Quantifying Salinity Habitat of Estuarine Species

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Abundance of numerous fish and invertebrate species of the Sacramento-San Joaquin estuary is correlated with delta outflow. Many have suggested that outflow affects species abundance through its effects on estuarine habitat (Moyle *et al* 1992), but attempts to quantify the effects of outflow on estuarine habitat have been limited.

Salinity is an important habitat factor and is strongly affected by outflow, so estuarine habitat often is defined in terms of a salinity range (Hieb and Baxter 1993). All estuarine species are assumed to have optimal salinity ranges, and life stages within a species often differ in salinity preference. Species survival may be determined partly by the amount of habitat available within their optimal salinity ranges. Because survival during an early life stage often determines the size of the year class, which in turn affects the size of the adult population, the optimal salinity habitat of this limiting life stage may be particularly important.

This article describes methods for quantifying salinity habitat of 10 fish and shrimp species in the estuary. To quantify the available salinity habitat of a species or life stage, it is necessary to determine the optimal salinity range, estimate the upstream and downstream limits of this range, and calculate the surface area or volume of water between these estuarine locations.

Optimal Salinity Range

Limits of optimal salinity ranges of fish and shrimp species investigated were defined as the 10th and 90th percentile of salinity distribution of all sampled larvae or young juveniles (or both) of the species. DFG provided the 10th and 90th percentile of salinity distributions for species other than striped bass and delta smelt. The 10th and 90th percentile for striped bass and delta smelt were computed using data from DFG's striped bass egg and larval survey. Table 1 lists estimated optimal salinity range for each of the selected species.

Location of Optimal Salinity Habitat

Upstream and downstream limits of the optimal salinity habitat were computed from monthly average outflow and the optimal salinity range of each species. Delta outflow was used to estimate X_2, the in-channel distance upstream of the Golden Gate Bridge, in kilometers, where the near-bottom salinity is 2 ppt. The distances (X) upstream from the Golden Gate Bridge of salinities representing the upper and lower limits of the optimal salinity range were computed from X_2 using a logistic equation derived from longitudinal salinity profiles presented by Monismith (1993).

Monthly (end-of-month) X2 was computed using Kimmerer and Monismith's (1992) regression equation for monthly data:

$$X_2(t) = 122.2 + 0.3278X_2(t-1) - 7.65LOG[Q_{OUT}(t)]$$

where $X_2(t)$ and $X_2(t-1)$ are the average 2-ppt positions for the current and previous months, respectively, and $LOG[Q_{OUT}(t)]$ is the log_{10} of the average outflow for the current month. Kimmerer and Monismith's (1992) equation for daily X_2 could have been used to provide daily estimates of estuarine habitat locations.

Monismith (1993) showed that when X_2 is known, the average position (X) in the estuary of other salinities can be estimated with little error. For a given ratio of X/X_2, mean salinity is nearly constant regardless of the value of X_2 (Figure 1). To derive an equation for estimating X, a logistic model was fitted to Monismith's data using nonlinear regression (SAS 1990).

Parameters of the regression model were modified slightly to im-

Table 1
OPTIMAL SALINITY RANGES AND MONTHLY WEIGHTING FACTORS FOR SELECTED ESTUARINE SPECIES

Species	Life Stage	Salinity Range: Upper Limit (ppt)	Salinity Range: Lower Limit (ppt)	Monthly Weighting Factors: Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Striped Bass (a)	Larvae (5-9 mm)	0.1	2.5	.00	.00	.00	.12	.52	.34	.02	.00	.00	.00	.00	.00
Delta Smelt (b)	Larvae and early juveniles	0.3	1.8	.00	.05	.10	.20	.30	.20	.10	.05	.00	.00	.00	.00
Longfin Smelt (c)	Larvae & early juveniles (< 50 mm)	1.1	18.5	.04	.44	.42	.09	.01	.00	.00	.00	.00	.00	.00	.00
Starry Flounder (c)	YOY (< 70 mm)	0.1	19.7	.00	.00	.04	.00	.03	.37	.24	.26	.05	.01	.00	.00
English Sole (c)	YOY (15-80 mm)	18.8	32.8	.00	.02	.04	.09	.20	.18	.15	.11	.07	.08	.03	.03
White Croaker (c)	YOY	18.1	32.4	.00	.00	.06	.04	.18	.24	.13	.10	.09	.17	.05	.00
Northern Anchovy (c)	YOY	21.3	32.1	.00	.00	.01	.04	.05	.17	.22	.11	.20	.13	.07	.00
Pacific Herring (c)	YOY	12.5	25.9	.26	.57	.12	.02	.00	.00	.00	.00	.00	.00	.00	.03
Crangon franciscorum (c)	Juveniles (< 26 mm)	1.6	21.6	.02	.01	.00	.02	.10	.24	.23	.16	.12	.05	.03	.02
Crangon nigricauda (c)	Juveniles (< 20 mm)	18.1	32.0	.09	.06	.03	.05	.14	.17	.09	.12	.07	.06	.05	.07

