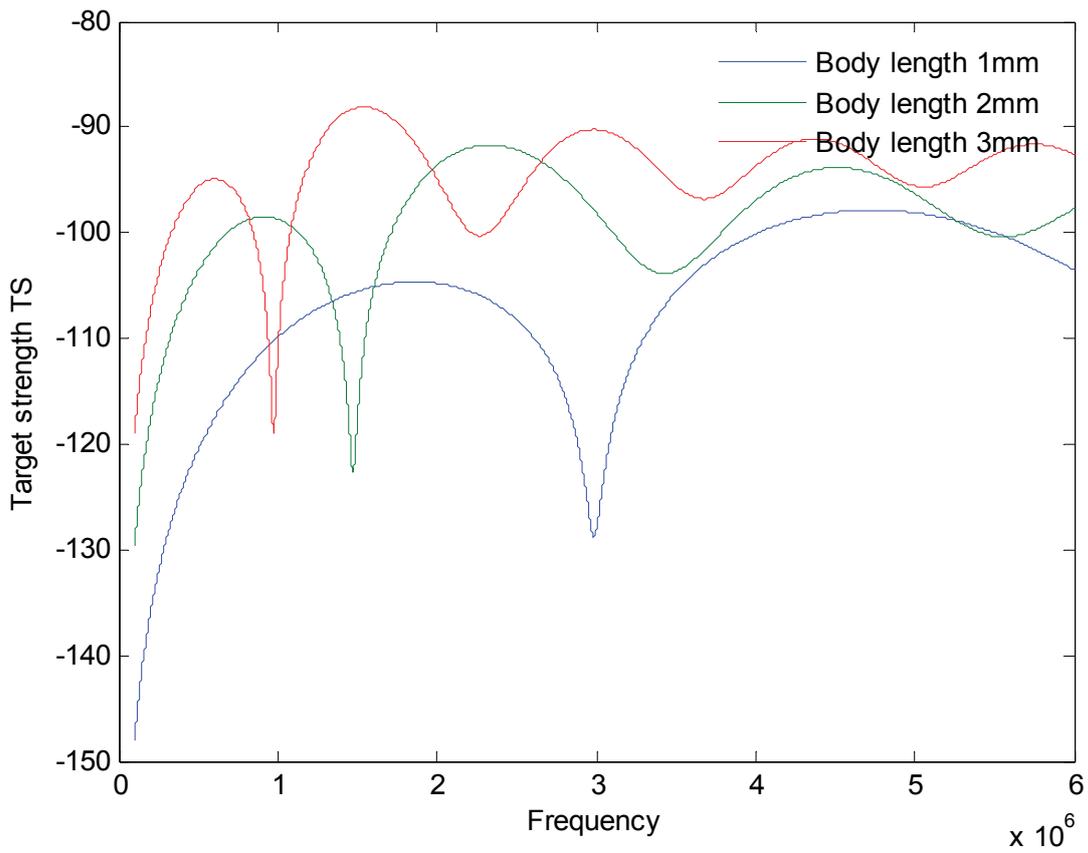
Figure 3.12.1 The calculated target strength at the plankton sizes 1, 2 and 3 mm in the frequency range from 0 to 6 MHz. TS is given in dB rel. 1µPa.

3.13 Passive measurements to remove background noise

As earlier mentioned it is possible use a signal threshold to remove noise but this method also removes any signal that is smaller than the threshold. The noise level also varies with time because the noise level in the sea varies according to the environment and the electronic noise in the echo sounder varies according to the temperature. This will make it necessary to make constant changes to the threshold value for it to be correct. The variation in the signal caused by noise will still be present when using a signal threshold. When measuring plankton we are interested in the reverberation caused by plankton and therefore a method based on the one proposed by Nunnallee (1990) where we measure the noise contribution with the transmitter switched of can be used. The method works by measuring the noise contribution in passive mode for the same time period as the echo sounder is used in receiving mode after each ping. The hypothesis is that the energy contribution caused by the noise is the same in the measured signal in active mode and the measured signal in passive mode. This means that the energy in the signal in passive mode can be subtracted from the energy in the signal in active mode, leaving only the energy caused by the reflections from the scatterers in the acoustic beam. When random noise with given amplitude is averaged over a series of samples then the average value will get a Gaussian probability density function where the average value is the most probable value. The variance in the signal decreases according to the number of samples used in the averaging. This means that the average value found in two independent random signals with the same amplitude will go against the same value accordance to an increasing number of samples used in the averaging. To assure that the variation in oceanic and thermal noise in the receiver are taken into account the measurement in passive mode should be taken after each ping. To be sure that the foregoing pulse has died out due to absorption and geometric loss before a new measurement in passive mode is taken a time gate should be chosen between the ping and the measurement in passive mode. When using the method the signal threshold should be set as low as possible if it can't be shut off. This is because the method has the potential of detecting signals below the noise floor, and therefore as much of the signal as possible should be included in the measurements.

In the APR system developed by NTNU it is measured 16 times at one frequency before measurements starts at a new frequency. These 16 measurements are then averaged against each other to get a better signal-to-noise ratio and to improve the linearity principle. The gain in signal-to-noise ratio is theoretically 12 dB (*see 3.10 Averaging*). In this case one should ideally perform passive measurements between each measurement in active mode, and then perform averaging of the measurements in passive mode. The results after averaging in both active and passive mode are then compensated for range with a TVG model. The energy is calculated in both signals and the energy in passive mode is subtracted from the energy in active mode. An alternative method can be to cut out the last samples of each measurement and assuming that the values found here only consists of noise. The average value of the samples is then compensated for range with a TVG model and subtracted from the values found after the range compensation with TVG of the whole measurement. This method is used in this report since the data is already collected in the traditional way. The danger in this method is that one has to be sure that the pulse has died out at the end of the measurement. This can especially be a problem at 200 kHz where the absorption is relatively small compared to the absorption at 710 kHz and 1 MHz. If the method is used at a later time the pulse repetition should therefore be slowed down to ensure that this problem doesn't occur.

The noise removal method is used by piecewise selecting windows of the signal and noise with a given range and then moving the window forward with the range of the chosen window length. This is done for the whole range of the signal. This method will give correct results and will ensure that abundance estimates are still a function of range, but the resolution will decrease in accordance to the window length. An alternative approach is to use a sliding window that moves the window only one sample value at a time forward. This method proves to give a better result in terms of resolution but at a much higher computational cost.

The echo integrator equation can be rewritten in the purpose of this method in the following way

$$\rho_{xf} = \frac{(E_{xf} - E_{N,xf})}{[P_0\, g_x]^2 [N_x P][\Omega c \Delta T / 2]\sigma_{bs}} \qquad (3.13.1)$$

Where E_{Nxf} is the energy of the noise contribution in the x range interval. Below in figure 3.13.1 the concept of the noise removal is shown. In the figure an integration length of 10 meters is suggested. The integration is performed between the diagonal lines for both the noise curve and the sonar data and the result of the integrated noise is subtracted from the sonar data. The noise curve is made by finding the mean average value for the last 600 samples of the measurement, which is then placed over the whole sonar data length and a TVG function is applied.
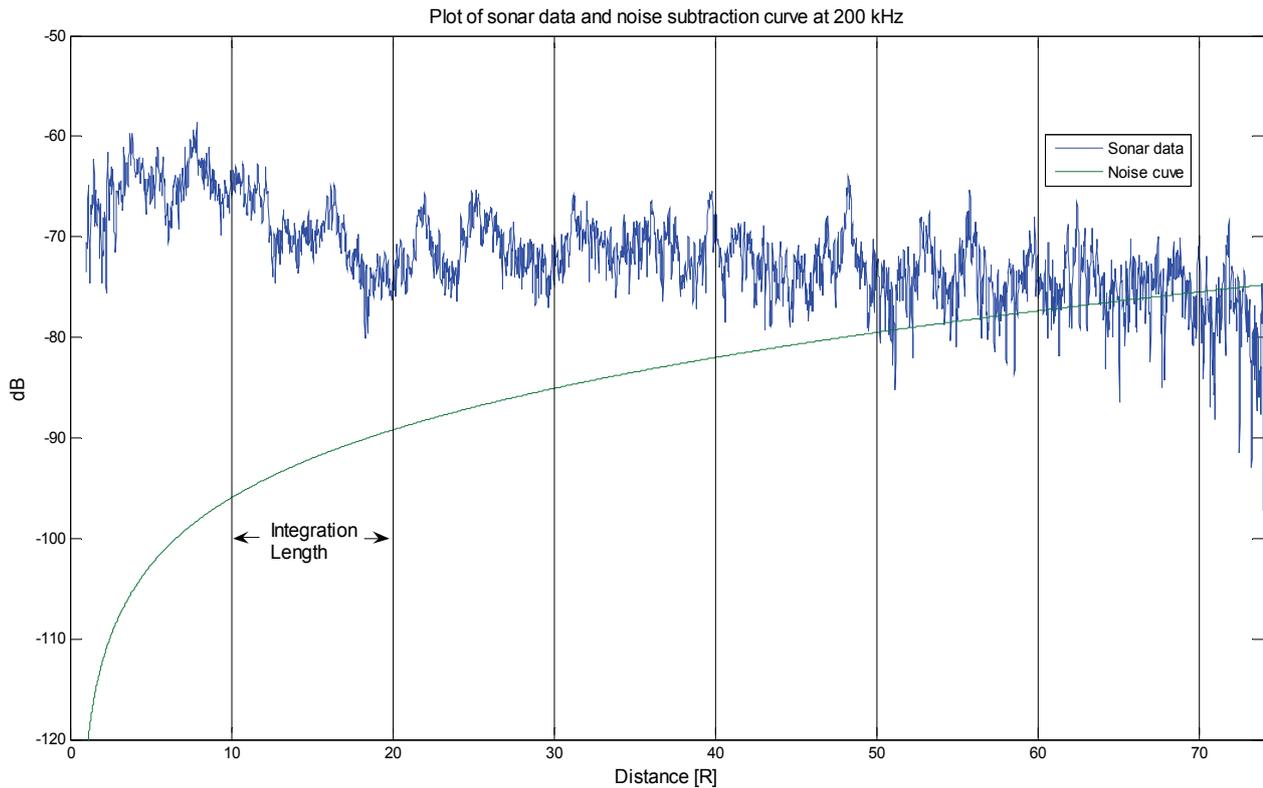

Figure 3.13.1 The TVG corrected sonar data together with the noise curve.

When short integration periods are used and the noise has to be completely removed from the measurements the maximum value in the windowed noise can be used instead of the average value. This will as told remove the noise, but it will also give a negative bias to the calculated result at higher signal-to-noise ratios and completely remove signals below the noise floor since the variation in the noise hasn't bin taken into account. Below in fig. 3.12.2 the concept of the two methods is shown together with the noise. The curves has bin made in the following way

- The last 600 samples has bin cut out of a measurement
- The 600 samples are laid side by side over the whole range of the measurement to reconstruct the noise and a TVG function is applied to construct the noise curve
- The average value of the 600 samples is calculated, and this value is allocated to the whole range of the measurement and a TVG function is applied to give the average value curve
- The maximum value is found in the 600 samples and this value is allocated to the whole range of the measurement and a TVG function is applied to give the average value curve
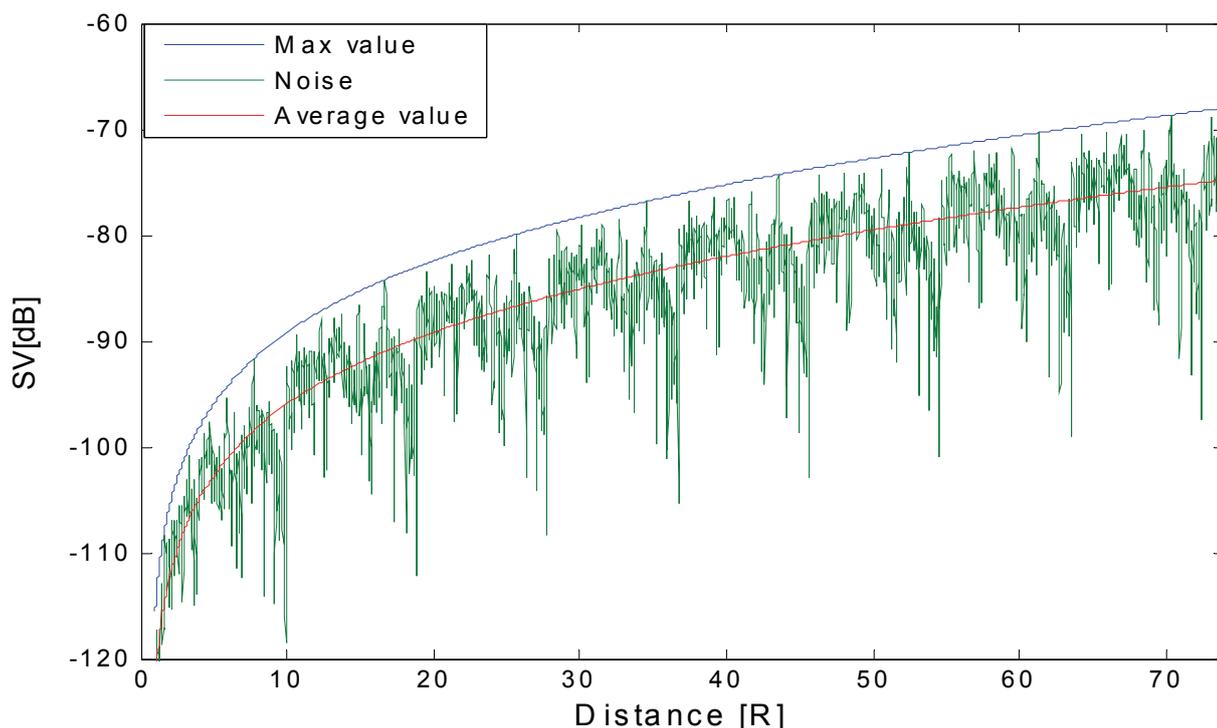

Figure 3.12.2 The concept of the average and maximum value constructed noise curves.

The average value and maximum value is found for a relatively long window. In this case 600 samples are used. This is because the noise can vary much with time and a representative value for the maximum and average value is needed.

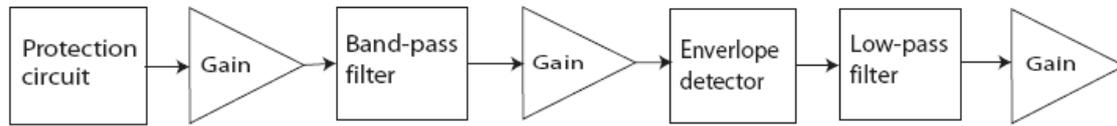## 3.14 The Receiver Electronics in the Acoustical Plankton Recorder

Figure3.14.1 The principle steps of the receiver electronics in the APR developed by NTNU.

The transducers are coupled to the sending and receiving electronics through a transformer. When the power of one channel is turned on from the acquisition system the sending and receiving circuits is connected to the batteries. The control unit controls this process as well as sending the signal from the active channel to the acquisition system and connecting the oscillator to the transmission circuit to make pulses with a specified length. The protection circuit in the receiver ensures that the system is not damaged at high pulse amplitudes. The band-pass filter removes noise in the system which results in a higher signal-to-noise ratio. The effect of the different steps on the received signal is evaluated in the following chapters.

3.14.1 The Band-pass Filter

The signal is band-pass-filtered before it is fed into the envelope detector. The bandwidth of the three frequencies are listed in Table 3.14.1.1

Table 3.14.1.1 The bandwidth of the band-pass filters used at each frequency in the APR developed by NTNU.

Frequency	Bandwidth
200 kHz	19 kHz
710 kHz	18 kHz
1 MHz	11 kHz

Below the backscattered signal to the transducer is modelled as a simple sinusoidal signal with amplitude of unity and a frequency of 200 kHz. A random number generator models the noise with amplitude of 10. The sinusoidal signal is then simply added to the noise to represent the total signal at the transducer.
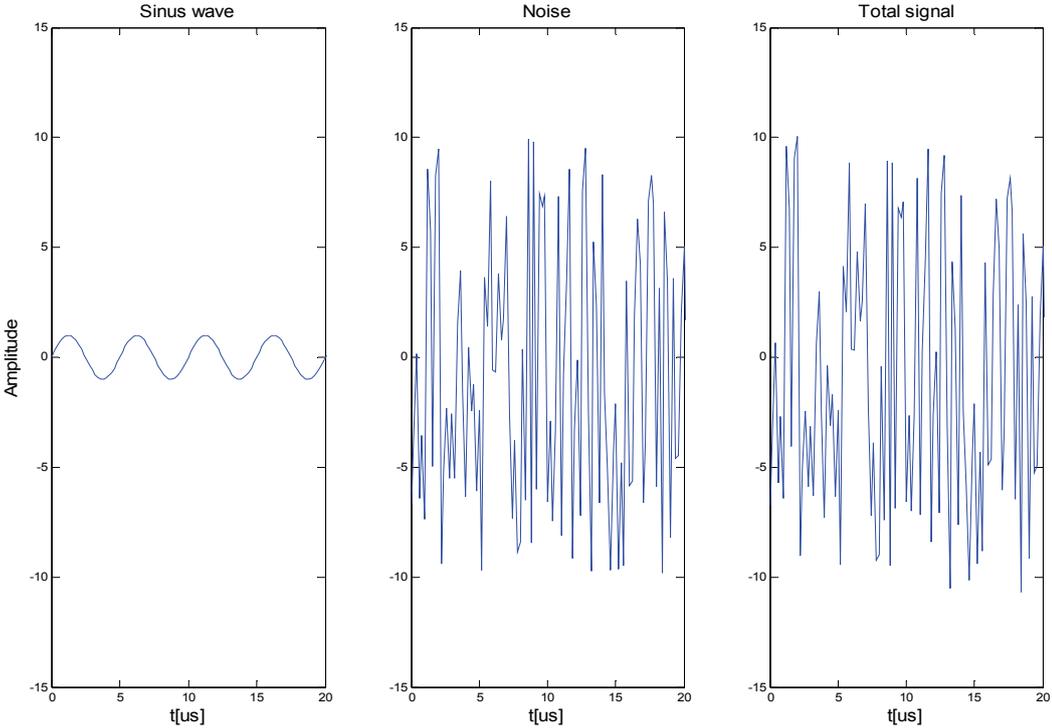

Figure 3.14.1.1 In the window to the right a signal is shown that consists of pure white noise with amplitude of 10 and a sinusoidal wave with amplitude of unity. In the window to the left and in the middle the sinusoidal wave and the noise parts are shown.

From the figure above it is evident that it is impossible to see that the signal contains a sinusoidal wave. The signal consisting of the sinusoidal wave and the noise is then filtered with a Butterworth band-pass filtered with a filter order 5 and a 3 dB bandwidth of 19 kHz to illustrate the effect of the band-pass filter in the system at 200 kHz. The results are shown below in fig. 3.14.1.2.
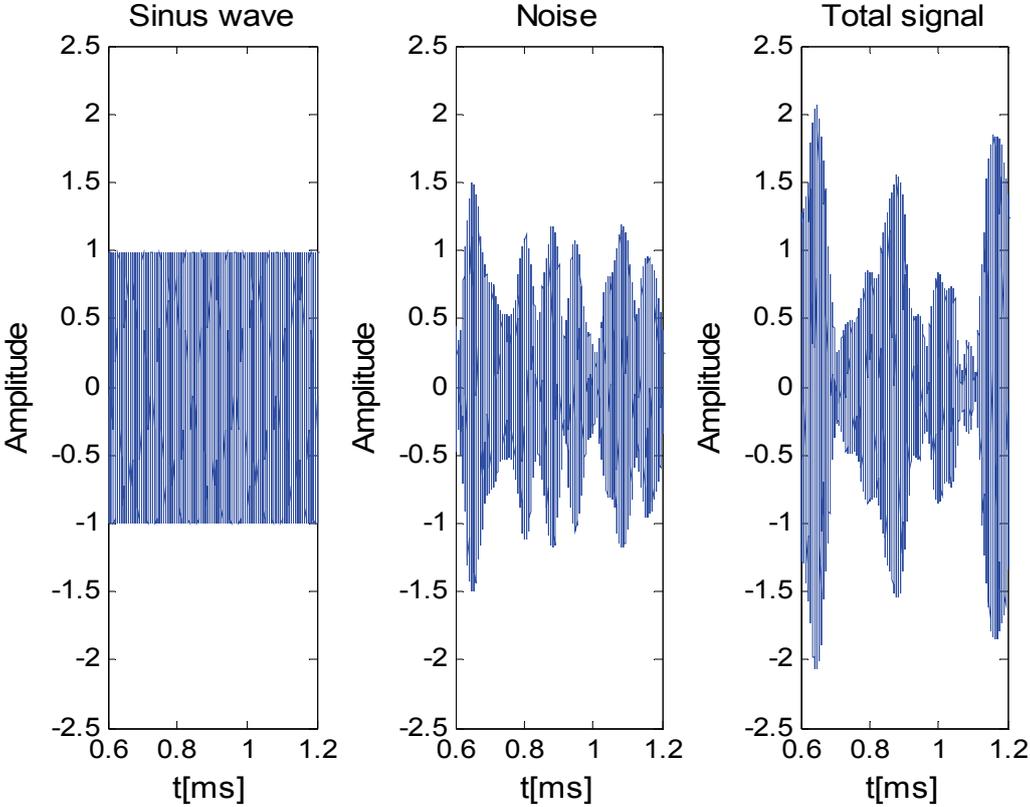

Figure 3.14.1.2 The effect of the band-pass filtering of a sinusoidal wave with amplitude of unity, the noise with amplitude of 10 and the total signal consisting of the sinusoidal wave and the noise.

The result of filtering the pure sinusoidal wave is as predicted a sinusoidal wave with the same amplitude. The noise after filtering is a wave that varies in amplitude with time. This is caused by the parts of the noise that lies inside the bandwidth of the band-pass filter. These parts will add and subtract incoherently with the sinusoidal wave. The total signal will vary as a result of the incoherent addition and subtraction of the noise together with the sinusoidal wave. The figure is plotted over 0.6 ms to illustrate this effect. After the band-pass filter the signals are fed into the envelope detector. The effect of the envelope detector on the signals given in fig. 3.14.1.2 is explained further under the "3.14.2 The Envelope detector" part of this report.

