Distribution and abundance of mesopredator fishes across the Kimbe Bay seascape: an initial analysis.

Overview

I sub-sampled from existing 30m DOV transects (2017 – 2019, 20-30m depth) to assess relative abundance and diversity of mesopredator fishes across 3 different habitat types: seamount, offshore and near-shore reef environments. In total, 60 transects were included, 20 on each of the target habitat types and 40 species of mesopredator fishes from 9 families were observed across all surveys (see Annex 1).

Abundance

Mesopredator abundance was calculated as numbers of fish counted per transect and was as follows:

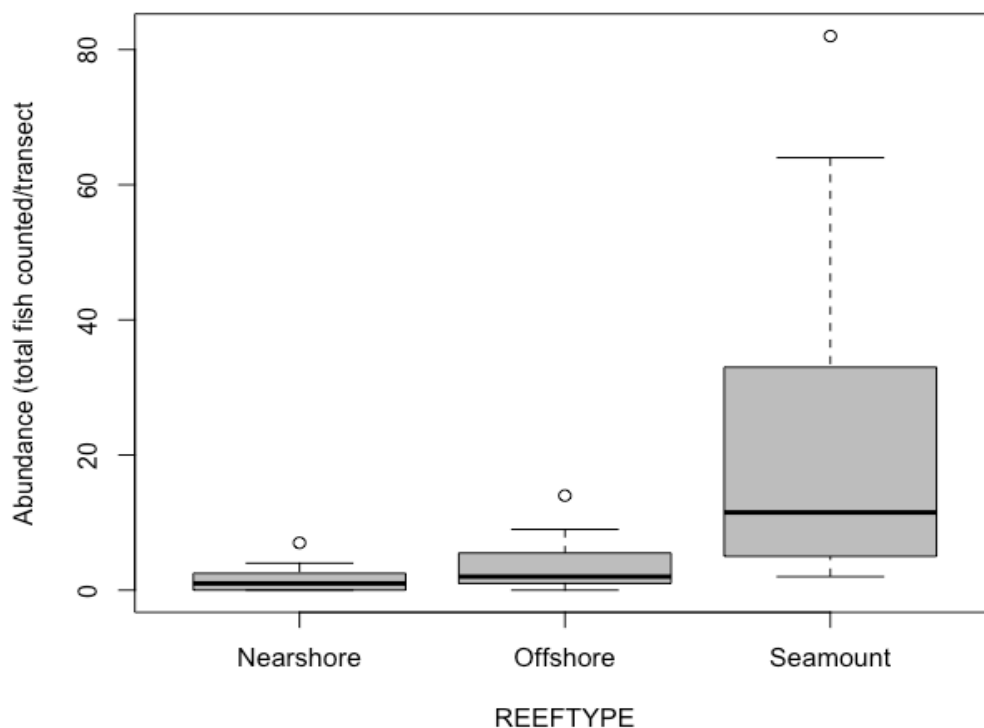| Habitat	Mean pred abundance / 30m transect	± SEM
Near-shore	1.45	0.40
Offshore	3.45	0.79
Seamount	19.9	4.88

Fig 1. Mesopredator abundance distributions across three habitat types. Dark horizontal lines indicate median values.

These data are not normally distributed (Fig 1 and Annex 2a) so transformation or non-parametric pairwise comparisons using Wilcoxon rank sum test are probably the best two avenues. The latter indicates significant differences between all habitat types:

Habitat Pairwise Differences	Different?	Significance
Near-shore – Offshore	Y	p<0.05
Seamount – Offshore	Y	p=0.001
Seamount – Near-shore	Y	p<0.001

Transforming the data

No form of transformation brings the data back into normal distribution (see Annex 2b for results of square-root transformation – this the nearest to, but still violating normality). Bootstrapping with 200 randomised resamples results in normal distributions for each habitat type (see Annex 3) and ANOVA on these concurs with the Wilcoxon test. I need to do some more reading around bootstrapping to check whether it's an appropriate method/step and would appreciate your thoughts?

Diversity and community structure

I've explored two avenues to investigate the mesopredator communities as a whole: 1. Using comparisons of Shannon-Wiener (H') diversity to see where the greatest amount of predator diversity is found (Hypothesis: on the seamounts); 2. Using cluster analysis to tease out similarities between sites and habitat types (Hypothesis: differences between all habitat types).

