TExNet workshop in Nuuk

14-19 May, 2025

Attending: Mathilde Le Moullec, Laura Barbero-Palacios, Amelia Keilbach, Théo Louis, Isabel C Barrio, Mathilde Defourneaux, Elina Kaarlejärvi.

The workshop was hosted by the Greenland Institute of Natural Resources (Kivioq 2, Nuuk 3900). The wokshop took place in Nuuk for the first two days at the facilities of GINR, while the last three days part of the team went on a writing retreat to Kapisillit. Funding to organize this workshop was provided by the 2024 UArctic Project Call for Networking Activities on UArctic Research and Education, for the project: *"Implications of changes in tundra herbivore diversity -West Greenland in a multiscale circumpolar experiment"*, and support for travel of early career researchers through the Nordic Borealization Network (NordBorN) funded by NordForsk (project nr. 164079).

An updated overview of the workshop agenda can be seen in **Table 1**.

Table 1. Updated agenda for the TExNET workshop in Nuuk

	Tues 13th	Wed 14th	Thurs 15th	Fri 16th	Sat 17th	Sun 18th	Mon 19th
9:00		Background presentations (EK, ICB, LBP, MD, MLM) Muskox room	Hands-on work	Departure to Kapisillit	Hands-on work	Hands-on work	Hands-on work
9:30							
10:00			Coffee break				
10:30		Coffee break	Hands-on work Muskox room				
11:00		Plan on analysis and task distribution Muskox room					
11:30							
12:00	Lunch EK arriving	Lunch (cantina)	Lunch (cantina)		Lunch	Lunch	Lunch
12:30				Lunch			
13:00	Resting time	Hands-on work Polar Bear room	Future of TexNet (EK) Muskox room	Hands-on work	Hike to reindeer area	Hands-on work	Departure to Nuuk
13:30							
14:00							
14:30		Coffee break	Coffee break				
15:00		Hands-on work Polar Bear room	Hands-on work Polar Bear room				
15:30						Resting time	
16:00				Hike around Kapisillit			
17:00	ICB and MD arriving	Lille Malene hike					
18:00			18.30 Dinner at Killut (covered)				
19:00	Dinner at the Annex (not covered)	Dinner at the Biology Station		Dinner	Dinner	Dinner	

Tuesday 13th May

Plans for Tuesday were delayed because of late arrival of the flight from Iceland. We had dinner together at the Annex.

Wednesday 14th May

9:00 – 10:30 Background presentations
[open to GN and online options]

TExNet: the Tundra Exclosure Network: ICB and EK gave a presentation of the Tundra Exclosure Network (TExNet) as a base for the discussions for the following days. TExNet is an initiative that started as part of the TUNDRAsalad project, funded by the Icelandic Research Fund (Rannís). The aim of the project was to understand the role of herbivore diversity on the functioning of tundra ecosystems, using complementary approaches. One of these approaches established a coordinated experiment that manipulates herbivore diversity across multiple tundra sites. TExNet proposes the use of size selective exclosures to isolate the separate and combined effects of different herbivores on tundra ecosystems. Setting up an experimental site requires an initial investment and a commitment of at least five years. To expand the geographical spread of sites, an observational protocol was proposed, that required a single visit to the sites. Data collected with the observational protocol is comparable to data collection in the initial year of the experiment. Data has been collected at observational and experimental sites since 2022, and currently there are six TExNET experimental sites and data has been collected at 20 additional sites using the observational protocol. More information about TExNet can be found here.

Herbivore diversity effects on Arctic tundra ecosystems: a systematic review: LBP presented a systematic review on the effects of herbivore diversity on tundra ecosystems. This work emphasizes the lack of studies specifically addressing the role of herbivore diversity on tundra ecosystems, highlighting the need for coordinated experimental manipulations like the one proposed in TExNet. The paper was published in Environmental Evidence (Barbero-Palacios et al 2024), also as a contribution of the TUNDRAsalad project.

The impacts of spatio-temporal shifts in vertebrate herbivore communities on the functioning of the Icelandic tundra: MD presented her PhD work on the changes over time and space in Icelandic herbivore communities, and the implications these changes have to the functioning of tundra ecosystems. MD's work assessed historical changes in the abundance of wild and domestic herbivores in Iceland and their impacts on Icelandic vegetation (Defourneaux et al 2024). In addition, MD developed tools to assess nutrient contributions by different species of herbivores (Defourneaux et al 2025) and assessed nutrient redistribution across the Icelandic tundra.