3.14.2 The envelope detector

In APR developed by NTNU the envelope detector works in the following way

- First a simple rectifier turns the signal into a pure positive signal
- The signal is then lowpass filtered at 20 kHz
- Then the signal is sampled with a sampling frequency of 50 kHz

The signals that has bin band-pass filter in the "3.14.1 The Band-pass Filter" part of the report are used further in the discussion of the effect of the envelope detector on the signal.
The signals are fed into the rectifier that makes a pure positive signal. This can be done by a simple If statement in Matlab that turns the negative values into positive values.
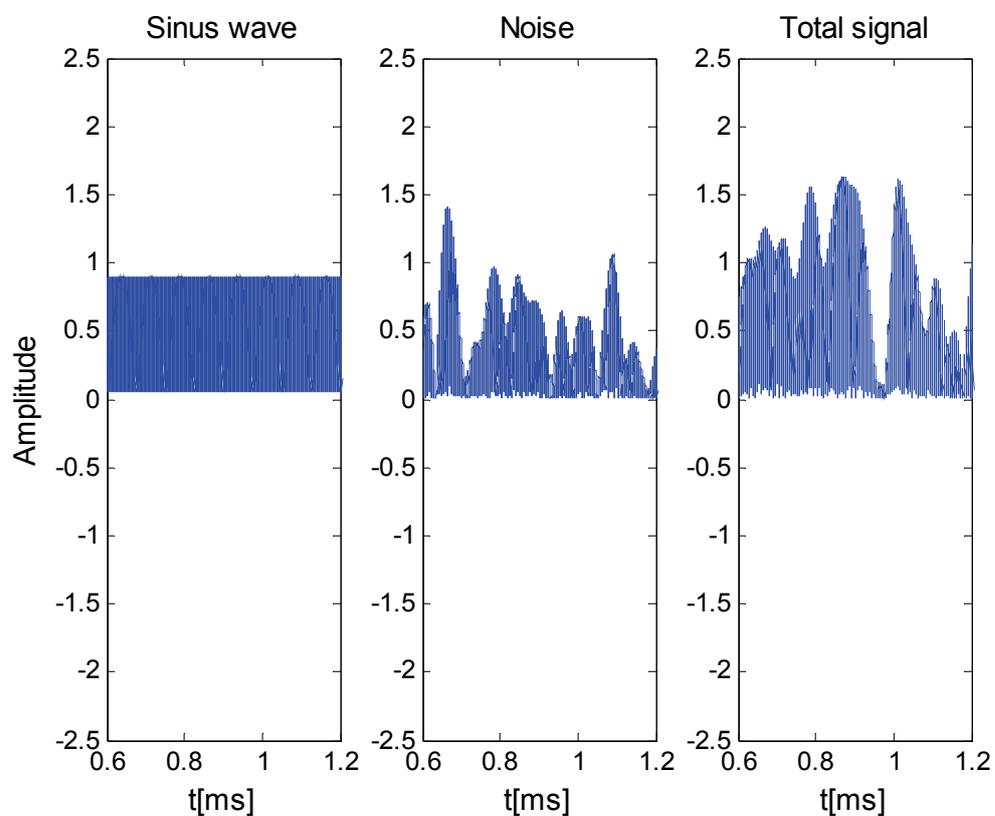The result is shown below.

Figure 3.14.2.1 The rectified signal for a band-pass filtered sinusoidal wave, white noise, and the total signal consisting of the band-pass filtered sinusoidal wave and the white noise.

After the rectifier the signals are low-pass filtered at 20 kHz and sampled at 50 kHz. This can be done in Matlab by using a Butterworth low-pass filter and the "decimate" function. This will filter and sample the signal so it corresponds to the real system.
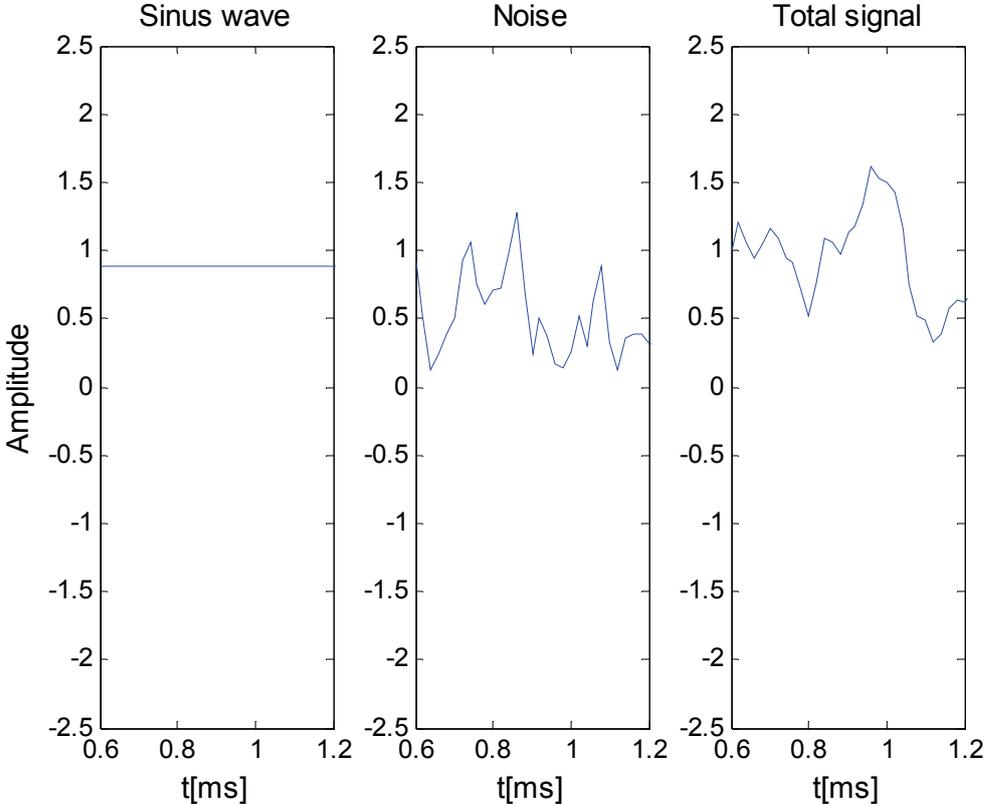

Figure 3.14.2.2 The result of the envelope detector. The sinusoidal wave, noise and total signal consisting of the noise and sinusoidal wave has bin rectified, lowpass filtered and down sampled to 50 kHz.

From fig. 3.14.2.2 the characteristic envelope is seen for the signal. The total signal has higher amplitude then the signal consisting of only noise. The values found here are used further in the "Evaluation of noise subtraction method" part of this report.

3.14.3 Evaluation of Noise Subtraction Method

Noise subtraction means that the noise energy found by echo integration over a time period is subtracted from the energy found by echo integration of a signal consisting of noise and scattered amplitudes from scatterers for the same time period. The hypothesis is that the result of this subtraction is the scattered energy from the scatterers.

By calculating the energy over the whole area in the three signals found in fig. 3.14.2.2 in "3.14.2 The Envelope Detector" and subtracting the noise energy from the energy in the total signal and comparing this result with the energy of the sinusoidal wave, it is possible to predict the error in the estimation.

$$Calculated\ value = energy_{\sin+noise} - energy_{noise} \qquad (3.14.3.1)$$

$$error_{dB} = 10\log\left(\frac{Calculated\ value}{energy_{\sin}}\right) \qquad (3.14.3.2)$$

Two different noise signals with the same amplitude are used in the signal consisting of the sinusoidal wave and noise and for the noise alone. This is done because in a real sonar system the variation of the noise amplitude in the signal of interest isn't known, and it is only possible to predict the energy level of the noise. When using this method to subtract noise from the signal containing noise and the sinusoidal wave the method will increase in accuracy with an increasing length of the time period the energy is determined from. This is because the standard deviation of the sum of the individual samples will decrease in the following way.

$$\sigma_{AV} = \sqrt{\left(\frac{\sigma_1^2}{n^2} + \frac{\sigma_2^2}{n^2} + ... + \frac{\sigma_n^2}{n^2}\right)} = \sqrt{\left(\frac{n\sigma^2}{n^2}\right)} = \frac{\sigma}{\sqrt{n}} \qquad (3.14.3.4)$$

This is the same equation that was used in averaging (see 3.10 Averaging). In this equation n is the number of samples and the standard deviation decreases with the square root of the number of samples. From this it is evident that with an increasing number of samples used to calculate the energy the variation in the calculated value will decrease. Below in table 3.14.3.1 the calculated value of the energy in the sinusoidal wave by noise subtraction from the total signal, the real value of the energy and the error is shown for 7 repeated calculations for the values found in fig. 3.14.2.2

Table 3.14.3.1 The calculated value of the sinusoidal wave when noise subtraction is used, the real value of the energy of the sinusoidal wave and the calculation error. The error is calculated as the dB difference between the two. In the calculations a window of 67 samples is used, and this corresponds to a length of 1 m with a sound speed of 1485 m/s and with a sampling frequency of 50 kHz.

Measurement	1	2	3	4	5	6	7	Average
Real value	0.3794	0.3794	0.3794	0.3794	0.3794	0.3794	0.3794	0.3794
Calculated value	0.315	0.3622	0.2354	0.5540	0.3758	0.2147	0.3579	0.345
Error in dB	-0.81	-0.202	-2.073	1.644	-0.041	-2.473	-0.254	-0.413

By comparing the result after the envelope detector at different signal-to-noise ratios and subtracting the calculated energy of the signal consisting of only noise from the signal consisting of the sinusoidal wave and noise, it is possible to get a picture of how large the bias is at the different signal-to-noise ratios. In fig. 3.14.3.1 and fig. 3.14.3.2 the energy is calculated over a distance of 1m and 10m for a signal consisting of a sinusoidal wave and noise, and for a signal consisting of only the noise. The energy in the signals is calculated by squaring the amplitude in each sample and adding the squared values over the length of the area of 1m and 10 m. Two different signal-to-noise ratios is calculated namely SNR_1 and SNR_2. SNR_1 is calculated as the difference between the sinusoidal wave and the noise after the envelope detector, and SNR_2 is calculated as the difference between the signal consisting of the sinusoidal wave plus the noise and the noise alone after the envelope detector. Notice that SNR_2 can never be less than unity in theory since the signal at this point will only consist of noise.

$$SNR_1 = 10\log(E_s / E_n) \hspace{4cm} (3.14.4.5)$$

$$SNR_2 = 10\log(E_{s+n} / E_n) \hspace{4cm} (3.14.3.6)$$

The SNR_2 is used because in the real sonar system there is no way of knowing the value of the sinusoidal wave alone because it will always be under the influence of noise. Therefore the only way of knowing the noise level is to measure the energy of the noise in passive mode. This level should then be compared to the energy for the same window in active mode to get the SNR_2.
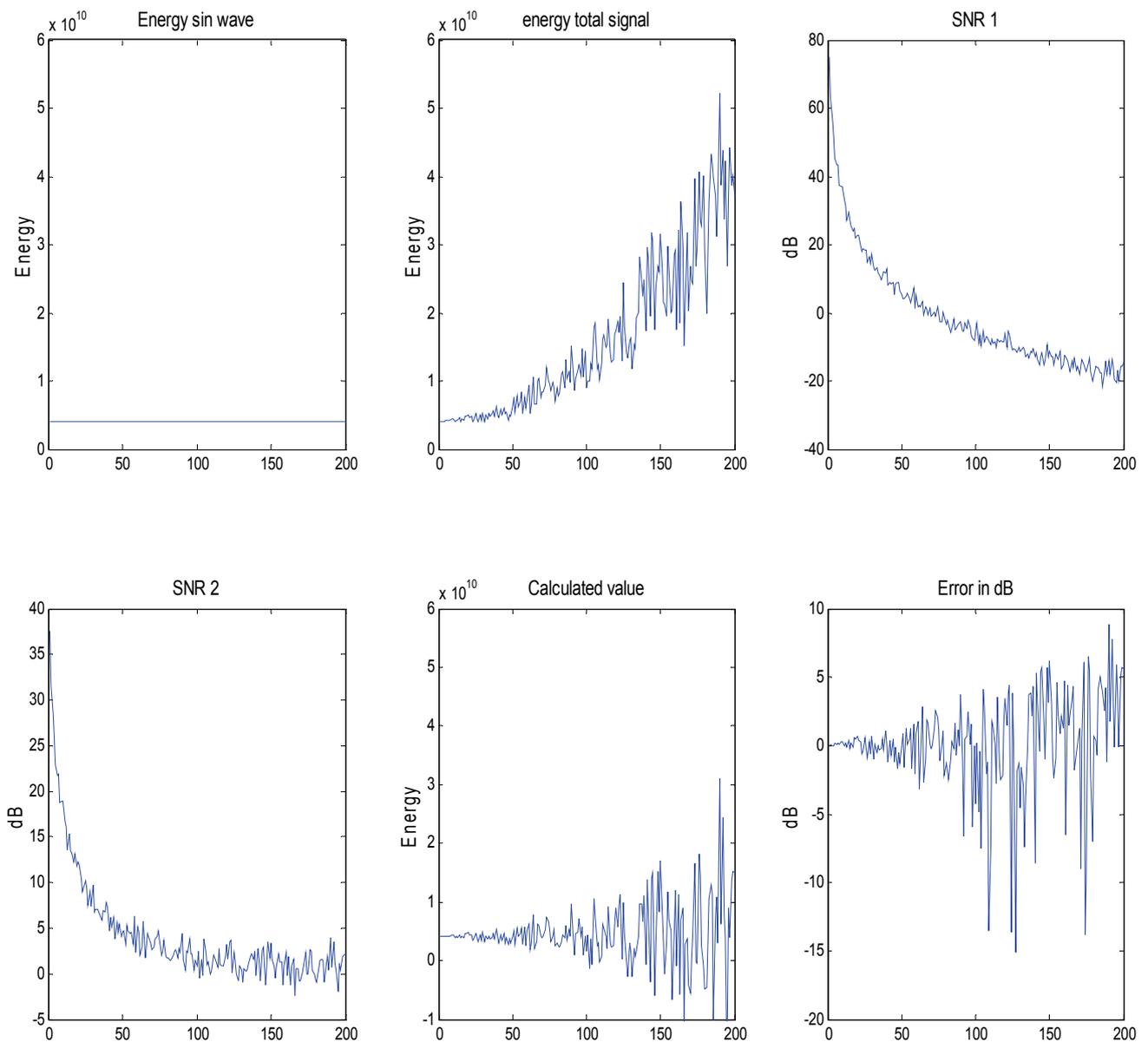
Figure 3.14.3.1 The energy in the sinusoidal wave, the energy in the total signal, the calculated value for the energy of the sinusoidal value, and the error at decreasing signal-to-noise values. The energy is calculated over a distance of 1m corresponding to 67 sampled values at a sampling rate of 50 kHz and a sound speed of 1485 m/s.

From fig. 3.14.3.1 the calculated value for the sinusoidal wave is exposed to large errors at low signal-to-noise ratios. The error is small at SNR_1 over 0 dB where the signal level is higher than the noise level. At decreasing values of SNR_1 below 0 dB the error increases and even negative values is calculated for the sinusoidal wave. These values have to be discarded in the solution by setting them to unity.
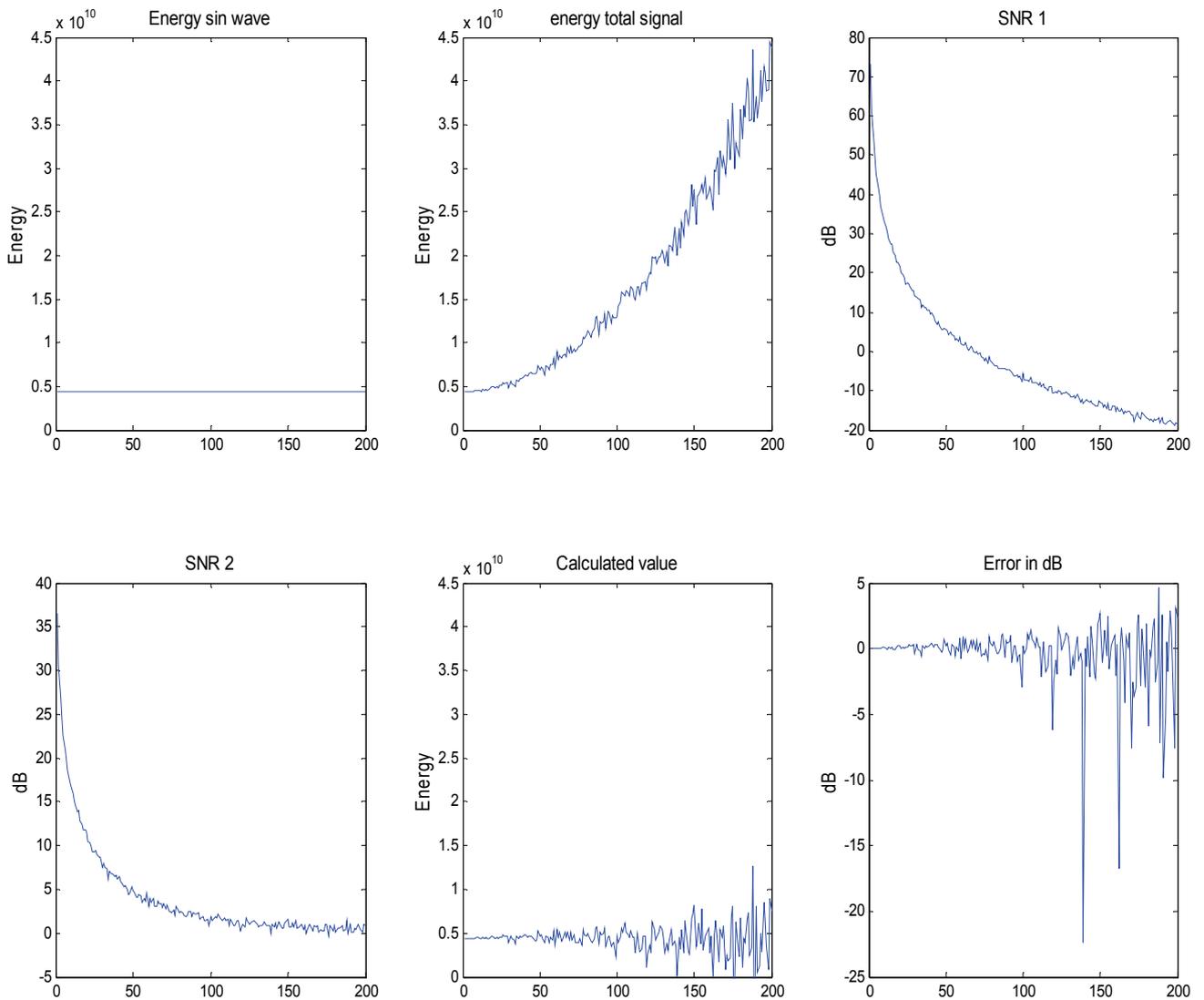
Figure 3.14.3.2 The energy in the sinusoidal wave, the energy in the total signal, the calculated value for the energy of the sinusoidal value, and the error at decreasing signal-to-noise values. The energy is calculated over a distance of 10m corresponding to 670 sampled values at a sampling rate of 50 kHz and a sound speed of 1485 m/s.

From fig. 3.14.3.2 it is clear that the error has bin reduced using a sampled distance of 10 meters compared to using a sampled distance of 1 m. The energy of the sinusoidal wave can be calculated with reasonable good accuracy up to SNR_1 values of about -10 dB. This shows the importance of a long sampled distance when high accuracy at low SNR_1 is needed.

3.14 Background noise removal by curve fitting

An alternative approach to the use of passive mode to remove noise is the use of curve fitting in the least square sense. The underlying background noise level follows the form of the exact TVG function, which can be scaled to the minimum volume backscatter (SV) in each layer during a transect and then subtracted from the entire data set to remove the background noise. In other words the smallest SV values are found for each integration layer for the whole transect to form a vector, namely the minimum volume backscatter (SV) that should have the form of the exact TVG function if a low or no threshold is used and long enough measurements are used in the transect. Curve fitting between the exact function and the minimum volume backscatter (SV) is then performed using a least square curve-fitting algorithm. The following equation is minimized in the least square sense.

$$F(x) = sv_{min} - (exact\ TVG \times x)^2 \qquad\qquad (3.14.1)$$

sv_{min} is a vector containing the linear minimum volume backscattering coefficients and x is the variable used to minimize the function. The absorption coefficient used to calculate the sv_{min} values are also used to calculate the linear *exact TVG* values.
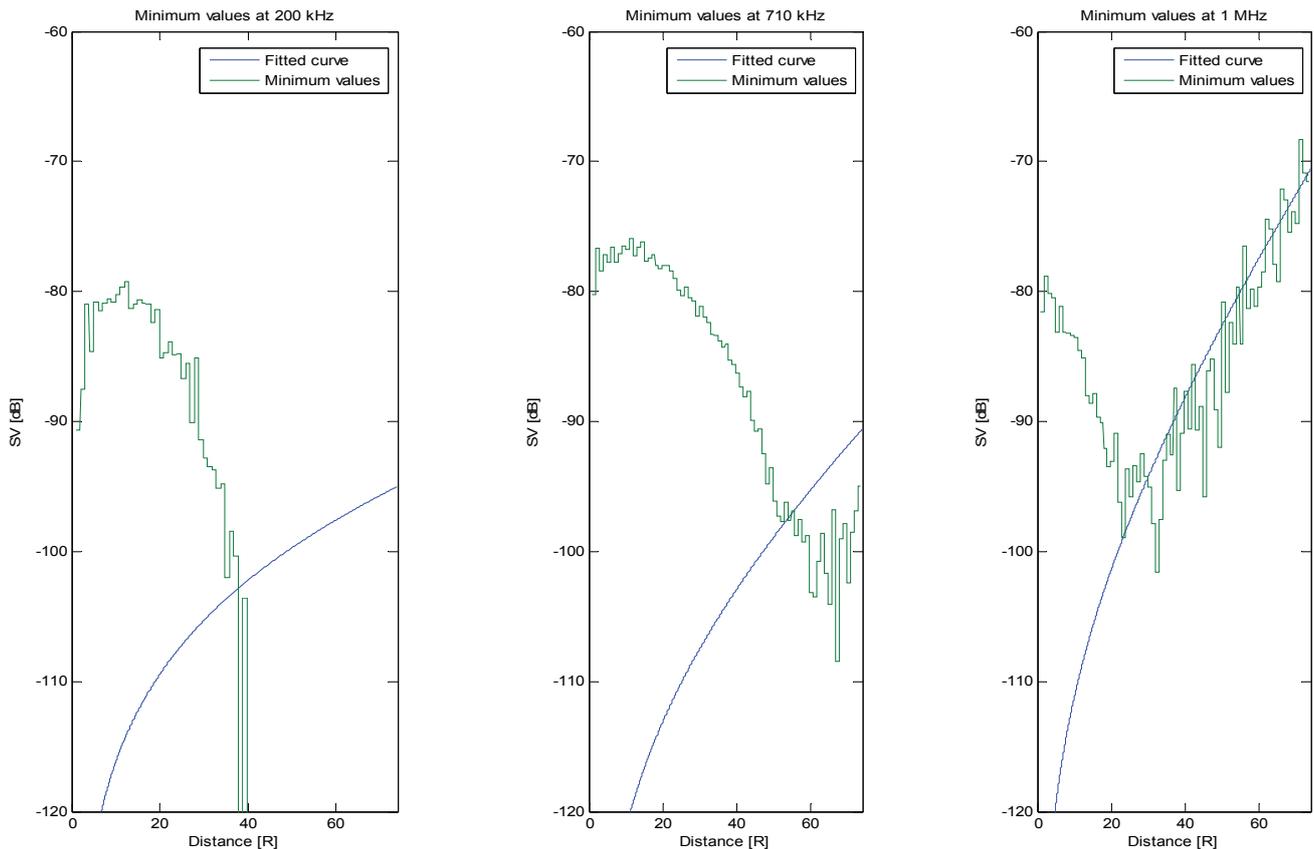

Figure 3.14.1 The minimum SV values found for the frequencies 200 kHz, 710 kHz and 1 MHz together with the fitted curve by the least square algorithm at each frequency.

