Ecosystem Model Indicators for the Beaufort Sea Shelf Region of the Beaufort Sea

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ABSTRACT

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Indicators are useful tools in detecting changes to an ecosystem over time. Here, an ecosystem model for the Beaufort Sea Shelf was created to represent local species and ecosystem linkages. This model was then used to calculate indicators at the ecosystem level and provide baseline values for future research.

Keywords: Beaufort Sea, Indicators, Food Web, Beaufort Sea Shelf, Ecosystem Model, Ecopath with Ecosim

RÉSUMÉ

Hoover, C.A. 2013. Ecosystem Model Indicators for the Beaufort Sea Shelf Region of the Beaufort Sea. Can. Data Rep. Fish. Aquat. Sci. 1249: vi +14 p.

Les indicateurs sont des outils utiles pour détecter des changements au sein d'un écosystème. Dans cette étude, un modèle écosystémique du plateau continental de la mer de Beaufort a été créé afin de représenter les espèces locales et comprendre leurs interactions. Ce modèle a également servi à calculer des indicateurs à l'échelle de l'écosystème et ainsi à fournir des valeurs de références pour de futures recherches.

Mots clés : Mer de Beaufort, indicateur, système trophique, plateau de la mer de Beaufort, Ecopath avec Ecosim

INTRODUCTION

Ecological indicators are an important tool in monitoring changes in ecosystems, allowing a representative species to represent ecosystem health. There have been numerous indicators proposed for the Beaufort Sea region; however these are primarily focused on species where data is readily available. While monitoring programs are useful in detecting changes in populations or health of populations, they often miss some components of the ecosystem as they tend to be centered on valued ecosystem components (VECs). A VEC is any component of the ecosystem that has scientific, economic, social or scientific value. In order to address potential gaps in important components to the ecosystem and food web, an ecosystem model was created to represent the Mackenzie Shelf area of the Beaufort Sea. This ecosystem model was then used to calculate ecosystem statistics in order to reveal important components of the system. The Beaufort Sea ecosystem model, created using Ecopath with Ecosim (Christensen *et al.* 2007; Buszowski *et al.* 2009) as part of the Beaufort Sea Shelf Ecosystem Research Initiative (BSS ERI), was used to estimate a variety of network analyses such as total system throughput, ascendency, redundancy, Finn's cycling index and keystoneness (uniqueness) of food web components. The results will be compared to other proposed indicators to potentially identify previously overlooked components of the food web to be considered for future monitoring.

The model represents the coastal area of the Mackenzie Shelf depicting the past (1970s) food web using parameter estimates from peer reviewed and grey literature. A total of 37 functional groups representing individual species or groups of species are included in the model, which is linked together through food web interactions. The statistics presented in this paper are centered on the mass-balance Ecopath model in order to serve as a baseline for comparison of future analyses.

MATERIALS AND METHODS

ECOSYSTEM MODEL

The Ecopath model representing the coastal food web is based on the Mackenzie Shelf area (Figure 1) containing the coastal area heavily influenced by flow from the Mackenzie River. The coastal area is designated where depth is less than 200m, as depicted in figure 1. The 200m depth was selected as the cut-off for the model for two reasons. First, the middle Canadian shelf reaches a depth of 100m with the outer shelf reaching over 200m (Carmack and Macdonald 2002). Second, changes in oceanography occur at the 200m isobath (Weingartner 2003). The model was created using Equation 1 (Christensen *et al.* 2007):

$$P_i = \sum_j B_j \cdot M2_{ij} + Y_i + E_i + BA_i + P_i \cdot (1 - EE_i) \qquad \text{(eq. 1)}$$

Where the production of each functional group (P_i) for each prey group (*i*) is calculated by including the biomass of predator group *j* (B_j), predation mortality ($M2_{ij}$) on group *i*, fisheries catches (Y_i), the net migration rate (E_i) as measured by emigration–immigration, the biomass accumulation rate (BA_i), and the ecotrophic efficiency (EE_i) or proportion of production that is consumed or exported out of the system. All species or functional groups are linked through trophic interactions compiled as contributions to the diet, so each predator's (j) diet is comprised of proportions of prey groups (i) totalling 1 (or 100%) as measured by wet weight. Detailed parameter descriptions for the Ecopath model are available in (Hoover unpublished data). Here a series of ecosystem calculations are used to provide information and baseline values of indices for future use.