1. Differences in diversity metrics

Species richness and Shannon-Weiner diversity were calculated for each transect with mean values as follows:

Habitat	Mean species richness / 30m transect	± SEM
Near-shore	1.2	0.30
Offshore	1.9	0.32
Seamount	5.5	0.72

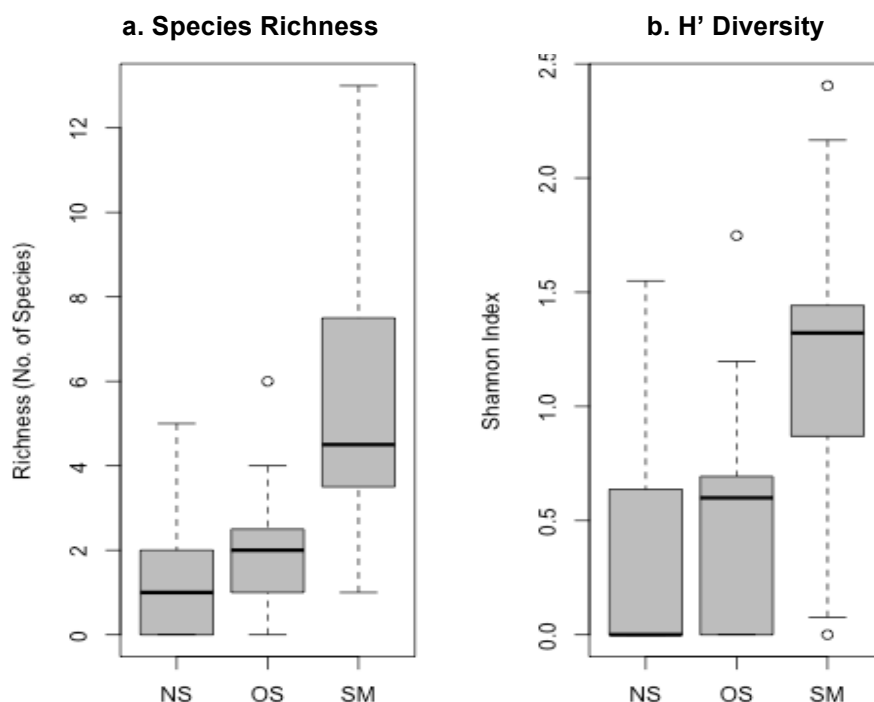| Habitat	Mean H' Diversity / 30m transect	± SEM
Near-shore	0.28	0.11
Offshore	0.48	0.11
Seamount	1.16	0.13

Fig 2. Mesopredator fish diversity across habitat types. Dark horizontal lines indicate median values.

Again, these data suffer from non-normal distributions. In this instance all transformations resulted in some form of NaN or Inf error. Bootstrapping the raw data might be an option again but for now a simple Kruskal Wallace test followed by Wilcoxon rank sum test on H' diversity indicates pairwise differences only between Seamount sites and both Near-shore and Offshore habitats (no difference between Offshore and Near-shore):

Habitat Pairwise Differences	Different?	Significance
Near-shore – Offshore	N	p=0.18
Seamount – Offshore	Y	p<0.001
Seamount – Near-shore	Y	p<0.001

2. Cluster analysis of community dissimilarity

The raw observations for DOV transects were converted into a distance matrix using the vegan package in R and the Bray method for calculating dissimilarities. Nine transects contained zero observations of predators (see Annex 5) and these required either a) removal from the matrix before analysis or b) some kind of substitution after matrix formation (basically they throw up NaNs in the matrix which prevent cluster analysis from working). Either way the clustering is pretty similar as you can see:
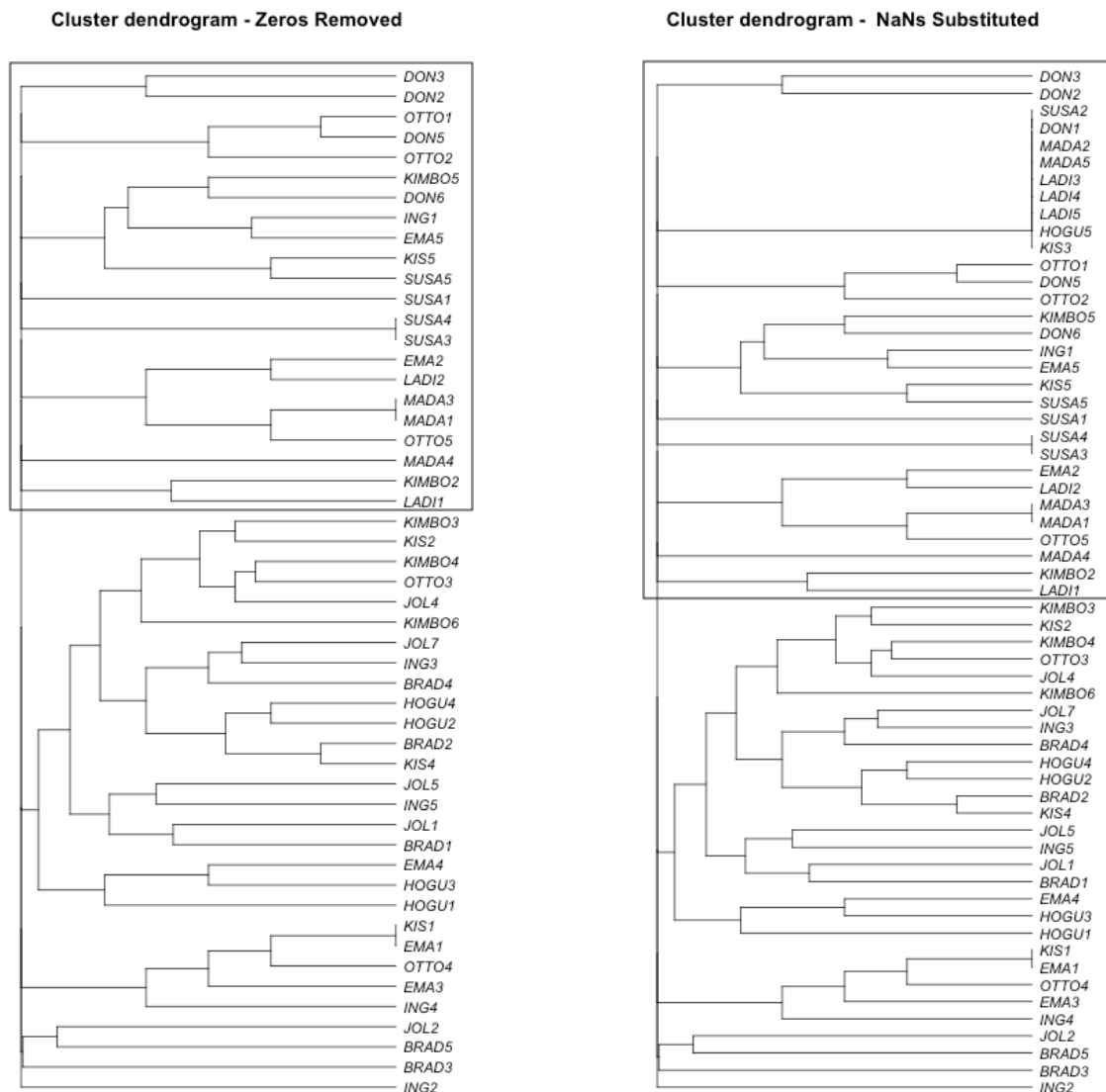

