HOW MANY LOBSTERS ARE IN THE SEA?

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ABSTRACT

A lobster fishery must have a reasonable estimate of the number of lobsters within the fishery in order to regulate the annual harvest. Stereological sampling procedures are used to estimate the number of lobsters in a defined region of the sea. From a given point in the fishery, a selective sample in a random direction to the boundary of the fishery is taken. This is repeated to generate a systematic sample from which the total population is estimated.

Keywords: lobsters, stereology, stochastic geometry.

INTRODUCTION

The lobster population off the east coast of Canada is currently an issue of critical interest. There is the possibility of increased fishing pressure due to a Supreme Court ruling on the rights of Native fishers. There has never been a proper assessment of the actual lobster population in the various fisheries. This knowledge is essential to the proper handling of the fishery. This paper hopes to remedy this by suggesting a procedure based on stereological methods to evaluate this lobster population.

A fishery F is a defined area of the sea. It is defined as the region of the sea where the concentration of lobsters is greater than some specified economically viable level, EVL. From any point within the fishery, labelled as B for the Buoy that would be placed there, we will sample at specified distances in a straight line until we pass the EVL. This will be repeated from B to generate a systematic sample from which the number of lobsters in the fishery will be estimated (see Enns and Ehlers, 1988, 1993; Gundersen and Jensen, 1987).

The process of sampling will involve a boat which takes a straight line trajectory from B and samples the sea floor at specified distances from B. At a point of sampling, the boat lowers a camera near the sea floor and photographs a circular region within which lobsters may be counted. How close the camera is to the sea floor depends on visibility. A flash would of course be necessary. At a sampling location let $h(r,\theta) =$ the number of lobsters/unit area a distance r in direction θ from B. We continue sampling on a straight line trajectory until $h(r,\theta) < c$ for the nth time where $n = 1,2,3...$ The EVL defines the concentration c.

While on a straight line trajectory from B we will consider two sampling spacings and take $n = 1$. These are:

a) Equal spacing:

b) In equal spacing, the boat samples distances r apart until we reach the EVL for the first time.

c) We specify concentration contours and using gradient estimates, sample as close as possible to concentration contours.

THE NUMBER OF LOBSTERS

$h(r,\theta)$ is the number of lobsters/unit area a distance r in direction θ from buoy B. A Fishery is defined as the region where $h(r,\theta) < c$. The total number of lobsters in the fishery is:

$$N = \int_0^{2\pi} d\theta \int_0^{R(\theta)} rh(r,\theta)\,dr \qquad (1)$$

$R(\theta)$ is the distance to the EVL measured in direction θ. If θ is defined as a uniformly distributed random variable on the interval $[0,2\pi]$, then we may write:

$$N = 2\pi\mathcal{E}_\theta\left[\int_0^{R(\theta)} rh(r,\theta)\,dr\right] \qquad (2)$$

In order to estimate (2) we will take a systematic sample of θ of size m, denoted by $\theta_1,\theta_2,...,\theta_m$. Then let:

$$N_i = \int_0^{R(\theta_i)} rh(r,\theta_i)\,dr \qquad (3)$$

and $\overline{N} = \sum_{i=1}^m N_i / m$ is an unbiased estimate of

$\mathcal{E}_\theta\left[\int_0^{R(\theta)} rh(r,\theta)\,dr\right]$.

The integral (3) must be estimated from sampling information obtained either in case a) or b). In both

cases, let $rh(r,\theta) = H(r,\theta)$ and $r_i h_i = H_i$ is the data from the ith sample from B. If we define $h(r,\theta)$ to be zero the first time it falls below the EVL, then this provides a sharp demarkation of the extent of the fishery. Hence $H_0 = H_n = 0$.
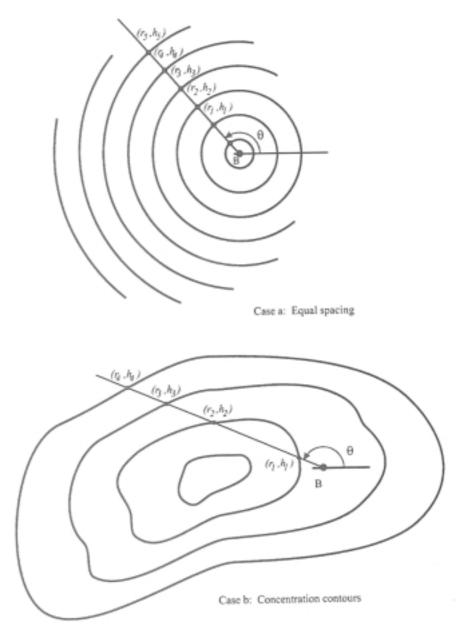

