the list for Cell 1. The commensals prevalent in Cell 4 are small clams and crabs associated with the ghost shrimp. Figure 31 shows that Cell 4 had many more infaunal taxa than epifauna or epiflora, and also more infauna than Cell 1.

Comparisons were made among sand beaches in Cell 1 (segments 56, 98, 107), Cell 2 (segments 125, 138, 147), and Cell 3 (segments 153, 159, 167) which are shown on Figures 32-34, and Table 8. The MDS plot shows that the sample points grouped separately with the Cell 1 points arranged vertically along the right side of the plot, Cell 2 points arranged vertically along the left side of the plot, and Cell 3 point arranged horizontally. A high global R-value and a low significance level support the observed difference. The results of pairwise tests are also shown and we note that Cells 1 and 3 are more similar than either Cells 1 and 2, or Cells 2 and 3. This is probably due to the high volume of fresh water input from Burley Lagoon which eliminated the sand dollar from the nearshore community. Without this active bioturbator the community structure shifts significantly. The similarity lists from the SIMPER analyses show *Dendraster excentricus* and ulvoids dominating the community in Cell 1 (85% combined contribution), *Spiochaetopterus costarum*, unidentified clam holes, and the burrowing anemone *Edwardsia sipunculoides* dominating Cell 2 (69% combined contribution), and *Dendraster excentricus* and the polychaete *Scoloplos armiger* dominating the community in Cell 3. From these lists, the only shared organism is the sand dollar in Cells 1 and 3. Figure 33 shows that the 3 sample groups are uniformly different in trophic class distribution with suspension feeders dominating in Cell 3, deposit feeders dominating in Cell 2, and carnivores dominating in Cell 1.

The analysis results for cobble beach communities in different nearshore cells are shown on Figures 35-37, and Table 9. Although only 2 samples were made in Cell 4, the MDS plot clearly shows the separation between groups of points representing Cells 1 and 4. The test for group difference is not significant but the high global R-value suggests that a difference exists. SIMPER analysis was not possible with only 2 samples in Cell 4. Figure 36 shows the trophic class distribution but note that any comparison should reflect that Cell 1 has 3 samples and Cell 4 has only 2 samples. In the discussion on species richness above, we showed that most of the taxa are accounted for in the first 30 samples so a difference of 10 samples between Cell 4 and Cell 1 will make a big difference in any frequency distributions.

Nearshore cells within a basin

The results from the 1997 study in Carr Inlet, and the 1998 analysis of modeled predictions, show that extrapolation of communities can be done with a high degree of reliability within nearshore cells (60%), but with mixed results when extrapolating among cells within a bay. The latter finding is likely caused by the steep gradients of salinity, water temperature, and wave energy within a bay, all creating a high diversity of physical heterogeneity among beaches in a small area. Conditions among nearshore cells in different bays may in some cases be more similar than within bays, which is the reason for carefully quantifying the nearshore ocean so that meaningful comparisons can be made among similar physical conditions over large spatial scales. For this analysis we

Community analysis of within-bay variation for sand beaches in Carr Inlet, South Puget Sound

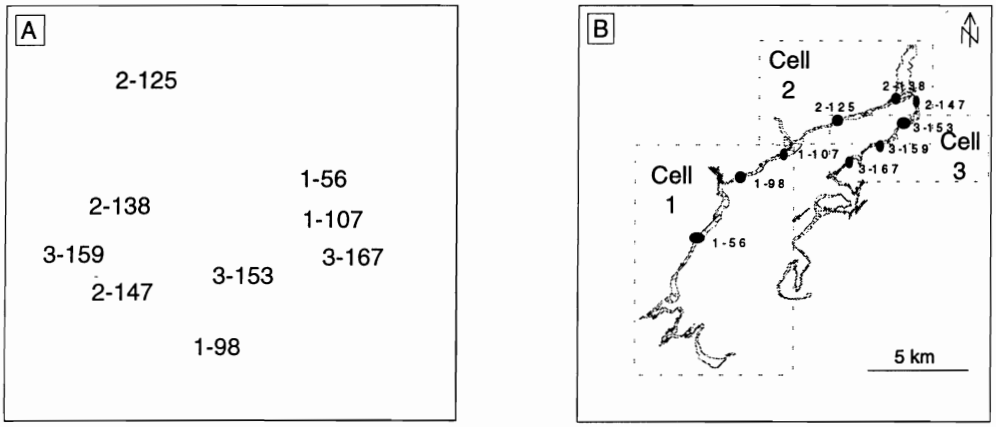

Figure 32. Analysis of sand beach biota within Carr Inlet. MDS ordination of community data collected from Segment Group 20 (107, 98, and 56 in Cell 1), Segment Group 21 (125, 138, and 147 in Cell 2), and Segment Group 11 (153, 159, and 167 in Cell 3) to assess within-bay variation, (stress=0.10). One-way ANOSIM with 280 permutations, global R=0.56 sig. level=6%; (pairwise tests with 10 permutations each: Cell 1 vs. Cell 2 sig. level=20%, Cell 1 vs. Cell 3 sig. level=80%, Cell 2 vs. Cell 3 sig. level=20%).

Table 8. Taxa contributing the most to within cell similarity (ranked by percent contribution). Listed taxa are the best indicator organisms for the cell group. The single taxa common to Cells 1 and 3 is highlighted in bold.

A. 1997 Cell 1 samples

Taxa (3 of 13)	%	Cum%
Dendraster excentricus	45.39	45.39
Ulvoids	39.84	85.23
Polysiphonia sp.	14.77	100

B. 1997 Cell 2 samples

Taxa (9 of 18)	%	Cum%
Spiochaetopterus costarum	32.69	32.69
Unid. clam holes	27.41	60.1
Edwardsia sipunculoides	8.64	68.74
Nephtys ferruginea	8.37	77.11
Notomastus lineatus	6	83.11
Gracelaria pacifica	5.05	88.16
Leptosynapta clarki	3.95	92.11
Punctaria lobata	3.95	96.05
Neotrypaea californiensis	3.95	100

C. 1997 Cell 3 samples

Taxa (2 of 16)	%	Cum%
Dendraster excentricus	79.12	79.12
Scoloplos armiger	20.88	100

Within-bay sand beach community variation for Carr Inlet Cells 1, 2, and 3

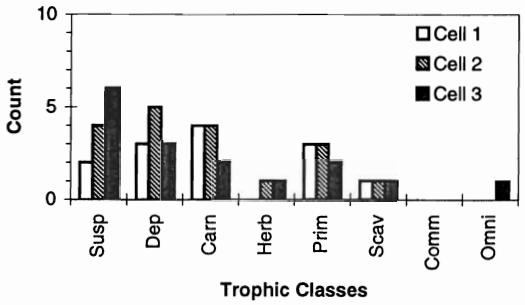

Figure 33. Community distribution by trophic class for Cells 1, 2 and 3 sand beach quadrat and core samples.

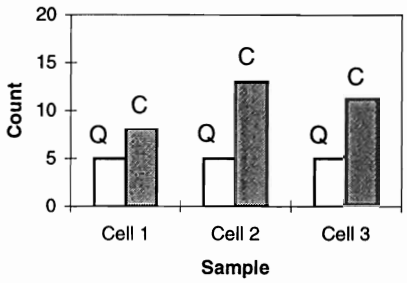

Figure 34. Comparison of organism counts by epifauna and epiflora (Q) and infauna (C). Total count=24 taxa, with 13 in Cell 1, 18 in Cell 2, and 16 in Cell 3. There are 9 taxa common to Cells 1 and 2, and 5 taxa common to Cells 1 and 3.

Community analysis of within-bay variation for cobble beaches in Carr Inlet, South Puget Sound

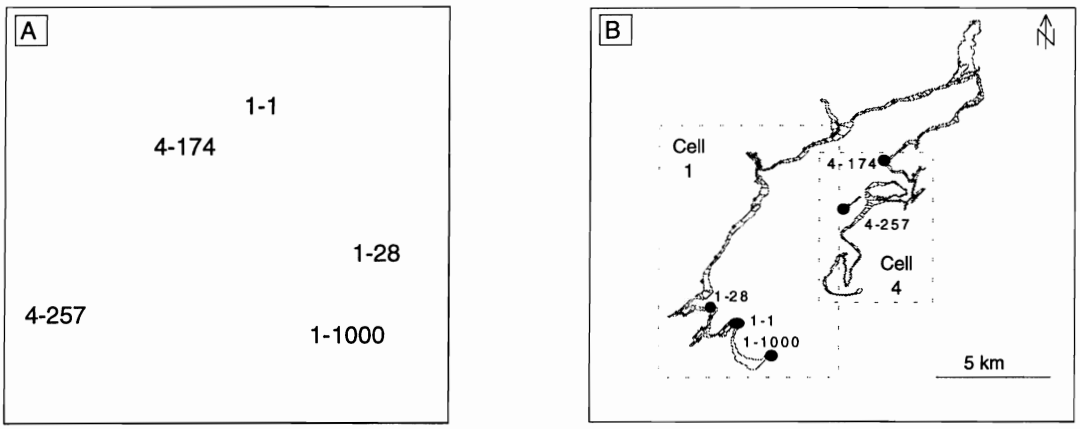

Figure 35. Spatial variation of cobble beach biota within Carr Inlet (A). MDS ordination of community data collected from Segment Group 56 (Cell 1) and Segment Group 55 (Cell 4) to assess within-bay variation (B), (stress=0.00). One-way ANOSIM with 10 permutations, global R=0.58, sig. level=10%.

