**-** No change through time indicates harbor seal foraging strategies able to compensate for dramatic changes in resources without altering foraging niche

-Dynamics that operate on more trophic level/community wide scales that may alter multiple species at the same time are a better predictor of harbor seal foraging abundance than individual prey species

-forward selection is bias towards type II error, but for the sake of this exercise we believe it is justified.

-Food web results represent a prey species that is both abundant in harbor seal diet and has experienced large scale changes in the system

-Sex does not appear to influence trophic position. While coastal harbor seals may exhibit different foraging strategies based on sex. This is contradictory to previous studies. Weight may be a better predictor than length but given the nature of this data was not possible to analyze. Or previous studies may have identified a more local phenomenon.

-Location is important, and variability may be the most important component of

**Methods**

Prey and isotope data was standardized around a mean of 0 and divided by the standard deviation.

*Trophic Position Calculation*

Bone collagen was decalcified, acid hydrolyzed, derivatized and analyzed for compound-specific stable isotope (δ15N) analysis (CSIA) of 12 individual amino acids (*SI Appendix 1*). δ15N was measured as:

Collagen samples were measured in triplicate with a laboratory standard containing a 12 amino acid mixture of known isotopic composition (mean reproducibility = ). Previous controlled feeding studies have determined the trophic discrimination factor (TDF) for harbor seals is substantially lower than the conventional literature value of 7.6‰ (Germain et al. 2013) and thus applying a harbor seal specific trophic discrimination factor is more ecologically realistic (McMahon et al. 2015). Therefore, trophic position was calculated using a harbor seal specific TDF, described by McMahon et al. (2015) as a "multi-TDF" approach, using the following equation:

where TDF(Tr-Phe) plankton is the difference between given trophic amino acid - phenylalanine pair of typical phytoplankton and lower food web species, specific for cyanobacteria and algae (Table 1, Chikaraishi et al 2010). TDF(Tr-Phe) harbor seal represents the harbor seal specific TDF for a given trophic amino acid - phenylalanine pair calculated from Germain et al (2003) controlled feeding study data (Table 1) and βTr is the δ15N difference between a specific trophic amino acid and phenylalanine of primary producers estimated by Nielsen et al. (2015).

Table 1:

|  |  |  |  |
| --- | --- | --- | --- |
| Trophic Amino Acid | β | TDF harbor seal | TDF plankton |
| Glutamic acid (Glu) | 2.9 | 3.4 | 3.4 |
| Alanine (Ala) | 2.8 | 2.5 | 3.2 |
| Proline (Pro) | 2.7 | 5.5 | 3.1 |
| Aspartic Acid (Asp) | 1.8 | 3.5 | 5.4 |
| Valine (Val) | 3.4 | 7.5 | 4.6 |