Seminary Diary

1) Deep-time evolution of biological responses to temperature changes

Dimitrios Georgios Kontopoulos - 10th October 2019

To better forecast the impacts of climate change we need to look at how biological traits respond to temperature. The measure of biological traits at different temperatures typically produces a unimodal thermal performance curve (TPC).

The Metabolic Theory of Ecology has been used mainly for large-scale comparisons of trait performance. There is limited within species or evolutionary application.

The literature details multiple TPC hypotheses. These range from strong thermal dynamic constraints (‘Hotter-is-better’) to weak thermal dynamic constraints (‘Perfect biochemical adaptation’). To test these hypotheses, a phylogenetic comparative approach was used, looking at the correlation structure of parameters and their phylogenetic signal.

Phytoplankton growth rates were used to obtain estimates of TPCs and showed a ‘Hotter-is-better-pattern’. Maximum growth rate increased weakly with thermal optimum, but general thermal responses were broad and showed weak thermodynamic constraints.

This project then tested two hypotheses regarding the evolution of thermosensitivity: that thermal sensitivity evolves around an optimum value or evolves in other ways. The phylogeny showed random bursts of trait evolution. There is no global optimum, instead species explore the parameter space through evolutionary time.

The effect of temperature on mutation was also explored. Simulations showed that mutations became more destabilising with temperature. Further simulations with multiple species at multiple temperatures indicated weak evidence that higher temperatures reduce mutation rate. We need to look at varying levels of organisation, from genome composition to how species interact. A multidisciplinary, multi-level approach is needed to develop a unified picture of thermal adaptation.

2) A manifesto for systematically describing consumer-resource interactions

Daniel Barrios-O’Neill, Leverhulme Trust, University of Exeter - 31st October 2019

Consumer-resource interactions are at the heart of ecology and worth quantifying. Capture rate contains information about the space in which the interaction occurs, whereas handling time relates to organismal biomechanics. Generally, larger, warmer animals have higher capture rates and shorter handling times.

Mutual interference suggests that as the density of predators in a patch increases, per capita consumption rate decreases. This may scale with body size, but more data is needed. It has also been shown that consumers moving through volume encounter each other more frequently than surface foragers, leading to a steeper scaling relationship of mutual interference.

When quantifying encounter rates, it is important to consider the impact of biomass, rather than units, and physical structure. Physical structure matters because we are changing it without understanding the consequences. Experimentally, it is necessary to work with artificial structures to precisely manipulate space.

In consumer-resource interactions, metabolic predictors are well established. However, the prevalence of model species skews the global data. To understand these interactions, modifiers of encounter rates are key and knowledge gaps must be addressed.

Experiments exploring consumer-resource interactions must consistently measure all appropriate variables, so that the data can be used by others. Opportunities to harvest that data are myriad, especially when combined with open access to data and tools. The large global ecological community must work together, and treat undescribed interactions with the same reverence as undescribed species.

3) 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

In recent decades there have been large shifts in biological events, including; flowering times, butterfly emergence and bird migrations. There is variation in the rate of these changes among species and events.

A major concern is phenological mismatch that may affect community function. Mismatch may have negative fitness consequences, as adaptive responses track seasonal optima, thus events have evolved to occur at optimal timings. Demographic consequences are comparatively understudied. A review of the literature indicated mixed demographic responses to climate change.

Plants and bees both exhibit an initial growth phase, followed by a switch to a reproduction stage. As production increases, optimal switching time moves closer to the end of the season.

Optimal switching time may be dependent on variation in seasonal production rate, as well as total growth capacity. Moreover, size dependent relative growth rates in plants and bees have shown that those species without exponential growth should reproduce earlier to increase productivity.

As season length increases, reproducing earlier would avoid competition, whilst switching later would lead to a larger population size. Different species may experience asymmetric shifts, thus resulting in changes to interspecific resource competition.

Demographic responses to climate change may show short term declines, but long-term population increases due to competitive release. However, phenological adaptation in one species may intensify competition. Adaptive responses may include evolutionary rescue to restore population sizes.

Overall, effects of climate change to community function will be varied and dependent on the unique features and adaptations of each system.