ECOSYSTEM INDICATORS

Total System Throughput

The Total System Throughput (TST) is measured by the sum of all flows in the ecosystem (Christensen 1995) and is also used in calculating the Finn Cycling Index. The TST accounts for all flows within the ecosystem including consumption, export, respiration and flows into detritus, with the value reflecting the size of the ecosystem (Baird and Ulanowicz 1993; Patricio *et al.* 2006). Odum (1971) considered the TST to be a surrogate for all power generated within the ecosystem. Equation 2 taken from Heymans *et al.* (2007) represents the TST or the sum of all flows within the ecosystem model measured in [t·km^{-2}·year-^{1}], where T$_{ij}$ is the flow between any two components in the model (*i* and *j*) and includes the flow (respiration, catch and export) from one component to the other:

$$TST = \sum_{i=1,j=1}^{n} T_{ij} \qquad \text{(eq. 2)}$$

System throughput can be useful on its own to determine changes in total ecosystem flows over time (Finn 1976; Heymans *et al.* 2007), however the calculation provided serves as a starting point to compare temporal simulation of the ecosystem model (Ecosim simulations).

Ascendency

Ascendency (A) measures the size and organization of flows within the ecosystem (Baird and Ulanowicz 1993), and is based on Odum's (1969) principles of ecosystem maturity. Ascendency increases in the absence of major perturbations as ecosystem matures, with ecosystems appearing to evolve to optimize ascendency (Ulanowicz and Norden 1990; Christensen 1995). Values are mathematically bound by 0 and C, where C (the capacity of development) is the maximum potential of developmental capacity (Rybarczyk *et al.* 2003). The difference between ascendency and capacity (C-A) is the system overhead, which indicates how much ascendency can increase (Christensen *et al.* 2007). Using Equation 3 ascendency is calculated as:

$$A = \sum_i \sum_j T_{ij} \cdot log \left(\frac{T_{ij} T_{..}}{T_i \; T_j} \right) \qquad \text{(eq. 3)}$$

Where T_{ij} is the flow form species i to species j, T_i is the sum of all flows leaving the ith component and T_j is the sum of all flows entering the jth component (Heymans *et al.* 2007). Changes in ascendency over time can be used to quantify system disturbances, growth or regressions (Patricio *et al.* 2006). Relative ascendency can be measured as the ratio between ascendency and the developmental capacity (Christensen 1994).

Redundancy

Redundancy (R) is a measure of ecosystem stability, also known as the overhead on internal flows. It measures the internal redundancy of the ecosystem (Christensen 1995). Redundancy reflects the number of parallel pathways and resilience within the ecosystem, so if a disturbance removed a connection between two compartments it could be replaced by a parallel pathway (Rybarczyk *et al.* 2003). Equation 4 taken from Heymans *et al.* (2007) calculates R as:

$$R = -\sum_{i=1}^{n} \sum_{j=1}^{n} (T_{ij}) \cdot log \left(\frac{T_{ij}^2}{\sum_{j=1}^{n} T_{ij} \cdot \sum_{i=1}^{n} T_{ij}} \right) \qquad \text{(eq. 4)}$$

Lower R values are representative of more fragile ecosystems being that broken pathways cannot be re-established between compartments, and there are no alternate routes for energy transfer in the system (Rybarczyk *et al.* 2003). Conversely, higher R values indicate energy flow is diversified among many alternative pathways and not concentrated in one or a few main pathways (Heymans *et al.* 2007).