Fig 3. Hierarchical cluster analysis of mesopredator communities. All near-shore transects contained within the black boxes outlined.

The only visual pattern emerging from this analysis is the clustering of all near-shore transects in the top part of the tree. This part of the tree also contains some offshore and seamount transects within it, these being transects where fewer predators were observed.

ANOSIM confirms some dissimilarity between groups (R=0.23, p=0.001), with a SIMPER analysis seeming to report larger differences in mesopredator communities (need to read around interpretation of these results some more though):

SIMPER Pairwise Differences	Difference (%)
Near-shore – Offshore	94.3
Seamount – Offshore	85.7
Seamount – Near-shore	96.1

Either way it looks like there may be interesting differences in mesopredator communities between these habitat types, maybe I do not yet have enough data/transects to support that hypothesis. An nMDS also confirms this:
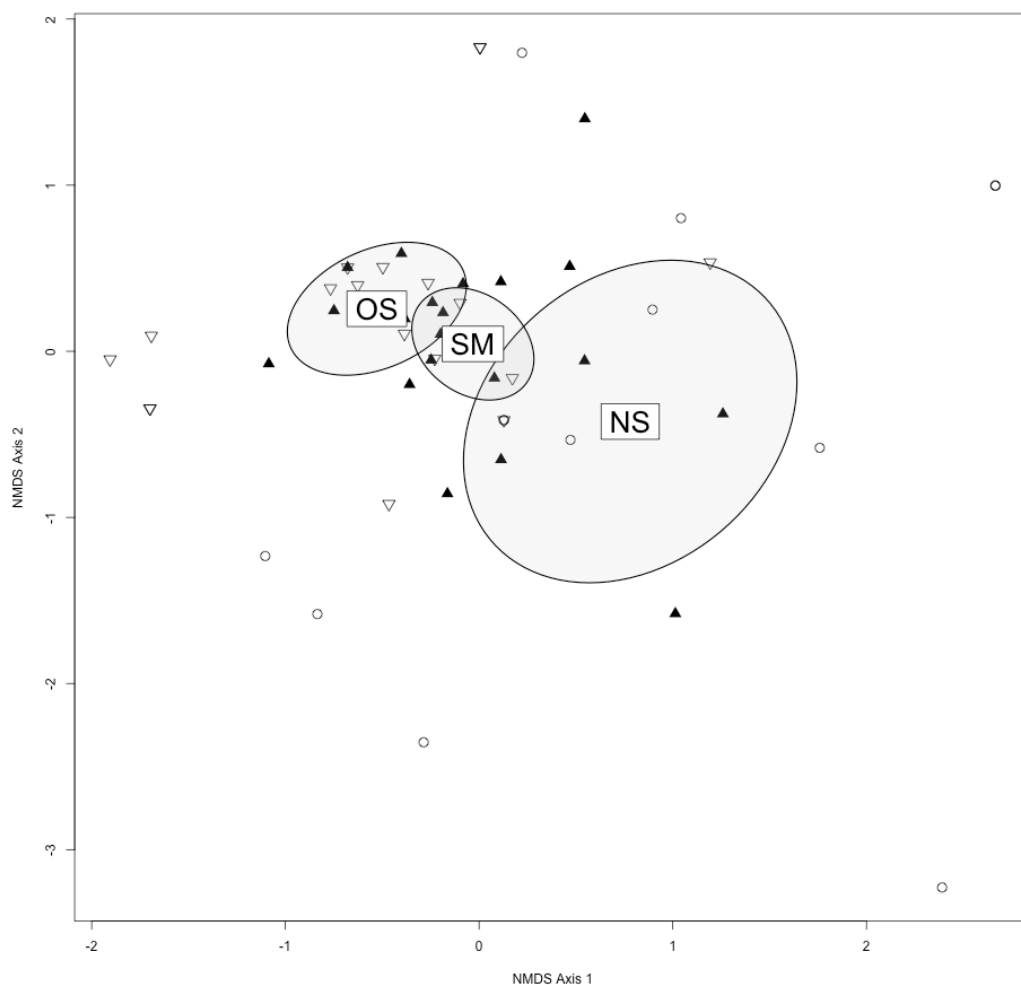