Implications of changes in tundra herbivore diversity - West Greenland in a multiscale circumpolar experiment: MLM presented an overview of the variables collected at two sites (KQN and KQS) in summer 2024 following the observational and experimental TExNet protocols. In summer 2024 the two sites were selected, one where caribou is the dominant large herbivore, and another one where muskoxen are more abundant. The two sites are dominated by graminoids, while KQS has also dwarf shrubs. At each site three patches were selected for the study. The plan is to set up larger exclosures than the ones required for the TExNet experiment, so that the design is comparable to other herbivory studies conducted near Kangerlussuaq. The fences for the experiment will be installed in summer 2025.

11:00 – 17:00 Plan on analysis and task distribution, and hands-on work
[continued on Thursday morning and during the writing retreat in Kapisillit 16-19 May]

The plan for the workshop is to advance the work on the first TExNet publication, which will include data from the observational protocol and from the initial year of the experimental protocol.

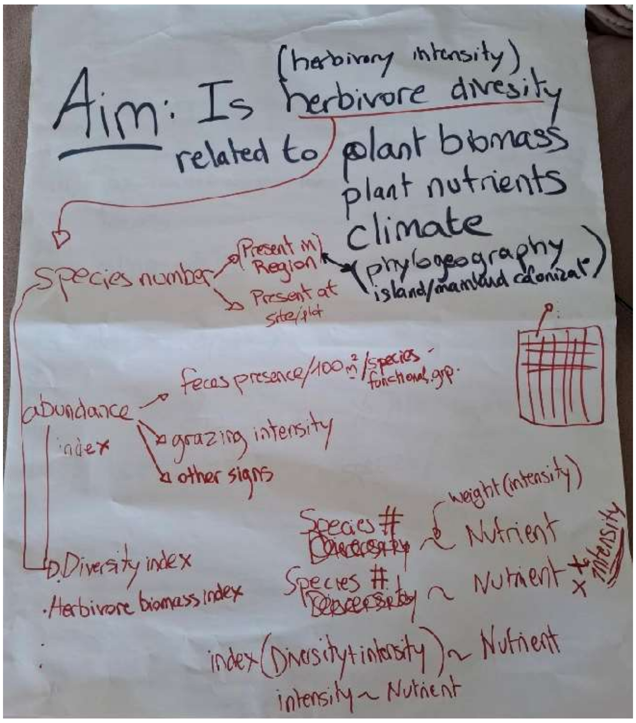

Figure 1. *Aim of the study*

Discussing the overarching questions: the aim of the study including data collected with the observational protocol and the first year of the experimental set up (year 0) is to assess the relative importance of aboveground biomass, nutrient content of vegetation and climate/weather and other environmental variables as drivers of herbivore diversity at the local scale and across the tundra biome (**Figure 1**).

The sampling design was such that herbivore diversity was measured in patches ca. 10 x 10 m, recording the presence/absence of herbivores in 100 plots of 1m^2 in each patch. At most sites, two habitats of contrasting productivity (one used by most herbivores, and the other used by some herbivores) were selected, and three replicate patches were sampled per habitat. We have a total of 27 sites across the tundra (**Table 2**).

Signs of the presence/absence of herbivore species (or higher taxonomic groups when not possible to identify at a higher resolution) that were recorded at the plot level (1m^2) included faecal pellets (faeces), or other signs of herbivore activity, including a variety of signs representing different strengths of evidence of herbivore activity, from bite marks and tunnelling to presence of feathers or hair. We classified these other signs as “bite marks” (signs of feeding activity), “signs of activity” (non-feeding activities by herbivores, like winter nests or burrowing) or “other” (other signs of presence, such as hair). One difficulty is that the taxonomic level differs between categories and sites (see further discussion below). These measurements allow quantifying the occurrence of herbivore species (or higher taxonomic groups) at the patch level, i.e., species richness, but can also provide an index of abundance (prevalence-based index of abundance as the proportion of plots per patch where herbivore presence is recorded). This index of abundance/intensity can be used in: 1) herbivore diversity index accounting for abundance (see discussion below on diversity index), 2) as some sort of model weight/offset, 3) as an interacting factor with some predictors e.g., anti-grazing plants components affecting nutrient levels in highly grazed sites, of different compensatory growth patterns/biomass in highly grazed sites. If herbivore intensity is used as a response variable in its own, we are addressing a different aim. An index of intensity of herbivory could also enable some approach like metabolic biomass of herbivores.

