Arctic Bivalve in the Chukchi Sea

I. Introduction:

Despite its polar conditions, the Arctic Chukchi Sea has been ranked one of the most productive seas in the world (Gosselin et al. 1997, Hill & Cota 2005). Of which, at least 10% has been attributed to the production of sea ice algae (Gosselin et al. 1997), which is a much higher proportion than any other shelf seas in the Arctic, with the exception of the Barren Sea (Sakshaug 2004). In the Chukchi Sea, sea ice algae production is directly transferred to the macrobenthic faunal community with little being consumed before reaching the sea bed (Dunton et al. 1989). The benthic production, then, support the higher trophic organisms such as Pacific walrus, grey whales and bearded seals (Grebmeier et al. 2006).

Given the importance of sea ice algae and sea ice coverage in general, it is particularly worrisome that unprecedented changes in sea ice extent and thickness have been observed in recent decades (Stroeve et al. 2007, Palmer et al. 2014, Zhang et al. 2015). For example,in 2007, the sea ice extent was 23% below previous low (Overland & Wang 2007). Between 1979 and 2014, there is a loss of approximate 1mil km^2 of summer sea ice coverage in the Arctic Ocean (Figure 1]) (Esri Canada Education and Research Group 2015). There is a high probability of a 40% reduction of summer sea ice extent in the Arctic by the year 2050 (Overland & Wang 2007). They are predicted to affect marine primary production in general (Palmer et al. 2014). However, little is known of how the benthic macrofauna responded to historic changes in sea ice cover and thus, prediction models lack the capacity to be thoroughly verified. Fortunately, bivalve shell growth has been shown to reflect changes in regional environmental parameters such as temperature and precipitation as well as food availability (Carroll et al. 2008).

In addition, the soft tissue materials from the specimens collected would be used in stable isotope signature studies to assess their food source and feeding relationships. The carbon isotopic signature ($\delta^{13}C$) reflects the relationship between an organism and its diet (Michener & Kaufman 2007). The nitrogen isotopic signature ($\delta^{15}N$) is enriched by +3.8‰ in the Arctic marine food web (Hobson & Welch 1992) and thus, could be used to trace the trophic level of an organism. Together, these two parameters could be used to outline food webs and follow the flows of nutrients in the system (Peterson & Fry 1987).

Here, we will attempt to use a dendrochronology approach (Black et al. 2005, Black 2009, Nguyen et al. 2015) to construct and analyze the historical growth record of twelve

Bivalvia genuses from the Chukchi Sea. The results will enable us to reconstruct past climatic events from the said records to study the effect of climate change, sea ice coverage in particular, on not only growth rate but also food web structure and energy flow. The outcome of this research would help consider the implications of environmental conditions predicted to occur in the future on benthic ecosystem within this region.

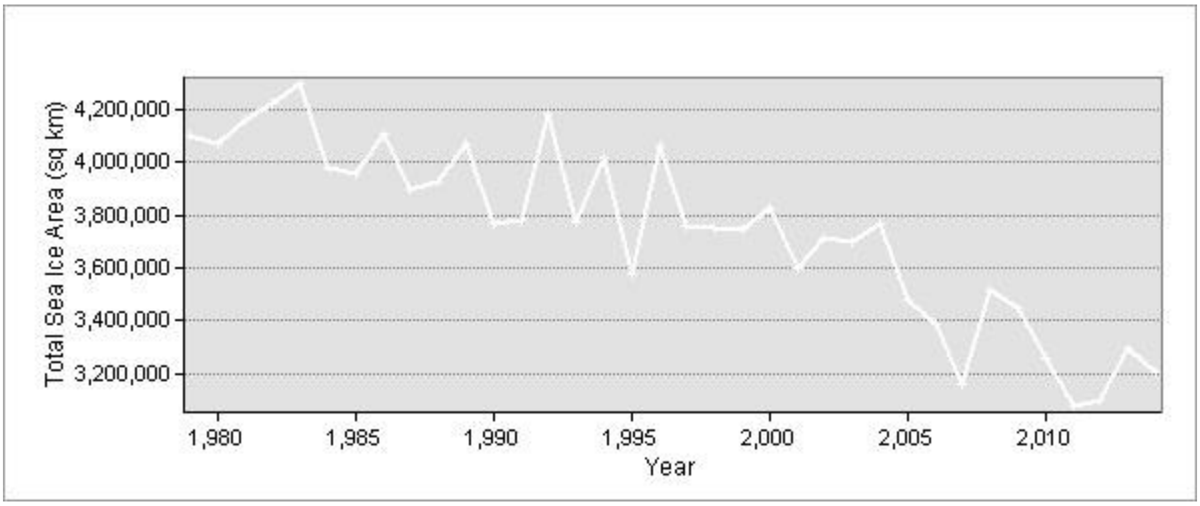

Figure 1: Sea ice coverage in summer in the Arctic Ocean from 1979 to 2014 (Esri Canada Education and Research Group 2015) with data from Meier et al. (2015).