Table 9. Taxa contributing the most to within group similarity (ranked by percent contribution). Listed taxa are the best indicator organisms for the Cell group.

A. 1997 Cell 1 samples			B. 1998 Cell 4 samples		
Taxa (13 of 24)	%	Cum%	Taxa	%	Cum%
Notomastus tenuis	12.86	12.86	**(not enough replicates)**		
Ulvoids	12.38	25.24			
Balanus glandula	11.36	36.6			
Ophiodromus pugettensis	10.3	46.9			
Hemipodus borealis	9.96	56.86			
Crepidula dorsi	9.37	66.23			
Micropodarki dubia	8.59	74.82			
Glycinde picta	8.03	82.86			
Cancer sp.	4.96	87.82			
Acrosiphonia sp.	4.01	91.83			
Unid. red crust	2.91	94.74			
Unid. Nemertea	2.82	97.55			
Nereis procera	2.45	100			

Within-bay cobble beach community variation for Carr Inlet Cell 1 and Cell 4

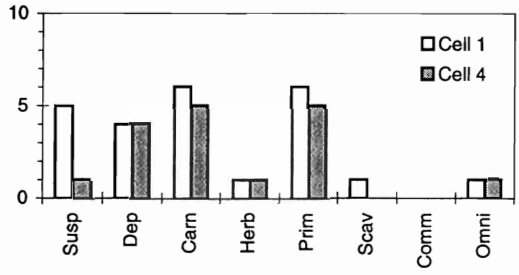

Figure 36. Community distribution by trophic class for Cell 1 cobble beach quadratand core samples.

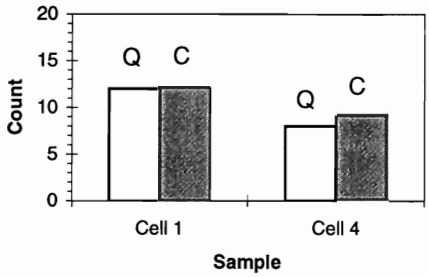

Figure 37. Comparison of organism counts by epifauna and epiflora (Q) and infauna (C). Total count=26 taxa, with 24 in Cell 1, 17 in Cell 4, and 15 taxa common to both Cells.

were interested in comparing the community structure of Carr Inlet biota to other geophysically similar beaches in Case and Budd Inlets in South Puget Sound. The results of the nested ANOVA tests were used to evaluate at which scales the variability of individual populations became significantly large.

The results of the comparison among mud beach segments from cells in Carr, Case, and Budd inlets are shown in Figures 38-40, and Table 10. The MDS plot shows the distribution of samples to be separated by nearshore cell. The 3 samples from Carr Inlet are grouped vertically along the right side of the plot, the Case Inlet samples are arranged horizontally across the top the plot, and the Budd Inlet samples are along the left side of the plot. Note that Budd Inlet samples 18 and 20 are separate from 101 and 19. We expected samples 18, 19 and 20 to be separate from the others because of the differences in physical conditions. The head of Budd Inlet is warmer, less saline, and more stratified (and probably more polluted) than any other nearshore cell. Sample 19 was taken from a beach covered with sandy dredge spoils, thus the community structure was expected to differ from the adjacent samples. Sample 101 was made in the boat basin of Boston Harbor where the water temperature is colder, more saline, and less stratified, thus the community was expected to be closer to those found in Carr and Case Inlets. The Case Inlet sample 12 is also separate from the others. This is the mud beach segment supporting an aquaculture operation and the surface biota was dominated by taxa found with oyster shells. Also this beach had been tilled for clams a year prior to the sampling. The global R-value is fairly low suggesting that the significance level is reliable. The high number of permutations also indicates that the test is meaningful. Therefore, the 3 cells do not show a significant difference, but the significance level is low enough to cast doubt on any conclusions of ecological similarity. Pairwise tests show that samples in the nearshore cells of Carr and Case Inlets are more similar than either one is to samples in the Budd Inlet cell.

SIMPER results strongly support this as shown by the list of taxa contributing to within group similarity. In Budd Inlet, only 6 of 14 taxa contribute to within group similarity, while in Carr Inlet there are 11 out of 33, and for Case there are 12 out of 32. Juvenile clams, *Mediomastus sp.*, ulvoids, unidentified clam or ghost shrimp holes, and *Punctaria lobata* dominated the samples in Carr Inlet (74% combined contribution). In Case Inlet, *Nereis procera*, unidentified clam or ghost shrimp holes, and ulvoids dominate the community structure (51% combined contribution). Budd Inlet mud samples are dominated by unidentified clam or ghost shrimp holes, a commensal crab *Scleroplax granulata*, and the clam *Macoma nasuta* (70% combined contribution).

The nested ANOVA tests showed that the variability for 8 out of 29 population abundances was not significant at any of the 3 scales of comparison, so that these taxa abundances can be scaled up from segment samples to all 9 beaches in the 3 nearshore cells of Carr, Case, and Budd Inlets.

The results of comparisons among sand beaches in the 3 nearshore cells of Carr, Case, and Budd Inlets are shown on Figures 41-43, and Table 11. The MDS plot shows that the

Community analysis of among-bay variation for mud beaches in South Puget Sound

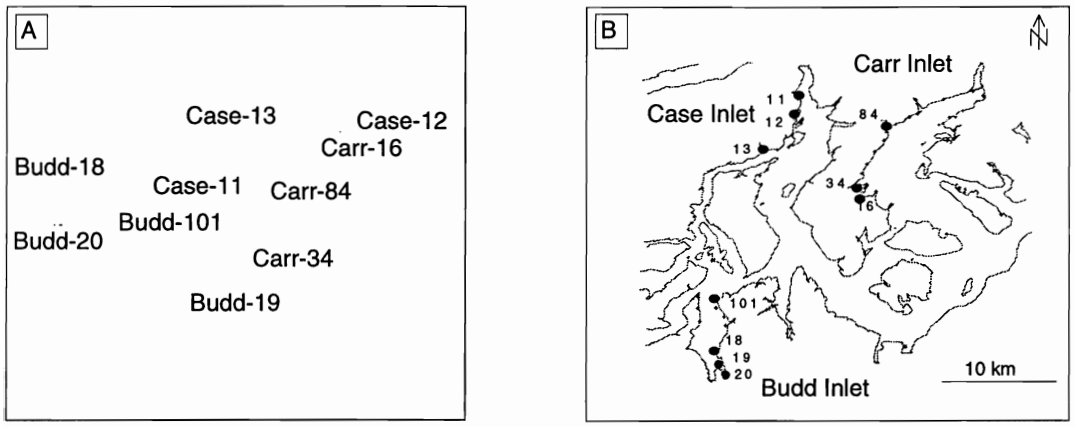

Figure 38. Analysis of mud beach biota among bays in South Puget Sound. MDS ordination of community data collected from locations shown in Carr, Case, and Budd Inlets to assess spatial variation, (stress=0.13). One-way ANOSIM with 280 permutations, global R=0.30, sig. level=8%; (pairwise tests with 10 permutations each: Carr vs. Case sig. level=50%, Carr vs. Budd sig. level 10%, Case vs. Budd sig. level=30%)

Table 10. South Puget Sound mud beach taxa contributing the most to within bay similarity (ranked by percent contribution). Listed taxa are the best indicator organisms for each bay group. Indicator taxa common to Carr and Case Inlets and indicator taxa common to Carr and Budd Inlet are highlighted in bold. S, C, and B refer to fully nested ANOVA tests of fourth root transformed taxa abundances within segment, within cell, and among bays respectively, where (n) indicates no significant difference, (+) indicates p-values < 0.05, and (*) indicates p-values<0.01 (degrees of freedom=36, 6, and 2). Totals refer to the number of non-significant p-values.

Carr Inlet						Case Inlet						Budd Inlet					
Taxa (11 of 33)		%	Cum%	S	C	B	Taxa (12 of 32)	%	Cum%	S	C	B	Taxa (6 of 14)	%	Cum%	S	C	B
Juvenile macoma		16	16	n	*	n	*Nereis procera*	20	20	n	n	*	**Unid. clam or shrimp holes**	44	44	n	*	n
Mediomastus sp.		15	31	n	n	*	**Unid. clam or shrimp holes**	18	38	n	*	n	*Scleroplax granulata*	14	58	n	*	n
Ulvoids		15	46	n	*	n	**Ulvoids**	13	51	n	*	n	*Macoma nasuta*	13	70	n	*	n
Unid. clam or shrimp holes		15	61	n	*	n	*Nassarius mendicus*	9	60	n	*	n	*Cryptomya californica*	10	80	n	*	n
Punctaria lobata		13	74	n	n	n	*Hemigrapsus oregonensis*	7	67	n	*	n	*Glycinde picta*	10	90	n	n	n
Leitoscoloplos pugettensis		5	80	+	n	n	*Nephtys caecoides*	6	72	n	n	n	*Pinnotherid sp.*	10	100	n	*	n
Protothaca staminea		5	84	n	n	n	Unid. Nemertea	6	78	n	n	n						
Spiochaetopterus costarum		4	89	+	*	n	***Spiochaetopterus costarum***	5	83	+	*	n						
Clinocardium nuttallii		4	93	+	n	+	**Juvenile macoma**	5	88	n	*	n						
Haminoea vesicula		4	97	n	n	n	*Hemipodus borealis*	5	93	n	n	n						
Leptosynapta clarki		3	100	n	n	n	*Notomastus tenuis*	4	97	*	*	n						
							Tellina bodegensis	3	100	n	*	n						

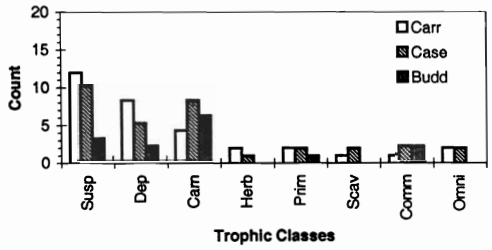

Figure 39. Community distribution by trophic class for comparison among mud beaches in South Puget Sound.