(a) Salinity range estimated by Jones & Stokes Associates from 16 years of DFG's Egg and Larval Survey data.

(b) Salinity range estimated by Jones & Stokes Associates from 2 years of DFG's Egg and Larval Survey data.

(c) Salinity range estimated by DFG from IEP Delta Outflow/San Francisco Bay Study Program data.

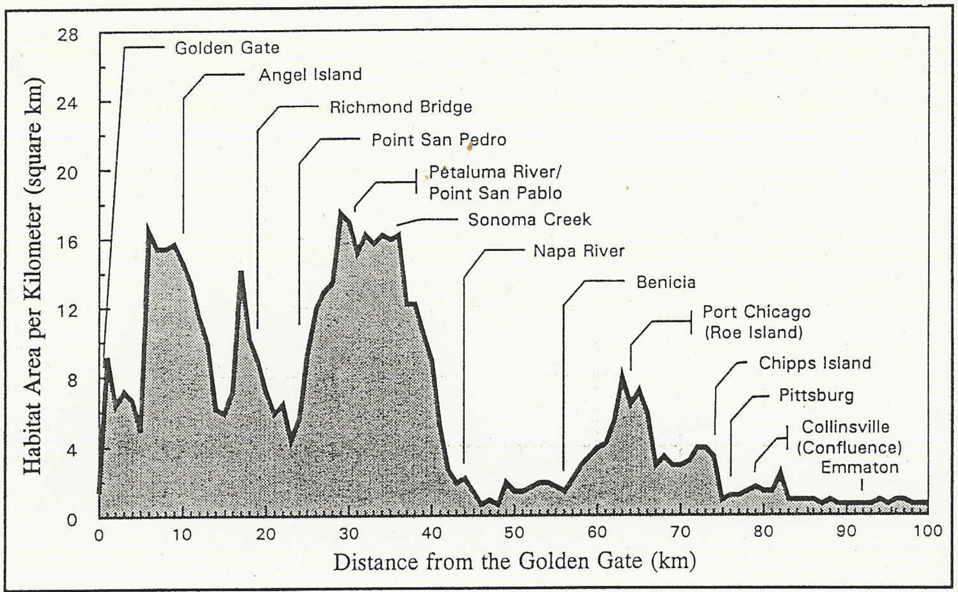

Figure 1
ESTUARINE HABITAT AREA UPSTREAM OF THE GOLDEN GATE

prove the fit in the low-salinity region of the curve with X/X_2 equal to about 1, because this region represents important habitat for many estuarine species. The logistic equation was solved for X so that the positions of the upstream and downstream limits of the optimal salinity habitat could be computed:

$$X = -X_2(\ln((31-S)/(515.67{*}S))/-7) - 1.5$$

where S equals mean (depth-averaged) salinity in practical salinity units (psu) of the upper or lower limit of the optimal salinity range. For the range of salinities found in the estuary, practical salinity units are nearly identical to parts per thousand (Monismith 1993).

Surface Area of Optimal Salinity Habitat

The Sacramento-San Joaquin estuary has a complex shape, so the area or volume of optimal salinity habitat varies greatly with its location. The surface area at different locations was estimated using tracings of nautical charts (prepared by USBR) to measure the shore-to-shore width perpendicular to the main shipping channel at each kilometer of distance along the channel upstream from the Golden Gate Bridge (Figure 2). Shorelines on the nautical charts represent mean lower-low tide position. Total surface area of optimal salinity habitat was computed by summing all the widths within the upstream and downstream limits of the habitat. South Bay was not included in the analyses.

Surface area rather than volume was used to quantify optimal salinity habitat, because habitat surface area was believed to affect most of the selected species more directly than habitat volume, and surface area is calculated more easily with available information.