4) Managing fisheries to protect dependent predators

Simeon Hill - 16th January 2020

Ecosystem-based management recognises that the fish species we exploit are embedded in complex ecosystems. Its goals are to maintain ecosystem productivity, health, resilience and services. To action this, we need to define safe ecological limits. Strategic ambiguity is often used to reduce the level of detail in defining safe ecological limits. Strategic ambiguity may foster conflicting opinions on management strategies between stakeholders. The Convention on the Conservation of Antarctic Marine Living Resources (CCAMLR) defines safe ecological limits as preventing changes to the ecosystem that are not reversible within two to three decades.

Traditionally, fisheries management has used a single species management approach. The aims are to maintain the harvested population and achieve socioeconomic goals. Fisheries management uses the harvest control rule, defining a relationship between the biomass of the fished organism and the amount of being caught.

Single species management relies on feedback loops derived from control theory. These loops are comprised of a variable (size of the fished population), reference points including targets (states to aim for), limits (boundary of states to avoid) and soft limits (boundary of states to avoid most of the time), as well as adjustment and implementation methods. A feedback loop can also be extended to include predators of the fished organism.

Many fisheries fail to use reference points. This may be due to uncertain objectives for predators due to strategic ambiguity. Moreover, fisheries are not the only factor in changing fish/predator populations. Climate change and other anthropogenic drivers play important, yet equivocal roles.

Precautionary measures may be used to limit fishery impacts on predators, albeit an ambiguous level of protection. Suitable reference points can also assist in protecting populations, but organism life-stage and data lag-time must be considered.

5) How shrinking glacier are affecting Alaska’s coastal ecosystems

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

University of Alaska Southeast – 20th February 2018

90% of Alaskan coastal glaciers are shrinking in mass, contributing considerably to global sea level rise and impacting downstream ecosystems. Glaciers provide a number of ecosystem services, including food, fisheries, tourism and recreation, as well as regulating water quality, outburst floods and hazards.

Rivers act as conduits between glaciers, ice fields and marine ecosystems. As these landscapes change, it is important to understand how rivers receiving runoff from glaciers contrast to those fed by forests. Forested streams receive stochastic discharges, where glacier fed streams receive deterministic discharge, in line with seasonal temperature change. These glacierized streams have consistently low temperatures and are less effected by air temperature during summer. They also exhibit greater turbidity.

Food webs are also affected by glaciation as glaciers provide rock derived elements including soluble reactive phosphorous and iron.

Glaciers provide one of three stream types found in Southeast Alaska, along with clearwater and brownwater. The physical removal of glaciers allows for new streams to develop. Whilst most salmon return to their natal stream, some stray and populate new streams, exploiting the habitat mosaic of varying resource availability.

Glaciated areas releasing cold, turbid water, are hotspots for ice associated species. Traditional thinking suggests that these waters provide low productivity, however, tidewater glacier fjords supply nutrients, increasing productivity and providing fertile hunting grounds for plunge feeding seabirds. Tidewater glaciers also produce ice bergs used by harbour seals as safe haul-outs and areas for pupping.

Climate driven changes to ice fields have far reaching impacts. In order to predict and protect against these changes we need coordinated, interdisciplinary systems thinking.

6) Arctic Microbes: Living in a Frozen Ocean

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

10th March 2011

The Arctic ocean is a unique habitat. It is smaller than other oceans, covered in saline ice and surrounded by land. Saline ice acts as an important ecosystem for microorganisms, as it contains microscopic pores and liquid water. A cubic meter of saline ice has between 10,000 and 100,000,000,000 pores and a surface area of between 100,000 and 1,000,000 square meters.

Salt trapped within the ice prevents some water from freezing and it has been estimated that all the brine, trapped in all the sea ice of the world, contains more water than all of the world’s rivers. It is this liquid water that supports microscopic life within sea ice.

One of the major microorganisms to inhabit sea ice are algae. Single celled algae can form long chains, meters long. These organisms provide an important source of food and are believed to support at least half of Arctic ecosystems.

Bacteria also help to recycle nutrients and maintain healthy systems, thus supporting larger Arctic species. These bacteria are halophilic to tolerate salt levels up to seven times higher than surrounding sea water. They also produce a protective substance around the cell wall to prevent penetration and damage from the volatile ice environment.

The ice caps cover between 3 and 6% of the Earth’s surface. This ice serves as an interface between the ocean and the atmosphere. It is important to understand the processes occurring within and around Arctic ice, as all the oceans are connected and impact the integrated planetary system.