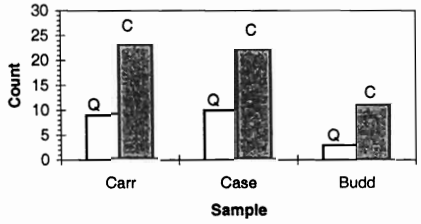

Figure 40. Comparison of organism counts by epifauna and epiflora (Q) and infauna (C). Total count=41 taxa, with 33 in Carr, 32 in Case, 14 in Budd Inlet. There are 23 taxa common to Carr and Case, and 10 taxa common to Carr and Budd Inlets.

Community analysis of among-bay variation for sand beaches in South Puget Sound

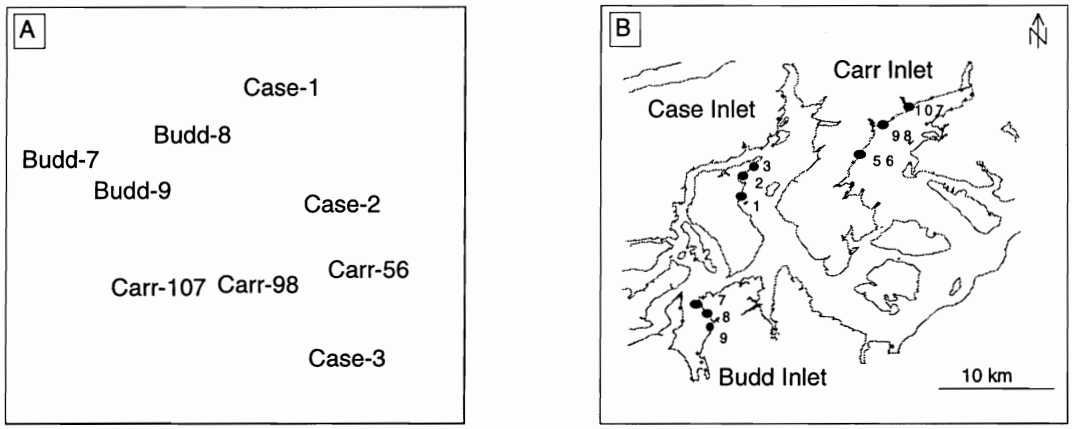

Figure 41. Analysis of sand beach biota among bays in South Puget Sound. MDS ordination of community data collected from locations shown in Carr, Case, and Budd Inlets to assess spatial variation, (stress=0.16). One-way ANOSIM with 280 permutations, global R=0.45, sig. level=4%; (pairwise tests with 10 permutations each: Carr vs. Case sig. level=50%, Carr vs. Budd sig. level=10%, Case vs. Budd sig. level=10%.).

Table 11. South Puget Sound sand beach taxa contributing the most to within bay similarity (ranked by percent contribution). Listed taxa are the best indicator organisms for each bay group. Indicator taxa common to Carr and Case Inlets and indicator taxa common to Carr and Budd Inlet are highlighted in bold. S, C, and B refer to fully nested ANOVA tests of fourth root transformed taxa abundances within segment, within cell, and among bays respectively, where (n) indicates no significant difference, (+) indicates p-values < 0.05, and (*) indicates p-values<0.01 (degrees of freedom=36, 6, and 2). Totals refer to the number of non-significant p-values.

Carr Inlet						Case Inlet						Budd Inlet					
Taxa (9 of 16)	%		Cum%	S	C	B	Taxa (3 of 13)	%	Cum%	S	C	B	Taxa (8 of 14)	%	Cum%	S	C	B
Dendraster excentricus	24		24	n	n	n	**Ulvoids**	56	56	n	n	n	*Balanus glandula*	24	24	n	n	*
Ulvoids	24		48	n	n	n	***Dendraster excentricus***	34	91	*	*	n	*Hemigrapsus oregonensis*	17	41	n	*	n
Notomastus tenuis	9		57	n	n	n	***Nephtys caeca***	9	100	n	n	n	***Dendraster excentricus***	17	57	*	*	n
Neotrypaea californiensis	9		65	*	n	n							*Armandia brevis*	15	72	n	n	+
Glycinde picta	8		74	n	n	n							**Ulvoids**	15	87	n	n	n
Nephtys caeca	8		81	n	n	n							*Nassarius mendicus*	5	92	n	n	n
Polydora kempi japonica	6		88	*	n	n							*Clinocardium nuttallii*	4	97	n	n	n
Spiochaetopterus costarum	6		94	n	*	n							Juvenile macoma	3	100	n	n	n
Unid. clam holes	6		100	+	*	n												

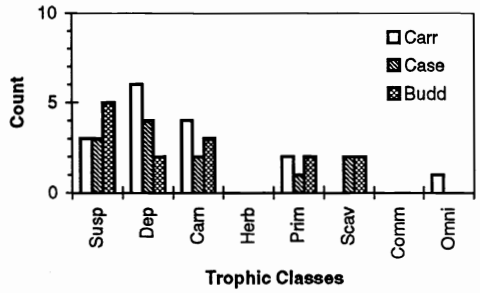

Figure 42. Community distribution by trophic class for comparison among sand beaches in South Puget Sound.

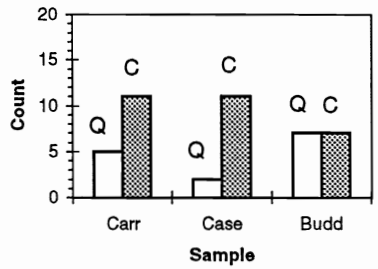

Figure 43. Comparison of organism counts by epifauna and epiflora (Q) and infauna (C). Total count=23 taxa, with 16 in Carr, 13 in Case, and 14 in Budd. There are 7 taxa common to Carr and Case, and 7 taxa common to Carr and Budd Inlets.

Budd Inlet sand beaches are tightly grouped and separate from the tightly grouped points for Carr Inlet. The Carr Inlet points are arranged linearly along the bottom of the plot, and the Budd Inlet points are clustered in the upper left portion of the plot. The Case Inlet points are not as tightly grouped but stay along the right side of the plot.

The ANOSIM test had enough permutations for a meaningful significance level but the global R-value is mid-range indicating that there are no clear similarities or differences in the sample groups. The pairwise tests show that the Carr and Case Inlet samples are more similar than Carr and Budd, or Case and Budd Inlet samples. There were no distinguishing characteristics of these beaches noted in the field to explain the group differences but the nearshore cell in Budd Inlet had lower salinities and higher water temperatures than either nearshore cells in Carr or Case Inlets (see Figure 10).

SIMPER results are listed on Table 11. Carr Inlet had 9 taxa out of 16 contribute to sample similarity, while Case Inlet had 3 of 13, and Budd Inlet had 6 of 14. The sand dollar *Dendraster excentricus* dominates the sand community in Carr, Case and Budd Inlets (33%, 34%, and 17% contribution, respectively), as do the ulvoids (32%, 56%, and 15% contribution, respectively).

The nested ANOVA tests showed that for 8 out of 18 population abundances, variability was not significant at any of the compared scales of observation. The trophic distributions (Figure 4.16C) showed no consistent patterns. Suspension feeders were highest in Budd Inlet and lowest in Carr, deposit feeders highest in Carr and lowest in Budd, carnivores highest in Carr and lowest in Case. There are 7 taxa common to Carr and Case, and 7 (different) taxa common to Carr and Budd.

The trophic distribution showed no consistent patterns. Suspension feeders were highest in Budd Inlet and lowest in Carr Inlet, deposit feeders highest in Carr and lowest in Budd, carnivores highest in Carr and lowest in Case Inlet. There are 7 taxa common to Carr and Case, and 7 (different) taxa common to Carr and Budd Inlets.

The results of the comparison of pebble beaches among nearshore cells are shown on Figures 44-46, and Table 12. The MDS plot shows that the Carr and Budd Inlet sample points overlap considerably and that the Case sample points stay horizontally along the bottom of the diagram. The mid-range global R-value indicates that the samples are not distinctly similar or different, even though the significance level is very low (1%). Despite this pattern, the pairwise tests show no greater similarities between any of the sample group pairs. This is an indication that the beaches and nearshore cells are well matched. The high number of permutations suggests that the significance levels are meaningful.