II. Methods:

a. Study area:

For this project, I collected 4,702 shells of multiple bivalve genuses from 31 sites in central and northern Chukchi Sea (Figure 2A-C) in summer 2015 (July 11th to July 22nd) on a research vessel funded by United States Geological Survey (USGS). These regions contain several bivalve hotspots and attract a large number of Pacific walrus as well as other large consumers (Grebmeier et al. 2006). The locations of sites were further justified by the historical distribution records of most abundant targeted families (Figure 2 A-C) (W.S. Beatty, U.S. Geological Survey, unpublished data).

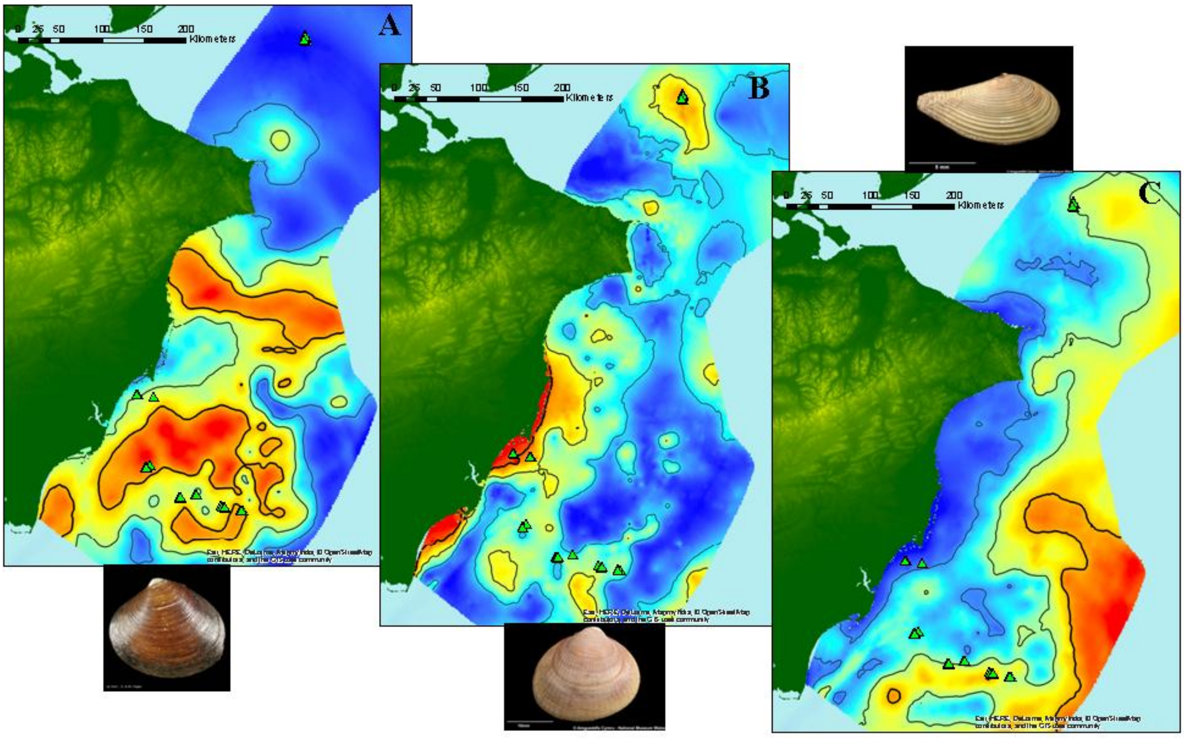

Figure 2: Historical distribution maps of three targeted Bivalvia families in the central and northern Chukchi Sea (W.S. Beatty, U.S. Geological Survey, unpublished data) with location of sites visited in Summer 2015. A: Artartidae, and representative species *Astarte borealis*. B: Cardiidae: *Serripes groenlandicus*. C: *Nuculanidae: Nuculana minuta*. Note: no legends available from U.S. Geological Survey dataset, color scheme from blue to red indicates distributions from lower than historical averages to higher than historical averages in all families.

b. Bivalve processing:

All specimens will be processed at the University of Texas – Marine Science Institute (UT-MSI), Port Aransas, Texas.

i. For biochronology development

Only the hinge plate will be processed as it is protected from erosion and thus provide the most complete records. The hinge area of one shell of each specimen would be thin-section (~100um), and polished with a sequence of sandpaper. The polished slides would then be viewed by a dissecting microscope with either reflected or transmitted light and have images taken (Black et al. 2008, Black 2009, Ambrose Jr. et al. 2011). Increments will be marked accordingly to the year they formed and have their with measure (See Figure 1 in Black et al. (2008) for details). The number of increments, indicating how old the specimens were, will be analyzed against the entire shell length records using either linear regression or von Bertalanffy growth functions (Ambrose Jr. et al. 2006, Ambrose Jr. et al. 2011) to study the age-growth relationships.