The function was minimized in this report by the use of a standard non linear least square algorithm in Matlab called "lsqnonlin". The *(exact TVG×x)^2* part of the function is the fitted curve where *x* is found by the algorithm. The technique assumes that within a given time period there will be some depth intervals where there are effectively no targets. This is more likely when integration layers and periods are small.

The data processed here is from a transect performed with the APR developed by NTNU (see Appendix A). In fig. 3.14.1 the minimum SV values are plotted with distance together with the fitted curve by the least square algorithm for the frequencies 200 kHz, 710 kHz and 1 MHz.

It becomes immediately clear that at 200 kHz there are no minimum SV values over 40 m. The reason for this can be that when the operator sets the working point of the sonar system to remove the DC level from the signal, the noise has also bin removed from one or several of the measurements. This means that there is no way of getting an accurate result with noise removal using this method at 200 kHz. At 710 kHz the background noise is kept in the measurements, and at a distance of approximately 65 meters the increase in the minimum SV value is caused by the *TVG* gain of the background noise. The fitted curve has got a positive bias compared to the minimum SV values. At 1 MHz the curve is nicely fitted to the minimum SV values and the method will therefore work correctly at this frequency.

To overcome the problems encountered at 200 and 710 kHz one should use a longer measurement time at each frequency. Although the method in this case will have a bias at 200 and 710 kHz the error will be small because the dB level of the fitted curve doesn't exceed more than -95 at 200 kHz and -90 dB at 710 kHz. It is therefore believed that the method will work satisfyingly although the curve isn't correctly fitted. A downside with the concept of the method is that it will not take account for the changing noise energy levels, caused by thermal noise in the receiver and the environmental noise. The method simply predicts that this level is constant for all the measurements during the transect, and as a consequence the noise energy level in each measurement will have a bias compared to the real level causing the predicted levels after noise removal to also have a bias.

3.15 Inversion

To find the number of plankton at different lengths we can use so called inversion. These are methods with varying complexity and accuracy. To test these kinds of methods we have to use known measuring data or we can use a synthetic model of the plankton population. Two different algorithms are used to find the abundance and size distribution of plankton in this report, namely a "Genetic Algorithm" and the "Least Square non Negative" algorithm.

3.15.1 Synthetic data

To test the inversion methods there has bin made synthetic data to illustrate the backscattering. Since Calanus finmarchicus is normally situated in a range from 1 to 3 mm a Gaussian synthetic model in this range zone has bin made with a centre point at 2 mm. The calculation of the synthetic data is done by multiplying the number of plankton at a given length with its corresponding backscattering cross section at a given frequency, and then the results at every length of plankton is summed together.

$$\text{Synthetic\_data}(f) = \sum_j n_{bj} \times \left| L_{bs,j}(f) \right|^2 = \sum_j n_{bj} \times \sigma_{bs,j}(f) \qquad (3.15.1.1)$$

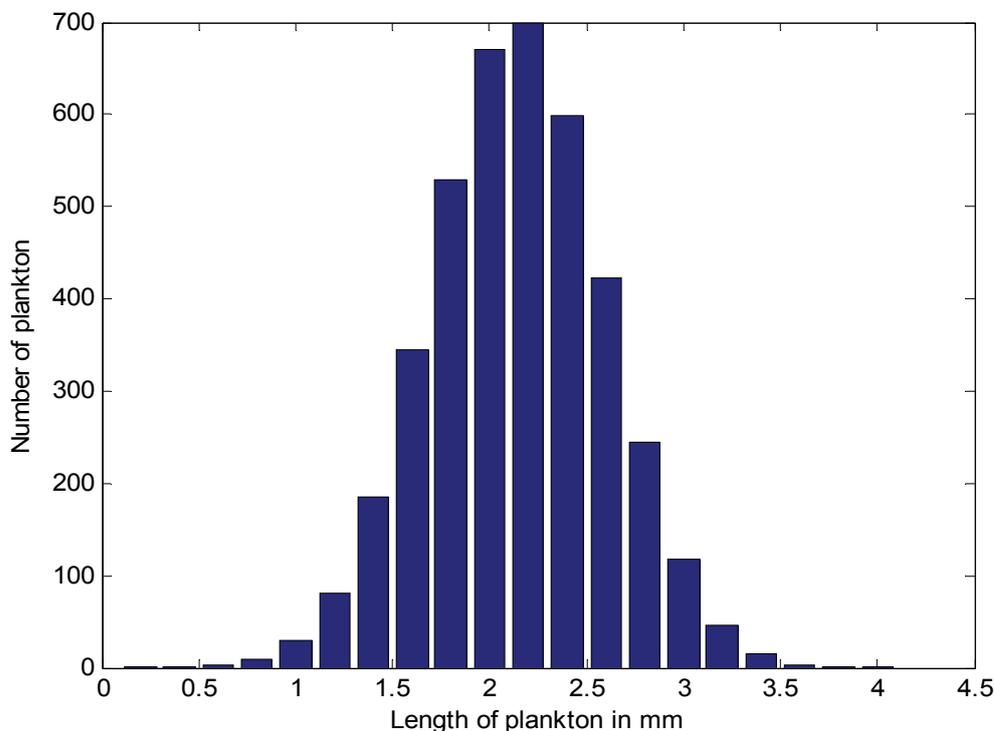Here j is the different lengths of plankton.

 Figure 3.15.1.1 A Gaussian distribution of plankton. The plankton is distributed in the area where the real Calanus is situated. The total number of plankton is 4000.

3.15.2 The "Least Square Non Negative" algorithm

When using three frequencies as in the case of the sonar system developed by NTNU we can write three equations on the following form.

$$\text{Synthetic\_data}(f_1) = n_1 \times \sigma_{bs}(f_1, a_1) + n_2 \times \sigma_{bs}(f_1, a_2) + n_3 \times \sigma_{bs}(f_1, a_3)$$
$$\text{Synthetic\_data}(f_2) = n_1 \times \sigma_{bs}(f_2, a_1) + n_2 \times \sigma_{bs}(f_2, a_2) + n_3 \times \sigma_{bs}(f_2, a_3) \qquad (3.15.2.1)$$
$$\text{Synthetic\_data}(f_3) = n_1 \times \sigma_{bs}(f_3, a_1) + n_2 \times \sigma_{bs}(f_3, a_2) + n_3 \times \sigma_{bs}(f_3, a_3)$$

Here n_1, n_2 and n_3 are the number of plankton for the corresponding sizes of plankton a_1, a_2 and a_3, and the frequencies used are f_1, f_2 and f_3. The problem can be rewritten on matrix notation in the following way

$$S = \begin{pmatrix} \sigma_{bs}(f_1, a_1) & \sigma_{bs}(f_1, a_2) & \sigma_{bs}(f_1, a_3) \\ \sigma_{bs}(f_2, a_1) & \sigma_{bs}(f_2, a_2) & \sigma_{bs}(f_2, a_3) \\ \sigma_{bs}(f_3, a_1) & \sigma_{bs}(f_3, a_2) & \sigma_{bs}(f_3, a_3) \end{pmatrix} \qquad (3.15.2.2)$$

$$s = \begin{pmatrix} \text{Synthetic\_data}(f_1) \\ \text{Synthetic\_data}(f_2) \\ \text{Synthetic\_data}(f_3) \end{pmatrix} \qquad (3.15.2.3)$$

$$n = \begin{pmatrix} n_1 \\ n_2 \\ n_3 \end{pmatrix} \qquad (3.15.2.4)$$

If there only are three sizes of plankton and their size where known we could solve this problem in the following way.

$$Sn = s \Rightarrow$$
$$S^{-1}Sn = S^{-1}n \Rightarrow \qquad (3.15.2.5)$$
$$In = S^{-1}s \Rightarrow$$
$$n = S^{-1}s$$

Since in practice this exact solution won't occur in nature one has to use some form of optimization to the problem to get as near as possible to the real solution. "Least Square non Negative" is an algorithm that finds the solution in the least square sense where negative solutions are discarded

$$\min_{x} = \frac{1}{2} \|Sn - s\|_2^2 \qquad x \geq 0 \qquad\qquad (3.15.2.6)$$

Here **S** and **s** coefficients in the objective function and **n** is solved for positive values. **S** is an m × n matrix.

Since the purpose of the method is to measure the backscattering from plankton one has to use low values in the approval of the solution. This means that the ratio **Sn-s** has to be very small before the algorithm approves the solution. When using the function. *LSQNONNEG* in Matlab one can use ratios in the area 10^{-320}. Experimental work has shown that the algorithm can allow solutions where the problem is under-determined by factors between 1.5 and 2.

3.15.3 The Genetic Algorithm

The GA will be used in this report to determine the size distribution of plankton in the APR developed by NTNU. The GA is a stochastic global search method that mimics the metaphor of natural biological evolution. The GA operates on a population of potential solutions and the principle of survival of the fittest is used to produce better approximations to a solution. At each generation, a new set of approximations is created by the process of assigning fitness to the individuals and then breeding them together by the use of operators borrowed from natural genetics. This is done in a probabilistic way, where the individuals with the highest fitness values will also have the largest probability of breeding. The process leads to the evolution of individuals in the population that are better suited to the environment then the individuals that they where originally created from. Although there are several different ways to make up the process of selecting individuals for breeding and the breeding process, only the methods used in this report is mentioned here.

The individuals are encoded as strings, *Chromosomes ,* composed over some alphabet, so that the genotypes (Chromosome values) are uniquely mapped onto the decision variable (*phenotypic)* domain. The binary alphabet is used to map the chromosome structure. For, example, a problem with two variables, x_1 and x_2 is mapped onto the chromosome structure in the following way:

$$1\ 0\ 1\ 1\ 0\ 1\ 0\ 0\ 1\ 1 \mid 0\ 1\ 0\ 1\ 1\ 1\ 0\ 1\ 0\ 1\ 0\ 0\ 1\ 0\ 1$$

$$\overset{\longleftarrow \qquad x_1 \qquad \longrightarrow}{} \qquad \overset{\longleftarrow \qquad\qquad x_2 \qquad\qquad \longrightarrow}{}$$
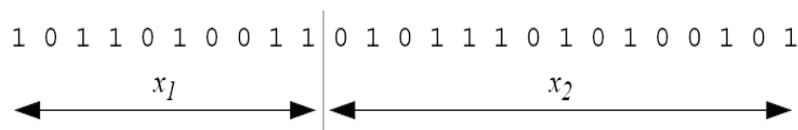
As seen the variable x_1 is represented by 10 bits and variable x_2 is represented by 15 bits. The amount of bits will determine the range or resolution of the individual variable. The search process will operate one these encoded binary values rather than on the decision variables them selves.

When decoding the chromosome representation into the decision variable domain, it is possible to asses the performance, or *fitness,* of the individual members of a population. This is done through an objective function that characterises an individual's performance in the problem domain. This is an analogy to the natural world where this would be the individual's ability to survive in its present environment. The objective function establishes the basis for selection of pairs of individuals that will be mated together during reproduction.

During the reproduction phase, the individuals are assigned a fitness value from its raw performance value that is given by the objective function. The highest fitness is given to the individual with the best raw performance value and the fitness thereafter decreases for the individuals according to their raw fitness. A highly fit individual has got a larger probability of being selected for mating whereas an individual with poorer fitness has got a lower probability of being selected as a parent.

When the fitness values has bin assigned to the individuals in the population they can bee recombined to form the next generation by a probability found according to the fitness value. Genetic operators are used to manipulate the genes of the chromosomes of the selected individuals for mating. The recombination operator is used to exchange genetic information between pairs, or larger groups of individuals.

Another genetic operator called mutation is then applied to the new chromosomes, with an execution probability of P_m when the pairs are chosen for breeding. After recombination and mutation, the individual strings are then, if necessary, decoded, the objective function evaluated, a fitness value is assigned to the individuals are selected for mating according to their fitness value. This process continues through a number of generations and the average performance of the individuals will increase since good individuals are kept and mated together, and less fit individuals will die out. The GA is terminated when some criteria is satisfied, e.g. a certain number of generations, a mean deviation in the population or when a particular point in the search space is encountered. The GA used in this report can be explained in the following steps.

1. Initialize population: An initial population is created of uniformly distributed random binary strings. The number of columns in the population matrix is given as the number of variables that we want to investigate multiplied by the precision. The precision is given as the number of bits that we want to represent each variable with. The number of rows in the matrix is given as the number of individuals in the population (*see datastructure)*.
2. The phenotypes are calculated from the binary values (*see phenotypes*). The first time the initial population is calculated and the consecutive times the offspring are calculated.
3. Evaluate objective function: The *objective function (see Objective Function)* is used to calculate the "raw fitness"
4. The least fit individuals are replaced by the children. The first time there will be no children and therefore this point is discarded.
5. Are optimization criteria met?: In the GA in this report the criteria will be satisfied when a certain number of iterations/generations are done. If the criterion is met the best individual in the population is displayed as the result. If the criterion is not met the GA will generate a new population.
6. Selection: The *fitness function (see The Fitness Function)* is used to calculate the "relative fitness" of the individuals using the "raw fitness". In this report a simple roulette wheel is used (see roulette wheel selection method) to select the parents. The parents are then paired together in a random manner.
7. The binary gray code (*see gray code*) is calculated for all the phenotypes in the parents.
8. Crossover: The probability Px is used to calculate which parents that is submitted to crossover. Single point crossover is then used (*see Recombination Operator: Single Point Crossover*) on the chromosomes of the selected parents.
9. Mutation: The probability Pm is used to calculate which bit that is submitted to mutation, and mutation is then performed on these bits in the chromosomes. (*see Background operator: Mutation*). The result is the children chromosomes.
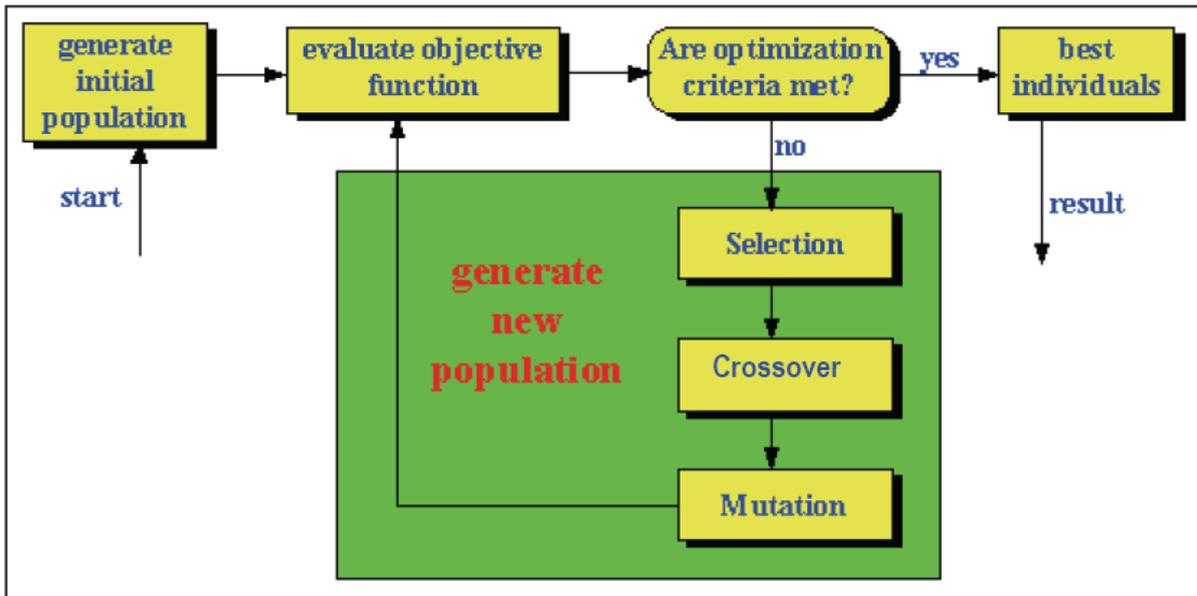10. Jump to point 2 and go through the process until the criterion in point 4 is met.

Figure 3.15.3.1 The sketch shows the simple genetic algorithm used in this report.

3.15.3.1 Genetic Algorithms versus Traditional Methods

The genetic algorithm differs substantially from traditionally search and optimization methods. The four most significant differences are:

- The Genetic algorithm search in an optimization space in parallel with several points with the use of a population, not in a single point.
- The GA's does not require derivative information or other auxiliary information because only the objective function and corresponding fitness levels will influence the direction of the search.
- GA's use probabilistic transition rules and not deterministic ones.
- GA's work on an encoding of the parameter set rather than the parameter set itself.

The GA can provide a number of potential solutions since it run in parallel and the choice of solutions can be done by the user if the best optimized solution is not chosen automatically. This can be useful in multi objective optimization where the GA can be used to identify alternative solutions simultaneously.

3.15.3.2 Phenotypes

Phenotypes are the real values of the parameters and the genes are the binary coding of these phenotypes

The genes can be decoded to phenotypes in the following way:

$$\theta_{j,i_j} = \theta_j^{min} + \Delta\theta_j i_j, \qquad i_j = 0,...,2^{n_j} - 1 \qquad\qquad (3.15.3.2.1)$$

$$\Delta\theta_j = \frac{\theta_j^{max} - \theta_j^{min}}{2^{n_j} - 1} \qquad\qquad (3.15.3.2.2)$$

θ_j^{min} and θ_j^{max} are the upper and lower real valued boundaries that is selected by the user.

$\Delta\theta_j$ is the resolution for the parameter j and n_j is the number of bits in parameter j.

The advantage of using Phenotypes is that the user of the GA can select the number of bits used in the solution thereby altering the resolution and the size of the chromosome matrix at wish. A large matrix will lead to time consuming iterations and therefore the choice of resolution should be made according to the problem at hand.

3.15.3.3 Data Structure

The chromosomes and the phenotypes are structured in the matrices shown below in fig. 3.15.3.3.1 and fig.3.15.3.3.2. The chromosome matrix consists of *Nind* individuals with *Lind* genes and the size is therefore Nind×Lind. The genes represented by g in the figure will consist of binary values with a length given by the precision in the solution. Each row in the Chrom matrix corresponds to one chromosome

$$
\text{Chrom} =
\begin{bmatrix}
g_{1,1} & g_{1,2} & g_{1,3} & \cdots & g_{1,\text{Lind}} \\
g_{2,1} & g_{2,2} & g_{2,3} & \cdots & g_{2,\text{Lind}} \\
g_{3,1} & g_{3,2} & g_{3,3} & \cdots & g_{3,\text{Lind}} \\
. & . & . & \cdots & . \\
g_{\text{Nind},1} & g_{\text{Nind},2} & g_{\text{Nind},3} & \cdots & g_{\text{Nind},\text{Lind}}
\end{bmatrix}
\begin{matrix}
\text{individual 1} \\
\text{individual 2} \\
\text{individual 3} \\
. \\
\text{individual Nind}
\end{matrix}
$$

Figure 3.15.3.3.1 The matrix containing the genes.

After the decoding of the Chrom matrix to phenotypes (*see phenotypes*) the result will be a matrix containing real values with the size Nind×Nvar

$$
\text{Phen} =
\begin{bmatrix}
x_{1,1} & x_{1,2} & x_{1,3} & \cdots & x_{1,\text{Nvar}} \\
x_{2,1} & x_{2,2} & x_{2,3} & \cdots & x_{2,\text{Nvar}} \\
x_{3,1} & x_{3,2} & x_{3,3} & \cdots & x_{3,\text{Nvar}} \\
. & . & . & \cdots & . \\
x_{\text{Nind},1} & x_{\text{Nind},2} & x_{\text{Nind},3} & \cdots & x_{\text{Nind},\text{Nvar}}
\end{bmatrix}
\begin{matrix}
\text{individual 1} \\
\text{individual 2} \\
\text{individual 3} \\
. \\
\text{individual Nind}
\end{matrix}
$$

Figure 3.15.3.3.2 The matrix containing the phenotypes

3.15.3.4 Gray Code

It has bin recommended that Gray code is used in stead of binary code. This is done to overcome the bias in ordinary binary code. In gray code the binary distance between adjacent numbers is constantly equal to one. The hamming distance is large in ordinary binary code and therefore the global minimum will be harder to find. Therefore it is preferable to use Gray code in the GA.