SIMPER results are shown on Table 12. The distinctive feature about these communities is their diversity and lack of dominating taxa. Note the large number of taxa represented on these lists. In Carr Inlet 63% of the taxa contribute to within nearshore cell similarity, in Case there are 77%, and in Budd Inlet there are 59%. The relatively small percentage

Community analysis of among-bay variation for pebble beaches in South Puget Sound

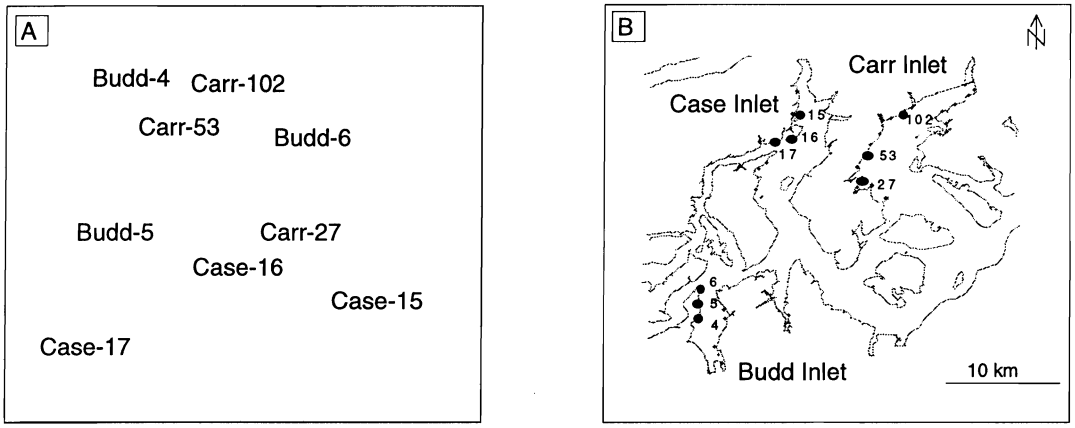

Figure 44. Analysis of pebble beach biota among bays in South Puget Sound (A). MDS ordination of community data collected from locations shown in Carr, Case, and Budd Inlets to assess spatial variation (B), (stress=0.16). One-way ANOSIM with 280 permutations, global R=0.45, sig. level=1%; (pairwise tests with 10 permutaions each: Carr vs. Case sig level=10%, Carr vs. Budd sig. level=10%, Case vs. Budd sig. level=10%.

Table 12. South Puget Sound pebble beach taxa contributing the most to within bay similarity (ranked by percent contribution). Listed taxa are the best indicator organisms for each bay group. Indicator taxa common to Carr and Case Inlets and indicator taxa common to Carr and Budd Inlet are highlighted in bold. S, C, and B refer to fully nested ANOVA tests of fourth root transformed taxa abundances within segment, within cell, and among bays respectively, where (n) indicates no significant difference, (+) indicates p-values < 0.05, and (*) indicates p-values<0.01 (degrees of freedom=36, 6, and 2). Totals refer to the number of non-significant p-values.

Carr Inlet						Case Inlet						Budd Inlet					
Taxa (25 of 40)	%		Cum%	S	C	B	Taxa (26 of 34)	%	Cum%	S	C	B	Taxa (22 of 38)	%	Cum%	S	C	B
Ulvoids		7	7	+	*	n	***Lottia pelta***	9	9	*	*	n	**Ulvoids**	8	8	+	*	n
Balanus glandula		7	14	+	*	n	***Balanus glandula***	9	18	+	*	n	***Hemigrapsus oregonensis***	8	15	n	*	n
Mytilus trossulus		6	20	n	*	n	***Hemipodus borealis***	8	25	n	*	n	Unid. red crust	7	23	n	*	+
Hemigrapsus oregonensis		6	26	n	*	n	***Notomastus tenuis***	7	33	n	*	n	***Pagurus sp.***	7	30	n	*	n
Mediomastus sp.		6	32	n	*	+	Unid. red crust	7	40	n	*	+	***Balanus glandula***	7	37	+	*	n
Armandia brevis		6	38	n	n	+	*Littorina scutulata*	7	46	*	*	n	*Mastocarpus papillatus*	7	43	*	*	n
Crepidula dorsata		6	43	n	n	n	**Juvenile macoma**	6	53	n	n	n	***Notomastus tenuis***	6	50	n	*	n
Lottia pelta		5	49	*	*	n	**Ulvoids**	6	59	+	*	n	***Leptosynapta clarki***	6	56	n	*	n
Pagurus sp.		5	54	n	*	n	***Leptosynapta clarki***	6	65	n	*	n	***Lottia pelta***	6	62	*	*	n
Notomastus tenuis		5	60	n	*	n	*Protothaca staminea*	3	68	*	n	n	***Mopalia lignosa***	6	67	n	*	n
Spiochaetopterus costarum		5	65	n	*	n	*Ophiodromus pugettensis*	3	71	n	*	n	***Spiochaetopterus costarum***	5	73	n	*	n
Unid. clam holes		5	70	n	*	n	***Polysiphonia sp.***	2	74	n	*	n	Unid. Sabellid	5	78	n	n	+
Unid. Nemertea		5	75	n	n	n	*Edwardsia sipunculoides*	2	76	*	n	n	*Crepidula fornicata*	3	81	*	*	n
Hemipodus borealis		5	80	n	*	n	***Hemigrapsus oregonensis***	2	78	n	*	n	***Nassarius mendicus***	3	84	+	*	n
Unid.scale worm		4	84	n	*	n	***Alia gausapata***	2	80	n	*	n	***Alia gausapata***	2	86	n	*	n
Alia gausapata		2	86	n	*	n	***Crepidula dorsata***	2	83	n	n	n	**Unid.scale worm**	2	88	n	*	n
Mopalia lignosa		2	88	n	*	n	*Leitoscoloplos pugettensis*	2	85	+	n	n	***Mytilus trossulus***	2	91	n	*	n
Polysiphonia sp.		2	90	n	*	n	***Mytilus trossulus***	2	86	n	*	n	***Crepidula dorsata***	2	93	n	n	n
Onchidoris bilamellata		2	92	n	*	n	***Lophopanopeus bellus***	2	88	n	*	n	Clinocardim nuttallii	2	95	n	n	n
Juvenile macoma		2	93	n	n	n	*Notomastus lineatus*	2	90	n	n	n	***Hemipodus borealis***	2	97	n	*	n
Lophopanopeus bellus		1	95	n	*	n	*Mastocarpus papillatus*	2	92	*	*	n	**Unid. Nemertea**	2	99	n	n	n
Nereis procera		1	96	+	*	n	*Scytosiphon lomentaria*	2	94	*	*	n	***Terebellid sp.***	1	100	n	+	n
Leptosynapta clarki		1	98	n	*	n	***Spiochaetopterus costarum***	2	95	n	*	n						
Terebellid sp.		1	99	n	+	n	***Nereis procera***	2	97	+	*	n						
Nassarius mendicus		1	100	+	*	n	**Unid. clam holes**	2	99	n	*	n						
							Pagurus sp.	1	100	n	*	n						

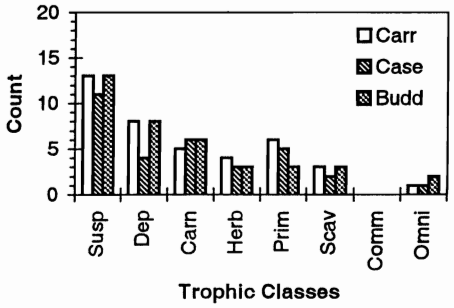

Figure 45. Community distribution by trophic class for comparison among pebble beaches in South Puget Sound.

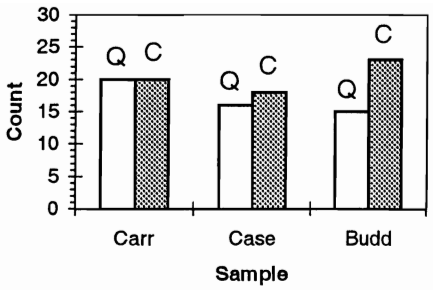

Figure 46. Comparison of organism counts by epifauna and epiflora (Q) and infauna (C). Total count=47 taxa, with 40 in Carr, 34 in Case, and 38 in Budd. There are 27 taxa common to Carr and Case, and 31 common to Carr and Budd Inlets.

that each taxa contributes to within sample group similarity indicates there are no distinct dominants. The highest taxa in Carr is ulvoids (7% contribution), in Case it is the limpet *Lottia pelta* (9% contribution), and in Budd it is also ulvoids (8% contribution). In Carr Inlet, 12 taxa are required to accumulate a combined contribution of 70%, in Case there are 11 taxa, and in Budd Inlet there are also 11 taxa. Taxa from the Carr Inlet samples can be extrapolated to the other nearshore cells with 17 of the 25 indicator taxa (68%) in Carr Inlet also appearing in Case and Budd Inlets where they comprise 65% and 77% of those indicator taxa, respectively.