Herbivore diversity can be defined in many ways (see discussion below), but generally refers to a measure of herbivore species number detected at a local scale relative to a herbivore species number detected at a larger spatial scale. With our study design, the patch-level is our smallest level of local species detection. We discussed what would be the most appropriate measure of ‘larger spatial scale’ of herbivore species detection to characterize herbivore diversity. It can be the number of species detected at the site level. In this case, if the number of species detected at the patch level matches the number of species detected at the site level, this patch has a high herbivore diversity index. Site-level may be appropriate when having low and high habitat productivity, however, it becomes problematic when only one habitat has been monitored and the number of patches per site differs, as the number of species detected at the site may increase with increasing number of patches (more investigations needed here). One way around may be to obtain the total number of herbivore species at the regional scale, asking PIs from each site.

One consideration discussed is the need to account for phylogeography. If the aim is to investigate herbivore diversity patterns at the tundra biome scale (i.e., the maximum level of diversity is higher than the regional scale), then we have to account for geographical limitations of dispersal of some herbivore groups, i.e., island/mainland.

Potential drivers of herbivore diversity (predictor variables; **Figure 2**) include measurements of plant productivity (total biomass, remote sensing NDVI or biomass map), plant nutrients (from NIRS) or plant diversity (from point intercept in some sites) and environmental variables related to weather (short term), climate (long-term), terrain features (slope, aspect), or other (e.g. predation, ask in the regional species list of PIs?). Further details below.

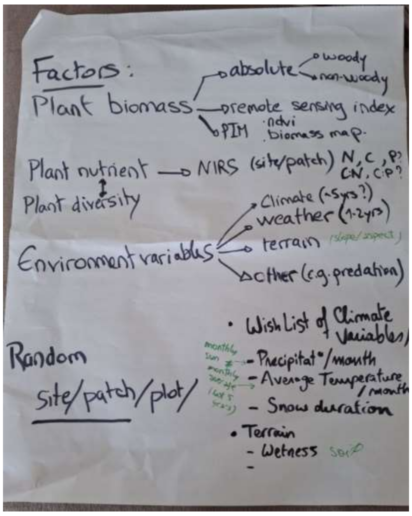

Figure 2. *Potential drivers of herbivore diversity*

Setting up a repository on GitHub for joint data analyses: a GitHub repository was set up: https://github.com/icbarrio/TExNet For now the repository is private (if you want access, please contact Isabel: isabel@lbhi.is).

Overview of the dataset: data for this project has been collected during the summers 2022 to 2024 and includes 27 sites across the tundra biome. For some of the sites there is data for all parts of the protocol, for some of them some parts are missing (**Table 2**), so some analyses will use specific subsets of the data. As well, different sites sampled one or two habitats, and the number of patches per habitat could also differ.

Table 2. Overview of sampling structure and measurements available.

Sampling levels and measurements		**Number**
Number of sites	Sampling two habitats	21
	Sampling one habitat	6
Number of sites	Observational protocol	21
	Experimental protocol	6
Number of patches per site		3-8
Number of patches per habitat		1-5
Number of sites with herbivory data		26
Number of sites with biomass data	Total aboveground biomass	25
	Separated woody/non-woody	12
Number of sites with plant chemistry data		26
Number of sites with plant community data		12

Cleaning the datasets: the data includes several types of data that require curating and homogenizing:

- **Information on sites, patches and plot names:** there were some inconsistencies in the naming of sites, patches and biomass harvest strips (**Figure 3**). The naming system we use within the project for the more detailed level (biomass harvest strip) includes: site name (three letters), patch name (some indication of habitat and patch number) and an indicator of the biomass strip, so it looks something like: *AUD_H1_Oa*. In the field, different names may have been used, and these are indicated in the data files with a name including “field” (e.g., field.code.plot).

  ⚠ This double coding system can create some confusion especially for the plant nutrient dataset, where either one system or the other was used when labelling the samples.