As proxy of the aforementioned biochronology analysis, I processed a subset of *Serripes* and *Clinocardia* specimens and used selected preliminary records from to present the results in this report.

ii. For stable isotope signatures:

All soft tissues from the above specimens will be extracted from the specimens above but only abductor muscle tissues will be used for stable isotope analysis (Dunton 2001). The tissues will be separated from the rest of specimens, dried overnight at 60^{o}C and manually ground. Samples will be then analyzed for carbon and nitrogen stable isotope signatures (Dunton 2001).

As proxy of the aforementioned stable isotope analysis, I selected 176 data points that belonged to my targeted genuses from the stable isotope synthesis comprised by Prof. Kenneth H. Dunton, Marine Science Institute – University of Texas at Austin, as part of the Pacific Marine Arctic Regional Synthesis (pacMARS) project to present the results in this report (Figure 3) (Dunton 2015, Grebmeier et al. 2015).

c. ArcGIS:

All maps presented in this report were projected in the GCS_WGS_1984 Geographic coordinate system using the D_WGS_1984 datum. The projected coordinate system was the North Pole Lambert Azimuthal Equal Area to maintain correct Earth surface area (D. Maidment, University of Texas at Austin, pers. comm.). The topographic/bathymetric data were from International Bathymetric Chart of the Arctic Ocean (IBCAO) Version 3.0 dataset (Jakobsson et al. 2012, 2015). The bivalve distribution record maps were imported into ArcGIS using the KML to layer tool with GroundOverlays selected in ArcGIS 10.3.1. The interpolation method chosen for this report was natural neighbor from the spatial analyst toolbox in Arc GIS 10.3.1 (Childs 2004) because it works well uneven points in distribution and density (Rodriguez 2015) like this dataset.