The lack of any dominantly abundant taxa makes it difficult to show quantitative similarity among these communities. This is also reflected by the nested ANOVA tests which show that most of the population abundances are not significantly different within segments (68%), but most are different among the segments in each nearshore cell (73%), and at the among nearshore cells scale most taxa are not different (89%). So population abundances on pebble beaches in South Puget Sound vary more from beach to beach than either within a beach or among bays even though the community members are very similar.

The trophic distributions (Figure 4.16E) are fairly consistent among bays with suspension feeders and deposit feeders highest in Carr and Budd, carnivores highest in Case and Budd, and primary producers highest in Carr and Case Inlets. Carr Inlet had an equal number of taxa found in quadrats and cores while Case and Budd had more taxa found in core samples than quadrats (Figure 4.16F). There were 47 total taxa found among all the pebble samples, with 27 common to Carr and Case, and 31 common to Carr and Budd Inlets.

Discussion

Communities among physically similar, replicate beach segments in one nearshore cell of Carr Inlet showed a high degree of similarity for each of the habitats sampled. Communities among replicate beach segments sampled both in 1997 and 1998 in Carr Inlet also showed a high degree of similarity within years. All communities changed to some extent among years, but often these shifts were in the same direction in all segments, suggesting parallel community responses to physical and biological interactions. The 1997 study in Carr Inlet showed that, for all 3 habitat types in Carr Inlet, the communities sampled from replicate beaches were different in nearshore cells with different water properties, thus supporting our hypothesis of the importance of nearshore cell conditions. In the small bays of South Puget Sound, it is difficult to find matching nearshore cells in the same bay because of the steep gradients in salinity, water temperature, and wave energy. But nearshore cells from different bays may in some cases be more similar than those within a bay, thus arguing for carefully quantifying properties of the nearshore ocean so that meaningful comparisons can be made over large spatial scales. We showed that biotic communities are similar among replicate beach segments in different bays if the nearshore cells have similar water properties.

Rahel (1990) argued that assessments of community persistence are appropriate only among comparable spatial, temporal and ecological resolutions. Communities are most persistent or stable when the absolute abundance of each taxon remains the same over scales of space and time. The data presented here show this most closely at the within-cell, within-year scale on sand and mud habitats. A lower level of stability would involve taxa abundances fluctuating but the relative rankings in the community staying the same. This occurred at the within-cell and among-year scale on sand, mud, and cobble habitats. The lowest level of community stability is when the population abundances and rankings in the community fluctuate but the same taxa are always present. This was found for sand, mud, and especially pebble habitats at the spatial scale different bays, when the nearshore cells have similar water properties. The least stable condition occurs when the presence and absence of taxa cannot be predicted, such as shown here within Carr Inlet in the comparison among cells with different water properties.

Intertidal communities are often chosen for studies of biological interactions (among taxa) and bio-physical interactions (between taxa and the environment) because the intertidal zone has particularly strong gradients in space and time, thus creating complex systems within spatial scales that are easily sampled. But these gradients also cause physical heterogeneity at small spatio-temporal scales. In fact, within any given beach polygon that may be classified as a single habitat, physical factors often vary substantially at small spatial scales. Bell et al. (1993) argue against ever assuming environmental uniformity because environments are heterogeneous at all scales and the variance in physical conditions tends to increase indefinitely with distance. Therefore, the likelihood of an organism encountering a different environment as it moves away from its original location will increase. If this is the case for nearshore ecosystems then generalizations about biotic communities and populations become increasingly inappropriate with distance.

Using SCALE

We have shown that water quality measurements need to be made at a high spatial resolution and preferably with a time series. The single point samples made by the Department of Ecology are not adequate for this type of mapping. We have also shown that identifying replicate beach segments does not work very well when the selections are arbitrarily made, and not based on the SCALE method of continuous shore segmentation, segment aggregation, and random selection from a replicate groups. Thus, we recommend that SCALE be implemented as a large spatial scale strategy to ensure sample comparability.

Indicator taxa

Every organism sampled has an indicator value [Dufrene, 1997 #11] calculated from its sampled abundance and frequency of observation. Organisms with high values are thus more characteristic of that habitat than those with low values. This is somewhat different from the "indicator taxa" calculated by the SIMPER program, which are the species most similar in indicator value among the segments sampled in a nearshore cell. The SIMPER

indicator taxa are those that make the segments similar. The other taxa found, but not appearing on the SIMPER lists, are those that make the segments dissimilar.

Species-area curves

Our analyses allowed an evaluation of how well the sampling protocol represents each habitat type. The discussion above indicates the low odds of finding exact duplicate communities even on replicate beach segments. But we were interested in how many beaches need to be sampled before the species-area curve reaches a maximum. We found that sampling communities on only two replicate beaches reveals a number of different species, since there is still a steep slope between 10 and 20 samples on the species-area curve. Thus it is difficult to compare only a few replicates in either space or time. But sampling over three segments is evidently sufficient to capture most of the species richness within a habitat type, especially for sand and mud beaches. This is only marginally true for the species-rich pebble beaches, leading to the poor performance of the nested ANOVAs; even though most of the taxa were similar among segments within the same nearshore cell. But when taxa abundances are considered in the comparison, higher richness makes it harder to find community similarity with only three samples.

Annual variation

Because all 3 habitat types showed changes over time, we know that (using the sampling protocols described here) there will be temporal variation at all spatial scales. However, it is useful to note that the annual variation for mud and sand segment communities is the same order of magnitude as the variation among segments. Only the cobble segments showed considerably more annual variation than the among segment differences. This is probably due to the diversity and high abundance of surface taxa which are more likely to change from year to year. In the nearshore systems that we have studied, most (95%) of the taxa broadcast propagules into the ocean. These are then carried by the prevailing currents to a location suitable for settlement and recruitment. As these propagules are transported, the chance of finding a suitable habitat for settlement becomes increasingly remote. Taxa have different tolerances for environmental variance, confounding our ability to make predictions about biotic communities in new places.

Simultaneous community shifts occurred through time on the mud and cobble beaches. A change was also detected on sand beaches in Carr Inlet, but segment 98 did not respond as strongly as segments 107 and 56, possibly because of the ground water seep found there. This is one indication of how sensitive the data are to detecting and explaining differences in community structure from predicted values. Interpretation of the ordination plots shows that when a community response to an event is manifested across all the samples simultaneously, then the cause is likely to be at scales larger than the area (or time) encompassed by the samples (e.g. the mud and cobble comparisons). When the response is not reflected by all the samples simultaneously, then the cause is likely to be at scales less than the area (or time) encompassed by the samples (e.g. the sand comparisons).

Model validation

The data show that the biota from mud and sand sample groups within a nearshore cell cluster tightly together. The mud segment communities would have grouped even tighter if segment 74 was classified correctly. Considering the general variability of sand communities regardless of spatial scale, the results of the validation were impressive. But the results are probably due to the dominance of *Dendraster* which forced community similarity by eliminating other organisms through the bioturbation of sediments.

Nearshore cells within a bay

Finding replicate nearshore cells within bays is difficult because of the steep gradients in water properties inherent to small estuaries. These gradients create a high degree of physical heterogeneity in a small area. Differences in water temperature, salinity, and circulation/stratification caused very clear differences among the mud beach segments in Nearshore Cells 1 and 4 in Carr Inlet. Differences found among sand beaches in Nearshore Cells 1, 2, and 3 can also be explained by nearshore ocean gradients. Thus within an inlet, the biota tightly reflect differences in nearshore water properties. Greater variation was detected within the mud and sand habitats than within the cobble habitats. This is probably because of aquaculture, subsistence, and recreational uses of these beaches, and a tendency for sand and mud communities to be radically altered by the presence (or absence) of a major bioturbator (*Dendraster* or *Neotrypaea*).

Nearshore cells within a basin

At the largest scale of our comparisons we found that mud beaches represent a relatively small percentage of the shoreline, and they tend to occur in the most sheltered parts of bays which are often the most developed (i.e. disturbed). These factors make finding comparable segments difficult over large scales of space and time. Sand beaches are also, in general, highly disturbed and should be avoided for change detection monitoring. Many of the sand beaches are used for commercial shellfish harvest and recreation. The nearshore wave energy of South Puget Sound is high enough to move sand size particles. Pebble and cobble beaches are relatively stable because wave energy high enough to move these grain sizes is infrequent over the time scales experienced by the biota. But sand grains are moved frequently (note transverse ripples on the sand flats in Carr Inlet), with the largest amount of sediment transport occurring in the winter, creating disturbances that are manifested seasonally and annually.

On-going mapping may show that pebble beaches are the most frequent and spatially extensive habitat in Puget Sound. If this is the case, then they become a strong candidate for monitoring. These beaches have high biotic diversity and no strong signal (dominance) from any specific taxa. In other words, no single taxon is driving the segment to segment similarity. Although we found the communities to show significant differences among inlets, this is probably due to the large number of taxa involved. Basically there are so many taxa that every pebble beach sampled was different when organism abundance was considered. Greater similarity would result for among segment comparisons if the data were transformed to presence/absence, but there would also be a loss of ecological resolution. This loss may be balanced by the high number of taxa in the pebble segment communities, thus retaining sensitivity to habitat change.