Fig 4. Non-metric multidimensional scaling (dimensions = 3) of differences between Seamount (SM), Offshore (OS) and Near-shore (NS) predator communities. Ellipses represent 95% confidence levels. Note overlap. Stress = 0.11

Thoughts and next steps

So it looks like there may be interesting differences in predator abundance, diversity and community structure emerging across these three habitat types. The data so far point in this direction, albeit perhaps inconclusively. I think supplementing the existing data set makes sense and I have the following ideas:

1. BRUV surveys: We already have BRUV videos for near-shore and offshore habitats that we obtained assisting Global Fin Print in 2017 (I think n ~ 50 for each of these). So I would like to conduct some of these surveys on the seamounts and see if this method clears up any of the above. I think this might be a September activity.

2. ROV surveys: G and I are already working on trying to standardise some ROV survey method for her project. It's been pretty challenging work but if we can get enough transects I should be able to extract predator data from the same videos. Current scenario is one of the motors has gone on the ROV – will be able to replace but will need to bring it back to Aus to change it out, so again a September activity I think.

3. eDNA: Will try to get some funding to contribute to the eDNA analysis that Gemma is planning to do. We have a new field pump prototype up here and a bunch of test kits so we should be able to get all the samples we need. We also now have Longmire's buffer which should preserve the low-copy DNA much better than ETOH so we should have a better chance of interesting hits on the next batch of samples.

4. Moving on, I think it would be worth extracting biomass estimates based on length estimates from the stereo-video – would be interesting to know if diversity and abundance also correlates to the biomass that can be supported at the top end of the trophic web (but this is moving a little bit into trophodynamics now which should be a separate avenue of investigation ☺)

Hope you both think there is an interesting story emerging, but maybe there are other angles on all of this? I clearly need to get my head around some of the multivariate analyses and probably do a bit more data-collection as well. Looking forward to your input and suggestions – please don't hold back!

Annexes

Annex 1: Species list

| Family	Genus	Species	Common Name
Carangidae	*Carangoides*	*bajad*	Orange spotted trevally
Carangidae	*Caranx*	*ignobilis*	Giant trevally
Carangidae	*Caranx*	*melampygus*	Bluefin trevally
Carangidae	*Caranx*	*sexfasciatus*	Bigeye trevally
Carangidae	*Elagatis*	*bipinnulata*	Rainbow runner
Carcharhinidae	*Carcharhinus*	*amblyrhynchos*	Grey reef shark
Carcharhinidae	*Carcharhinus*	*melanopterus*	Blacktip reef shark
Cirrhitidae	*Paracirrhites*	*forsteri*	Blackside hawkfish
Haemulidae	*Plectorhinchus*	*picus*	Dotted sweetlips
Lethrinidae	*Lethrinus*	*erythracanthus*	Yellow spotted emperor
Lethrinidae	*Monotaxis*	*grandoculis*	Big eye bream
Lethrinidae	*Monotaxis*	*heterodon*	Red fin emperor
Lutjanidae	*Lutjanus*	*biguttatus*	Two-spot banded seaperch
Lutjanidae	*Lutjanus*	*bohar*	Red bass
Lutjanidae	*Lutjanus*	*carponotatus*	Stripey seaperch
Lutjanidae	*Lutjanus*	*ehrenbergii*	Ehrenberg's seaperch
Lutjanidae	*Lutjanus*	*gibbus*	Paddletail
Lutjanidae	*Lutjanus*	*kasmira*	Bluestripe snapper
Lutjanidae	*Lutjanus*	*monostigma*	One-spot snapper
Lutjanidae	*Lutjanus*	*semicinctus*	Black-banded snapper
Lutjanidae	*Macolor*	*macularis*	Midnight snapper
Lutjanidae	*Macolor*	*niger*	Black-and-white snapper
Lutjanidae	*Pinjalo*	*lewisi*	Slender pinjalo
Scombridae	*Grammatorcynus*	*bilineatus*	Double-lined mackerel
Scombridae	*Gymnosarda*	*unicolor*	Dogtooth tuna
Serranidae	*Anyperodon*	*leucogrammicus*	Slender grouper
Serranidae	*Cephalopholis*	*argus*	Peacock grouper
Serranidae	*Cephalopholis*	*cyanostigma*	Bluespotted grouper
Serranidae	*Cephalopholis*	*leopardus*	Leopard grouper
Serranidae	*Cephalopholis*	*microprion*	Freckled grouper
Serranidae	*Cephalopholis*	*miniata*	Coral grouper
Serranidae	*Epinephelus*	*areolatus*	Areolate grouper
Serranidae	*Epinephelus*	*coeruleopunctatus*	Whitespotted grouper
Serranidae	*Epinephelus*	*fasciatus*	Blacktip grouper
Serranidae	*Epinephelus*	*polyphekadion*	Camouflage grouper
Serranidae	*Gracila*	*albomarginata*	Masked grouper
Serranidae	*Plectropomus*	*leopardus*	Coral trout
Serranidae	*Plectropomus*	*maculatus*	Barred-cheek coral trout
Serranidae	*Plectropomus*	*oligacanthus*	Highfin coral trout
Serranidae	*Variola*	*albimarginata*	Lyretail trout
Sphyraenidae	*Sphyraena*	*qenie*	Chevron barracuda