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

Dr Bonnie Bassler, Princeton University, 28th January 2013

Bacteria have existed on Earth for 4 billion years and can be both virulent and beneficial to other organisms. They carry out these processes is by talking to each other with a chemical language. They recognise when they are among others of their species, they can count themselves and carry out behaviours as a multicellular group.

Bacteria exist in two modes: social and a-social. A single cell detects if it is alone by producing small, hormone-like molecules called autoinducers. These are released into the environment and if they are not returned by sibling cells, a-social traits are expressed.

As the cell divides, it’s sibling cells begin to release their own autoinducers. Once a certain threshold is met these molecules can be detected by a receptor protein within the cell membrane and the population alters gene expression in unison. This is known as quorum sensing. Interspecific differences in autoinducer molecules infers intra-specific communication properties.

Bacteria are also capable of multilingual quorum sensing. A second enzyme produces a universal communication molecule allowing for interspecific communication. It is believed that whilst bacteria use hormonal sensing to detect whether they are alone or in a group, they may also measure the ratio between the ‘self’ and ‘other’ molecules to infer if they are in the minority or majority in a given environment.

Understanding of quorum sensing may lead to new approaches in antibiotics. In order to be successfully virulent, bacteria must act as a group. By modifying the shape of autoinducers we may be able to jam bacterial receptors, inhibiting group behaviour. Behaviour modification could also be used to increase the impact of autoinducers, leading to beneficial industrial applications.

Studying the quorum sensing process in bacteria can help us understand the evolution and robustness of multicellularity in higher organisms, as well as tackling some of humanities most pressing medical and industrial issues.

8) Astrobiology and Space Exploration Introduction

Seth Shostak, Senior Astronomer at the SETI Institute, 27th August 2009

Throughout history, humans have held varying beliefs about the Solar System and what lies beyond. Central to refining these ideas has been the ability to measure the distances of celestial bodies, allowing us to look back into the past and speculate on the future.

In 1823 Heinrich Olber described Olber’s paradox, whereby the darkness of the night’s sky was in conflict with an infinite and fixed universe. The stars should constantly illuminate the point of view of the observer. The paradox allowed astronomers to hypothesise that all matter in the universe must be moving away, causing the light of distant stars to appear redder and dimmer.

In the early 20th century, astronomer Henrietta Leavitt discovered that the brightness of a nebula could be calculated by measuring the length of its luminosity cycle. Edwin Hubble further developed the work of Leavitt and used stars with known distances and luminosities, known as Cephid Variables, to estimate the distance of extra-galactic nebula and assert that they were other galaxies moving away from us.

By working the expanding universe backwards, astronomers were able to suggest that there was a time when all matter was tightly condensed. This theory became mockingly known as the Big Bang. Despite the success of this theory, there remain many questions: what existed before the Big Bang? What did the universe expand into? The answers to these questions we may never know.

There are several theories concerning the future of the universe. By looking at supernovas, astronomers have calculated that the expansion of the universe is speeding up due to dark energy. It may be that dark energy continues to expand space until all matter is pulled apart. There may come a time when the universe begins to re-condense. Ultimately, after a finite period of habitability, it seems the universe will become an infinity of nothingness.

9) Astrobiology and the Very Small

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

Astrobiology seeks to understand the origins of life on Earth and its existence elsewhere. Defining life can be challenging as many non-living things share living properties. NASA scientist Gerald Joyce defines life as, “a self-sustaining chemical system capable of undergoing Darwinian evolution”.

Habitability is an important concept in astrobiology, informing policy and mission planning. The NASA Astrobiology Roadmap defines habitability as an environment with, ‘extended regions of liquid water, conditions favourable for the assembly of complex organic molecules, and energy sources to sustain metabolism’. Water is key to habitability due to the low density of ice insulating aquatic ecosystems that would otherwise freeze. It is also abundant and an excellent solvent.

Other planets in our Solar System present extreme habitats. Study of terrestrial extremophiles can help us understand the lifeforms that may exist elsewhere. Microorganisms, such as *Methanopyrus kandleri*, found living around oceanic black smokers, can survive in temperatures up to 121 °C. Microorganisms also thrive in extreme cold environments. Lake Vostok, Antarctica, is buried under ice, with temperatures reaching minus 13°C and contains upwards of 4000 species. *Deinococcus radiodurans* thrives in highly radiated environments, surviving exposure to 1.5 million rads.