CONCLUSIONS

The objective of this study was to test for a deterministic organization of communities among replicate soft-sediment beach segments in South Puget Sound. We hypothesized that benthic communities of macroalgae and invertebrates should be similar within groups of segments that are "replicates" in terms of having similar geophysical characteristics. The results support this hypothesis; reducing physical and chemical differences among biological sample sites reduces the environmental variation that inevitably results in biotic variation. Because the sampled communities show significant fidelity to their physical habitat type, we can scale up localized biological data to larger regions. But any attempt to force natural gradients into discrete categories is going to encounter problems since ecosystems are multidimensional continua (Bell et al., 1993). When we infer to larger spatial scales, the number of potentially interacting small scale spatial and temporal gradients can increase system complexity (Rastetter et al., 1992). Therefore, predictions about coarse-scale systems will not be able to retain the degree of detail and ecological resolution used in models of fine-scale systems. Our studies in Puget Sound have demonstrated that as we scale up our observations, we are adding new sources of variation to the data, and thus more statistical uncertainty. Predictions of community structure are most likely to be valid among replicate segments within the spatial range of nearshore cells with similar water properties.

Recommendations

Important issues have been identified by this study that need to be addressed by a large scale sampling program for detecting change in the health of Puget Sound.

Nearshore cells

What water quality attributes should be sampled? The purpose of measuring water temperature and salinity is to quantify gradients and the motion of water in the study estuaries. Locating and mapping the extent of persistent patterns in circulation is important because the ocean is likely to be a major force in controlling large spatial and temporal variability in nearshore communities. There are many properties of the ocean that could be measured to acquire this information but many co-vary in time, and at this point we can justify measuring the least expensive attributes (temperature and salinity). Once the persistent spatial and seasonal water patterns have been determined, then we can begin to evaluate boundary variability. The current methods rapidly and cheaply characterize circulation patterns and fulfilled our information requirements. Further decisions of which attributes to measure will need to be based on available resources. Continuous recordings of nutrients, chlorophyll, current speed and direction are candidates to be considered.

The current program by the Department of Ecology for monitoring water quality in Puget Sound is adequate for identifying seasonal patterns in ocean temperature and salinity, and proved valuable for this study by showing that nearshore sampling should consider

differences between the winter mixed period, the summer stratification period, and the spring and fall transition periods. Comparisons among replicate beach segments should be made only within one of these periods and not across periods.

How should a monitoring program account for the temporal variability of nearshore cell boundaries? We have shown that taxa on replicate beaches are more similar within years than among years. This is likely to reflect spatial and temporal changes in propagule distribution caused by regional and local effects of the ocean. While the exact boundaries between nearshore cells may vary seasonally, annually, and even episodically (e.g. following a rain storm), the physics that establish the relative patterns are unlikely to change. We know for example that there always be a gradient in these estuaries, but the range of the gradient will fluctuate over time. The bathymetry largely controls the local ocean mixing pattern, and these data should be considered when nearshore cells are initially delineated. If it becomes necessary to find permanent boundaries for nearshore cells, we recommend that the bathymetry be considered since this will ultimately control the spatial patterns of local ocean mixing.

What about the methods of cell delineation? The methods described in this report are based on the water temperature and salinity gradients measured prior to intertidal sampling. Our results show that, for Puget Sound, using a criterion of 2 units of difference for each attribute per nearshore cell is evidently a sufficient resolution in terms of effects on the biota. However, we should expect better results if the criteria were made more strict by narrowing the range to 1 unit of change per nearshore cell (such as used on the outer coast). But this would create many more nearshore cells, each with less spatial extent, and the high likelihood of not finding replicate segments within these small cells.

Beach segment selection

This study describes a model for determining landscape scale patterns in nearshore biota based on the physical characteristics of shoreline partitions. The selection of replicate beach habitats is the first step in designing a sampling protocol for comparative analyses of nearshore community structure and population abundances across scales of space and time. The justification for using the SCALE approach is that the range of available habitats is quantified *a priori* and selections for sampling can be made from the resulting distributions based on habitat frequency, cumulative shoreline length, or area. Comparability among sample sites is of utmost concern for measuring ecological change over space and time. When unquantified physical variability exists among sample sites, then unexplained biological variability will also increase. In reality, exact replicates in nature are extremely rare and no two beaches will be physically identical at all scales of observation. The limitations of this model must therefore be recognized, especially in terms of making large scale inferences about community similarity and population abundances. The degree of physical similarity among replicate beach segments will depend on the number and choice of attributes used to characterize a beach, the effort involved in quantifying segment attributes, the number and range of increments used to categorize each attribute, and the number of attributes chosen for segment aggregation.

Biological sampling

We have shown that in order to capture the variability (in space and time) in shoreline biota it is important to quantify the range of organisms most likely to be found on any given habitat type. The particular combination of taxa that make a community is probably unique to any given beach and the likelihood of finding that exact community combination anywhere else is inversely proportional to distance from the point of origin because the physical environment changes incrementally, both within categories of attributes we measure but also in attributes that are not measured. Even though we found that over 95% of the populations sampled in South Sound contribute propagules to the plankton, communities will be similar only if segments at increasing distance are exactly the same, and the water mass transporting the propagules remains exactly the same enroute between suitable habitats. Given the environmental variance in Puget Sound, the issue of change detection is compounded by the low odds of finding the exact community in any two places at the same time.

While more beach replicates are needed to adequately capture species richness and mean abundances, any increase comes at a high cost in field time and logistics; does the need justify the cost? Change detection will require statistical power which can be achieved by increasing the number of replicate beach segments sampled. At small spatial scales (i.e. quadrats and cores), population abundances are constantly changing in response to physical and biological interactions. This creates patchiness at the sampling scale and often at multiple scales of space and time. Thus, it is generally not adequate to sample with quadrats and cores at one site over time with the intent of resolving larger spatial scale differences; A one-site design would be unable to distinguish between natural variability and a signal indicating meaningful change. The currently used design of 10 samples per beach provides adequate power to detect change within a segment (because we have 10 replicates). We also use this design because it is logistically convenient and when we pool the samples we get values that characterize the community structure on a beach segment. But for Puget Sound, the question of interest is likely to be at larger spatial scales. For example, a more important issue may be how to determine if the entire shoreline is changing. In this case more replicate beach segments will be required.

What is the justification for choosing pebble beaches for community monitoring when the significance levels are all very low for this habitat? Of all the habitat types sampled in South Sound, the pebble and cobble beaches do not have dominant taxa forcing among-replicate similarity. The mud and sand segments sampled have strong bioturbators (*Neotrypaea* and *Dendraster*), therefore, natural fluctuations in these population densities will completely control the presence/absence of other taxa. By monitoring these habitats for change, we are really only monitoring the considerable population effects of bioturbators. Compounding these natural fluctuations in the biota, are the local effects of human populations in terms of selecting these habitats for aquaculture, subsistence and recreational harvests, and trampling. In addition, pebble beaches appear to be more common than either sand or mud; sand flats are common in Carr Inlet but are not as ubiquitous in other inlets, and mud beaches are widely distributed but small in spatial extent. Further application of SCALE mapping will quantify the distribution of habitats in

Puget Sound, and will provide selection criteria for the most appropriate habitat to monitor.

What research should be done on mechanistic links? We should consider establishing some experimental evidence that links changes in community structure to changes in water temperature and salinity. This can be done in the lab under controlled conditions and simultaneously in the field on a series of replicate beach segments.

Based on the South Sound work, what major recommendations would we make for future work in the greater Puget Sound area? The overall monitoring issue concerns the detection of change in nearshore biota following an unnatural perturbation. There are many perturbations (natural and artificial) that can affect nearshore community structure. These can occur over all scales of space and time from large scale oceanic changes caused by an El Nino every 5-10 years, to intermediate scale effects of oil spills that occur episodically, to the effects of point source contaminants continually emitted from industrial and municipal outfalls. For this discussion, and for the proposed monitoring program, we cannot explicitly define the perturbation and therefore must assume that an effect needs to be detected at all scales of space and time. Since we are monitoring the nearshore biota for a signal of change by comparing community structure among replicate beach habitats, the specific mechanisms of perturbation may remain undefined unless experiments determining causal effects are conducted.

The scale of monitoring must depend on the scale of the expected perturbation. If the interest is one specific beach (10's of meters), then spatially independent replicate beaches must be found within the same nearshore cell for comparison. If the interest is in cell-scale perturbations (10's of kilometers), then at least 3-5 replicate beach segments in the disturbed nearshore cell, and another 3-5 replicate beach segments in a replicate nearshore cell, would need to be sampled. An example is when the concern is over all the beaches of a certain shoretype within a nearshore cell (i.e. how is aquaculture affecting the community structure on mud beaches in Case Inlet Cell 9?). Then replicate beach segments (5) need to be found in Case Inlet Cell 9, and another 5 replicates in a replicate nearshore cell (i.e. five replicates would give 126 permutations over 2 nearshore cells). If 5 replicates in 2 nearshore cells cannot be found, then 3 replicate beach segments in 3 replicate nearshore cells could be substituted.

We have shown that when a community response to an affect is manifested across all the samples simultaneously, then the cause is likely to be at scales larger than the area (or time) encompassed by the samples. When the response is not reflected by all the samples simultaneously, then the cause is likely to be at scales less than the area (or time) encompassed by the samples.