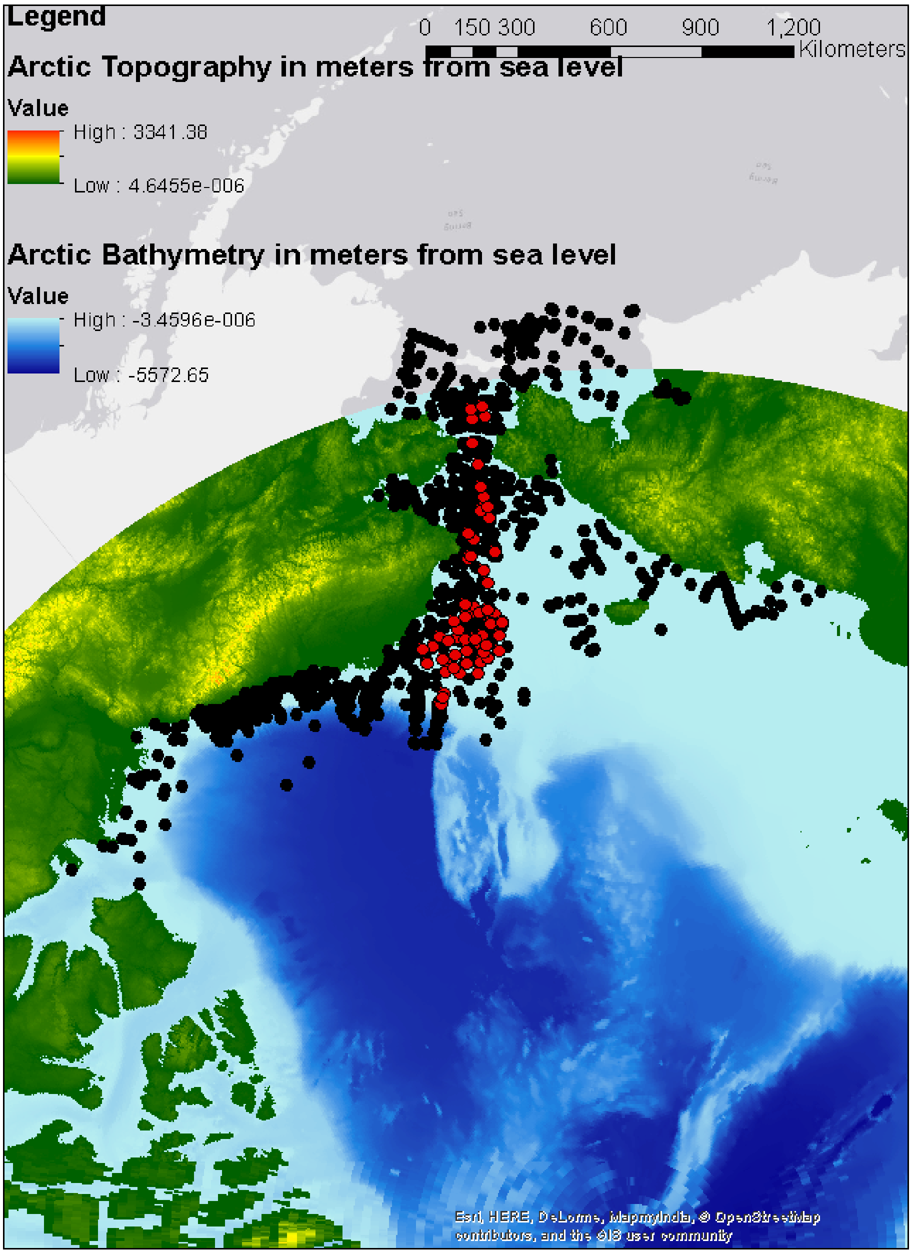

Figure 3: Map showing locations of all PacMARS stable isotope samples (black points) and the selected locations of samples belonging to targeted Bivalvia genuses in central and northern Chukchi Sea (red points).

d. Other statistical analyses:

Other statistical analyses, including growth functions on shell increments and fitting principal component analysis on stable isotope signatures, were performed by R Statistical package version 3.2.2 (R Development Core Team 2013)

III. Results and Discussions:

a. Age-growth relationships

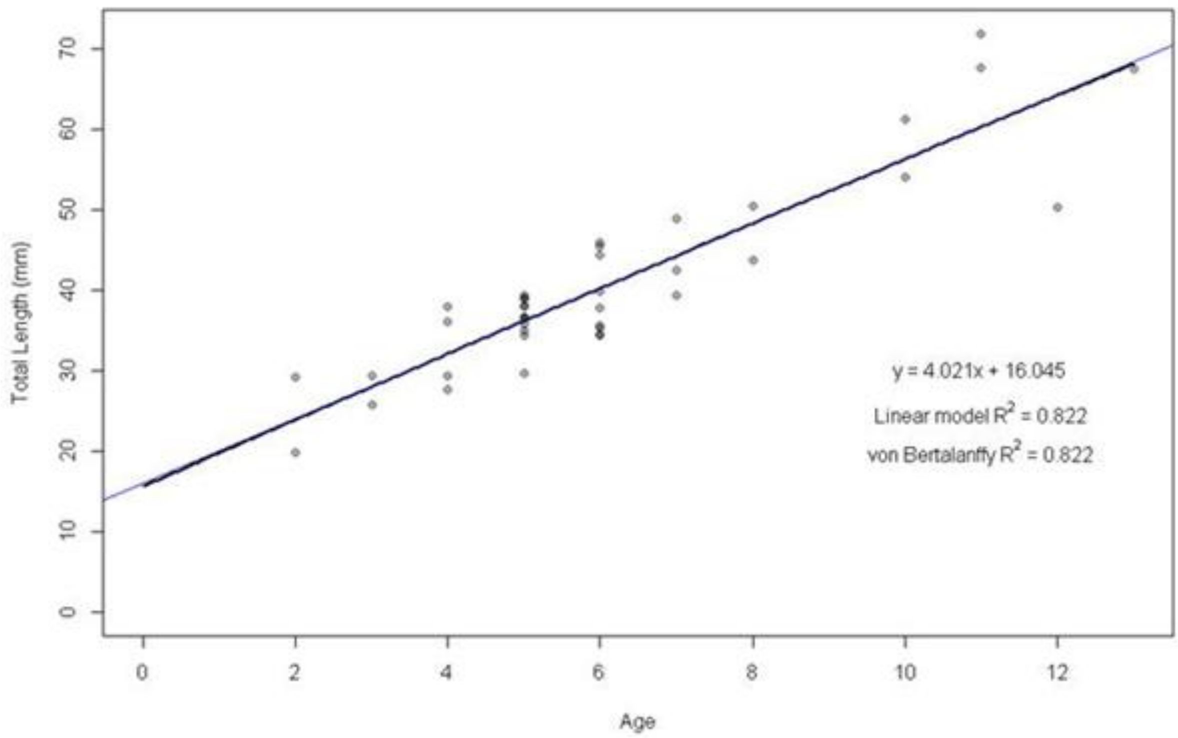

Figure 4: Age and growth relationship in *Serripes* specimens collected from central and northern Chukchi Sea in Summer 2015. The two functions plotted against the data are linear regression model (blue line with full equation and coefficient of determination included) and von Bertalanffy model (black line with coefficient of determination included).