Results of Historical Comparisons

Mean monthly outflow for 1922-1993 from the DWR (1994) DAYFLOW database were used to estimate optimal salinity habitat area for different species under a variety of outflow conditions (1922-1929 data were estimated by Jones & Stokes Associates). The database included many outflows greatly exceeding those that would produce the minimum X_2 value (X_2=58

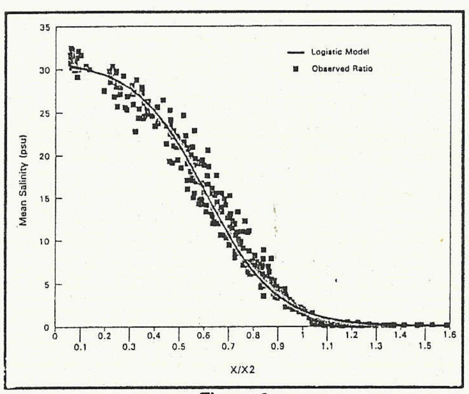

Figure 2
MEAN SALINITY AS A FUNCTION OF X/X_2

km) included in the data Monismith (1993) used to investigate the relationship between X/X_2 and salinity, but it was assumed that the relationship between X/X_2 and salinity was unchanged at low X_2 (*ie*, higher outflows).

Computed optimal salinity habitat area for delta smelt, longfin smelt, striped bass, and the shrimp *Crangon franciscorum* are plotted against outflow in Figure 3 and against X_2 in Figure 4 (both on page 9). The species show important differences in response of computed habitat area to changes in outflow or X_2. For example, computed habitat areas for striped bass and delta smelt increased rapidly as X_2 moved downstream of 100 km, but the habitat area for longfin smelt and *C. franciscorum* changed little until X_2 was below 80 or 90 km. At X_2 below about 60 km, habitat areas for striped bass and delta smelt leveled off or declined, while those for longfin smelt and *C. franciscorum* increased continuously.

If surface area of optimal salinity habitat is an important contributor to survival in estuarine species and if the method described above for estimating this area is reliable, then variation in computed habitat area of the limiting life stage should explain a significant portion of the observed variation in annual abundance indices for these species. The relationship between abundance and habitat area was examined for the ten species by linear regression analysis of annual indices of abundance on annual indices of optimal monthly salinity habitat area. Annual indices of optimal monthly salinity habitat area were computed by weighting monthly habitat areas by the average proportion of the limiting life stage present in each month (Table 1). Thus, the annual habitat area indices give weight to habitat area according to the presumed relative importance to the species of the month in which the habitat area was present. The proportions of the limiting life stage present in each month were computed from DFG survey data (Baxter, Hieb, Mecum, Sweetnam, pers comm).

Regressions were significant ($p<0.05$) for all the species whose limiting life stages inhabit relatively fresh

