Seminar Diary

* Write a half-page on 10 seminars and create a “seminar journal”.
* Due: 1st July 5pm, email pdf to Samraat.
* The diaries are not assessed for beauty of prose or scientific rigour, but on the basis of how good the logical structure of the entry/account for each seminar is.
* Please do not exceed 1/2 page per seminar's entry/account.

Model Examples

Adaption to Environmental Change in Communities of Aquatic Microbiota

12/10/17 - Dr Etienne Low-Decarie - University of Essex

Organisms are fundamentally driven towards fulﬁlling particular ecological niches, extreme or otherwise. If we understand and can quantify the niche that a particular organism is adapted to we can predict not only its location and range, but also its potential ranges and tolerances to change. However, diﬀerent models can predict wildly diﬀerent niches, and are often speciﬁc to the particular dataset they were developed from/for.

Low-Decarie et. al used lab experiments along with Amplifying Bioreactors (ABRs) to evaluate community rescue and extremophile abundances. When communities are exposed to sub-lethal levels of stressors prior to exposure to typically lethal doses, they can often recover to pre-stress states. This recovery is dependent on the diversity, disparity, dispersal, and level of sub-lethal exposure. Highly adapted organisms survive well in benign conditions, however as stressors (such as pH or temperature) are increased, adapted organisms fare better. Overall adaptations to benign changes are less likely than adaptations to sub-lethal stressor changes.

Impacts, Spread, Evolution and Virulence of “Frog Ebola” Viruses

19/10/17 - Dr Stephen Price - UCL

Ranavirus is an emerging infective disease that aﬀects all of the 6 major UK amphibians. It damages individuals at all life stages, and can spread past amphibians. Price et. al showed that salamander pets are a likely source of pathogen pollution, with frog and salamander farms in China acting as disease incubators. To assess the spread of disease through the United Kingdom, they started an ongoing frog mortality citizen science project. In addition to live data, Price carried out in vitro experiments to test the viability of temperature as a predictor of ranavirus status. FE3-like strains of ranavirus were particularly well-adapted to high temperature (shown later in vivo)

From genomic analysis, ranavirus seems to have a signiﬁcant variation in terms of genome arrangement and content. The genome has undergone widespread gene recombination and horizontal gene transfer, and is currently undergoing positive selection.

Seminar One

Deep-time evolution of biological responses to temperature changes

Dimitrios Georgios Kontopoulos

10th October 2019

* What is the topic?
* Why is it important?
* What experiments/investigations have been done to learn more about this topic?
* Any conclusions?

Species at risk from climate change, one of the major threats to global biodiversity today. If we are to better forecast how different kinds of species will respond to climate change we need to develop a thorough understand of how physiology responds to temperature change over shorter or longer time scales. One way of looking at that, is to look at how biological traits respond to temperature changes. If you measure biological trait such as growth rate or photosynthesis or respiration, if you measure these at different temperatures you typically get this unimodal curve. So, this curve is called the thermal performance curve. Trait values typically slowly increase with temperature until an optimum temperature (which is called Tpk) they steeply decline. The maximum height of this curve is called Bpk, and it’s a measure of the performance of the organism. Understanding how these curves vary between different individuals, populations or different species is important because for example we know that interacting species tend to have systematic differences in those kinds of curves and if we know the processes that generate variation in these curves then we can better forecast what will happen under different scenarios.

Throughout this talk I will be using this mathematical model, the Sharpe-Schoolfield model, to quantitatively characterise different aspects of the shape of these curves. As you can see the numerator of this model is just an araneous equation and captures how smoothly the curve rises until the thermal optimum. Whereas the denominator captures how steeply the curve declines about the optimum. The basic assumption of this model is that the biological traits of growth rate here is being determined by the effects of temperature on the activity of a single rate limiting enzyme. So, this rate limiting enzyme is deactivated at very high temperatures whereas at low temperatures it operates at very low rates because of low kinetic energy. This model can be considered as mechanistic but you can also use it as a phenomenological model just to capture the statistical relationship between trait performance and temperature. This model has four main parameters, Tpk –thermal optimum, E – captures how smoothly the curve rises up to the optimum, a measure of thermal sensitivity near the range of temperatures in which organisms typically operate. Ed – captures how smoothly the curve declines after the optimum and then B0 – which is approximately the trait value at a low normalisation temperature. After getting estimates of these four main parameters we can also estimate two more parameters: Bpk, the maximum height of the curve, and Wop, the difference between the thermal optimum and the temperature at the rising part of the curve where the performance is half of the maximum (operational niche width), another way of looking at thermal sensitivity. Both E and Wop are measures of thermal sensitivity. For this reason we would expect them to be correlated, so imagine you have a very steep slope of the rising part, then by definition your niche width would necessarily become narrower (Wop would become smaller).

At this point I’d like to introduce the Metabolic Theory of Ecology, which is arguably the most popular macroecological framework. It makes a lot of explicit predictions regarding how these curves, and also other macroecological patterns, will vary with temperature. So, the metabolic theory has been used mostly for large-scale comparisons of trait performance for example across multiple taxonomic groups, but very few people have looked at what these predictions hold when you look at within species for example or when you look through evolutionary time. So, my goal throughout this PhD and this presentation is to understand whether the predictions of this framework hold when we look at the evolution of species.

In my talk I will tell you about how thermodynamic constraints influence the shape of thermal performance curves. How thermal sensitivity evolves and near the end I will tell you a bit about what we can do to link those kinds of approaches with other fields and other search traditions to develop a thorough understanding of thermal adaptations from multiple ecosystems.

For the first part if we look at the literature for hypothesis of thermal performance curve evolution, we find that a lot of different hypothesis that can be broadly placed along the continuum that ranges from strong thermodynamic constraints to weak thermodynamic constraints that can be at least to an extent be overcome by adaptation. So, at the strong thermodynamic constraint extreme we have ‘Hotter-is-better’. So this hypothesis assumes that due to very strong thermodynamic constraints these curves can only differ in the thermal optimum, the maximum performance and as you can see the vertical lift is the same for all these curves and the slope of the rise is the same. So, in this hypothesis we expect a very strong positive correlation between the thermal optimum (Tpk) and maximum performance (Bpk). This hypothesis basically assumes that at higher temp the activity of the underlying enzyme is accelerated because of the higher kinetic energy and this is why they would get an increase in the max performance.

If we relax those assumptions then we get to a ‘Weak hotter-is-better’. Where we either have variation on the vertical lift of these curves, variation in the slope of the rising part or in both. So if we assume that the vertical lift of the curves vary, then this is very close to what the metabolic theory of ecology expects.

The metabolic theory of ecology suggests that variation either here, at the offset, or at the max height, is associated with body size. So, imagine that you have a v high body size therefore you need to invest a lot of energy into maintaining it, therefore this leaves you with a lower maximum performance and vice versa. Small body size = higher max =energy to increase max performance. So in this case we would have a weak positive correlation between thermal optimum (Tpk) and max performance (Bpk).

Next, moving towards weak thermodynamic constraints we have the specialist-generalist hypothesis. This hypothesis assumes that for species to achieve a very high trait performance they need to become thermal specialists. So they need to operate at a very narrow range of temperatures, whereas if you are a thermal generalist and you need to operate over a wide range then you would have to pay a metabolic cost and this would decrease your maximum performance. So in this case we would have a negative correlation between Bpk and Wop.

And finally the last hypothesis is the perfect biochemical adaptation hypothesis which suggests no matter which environment a species is found, adaptations should be able to maximise its Bpk. All species would have the same maximum Bpk, across different enviros.

To test this hypothesis we need to look at two things, the correlations between thermal response parameters and understand how some of those parameters, how they offset the slope of the rise or the maximum height, how these parameters evolve across species, what is the kind of variation across species?

My approach was to take a phylogenetic comparative approach and examine the correlation structure of these parameters but also examine the phylogenetic signal of its parameters separately. So basically the phylogenetic signal is the measure of whether close related species have more similar trait values than species chosen at random. If, for example Bpk is held constant, then it should vary like random noise across species and it shouldn’t exceed the phylogenetic signal. Currently we have big databases of thermal performance curves where we can examine these questions and answer these questions.

My data comes from the literature. They are phytoplankton growth rates. Typically, people go to the environment, isolate the strain of phytoplankton, take it back to their lab and grew it under a range of temperatures under light and nutrient saturated conditions. Before measuring the growth rate at every temperature, we first allow the species to acclimate. What I did was I took all of those data and feed the model to each species or strain separately. This allowed me to obtain estimates of the thermal performance parameters for each species/strain. To analyse these, I feed it a phylogenetic regression model where I estimated the covariance structure of four thermal response parameters, controlling for the phylogeny of the species and local environmental effects – temp variation and habitat. By doing that I managed to identify two correlations between thermal performance curve parameters. One was between the two measures of thermal sensitivity, a negative correlation between the slope of the rise and the operational niche width which is what we expect to find. The other correlation was indeed a weak correlation between the thermal optimum and the maximum performance. As you see here, as temp increases (the thermal optimum), the max performance of species weakly increases as well. However, if you just discard these three data points here, then this correlation is no longer significant. This means that most of this pattern is driven by species at low temperatures. There is an increase then it levels off. These results are consistent with a very good ‘hotter is better’ pattern.

The next thing I did was I measures the phylogenetic signal for these parameters and you can see it here. The phylogenetic signal or phylogenetic heritability ranges from zero to one. You see that all of these parameters have at least some amount of phylogenetic signalling. The strongest amount of signalling is in the thermal optimum which evolves fairly gradually across species. Whereas some other parameters may make larger jumps in parameter space. These results all tell us that there is variation in the intercept and the slope of the rise and there is also variation in the maximum performance. The final thing to test this hypothesis was to look at the effect of body size so I obtained estimates of cell volume and I looked at whether these correlate with the offset of the curve or the maximum height of the curve. The result is the only significant correlation was the max height of the curve. As cell volume increases the max height of the curve weakly declines. Cell volume explains 15% of this variation and if we add species identity in there then this gets all the way to 72% of the variation being explained.

These results tell us 1) the max performance weakly increases with the thermal optimum. Some of this variation is driven by cell volume, but there is variation in both the intercept and the slope so with all this in mind we can say that phytoplankton thermal responses are broadly here nearer to weak thermodynamic constraints.

Next, we will focus on thermal sensitivity. A big debate in the lit. The metabolic theory of ecology suggest thermal sensitivity should not vary across species due to thermodynamic constraints. It should be almost held constant. However, I found that there is some phylogenetic signals in this parameter. In 2011 this paper came out – Systematic variation in the temperature dependence of physiological and ecological traits – it looked at thermal sensitivity across a large variety of species and different traits. They found that thermal sensitivity is not fixed, it has a distribution. This distribution isn’t gaussian. It has a long tail towards high values. They found some evidence that prey traits may have lower thermal sensitivity that predator traits. They called this the life-dinner principal. Prey traits should be under stronger selection for being less dependent on temperature than predator traits. Even in this paper there wasn’t a clear evolutionary explanation on how this variation came to be given that we expect thermosensitivity to be fixed because of thermodynamic constraints. In this project we would like to test two hypothesis regarding the evolution of thermosensitivity. The first hypothesis agrees with the metabolic theory of ecology and it is that thermal sensitivity evolves around an optimum value. This value is set because of thermal dynamic constraints. Occasionally some species are able to break free from those constraints and maybe have variation in thermal sensitivity but because of selection, other closely related species will move very quickly back to the optimum value. The second hypothesis is that thermal sensitivity may evolve in other ways. Maybe there is a global optimum but its attraction is very weak. It allows species to explore a v wide area of the parameter space around it. Or maybe certain clades have a higher rate of evolution in thermal sensitivity and better able to explore the parameter space.