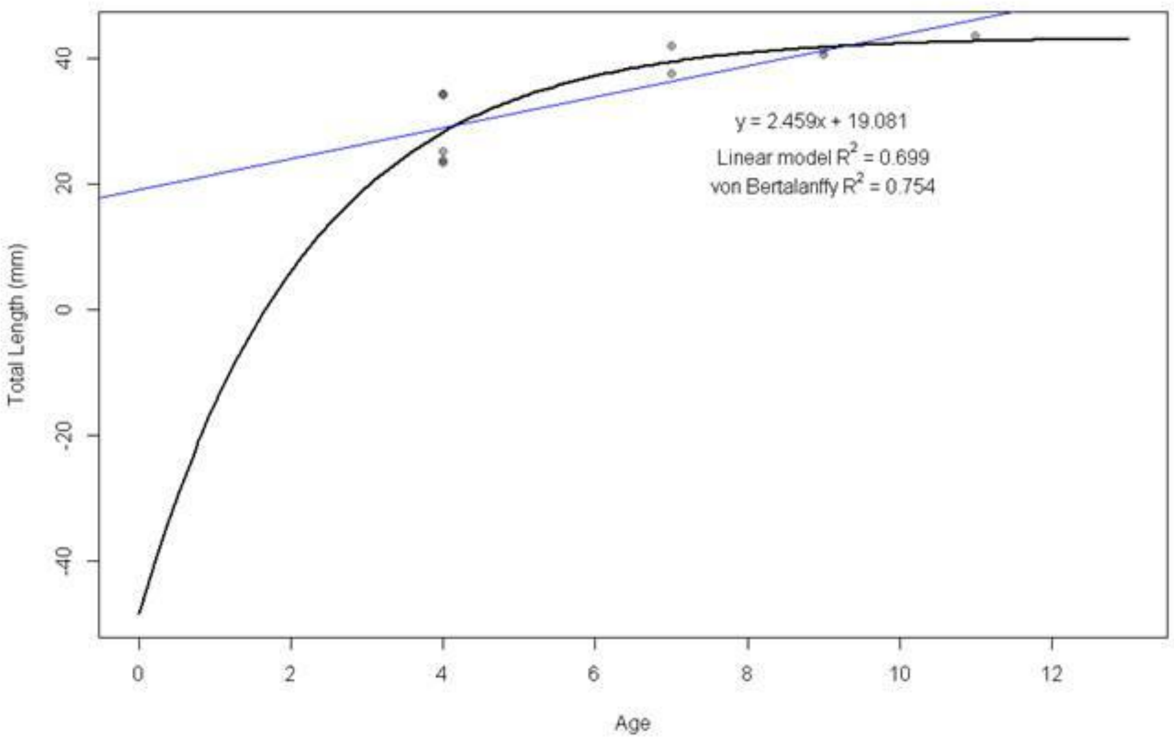

Figure 5: Age and growth relationship in *Clinocardia* specimens collected from central and northern Chukchi Sea in Summer 2015. The two functions plotted against the data are linear regression model (blue line with full equation and coefficient of determination included) and von Bertalanffy model (black line with coefficient of determination included).

There is little to none difference between using linear regression function and von Bertalanffy function to illustrate the age and growth relationship among *Serripes* specimens collected in this project. Both gave a significant output of R^2 = 0.822 and produced near identical line of best fits (Figure 3). The results indicate a strong relationship between the number of increment a *Serripes* shell has, i.e. how old the organism was when it was collected, and its entire length. In *Clinocardia*, although both linear regression function and von Bertalanffy function produced high correlation coefficients (R^2 = 0.699 and 0.754 respectively), only 10 data points were available and the results therefore were not highly reliable. Furthermore, while both functions produced significant results as expected, it is worth noticed that there are other growth functions that have been utilized in biochronology studies (Chen et al. 1992) and thus should be investigated.

Stable isotope signatures:

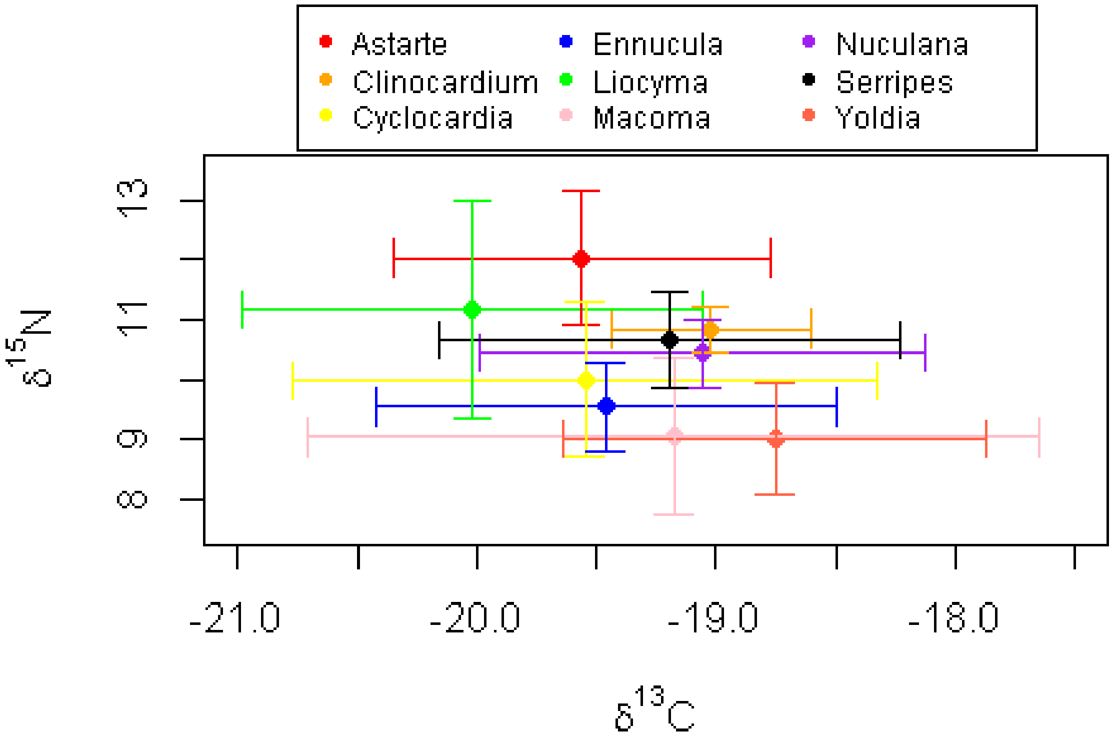

Figure 6: Stable isotope signatures ($\delta^{13}C$ and $\delta^{15}N$) values (average over all years ± SD) for all targeted genuses.

There is no distinguishable signature among the targeted genuses from PacMARS dataset. Signals vary between -21 to -18‰ for $\delta^{13}C$ and between 8 and 13‰ for $\delta^{15}N$. The ranges are similar to those recorded by previous studies in the Arctic Ocean (Hobson & Welch 1992, Dunton 2001). These data fit in the narrative that all targeted Bivalvia genuses in the central and northern Chukchi Sea have similar food sources and a disruption in sea ice algae productivity would likely affect equally. Spatial interpolation results show values also within comparable ranges (Figures 7 and 8). There is a higher enrichment in $\delta^{13}C$ in the central region of the Chukchi Sea (Figure 7) which indicates organisms with faster growth. Furthermore, specimen from central Chukchi appears to have higher $\delta^{15}N$ enrichment which means they feed on higher trophic level (Figure 8). Both phenomena could be explained by the warmer water temperature leaked through the Bering Strait from the Pacific Ocean, thus produce better conditions for growth.