Case a: Equal spacing

Case b: Concentration contours

Figure 1

N_i as described in (3) may be rewritten as:

$$N_i \cong \sum_{j=1}^{N} (r_j - r_{j-1})(H_j + H_{j-1})/2. \qquad (4)$$

This reflects fitting linear segments between contour values of $H(r,\theta)$. (4) can be simplified to:

$$N_i \cong \sum_{j=1}^{n-1} H_j (r_{j+1} - r_{j-1})/2 \qquad (5)$$

At this point we must consider the two cases:

a) The Equal Spacing Case:

The boat will leave the Buoy B and sample at regular intervals a distance r apart. Then $H_i = r_i h_i = irh_i$ and (5) becomes:

$$N_i \cong r^2 \sum_{j=1}^{n-1} jh_j. \qquad (6)$$

b) The Concentration Contour Case:

In this case we will use the gradient in the sampling direction to estimate how far the boat should travel between sampling points. Specifically $\partial h(r,\theta)/\partial r$ gives us the concentration gradient. Since we only know $h(r,\theta)$ at sampling points, we will estimate $\dfrac{\partial h(r,\theta)}{\partial r}$ by $(h_j - h_{j-1})/(r_j - r_{j-1})$ for $j = 1,...,n$. If we wish to estimate the distance to a concentration contour a value c, above or below, our present concentration, then the boat should proceed a distance $c\left(\dfrac{r_j - r_{j-1}}{h_j - h_{j-1}}\right)$ from the jth sampling point.

We will not be fortunate enough to always sample on the next concentration contour, hence we can only simplify (5) by using $H_j = r_j h_j$ to obtain:

$$N_i \cong \sum_{j=1}^{n-1} r_j (r_{j+1} - r_{j-1})h_j/2. $$

SIMULATIONS

We consider a fishery of lobsters. The actual number of lobsters in the fishery will be 100,000 lobsters for the purpose of the simulation.

The positions of 100,000 lobsters were simulated from a bivariate normal distribution with means zero, variances one, and a covariance of 0.814. This implies the ratio of the major to minor axes of a confidence ellipse is approximately 10:1.

The local concentration $h(r,\theta)$ was estimated as the number of lobsters within a disk of radius dr centered at (r,θ). The number of systematically sampled angles was

m, and the number of points sampled along a ray was n. In both the equal spacing and concentration contour case, sampling was begun at the origin. In the equal spacing case the spacing was taken as $4/n$, and in the concentration contour case, the concentration interval c was taken to be the initial concentration estimate at the origin divided by n. The second sample along each ray was taken at radius $4/n$, after which radial sampling positions were estimated as described above. In each of these schemes, the total area sampled was $A = mn\pi dr^2$. With the simulation parameters used, a complete enumeration of the stock would require examination of approximately 9π square units.

Twenty independent simulation batches were run at each of $m = 6,12,18,24$, $n = 10,20,40$, and $dr = 10,5,.1,.5$. Table 1 lists the estimated mean (μ_e) and standard deviation (σ_e) for the equal spacing case together with the estimated mean (μ_c) and standard deviation (σ_c) for the concentration contour case.

The total area sampled A is reported is in units of 10^{-6}, which corresponds to the lobster co-ordinates being measured in kilometers, and the radius of the sampling region being measured in metres.