Annex 2a: Distributions of abundance observations – raw data. Not normally distributed.
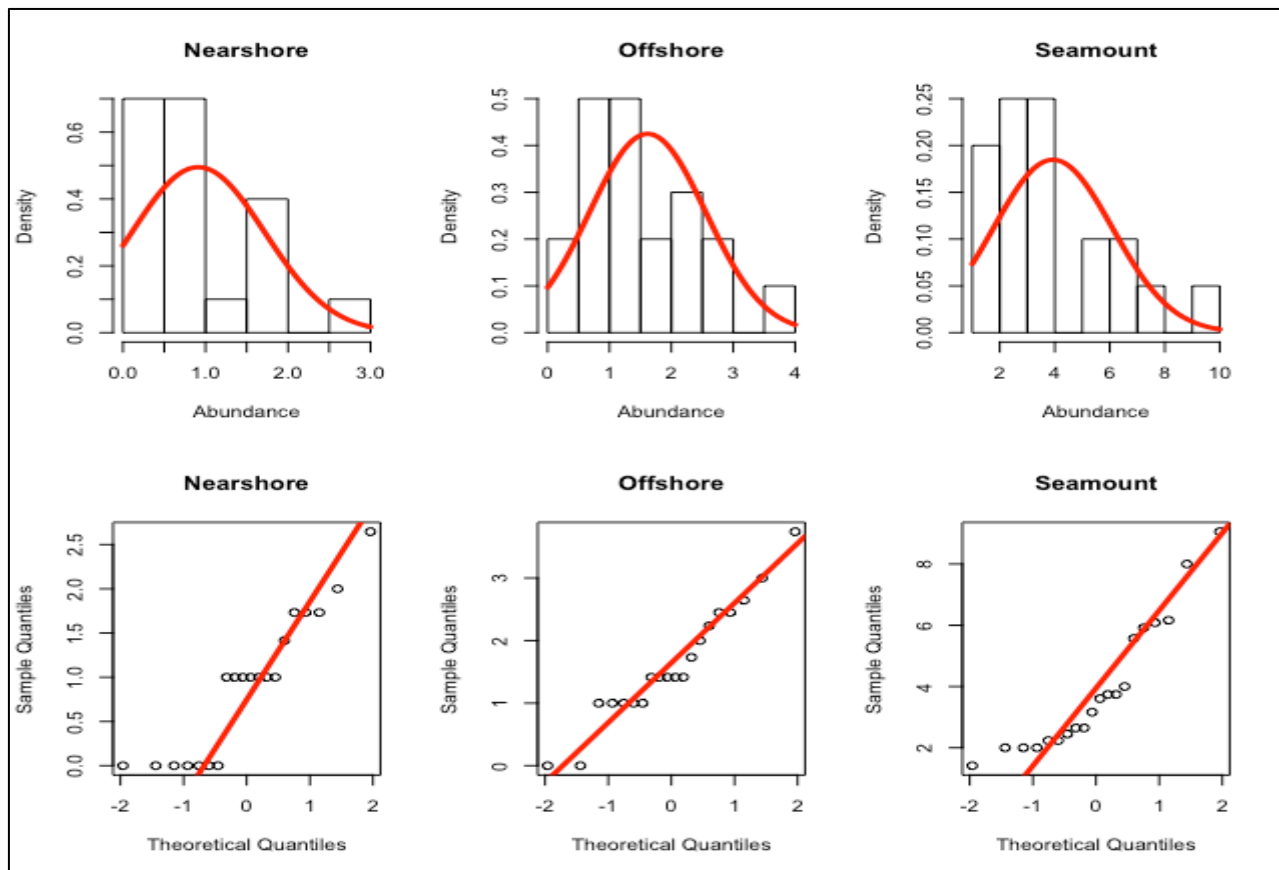
Annex 2b: Distributions of abundance observations – square root