Table 1 Ecosystems, prey species, and food web models used

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| **Ecosystem** | **Region code** | **Prey functional groups** | **Food web model** |
| North Sea | NORT | Atlantic herring, Lesser sandeel, Norway pout, Common sole, Whiting | (Mackinson and Daskalov, 2007) |
| Barents Sea | BS | Atlantic herring, Capelin | (Blanchard *et al.*, 2002) |
| Baltic Sea | BALT | Atlantic herring, Sprat | (Harvey *et al.*, 2003) |
| Western Scotian Shelf | WSS | Atlantic herring, Other pelagics | (Araújo *et al.*, 2011) |
| Eastern Scotian Shelf | ESS | Northern sand lance, small pelagics | (Bundy, 2004) |
| Gulf of Maine | GoM | Commercial pelagics, Other pelagics | (Link *et al.*, 2006) |
| Georges Bank | GB | Commercial pelagics, Other pelagics | (Link *et al.*, 2006) |
| Hecate Strait | HS | Pacific herring, Flatfish | (Ainsworth *et al.*, 2002) |
| Gulf of Alaska | GoA | Pacific herring, Walleye Pollock, Capelin | (Aydin *et al.*, 2002) |
| Eastern Bering Sea | EBS | Pacific herring, Walleye pollock, Capelin, Yellowfin sole, Pacific sand lance | (Aydin *et al.*, 2002) |

Fig. 1 Schematic showing how multiple time series of predator abundance (dotted lines), all with a mean of zero, sum together into a single predator index (thick solid line). Component species can be either synchronous (resulting in black line, most variable), statistically independent (resulting dark gray line, moderately variable), or asynchronous (resulting in light gray line, least variable). The three different cases all have identical random generator seeds, and only differ in the correlation structure of the component species.

../figs/prop-quantified.pdf

Fig. 2 Histogram of proportion of predation mortality in the mass balance model for which time series data were available.

../figs/pred-props.pdfFig. 3 Histogram of proportion of predation mortality accounted for by the most important (dark gray) and second-most important (light gray) predators based on static analysis.

../figs/pred-indices.pdf

Fig. 4 Predator index for all prey species in all regions. Each color slice represents a different predator species. For simplicity, only the predator index of the top ten predators is plotted. These species makes up at least 90% of the total index, and an average of 99%. See appendix for predator species labels.

../figs/variance-factors.pdf

Fig. 5 Variance ratio of predator index for (a) all predator species and (b) the minimum number of species to account for 90% of the total predator index (i.e., core species only), versus species richness. Black horizontal line is at 1. Red dashed line is best-fit linear model forced to go through (1,1). Note four points are over-plotted in panel (b) at (1,1). Bars on the right-hand side are histograms aggregated over species richness. See table 1 for region codes.

../figs/violin-plots.pdf

Fig. 6 Distribution of bootstrapped variance ratios for core species under the null assumption that predator populations are independent, and observed variance factors (points). Horizontal line is where the variance ratio equals one, the theoretical mean of the distributions. Numbers on top indicate number of predators. Points without distributions have one predator that accounts for >90% of predator index, and thus the variance factor must equal one. Points in the tails of the distributions indicate evidence for synchronous (above) or asynchronous (below) predator assemblages. See table 1 for region codes.

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