Finns Cycling Index

Finn's Cycling Index (FCI) is calculated as the proportion of TST (from Equation 2) that is recycled in the system, and measures the magnitude of recycled activity (Christensen 1995; Patricio *et al.* 2006). A modified version of this index, not used in this paper, is the predatory cycling index which is calculated in the same manner, with the exception that detrital groups are excluded (Christensen and Pauly 1992; Christensen 1995). The FCI (Equation 5) can be used to identify structural differences between models or for one model throughout time (Finn 1976; Heymans *et al.* 2007).

$$FCI = \frac{TST_c}{TST} \qquad \text{(eq. 5)}$$

TST is the total system throughput (as measured in Equation 2), and TST_c is the total recycled flow. Higher FCI values indicates higher retentiveness in the system or more recycling, reflective of more mature/less stressed ecosystems (Odum 1969; Baird and Ulanowicz 1993). Systems with higher FCI values are expected to recover faster from perturbations than more degraded systems with lower FCI values (Shannon *et al.* 2009). As part of FCI, path lengths can be calculated from the TST and respiration (Christensen 1994). The mean path length is dependent upon the total number of trophic links divided by the number of pathways. (Christensen *et al.* 2007). The mean path length is calculated by Equation 6:

$$Path\ Length = \frac{TST}{(\sum Export + \sum Respiration)} \qquad \text{(Eq.6)}$$

Keystoneness Indices

Keystone species are defined as impacting the food web disproportionately to their abundance or biomass (Power *et al.* 1996). Here, keystoneness is calculated through two indices in Ecopath; keystoneness index #1 and keystoneness index #2. Although temporal simulations are not utilized in this paper (through Ecosim), they can be useful in validating the ranking of functional groups based on their keystoneness or identifying

changes in ranking over time. Keystone index #1 (KS$_{i1}$) combines the overall effect of each species group on the ecosystem (ε$_i$)[1] and the contribution of each group to the food web *(p$_i$)*[2] in Equation 7, for each species or functional group *i* (Heymans *et al.* 2012):

$$KS_{i1} = log[\varepsilon_i(1 - p_i)] \qquad \text{(eq. 7)}$$

Where p$_i$ is the production for group *i* and ε$_i$ represents the overall effect of group *I,* accounting for positive and negative contributions as based on the mixed trophic impact (Libralato *et al.* 2006). Groups with low biomass and high effects have high keystoneness (#1) values, however with this calculation species groups with high effects and high biomass are assigned a lower keystoneness value (Libralato *et al.* 2006). A KS value close to or above 0 indicate that a species or species group would be considered a keystone species (Heymans *et al.* 2012). A previous version (Keystoneness index #2) of this equation was derived based on Power *et al.* (1996) in Equation 8, which provides an alternative calculation for keystoneness:

$$KS_{i2} = log\left[\varepsilon_i \cdot \left(\frac{1}{p_i}\right)\right] \qquad \text{(eq. 8)}$$

However, this calculation (Equation 8) assigns high keystoneness values to groups with low biomass and low overall effect, whereas index #1 (Equation 7) assigns high keystoneness values to groups with low biomass and high effects (Libralato *et al.* 2006). Again, values close to or above 0 indicate a keystone species. While both indices can

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[1] ε$_i$ is calculated as $\varepsilon_i = \sqrt{\sum_{j \neq i}^{n} m_{ij}^2}$ where m_{ij} is the mixed trophic impact (the product of all net impacts) or the direct and indirect impacts that each impacting group (*i)* has on each impacted group (*j*) in the food web. Here the contributions of the overall effect of each group can be interpreted as top-down (where m_{ij} is negative) or bottom-up (where m_{ij} is positive) (Heymans *et al.* 2012).

[2] Pi is calculated as $P_i = \frac{B_i}{\sum_k B_k}$ where P$_i$ is the production of group *i*, B$_i$ is the biomass of group *i*, and B$_k$ is the biomass of group *k* (Power *et al.* 1996; Libralato *et al.* 2006)

be useful, higher priority should be given to index #1 (Equation 7) for looking at important species within the food web.