A realistic scenario to consider is if a perturbation occurs randomly on a shore or beach type with no sampled or modeled data. Then replicate beaches and nearshore cells would need to be selected and sampled as close to the time of the perturbation as possible to determine the undisturbed community structure under the same ambient conditions. The

SCALE model was designed to address this exact issue. But this type of rapid response monitoring only works if the SCALE database is complete for the region of concern. Trying to select beach segment replicates in a non-systematic way has not proved to be accurate and can lead to misclassification of beaches and poor or misleading comparisons.

If the scale of the perturbation is not explicitly known, then we are forced to monitor at all scales simultaneously. In that case, the ideal program would be a nested design sampling matched segments in each nearshore cell, for each cell in a bay, for each bay in a district, for each district in Puget Sound. This would be for every habitat type of interest, and preferably at least twice per year to account for seasonal variability of the ocean. Since that is unlikely, a minimalist alternative is to identify the most common nearshore cell type, and select for monitoring within that nearshore cell type the most common beach habitat representing either the longest shore length or largest shore area. This type of monitoring program can be supplemented by the rapid response monitoring for beaches not included in the monitoring program.

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APPENDIX

Taxa Names

CODE	PHYLA	CLASS	FAMILY	SPECIES (sorted on genuis)	TROPHIC
Acro(Q)	Chlorophyta	Ulvophyceae	Acrosiphoniaceae	Acrosiphonia coalita	Prim
A_gausa(C)	Mollusca	Gastropoda	Columbellidae	Alia gausapata	Carn
A_salm(C)	Arthropoda	Malacostraca	Corophiidae	Americorophium salmonis	Scav
A_aga(C)	Arthropoda	Malacostraca	Ampeliscidae	Ampelisca agassizi	Scav
A_labr(C)	Annelida	Polychaeta	Ampharetidae	Ampharete labrops	Dep
Amph(C)	Echinodermata	Ophiuroidea	Amphiuridae	Amphiodia urtica	Scav
A_eleg(Q)	Cnidaria	Anthozoa	Actiniidae	Anthopleura elegantissima	Carn
Aphelo(C)	Annelida	Polychaeta	Cirratulidae	Aphelochaeta multifilis	Dep
A_brev(C)	Annelida	Polychaeta	Opheliidae	Armandia brevis	Dep
A_rubr(C)	Annelida	Polychaeta	Maldanidae	Axiothella rubrocincta	Dep
Gland(Q)	Arthropoda	Cirripedia	Balanidae	Balanus glandula	Susp
Bitt(C)	Mollusca	Gastropoda	Cerithiidae	Bittium eschrichtii	Herb
Canc(Q)	Arthropoda	Malacostraca	Cancridea	Cancer sp.	Scav
Cap_c(C)	Annelida	Polychaeta	Capitellidae	Capitella capitata	Dep
Ceram(Q)	Rhodophyte			Ceramium sp.	Prim
Cereb(C)	Nemertea	Anopla	Lineidae	Cerebratulus sp.	Carn
C_rob(C)	Annelida	Polychaeta	Cirratulidae	Cirratulus robustus	Dep
Cirr_sp(C)	Annelida	Polychaeta	Cirratulidae	Cirratulus spectabilis	Dep
Cirri_A (C)	Annelida	Polychaeta	Cirratulidae	Cirriforma sp.A	Dep
Clino(C)	Mollusca	Bivalvia	Cardiidae	Clinocardium ciliatum	Susp
C_nut(C)	Mollusca	Bivalvia	Cardiidae	Clinocardium nuttallii	Susp
Comp(C)	Mollusca	Bivalvia	Veneridae	Compsomyax subdiaphana	Susp
Crass(Q)	Mollusca	Bivalvia	Ostreoida	Crassostrea gigas	Susp
C_dors(Q)	Mollusca	Gastropoda	Calyptraeidae	Crepidula dorsata	Susp
C_forn(Q)	Mollusca	Gastropoda	Calyptraeidae	Crepidula fornicata	Susp
Crypt(C)	Mollusca	Bivalvia	Myidae	Cryptomya californica	Comm
Decam(C)	Annelida	Polychaeta	Capitellidae	Decamastus gracilis	Dep
Dendr(Q)	Echinodermata	Echinoidea	Dendrasteridae	Dendraster excentricus	Susp
D_orn(C)	Annelida	Polychaeta	Onuphidae	Diopatra ornata	Carn
Edw_sA(C)	Cnidaria	Anthozoa	Edwardsiidae	Edwardsia sipunculoides	Susp
Edwar(C)	Cnidaria	Anthozoa	Edwardsiidae	Edwardsia sp.	Susp
Endo(Q)	Rhodophyta			Endocladia muricata	Prim
E_pacif (C)	Annelida	Polychaeta	Phyllodocidae	Eteone pacifica	Carn
Euc_sA(C)	Annelida	Polychaeta	Maldanidae	Euclymene sp.A	Dep
Euc_z(C)	Annelida	Polychaeta	Maldanidae	Euclymene sp.B	Dep
Eupol(C)	Annelida	Polychaeta	Terebellidae	Eupolymnia sp. A	Dep
Free(C)	Platyhelminthes	Platyhelminthes	Childiidae	Freemania litoricola	Carn
Fucus(Q)	Phaeophyta			Fucus gardneri	Prim
Gelid(Q)	Rhodophyta			Gelidium spp.	Prim
Gsiph(C)	Annelida	Polychaeta	Glyceridae	Glycera siphonostoma	Carn
Gten(C)	Annelida	Polychaeta	Glyceridae	Glycera tenuis	Carn
G_picta(C)	Annelida	Polychaeta	Goniadidae	Glycinde picta	Carn
Gpoly(C)	Annelida	Polychaeta	Glyceridae	Glycinde polygnatha	Carn
Gnori(C)	Arthropoda	Malacostraca	Sphaeromatidae	Gnorimosphaeroma oregonense	Scav
G_ann(C)	Annelida	Polychaeta	Goniadidae	Goniada annulata	Carn
Grac(Q)	Rhodophyta			Gracelaria pacifica	Prim
Scale(Q)	Annelida	Polychaeta	Polynoidae	Halosydna brevisetosa	Carn
Hami(C)	Mollusca	Gastropoda	Atyidae	Haminoea vesicula	Herb
Hem_n(Q)	Arthropoda	Malacostraca	Grapsidae	Hemigrapsus nudus	Scav
Hem_o(Q)	Arthropoda	Malacostraca	Grapsidae	Hemigrapsus oregonensis	Scav
Hemip(C)	Annelida	Polychaeta	Glyceridae	Hemipodus borealis	Carn
H_comp(C)	Annelida	Polychaeta	Polynoidae	Hesperonoe complanata	Carn
H_arc(C)	Mollusca	Bivalvia	Hiatellidae	Hiatella arctica	Susp
Hipp(C)	Arthropoda	Malacostraca	Hippolytidae	Hippolyte clarki	Scav
L_vin(C)	Mollusca	Gastropoda	Lacunidae	Lacuna vincta	Herb
L_sac(Q)	Phaeophyta			Laminaria saccharina	Prim
Leito(C)	Annelida	Polychaeta	Orbiniidae	Leitoscoloplos pugettensis	Dep
L_squa(C)	Annelida	Polychaeta	Polynoidae	Lepidonotus squamatus	Carn