To test this hypothesis, I used the phytoplankton growth rate dataset but also another dataset of prokaryote growth rates. First, I examined how the variation in thermal sensitivity is distributed along the phylogeny. This method allows us to differentiate between random evolution between an increasingly overlapping parameter space of different lineages and between a segregation of lineages with the parameter space, similar to adaptive radiation. Here on the x axis we have time, 0 is the root of the tree, 1 is the present time. Here (y-axis) is the mean clade disparity in thermal sensitivity. These shaded areas are the expected disparity line that we would get from 10,000 simulations of random evolutions. If a trait was evolving randomly on our tree, what it’s disparity would be. If our actual disparity line is above shaded area then this means lineages overlap in parameter space. If it is below then different lineages occupy distinct areas of the parameter space. We calculated the disparity line and we found as we move towards the present we have an increase in overlap in the parameter space by different lineages. Species that come from very different clades may have v similar values of thermal sensitivity. This suggests that it’s not the evolutionary history that matters that much, it’s that the environment selects for particular values of thermal sensitivity. No matter what clade you are from you can adapt.

You can see better if we look at the major phyla in this analysis. There are the main phyla. You can see that for example Dinophyta and Cyanobacteria are very far away from each other in their phylogeny but they have similar distributions of thermal sensitivity.

We tried to see if different clades vary in their rate of evolution of thermal sensitivity. We mapped the rate of evolution on each different branch of the phylogeny. High rates of evolution shown in red/brown. Pattern is very patchy. No one particular clade with high/low evolution of thermal sensitivity. All over the phylogeny we get random bursts of trait evolution of thermal sensitivity. Leads to the pattern we saw before. To better understand the results, I performed a visualisation of the thermal sensitivity evolution. Time (x-axis) and values of E (y-axis) Yellow lines are median estimated values of thermal sensitivity, red areas are confidence intervals. As we move from root to present there is an increase in range of trait values. There is not one global optimum, but species are able to explore the parameter space. When we saw this result we said okay this is population growth rate, it is a relatively higher order trait and maybe there are a lot of processes going on. What would happen if we looked at different traits that are closer to the physiology. I tried to do the same analysis with lower physiological traits, such as photosynthesis and respiration of algae, aquatic and terrestrial plants and the data sets were a bit smaller but the results were pretty much to same. We can see the thermal sensitivity even for those traits. Typically explores a wide area of the parameter space and can vary a lot even between closely related species.

All these results suggest thermal sensitivity responds to selection. It’s not just fixed because of thermal dynamic constraints. Nobody else has shown how thermal sensitivity may vary across different environments across such a macroevolutionary scale. One thing we would expect would be that thermal sensitivity should vary with latitude. Near the equator you would expect selection for thermal specialists with very high values of thermal sensitivity. As we go to middle latitudes we would expect increasing selection for thermal generalists because of the variation of temperature with latitude. What I did was I took the thermal sensitivity values of all those traits, population growth rate, photosynthesis and respiration, and I tried to see if they all varied with latitude. The result is exactly as we would expect. You find high values of thermal sensitivity at the equator and as we move away we get a decrease in thermal sensitivity.

Latitude and trait identity explain 23% of the variation in thermal sensitivity and when we add species identity we get to 58% of the variation being explained. The traits have different intercepts but the same slopes for latitude, but this may be a fact of the small sample size. This result hasn’t been shown before because the metabolic theory of ecology assumes that thermal sensitivity is fixed across species.

I’d like to tell you about how we can take these kinds of approaches and link them to our other levels of organisation in order to develop a more unified picture of thermal adaptation. So when I think about the effects of temperature on biological systems I don’t just think about biological traits. I tend to think temperature affects all levels of biological organisations. Here is a simplified version of a community of three species interacting. Each species is composed of a population. Each pop has individuals. Each individual is composed of different cells and tissues. Each cell has a copy of the genome, mitochondria that produce energy and also expresses proteins. Temperature effects every single thing on this figure. It affects probably genome composition, amino acid composition in proteins, how different species interact with each other. Most frameworks tend to focus on one particular level of organisation. Then they assume that levels below or above tend to fall apart. Whereas my argument is that if we are to develop a thorough understanding of how organisms will be affected we need to embrace all of this complexity and understand how temp affects each level separately and hwo they interact with each other. One approach that we could follow is to get some ideas from the complexity science field. For example, we can assume that each level of biological organisation is a complex system which is composed of agents. A gene within a genome can be its own agent and respond to temperature and other genes in different ways. By doing that we will be able to predict properties of those systems that can’t be identified by studying each agent in isolation. Obviously this is no easy task and this is a very long in the future idea. What we can d for now is we can look at different pieces of the puzzle and see how they respond to temperature.

Besides physiology I looked at how temperature affects the effects of mutations. Here on the left you see a protein stability curve with temperature. Mutations tend to decrease the stability fo the protein. Conventional assumption in lit is mutations should have same affect regardless of temperature. Whereas from biophysical pov we would expect that mutations would be more detrimental at higher temperatures. Imagine a thermophilic enzyme. If a mutation happens there, because of the high energy of protein atoms, then this mutation would strongly destabilise the protein. Wheras if we lowered the kinetic energy of those atoms the effects of this mutation wouldn’t be so sever. We expect mutations would be more detrimental at high temp, implications for the rate of evolution at those temps. I used adenylate kinase, this is an essential enzyme, found in all organisms, it catalyses an essential biochemical reaction. I got seventy structures of this enzyme from bacteria and archeae. I then divided them into thermal groups, psychrophiles, moderate temperatures, thermophiles. Then I performed molecular dynamic simulations, biophysical simulations, put this enzyme under a forcefield surrounded by water molecules and some salt molecules. You simulate how this enzyme moves in the solution under the temp that’s close to it’s environment. Finally, once you do those simulations you can extract confirmation of these enzymes, see how they move, find conformational structures. Take those confirmations and submit to server that performs all possible mutations. It tells you what the mutations would be like, beneficial or detrimental. Results showed that mutations become more destabilising with temperature.

I then wanted to see if these results hold if we look within species. I took five species and performed these biophysical simulations at multiple temperatures. You get a similar relationship within species, although there is a change is shape of the relationship. These results suggest that mutations become more detrimental to proteins stability both within and across species. Like I previously said, we would expect these to have some implications for the rate of molecular evolution trait temperatures. So using this I build a phylogeny using 44 genes for those 70 species and then I allowed each branch of this phylogeny to have a different rate of molecular evolution, a different substitution rate. By doing that I was able to get substitution rates for those seventy species. I corrected those substitution rates for generation time and tried to see whether you see an effect of temperature. There is a strong relationship between temperature and substitutions. This suggests that at higher temperatures substitution rates are lower, possibly due to lower mutation rates or effective population size. It’s a result that people haven’t shown before. There is v weak evidence that when you move to higher temp your mutation rate may decline, but few studies have looked at that, and only a few species. Result is very interested for another reason, it is completely opposite to what the metabolic theory of ecology predicts. It predicts that at higher temps you would have high rates of molecular evolution because you would have a higher production of oxidated free-radicals that would lead to mutations.

This is another point in m argument at least that we need to embrace all of the complexity, not focus on one particular level like metabolic theory does.

Other things to be done in the future: look at the genetic basis of thermal response curves. We don’t really know what drives shift in thermal optimum, what drives shifts in thermal sensitivity at the genetic level. One way someone could approach this would be to grow different strains of the same species at multiple temperatures. So you get thermal performance curves for a lot of different genotypes for the same species. Then using a genome wide association study, identify the genetic drivers of variation in all those different thermal response curve parameters. Other things that could be done would be for example to see how these species interact and whether these interacts are driven by temperature and whether such variation is also associated with changes in the physiological and other levels.

The take home message from this talk is that contrary to what we would expect from the metabolic theory of ecology, thermodynamic constraints have a very weak influence on the shape of thermal performance curves. The various TPC components evolve in different ways (e.g. gradual vs non-gradual exploration of the parameter space). Mutations become more detrimental to protein stability as temperature increases. Linking approaches from diverse fields and research traditions is key for developing a unified picture of thermal adaptation.

Seminar Two

A manifesto for systematically describing consumer-resource interactions

Daniel Barrios-O’Neill, Leverhulme Trust, University of Exeter

31st October 2019

**picture of log** Why is it in the open ocean, fish associate with the only habitat structure available to them?

Study functional responses. Everyone has a two liner about why functional responses or what they study matters. Everything that is interesting and consequential in ecology turns on the capacity of organisms to survive and grow and reproduce and that turns on their ability to acquire resources. Consumer resource interactions are at the heart of ecology. The currency of ecology. That’s why they are worth quantifying.

Consumer-resource interactions. Pac man consumes resources in proportion to the rate that he encounters them. He has no handling time. That produces a relationship between the prey/resource density in the enviro and the consumption of that resource that’s linear. A type 1 functional response. But, we all at some point have to spend time handling our food resources. We have to ingest them, we have to digest them. This limits the rate at which we can consume resources. Leading to a saturating relationship – type 2 functional response. Third type – type 3 – effectively describing the same phenomenon but with an inflection at low resource densities, to reflect things like learning.

In terms of the way we fit data and model these functional responses, there are two quantities to keep in mind. The attack or space clearance rate or capture rate, and the second is the resource handling time. Useful heuristic for describing two parts of the function resource curve along that gradient of resource density. You can think of capture rate as containing some information about the space through which consumers and resources move. Info about the physical world. Handling time is limiting resource consumption at high densities because it relates to biomechanics to some degree, to physiology and metabolism.

Size and temperature define a lot across the biosphere. Roughly speaking, larger animals and warmer animals have higher attack/capture rates and shorter handling times. Warmer and bigger = eat more. Metanalyses: 1000-2000 data points, not much. Distribution among marine, freshwater and terrestrial systems, highly skewed. Marine systems underrepresented. Sudo replication in data. Currently limited position to be able to say anything meaningful.

Differences in taxonomic groups. Placeholder for strategy. Collected lit on marine benthic consumers. An underrepresented broad group. I’ve augmented what I could find in the lit with new experimental data, to target underrepresented groups, like obligate sit-and-wait predators. You can consider that organisms adopt either active encounter strategies, they more around the find resources, or they sit and wait for things to come their way. You can consider these to be categorical predictors of some of those patterns in the previous slide. Taxon is kind of opaque to changes in strategy. A crab could employ several strategies. If we describe just in terms of taxonomic groups we don’t necessarily get all the useful information about changes in strategy which can happen moment to moment in real terms.

So, when you put all that data together what you get is highly skewed results. There are lots of data for the active static group, for the active mobile group, for filter feeders. Literally only two of three data points for marine benthic grazers, deposit feeders and obligate sit and wait. The overall pattern is filter feeders have lower size specific feeding rates than those other key groups. That’s a pattern that warrants some kind of explanation.

Mutual interference. This is something that has occupied many lines of papers, particularly in 80s and 90s. A debate that continues. Idea is that as the density of predators foraging on a patch increases, the per capita rates of consumption go down, this is mutual interference. The fact that this occurs is almost unambiguous, although the effects are subtle. The best models to describe it have been the focus of a lot of the debates, whether we should use ration or prey or predator dependent models. My position on that whole thing is that it is a little bit academic and here’s the reason: this is a recent paper looking at Ostracods, going from one predator to four predators and these are the per capita functional responses. The first thing to note is that the difference between per capita functional responses in one and four are extremely subtle. Not statistically significant. You can barely see, but the competing models, largely predict the same thing. In terms of consequences for energy flow, consequences for stability of populations, this seems like something of a side point.

A better question to ask about interference might be something like, is there a size bases for understanding interference? Does interference scale with bodysize? I’ve been trying to address that question using reasonable large datasets. Three sizes with crabs, crosses with 3 sizes of mussels, crossed with 3 densities of predators. From that data you get quite a subtle effect as the number of predators increases, the scaling with body mass ratio flatterns out. The data is really messy. This demands, three to four times as many data points. If we want to ask meaningful questions about the scaling of interference, we can’t do it without doing the experimental work.

Thinking on about patterns which aren’t necessarily grounded in size and temperature but are generalisable. This is a pattern of Samraat’s, influential because my take home from this is, well here’s a generalisation that we can make about consumer resource interactions across species and systems which has a size basis but is fundamentally about the physical space in which consumers and resources interact. That is a pattern that is just sat there in the data and there’s a mechanism underpinning that. Consumers that move and forage through volume tend to encounter each other more frequently than consumers that forage over surface, so that leads to a slightly steeper scaling relationship of those feeding interactions. It suggests to us that encounter rates are important for improving our understanding. We need to start thinking about the interaction space to improve our understanding.