DATA PRESENTATION

Total System Throughput for the base year of the model was $1940 t \cdot km^{-2} \cdot year^{-1}$. Figure 2 identifies the contributions of consumption ($608 t \cdot km^{-2} \cdot year^{-1}$), exports ($96 t \cdot km^{-2} \cdot year^{-1}$), respiration flows ($329 t \cdot km^{-2} \cdot year^{-1}$), and flows to detritus ($907 t \cdot km^{-2} \cdot year^{-1}$), to TST. Ascendency was calculated for each species group (Table 1), with the total ascendency for the ecosystem calculated to be 2743 flowbits or 26.9% of system capacity, with the system capacity (C) calculated as 10197 flowbits. Total system overhead is 7454 flowbits. Figure 3 shows the different contributions to ascendency; internal flow (68%), export (12%), and respiration (20%) with no contributions from imports. The redundancy of the ecosystem or overhead on internal flows of the ecosystem was measured to be 5870 flowbits or 57.6% of internal flow overhead. The Finn's Cycling Index was calculated to be 3.7% of total throughput, with a TST_c value of $71.4 t \cdot km^{-2} \cdot year^{-1}$ including detritus. It should be noted that the TST_c value would drop to $3.7 t \cdot km^{-2} \cdot year^{-1}$ if detrital groups were excluded. The mean path length is 4.56 for the ecosystem.

Keystoneness indices are presented in Table 2, and visually in figure 4. For keystoneness index #1 the top five ranking species or species groups are: smelt (KS_{i1}= 0.078), cods (KS_{i1}= 0.011), echinoderms (KS_{i1}= -0.044), arthropods (KS_{i1}= -0.092), and macro-zooplankton (KS_{i1}= -0.140). From these values, smelt and cods should be considered keystone species; however echinoderms, arthropods and macro-zooplankton may need more investigation due to their negative values of this index. For keystone index #2 the top five ranking species or species groups are: polar bears (KS_{i2}=4.165), ringed seals (KS_{i2}=3.517), bearded seals (KS_{i2}=3.025), beluga (KS_{i2}=2.827), and bacteria (KS_{i2}=2.482).

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Table 1: Ascendency as calculated for each functional group within the model and ecosystem totals.

Group Number	Group Name	Ascendency (t/km²/year * bits)
1	Polar Bears	0.022
2	Beluga	2.330
3	Bowhead	7.301
4	Ringed Seals	0.337
5	Bearded Seals	1.061
6	Birds	0.018
7	Char & Dolly Varden	0.834
8	Ciscos/ Whitefish	7.597
9	Inconnu	2.102
10	Salmonids	0.962
11	Herring	1.711
12	Cods	18.280
13	Smelt	19.310
14	Flounder	2.380
15	Sculpins/Zoarcids	8.976
16	Other Fish	8.971
17	Arthropods	49.520
18	Bivalves	36.190
19	Echinoderms	74.590
20	Molluscs	28.900
21	Benthic Worms	35.280
22	Other Benthos	13.630
23	Jellies	43.970
24	Macro-zooplankton	20.180
25	Pseudocalanus	46.440
26	Large Copepods	127.000
27	Other Meso-zooplankton	47.420
28	Micro-zooplankton	140.400
29	Heterotrophic Protists	41.060
30	Primary Producers >5um	122.900
31	Primary Producers <5um	608.000
32	Ice Algae	464.300
33	Benthic Plants	19.840
34	Bacteria	176.100
35	DOC	0.000
36	Pelagic POC	105.200
37	Ice Detritus	460.000
All	Total	2743.000
All	(%)	26.900

Table 2: Keystoneness Indices as calculated for each model group

Group #	Group Name	Keystone Index #1	Keystone Index #2
1	Polar Bears	-0.288	4.165
2	Beluga	-0.249	2.827
3	Bowhead	-1.010	1.078
4	Ringed Seals	-0.448	3.517
5	Bearded Seals	-0.305	3.025
6	Birds	-3.287	2.467
7	Char & Dolly Varden	-1.003	1.566
8	Ciscos/ Whitefish	-0.198	1.571
9	Inconnu	-0.348	1.580
10	Salmonids	-0.845	1.708
11	Herring	-1.333	1.193
12	Cods	0.011	1.360
13	Smelt	0.078	1.566
14	Flounder	-0.736	1.407
15	Sculpins/Zoarcids	-0.249	1.353
16	Other Fish	-0.787	0.830
17	Arthropods	-0.092	0.933
18	Bivalves	-0.201	1.220
19	Echinoderms	-0.044	0.980
20	Molluscs	-0.470	0.635
21	Benthic Worms	-0.666	0.569
22	Other Benthos	-0.757	0.784
23	Jellies	-0.492	1.444
24	Macro-zooplankton	-0.140	2.136
25	Pseudocalanus	-0.570	1.272
26	Large Copepods	-0.230	0.953
27	Other Meso-zooplankton	-0.555	0.969
28	Micro-zooplankton	-0.319	1.611
29	Heterotrophic Protists	-0.324	1.666
30	Primary Producers >5um	-0.415	0.871
31	Primary Producers <5um	-0.243	0.927
32	Ice Algae	-0.352	0.730
33	Benthic Plants	-1.000	1.008
34	Bacteria	-0.320	2.482