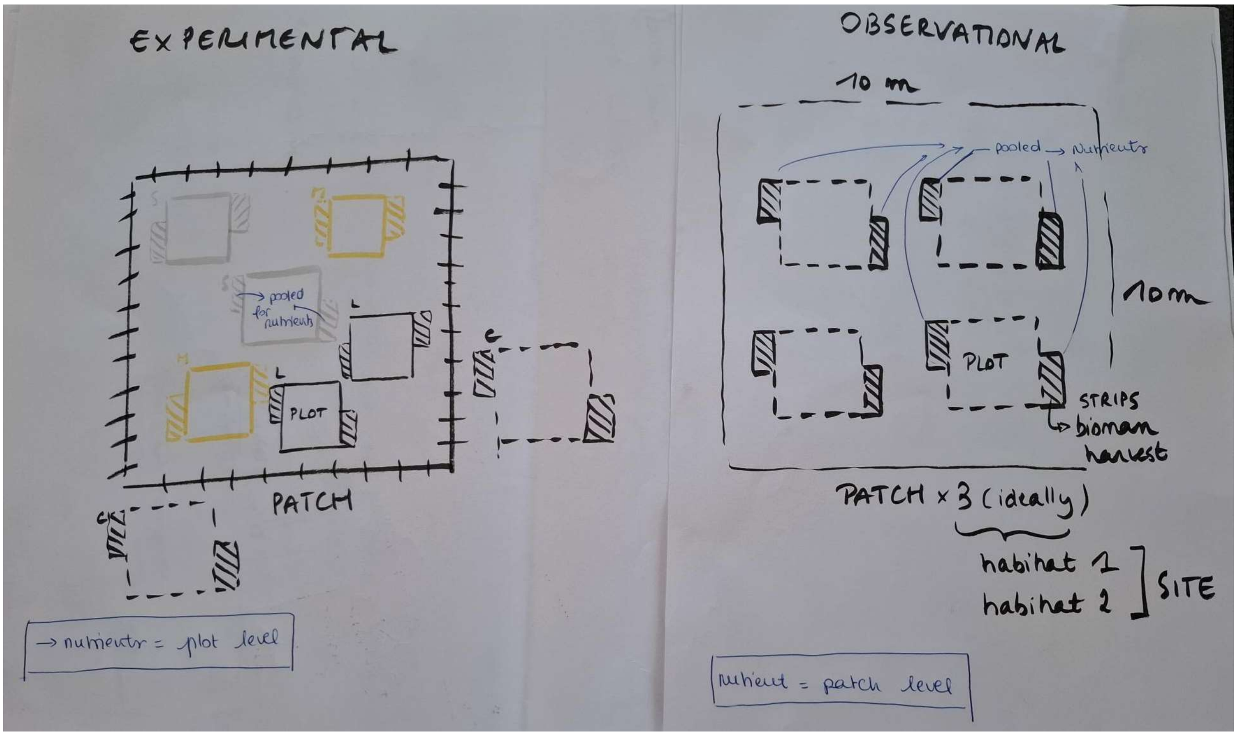

Figure 3. *Diagram of the experimental and observational sampling design.*

- **Location of study sites:** geographical coordinates of sites were reported in different formats and required conversion and careful checking. There were some coordinates missing at the patch level. The overall distribution of sites to be included in the study is shown in **Figure 4**.