3.15.3.5 Roulette Wheel Selection Method

A simple roulette wheel is used for selection of the individuals for mating. A real valued interval *Sum*, is determined as the sum of the individuals relative fitness that is given by the *fitness function*. The fitness value of the individuals will then determine the size of its interval on the roulette wheel. A high fitness value will give a large interval on the roulette wheel. Below in fig. 3.15.3.5.1 a simple roulette wheel is shown where the fitness of individual 5 is largest and the fitness of individuals 4 and 6 are smallest. To select an individual, a random number is generated in the area [0, *Sum*] and the individual whose segment spans over the random number is selected.
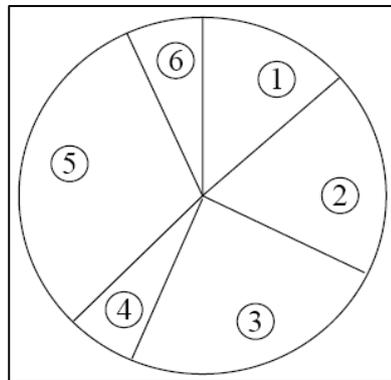
Figure 3.15.3.5.1 The principle of the roulette wheel selection method

The roulette wheel is spun a specified times according to the number of new individuals that are needed in the population specified by the generation gap GGAP.

3.15.3.6 Recombination Operator: Single Point crossover

Below the recombination operator single-point crossover is shown.

We have two binary strings representing parents:

Parent	Binary code
P_1	1 0 0 1 0 1 1 0
P_2	1 0 1 1 1 0 0 0

An integer position i is selected randomly between 1 and the string length l minus one $[1,l-1]$, and the genetic information is exchanged about point i between the two individuals and this will produce two new offspring strings. Below two new offspring are produced with crossover point $i=5$.

Offspring	Binary code
O_1	1 0 0 1 0 0 0 0
O_2	1 0 1 1 1 1 1 0

The crossover is not necessarily performed on all strings in the population. Instead, it is applied with a probability P_x.

3.15.3.7 Background Operator: Mutation

In the binary string representation, mutation will cause a single bit to change state, $0 \rightarrow 1$ or $1 \rightarrow 0$. Mutation on the fourth bit of O_1 leads to a new string O_{1m}.

Offspring	Binary code
O_1	1 0 0 1 0 0 0 0
O_{1m}	1 0 0 0 0 0 0 0

The mutation has the effect of tending to inhibit the possibility of converging to a local optimum, rather than the global optimum. The mutation is performed with a probability Pm on every bit. The reason for the mutation is that it will prevent the solution from getting stuck in a local minimum. This will increase the GA's chances of finding the global minimum.

3.15.3.8 The Fitness Function

The objective function is used to determine how well the individuals have performed in the problem domain. When a minimization problem is used the most fit individuals will have the lowest numerical values of the objective function. This value is called the raw-fitness and is only considered an intermediate state in determining the relative performance of the individuals in GA. After the objective function the raw-fitness values is treated with the *fitness function* that transforms the raw-fitness values into relative fitness, thus:

$$F(x) = g(f(x)) \qquad (3.15.3.8.1)$$

Here *f* is the objective function and *g* will transform the value of the objective function into a non-negative number, and *F* is the relative fitness.

It has bin found that by limiting the reproductive range so that no individuals generate an excessive number of offspring, it will prevent premature convergence. This can bin done by assigning fitness values according to their rank in the population rather than according to their raw performance. Only one variable *MAX* is used to determine the bias towards the most fit individuals and the fitness of the other individuals is determined in the following way:

- *MIN=2.0 – MAX*
- *INC=2.0×(MAX-1.0)/N$_{ind}$*
- *LOW=INC/2.0*

MIN is here the lower bound, *INC* is the difference between the fitness of adjacent individuals and *LOW* is the expected number of trials (number of times selected) of the least fit individual. *MAX* is normally chosen in the range [1.1, 2.0].

The fitness of the individuals can be calculated directly by the following equation

$$F(x_i) = 2 - MAX + 2(MAX - 1)\frac{x_i - 1}{N_{ind} - 1} \qquad (3.15.3.8.2)$$

x_i is the position in the ordered population of individual *i*. The individuals are ordered in the population according to their deceasing raw fitness.

3.15.3.9 The objective function

In the case of the APR developed by NTNU the following objective function is minimized.

$$f(x) = \|Sn - s\| \qquad (3.15.3.9.1)$$

The matrix **S** and **s** are the same as in (3.15.2 The "Least Square non Negative" Algorithm) part of the report. The vector **n** contains the numbers of plankton at each size and this vector is changed and fed to the equation after each generation by the GA. Since the object function only has to determine which size group that fits the equation best when using linear ranking in the fitness function, it can be made in this simple way.

3.16 Processing of real sonar data

The sonar data is given in a matrix with dimensions 4981×304. The measurements are structured in the following way in increasing column number: 200 kHz, 710 kHz, 1 MHz, 200 kHz and so on. The last measurement in the matrix is discarded so the result is 101 measurements at each frequency. Each measurement is given on a scale from 0-10 volt. The first meter in the measurements is discarded. This is because the receiving and sending electronics are activated at the same time when the sender electronics is sending the pulse. The received signal can therefore not be used in this time period, which corresponds to approximately 0.9 meters. The transducer will also oscillate for a short time period as a consequence of the sending. In addition the signal in the near field (below approximately the Rayleigh distance) can't be used, since the sonar system is calibrated for use in the far field. Below in fig. 3.16.1 the first measurement is plotted as it is given in the matrix together with its TVG corrected counterpart.
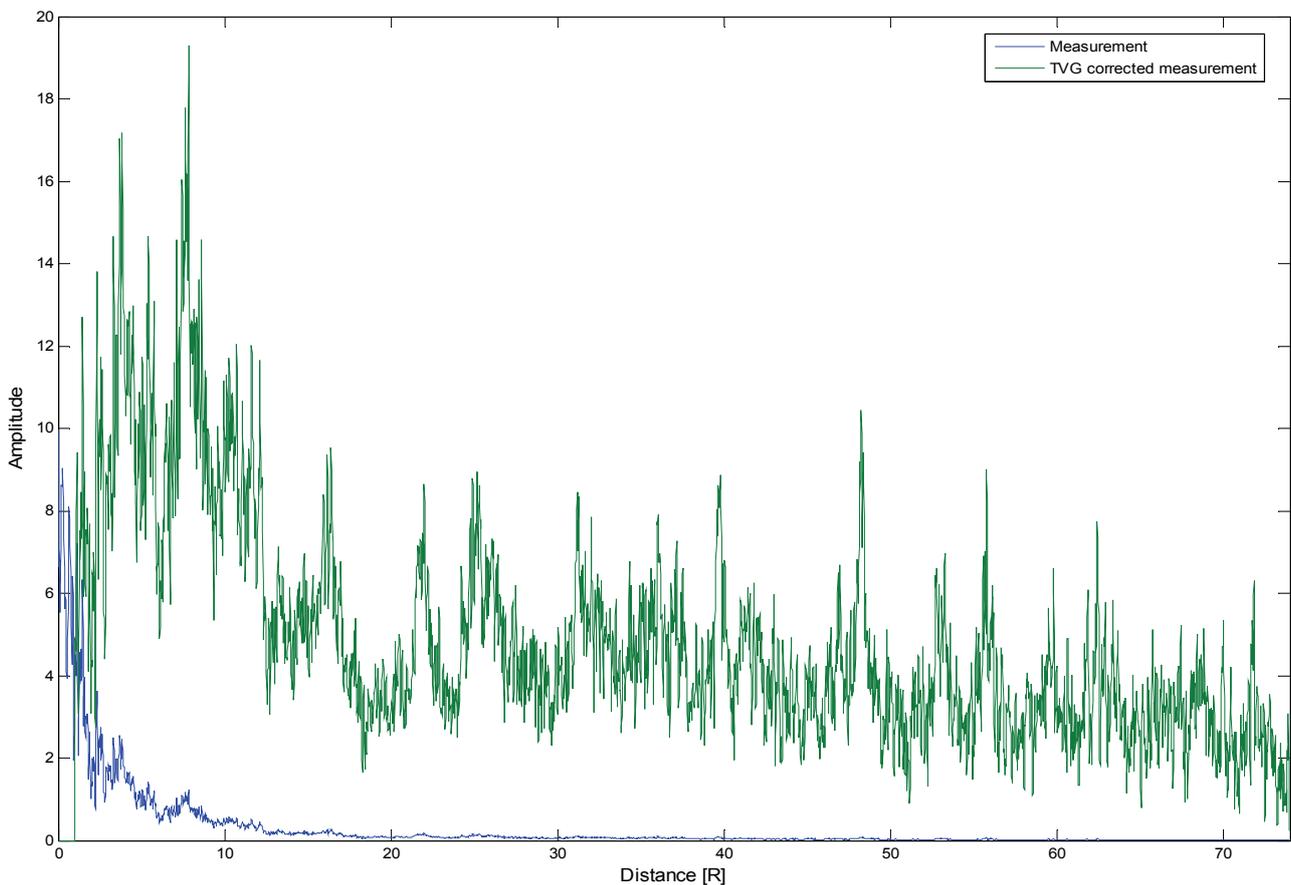
Figure 3.16.1 The first measurement at 200 kHz as blue together with its TVG corrected counterpart shown in green.

3.16.1 Echogram of signal data without echo integration

The echogram is made in the following way for each frequency

- The measurement values from 0-10 volts are TVG corrected with an exact TVG function
- The echo integrator equation is used to calculate the sv (scattering volume) values in each measurement in amplitude.
- Interpolation between the measurements is performed to get a smoother surface and SV(scattering volume) values in dB rel. 1μPa is then calculated.
- The calculated SV values for each measurement are plotted side by side to get the 2-D echogram plot.

The echogram in fig. 3.16.1.1, fig. 3.16.1.1 and fig. 3.16.1.1 are done without echo integration. In other words the P and N_x terms in the echo integrator equation are set to unity and the integration is only performed over one sample. Since there hasn't bin performed any echo integration there can't be performed any noise removal either. The TVG function will cause the noise level to rise with distance. This is especially the case at 1 MHz, where the absorption is high and therefore the gain of the TVG function is also high. The colour bar below the figures represents the SV value from -60 to -100 dB. The SV values in the bar represented by different colours are equivalent to the SV values in the figure. All the echograms are interpolated to give a smother surface and a clearer picture.
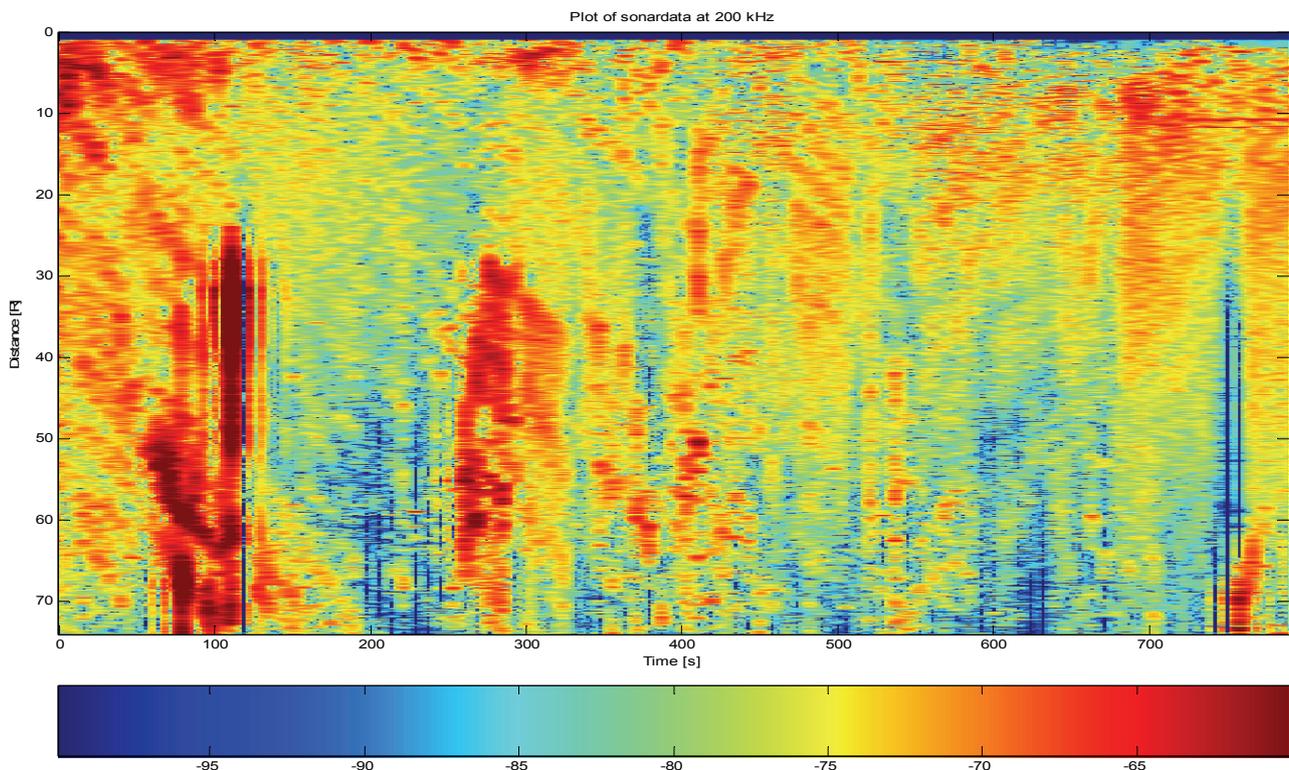
Figure 3.16.1.1 Echogram of the signal data at 200 kHz. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.

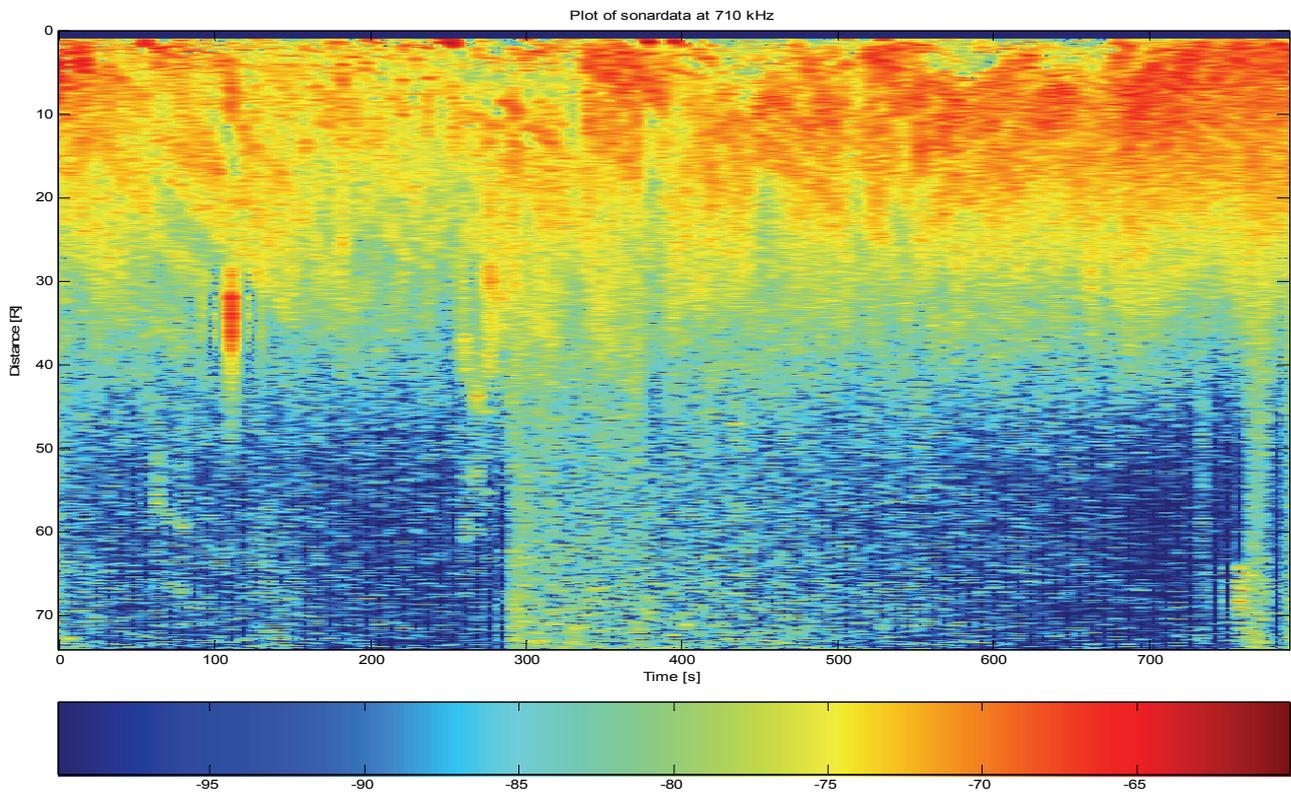**Figure 3.16.1.2** Echogram of the signal data at 710 kHz. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.
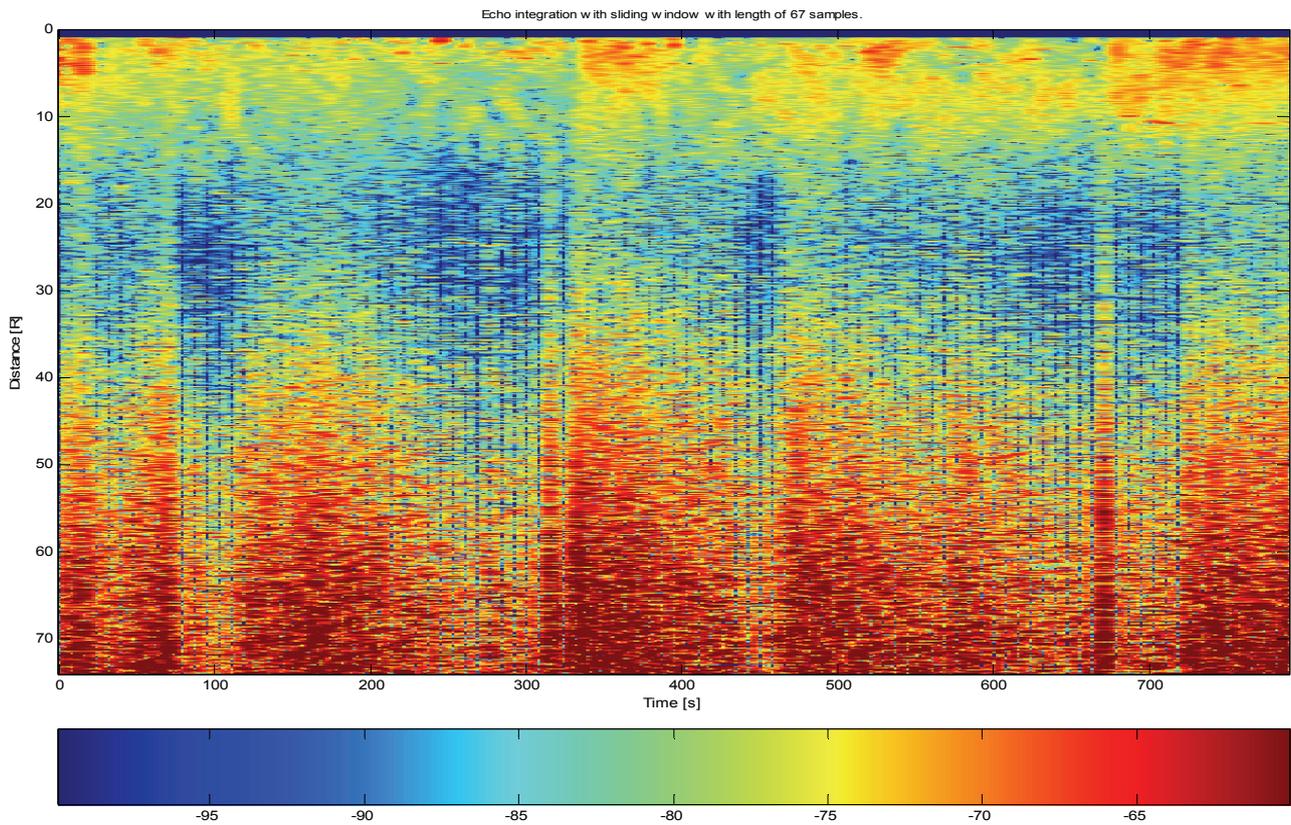

Figure 3.16.1.3 Echogram of the signal data at 1 MHz. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.

4 RESULTS

This chapter is divided into three parts. In the firs part "4.1 Results of Echo Integration" the results from the different types of echo integration with noise subtraction are shown.
In the second part "4.2 Results from Inversion of Synthetic data" the results from the tests of the GA and the "Least Square non Negative" algorithm by the use of synthetic data is shown.
In the last part "4.3 Results from Inversion of Real Sonar Data" the results from inversion of the real sonar data (see Appendix A) that was collected with APR developed by NTNU are shown

4.1 Results of Echo Integration

4.1.1 Results: Noise subtraction by the use of passive mode

As explained earlier noise can be removed from the measurements by the use of echo integration and by the calculation of noise energy for the equivalent integration period. In fig. 4.1.1.1, fig. 4.1.1.2 and fig. 4.1.1.3 the echograms are made in the following way.