The sampling actually carried out by the Department of Fisheries and Oceans, Canada, is based on occasional trips with lobster fishers, and observations of catch. At present, the department samples about 1 in 6000 boat trips (personal communication, DFO). The lobster density is thought to be in the hundreds or thousands per square kilometer, and the fishing region in many parts of the east coast of Canada, extends up to several hundred kilometers offshore in areas where the continental shelf is wide. Physical sampling devices are sometimes used which have a field of vision of approximatley 30 metres. Given these numbers and the units of the simulation, it is perhaps resonable to consider one of the small values of dr as being plausible. See (Chadwick, 1998) and (Lanteigne et al., 1998).

In these simulations the equal spacing method has little bias while the equal concentration method is biased downwards. In contrast to this, the variability of the equal concentration method is almost always lower than the equal spacing method.

We conjecture that the bias in the equal concentration method is due to inaccurate estimates of the derivative, leading to inaccurate estimates of the next concentration contour. The inaccuracy in the derivative stems from the fact that, at many points, the estimate of $h(r,\theta)$ is based on only a few lobsters contained in the sampling region.

TABLE I

m	n	dr	A	μ_e	σ_e	μ_c	σ_c
6	10	10.00	0.01885	102293	22333	63053	12749
6	10	5.00	0.00471	91307	31128	57201	17673
6	10	1.00	0.00019	77333	93943	40000	64455
6	10	0.50	0.00005	138667	399260	96000	342419
6	20	10.00	0.03770	95480	14987	75793	11393
6	20	5.00	0.00942	100667	15790	81164	15569
6	20	1.00	0.00038	106000	112513	82067	97353
6	20	0.50	0.00009	154667	216053	120000	180551
6	40	10.00	0.07540	99945	18140	85009	12990
6	40	5.00	0.01885	97327	16720	82741	16139
6	40	1.00	0.00075	105667	46718	94273	47175
6	40	0.50	0.00019	119333	156779	102667	140848
12	10	10.00	0.03770	96653	11964	63723	6552
12	10	5.00	0.00942	101493	15609	62816	15413
12	10	1.00	0.00038	90667	101783	50200	71645
12	10	0.50	0.00009	64000	135809	37867	105791
12	20	10.00	0.07540	93983	8044	75080	8711
12	20	5.00	0.01885	97960	13988	83904	11404
12	20	1.00	0.00075	93667	56464	66667	47977
12	20	0.50	0.00019	69333	105040	73268	146312
12	40	10.00	0.15080	100821	8898	85314	7207
12	40	5.00	0.03770	99083	10866	87541	9940
12	40	1.00	0.00151	102250	49071	90588	45562
12	40	0.50	0.00038	77667	63918	69367	62734
18	10	10.00	0.05655	98498	8413	63639	5756
18	10	5.00	0.01414	94791	15219	62154	14937
18	10	1.00	0.00057	100444	97078	66316	78034
18	10	0.50	0.00014	67556	167129	39111	118712
18	20	10.00	0.11310	101140	4621	77748	3503
18	20	5.00	0.02827	97573	10260	77875	7419
18	20	1.00	0.00113	95111	55910	69561	48691
18	20	0.50	0.00028	90667	81957	61333	66136
18	40	10.00	0.22619	99518	4803	85263	4688
18	40	5.00	0.05655	102056	9588	87631	6553
18	40	1.00	0.00226	100722	31999	94674	39259
18	40	0.50	0.00057	81556	72347	70114	65541
24	10	10.00	0.07540	97313	7360	62808	4175
24	10	5.00	0.01885	97040	13063	58370	11881
24	10	1.00	0.00075	78000	59357	37333	42955
24	10	0.50	0.00019	77333	95523	37333	77577
24	20	10.00	0.15080	99485	5133	77998	3768
24	20	5.00	0.03770	99527	9375	79877	6554
24	20	1.00	0.00151	98000	43264	68421	38106
24	20	0.50	0.00038	86667	83154	62667	67448
24	40	10.00	0.30159	98910	4843	83624	4191
24	40	5.00	0.07540	99378	8922	85909	6264
24	40	1.00	0.00302	106000	27551	91813	26315
24	40	0.50	0.00075	94333	67988	80167	62860

A preliminary report of some of the data (Enns, 1999) was presented at the Xth International Congress for Stereology, Melbourne, Australia, 1-4 November 1999.

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