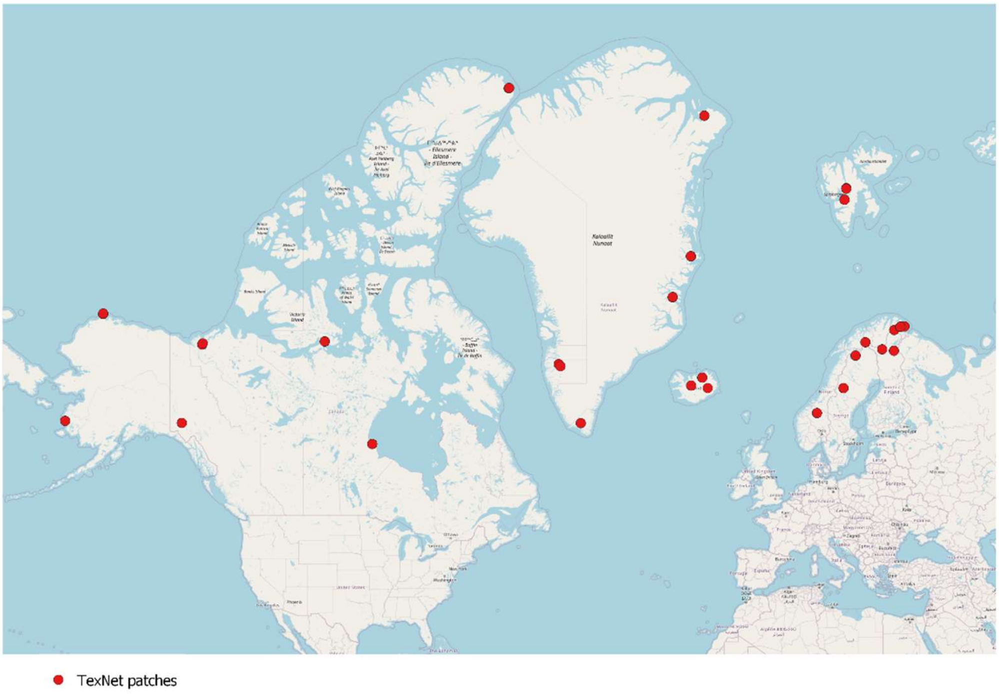

Figure 4. *Location of study sites.*

- **Data on herbivore presence (i.e., pellets, bite marks and activity):** at each patch we recorded signs of herbivore presence, whenever possible associated to a specific species of herbivore, but to higher groupings when it was not possible to assign to a species. In the database, signs are recorded as either 'pellets' or 'other signs of herbivory'. However, the latter category includes signs that have different meanings. For example, a feather could have been blown from somewhere else, but a lemming nest is a strong indicator of lemming presence in the patch, and bite marks or grubbing are a clear sign of herbivore activity in the patch. Some issues arise from the fact that the instructions in the protocols advised on focusing on pellets, and (secondarily) record other signs of herbivory, so these other signs may not have been recorded as consistently as pellets. It was decided to provide more details about these other signs of herbivory and separate them into: 'feeding marks' (e.g., grubbing, bite marks), 'activity' (e.g., burrows, winter nests) and 'other' (e.g., carcass, hairs, feathers).
  Pellets of large herbivores were attributed to specific species across all sites, while it was often attributed to coarser groups for small mammals and different goose species. However, the other signs of herbivory can come at even coarser taxonomic resolutions (e.g. bite marks by herbivores but not known whether the herbivore is a goose or a sheep). This poses challenges when pooling data across sign types at the patch level, because we do not want to lose information for the species. One suggestion was to look at the prevalence of different types of signs, and if the prevalence is too low, ignore the signs with very coarse **taxonomic resolution** (if prevalence is high, then we need to think more about it and decide if we infer a taxonomic level from what we know is present in the patch). In addition, in each patch we may have **different signs for the same species or group of herbivores** (e.g. pellets and grubbing by geese). We need to make sure that those are only counted once. We can also check whether there is a correlation between different signs of herbivory, as it is likely that pellets and signs of activity like nests or tunnels are highly correlated for small mammals, whereas for larger mammals this correlation may be expected for pellets and bite marks, but likely less strongly than for small mammals.

***Calculation of herbivore diversity:** a coarse measure of herbivore diversity would be the number of species detected in a patch (species richness). As well, this could be expressed as a relative value, taking into account the number of species detected at the site level or even regional level as a measure of the species pool, e.g., 3 species detected at the patch out of 4 known to be present in the area. This measure of the species pool could be calculated based on the total number of herbivore species detected across all patches in a site (here it would be good to compare the species richness for each habitat type for sites that included two habitats and see if it is comparable for sites that only sampled one habitat). As well, we could ask site PIs for information on the potential maximum number of species (and which ones) at their sites.

Other indices of diversity discussed, and to be investigated further, include the ones with information on abundance (prevalence-based, exponential of Shannon: Jost 2006, Oikos) or functional diversity indices (Speed et al 2019, Ecography – check with James), such as multivariate traits with different weights (Laliberté & Legendre 2010). EK's suggestions:

How many equally abundant species within a patch? = How similar are species abundances within a patch?

- After curating data so that it does not contain any nested taxa, compute prevalence for each taxon in each patch by considering the observation of any sign of herbivory (herbivory_type) equally valuable (or ignore 'other_signs_herbivore', in case it does not tell anything about the presence of a species in the patch).
- Calculate Shannon entropy (Jost 2006, Oikos) using the function 'diversity' in the *vegan* package (the diversity function in *vegan* gives H, take exp of it).

$$ {}^{1}\mathrm{D} = \exp\left(-\sum_{i=1}^{S} p_i \ln p_i\right) = \exp(\mathrm{H}) $$

Functional diversity

- Functional diversity tells how different or similar are the characteristics (= functional traits) of the herbivore community using each patch. Functional diversity can be measured with single or multiple traits, and either by giving species equal weight or by weighting species' traits with their relative abundance.