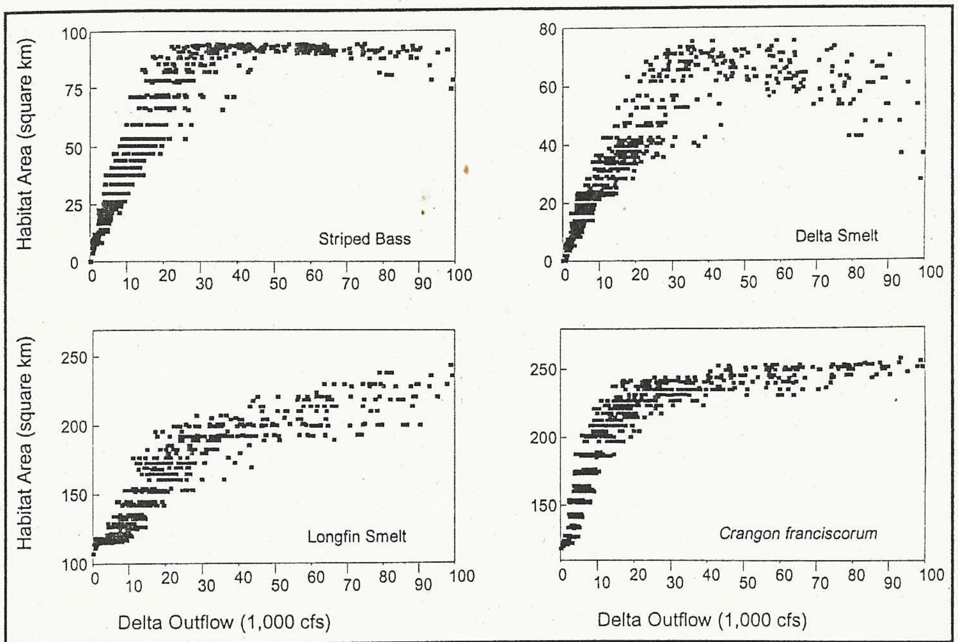

Figure 3
OPTIMAL SALINITY HABITAT AREA AS A FUNCTION OF DELTA OUTFLOW

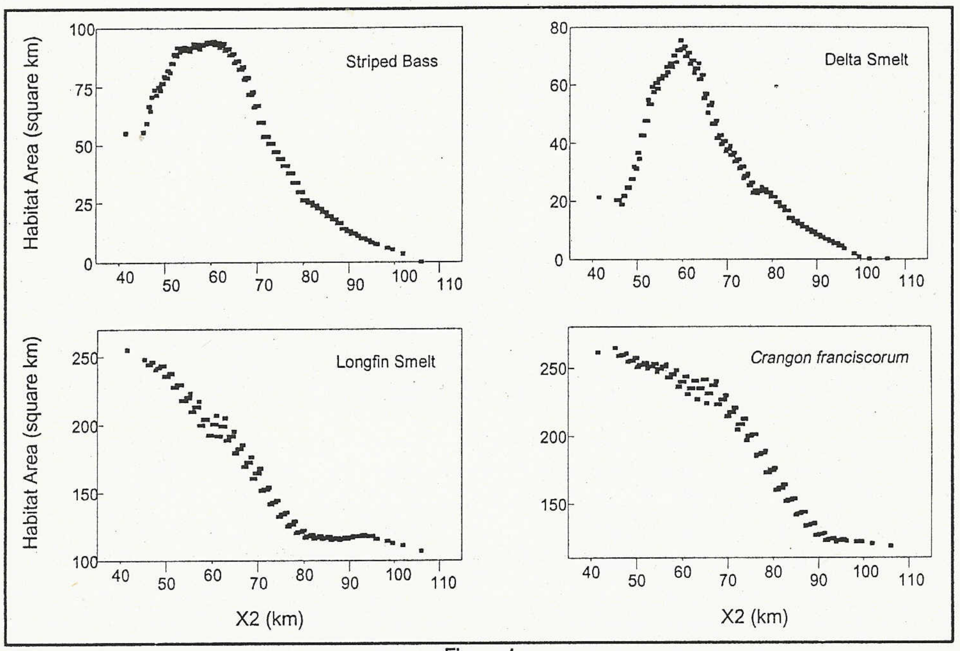

Figure 4
OPTIMAL SALINITY HABITAT AREA AS A FUNCTION OF X_2

or brackish water, except delta smelt (Table 2). The regression for delta smelt gave a p-value of 0.08, which is close to the significance level. Regressions were not significant for all the more marine species, presumably because abundance of these species is determined largely by habitat conditions in the ocean (Baxter, Hieb, pers comm).

Table 2
COEFFICIENTS OF DETERMINATION AND REGRESSION EQUATIONS FOR SELECTED SPECIES

Species	r2	Regression Equation*
Striped bass	0.43	Y = 1.189 + 0.784 (OSHA)
Delta smelt	0.13	Y = 2.377 + 0.008 (OSHA)
Longfin smelt	0.70	Y = 0.393 + 0.016 (OSHA)
Starry flounder	0.57	Y = -1855.737+ 15.435 (OSHA)
C. franciscorum	0.75	Y = -272.923+2.304 (OSHA)

* OSHA = Optimal Salinity Habitat Area
For striped bass, Y = 38-mm index.
For delta and longfin smelt, y = Log10(MWT index).
For starry flounder, Y = Log10(following year's bay survey yearling index.
For *C. franciscorum*, Y = Bay survey juvenile index.

Conclusions

The method described for quantifying optimal salinity habitat surface area should be useful for predicting optimal salinity habitat area available at a given flow and for evaluating salinity habitat conditions of any estuarine species whose optimal salinity range is known. Hieb and Baxter (1993) presented results of analyses relating abundance of three estuarine species to estimated optimal salinity habitat area. They estimated habitat area by extrapolating from measured salinities. The method presented here relies on general relationships between outflow and salinity and, therefore, can be used to predict habitat area from outflow.