- The last 600 samples of each measurement are used to calculate the average/maximum value of the noise and the average/maximum value is allocated to the whole range of each measurement.
- The measurement values from 0-10 volts and the allocated noise values are TVG corrected with an exact TVG function
- An integration length is specified and the echo integrator equation with noise subtraction eq 3.13.1 is used to calculate the sv (scattering volume) values in amplitude in each measurement. When integration is performed over the specified integration length one value is found and this value is placed in every sample position within this range. This is done for every integration distance. If a sliding window is used the integration window only moves forward with one sample at a time and the value found is placed in the middle of the integration area.
- Interpolation is performed between the samples to give a smother surface and SV(scattering volume) values in dB is then calculated
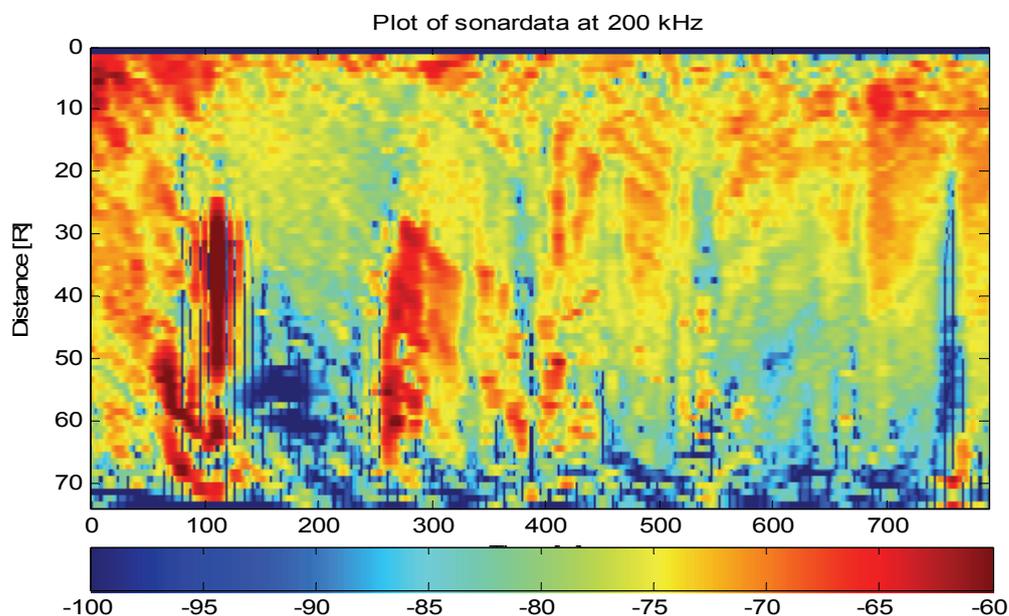- The calculated SV values for each measurement are plotted side by side to get the 2-D echogram plot.
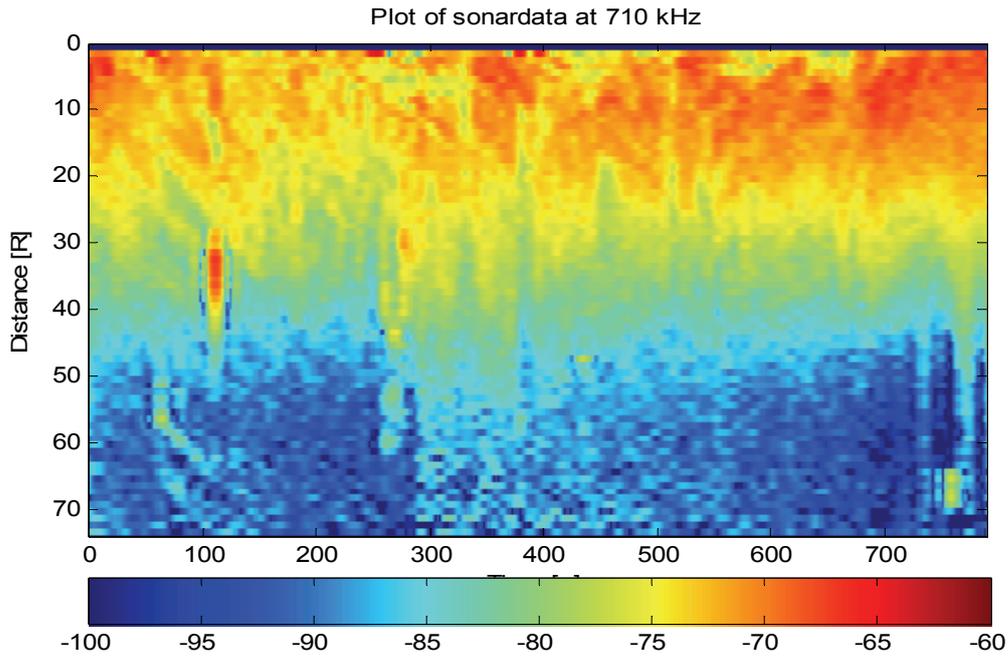

Figure 4.1.1.1 The result of echo integration with noise removal using the average value of the last 600 samples at 200 kHz. The integration length is 1 m. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.

Figure 4.1.1.2 The result of echo integration with noise removal using the average value of the last 600 samples at 710 kHz. The integration length is 1 m. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.
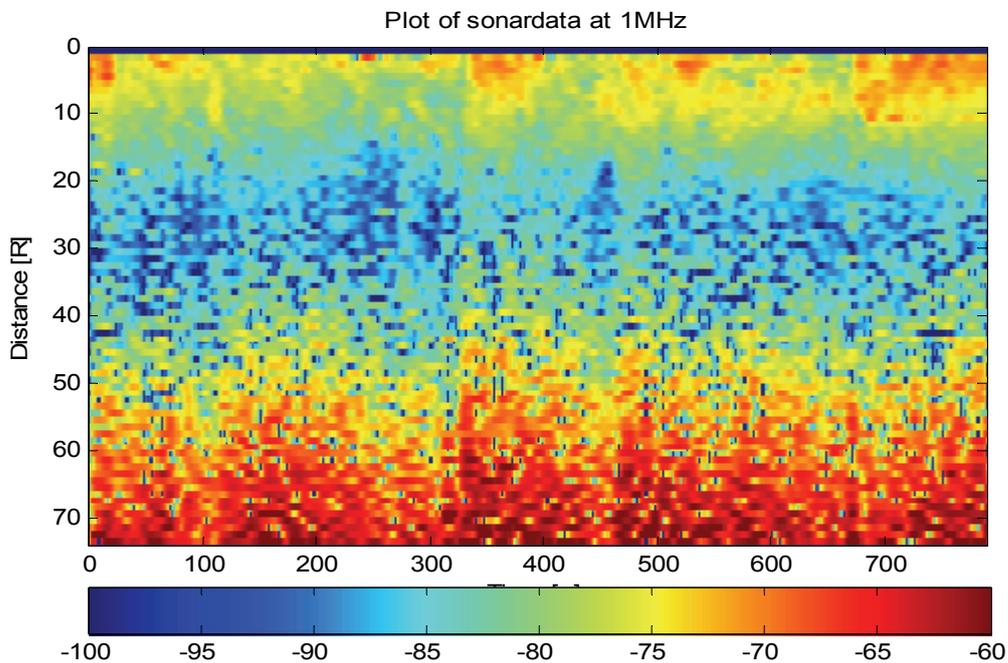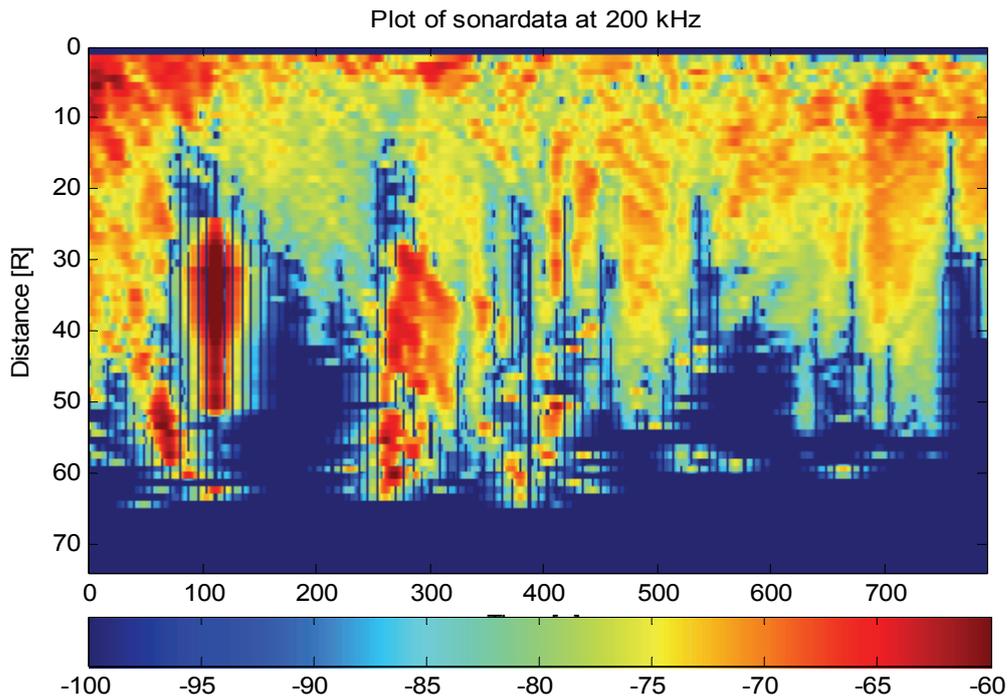

Figure 4.1.1.3 The result of echo integration and noise removal using the average value of the last 600 samples at 1 MHz. The integration length is 1 m. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.
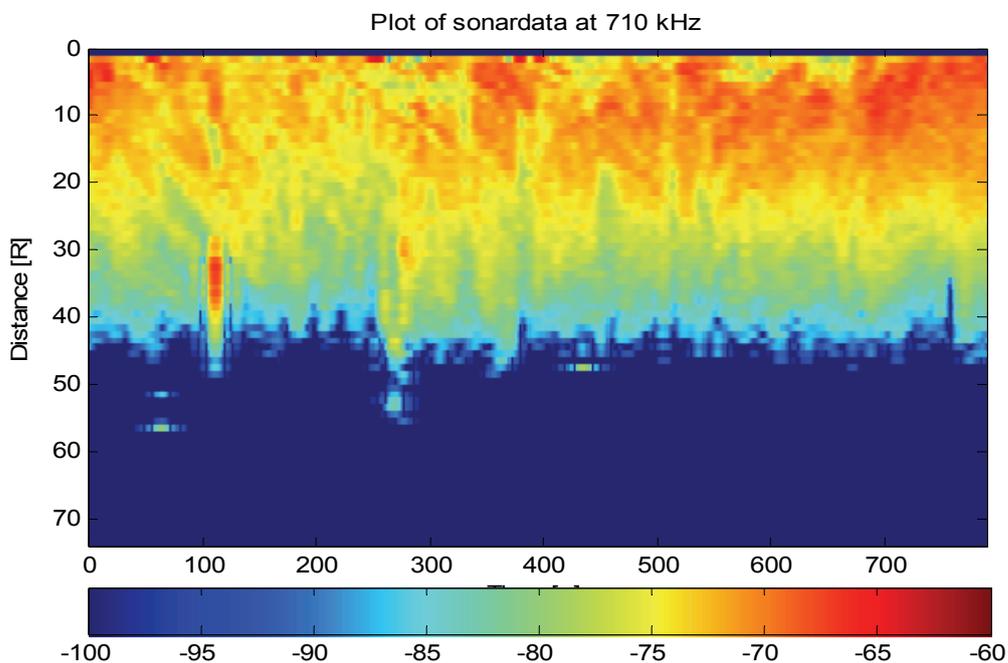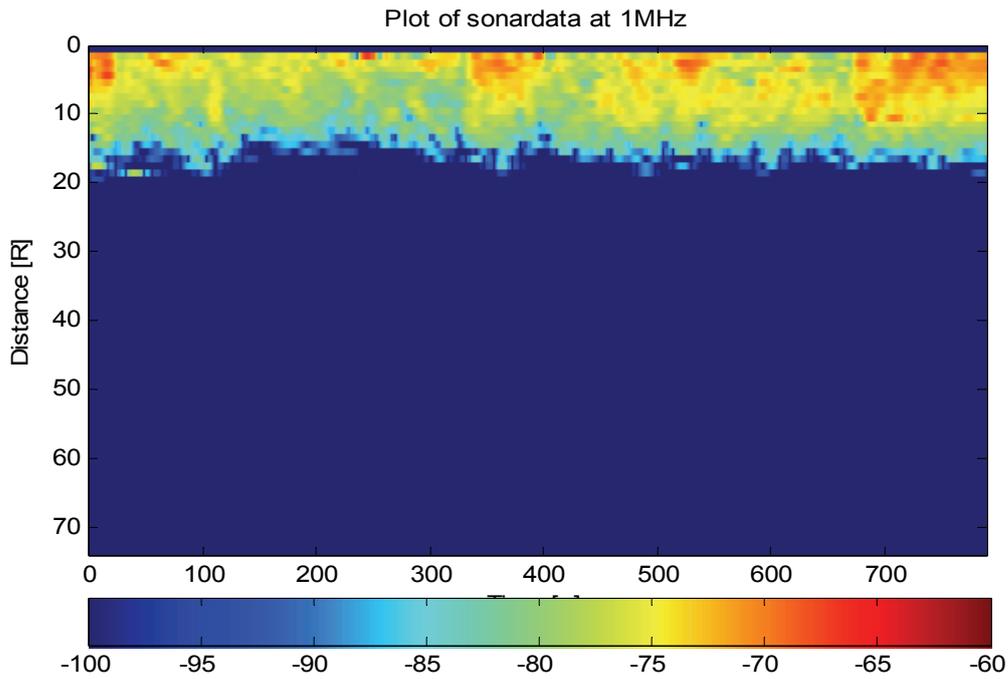
Figure 4.1.1.4 The result after echo integration and noise removal using the maximum value of the last 600 samples at 200 kHz. The integration length is 1 m. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.

Figure 4.1.1.5 The result after echo integration and noise removal using the maximum value of the last 600 samples at 710 kHz. The integration length is 1 m. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.

Figure 4.1.1.6 The result after echo integration and noise removal using the maximum value of the last 600 samples at 200 kHz. The integration length is 1 m. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.
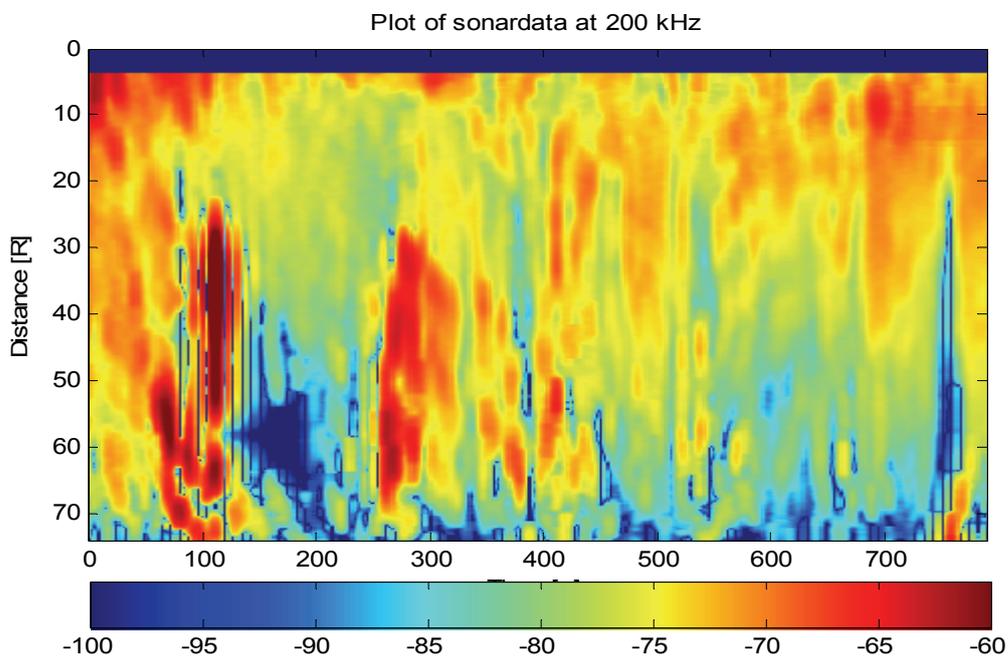

Figure 4.1.1.7 The result after echo integration and noise removal using the average value of the last 600 samples at 200 kHz. The integration length is 5 m and a sliding window has bin used. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.
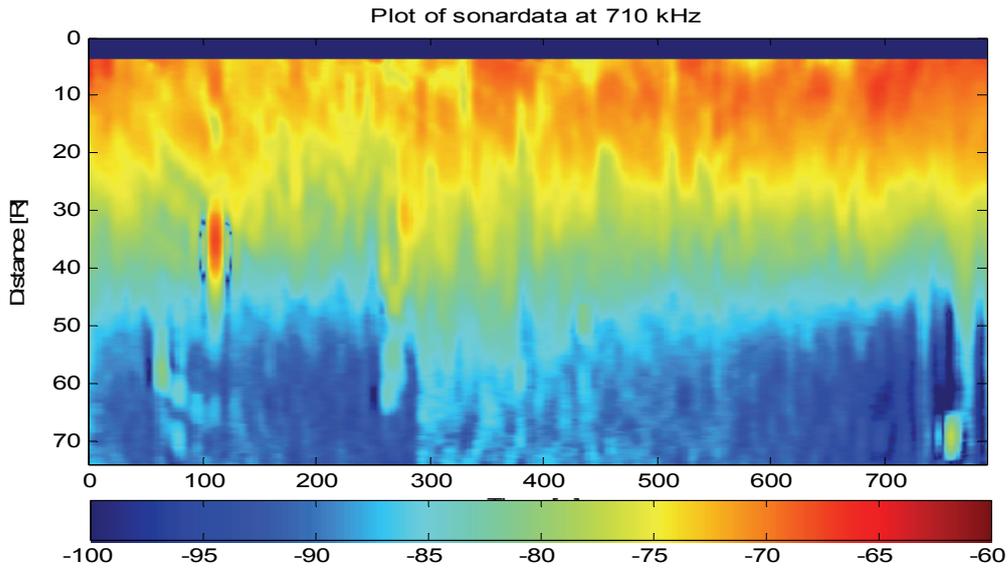
Plot of sonardata at 710 kHz

Figure 4.1.1.8 The result after echo integration and noise removal using the average value of the last 600 samples at 710 kHz. The integration length is 5 m and a sliding window has bin used. The colour bar specifies the SV value from -60 to -100 dB rel. 1μPa.
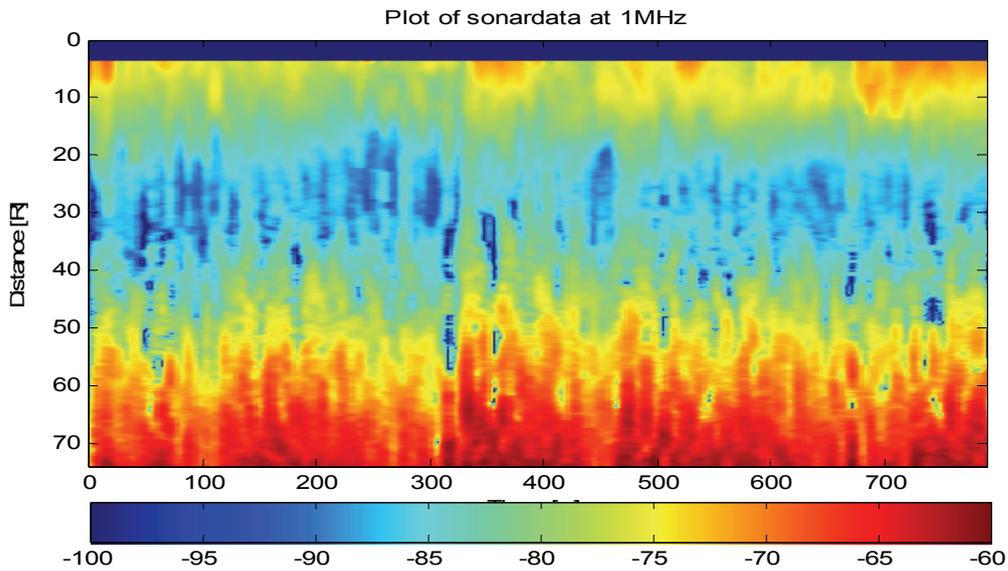

Plot of sonardata at 1MHz

Figure 4.1.1.9 The result after echo integration and noise removal using the average value of the last 600 samples at 1 MHz. The integration length is 5 m and a sliding window has bin used. The colour bar specifies the SV value from -60 to -100 dB dB rel. 1μPa.

4.1.2 Results: Noise subtraction by the use of curve fitting

Earlier the principle of curve fitting to the minimum values found in a transect is explained.
Below in fig. 4.1.2.1, fig. 4.1.2.2 and fig. 4.1.2.3 the result of this method is shown for the
frequencies 200 kHz, 710 kHz and 1MHz. The echograms are made in the following way

- The measurement values from 0-10 volts are TVG corrected with an exact TVG
  function
- The sv values are calculated at each frequency
- Echo integration is performed with an integration length of 1 m.
- The minimum sv values is found for each frequency in the transect
- Curve fitting is performed in the least square sense between the TVG function and the
  minimum sv values at each frequency.
- The fitted curve at each frequency is then subtracted from the transect
- Interpolation is performed between the sv values at each frequency, and the SV values
  in dB are calculated.
- The calculated SV values for each measurement are plotted side by side to get the 2-D
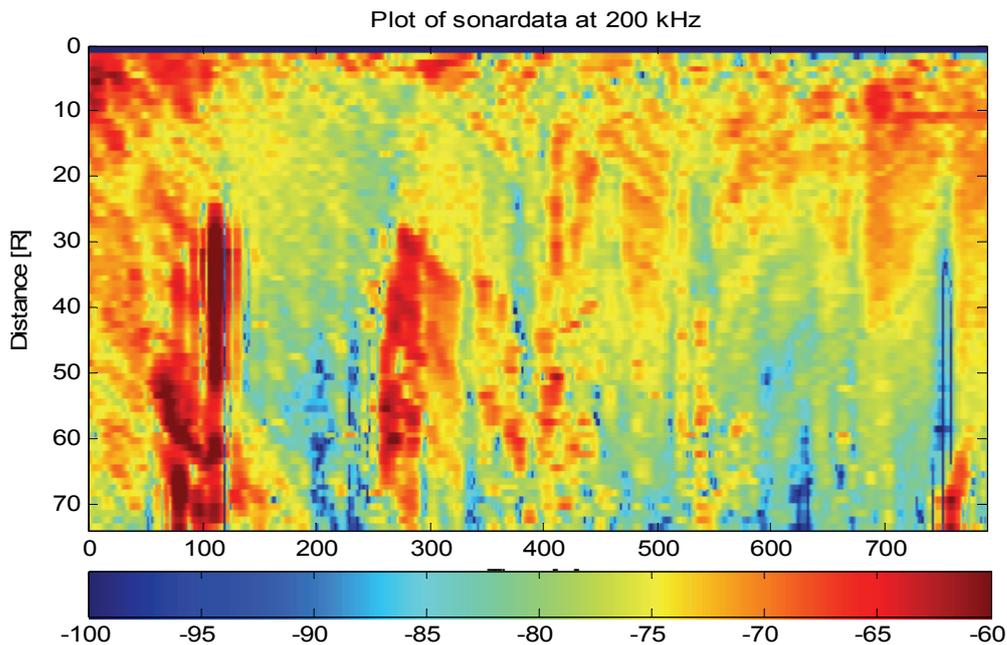 echogram plot.