transformed. Not normally distributed.
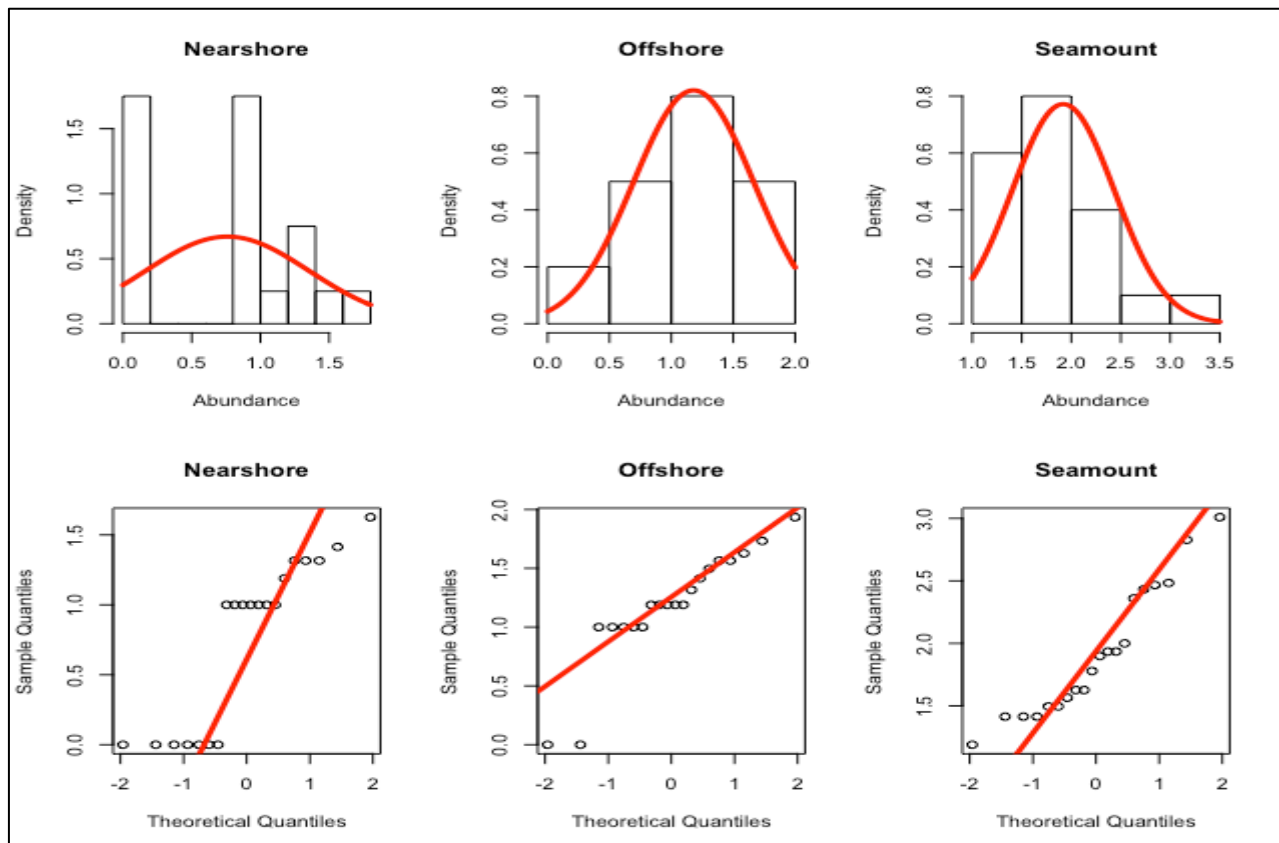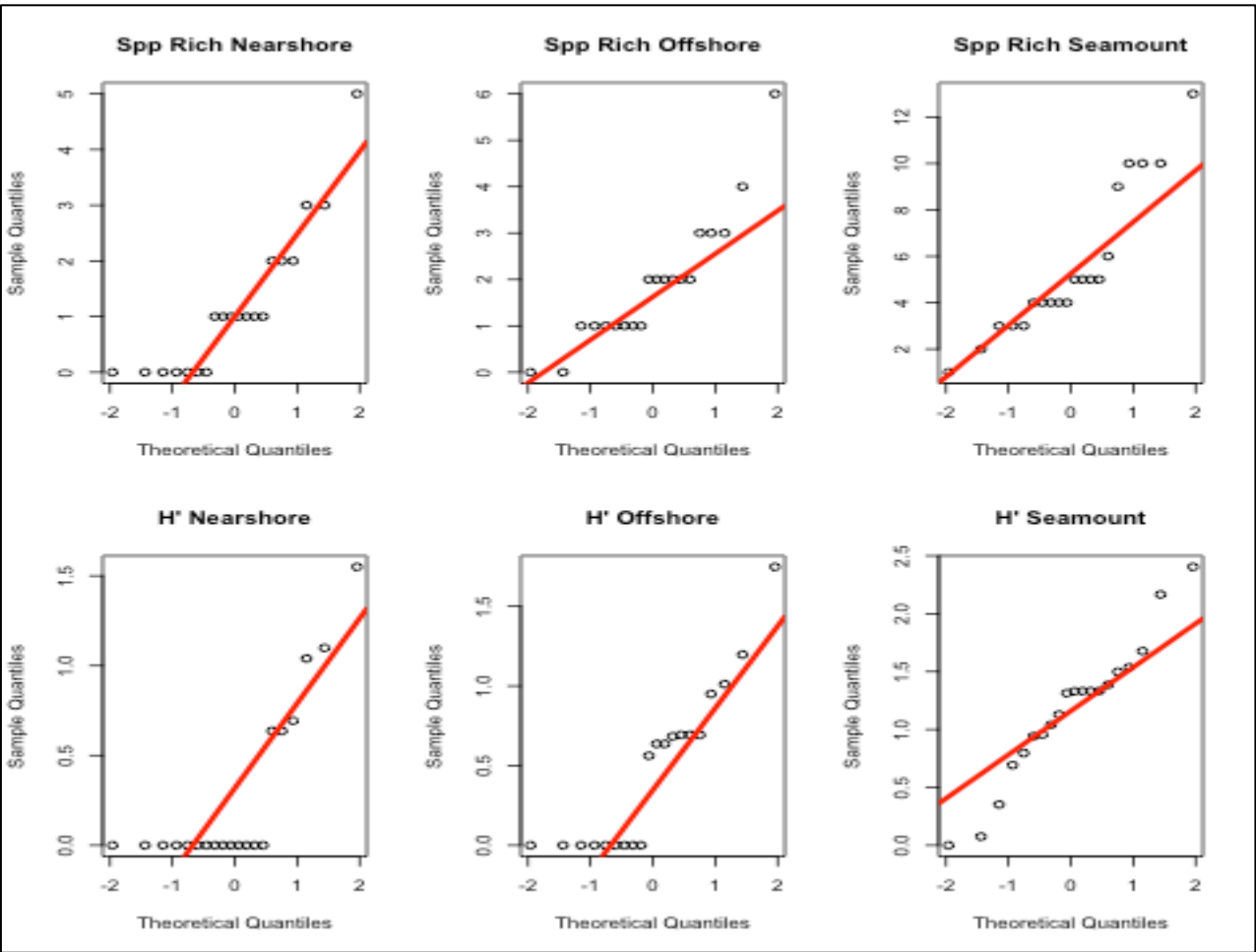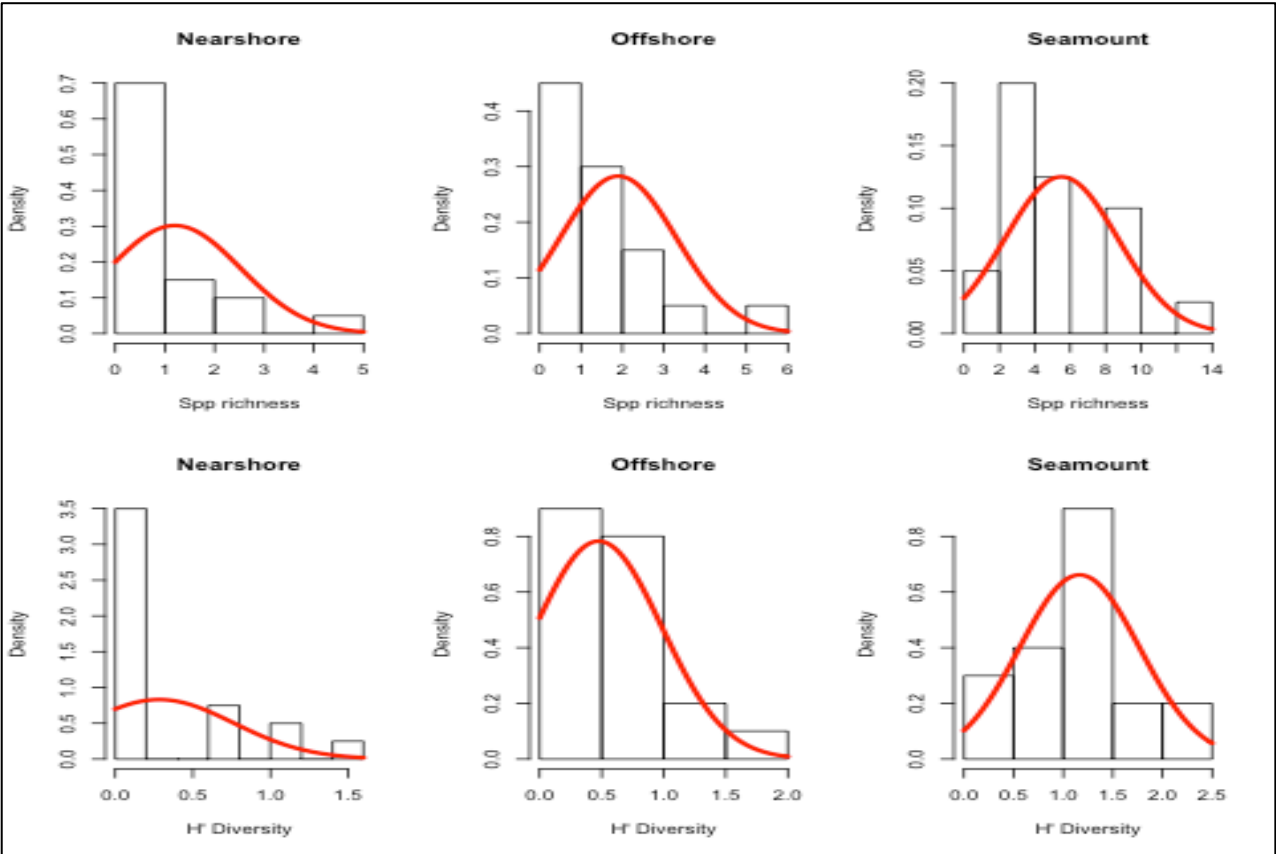
Annex 3: Distributions of