Figure 1: Beaufort Sea Shelf and surrounding communities. Model area includes the coastal shelf up to a depth of roughly 200m and is outlined in black.
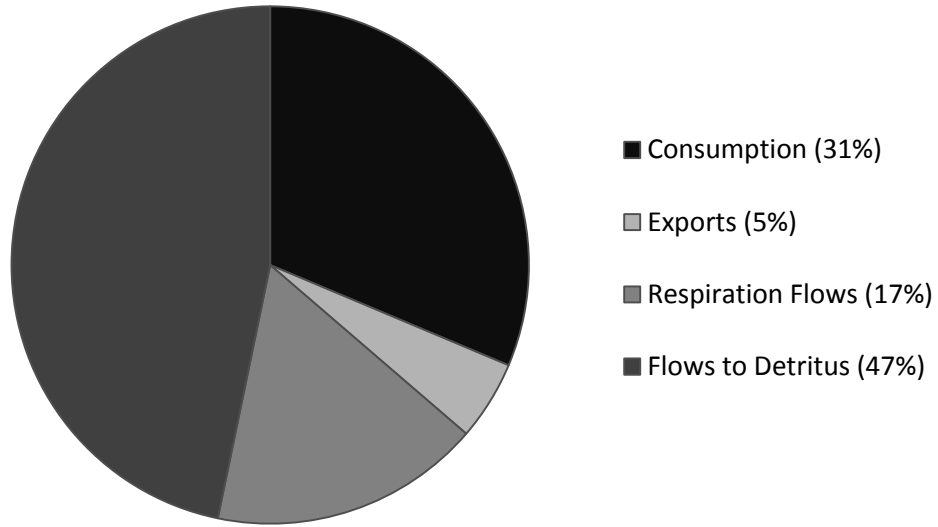
Figure 2: Contributions of consumption, exports, respiration flows and flows to detritus to Total System Throughput.
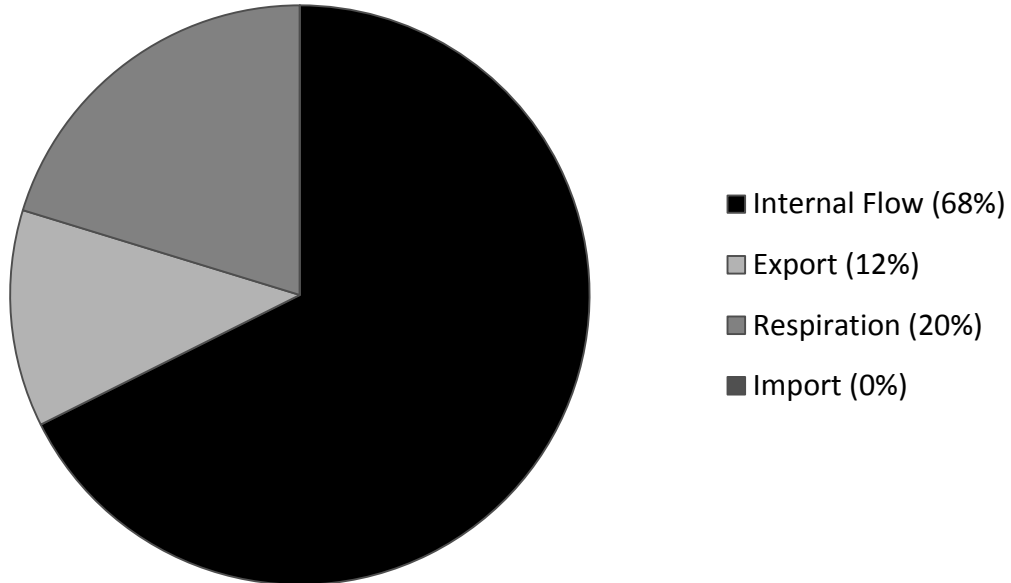