I’ve been trying to do that a little bit with this big marine meta-analysis. I’ve been developing agent based models that basically assume that consumers and resources that move, go on random walks, at velocities that scale with their size, that they have reaction distances and detection regions that also scale with their size. And then just asking, basically, fully empirically parameterising these models with the prey density and prey size data from that data set of marine benthic functional responses. The questions that I would have, given what we know about the strategy and the movement of these consumer resource pairs and essentially the biomass density of resources of resources that they’re going after, are there any hard limits to the rate at which these different strategies can expect to encounter resources before anything else has happened, before any attacks have happened. I’ve been doing that in NetLogo.

When you look at consumer mass and you look at resource biomass, rather than units, it’s obvious that at a first pass filter feeders cannot encounter as much resource biomass as other strategies. Seems like a trivial result. However, when you consider that result in the context of how we think about filter feeders in the literature, it is interesting because this is what you see in the classical lit, this is how functional responses are presented. Type 1 pac man, feeding optimally. Epople talk about the adptive significance of filter feeding as a strategy because of the difference between type 1, 2 and 3. The problem with these kinds of analyses are, they bring together lots of different type of filter feeders (whales and daphnia). Whales swim to exploit concentrations of resources, different to being stuck in one place and having to accumulate resources in the environment come what may. Fundamentally a filter feeding that is static is more akin to something like a tree than a filter feeding that moves through the environment to exploit concentrations of resources.

Habitat Structure. Back to the log. Thinking about movement through space. This log, things accumulate round it. Like a stone in your garden, things crawling. The physical structure of the world is consequential to species survival. What we need to do is get to a position where we understand from first principals how physical structure modifies those encounter rates and modifies interactions, without being qualitative about it.

Looking at this since PhD. This is a piece of work, big piece of experimental work, where I took an invasive corophid arthropod you can find drifting in the water column, you can find established in a simple habitat or in complex habitats. 3 different contexts for potential predators to forage for this prey. My approach here was to try and get as many animals as possible. This is the largest stand-alone functional response experiment. Going from very large to small animals, across several orders of magnitude. Exposing them to three different experimental contexts. They are three dimensional swimmers, with three dimensional interactions. With substrate they settle. Not a neat test of dimensionality because when they settle their behaviour changes. My question is, how does this foraging context alter the scaling of the feeding interactions of a potential community of predators.

It’s worth noting, that although we expect positive scaling of capture rates with consumer size across the biosphere, we find hump shaped things across the global trend, and that is because essentially, consumers that forage for relatively small resources and those that foraging for relatively large resources, forage sub-optimally.

When you look at the drifting 3-D content you find that hump shapes distribution. This is log predators prey mass ratio plotted against capture rates. When you look at the simple and complex habitats, you see a collapse in that hump shaped distribution. My take is this, these are large differences in capture rates that are potentially occurring over v small spatial scales. When you consider that as compared to all the work that’s been done on interference, those differences are subtle. If this is a characteristic of interactions in other systems, then we’d like to know about it. This is fundamentally going to change the outcomes of any models that you might wish to parameterise. In particular the strongest interactors, do the work relative to their position in the drifting context.

Interactions are ‘Context-dependent’ this is an experiment where I’m doing a functional response in situ with shrimp that are migrating up and down a lake water column. I’m taking them and doing experiments in situ, in shore and off shore, on the surface, on the bottom, in the day and in the night. You can see that the attack rates and handling times change a lot. As organisms move through the world, these interactions with their resources are always changing depending on the context in which they forage.

A wider take on why the physical structure of the world matters. We are changing it, in a lot of ways. We are introducing complex habitats, where before there were none. We’re changing structure in ways that we don’t understand the consequences of from first principals. We need to get to a position where we understand the effects of habitat structure in first principals.

Parsing habitat structure. When we do these experiments we do reference treatment, then single unit treatment, then double unit treatment. This covaries lots of things at the same time, volume, surface area, potential for camouflage. We can measure the overall effect size of changing context. We cannot ascribe easily the reason for the changes. To do that we need to get away from assuming working with natural structures is the best thing to do. Need artificial structures to precisely manipulate space/structures in known ways and scale those manipulations so that we can test specific hypotheses.

Increasing predator-free space. Reef schematics. Moving from left to right, increase in predator free space/refuge space. Manipulating refuge space and maintaining surface area and volume of system. Certainly, better than throwing mussels on a bucket. Magnitude of functional response changes as well as shape, along that gradient. Change along continuous, quantifiable dimension of habitat structure. Fractal dimensions of these habitats are all the same. Don’t necessarily tell us anything useful about the space in terms of how consumers and resources might use it.

Consider another dimension of habitat complexity, for example, how the density of obstacles in an environment might affect an interaction. You need to be very precise about how you change structure. Errors lead to the creation of refuge space, can’t isolate effects. 3-D printing! V precise, scale the system. Resin good for printing small scales. Printing time scales with length. Minutes to hours to days. Generating lots of data about structure!

Process: Agent based models > 3D habitats > experiments > interpretation > model fitting.

Beyond size, available data limits what we can know: metabolic predictors are well established. Model species and systems skew limited global data. Modifiers of encounter rates are key. Structure cannot be understood without new data.

Down with model species and systems! Crabs and mussels only going to cut it for so long. Lacking data points for important, underrepresented groups. Address knowledge gaps.

We need to get Linnaean! Being arbitrary at the moment. When we do these experiments, we need to know all the variables in ways that other people can use. We’re not consistently doing that.

Opportunities to harvest data are myriad. E.g. cameras on the backs of turtles. New pipelines of data.

Open access data and open source tools.

Ecologists are legion. More ecologists working today that 50s and 60s.

Undescribed interactions are as exciting as undescribed species. Treat interactions and knowledge gaps as something to be discovered.

Seminar Three

Flowers, bees and shifting seasons – how to adapt when Nature’s calendar goes out of sync in a warming world

Jacob Johansson, Theoretical Population Ecology and Evolution Group (The PEG), Lund University, Imperial College London

21st November 2019

I want to talk about flowers and bees and shifting seasons and how they adapt when Nature’s calendar goes out of sync in a warming world. Background to this is as you may be well aware of many biologicals events now occur earlier. In the last decades we have seen big shifts. Flowering times, bird migrations, butterflies appearing earlier. Well establish examples. Another pattern we also see if the large variation in rates of change among species and events. Some species have shifted a lot, others appear not to be shifting, other going in the other direction. Question is how do we interpret these patterns? Are these responding strongly, are they doing well? Those that don’t respond doing less well?

One of the big fears is called phenological mismatch. Phenology is seasonal timing of biological events. You do your thing, reproduction/growth, in a time which is suboptimal. E.g. snowdrop tricked into flowering early and got stuck in ice. Mismatches or asynchronies highlighted early on in IPCC reports. 1990s. Crucial importance in community function, interaction between plants, animals, soil organisms. Changes in climate can disrupt these synchronies. Big networks collect phenological data but volunteers. Not all species change at the same rate, leading the mismatch.

Mismatch concept: 1. Mismatch has negative fitness effects + 2. Best response is to track seasonal optima. If you characterise it a bit, the idea could be that before climate was changing, biological events by evolution were take place at optimal timings. Now if these seasonal optima and changing you would expect to see negative fitness effects and adaptive response would be to track the seasonal optima.

If you look at demographic consequences they are less studied than the shifts themselves. One paper, 400,000 phenological time series in one paper. 75% showed response to climate change. Not so much done on the actual consequences. We did a review and four 4 other studies that mentioned demographic consequences, and 62 mentioned something. Either effects on pop size/reproduction/survival. These show mixed responses. Advancing phenology’s would have no negative effect on survival/reproduction in some cases. Pop decline/growth in some cases. Unclear what’s going on!

Clarkia rubicunda – native plant in California. Bombus terrstris – bumble bee. Similarities in how they grow. Both annual. They have first growth phase, vegetative growth. Then switch, flower and start investing resources into reproduction. Bumble bee shows similar thing. First to grow colony with workers, more workers = more growth. Switches to produce sexuals. In this case males. The kind of model which was developed in the 70s to describe this is called the dynamic energy allocation models. Flowers would have vegetative part and reproductive part. The vegetative part increases your production. Measure in the end reproductive output. This results in vegetative growth phase then switching time then investing in reproduction. Similar model developed for bees. Optimal switching time = length of season – 1 / production. This means that when p is high you should wait to grow, closer to end of the season. Invest as long as you can, towards the end your switch.

We have extended this in various ways. Firstly, we have looked at seasonal variation in production rate (p not being constant). Size dependent relative growth rates, where productivity doesn’t increase linearly with size. E.g. because when you get bigger plant you start shading yourself, interfering with yourself. Intraspecific resource competition where the production depends on how many individuals are competing for that resource. Also, interspecific resource competition, multiple species competing for resource.

Seasonal variation in production rate. Example, bumble bees how in different environments, semi-natural, agricultural dominated, different distributions of seasonal resource. To get a different understanding of this we normalised the timescale from zero to one, extracted the shape function – the area under the curve is one – describe this as shape x total productivity. From there you arrive at a general graphic solution to this problem. This is your shape function. You can calculate the cumulative integral of that shape function. You can just plug in your productivity level here, then you invert that and you can kind of get your optimal flower term as functional productivity for any shape in the end. So this we can get the complete overview of how changes in seasonal productivity rates is affective optimal timing. For example, is this is the relative growth rate, then if you just increase the growth capacity, which is the total productivity, you will see that that always increases regardless of the shape. You can look at the different components of this shape function for some change in the resource peak level and we look at that one on its own you see that the optimum timing increases, late peak, late optimal timing. We looked at the spread for example, it depends on the productivity level. If you have low productivity and you increase the spread you should flower earlier. Whereas if you have high productivity and increase the spread you should flower later. That’s the main results.

We can then try to look at how if you change different components of this shape then, we can see what happens. If we at the same time change this total growth capacity and the productivity peak date, then actually in this case the optimum time shouldn’t change. It should advance because you have an earlier peak, but at the same time increased productivity should make you flower later. It’s possible that not changing is an adaptive response.

Size dependent relative growth rate. In some cases, you find exponential growth. At some point you would have some limitations setting in. Self-shading in plants, social insects – growth which levels off with size, possibly due to increased metabolic cost when larger, harder to get round the colony, more social unrest. If we have plants that do not have exponential growth, we see that increased productivity should reproduce earlier. This is because with limitations you don’t get so much back if you grow more. Might as well switch to reproduction. Internal growth constraints switch direction of optimal response to change.

Colony growth experiments. Working with colonies in lab in different conditions, different levels of nutrition/pesticides. When colony grows, consumption rate levels off. Indicates levelling off of production rates with colony weight. Should expect that if we increase productivity, amount of resources, you should switch to reproduction earlier – experiment showed this.

Effects of resource competition. When bee has emptied flower, it will be less food for others on that flower. Can expect if you have lots of bees foraging, the amount of forage will decrease. Resource per capita decreases. As workers get more numerous, resource per individual decreases. Interested in optimal switch point. If pop switches early there will be lots of resources left. If colony grow for long time, less resources left, will not be able to reproduce so much = more resources. System can be invaded by a strategy using an earlier time. Link together many years. Reproductive output gets fed into next year’s dynamics. Higher the sexual output in year one, more established year two = strong competition.

Max pop size you should reproduce earlier to reduce competition. ESS = evolutionary stable state. Somewhere in between. If you start thinking from this point, the pop reproducing early. Can be invaded by late reproducing strategies that use more resources. If you start here, reproduce v late, would grow so big they would deplete resources, making it advantageous for earlier strategy to come in. If season length increases, reproduce earlier to avoid competition, a bit earlier to reach ESS and later to increase pop max. Depending on how strong the resource comp is, you get dif responses. None of them are tracking resource perfectly, because if the trade-off between growth and reproduction. Need some time to grow and some time to reproduce. Also look at pop size. As resource peak date increases, pop size and timing of production increases.

We start at evolutionary equilibrium, pop growth, at some point grows slow due to increases comp, switches to reproducing sexuals. Later flowering peak, immediate response is more energy for sexuals, higher reproductive output. Leads to more colonies. Some evidence if you introduce red clover flowering late gives big boost in reproductive output. If you add adaptive response, use resources to increase colony growth rather than reproduction. Reproductive output goes down. Long term the system may be invaded by late reproducing species.