- Speed et al 2019 lists multiple traits of Arctic herbivores (Suppl Table A3). The following traits included in the table could be related to habitat use: diet type (3 categories: obligate generalist, obligate specialist, facultative generalist), body mass (continuous), diet breadth index (continuous; as a sum of 5 diet column values).

- To calculate functional diversity we would need to build a trait file, which lists all herbivore species as rows and functional traits as columns. For higher taxonomic levels, we could calculate a mean trait value or assign the most common categorical trait value (if that makes sense).

- To calculate functional diversity index, we can use the *FD* package:

- Check first the correlations among the three traits. If they are not strongly correlated, all of them can be used for calculating multi-trait functional dispersion.

    - Use dbFD function in package *vegan*. It allows both continuous and categorical traits, but no missing values. Use species prevalence (as vector w) for weighing the traits with species abundances. dbFD function calculates many functional diversity indices at the same time, but FDis has many properties making it more useful than the others.

- **Data on aboveground plant biomass:** for most sites we have information on total aboveground plant biomass (AGB). In some cases, weights are provided separately for the woody and non-woody fractions.
  We considered using the new Arctic plant biomass map (Orndahl et al. 2025) for additional information and possible comparison. The map provides total aboveground biomass (AGB) and woody AGB values for most of our sites (except the three sites in Iceland) with a 30x30m resolution. However, total AGB includes bryophyte biomass and woody AGB includes the entire woody plant, not just the woody fraction. It was therefore decided to **focus on the field measurements at the local scale for now** and potentially use the biomass map for information on woody plant dominance if needed. Additionally, we discussed using NDVI as a proxy for biomass. However, since this study is not focused on a large scale, we dismissed that idea for now.

  ⚠ AGB might have been weighed differently across sites! In some cases, researchers weighed biomass themselves, and woody biomass may refer to "woody species", including leaves and wood of those species, whereas in others woody biomass includes only "woody fractions". Some samples were weighed in Iceland. In those cases, the total weight is reported first, and the woody fraction and non-vascular biomass were separated after the initial weight, when preparing the samples for nutrient analyses. In those cases, total weight includes woody and non-vascular, but the column for non-woody is not reported (= total – (woody + non-vascular)).

- **Data on plant nutrient content:** the non-woody fraction of aboveground biomass was pooled per patch (observational sites) or per plot (experimental sites), ground and scanned with NIRS. N, C and P were estimated (% dw) using existing models (Murguzur et al 2019); in addition, C:N and C:P ratios. Some samples (1-2 per site) will be analysed with wet chemistry to validate the application of the models to vascular plant communities, as the original models were developed for single plant species (ICB to contact Jonas about this). A consideration in this dataset is that biomass samples were pooled per *plot* (2 biomass harvest strips) in the experimental protocol, and per *patch* (8 biomass harvest strips) in the observational protocol, so we will have different sample sizes (and potentially random structures in the models).
  ➔ Preliminary analyses indicate that including P might not be feasible because the models estimated negative values in ca. 26% of the cases and have to be removed (this is a common issue for P).

- **Data on plant community composition:** assessment of plant community composition was marked as optional in the observational protocol. Still, 12 sites collected data on plant community composition using the point intercept method (and an additional site had detailed plant community data from nearby plots that could be used). From this dataset we can calculate plant diversity and assess its role as a local driver of herbivore diversity.

- **Other environmental variables:** based on the geographical coordinates of each site, we extracted information on:

  - Average surface temperature: for each season and at site level, we used MODIS radiometer data (Earth Observing System satellites) over the period 2012-2022. The data was extracted using Google Earth Engine.
  - Average precipitation per year was extracted for each of the sites, using the ERA5 database over the period 2009-2019.