Astrobiology research has focused on Mars and Jupiter’s moon, Europa, as potential habitats for life. Images of the Martian Gale Crater suggest the area was once a freshwater lake, providing conditions favourable to life. The Martian Meteorite Yamato found in Antarctica, indicated there had once been liquid water on Mars and it may have been exposed to biological processes. Europa’s subsurface ocean is warmed by tidal heating and may host aquatic life.

Astrobiology provides a cosmic context in which to understand the origins of life on this planet, its future, and the possibility of life on other worlds.

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

Tom Smith – 23rd January 2020

Microbes play an essential role in biogeochemical cycling. In order to construct accurate climate models, we need to understand the impacts of temperature change on microbial metabolic rates.

A variety of microbial thermal performance curves (TPCs) can be found in the literature. By fitting the Schoolfield-Sharpe model, the parameter E (thermal sensitivity) can be recovered.

Analysis of a large range of macroorganism TPCs reveals a global average E of 0.65. Research reveals that species follow similar patterns of inter- and intra- specific E. Do microorganisms conform to the same rules? Digitisation software was used to extract 542 microbial TPC datasets from the literature. E for bacteria and archaea was found to be greater than the macroorganisms global average. Environmental data supports these findings, as habitats with higher proportions of microbes have higher E overall.

How do these short-term responses link with long-term responses, such as climate change? Generally bacterial species show increased metabolic rate with temperature. We may then expect climate change to increase microbial metabolic rates.

Some species may experience a decline in metabolic rate, unless they can adapt to higher temperatures. Lab settings have shown rapid adaptation to temperature change, but can this be replicated in natural environments? Genetic and phenotypic variation within microbial communities may facilitate species sorting, as an alternative to adaptation. Evidence supports species sorting over adaptation, with changes in optimum temperature phylogenetically dependent. Climate change will likely cause a shift in microbial community thermal optima through either or both of these processes. Understanding the extent to which climate change may increase ecosystem respiration depends on the relative abundances of autotrophs to heterotrophs, and eukaryotes to prokaryotes. Global estimations of these proportions vary greatly.

Future work could benefit from empirical data collection through mesocosm manipulation.

11) Coronaviruses

Dr Michael Tristem – 20th February 2020

The coronavirus group is named after the Greek word for crown, halo or wreath, in reference to their distinct morphology. They possess +ssRNA genomes, similar to polio, and envelopes similar to influenza. Nucleoprotein forms a helical shape around RNA in the viral core. The group exhibit unusually complex genomes, larger than other RNA viruses, but smaller genomes than dsDNA groups.

Within the Coronavinae subfamily, the beta virus genera are of the most clinical importance to humans. It typically infects mammalian and avian hosts, specifically bats which act as an important viral reservoir for humans.

Beta human coronaviruses are common, accounting for a quarter of common colds, and are rarely pathogenic. SARS-CoV (Severe Acute Respiratory Syndrome Coronavirus) and MERS-CoV (Middle East Respiratory Syndrome Coronavirus) represent recent pathogenic beta human coronavirus outbreaks. SARS-CoV 2 and SARS-CoV are so closely related to have only 380 amino acid differences. It is believed the initial SARS-CoV outbreak was transmitted from bats via civets as intermediaries, and the most recent SARS-CoV 2 transmitted via pangolin intermediaries.

ACE2 (Angiotensin-converting Enzyme 2) is the cellular receptor utilised by SARS-CoV, and likely SARS-CoV2. The distribution of ACE2 in the host body determines the maximum tissue tropism that infection can cause. ACE2 is generally found in the lungs, kidneys, heart and gastrointestinal tract of humans, thus infection can lead to multiple organ failure.

Initial SARS-CoV2 cases were reported from Wuhan wet market in December 2019. It is believed close human contact with infected animals lead to the transmission of the virus to humans.

Initial stages of the virus are similar to many other conditions and must be confirmed with genetic testing. Many are asymptomatic and at low risk of transmitting adequate viral load to infect others.

Viral particles travel in oral droplets that can be absorbed through the eyes, inhaled or ingested. Survival of viral particles on materials varies, but transmission is most likely from hard surfaces.