Statistically significant relationships have been demonstrated between abundance indices of the species listed in Table 2 and outflow or X_2 (*eg*, see Jassby 1992). Optimal salinity habitat area of these species also generally increases with increased outflow (*ie*, reduced X_2) (Figures 3 and 4). The effect of habitat area on species abundance is difficult to separate from effects of other factors related to outflow, such as residence time, nutrient input, sediment transport, transport of eggs and larvae, entrainment in diversions, and dilution of toxins. Nevertheless, the ability to quantify habitat area separately from other factors makes possible more refined analyses of the effects of outflow on estuarine species.

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Literature cited in this article is provided on page 10.

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Decline of the Opossum Shrimp, *Neomysis mercedis*

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Neomysis mercedis is an estuarine and freshwater shrimp native to the Pacific Coast from Alaska to below Santa Barbara. In the Sacramento-San Joaquin estuary, it is most abundant in the entrapment zone but ranges from fresh water to near-oceanic salinity. *Neomysis* is eaten by the bay shrimp *Crangon franciscorum*, the oriental shrimp *Palaemon macrodactylus*, and many fish species including striped bass and delta smelt. Because of its importance to fish, DFG has monitored *Neomysis* abundance since June 1968. Abundance has declined greatly over the years, especially during the 1987-1992 drought (Figure 1). Abundance is now so low that *Neomysis* is unlikely to be a significant food resource for striped bass or any other fish or invertebrate species.

Several factors can explain the decline, but food limitation caused by reduced phytoplankton concentrations is the most probable. Correlations between abundance and chlorophyll *a* are significant and curvilinear in all seasons for the 1968-1993 period (Figure 2), providing statistical evidence for food limitation. R-square analyses for each season for 1972-1993 using chlorophyll *a*, outflow, outflow squared, temperature, and logs of rotifers and copepods showed that only chlorophyll *a* explained a significant amount of the variance in abundance (Table 1).

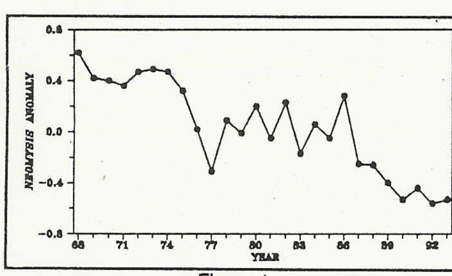

Figure 1
NEOMYSIS ABUNDANCE ANOMALIES, MARCH-NOVEMBER, 1968-1993

Abundance anomalies are logs of numbers/m³ corrected for salinity and month.

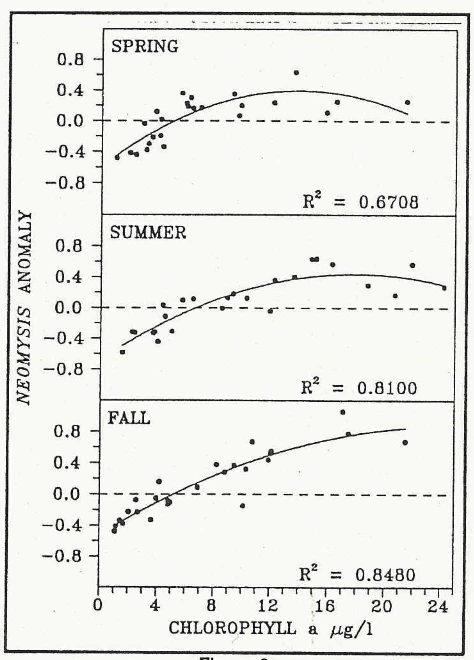

Figure 2
ABUNDANCE ANOMALIES VERSUS CHLOROPHYLL *a*, 1968-1993

If low phytoplankton concentrations are limiting *Neomysis*, this limitation would probably cause lower juvenile growth rates. This would result in smaller adults and, because brood size depends on female size, egg production would be lower. Adults may also be directly affected by food limitation because one of their food sources, rotifers, has declined over the years. The other food source, copepods, has remained high due to the introduction of exotic copepods.

In support of the food limitation hypothesis, adult females were smaller in July and August during 1989-1993, years of very low chlorophyll *a* concentrations (Figure 3). This indicates juvenile growth rates were lower, but brood size of females was not lower in these years when effects of length on brood size was corrected for. This indicates adults were not food limited. Since small mysids are more dependent on phytoplankton than adults are, the results are reasonable. Birth rates, as measured by neonate (newly released young) abundance, were lower from 1987-1993 as compared to earlier periods. The birth rates were particularly reduced in fall the variance in abundance (Figure 4).

Other factors that could have caused the abundance decline are high temperature, rice herbicides, and export pumping. Mortality from high temperature would be expected only