Figure 3: Contributions of internal flow, export, respiration, and imports to total ascendency.
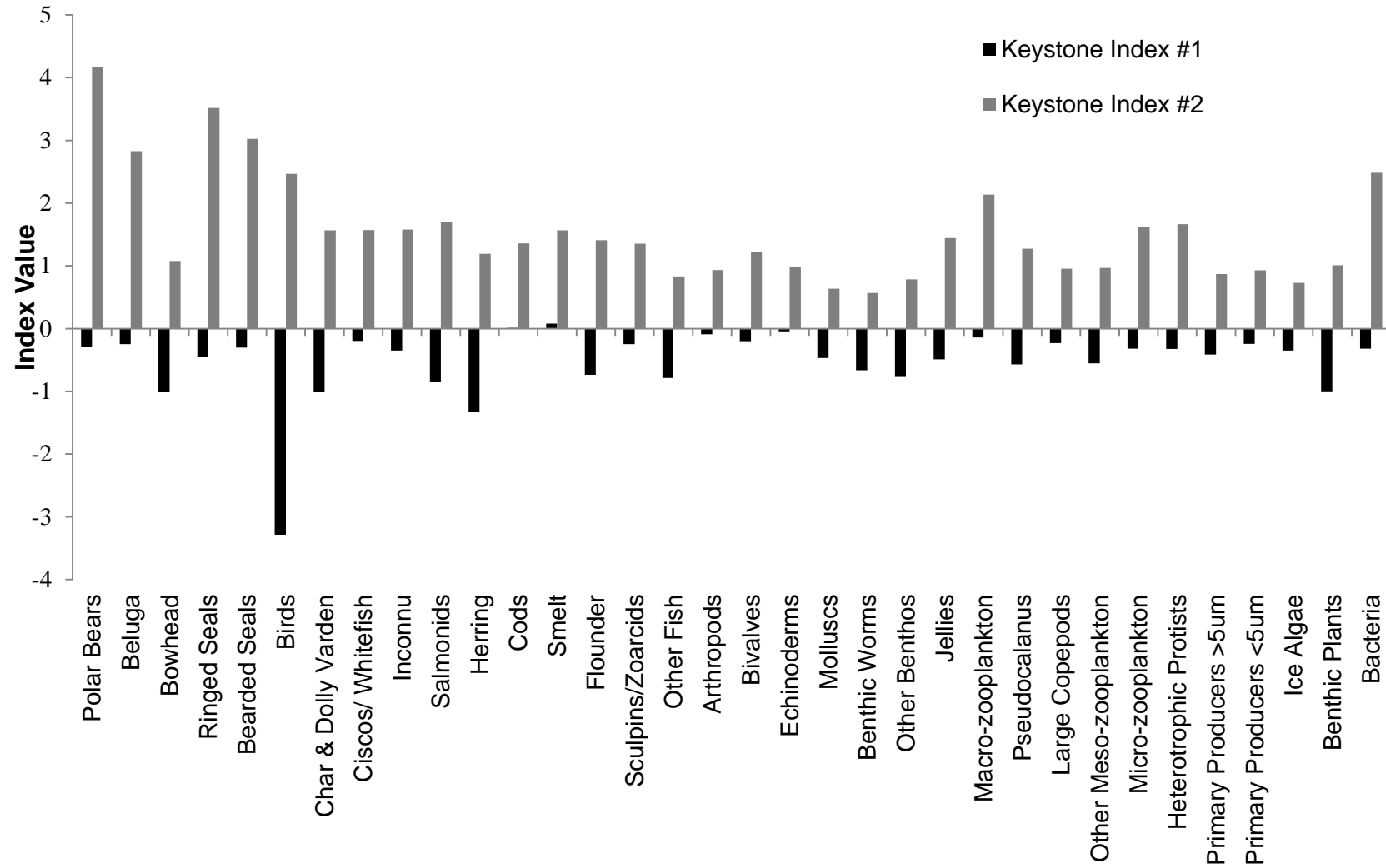
Figure 4: Keystone Indices measure by each species group within the model.