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Lepto(C)	Echinodermata	Holothuroidea	Synaptidae	Leptosynapta clarki	Dep
Lig_o(Q)	Arthropoda	Malacostraca	Ligiidae	Ligia occidentalis	Scav
Litt_s(Q)	Mollusca	Gastropoda	Littorinidae	Littorina scutulata	Herb
L_bel(Q)	Arthropoda	Malacostraca	Xanthidae	Lophopanopeus bellus bellus	Carn
L_pelta(Q)	Mollusca	Gastropoda	Lottiidae	Lottia pelta	Herb
L_strig(Q)	Mollusca	Gastropoda	Lottiidae	Lottia strigatella	Herb
L_pal(C)	Annelida	Polychaeta	Lumbrineridae	Lumbrineris pallida	Dep
M_inq(C)	Mollusca	Bivalvia	Tellinidae	Macoma inquinata	Dep
Macom(C)	Mollusca	Bivalvia	Tellinidae	Macoma juv	Dep
M_nas(C)	Mollusca	Bivalvia	Tellinidae	Macoma nasuta	Susp
M_sect(C)	Mollusca	Bivalvia	Tellinidae	Macoma secta	Susp
Magel(C)	Annelida	Polychaeta	Magelonidae	Magelona hobsonae	Dep
M_sar(C)	Annelida	Polychaeta	Maldanidae	Maldane sarsi	Dep
Mal_ban(C)	Annelida	Polychaeta	Polynoidae	Malmgreniella bansei	Comm
Masto(Q)	Rhodophyta			Mastocarpus papillatus	Prim
Med_a(C)	Annelida	Polychaeta	Capitellidae	Mediomastus sp. A	dep
Metrid(Q)	Cnidaria	Anthozoa		Metridium senile	Susp
M_dub(C)	Annelida	Polychaeta	Hesionidae	Micropodarke dubia	Carn
Holes(Q)		Miscellaneous		Miscellaneous unidentified holes	Misc
M_acher(C)	Arthropoda	Malacostraca	Corophiidae	Monocorophium acherusicum	Scav
Mopal(Q)	Mollusca	Polyplacophora	Mopaliidae	Mopalia lignosa	Herb
M_tross(Q)	Mollusca	Bivalvia	Mytilidae	Mytilus edulis	Susp
Nassa(C)	Mollusca	Gastropoda	Nassariidae	Nassarius mendicus	Scav
N_perp(C)	Mollusca	Gastropoda	Nassariidae	Nassarius perpinguis	Scav
Callia(C)	Arthropoda	Malacostraca	Callianassidae	Neotrypaea californiensis	Dep
N_ca(C)	Annelida	Polychaeta	Nephtyidae	Nephtys caeca	Carn
N_caec(C)	Annelida	Polychaeta	Nephtyidae	Nephtys caecoides	Carn
N_ferr(C)	Annelida	Polychaeta	Nephtyidae	Nephtys ferruginea	Carn
N_long(C)	Annelida	Polychaeta	Nephtyidae	Nephtys longosetosa	Carn
Neph(C)	Annelida	Polychaeta	Nephtyidae	Nephtys sp.	Carn
N_bran(C)	Annelida	Polychaeta	Nereidae	Nereis brandti	Omn
N_limn(C)	Annelida	Polychaeta	Nereidae	Nereis limnicola	Omni
N_proc(C)	Annelida	Polychaeta	Nereidae	Nereis procera	Omni
N_vex(C)	Annelida	Polychaeta	Nereidae	Nereis vexillosa	Omni
N_zon(C)	Annelida	Polychaeta	Nereidae	Nereis zonata	Omni
Nothr(C)	Annelida	Polychaeta	Onuphidae	Nothria conchylega	Omni
N_linea(C)	Annelida	Polychaeta	Capitellidae	Notomastus lineatus	Dep
Noto A (C)	Annelida	Polychaeta	Capitellidae	Notomastus sp. A	Dep
N_tenu(C)	Annelida	Polychaeta	Capitellidae	Notomastus tenuis	Dep
Nuc_l(Q)	Mollusca	Gastropoda	Nucellidae	Nucella lamellosa	Carn
O_bil(C)	Mollusca	Gastropoda	Onchidoridídae	Onchidoris bilamellata	Carn
Onu_hol(C)	Annelida	Polychaeta	Onuphidae	Onuphis 'holobranchiata'	Omni
O_pug(C)	Annelida	Polychaeta	Hesionidae	Ophiodromus pugettensis	Carn
O_lut(C)	Echinodermata	Ophiuroidea	Ophiuridae	Ophiura lutkeni	Carn
P_ber(C)	Arthropoda	Malacostraca	Paguridae	Pagurus beringanus	Scav
Pagur(Q)	Arthropoda	Malacostraca	Paguridae	Pagurus sp.	Carn
Paran(C)	Nemertea	Enopla	Emplectonematida	Paranemertes peregrina	Carn
P_pin(C)	Annelida	Polychaeta	Spionidae	Paraprionospio pinnata	Dep/Susp
Pectin(C)	Annelida	Polychaeta	Pectinariidae	Pectinaria granulata	Dep
Pect_m(C)	Annelida	Polychaeta	Pectinariidae	Pectinaria moorei	Dep
Petal(Q)	Rhodophyta			Petalonia sp.	Prim
Petro(Q)	Rhodophyta			Petrocelis sp.	Prim
Phas(C)	Sipuncula		Phascolosomatida	Phascolosoma agassizii	Dep
Pholo(C)	Annelida	Polychaeta	Pholoidae	Pholoe sp.	Dep
P_harm(C)	Phoronida		Phoronidae	Phoronopsis harmeri	Susp
Pidd(Q)				Piddock clam	Susp
Pin_eb(C)	Arthropoda	Malacostraca	Pinnotheridae	Pinnixia eburna	Comm
Pin_tu(C)	Arthropoda	Malacostraca	Pinnotheridae	Pinnixia tubicola	Comm

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Pinno(C)	Arthropoda	Malacostraca	Pinnotheridae	Pinnotherid sp.	Carn
P_wui (C)	Annelida	Polychaeta	Terebellidae	Pista wui	Dep
Platy(C)	Annelida	Polychaeta	Nereidae	Platynereis bicanaliculata	Omni
P_glab(C)	Annelida	Polychaeta	Hesionidae	Podarkeopsis glabrus	Omni
Podo(C)	Mollusca	Bivalvia	Anomiidae	Pododesmus cepio	Susp
Polin(C)	Mollusca	Gastropoda	Naticidae	Polinices lewisii	Carn
Polycir(C)	Annelida	Polychaeta	Terebellidae	Polycirrus n. sp. (L. Harris)	Dep
P_brac(C)	Annelida	Polychaeta	Spionidae	Polydora brachycephala	Dep/Susp
P_card(C)	Annelida	Polychaeta	Spionidae	Polydora cardalia	Dep/Susp
P_colu(C)	Annelida	Polychaeta	Spionidae	Polydora columbiana	Dep/Susp
P_kem(C)	Annelida	Polychaeta	Spionidae	Polydora kempi japonica	Dep/Susp
P_soc(C)	Annelida	Polychaeta	Spionidae	Polydora socialis	Dep/Susp
P_siph(Q)	Rhodophyta			Polysiphonia sp.	Prim
Punct(Q)	Rhodophyta			Porphyra sp.	Prim
Prion(C)	Annelida	Polychaeta	Spionidae	Prionospio steenstrupi	Dep/Susp
Pro/Tap(C)	Mollusca	Bivalvia	Veneridae	Protothaca or Tapes	Susp
Proto(C)	Mollusca	Bivalvia	Veneridae	Protothaca staminea	Susp
Pseud(C)	Mollusca	Bivalvia	Montacutidae	Pseudopythina rugifera	Comm
Puget(Q)	Decapoda		Majidae	Pugettia gracilis	Scav
Sacco(C)	Hemichordata	Enteropneusta	Unid	Saccoglossus sp.	Dep
S_gig	Mollusca	Bivalvia	Veneridae	Saxidomus giganteus	Susp
Scler(C)	Arthropoda	Malacostraca	Pinnotheridae	Scleroplax granulata	Comm
S_armig(C)	Annelida	Polychaeta	Orbiniidae	Scoloplos armiger	Dep
Scol_sp(C)	Annelida	Polychaeta	Orbiniidae	Scoloplos sp.	Dep
Scyto(Q)	Phaeophyta			Scytosiphon lomentaria	Prim
Cario(Q)	Arthropoda	Cirripedia	Archaeobalanidae	Semibalanus cariosus	Susp
Serpul(Q)	Annelida	Polychaeta	Serpulidae	Sepulid sp.	Susp
Sigam(C)	Annelida	Polychaeta	Pilargiidae	Sigambra tentaculata	Carn
Spio(C)	Annelida	Polychaeta	Spionidae	Spio. sp.	Susp
Spio_c(C)	Annelida	Polychaeta	Chaeotopteridae	Spiochaetopterus costarum	Susp
S_berk(C)	Annelida	Polychaeta	Spionidae	Spiophanes berkelyorum	Dep/Susp
Tape(C)	Mollusca	Bivalvia	Veneridae	Tapes philippinarum	Susp
T_bod(C)	Mollusca	Bivalvia	Tellinidae	Tellina bodegensis	Susp
Telli(C)	Mollusca	Bivalvia	Tellinidae	Tellina sp.	Dep
Ter_sp(C)	Annelida	Polychaeta	Terebellidae	Terebellid sp.	Dep
T_calif (C)	Annelida	Polychaeta	Trichobranchidae	Terebellides californica	Dep
T_strom(C)	Annelida	Polychaeta	Trichobranchidae	Terebellides stroemii	Dep
Thary(C)	Annelida	Polychaeta	Cirratulidae	Tharyx parvus	Dep
Turbon(C)	Mollusca	Gastropoda	Pyramidellidae	Turbonilla sp.	Herb
Ulvo(Q)	Chlorophyta			Ulvoids	Prim
Capit(C)	Annelida	Polychaeta	Capitellidae	Unid	Dep
Mald(C)	Annelida	Polychaeta	Maldanidae	Unid	Dep
Nemer(C)	Nemertea	Nemertea		Unid	Carn
Ner_sp(C)	Annelida	Polychaeta	Nereidae	Unid	Omni
Oligo(C)	Annelida	Oligochaeta		Unid	Dep
Polyn(C)	Annelida	Polychaeta	Polynoidae	Unid	Carn
Talit(Q)	Arthropoda	Malacostraca	Talitridae	Unid	Scav
Tana(C)	Arthropoda	Malacostraca	Tanaidacea	Unid	Scav
Rnd_oys(Q)	Mollusca	Bivalvia	Ostreoida	Unid	Susp
Sabell(Q)	Annelida	Polychaeta	Sabellidae	Unid	Susp
flat(C)	Platyhelminthes			Unid. Flat Worm	Carn
Myi(C)	Mollusca	Bivalvia	Myidae	Unid. Myidae	Susp
Siph(C)	Mollusca	Bivalvia		Unidentified clam siphons	Susp
Red_cr(Q)	Rhodophyta			Unidentified encrusting red alga	Prim
Upog(C)	Arthropoda	Malacostraca	Upogebiidae	Upogebia pugettensis	Dep