Effects of interspecific competition. More species competing. Niche diversification. Different species use different resources. Classic example, short and long tongue bees. Short corolla, long corolla. Also use different parts of the season. Depending on tongue length you can access different numbers of flowers at different times of the year. Different amount of resources available. Plug in the bumblebee model. Consider colony initiation (by queen who lays worker eggs) and switch to reproduction.

Consider how these strategies evolve in the resource landscape. Might expect not much point starting colony earlier but should evolve to use different resources. Finding the ESS using adaptive dynamics. Use adaptive dynamics to calculate evolutionary change.

Four plants flowering at different times. Simplest case everything shifts forward. What if you have a-symmetric shifts of resource, affecting species differently.

Adaptations to shifting seasons. Classic thinking is that you should just track another event. This could be some related event. Could be start of spring, snow melt, flowering time. What we see if that it might be perfectly adaptive to trail behind, or not change. Also see phenological responses in different directions. Plant and bee might shift in different directions. We could interpret it as a mismatch.

Demographic responses. Short term pop declines expected, but pop increases may occur due to competitive release.

Adaptive responses. Expected to restore population sizes (evolutionary rescue), but may cause pop declines (intensified competition).

Interspecific competition. Uneven shifts of seasonal resource distributions can cause asymmetric pop responses. Asymmetry reinforced by adaptation later. Phenological adaptation in one species may cause population declines in (or extinction of) another.

Adative phenological responses can be quite variable. Associated pop trends can also vary. Depends on life history trade-offs and competitive effects. Eco-evolutionary modelling can help us understand and analyse apparently idiosyncratic responses.

We have Ana and Richard, they are doing these kind of big colony experiments. Developing more detailed demographic model to capture dynamics within the colony because it’s when you know a lot about the system you realise it’s not so simple. Bees – one important thing is that the Queen lays egg and then that could take 20 days before that worker comes out. Might mean a lot of things when you think about how to adapt to seasonal shifts.

Seminar Four

The complex consequences of simple sociality in the wild

Josh Firth, Oxford University, Department of Zoology

5th December 2019

Seminar Five

Reconstructing the spread of bacterial mobile elements in space and time

Francois Balloux, Sillwood Park, Imperial College London

10th January 2020

Seminar Six

Managing fisheries to protect dependent predators

Simeon Hill

16th January 2020

So, the broad concept that I’m talking about today is called ecosystem-based management. IT’s difficult to define. It’s got something to do with recognision of the fact that the fish species we exploit are embedded in ecosystems which are complex. Other things depend upon them that we need to take knowledge of the ecosystems into account in managing those fishers. We need to manage the impacts on those fisheries on other components of the ecosystem. There’s a few definitions of that concept in international treaties. Maintenance of the ecological relationships between harvested, dependent and related populations of Antarctic marine living organisms. Management measures should not only ensure the conservation of target species but also of species belonging to the same ecosystem or associated with or dependent upon the target species. It is not sufficient to manage the fishes you rely on, you must not unnecessarily disrupt the relationship between that species and other species that depend on it. By 2020 all fish and invertebrate stocks and aquatic plants are managed and harvested sustainably, legally and applying ecosystem based approached, so that overfishing is avoided, recovery plans and measures are in place for all depleted species, fisheries have no significant adverse impacts on threatened species and vulnerable ecosystems and the impacts of fisheries on stocks, species and ecosystems are within safe ecological limits.

There are other definitions of ecosystem-based managemen. I find this one quite useful. This is effectively a group of academics and conservationists who’ve come up with a definition that identifies a number of goals of ecosystem based management which are to maintain ecosystem productivity, maintain ecosystem health, maintain ecosystem resilience, and maintain ecosystem services.

What does safe ecological limits mean? Not sure I have a particularly good answer. Really important for achieving this object to understand what it means. Many legalistic documents are written by lawyers etc, not practising fisheries managers and ecologists. They use technique called strategic ambiguity. Reduce the level of detail to something everyone can agree to without feeling threatened. Fair to say that a lot of the world supports the general principal of ecosystem-based management. Few people know what it actually means in practise.

One of the consequences of this strategic ambiguity was revealed in this study where we looked at the objectives of stakeholders in the Antarctic krill fisheries: conservation professional, the fishing industry itself, scientists involved in the management of conservation. Identified what they considered the most important of various potential objectives. Effectively the group split into two broad categories: coalition of conservation ngos and likeminded scientists, the other was a coalition of fisheries and likeminded scientists. One of the things that they differed on was their preferred management strategy for the krill fishery. One preferred, marine protected area, effectively, areas of the sea which have a higher level of protection than surrounded areas, greater restriction on fishing. The other approach is feedback management. None of them thought that research into the effectiveness of these measures was particularly important. Suggests that it’s easier for people to identify solutions, even when they are not clear on what particular problem that solution is supposed to be solving.

The Convention on the Conservation of Antarctic Marine Living Resources (CCAMLR) provides a clue to safe ecological limits. Prevent changes to the ecosystem that are not potentially reversible within two to three decades. Able to recover to original level in two the three years, impact is considered safe. Below that level is in unsafe zone. Some attempts to clarify what safe ecological limits might mean. Very tricky to convert that into practice.

Take home message: complicated, not obvious exactly how you achieve it.

Fisheries management as a discipline has been practised for at least 70 years. Effectively it used an approach called single species management – two main objectives. One, to maintain pop that’s being harvested, to achieve socioeconomic goal – to allow fishing/profit. Over 70 years fisheries managers, where they are effective become good at achieving these goals. Core of the approach to fisheries management is called the harvest control rule. A relationship between the biomass of the fished organisms, and the amount that the fishery is allowed to catch. Can be more complicated. If your organism biomass in a safe zone you have a direct linear relationship between how much you can catch and spawning stock biomass. Antarctic krill has fixed catch limit, no regular stock assessment. Benefits – very low limit! 1% of estimates of spawning stock biomass in the area of the fishery.

Single species management tends to rely on feedback loops which are derived from control theory and consist on the numbered components here (screen). We have a variable (the size of the population). We need to collect data on that, which we convert into an estimate. We have a set of objectives, known as a reference. We have some method for adjusting fishing activity in response to the difference between he estimates and what we’re trying to achieve. We need a process for making sure whatever decision we make are implemented. Analogous to domestic central heating system.

Reference points: Target (states to aim for). Limit (boundary of states to avoid). Soft limit (boundary of states to avoid most of the time – in simulations).

Is it possible to implement for ecosystem-based management? Extend feedback loop to include more variables (e.g. predators).

Does it work in a model system? Spatially structured (area 1 and 2), linked by transport of main organisms (krill) between them. Carrying capacity of krill varies over time. Fed upon by predators and fishery. If we implement this feedback control and apply it to the model, we want to add uncertainty to estimates of predators.

Works in theory, does it work in practise? Assed the two feedback loops previously discussed. How far they progressed with developing and implementing the single species feedback loop. Good set of scores!

How far have they got with implementing the second feedback loop (predators)? Poor set of scores! Fisheries bad at adjusting for predator pop levels.

Of the things that we have identified as missing, I think that reference points is a real significant impediment to progress. If we can’t define reference points then we have no basis for adjusting fishing activities to achieve our reference points.

So, there is a question about, firstly, why the fishery managers do not use reference points. Our study wasn’t sufficient to identify the exact suite of reasons, but the things that we came up with were: firstly, these fishery managers are always working with uncertain objective for predators, because they are working within legalistic frameworks which use strategic ambiguity. Secondly, there’s uncertainty about the nature and extend of fisheries impacts. In most cases, fisheries are not the major thing that influencing the predator populations. If we see a pred pop being influenced it’s quite difficult to tease out the part of that impact which is due exclusively to fishing. That’s all the fisheries manager s are tasked with managing. Another issue is the adversarial nature of debate between fisheries advocates and conservation GNOs. Often evidence of stress in pred pops is conflated with evidence of fisheries impact. Generally, it’s unclear what contributions to that stress the fisheries is making. Likely that fisheries managers are reluctant to implement predator reference points, that is specific definitions of what they are trying to achieve for preds, because there is a concern that if external influences cause a breach of those reference points, they will be interpreted as a failure of fisheries management. Then, there is another thing, the attractiveness of simpler implementation targets (e.g. changing targets for how much ecosystem will be protected by what date). May have common-sense behind them, but object to achieve the measure than the achieve some conservational objective. They are more attractive to a suite of people.

Are predator reference points available? Yes!

Are there other way to limit fisheries impacts on predators? Precautionary measures, infers protection, not sure what level but better than doing nothing. Include, fixed biomass for predators, restrictions near breeding sites, spatial closures, low catch limits. No clear picture of if these measures are reducing predator impacts.

Suitable reference points. Need reference points for something to assess against and adaptive management strategies. Qualities of appropriate reference points: many of the preds are worst affected by potential fisheries impacts in early life stages. Don’t generally join adult pop for 5 years, effectively if our reference points are based on adult pop size, there’s a risk we will identify impacts 5 years too late. Need something that accounts for this lack time. Need leading indicators that provide prior warning of potential impact.

If we’re interested in keeping impacts within safe limits, we need to define limits of impact – limit reference points. Another consideration, pred pops changing in response to external influences: climate change. Important debate about whether you adjust your reference points for fisheries, lowering expectations about how small their impacts should be, over time, so that you are not unduly penalising fisheries for changes being driven by other influences. Fishing needed to support people’s nutritional needs.

Policy goals for ecosystems are ambiguous. This results in a preference for ‘implementation pargets’ than objective for ecosystem state. It is 2020 and we cannot be sure that fisheries impacts are within safe limits because there is no clear definition of safe limits Many fisheries managers have access to data for predators but do not use them. Clear objects for predators are feasible. Using predator reference points in management might increase out knowledge of ecosystem response to impacts.

Seminar Seven

Effects Temperature on Microbial Metabolic Rates: Linking Individual Responses to Ecosystem Impacts

Tom Smith, Imperial College London

23rd January 2020

Seminar Eight

The phylogenetic signature of interspecific competition in birds

Jonathan Drury, Durham University

30th January 2020

Seminar Nine

Sex, Drugs and Ecosystem Services: the paradox of plant toxins in nectar

Philip C Stevenson, University of Greenwich, Kew Botanical Gardens

6th February 2020

Seminar Ten

Conserving Genomic Diversity in a Changing World

Mike Bruford, Cardiff University

13th February 2020

Seminar Eleven

Evolutionary causes and consequences of avian dispersal syndromes: the importance of individual variation in colonisation processes

Marion Nicolaus, University of Groningen

27th February 2020

How shrinking glaciers are affecting Alaska’s coastal ecosystems

Eran Hood, UAF Geophysical Institute Presents Science for Alaska Lecture Series, University of Alaska Southeast

20th February 2018

What I want to do today is talk to you about changes in glaciers and ice field and basically how those changes that we’re seeing in the ice fields are impacting downstream ecosystems.

So I’d like to start off by showing a diagram that a group of us came up with recently that look at what are the ecosystem services that glaciers provide. We can categorise these in a number of areas, provision things like food supplies, fisheries, culture amenities such as tourisn and recreation and regulation ecosystems and that would eb things like water quality, outbust floors, hazards and this of that nature.

Example from coastal Alaska, impacts that changing glaciers are having. Started with a basic question. How much water is running from the land here along the Gulf of Alaska into the marine ecosystems in the Gulf of Alaska. Yukon drainage basic, twice the size of the Gulf of Alaska drainage basin, Looked at the meteorological data and calculated the amount of freshwater that’s discharged into the ocean and it turns out there’s a tremendous amount of runoff coming into the Gulf of Alaska. Four times was much discharge, 870 cubic kilometres water discharging into the Gulf of Alaska. 50% derived directly from glaciers. Important because we know – work by Chris Larson – changing glaciers along the Gulf. Overall 90% glaciers in coastal Alaska hinking in mass. For all classes of glaciers, terminating in land or lakes or tidewater. If we add all three together we get about minus 75 gigatons per year, 75 cubic kilometres of water excess in the lost volume from these glaciers. Important at global scale. Alaskan glaciers one fo the bigger contributors to global sea rise.