Other variables that were discussed at the workshop were (more as a wish-list of climate and environmental variables, some might not be available at adequate temporal/spatial resolution):

  - Monthly precipitation
  - Average monthly temperature (averaged over the last 5 years)
  - Snow duration
  - Terrain wetness

- **Exploratory analyses:**
  The first step is to run univariate exploration of variables, to detect outliers (plot histograms) and also boxplots separated by site, by habitat type and by patch to see variability. Also, quantify variability at the different sampling levels (e.g., partition the variance from the random effects of GLMM: biomass ~ 1 + (1|site/patch/plot)). Do this for biomass, nutrients and plant diversity measures.
  For biomass, where available, check the relationship between woody vs total biomass. Eventually, generate summary tables with descriptive statistics for each variable: mean (min, max, SE). Also, explore relationships between the different signs of herbivory (see above) and look at relationships between variables, e.g., biomass ~ nutrients (**Figure 5**). This relationship may not be linear and could influence herbivore diversity differently because different herbivores may favour different ranges of biomass and nutrients. For example, we can expect large herbivores to use more patches with high biomass but relatively lower nutrient levels, while small herbivores may target patches with high nutrient but relatively lower biomass. Geese may be somewhere in between. We need to think of specific hypotheses to support predictions.

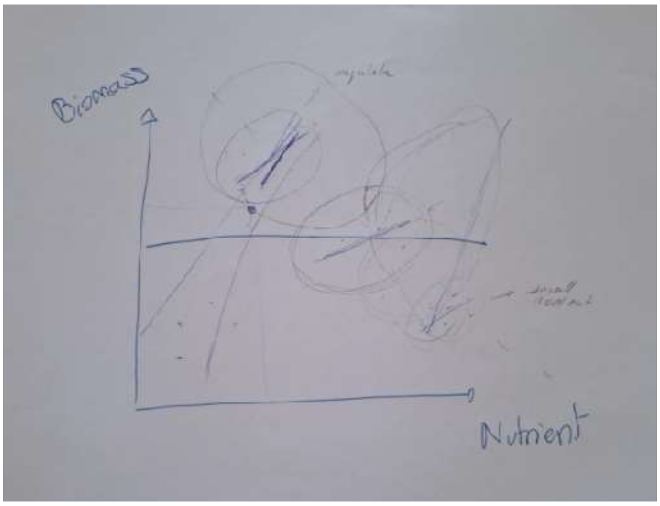

Figure 5. *The relationship between biomass and nutrient availability might vary for different herbivores (not super clear figure, but just so that we remember our discussions ;))*

- **Modelling approach:** probably Generalized Linear Mixed Effect Models, with site/patch/plot as random effect where relevant. The main model would probably be (measurements at patch level):
  [herbivore diversity] ~ biomass + nutrients + plant diversity + environmental variables + (1|site)

- **Writing up:** a manuscript draft is available: TExNet_Y0_ms.docx. So far, the manuscript mostly describes the methods, as explained in the protocols, but it is to be populated over the next months once we start getting some results 😊

After the workshop most of the data are compiled and cleaned, and some of the exploratory analyses were initiated. The next steps will include more exploration (also regarding the indices of diversity and functional diversity). It would be great to compile into a single document the results (figures) from these exploratory analyses, and thoughts that arise from them that we can discuss later.

Thursday 15th May

13:00 – 14:00 The future of TExNet, online participation option

EK opened the floor for discussions about the future of the TExNet experimental sites, which questions we could address within the TExNet network, what data collection would be possible or relevant, which funding sources to target and how to attract new contributors.

Kangerlussuaq (KQS and KQN) was the last site to be added to the network. One of the conditions that made this possible was the opening of a suitable funding call (UArctic) and the assistance with writing the grant application by the TExNet team. As well, the focus of the research suited the overall research interests of the PI, and allowed room for combining the experimental set up with other experimental manipulations of interest (e.g., icing experiments), by building larger fences. Maybe this could also be attractive to other researchers.

Funding opportunities seem to be opportunistic, e.g. through UArctic, maybe there are some suitable calls through NordForsk or NPA, or the national research councils. Other synergies that were mentioned are the toolkits for monitoring being developed by CBMP.

Some TExNet sites started already in 2022 (NAR, NII), others started later (ICE, KIL) and others will set up fences this summer (KQN, KQS). Thus, for comparable measurements, visits to the sites will have to be staggered over time – which in a way could be beneficial, for example if the measurements are part of a PhD thesis, so that not all sites need to be visited simultaneously. However, this may impose some constraints on adding more sites, if that means a much more extended period to collect comparable data across sites.

Some of the additional measurements that could be included are plant phenology, C dynamics, invertebrate herbivory and/or pitfall traps, drones for hyperspectral data, cameras to capture abundance of herbivores and environmental variables. Suggestions from other TExNet colleagues (THMK) include detailed assessment of bryophytes and lichens in year 5 and maximum plant height.