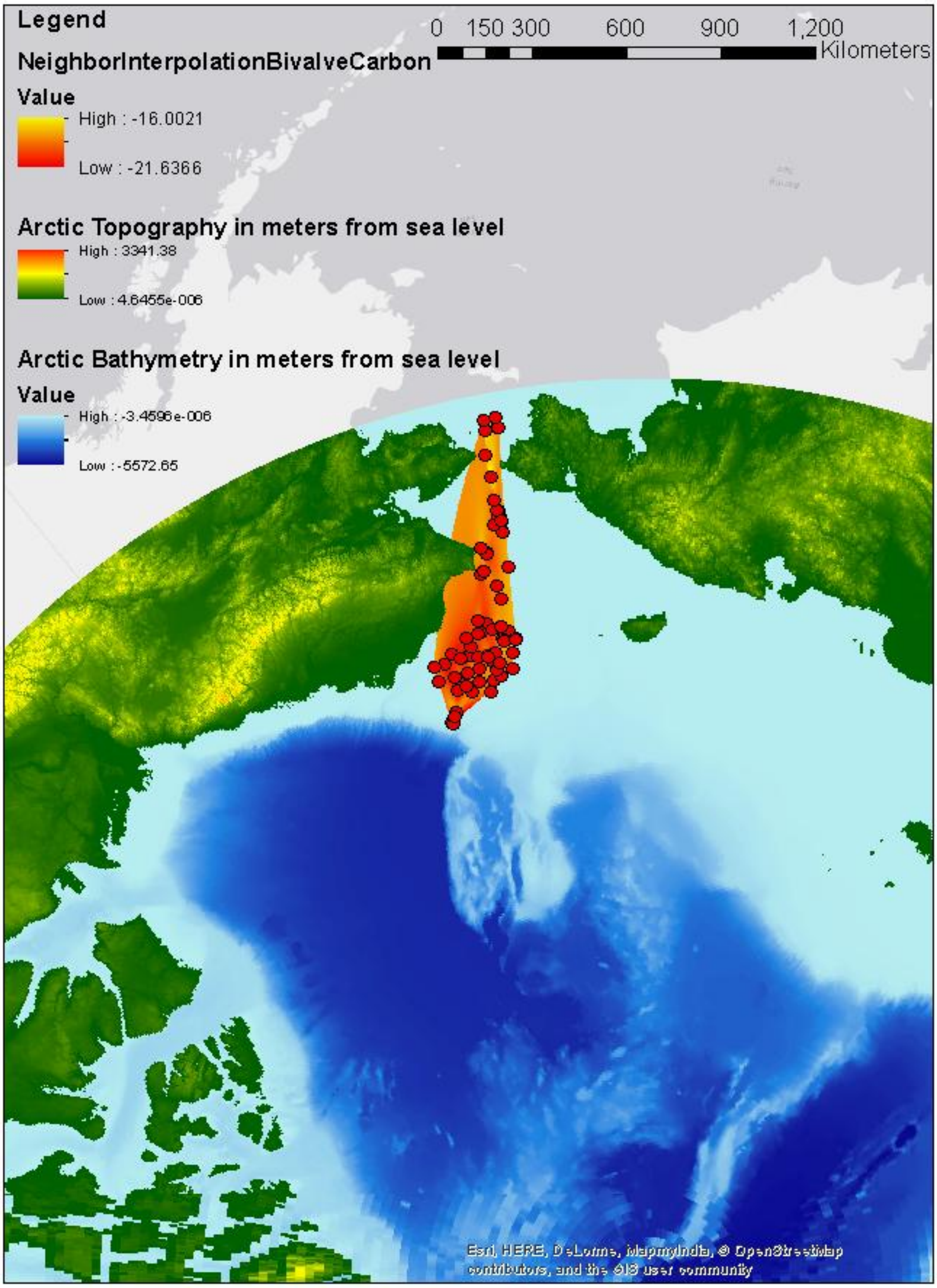

Figure 7: Raster created from natural neighbor interpolation method in ArcGIS 10.3.3 for carbon stable isotope signature ($\delta^{13}C$)