Example from recent study of Juneau ice field. 4000km squared, the ice thickness Taku glacier exceeds 1000 meters in some places. Projecting forward the icefield will about two thirds of it’s mass, two thirds surface area by end of the century. V different landscape around Junaeu, less dominated by glaciers. Important for us to understand from an ecosystem perspective what are the services glaciers are providing these ecosystems that may be lost or alternatively what are some of the opportunities that may arise from changes in these glaciers.

Video, cameras take a pic every hour, every day. Notice deflation and thinning of glaciers.

Landscape change. All kinds of valleys see trim lines where glaciers are thinning. Forest reoccuping area that becoming deglaciated. Losing ice rapidly. Seeing landscape change. One of the questions I’m particularly intereste in, the rivers conduits between glaciers, the ice fields and the marine ecosystems downstream. Important for us to understand what are the fundamental difference between rivers receiving runoff from glaciers, vs rivers receiving run off from forested ecosystems that are very different.

Streamflow/discharge – forested streams fairly stochastic discharge. Small peak assicated with snow melt, after than stochastic, depends on rainfall. Pulse delivery of water in smaller coastal streams. In contrast, glacier Rivers discharge looks very much like air temperature. It gets warm in summer, cooler in fall. See this deterministic pattern, from an ecosystem perspective, if you are adapted to this downstream, you have one deterministic pattern where no matter the weather, you’re always going to fill the river with glacier water. In forested case if you have little/lot of rainfall you’re going to have dramatic swings in the amount of water that’s available.

Physical properties of these systems also very different. Series of watersheds that have either more glacier coverage in the watershed or less of either no glacier cover in the watershed. Glacierised streams = lower temperature, unresponsive to air temperature in summer months. Streams with little/no glacier responsive to air temp in summer months. Different sort of physical seeting in the systems depend on how much glacier present in watershed. Similar with turbidity (water clarity – important for life penetration and primary productivity). Glacier streams = higher turbidity (less clear). Less glacier = clearer water.

Heavily glacierised rivers for the whole year spent 100% of time less than 5degrees. Whereas small low elevation rain fed streams have periods of time where temp is above 15 degrees +. Warmer streams = optimal thermal range for sockeye salmon. Glaciated streams generally below optimal salmon range. Global warming will push some cooler streams into optimal range, and push some up and out of the optimal range.

Alaska has a lot of thermal heterogeneity that helps adaptability and resilience for salmon populations.

What is the chemistry of glacier runoff? Originally glaciers were thought fo as sort of inert blocks of ice that were sitting there melting and served almost like an icy desert. What we can see now is that people have done a lot of sampling under and on top of the glacier and it is a really vibrant ecosystem in term fo microbial ecology. Samples show finger print of microbes that are working and transforming elements coming out and so in this context we think about glaciers more as ecosystems than sort of these inert blocks of ice. Soluble reactive phosphorous (SRP) a limiting nutrient for primary productivity in many aquatic ecosystems. We have the same kind of scheme here where zero is a watershed with no glacier, 25% glacier and 55% heavily glaciated. What this plot tells you is that per area of watershed you’ll get more kg of phosphorous out if you’re in a heavily glacierised system than a non-glacierised system. Particularly during summer when temp and melt at peak. There’s no appreciable atmospheric source of phosphorous and glacier are good at grinding up rocks. Glacier runoff could be a potentially important source of phosphorous if that’s limiting in either freshwater systems downstream or in nearshore marine ecosystems.

Iron export to marine ecosystems. Another rock derived element that glaciers are thought to be an important source of iron. And so many marine ecosystems especially as you go more offshore are what are called high nutrient low chlorophyll which means there’s enough nutrient to support primary productivity but there’s typically a lack of some micronutrient which is a lot of cases is iron. So the glacier rivers deliver this crushed up rock in these sediment plumes and that can be a source of dissolved iron. We also have cases where the sediments settle but then they’re resuspended during storms and that’s another opportunity to solubilise. Finally, glaciers also contribute through dust storms. During the winter time you have the strong outflow wings and there’s all this glacier flower fitting around in these river valleys and that can be blow out into the Gulf where it can help provide iron to these marine ecosystems. In terms of among other things glaciers can be a really important source to some of these rock derived elements.

Glaciers and freshwater food webs. Kowee Creek – one of ther questions we’re asking, we’re looking from the glacier down into the watershed, from a food web perspective, in the watershed does it matter that this glacier is here or not? Need to understand to see how these food webs might change as these relatively small glaciers in the Creek disappear over time. Have three generic types of streams (glacial, clearwater – snowmelt, brownwater – rainfall) in Southeast Alaska. Long term datasets tell us about how the chemical and physical characteristics vary. Habitat mosaic within watershed. Evaluate value of habitat mosaic from ecosystem services perspective. Organic matter from vegetation, biofilms, algae > supports invertebrates > supports fish. Can you what we klnow about chemical and physical characteristics as drivers to run this model and look at the potential to support fish growth. Juvenile coho salmon – glacier water provides less resources for growth potential. Too cold for fish productivity. Fish best in rainfed stream. But fish mobile consumers, make use of different provisions at different times of year.

Stream physiochemistry tells us about resource availability which tells us about fish capacity. We now have some hypotheses that the model that we can go out and test on the ground by sampling food webs/streams to explore idea of habitat mosaic.

In addition to influencing rivers, the physical removal of glaciers from the landscape is also creating opportunities for salmon. New streams come out from under the ice, providing new salmon streams along the coast of southeast Alaska. Although salmon go back to their natal stream, a certain percentage stray, which allows them on sub-decadal timescale to repopulate new streams. Roughly 500 new salmon streams along the coast of south east Alaska.

Impacts on marine ecosystems. Glacial plums provide a certain chemistry and structure to these marine ecosystems. One way we can map the sort of extent of this glacier influence is to use water isotopes, looking at the water molecule, at the isotopic signature. Fords with lots of glacier and snow melt run off are dominated by freshwater. You can use isotopes to see fresh water and see it in the chemistry. You can see the signature 10+ km away from these glaciers, where the glacier water is coming out into marine ecosystems.

Ice associated species appear in high densities in these heavily glaciated areas, turbid and cold waters. Traditional thinking says not much productivity in these waters. Krill, really pronounced hot spots in the trawls in the upper reaches of bays dominated by glacier run-off. Surprising. Tells us that there’s something there that is increasing productivity and sustaining these aggregations of prey species or plunge feeding seabirds.

Example of a modelling effort to look at this, we can use isotopes, take a sample from any animals mentioned, look at the carbon and hydrogen nitrogen isotopes in the sample and you can use a mixing model that allows you to deduce where the resources that the animal is utilizing are derived from.

Tidewater glacier fjords. Specialized glacier, endangered species with unique characteristics. Throughout Alaska there are 36 tidewater glaciers remaining, down from 50 in 1975. Interesting pattern that you see in these tidewater fjords - number of different circulation patterns. Idea if that the freshwater, instead of being discharged in a lens on top, that you’d get from a land terminating glacier. Discharge coming from underneath the glacier. The freshwater is buoyant. Rises up and entrains warm ocean water, adds to melt of glacier. Entrains organisms like krill and they can be killed by the osmotic shock from exposure to freshwater brought to the surface. Brings up nutrients to the surface as well. Increases productivity and oftentimes in you go into these tidewater glaciers you’ll see a lot of plunge feeding seabirds that are aggregated in these areas because of all the material that’s being brought up by that upwelling and the sort of convection loop circulation that you have in fjords that have tidewater glaciers.

Tidewater habitat. In addition to that circulation tidewater glaciers are also important for providing habitats. The icebergs that calve off the tidewater glaciers provide haul outs for harbour seals. Provide areas for pupping, raising young. Safe environments from Orca’s and other predators. Seals concentrate around tidewater glaciers during breeding season.

Glacier tourism. Tidewater glaciers good for tourism! More dynamic and interesting for tourists. Land glaciers not as interesting, more static.

Glacier hazards. Climate driven glacier hazards. Detached, remnant ice. Melt water comes down, fills basin, main glacier acts as a dam – regular outburst floods.

Systems thinking - Need to think of coastal ecosystems as extending all the way from the ice field to the ocean and try to study these as one big linked ecosystem. What we understand now is that the changes in the icefields are propagating to rivers which are propagating downstream and have a whole variety of impacts many of which in terms of chemistry and food webs and Alaskan coastal current. Interdisciplinary approach needed. Coordination to tell a story that extends across the whole ecosystem.

Arctic Microbes: Living in a Frozen Ocean

Marcela Ewert, University of Washington’s School of Oceanography and Astrobiology

10th March 2011

Arctic Ocean. What is different about this ocean compared to others? Properties? Covered in ice. Much smaller. Surrounded by land. Very special place. Different from other oceans. How does the arctic ocean get ice on it? By freezing ocean water, going to make a difference in the kind of ice formed there. Greenland is also covered in ice, but Greenland is covered in ice made out of freshwater. Compilation of snow. Ice in the arctic ocean made out of ocean water. What could be a difference in composition of the ice? Salty! So a different kind of ice. Salt water ice looks different from fresh water ice. One of the most important properties of saline ice/sea ice is full of channels and pores with liquid water inside. This makes it a very special environment for microbes to live. Imagine you are very small, you can fit in one of those channels.

The three things we should remember is that saline ice is different from freshwater ice. The second is that this topic is important because there is a lot of it. A whole ocean is covered with saline ice. The third thing we should keep in mind is that this ice is floating on top of the ocean and the oceans are connected, all of them. Whatever is happening in this ice is connected to the rest of the planet. It is not an isolated system. Things that happen all over the planet will affect what is happening to this saline ice.

I want you to imagine a cubic meter that is approximately 35 cubic feet. Around a block of ice that is three foot by three foot by three foot. How many pores are inside? Between 10,000 and 100,000,000,000 of tiny little holes that could be used by microbes. There is plenty of room for microbes. These channels have a surface in which microbes can potentially attach. The surface of these 35 cubic feet piece of ice, can be between 100,000 and 1,000,000 square meters. Huge. Size of a small farm. Plenty of room for microbes to attach to surface of ice. This is not the same situation in freshwater ice. Not the same space/room inside.

Not all the water in saline ice is frozen. This is because of the salt. Salt doesn’t let all the water freeze. There is liquid water. There is a lot of liquid water. It has been estimated that the amount of liquid brine in all of the sea ice in the world would be bigger than four times the volume of the water contained in rivers. Imagine the Arctic Ocean. IT is made out of salty ice and you just learned that salty ice has liquid brine inside. If you were able to collect all of the brine contained in the ice in the Arctic, all of that liquid, that volume would be bigger that the volume of water in the rivers on the land. So there is a lot of liquid water entrapped in the ice. That is good if you are a living organism because all life on Earth, all the life we know about, needs water to survive. Knowing sea ice has so much water helps us understand why it is such an important environment. How do we study this liquid water in the field? You can just open a hole in the ice and overnight the hole will be filled with the water that is flowing from the ice. Then we take samples and study them and find microbes in there.

The other organisms are algae, there is plenty of room and plenty of water and they just start growing. Microscopic algae. If you want to see the organisms you need to take a piece of ice and put it under a microscope and you will see the algae, tiny cells. Sometimes they make chains, long chains. Sometimes they overgrow and form chains that can be meters long. There is a lot of algae growing in the Arctic. What can happen to the algae is it becomes food. They are like plants of the ocean. They get eaten by other organisms. Many organisms depend on the algae to produce their food. Half of these Arctic ecosystems are sustained by algae that grow inside the ice.

When we think about the Arctic ecosystems, most people think about polar bears, but what we focus on are the smallest ones nobody notices – bacteria. They are helping, recycling the nutrients in the system, keeping the system healthy so to speak.

But it is not easy to live inside the ice. You have to be adapted to living there. There are many reasons how or why would it be difficult to live inside an ice pore. You are in a pore, you are surrounded by solid ice, that as the season gets colder, the ice grows and gets closer. As the ice is growing the salts start to concentrate. The environment becomes saltier – a halophilic environment. The salinity here can be seven times higher than the normal salinity of sea water. V small, v salty, ice crystals grow and poke the cell. Not a great environment. You need to be protected to be able to survive there. Life is very amazing! Life has found ways to live in there. These organisms have adaptations that allows them to live in this salty, cold, icy place. They produce a goopy substance that the cells cover themselves in, like a cushion that protects them against the ice and salt.