bootstrapped (n=200) abundance observations.. Normally distributed.
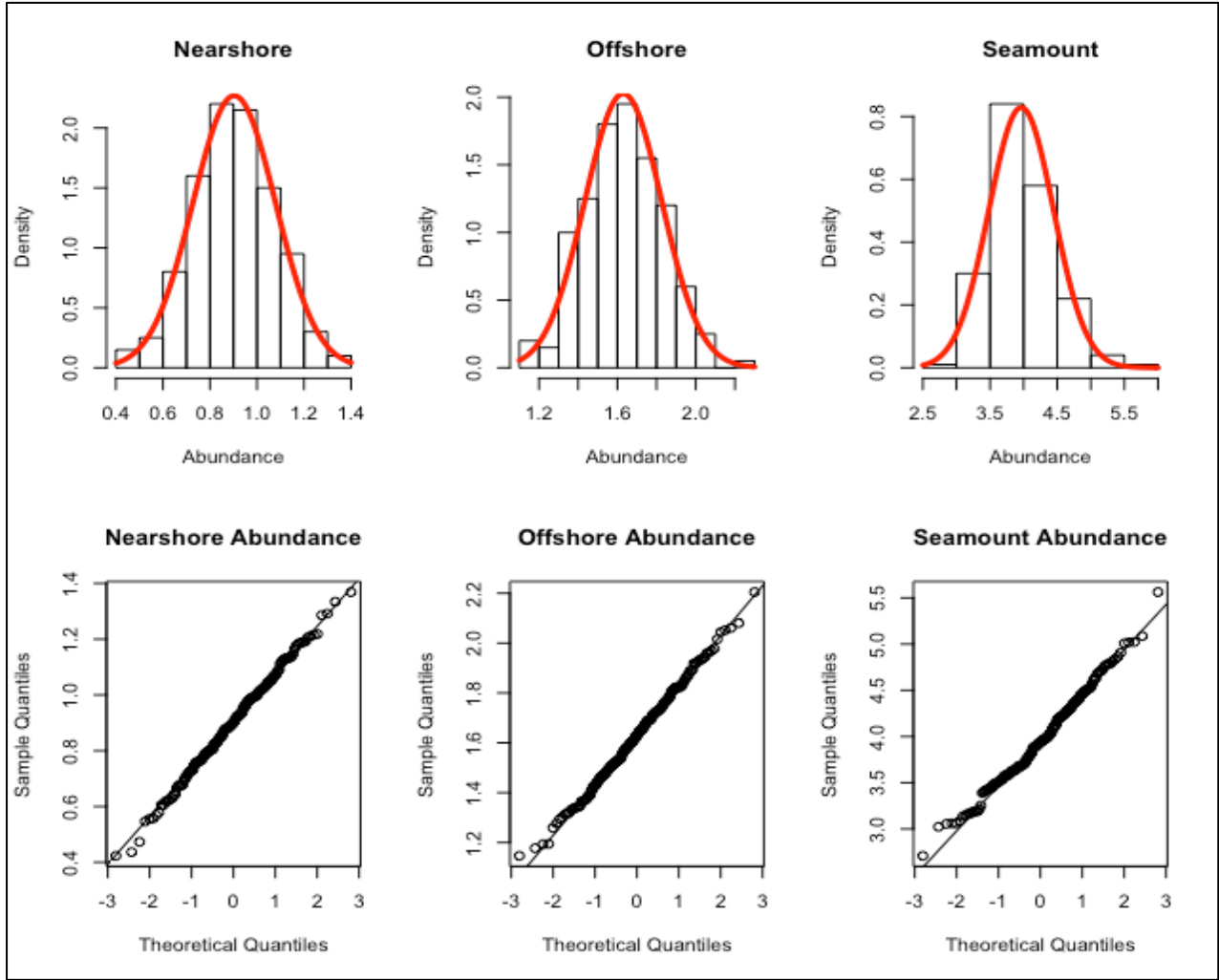
Annex 4: Distributions of diversity observations – raw data. Not normally distributed.

Annex 5: Stereo video transects with zero observations of predators:

1. Donna T1
2. Susan T2
3. Madaro T2
4. Madaro T5
5. Lady Di T3
6. Lady Di T4
7. Lady Di T5
8. Hogu T5
9. Kimbe Island T3