Figure 4.1.2.1 The result after echo integration and noise removal by curve-fitting at 200
kHz. The integration length is 1 m. The colour bar specifies the SV values from -100 to 60 db
rel. 1 μPa.

Figure 4.1.2.2 The result after echo integration and noise removal by curve-fitting at 710 kHz. The integration length is 1 m. The colour bar specifies the SV values from -100 to 60 db rel. 1 µPa.

Figure 4.1.2.3 The result after echo integration and noise removal by curve-fitting at 200 kHz. The integration length is 1 m. The colour bar specifies the SV values from -100 to 60 db rel. 1 µPa.
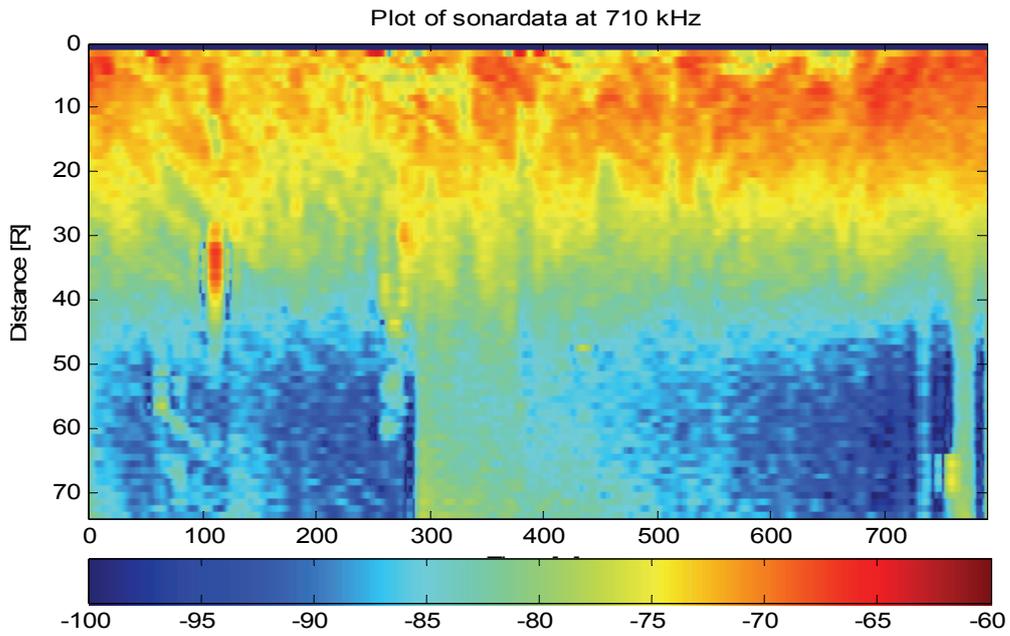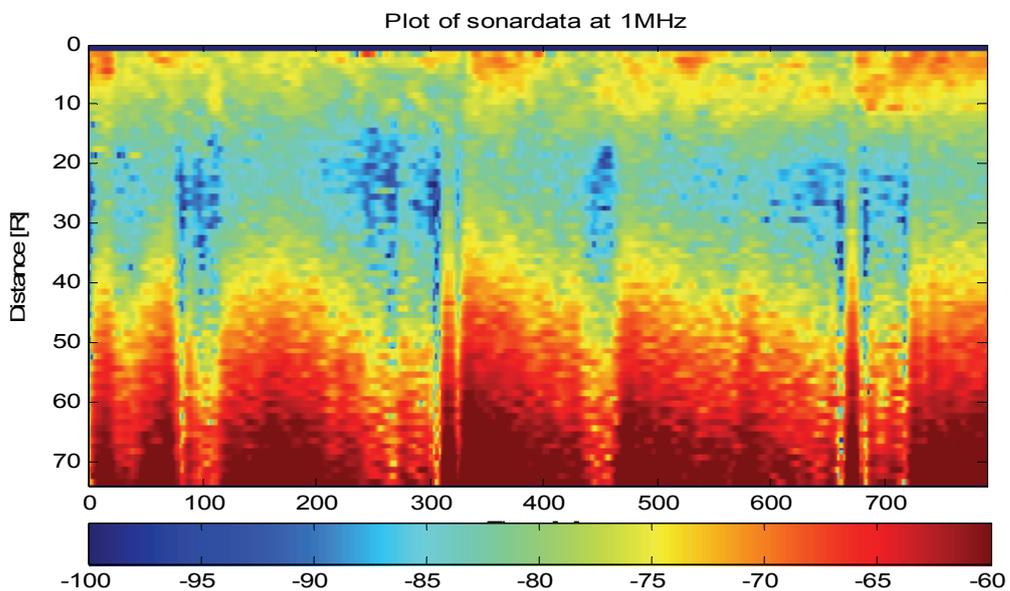
4.2 Results from Inversion of Synthetic Data

In this part of the report the inversion methods are compared and their abilities will be exposed. A deviation estimate is calculated on the basis of the difference between the estimated population and the amount of plankton in the synthetic model. To calculate the total deviation the following equation is used.

$$\Delta_{total} = \left| \frac{\text{Estimated population} - \text{Real population}}{\text{Real population}} \right| \qquad (4.2.1)$$

The distribution of the plankton at different plankton lengths for the estimated data can be seen in the figures that are given by each inversion.

The Genetic Algorithm and the "Least Square non Negative" algorithm will be evaluated by the use of synthetic data. The synthetic model that is used here is the Gaussian distributed population that is shown under the "synthetic model" chapter in fig. 3.15.1.1. The frequencies that are used are 200 kHz, 710 kHz and 1 MHz. These are the same frequencies that are used in the APR developed by NTNU.

The testing of the different methods is done in the following way.

- Synthetic data is generated from the Gaussian model using the frequencies (200 kHz, 710 kHz and 1 MHz) using eq. 3.15.1.1 and generating the **s** matrix
- The matrix **S** (eq 3.15.2.2) that contains the predicted values for the backscattering is generated
- Inversion is performed using the Genetic Algorithm and the "Least Square non Negative" algorithm.

The inversion by the two algorithms is first tested by setting the lengths of plankton to 1, 2 and 3 mm in the **S** matrix. The genetic algorithm uses the following fixed settings:

- Koding: Gray
- Px=0.8
- Pm=1/n ,where n is number of bits in the resolution
- GGAP=0.9
- n=12
- Max gen=200
- Population=80
- Range=0 to 4095

The number of bits n is the resolution in the solution. In this case the number of bits is 12 leading to a resolution in size increments of 1. Therefore the solution of the GA can tell the difference in increments of one plankton.
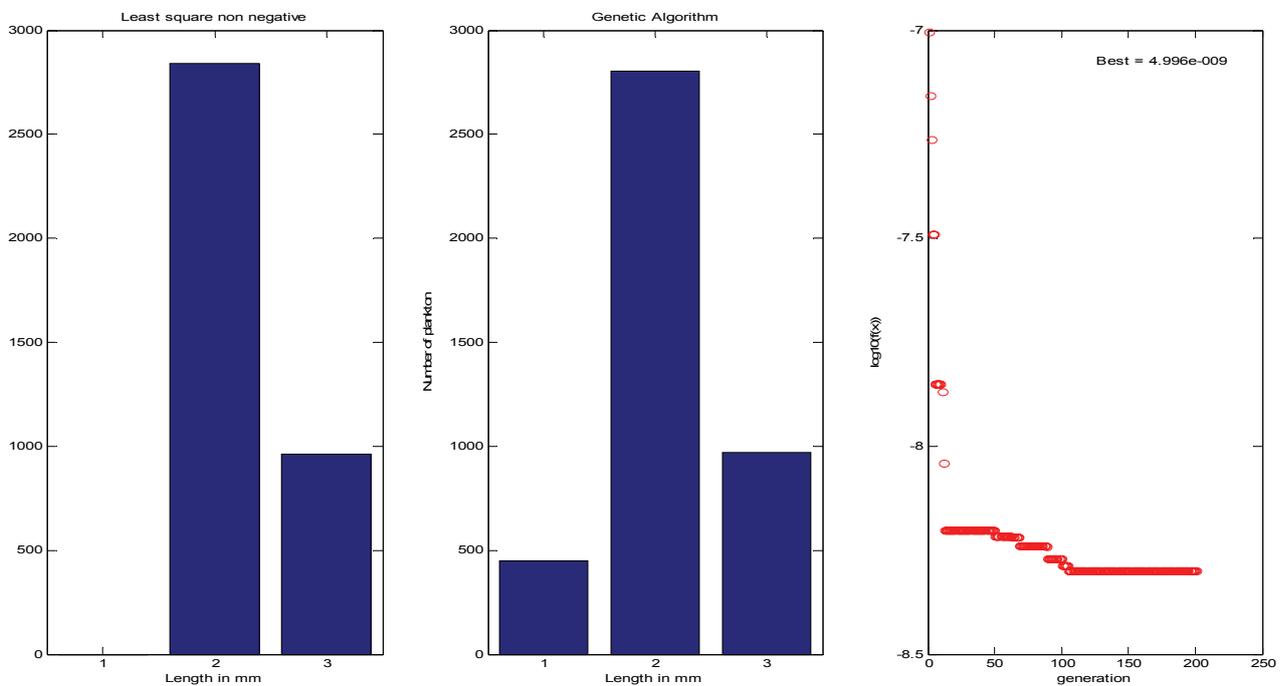

Figure 4.2.1 The result of inversion of a Gaussian population using the "Least Square non Negative" and GA algorithms together with the GA's selection. The size groups 1, 2 and 3 mm are used in the inversion.

Both methods will give an accurate result in terms of the total population. It should be noted however that the total number of plankton in the GA can vary from inversion to inversion since it's a stochastic optimization method, and especially at shorter lengths of plankton. Below the deviation is calculated for the two methods.

Methode	Least Square Non Negative	Genetic Algorithm
Δ_{total}	0.046	0.056

Inversion using the two algorithms in the over determined case will be tested here, which means that we are using more frequencies than size groups of plankton. In the APR developed by NTNU it is expected that the lengths of plankton in the area from 4-8 mm will be resonant at 200 kHz while individuals from 1-3 mm will be resonant at 1 MHz and 710 kHz. The size groups 2 and 5 mm is therefore chosen as the lengths of plankton in the solution. The same fixed settings are used in this GA as in the case of the foregoing result where the plankton lengths 1, 2 and 3 mm was used.
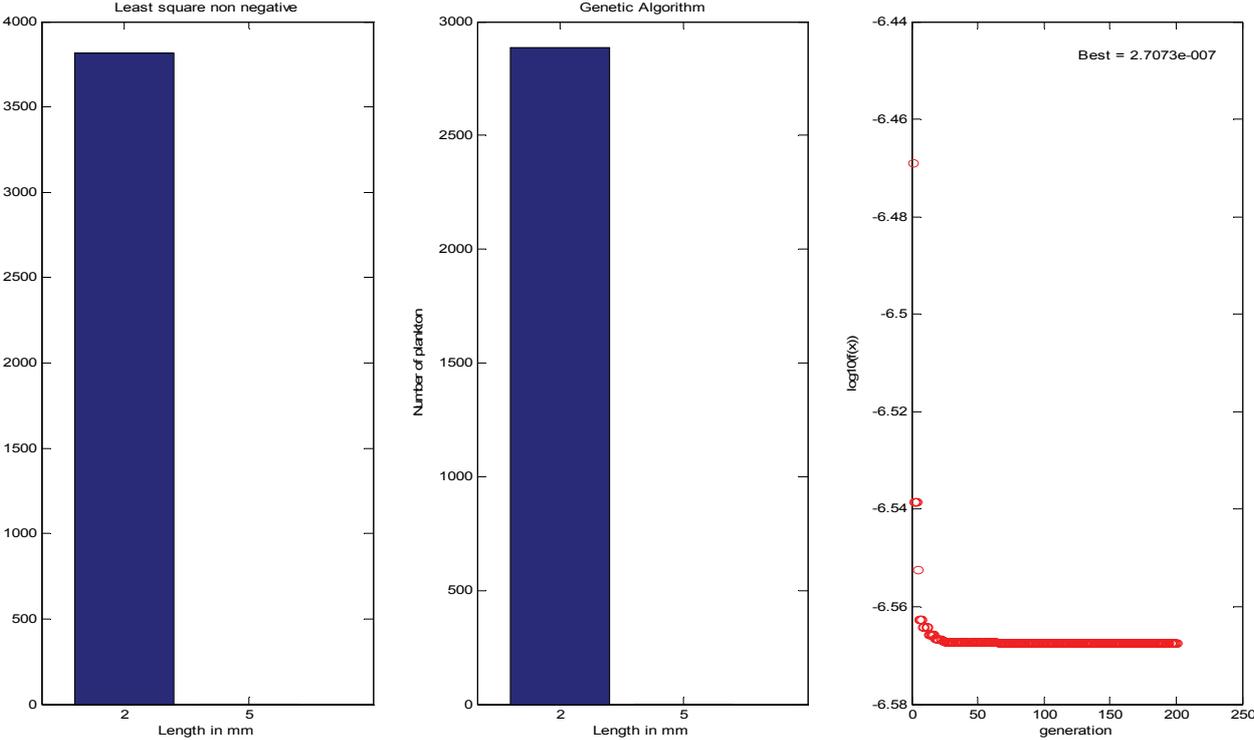

Figure 4.2.2 The result of inversion of a Gaussian population using the "Least Square non Negative" and GA algorithms together with the GA's selection. The size groups 2 and 5 mm are used in the inversion.

From the figure it is evident that the "Least Square non Negative" algorithm will give the most accurate result in terms of the total population while both methods indicate that the plankton is in the area around 2 mm. Below the deviation is calculated for the two methods.

Methode	*Least Square Non Negative*	*Genetic Algorithm*
Δ_{total}	0.046	0.28

Now the under determined case where more size groups are used than there are frequencies is tested. The plankton lengths (1, 2, 3, 5 and 8 mm) are used in the inversion. Since this is a more difficult problem to solve the following fixed settings are used in GA:

- Koding: Gray
- Px=0.99
- Pm=1/n ,where n is number of bits in the resolution
- GGAP=0.9
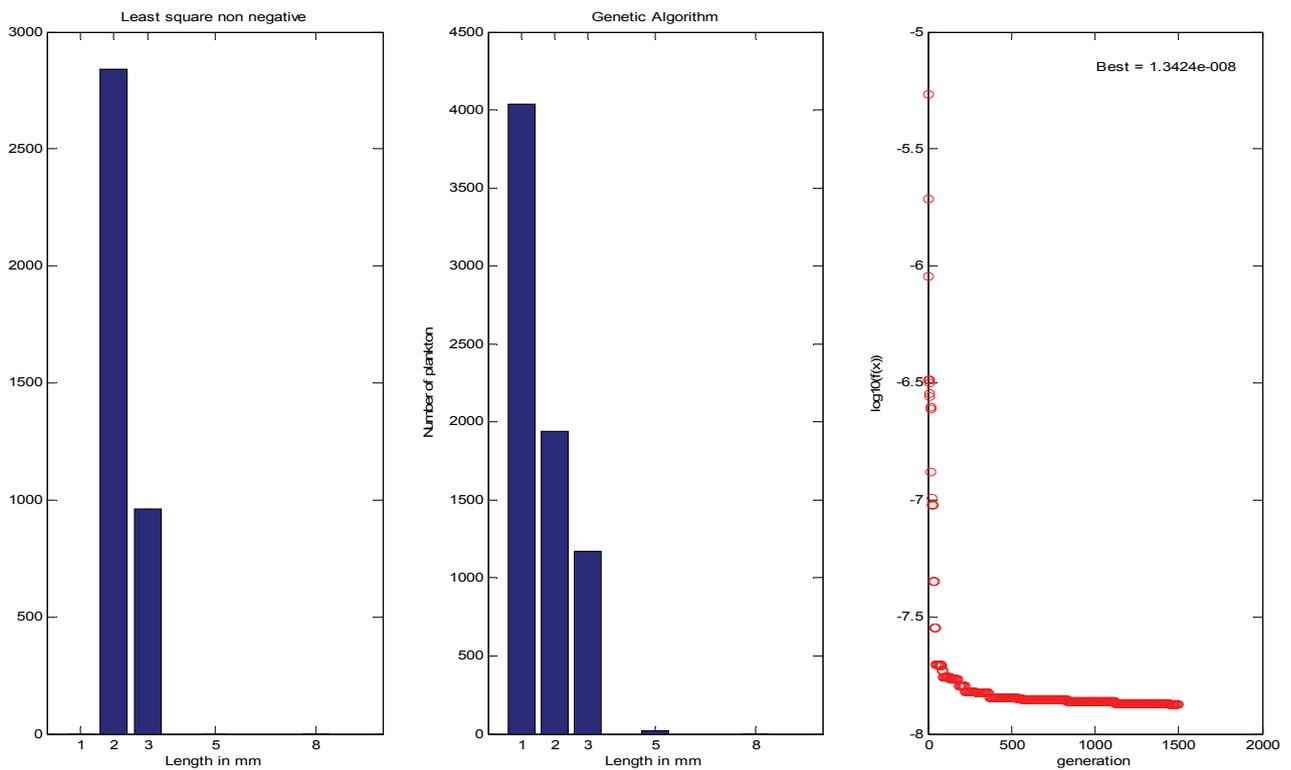- n=12
- Max gen=1500
- Population=80
- Range=0 to 4095

Figure 4.2.3 The result of inversion of a Gaussian population using the "Least Square non Negative" and GA algorithms together with the GA's selection. The size groups (1, 2, 3, 5, 8 mm) are used in the inversion

The two algorithms will also in this case indicate that the plankton is situated in the area from 1 to 3 mm. However the GA will give a large error in the estimated plankton abundance at 1 mm leading to large error in the predicted total number of plankton. Below the deviation of the two methods is calculated. See appendix B for more results.

Methode	Least Square Non Negative	Genetic Algorithm
Δ_{total}	0.046	0.791

4.3 Results from Inversion of Real Sonar Data

Since it is believed that the best results are obtained when noise removal by curve fitting is used, the result of the processing of the signal data by this method will be inverted in this chapter. Only the first 20 meters at each frequency will be used in the inversion since the maximum distance of the sound wave at 1 MHz is approximately 20 meters. The first 20 meters are shown below.
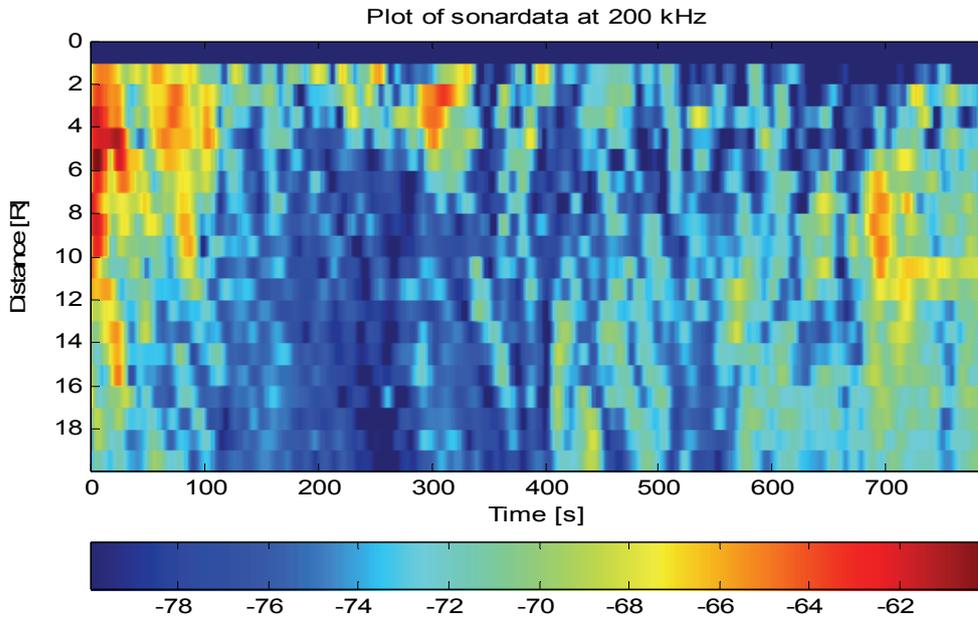

Figure 4.3.1 The result of echo integration with noise removal by the use of curve fitting for the first 20 m. The colour bar specifies the SV values from -80 to -60 dB rel 1 μPa.

Figure 4.3.2 The result of echo integration with noise removal by the use of curve fitting for the first 20 m. The colour bar specifies the SV values from -80 to -60 dB rel 1 μPa.