We’ve been talking about small scale, but there is a lot of this ice over the planet. The ice caps can cover the planet, between 3 and 6 percent of the surface of he planet at any given moment. There is a good percentage of the planet that will be covered by this sea ice. Also remember that this sea ice is floating on top of the ocean. This is something that people tend to forget. This ice serves as an interface between the atmosphere and the ocean below. If there are things in the atmosphere that are falling, they will stay on top of the ice, it will not get to the ocean. As the ice is forming it will expel a lot of salt. The salt will sink and this promotes circulation. There are many ways the ice is relating the atmosphere to the ocean below. It’s not an isolated thing. It communicates with the rest of the planetary systems.

The Secret Language of Bacteria – An ASM “Microbes After Hours” Event

Dr Bonnie Bassler, Princeton University

28th January 2013

Brief introduction to bacteria and bacterial communication. What’s special about bacteria is they are single cells, they are very single. They are the first organisms to appear on Earth, been on Earth for 4 billion years. Made up of a membrane that keeps the outside out and the inside in. Inside cytoplasm where all biomolecules roll around and keep them alive. Bacteria only have one chromosome, one piece of DNA. So they only have a few thousand genes. The question that has driven microbiologists is how do bacteria do what they do, what can they do, given that they only have one piece of DNA, so not very much genetic information to work with. Thought to be simple, primitive organisms.

We know that there are all these virulent bacteria in the environment that if they can get in or on you or on an animal or plant they can make you sick of kill you. What we are starting to learn more about now is that there’s also all of these beneficial bacteria. Bacteria that are essential to make life happen, digest food, make vitamins, educate immune system. We need to think about both personalities of bacteria. The question at the centre is how do they manage to do either of these things? How can it be that they either keep us alive or have the capacity to kill us? The way that bacteria manage these amazing feats, for good or bad, is by talking to each other with a chemical language. They count their numbers, they recognise when they are in groups, and if they do things in unison, as a multicellular unit, they can accomplish tasks they never could if they functioned as individuals. This is what we think bacteria are doing and why they are so successful on earth.

Bacteria live in two modes: a-social mode, and social mode.

When bacteria are alone in a big world, they want to have the program of gene expression going that’s good for acting as individuals. They are carrying out or expressing traits that are good for being along. Among those things they make and produce small molecules that you can think of as hormones. We call these autoinducers. They make and release these molecules and since the bacteria are basically alone, these molecules float away, the bacteria can’t detect them and that says act as an individual.

As bacteria grow and divide, if they are ion a particular environment sort of near each other since all the members of the group are participating in making their share of these hormones, these autoinducers, the autoinducers that are outside of the cells accumulate in proportion to cell number and so when the molecules hit a particular threshold concentration the bacteria detect them and it tells them that there’s neighbours around and then all of the bacteria change their gene expression or their behaviour in unison. So, what they begin to do is to carry out group behaviours. What we think then is that by measuring the concentration of these chemicals, bacteria can detect then they’re alone and when they’re in groups and so different jobs. So, microbiologists brought the tools of molecular biology to this game to understand how does this work. What we found is that there’s an enzyme that makes that hormone that autoinducer molecule and that diffuses out of the cells. Then the autoinducers when it increases to a particular amount it can get detected by a protein that’s on the bacteria membrane, a receptor protein. This protein is just like the hormone receptors that sit on your cells surfaces. That molecule can slot into that receptor and that sends a signal into the cells to tell that cells to turn on the genes that underpin group behaviours. So the more cells there are the more that autoinducer molecule there is and a particular amount all the bacteria change their genes and turn on and off genes that allow them to carry out group behaviours. We call it quorum sensing. The bacteria vote with these chemical votes, the vote gets counted and that the group goes along with these Democratic solutions.

A chemist began to look at what these molecules are. Looking at the molecules that bacteria make we see that the left hand part of the molecule is identical in ever case, but the right hand side is different. What those differences do is to confer exquisite species specificities to each of these molecules. These molecules really do fit like locks and keys into their partner receptors and so they allow the bacteria to speak within their own species. These chemical differences make these molecules have intra- species communication properties. Sort of private, secret conversations that bacteria carry out with their siblings and it tells them and their clones when to do something.

Multi-lingual bacteria. In addition to this system that allows intra-species communication, there’s a second quorum sensing system in bacteria. There’s a second enzyme that makes another molecule. It has a partner receptor as well. All of that information comes in both from the first molecule and the second molecule to tell the bacteria to turn on group behaviours. What’s the point of having two molecules if these chemicals don’t encode different pieces of information. Having two molecules isn’t better than one. So what we found when scientists purified the second molecule was that it was one molecule. A universal communication molecule. Made by all bacteria. We think this since it’s one molecule that’s made by all different bacteria we think this is the molecule that allows interspecies communication. This is the trade language or the bacteria Esperanto that allows bacteria to talk across their species boundary. We think now that bacetria must be at least bilingual. There’s probably lots more to it. We think that they all have some molecule that says self and then they use this universal molecule to say other. The computation that we think bacteria do now is the following: we think the first thing they do is that they just scan the environment and they ask is there any molecule out there and so tat begins to tell them you’re alone or you’re in a Group. Based on whether or not they detect the molecule they start turning on and off genes. But then the more sophisticated computation that we know they do is that they actually measure the ratio of those two molecules. They turn on different genes based on whether they’re in the majority and you’re in the minority or the reverse. So sort of like what we do they figure out is it my family or is it somebody else out there and then I change my behaviour based on the blend of this case of bacteria that are in the vicinal community.

What do they do? Quorum sensing behaviours. Scientists have looked at the kinds of behaviours controlled by this chemical communication process. This quorum sensing process (biolumenescen, virulence factors, biofilms). Bacteria need to be able to act in a group to be virulent. What we think is that when a bacterium, one or a few bacteria, get into you or into a big host, the stupidest thing bacteria could do is to secrete their virulence factors if there’s only a few bacteria those factors won’t do any good and furthermore they’re a red flag for the immune system. What we thing is that the better idea from the bacterium’s POV is to wait, to count your members and to decide when there’s enough of you there that if everyone secretes these virulence factors together they can overcome a huge host. Now we have many clinically relevant cases of bacteria that if you make mutants so that they can’t talk or they can’t hear, those bacteria are a-virulent. The group-wide production of virulence factors is a big quorum sensing control trait also biofilm formation is also controlled by quorum sensing. We know now that bacteria sit on surfaces like on your teeth on your skin and your intestine, they sit in biofilms and these of course are communities of bacteria of bacteria that do things together and so this list goes on and on of the different traits. I think the idea that you can think of is whenever a bacterium is gonna give something away to the world, some protein, some factor, it’s never gonna get it’s own back. The world is too big, so it’s only when they do these things as a collective, that these kinds of behaviours become effective. That’s quorum sensing. Now we know bacteria talk, we know bacteria have multiple languages, we know that they both do good things but then a lot of bad things through quorum sensing. The sort of practical place that the field is moving to is trying to understand whether we could manipulate these quorum sensing languages so could we stop harmful bacterium from communicating so make new therapeutics and likewise could we make the beneficial bacteria that we know are essential for life could we make them better at communicating to make our lives healthier?

New approaches to antibiotics. The idea is to take these molecules, with chemistry we can change them so we can change their shapes a little bit. We have the signal molecule and then we have a molecule that would be an antagonist. You could put say a bump on the molecule and try to make a new molecule that would jam the receptor and so the question is, can we make such molecules and shut down virulence? The experiment that’s been done which seems to be working in model animals, is that we can take virulent bacteria to kill that animal (put yourself here). You need quorum sensing to make that happen. The question is whether we can make molecules that can make bacteria unable to communicate and get these animals to live. This is done for sure we can do this in the lab. These are not drugs yet, these are lead molecules. But it is very exciting because this would be a new way t think about antibiotics. Instead of killing bacteria, instead of stopping their growth, if we could just do behaviour modification maybe that would be a really nice way to go forward in thinking about therapeutics. Likewise, to give a plug for the good bacteria, if we could make quorum sensing better by making super autoinducers, maybe that would be useful for industry and for health purposes. There’s sort of this basic part of the science to learn how collective behviours evolved on this Earth, and then this practical part of the science to see if we can do something about it.

To summarize, my 9 minute talk in one minute, I hope what you think is that bacteria can talk to each other. They use chemicals as their words. What we think is that this made bacterium multicellular. This was the invention of multicellularity. When microbiologists study quorum sensing bacteria, what we hope is when we find these ancient principles that allowed collective bevavihours, that allowed robustness, that allowed bacteria to act in synchrony, we hope we’ll be able to help our colleagues who study higher organisms to understand how multicellularity can be robust. We think the secrets are hidden in these bacteria. With the molecules that I told you we think that bacteria can tell self from other. Again we would argue this is what happens in higher organisms but we think bacteria evolved this ability billions of years ago. So, we’ll be able to learn about higher organisms by studying this process. To go back to this practical part, we would love to be able to impede quorum sensing in harmful bacteria and improve quorum sensing in beneficial bacteria. Lots of scientists have ponies in that race, it’s a really exciting time in the field. Natural anti- and pro-quorum sensing strategies already exists among bacteria. Those strategies have won over billions of years of evolution. Maybe we should use this as our starting point.

Astrobiology and Space Exploration Introduction Seth Shostak Senior Astronomer SETI Institute Standford University

Cosmology – means everything, the whole universe, cosmology is just, what is it? How does the universe work?

The Greeks view of the universe really simple. There was the Mediterranean and clifts and everything was floating in a big bowl somewhere. Some cultures believe the world is on a waterfall on top of a turtle on top of a turtle. Cosmology very old discipline. Science that for a long time didn’t have a way to measure anything expect looking at it. Cosmology was looking up at the sky for patterns. Had attitude that if you have idea, you need observations to back it up. For astronomers you can have any idea you want, but if it doesn’t predict something we can see if a measuring device, it’s not worth very much. The old Copernican model had the longest run. Cosmos consted of the solar system with the earth in the middle. Stars were backdrop to planets of the solar system. This predicted things. Could use it depending on how fast things moved around in the sky. IF there was regularity to that you could predict where planets were going to be. Developed elaborate systems based on this cosmology to predict movement of the planets. They worked pretty well. Not perfect, but well enough. Copernicus 1450 – system didn’t work as well. Took a while to refine the system. Better scheme because closer to the truth.

These ideas went away in 1500 when people started measuring positions of sun and moon. No telescopes just giant protractors aimed at the sky. Tycho Braye – Dane, missing nose. Measurements led to Copernicus and Newton’s revolution in how the solar system worked.

In the last two centuries the question has become different. Beginning in 1800s were able to measure how far away the starts were. How? Planets used geometry. They had to build better instruments. Fredrick Vessell in 1858(?) measured the distance to a nearby star. About 11 lightyears. 1 lightyear = approx 6 trillion miles. The universe was far larger than they thought. One of the nearest half douzen starts. Nearest star about half that. Blaise Pascal who about how terrifying these enormous spaces are.

You can learn something about cosmology by doing a simple experiment, by going out at night and seeing what is it about the night-time that’s different than the day time: it’s dark. Not trivial. Tells you about the universe. Imagine the universe is infinite. IT probably goes on forever. If it doesn’t there must be some place you get to where there’s a sign, last gas before the end of the universe. Some people have a philosophical problem with that. Imagine that stars go on forever, you can see that no matter which direction we look at, sooner or later it’s going to hit a star. That means that the whole night’s sky should be as bright as a pinprick star. It should be the same surface brightness as the sun. Overous paradox – pointed it out.

How could you have a night’s sky without having the universe be finite? Could you have an infinite universe and still have a dark sky? If the universe is expanding you’ll have a dark sky even if it’s infinite because the stars than at farther away are moving away from you, their colour changes, a Doppler shift. Light gets stretched out as the stars move further away, it gets redder, then infrared then radio waves. By having the universe expanding you account for the sky being dark at night. So universe is finite or expanding.