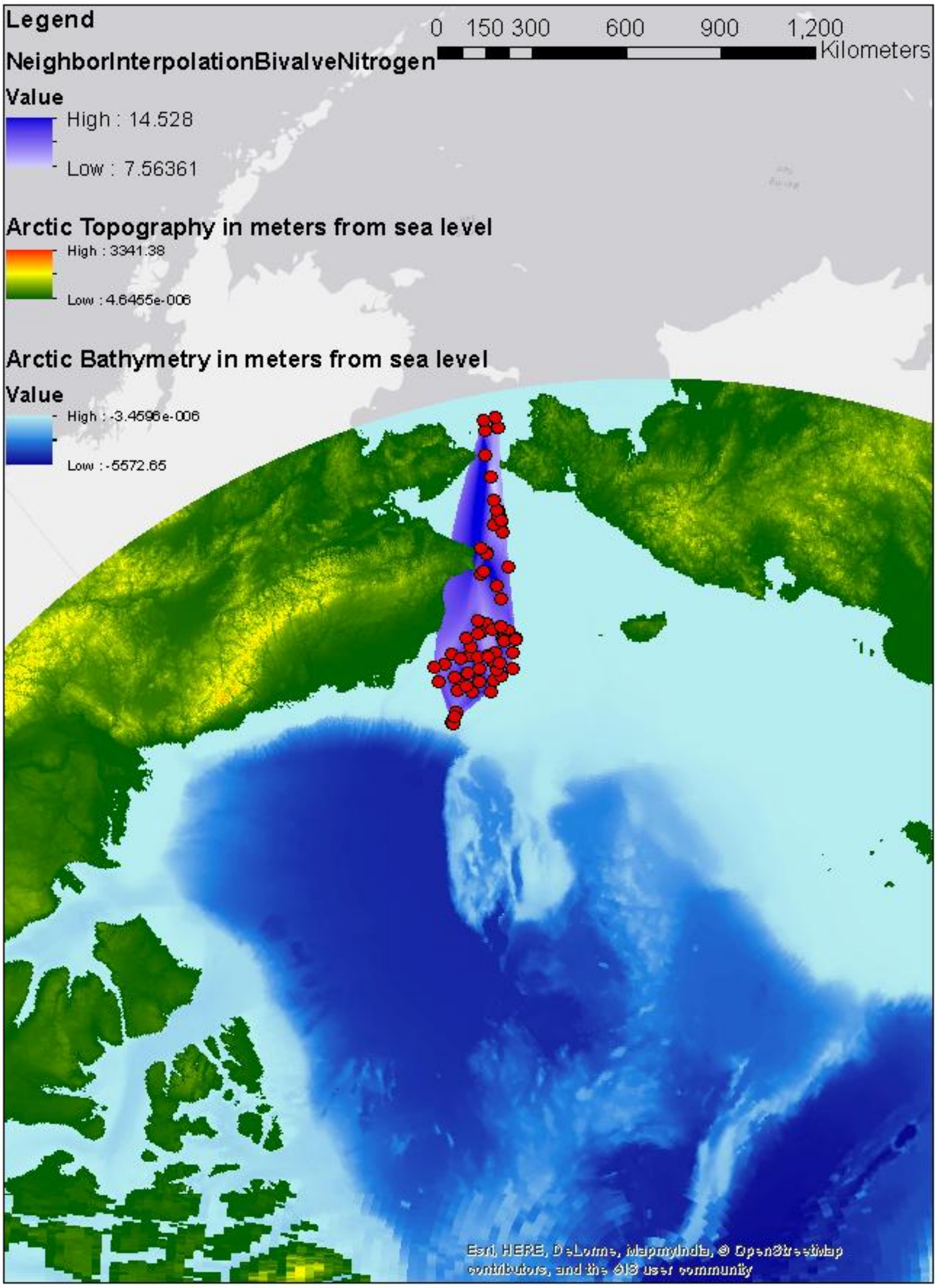

Figure 8: Raster created from natural neighbor interpolation method in ArcGIS 10.3.3 for nitrogen stable isotope signature ($\delta^{15}N$)

The pattern of stable isotope signatures above are again observed in principal component analysis output (Figure 9). Latitude and longitude values are negatively correlated with $\delta^{13}C$ and $\delta^{15}C$ signals. More importantly, the year the specimens were collected is correlated negatively with stable isotope signature of nitrogen but positively with that of carbon. This indicates a shift in food web toward more basal food sources but with higher nutrient contents for bivalve in the studied region. The signals coincide with the warning of global warming at lower latitudes. A warmer climate could affect the flow of the Bering Under Current which brings nutrient-rich water from the Bering Sea northward (Dunton et al. 2006).

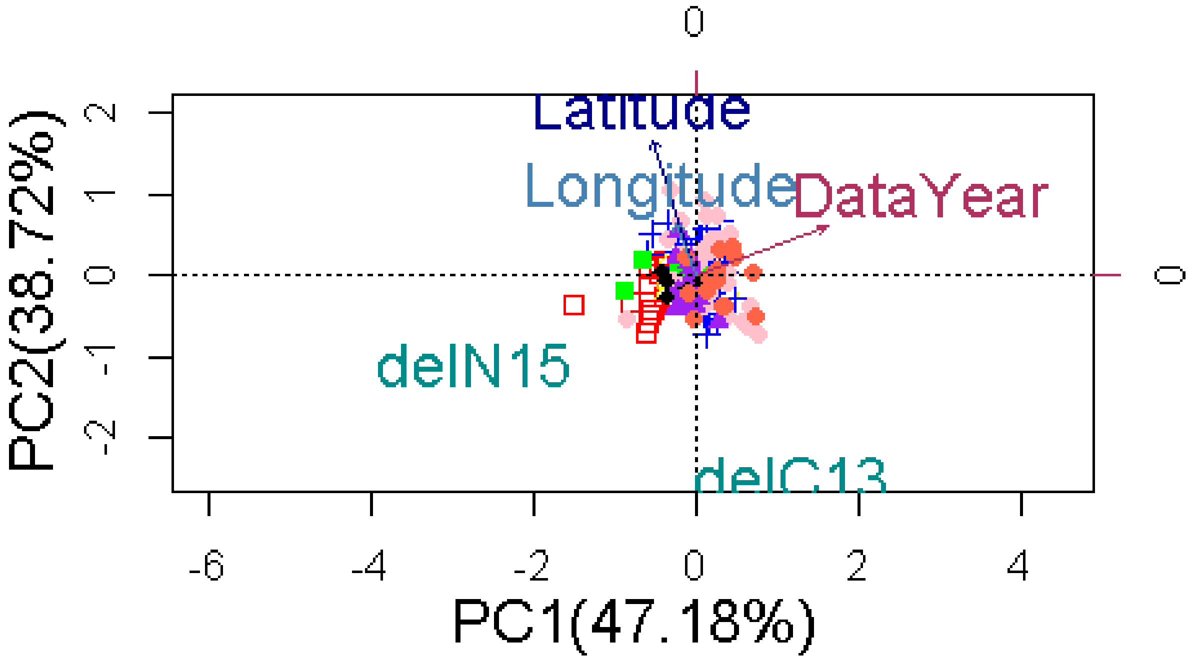

Figure 9: Biplot of the (scaled) two principal components (PC1 and PC2) of the δ^{13}C, δ^{15}N composition variables of bivalve samples with the geographic coordinates and the year they were caught. *Note*: the left and bottom axes show the loading of each variable on the two principal components; the top and right axes show the principal component score of each sample.

IV. Conclusion and future work:

Arctic bivalves from the Chukchi Sea, a marginal sea of the Arctic Ocean, have shown signs to be affected by the changing in climate. Together with ArcGIS and other analysis tools, biochronology and stable isotope analyses promise an in-depth understand of historical bivalve growth records which could be used to reconstruct past climatic. There are data already available from other studies but remain in inefficient volume. Future work including processing the nearly 5,000 bivalve samples from Summer 2015 field trip would certainly help fill in the gaps to provide a better picture of the imminent global warming effects on the regional productivity.

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