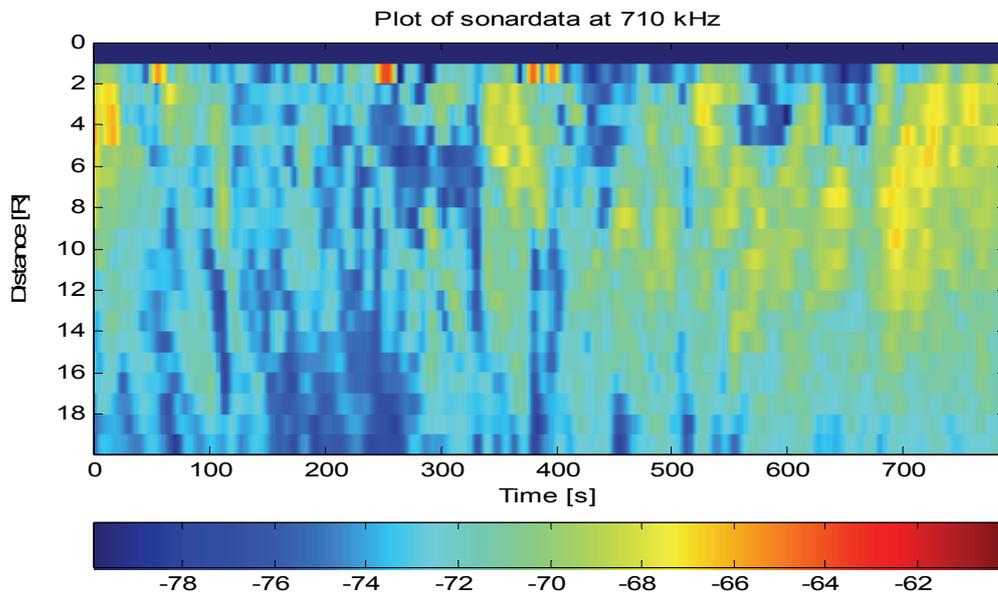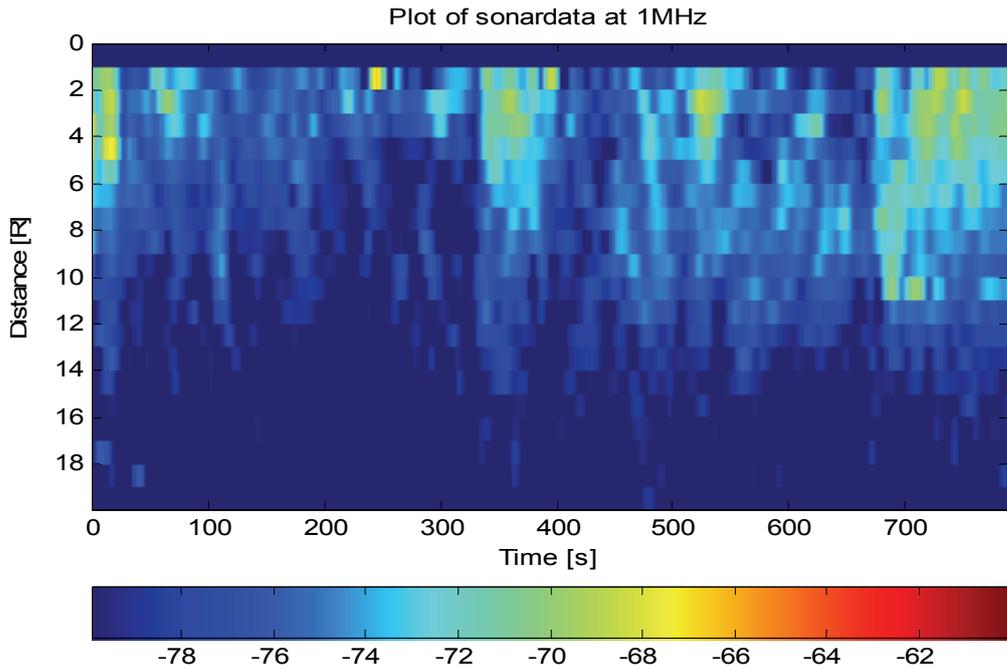**Figure 4.3.3** The result of echo integration with noise removal by the use of curve fitting for the first 20 m. The colour bar specifies the SV values from -80 to -60 dB rel 1 μPa.

Below the result of the inversion is plotted. The lengths 2, 3 and 6 mm are used in the inversion and the "Least Square non Negative" algorithm was used in the computation of the plankton distribution. The lengths 2, 3 and 6 mm where chosen because they proved to be the most robust when larger plankton or air bubbles are present.

Figure 4.3.4 The plankton distribution found by inversion with the "Least Squared non Negative" algorithm around 2 mm. The colour bar specifies the number of plankton per m^3.

Figure 4.3.5 The plankton distribution found by inversion with the "Least Squared non Negative" algorithm around 3 mm. The colour bar specifies the number of plankton per m^3.
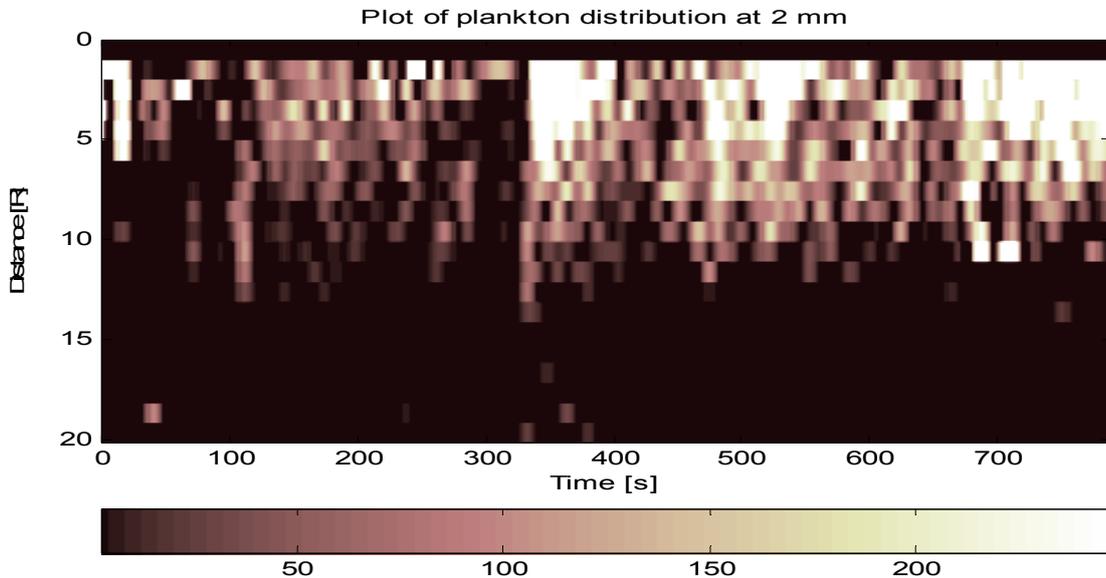

Figure 4.3.6 The plankton distribution found by inversion with the "Least Squared non Negative" algorithm around 3 mm. The colour bar specifies the number of plankton per m^3.
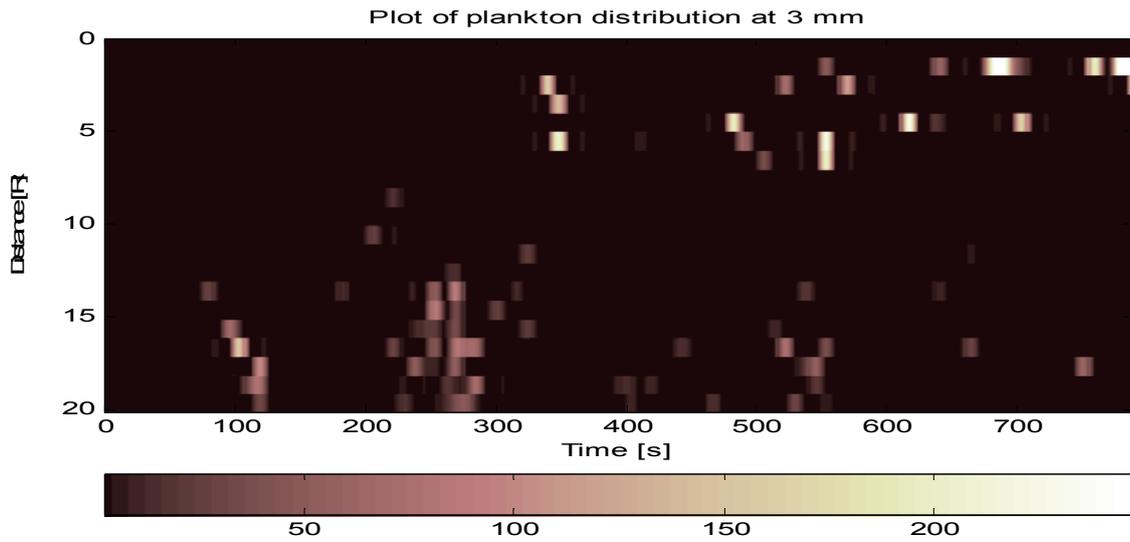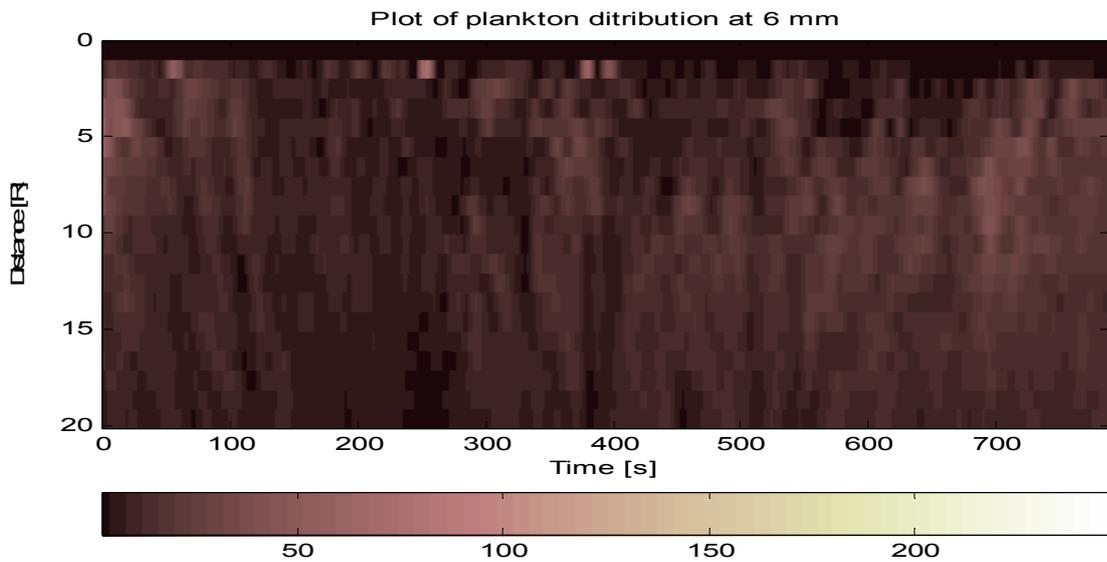
Since echo integration is used over 1 m increments the number of inversion points will be reduced with 67. This is because it is only necessary to perform inversion one time for a range increment of one meter which means every 67'Th sample. It is therefore possible perform inversion by the use of the GA algorithm at an overcoming computational cost. The inversion of all the points performed here took about 3 hours on a Pentium 4 3.0 GHZ with 2.0 GB RAM. The following fixed setting in the GA algorithm was used

- Koding: Gray
- Px=0.8
- Pm=1/n ,where n is number of bits in the resolution
- GGAP=0.9
- n=8
- Max gen=300
- Population=80
- Range=0 to 255

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Figure 4.3.7 The plankton distribution found by inversion with GA algorithm at 2 mm. The colour bar specifies the number of plankton per m^3.

Figure 4.3.8 The plankton distribution found by inversion with GA algorithm at 3 mm. The colour bar specifies the number of plankton per m^3.

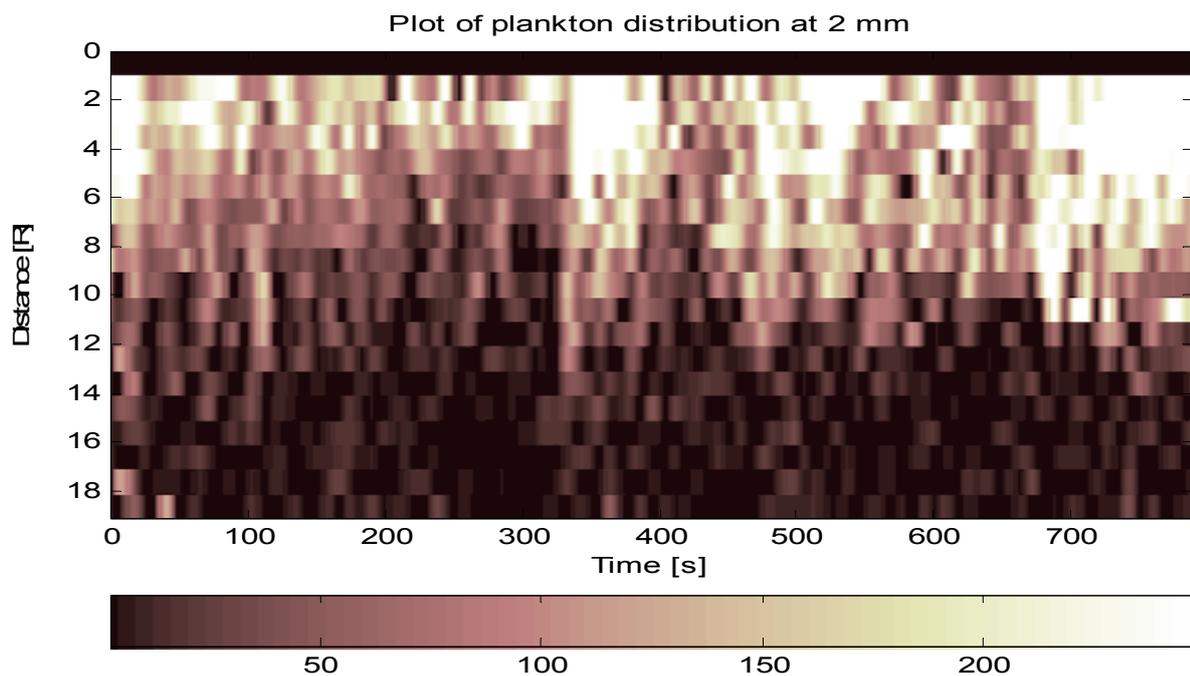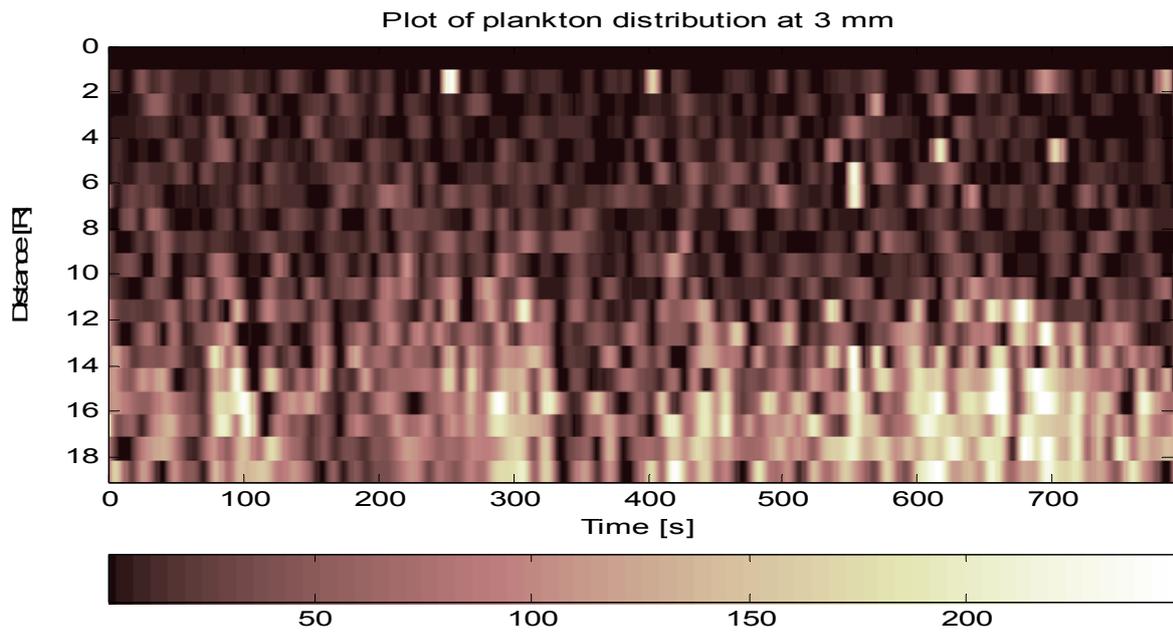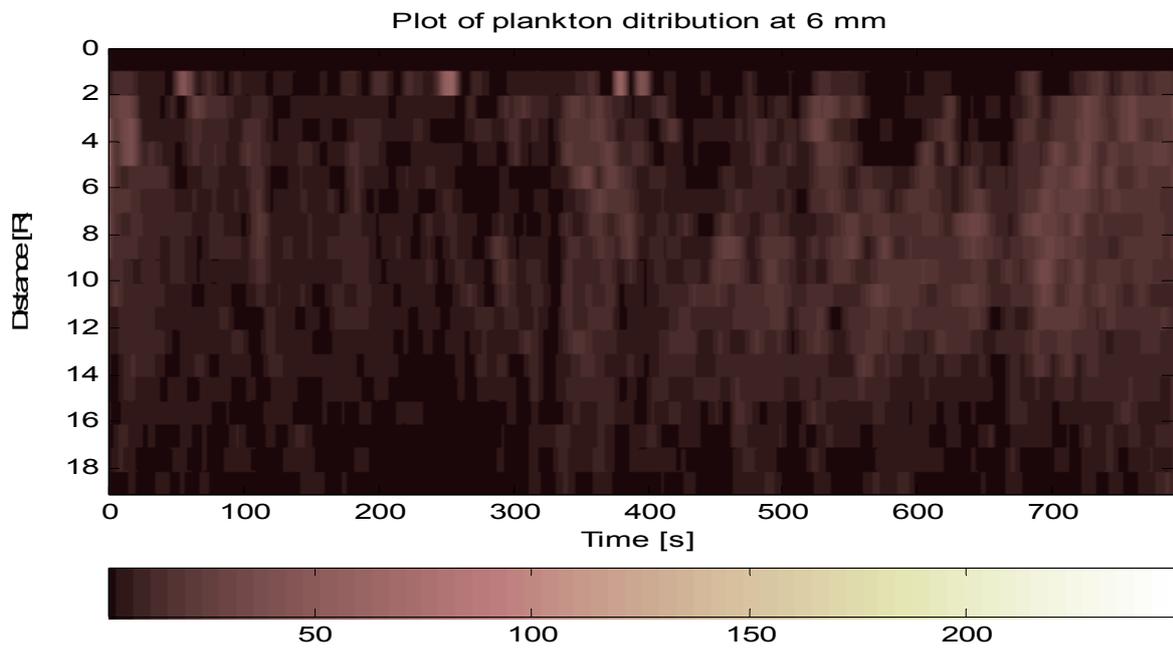**Figure 4.3.9** The plankton distribution found by inversion with GA algorithm at 6 mm. The colour bar specifies the number of plankton per m^3.

5 DISCUSSION

In this part of the report the results will be discussed. First the results from the echo integration will be discussed, then the results from the inversion of the synthetic data, and at the end the results from the inversion of real data.

5.1 Discussion: Results of echo integration

Since the wave at 200 kHz is believed to propagate longer than to the last 600 samples scatterers and possible the bottom will be treated as noise in the case of echo integration with noise subtraction in passive mode. The result will be that a higher noise level is predicted than what actually is encountered. This will lead to a lower predicted signal level than the real level. The same problem will probably to some extent exist at 710 kHz, but at 1 MHz this is not believed to be a problem.

It is difficult to predict that the noise subtraction method really works just by looking at the echograms since the method works best at lower noise levels (*see 3.14.3 evaluation of the noise subtraction method*) where the signal level itself is relatively high. The result should be that the scatters will give a somewhat clearer mark on the echogram compared to echo integration without noise removal, and the predicted scattered value should be closer to the real value. The noise level is still large at longer ranges when the average value of the noise is used and this is especially the case at 1 MHz. This shouldn't be of concern since this result was predicted in the evaluation of the noise subtraction method. When the noise subtraction method is used samples after the distance where the sound wave is believed to have "died" out as a result of absorption should be removed and therefore the problem with the presence of noise at larger lengths is eliminated.

In the case where the maximum value of the noise is used to calculate the noise subtraction curve the echogram shows that all the noise has bin removed. In this case some amount of the energy in the scattered signal is also removed giving a negative bias to the scattered signal. Although the method works well in removing the noise it will also remove an amount of the scattered signal and therefore this will lead to problems in the case of the abundance and size distribution of plankton.

When curve-fitting is used to remove the noise it will in this case not predict noise curves that coincide with the real noise curves at 200 kHz and 710 kHz. However the curves are believed to be better fitted than in the case of passive mode since the measured noise level in this case isn't strictly passive at 200 and 710 kHz. As a consequence of this evaluation the data that will be submitted to inversion to find the abundance and size distribution of plankton is the signal data that is processed with noise removal by curve fitting.

5.2 Discussion: Results from Inversion of Synthetic data

In the two algorithms it has bin found that both has its own characteristic weaknesses and strengths. The "Least Square non Negative" algorithm has the least computational cost and has proven to bee much faster that the GA. The GA algorithm on the other hand seems to give better results when the populations of plankton are complex, meaning that when there are a lot of different size groups at once it will give a better result, and especially in the underdetermined case.

When the population of plankton is situated at larger lengths 6-8 mm the GA will have problems in predicting the true population and predicts plankton at lower lengths as well. This is not a problem when the real population is situated at lower length (1-3 mm) .in this case the GA predicts the population satisfactory.

In the underdetermined case the "Least Square non Negative" algorithm predicts the population better then the GA in the case where just large individuals occur but in the case where both large and small individuals (1-3 and 4-8 mm) exists it will in some cases only predict one of the clusters, so the result will be either the 1-3 or 4-8 mm cluster. In this case the GA seems to work better and gives a smaller deviation in the predicted abundance. The problem involving only the higher or the lower lengths of plankton decreases by increasing the number of frequencies used.

The solutions are very sensitive in the 1 mm region where it's very difficult to get accurate results. This is due to the ill-conditioned objective function meaning that a small change in the measured level can give large changes in the predicted number of small plankton.