1908 if you had asked astronomers, what is the cosmology of the universe they would have said it consists of a big ball of stars (milky way galaxy) and that’s it. Outside that there’s nothing. That was the picture. Only 100 years ago. That picture became a problem when people began to study things like nebulae which is latin for cloud. Some sort of fuzzy thing. The question was what were these things? They could see them in the 1700s. Question was is it some sort of gas and dust? Forming a star? Making planets? Other people said maybe this is something really far away, beyond the galaxy. In order to tell whether that’s true or not, you need to be able to measure the distance to one of these nebulae. A big triumph of the early 20th century. Figured out how to measure distances to these far away objects. What you want to do is find a standard candle. All it means is something in space that you know how bright it is. For example, if I had a hundred watt lightbulbs are about the same brightness, irrespective of brand. Use light meter to measure the light, move it twice as far away, the light goes down by a factor of 4. You could turn this experiment around, measure the light and tell how far away the lightbulb is based on it’s brightness. But you need to know the strength of that lightbulb.

Astronomers looking for things that might be standard candle to use to measure nebulae. Used big bright stars known as Cepheid Variables. These have been studied by a woman down in south Africa Henrietta Levin. Did this work in early half of 20th Century. Not well know because done by a woman. She provided the whole key for figuring out how to determin the distances to these galaxies. Able to say these guys are not only bright stars in smudges, but they were unstable. Means they would get brighter and dimmer and brighter and dimmer. Unstable if too big, gravity fighting with nuclear engines. But she found that the bigger ones got brighter and dimmer slowly. Smaller ones got brighter and dimmer much more quickly. Looking at a bunch of them, more or less at same distance. Established that if you plot brightness verse how long it takes for them to go through one cycle. Dim = short period, Brighter = longer period. Had profound implications. Meant that if you found one of these guys, just sit around and see how long it took to go through one cycle of getting bright and dim and now you know how bright it is, what wattage bulb it is. Edwin Hubble realized this and found some Cepheid Variables in nearby galaxies, in particular the Andromeda Galaxy and he could figure out how far away they were.

Hubble not such a nice guy, but everyone forgot about Henrietta Leavitt.

Hubble plotted smudges (galaxies) measurement on a smudge and he was able to find some of these Cepheid Variables so that he can figure out how far away they are. The light was redder – so figured out galaxies are moving away from us. What does that have to do with anything else? The data show that the farther away one of these smudges is, the faster it’s moving with respect to us. They’re all moving away from us, with the exception of a few. This is the expanding universe.

The cosmos looked like it was blowing up. Fundamentally new idea. Einstein tripped across the idea but didn’t believe it himself. Astronomers told him the universe stays the same.

What happens if we run that expanding universe backwards? Must be a point where everything comes together. We can use mathematics to work out when the universe started expanding. Approx 2 billion years ago. Clearly there must have been a beginning to this. People thought it was a problem. Tried to make fun of the idea by calling it the big bang.

Heisenberg Uncertainty Principal – means that you know the universe wasn’t completely uniform even in the early days. Very small, hot, dense. Slightly inhomogeneous, so by the time the universe blows up there are clumps. Clumps can collapse under their own weight to form galaxies of stars which when they form almost always make planets and then you get a little bit of dirty chemistry.

Who pulled the pin? Universe it only 13.7 billion years old. Can’t see anything beyond that many light years away as it hasn’t had time to get to you yet. The universe looks pretty much the same no matter which direction you look. How do those galaxies know to be arranged similarly to those guys? Why is there uniformity between vastly remote areas?

BB questions: galaxies all moving away from us, so are we in the centre? Old raison pudding analogy – big bowl of batter, raisin, into oven, raisin = galaxies, heat = expansion so all raisins move away from you regardless of where you start off. What did the universe expand into? There was no outside that, no space on the outside. What was before the Big Bang? Was there any time? The universe is also particularly set up for life. Atomic constants that make stars work is just right. The laws of physics don’t allow the numbers to be different than they are? Universes are cheap, all the energy in the universe = zero, ultimate free lunch. Maybe very common? Born with random properties. Most of them not suitable for life. Anthropic principle says of course we’re in the winning universe because if we weren’t we wouldn’t be here.

Stars don’t exist everywhere, they tend the be in organised structures called galaxies. Looking at galaxies further away they have different shapes, but we’re also looking back in time. If there was no big bang the galaxies should look the same. Different shapes support changes through time/big bang. Satellites discovered the background radio glow from the big back to support the theory.

What was happening in the first second of the universe? The physics stops working before a certain point (10^-43 secs after the big bang). So small, hot, dense means uncertainty principals says you don’t know anything.

The future of the universe. We’ve had 13.7 billion years, had stars for most of that time, we’ve had the elements. Universe is ¼ helium by weight and ¾ hydrogen and a little bit of all the other stuff created by stars. But, what’s going to happen in the future? You need to figure out how much STUFF is in the universe. Lots of stuff = slowing expansion and eventually, the big crunch. Possibly isn’t enough stuff out there to stop the expansion = open universe, getting bigger and bigger. The universe is mostly empty.

Astronomers looking at supernovas, would tell them to what degree the universe was slowing down. They found that the universe was speeding up. No body had anticipated. Something must be pushing the universe apart, acting as antigravity. DARK ENERGY! Leading to the big rip? Everything finally pulls apart? 30 billion years from now. Before then the sun will run out of fuel. 5.5 billion years the sun will start running down. It will swell up, 10 times current size, energy output will go out, Earth will be cooked. But we can move, not a problem. But eventually all the stars will go out. The universe keeps expanding, it goes on forever. Eventually everything that can happen will happen. 10^100 years time at that point the last thing has happened, after that nothing more happens. No more energy sources. Bottom line, in high school made timelines of earth, development of life, dinosaurs then people, timeline goes around the room. 100 billion years of excitement in the universe, then infinite amount of time of nothing…

Astrobiology and the Very Small

Professor Ken Kubo, American River College, Sacramenta 1st April 2014

I’m going to talk about astrobiology and the very small. I know microbiology and molecular biology. I’m a biologist at a physics/astronomy lecture. Why? Are we alone in the universe? Neil deGreasse Tyson, “more than likely the first life we find would be microbial”.

Today’s topics:

* Definitions
* What can microbes teach us about astrobiology?
* Life elsewhere in the Solar System?

Are we alone in the universe? A major topic in astrobiology? Astrobiology addresses the study of the origins, evolution, distribution and future of life in the Universe. Astrobiology seeks to understand life in a cosmic perspective.

Some topics in astrobiology: combines lots of different areas of science. All of us have something to contribute. The origin and emergence of life – this planet as well as other worlds. What are the limits of life (extremophiles)? The possibility of life elsewhere besides Earth? Future of life on Earth and beyond.

What is LIFE? IF we’re looking for life elsewhere we need to be able to say what we’re looking for. Some properties: it grows, it divides (replicates), it metabolises, it can store instructions. There is another property of life – it evolves. This idea of evolution is used as a working definition of life.

Gerald Joyce, NASA scientist, 1994 ‘Life is: a self-sustaining chemical system capable of undergoing Darwinian evolution.’

Defining life is complicated. It grows – non-living things like salt crystals grow. It divides – computer files divide and multiply. It metabolises – fire metabolises. It can store instructions – computers. It evolves – algorithms capable of evolving – Jnetic: Evolution of Stylized Images. Although life is complicated to define, we know life when we observe it.

Habitability: ability of a world to develop and sustain life. This is one of the basic concepts of astrobiology. What makes a world habitable? NASA definition: Habitability - extended regions of liquid water, conditions favourable for the assembly of complex organic molecules, and energy sources to sustain metabolism. Important from policy perspective, informs what they send up into space to look for evidence of life. From the NASA Astrobiology Roadmap.

Why water for habitability? Water expands when it freezes (solid/liquid density <1). Why is this important? When water freezes it floats, so aquatic organisms survive. Water absorbs heat well (high specific heat). Water also excellent solvent, can dissolve things in water, good for dispersing out molecules important for life. Water takes part in many chemical reactions. Water is abundant! Not only on Earth, but also in the Universe? What is water made of, hydrogen and oxygen. How abundant are those elements? Hydrogen is extremely abundant in the universe.

The challenge of heat. We can use microbiology to understand astronomy. What we’re going to look at is organisms here on earth that can help us understand how life may develop beyond Earth. What are the limits of life? Black smoker: found pyrococcus furiosus, optimal growth 100 degrees, boiling point of water. Range from 70 to 103 degrees. Geogemma barossii, optimal growth 115 degrees. Range of 85 to 121 degrees Celsius – thrived after subjected to autoclave. Methanopyrus kandleri optimal growth 98 degrees, range 90 to 122 degrees. Extremophiles!

The challenge of cold! Vostok Station, Antarctica – Lake Vostok underneath sheet of ice. Is there anything living down there? How cold is it? Minus 13 degrees. Below freezing. Not frozen because of pressure and salt. Five times saltier than the ocean. Take ice cores. Looking back in time. Sealed off from the rest of the world. Are there any organisms? Yes! They’ve been able to determine what kinds of organisms live in that lake. What they found is 1500 different types of organisms in one sample. There’s over 3300 that they can’t identify. DNA barcoding used to identify species. Fish have other organisms living on them. If these microbes have to depend on living fish, then are they living fish living down there?

The challenge of radiation. Can’t tolerate a lot of radiation. Human lethal dose 500-1000 rads. Deinococcus radiodurans “Conan the Bacterium” – thrives after 1.5 million rads. Has many copies of its DNA, back up files, it can stitch back together it’s genetic instructions when DNA is destroyed by radiation. It might be possible one day to do the same with our DNA.

Organisms here on Earth challenge our definition of the habitable zone.

Does life exist elsewhere in the Solar System? Just going to focus on a few worlds. Habitability of Mars? Curiosity is exploring Mars. Has made exciting findings about habitability. Images seem to suggest that once water flowed over the surface of Mars. Suggests the Gale crater was once a lake. Jim Bell (ASU) at American Geophysical Union meeting Dec 2013: “Previous results from Spirit and Opportunity pointed to very acidic water, but what we’re seeing in gale Crater is evidence of fresh water. Very neutral. Drinkable.” The kind of microbes we have on Earth could have lived on Mars under these conditions.

Jupiter’s moon Europa. Has subsurface ocean. Liquid water underneath the surface. Under a lot of gravitational pressure, tidal heating keeps it warm. Is there water at the surface? Leakage to surface shown by spectral data from WM Keck Observatory. Hubble Space Telescope showed Geysers. Big space exploration indication from this. To get to the ocean we’d need a bit drill. But now we could send something with a cup! Provocative.

Meteorites as interplanetary samples. Easy to find in Arctic regions as they stand out! Finding meteorites from Mars. Martian Meteorite Yamato (000593). Formed 1.3 billion years ago. Water evidence in meteorite, based on the structure within the meteorite. This is why the science is interdisciplinary – need a geologist to see these things. Carbon rich structures that could have been caused by biological processes. Need to be careful what we infer about these signs.

Astrobiology and the Future. How are we going to explore these two worlds? Mars sample return. Sending a probe to Europa (Europa Clipper).

What about other stars? Could they have habitable planets. NASA Kepler famous spacecraft for planet hunting around other stars. Finding a large number of exoplanets, as well as exoplanets in the habitable zone.

Will Earth’s habitability change? Earth’s history of mass extinctions. Last one 75 million years ago, meteorite crashed into the Earth. We are currently going through the 6th mass extinction. Book by Elizabeth Kolbert – The Sixth Extinction. Anthropogenically driven.

Summary, defining life and habitability is complicated. But what we have learned expands life’s limits. Extremophiles on Earth have greatly expanded the limits of possible life in the Solar System and beyond. Astrobiology provides a context for understanding Earths history and its future.

Effects of Temperature on Microbial Metabolic Rates: Linking Individual Responses to Ecosystem Impacts

Tom Smith

Prokaryotic microbes – bacteria and archaea. Eukaryotic microbes – protists. Tom’s work is mostly bacteria related. Microbes super important in various biogeochemical cycling, particularly carbon cycling in soils, super abundant, represent lots of biomass in soils. They sit at the bottom of the food chain, tying over carbon. Important in wetland systems, produce methane. Cyanobacteria important for photosynthetic. In order to predict the impacts of climate change its important to understand how temperature effects microbes and thus biogeochemical cycles.

Looking at the direct effects of temperature on growth rates. I’m going to be looking at the direct effects of temperature.

How does temp directly affect microbial metabolic rates and are these effects constrained across taxa and timescales? How does temperature alter the composition of microbial communities? What more complex effect are these changes likely to have on community or ecosystem functioning?

The way I’ve been looking at how temperature affects microorganisms is through thermal performance curves. Find these throughout the literature for all sorts of different traits of organisms. Take biological rate and measure against loads of different temperatures.

Looking at microbial growth rates because they are quick and painless to measure compared to other traits in other organisms. There’s hundreds of thermal performance curves for different bacterial species in the literature. There’s a good set of data to compare across organisms. Can be used as a proxy for fitness.

Been fitting schoolfield-sharpe model which gives a good approximation of the shape of the curve. Parameter E – thermal sensitivity (steepness of the curve). High E = high thermal sensitivity. Every stepwise increase in temperature comparatively increases your biological rate more than if you had a low E. T peak = optimum temperature. P peak is the maximum growth rate.

A much simpler model that’s been used for decades in metabolic ecology is the Boltzmann-Arrhenius model.

Variation in E across taxa and traits. Collected 100s tpc from dif org for dif traits, looked at variation in thermal sensitivity. Global average 0.65. Variation across groups but there is a global average. Didn’t use bacteria in this study. Interesting to know if bacteria conform to these rules.

Interspecific E. Seminal paper on metabolic theory of ecology 2004 brown et al. Across species thermal performance curves. Across species shows similar thermal sensitivity as within species. Universal temperatures dependence. Everything governed by same sort of thermal constraints. How temp affects these organisms. But no bacteria.

If each point represents different species, are we looking at global line or thermal constraint which constrains how different species respond to temperature and are the individual species responses different points along a global continuum.

Do bacteria/archaea conform to the same intra/inter- specific E rules? Collected TPC for literature. Can we use these data to understand how intra and inter- specific thermal sensitivity is linked?

Used digitisation software (plot digitizer) to collect TPC data from the literature. Digitized 542 growth rates TPCs, across all temps 0 to 122 degrees. Entire range of habitable global temperatures.

High E for prokaryotes in general. Mean E for bacteria and archaea 0.88 eV and 0.95 eV respectively. E > 0.65 consistent pattern across low tax groups. Global average don’t extend to these organisms.

Evidence from environmental data – enviro with higher proportion of microbes to other organism tend to have higher thermal sensitivity overall. Tundra/boreal forest/temperate forest.

Linking long and short-term responses. These data short instantaneous thermal response. What about long term? Evolutionary responses which are likely to come into play over time-scales involved in climate change? How will a TPC change over time?

If hotter is better, fitness will increase. Selection may override thermos constraints << Equalisation of fitness. Or fitness increases but within and scross species R is not couples < Weak biochemcical adaptation.

Results from bacteria. Mesophiles: 42 degree optimum growth. Hotter is better idea. Hotter is better bacteria show no increase in metabolic rate with temperature.

For biologically relevant temp prokaryote metabolic rates fit with the hotter is better hypothesis. Across species peak meta rate increases with temp. With climate change driven temp increases, may we therefore expect microbial communities to have higher metabolic rates?

Long-term effects: considered a species with a defined TPC, which normally experiences temp below it’s tpk. IF temp moves beyond tpk this may cause a decrease in metabolic rate.

IF species can adapt to higher temptpk will increase along global thermodynamic line and meta rate increase at new adapted temp.

Micro com contains vast amount of genetic and phenotypic diversity which may extend to diversity in thermal performance. Can species sorting give the same overall effect at the community level as adaptation?

Adaptation of bacteria to higher temperatures over short absolute timescales, in as few as 200 gens. Easy to adapt bacteria to a new temperature. Done in lab setting on model organisms. Can this occur in the natural environment?

Diversity of microbe coms, thousands of taxa present in small environ samples. Unexpected phenotypes can be found. Extremophile coms, adapted to high salt, acid, from freshwater lake. Gradient of phenotypes constantly under selection.

Phylogenetic evidence for species sorting over adaptation. Strong phylogenetic signal in peak temperature of strains. Had strains rapidly adapted to new temp regimes over the duration of experiment, tpk may be expected to be independent of phylogeny.

Ecosystem impacts: climate warming likely to result in a shift in microbial community thermal optima, either through adaptation or species sorting of existing phenotypic diversity (or both).

Shifts in thermal optima necessitate an equivalent increase in metabolic rate (as per hotter is better).

Results in increased metabolic rates of microbial community with temperature increase.

Increased E enhances this effect in prokaryotes versus eukaryotes.

Simple model to illustrate impacts of this. Model each component as a Boltzmann-Arrhenius function. Parametrise using new estimate of prokaryotic E. Alter proportions of autotraophs:heterotrophs and eukaryoitkes:prok within ecosystem. Work out how overall ecosystem respiration may increase.

How to paramaterise? What proportions of ecosystem is made up of these different components? Prokaryotes up to 50% of total biomass of planet? Distribution of biomass on earth – bacteria second largest component? Made distribution of different possible ecosystem compositions. Varied abundance of autotrophs (25-75%) varied comp of prokaryote heterotrophs (25-75%). Range of different possibilities.

What difference does including prokaryotic thermak sensitivity/eukaryote sensitivity, change how much respiration may come out of ecosystem with climate change warming scenario?

Differences in temperature preference. High tpk strains = all Firmicutes (one phylem). Shifts in com compositions based on changes in temp if particular phyla have propensitiy to grow at certain temp than others.

Differences in growth strategies. Firmicutes – high growth rate, low carrying capacity, r-specialists.

Proteobacteria – low growth rates, high carrying capacity, K-specialists. Continum between growth specialist and carrying capacity specialists. Either grow super fast and waste resources = low carrying capacity = low efficiency. Or grow slow but efficiently = high carrying capacity. Dif strategies associated with different lifestyles of microbes. High CC strains tend to be high carbon use efficiency, oligotrophic, found in spcially structures enviro (soil). GR specialists, low efficiency coperotrophic, high temp things at this end of the spectrum. Increase temp change ecosystem functioning at that scale? Push communities towards being more copeotrophic, less carbon efficient?

Some papers have seen these results, warming studies on ecological data, increase firmicutes, not clear how shifts in these community comps relate to functioning.

Future work: changes in community with temperature and link to functioning – mesocosms could provide both. Various warmed ponds being samples for microbial community composition. See if the community composition changes the same way with warming. Could look at the respiration to see if the community function is relatable to the changes in community diversity.

Coronaviruses

Michael Tristem – 20th February 2020

Corona = crown/halo/wreath

Morphology: + ssRNA genomes like polio. Have envelope like influenza viruses. Odd shaped core, with nucleoprotein surround RNA in a helical arrangement. Nuclear protein binds to RNA of virus. Not much complexity inside. Spike glycoprotein trimers on outside. E protein involved with assembly inside the cell. Very complicated genome for RNA virus. Each protein has multiple functions. Complex virology.

Viral RNA contains a cap and poly A tail=translated directly by host ribosomes upon cell entry. Main (spike), receptor binding (Env) protein is a pretty standard trimer in terms of structure.

Taxonomy and phylogenies. Coronavirus genomes are much bigger than other RNA viruses (although a LOT smaller than many dsDNA viruses). Coronaviruses are members of the viral order Nidovirales = ‘nest=nested subgenomic 3’ RNAs=animal viruses.

Look at the subfamily Coronavinae: alpha, beta, gamma and delta virus genera. We are mainly interested in the different beta CoVs (and a bit on the alpha CoVs) Mammalian and avian hosts, with a lot of bat hosts. Bats are very common reservoir hosts for human viruses (e.g. ebola, nipah). Rare for human coronavirus to be pathogenic in humans. Common colds caused by lots of different viruses. ¼ of colds caused by coronaviruses. Mortality rate for cold close to zero. Non-pathogenic coronaviruses, have same cellular receptor as SARs. Some of the non-pathogenic viruses have the same receptor and so similar tissue tropism. Often not direct from bats, often there is an intermediary host.

Human and related coronaviruses: Only a subset of the beta human corona are pathogenic, the other cause colds. SARS-Cov and MERS = other recent, pathogenic cornoa outbreaks. This excluded SARS-CoVs (the Wuhan coronavirus). Notes the host cellular receptor=maximum tissues tropism (unlikely to be met). SARS2 from bats via armadillos.

Origins: SARS-Cov2 is basically a variant of the original SARS. Both are closely related to viruses in bats although both likely have intermediate hosts (SARS-Cov = civet, SARS CoV2 = pangolin). MERS has a camel reservoir. Bats form backbone of transmissions into humans.

380 amino acid differences between SARS 1 and 2. Closely related! Also closely related to MERS.

Origins of pathogenic human corona. MERS and SARS1 originate in different bats via and intermediate host, may well be/have been cycling back into the intermediate host, may also be acquired directly from the original bat reservoir. Complex evolutionary histories.

Genomic organization. Corona longest genomes of any RNA viruses. Monopartite linear + ssRNA (27-32kb). Capped and tailed. Virion RNA is infectious. 5’ end = viral polymerase complex (PL Pro, RdRp and various non-structural proteins). S=Spike protein binds to cellular receptors. Proteins used in overcoming host defence, likely have multiple functions. Some gross difference between sars1 and 2. Still pretty closely related.

ACE2 (Angiotensin-converting Enzyme 2): cellular receptor for at least on non-pathogenic coronavirus as well as SARS and likely SARS2. The distribution in tissues thus determines the maximum tissues tropism for these viruses. Expressed in the lungs, kidneys, gastrointestinal tract and the heart. SARS in present in all these tissues. SARS2 spike protein is almost identical in sequence to SARS and so presumably has the same tissue tropism. Dissemination from the initial site of infection (lungs) could therefore cause multiple organ failure. 3-4 weeks to die – fairly long time.

Life cycle. Relatively standard BASIC life-cycle but lots of the non-structural genes are likely to have a major impact on the pathogenicity of the virus. This is SARS but likely similar in SARS2.

SARS mortality rate around 10%. Pathogenesis complex: sever injury to lungs and dissemination to other organs. Reproductive number 2-5. This compares with a recent estimate of SARS2 of 3.

SARS – flue like symptoms, fever, chills, then shortness of breath, presisten fever. 70% recovery at this stage. 20-30% then require intensive care including mechanical ventilation. 6.8% fatality rate for less than 60 years of age, 43% above this age. Major lung injury, major pulmonary injury, sever impact on other organs also. The symptoms, if not the % are very similar to SARS2. Airborne droplets can be inhaled or ingested.

SARS2 Wuhan wet market early December 2019. Animals traded. SARS2 origin. Some early cases not linked. Best guess is that one or a few people in the animal trade contracted the virus and then passed it on to workers in the market who passed it on to others. The workers ended up with unusual symptoms and that is when the first alarm was raised.

Li Wenliang told doctors that several cases of disease similar to SARS has been confirmed. They were linked to a seafood market in Wuhan.

SARS2 symptoms. Symptoms similar to lots of other diseases in the early stages – it must therefore be diagnosed with a genetic test or similar. There is no other way to confirm it. Need viral load of about 100. Need symptoms to spread it to other people. Asymptomatic people not very good at passing it on. First symptoms usually occur within eight days.

Infectious routes of SARS2. Infectious dose of the virus likely to be around several hundred. PFU number refers to the tissue culture infection, that is not the same as infecting a human. Infected by eyes, lungs and mouth. Travels <1m in oral droplets. Can get on hands and bedding.

How long do viral particles last. Survival of SARS2 viral particles. No data yet but data on SARS is good and the two viruses are physically so similar it is likely a good guide. 4 days stool, 4 days urine, 60 hours soil/water, 1 day hard surfaces, 48 hours plastic. Inactivated by hand disinfectants. Doesn’t survive well on paper, lasts a little longer on cotton. Transmission on hard surfaces most likely for transmission.

What happens if you loss control? Cruise ship infections, on going transmission, quarantine not stopping spread of virus. Ship workers spreading virus via food. Mild symptoms can spread it.