When the sizes of plankton are set to e.g. 2, 3 and 6 mm in the inversion and only plankton sizes of over 6 mm are present in the population the result won't be that these planktons occur at 6mm, but the result will be spread out over all the three sizes. Only in isolated instances does this give a satisfying result. Since the backscattering cross section is much larger for plankton of a size over 6 mm than at 2 and 3 mm the inversion will calculate a much larger total population as a cause of an estimated presence of large amount of plankton at 2 and 3 mm. However it seems that these values will give the overall best results when a realistic population is investigated.

The most robust results seems to appear when one assumes that no plankton sizes greater than 3 mm are present and the lengths 1, 2 and 3 mm of plankton are chosen in the inversion. This will give good results in terms of the total abundance as well as a reasonable good calculated distribution between the three sizes. Problems will occur in this situation when lengths of plankton longer than 3 mm occur in the real measurements since the backscattering from these are much larger than the smaller plankton. Another thing that will probably cause problems are air bubbles in the water that will give large backscattering compared to backscattering from the plankton. These two conditions will cause the population of plankton in the 1-3 mm area to be predicted with a large bias.

5.3 Discussion: Results of inversion of real sonar data

When the inversion is performed on the real sonar data it seams that the result will always contain values for longer plankton lengths than 3 mm. The problem is that when using only one larger plankton length in the inversion this wont' be enough to "describe" the larger lengths. The result will be that some of the larger plankton values leaks into the smaller values resulting in a larger predicted value at the smaller lengths than what's really encountered.

It seems that the "Least Square non Negative" algorithm will in some cases choose the area with the largest abundance of plankton. So if the predicted value is large at higher plankton lengths the values at the lowest lengths are discarded even though they are present. This problem does not occur with the GA algorithm. On the other hand when large plankton/air bubbles are present these plankton/air bubbles that should have bin predicted at longer values in the solution are easier shifted over in the calculated smaller values with the GA algorithm. The result is that the GA algorithm will predict larger values of small plankton than it really is. In this case the "Least Square non Negative" algorithm will predict smaller amounts of plankton than what is really present and only the larger values will to some extent be calculated satisfyingly. When comparing the figures representing the plankton distribution by the two methods it is evident that the characteristics of the two algorithms are present.

6 CONCLUSION

When measurements below ten meters are used in the APR system developed by NTNU an exact TVG function should be used. When using an ordinary TVG function it will amplify the signal to much in this area causing a larger value to be predicted than what is really encountered.

The echo integration will improve the linearity principle since more plankton is included due to the integration window. If no echo integration is applied then only the plankton in the reverberation volume contributes to the linearity principle. When noise subtraction is included in the echo integration the accuracy of the result is dependent on the integration length, giving an increasing accuracy in the results with an increasing integration length. The echo integration will lead to less computational cost when inversion is performed since the inversion is only needed once for every range increment. The resolution will decrease when echo integration is used and therefore the length of the integration window should be chosen on basis of the resolution and accuracy needed.

The pulse repetition rate should be slowed down in the APR developed by NTNU to get long enough measurements at each frequency so more accurate measurements for the noise level can be taken. This should also remove the problem with no clear rising noise curve at 200 and 710 kHz when noise removal by curve fitting is applied.

It is difficult to get satisfying results from the inversions performed by the "Least Square non Negative" algorithm and the GA algorithm in the case of realistic data when only three frequencies are used. Both methods will rarely give a correct result when it comes to the estimation of the abundance of plankton in the 1-3 mm area. Test done on synthetic data with a more complex plankton distribution with plankton lengths in the area from 4-10 mm shows that leakage to the smaller lengths in the solution will occur.

the "Least Square non Negative" algorithm will in some cases pick the size range where the most plankton is present and discarding the rest of the plankton sizes even though they are represented in the real data. This is especially a problem in the underdetermined case. This is not the case with the GA algorithm. However the GA algorithm has problems when only long lengths of plankton are present. In this case it seams that always some shorter lengths will be calculated as well. Based on this it is believed that the system will work satisfyingly in predicting the abundance of plankton in the 1-3 mm area when small abundances of plankton over 4 mm is present and poorly when large abundances in this size range is present.

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APPENDIX A

Environmental, biological data and sonar system variables

The APR developed by NTNU has bin used to collect the signal data processed in this report. Data concerning the measurement are listed in the tables below. The depth at the measurement place varied between 64 and 50 meters. The cylinder containing the electronics was lowered in the water so it had a horizontal level in the water +- 1 degree. There was a lot of jellyfish at the place. Measurements below 7 meters were not possible because the winch cable wasn't longer. The weather was shifting between snatches of sunshine, hail showers and rain showers. The measurements were performed in a short period of good weather right after a hail shower.

Table A.1 The coordinates of the place where the measurements where taken, the date and the start and end time.

Coordinates, date, start and end time of measurement	
Coordinates of the measurement place	63.48.757,8.44.458
Date of signal data collection	19.05.05
Start time	9.55.40
End time	10.10.10

Table A.2 The depth of the steal cylinder with time

Depth of sonar with time	
time	depth
9.55	Just below surface
9.58	2 meters
10.02	3 meters
10.04	4 meters
10.06	7 meters

Table A.3 The biological data collected at the measurement place

Biological data from the measurement place		
Depth	Calanus	Jelly fish
0	15 ml/m^3 corresponds to 500 ind/m^3	
5	20 ml/m^3 corresponds to 1500 ind/m^3	7 ml
10	8 ml/m^3 corresponds to 600 ind/m^3	30 ml
15	0.5 ml/m^3	67 ml
20	0.5 ml/m^3	10 ml

Table A.4 The temperature and salinity measured in the surface of the water.

Environmental variables	
Temperature	10 ^{0}C
Salinity	35 $^0/_{00}$
Depth	0 m

Table A.5 The variables needed to calculate the echo integrator equation for sv values.

Variables used in the echo integrator equation			
Frequency	200 kHz	710 kHz	1MHz
Source level SL	221 dB	217.5 dB	211 dB
Total gain G_X	-115.5 dB	-112.6 dB	-120 dB
EBA Ω	-20.62 dB	-20.62 dB	-17.72 dB
Pulse length	0.0012 s	0.0012 s	0.0012 s

APPENDIX B

Inversion of realistic measured plankton data

Here inversion is performed by the use of the GA and the "Least Square non Negative" algorithm on a realistic plankton distribution collected by measurements performed in the sea on Calanus finmarchicus. Below the measured Calanus lengths are shown in a table

Table B.1 The table shows the plankton distribution collected in measurements performed by with a landing net from the bottom to the surface. The data is given by Nils Tokle at NTNU. The measurements where taken in the Trondheim fjord over 12 sortie days distributed over 2002-2003. The total number of plankton is 4859.

Størrelsesfordeling av calanus				
Length[mm]	CIV	CV	CVI female	CVI male
1,428				
1,5232	3			
1,6184	53			
1,7136	200			
1,8088	24			
1,904	192	11		
1,9992	1	26		
2,0944	1	557		
2,1896		1099	3	
2,2848		166	2	2
2,38		1675	77	69
2,4752		99	75	21
2,5704		199	52	74
2,6656		125	8	40
2,7608				1
2,856		1	3	

In addition to the measurements of the calanus some length distributions are added to the synthetic model in the area from 4-8 mm. This is done to see if the inversion methods can separate the plankton in the area from 1-3 mm from the plankton in the area from 4-8 mm. In fig. B.1 the plankton distribution that is used is shown.
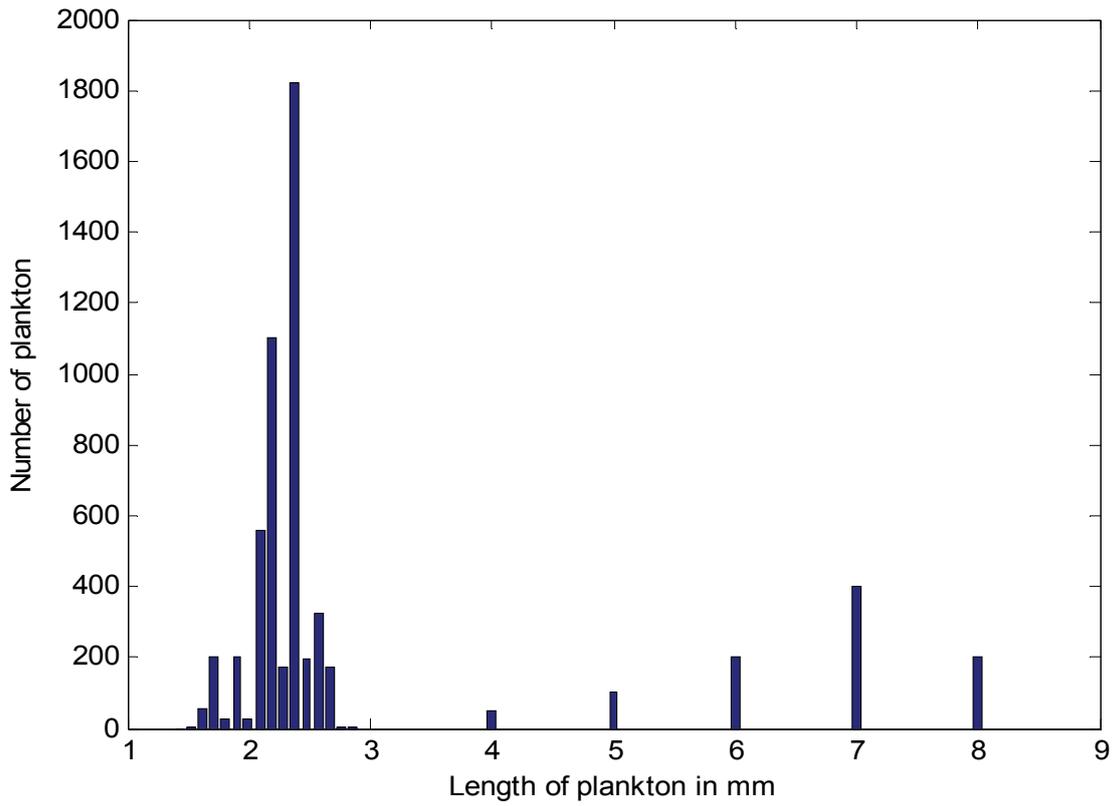
Figure B.1 The plankton distribution used in the synthetic model. The total number of plankton is 5809. 950 planktons are added to the realistic distribution in the area from 4 to 8 mm.

The "Least Square non Negative" and the GA algorithm are used in the inversion. First the lengths 2 and 8 mm are used in the inversion and we have a underdetermined system. The following fixed settings are used in the GA:

- Koding: Gray
- Px=0.99
- Pm=1/n ,where n is number of bits in the resolution
- GGAP=0.9
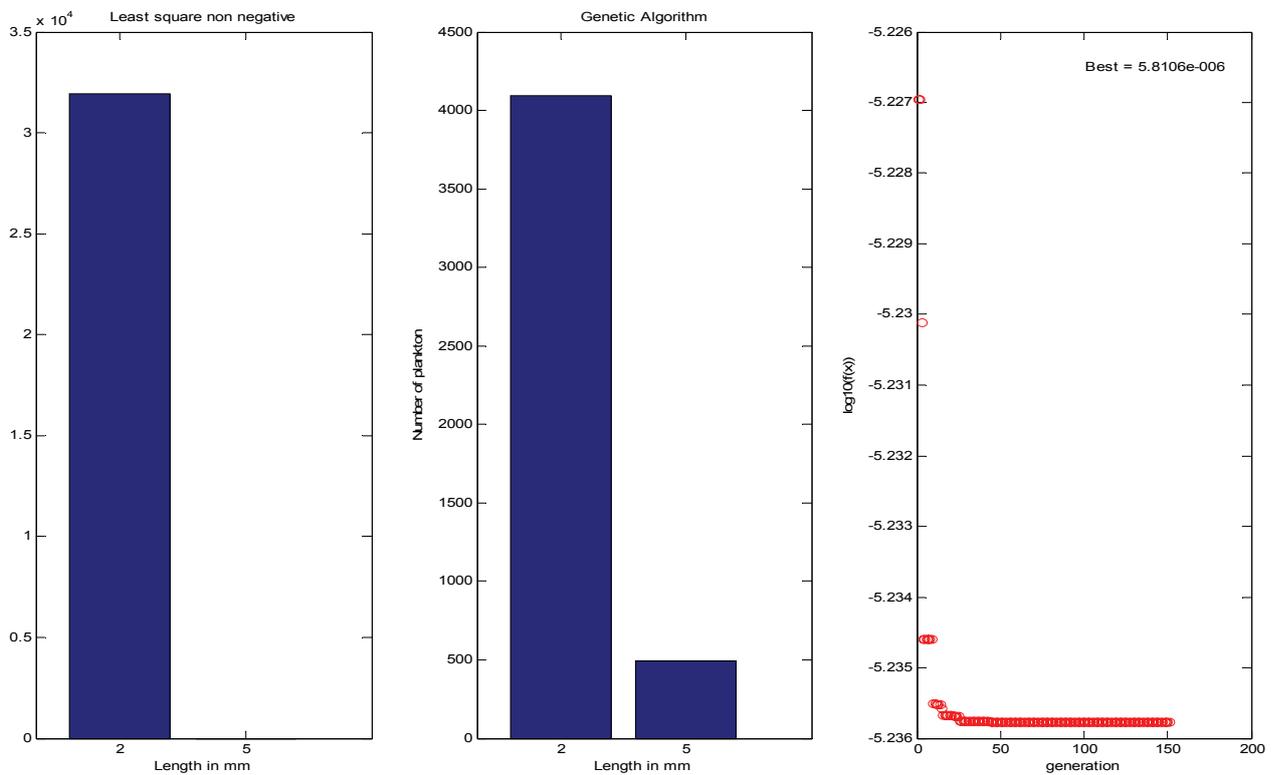- n=12
- Max gen=150
- Population=80
- Range=0 to 4095

Figure B.2 The result of inversion of a realistic population using the "Least Square non Negative" and GA algorithm together with the GA's selection. The size groups 2 and 5 mm are used in the inversion.

The result shows that the Least square non negative algorithm only gives results at 2 mm and no plankton at 5 mm in this case. While the GA gives results at both 2 and 5 mm with a reasonable accuracy. The maximum value at each size group in the GA has limited the result at 2 mm. The deviation in the two methods is calculated below.

Methode	Least Square Non Negative	Genetic Algorithm
Δ_{total}	5.025	0.21

The case where 3 size groups and 3 frequencies are used will now be investigated. The plankton lengths are 2, 3 and 6 mm. The fixed settings in the GA algorithm are the same as in the foregoing example. This will give the result shown in the figure B3.
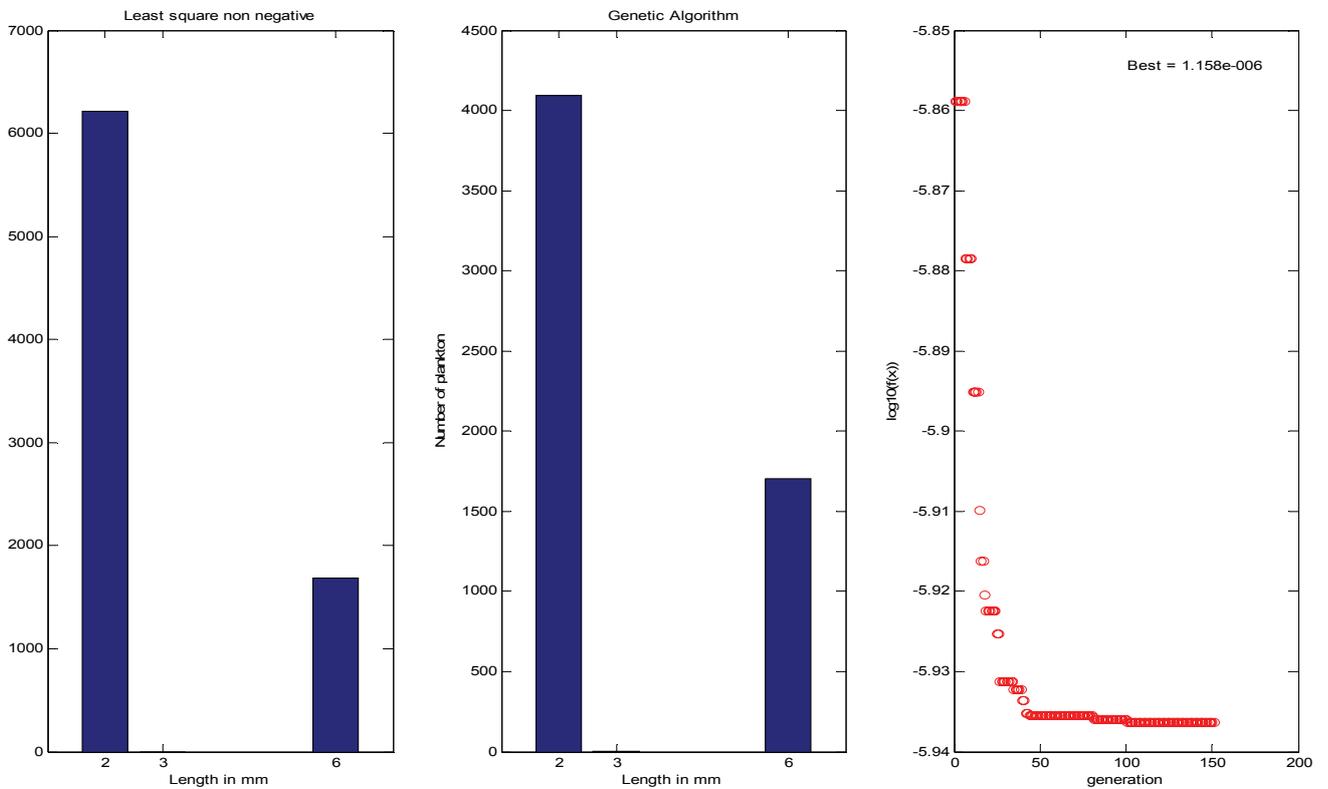

Figure B.3 The result of inversion of a realistic population using the "Least Square non Negative" and GA algorithm together with the GA's selection. The size groups 2, 3 and 6 mm are used in the inversion.

From the result we see that the GA has limited the result for the plankton length 2 mm at 4095 individuals. Both methods will give a result at 2 and 6 mm but the "Least Square non Negative" algorithm will give a larger result at 2 mm and a lower result at 6 mm compared to the GA. The deviation is given below.

Methode	Least Square Non Negative	Genetic Algorithm
Δ_{total}	0.956	0.124

In the underdetermined case there are more size groups than there are frequencies. The lengths (1, 2, 3, 4, 5, 6, 7 and 8 mm) are used in the inversion. The same fixed settings in the GA algorithm that has bin used in the previous example is also used here.
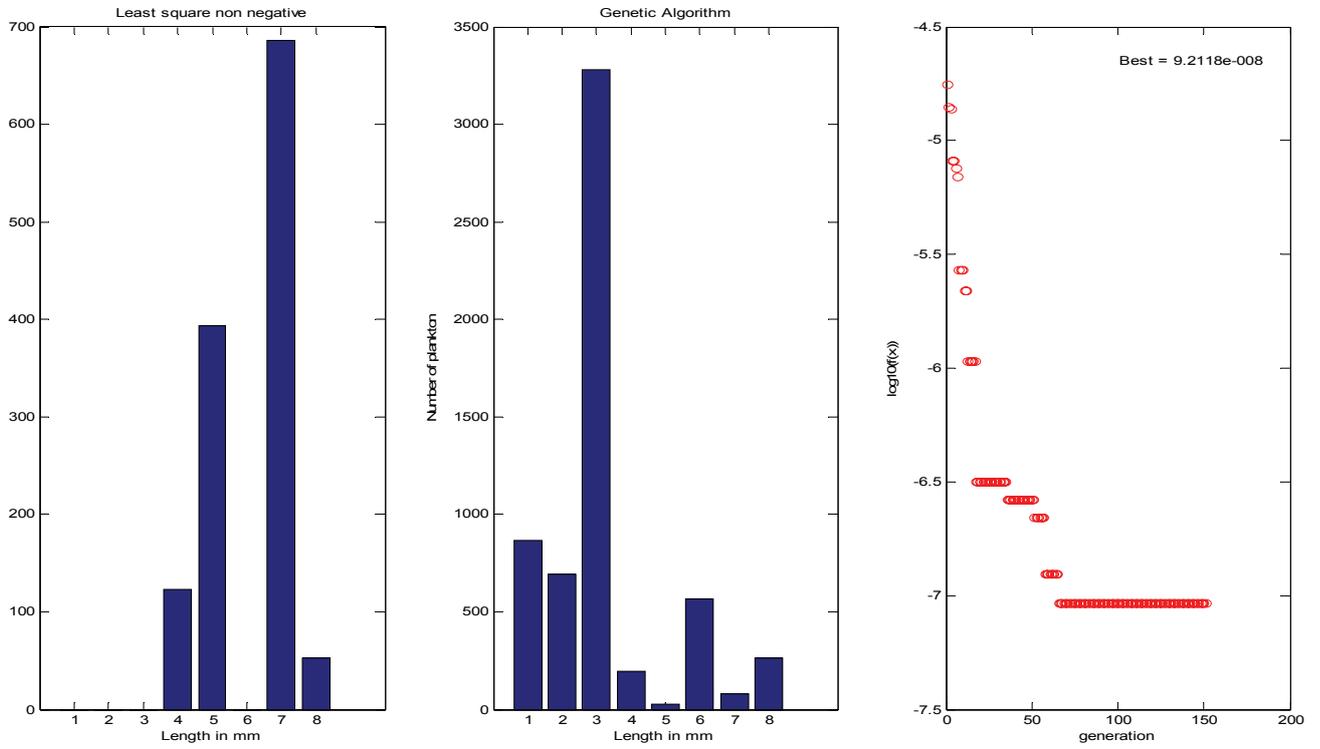

Figure B.4 The results of inversion of a Gaussian population using the "Least Square non Negative" and GA algorithm together with the GA's selection. The size groups (1, 2, 3, 4, 5, 6, 7 and 8 mm) are used in the inversion

From this result we can see that the Least square non negative algorithm will get problems with finding the position of the plankton population and also the total number of plankton will be biased. The genetic algorithm will position the plankton population with a relatively good precision and the bias in the total abundance is small.

Methode	Least Square Non Negative	Genetic Algorithm
Δ_{total}	0.784	0.028