



# **Netherlands Annual Ecology Meeting (NAEM)**

**8 & 9 February 2011**

**Congrescentrum De Werelt, Lunteren**

## **Handout**

# Programme

## Tuesday 8 February

TIME	Main Entrance Hall			
08:30	Registration and coffee in the Lounge and setting up posters			
	Europe Hall			
10:15	<b>Word of Welcome</b> (Louise Vet, Chair NERN, Director Netherlands Institute for Ecology)			
	Plenary 1: " Species interactions under environmental change "			
10:30	1. Environmental change and the ecological and evolutionary dynamics of predator-prey interactions (Anthony Ives, University of Wisconsin)			
11:15	2. The effect of trait plasticity on community dynamics (Jacintha Ellers, Vrije Universiteit)			
12:00	Lunch in the restaurant			
Location	America Hall	Europe Hall	Asia Hall	Africa Hall
13:30	<b>Parallel 1a: Innovative understanding of biodiversity and ecosystem functioning</b>	<b>Parallel 1b: Element cycles in aquatic systems under global change</b>	<b>Parallel 1c: Interface between ecology and paleo-ecology</b>	<b>Parallel 1d: Ecology regarding genetically modified organisms</b>
	<i>Conveners:</i> 1. Joana Salles (University of Groningen) 2. Britas Klemens Eriksson (University of Groningen)	<i>Conveners:</i> 1. Sarian Kosten (Wageningen University) 2. Dick van Oevelen (Netherlands Institute of Ecology)	<i>Conveners:</i> 1. Henry Hooghiemstra (University of Amsterdam) 2. Gert-Jan Reichart (Utrecht University)	<i>Conveners:</i> 1. Patrick Kabouw (Netherlands Institute of Ecology) 2. Emilia Hannula (Netherlands Institute of Ecology) 3. Martine Kos (Wageningen University)
13:30	Integrating complexity into BEF research (Helmut Hillebrand, University Oldenburg, Oldenburg-Wilhemshaven, Germany)	Influence of warming and macrophyte presence on lake denitrification across climatic regions (Annelies Veraart, Wageningen University)	Climate forcing due to optimization of maximal leaf conductance in subtropical vegetation under rising CO2 (Hugo de Boer, Utrecht University)	Quantitative aspects of field studies of risk assessment of GM plants (Joe Perry, Rothamsted Research, United Kingdom)
13:50	Plant diversity and composition as driver of ecosystem multi-functionality in grassland ecosystems (Gerlinde De Deyn, Netherlands Institute of Ecology)	Setting critical values for nutrient loading in ditches with an ecological model (Jeroen de Klein, Wageningen University)	How will peat bogs respond to climate change? Results of combined palaeo-ecological, experimental and model research (Monique Heijmans, Wageningen University)	The baseline across soils: transformation of plant-borne organic matter (Agnieszka Szturc-Koetsier, Utrecht University)
14:10	Unexpected consequences of diversity loss (Andrea Downing, Wageningen University)	Aquatic herbivores as a regulating factor of methane emission in the land-water transition zone of shallow lakes. (Paul Bodelier, Netherlands Institute of Ecology)	Non-pollen palynomorphs: towards more complete ecological information in Quaternary studies (Bas van Geel, University of Amsterdam)	Quantifying stochastic introgression risks with hazard rates (Atiyo Ghosh, Leiden University)
14:30	break			

## Parallel Session 1 Continued

	<b>Parallel Session 1 Continued</b>			
<b>14:40</b>	Consequences of species loss for the ability of communities to recover from a simulated heat wave (Karin de Boer, University of Groningen)	Hypoxia in a changing world (Lorenz Meire, Netherlands Institute of Ecology)	Identification and distribution of intact polar branched glycerol dialkyl glycerol tetraether lipids in a Swedish peat bog (Francien Peterse, Royal Netherlands Institute for Sea Research)	How non-native plants affect natural ecosystems (Thomas van Hengstum, University of Amsterdam)
<b>15:00</b>	Recovery from eutrophication in times of global change: interactive drivers of phylogenetic and functional plankton diversity (Francesco Pomati, Netherlands Institute of Ecology)	C:N:P ratios of individual bacteria: an explanation for enhanced regeneration of P relative to carbon from marine sediments? (Anne Steenbergh, Netherlands Institute of Ecology)	Differences in cyclopentane distribution amongst intact polar tetraether lipids: implications for the tex86 paleothermometer (Sabine Lengger, Royal Netherlands Institute for Sea Research)	Introgression of crop (trans-)genes into wild relatives: Environment specific effects in <i>Lactuca</i> . (Yorike Hartman, University of Amsterdam)
<b>15:20</b>	MECOMECON: MEthanotrophic diversity and gene expression as a CONtrolling factor of global MEthane CONsumption (Sascha Krause, Netherlands Institute of Ecology)	Stoichiometric effects of food on growth and movement decisions in zooplankton: implications for competitive ability (Tibor Bukovinszky, Netherlands Institute of Ecology)	Evidences for silicic acid leakage to South East Australia during interglacials and MIS 3 (Raquel Lopes dos Santos, Royal Netherlands Institute for Sea Research)	Comparison of the whole-genome response to perturbations and its ecological applications. (Benyamin Houshyani, Wageningen University)
<b>15:40</b>	<b>Time to stretch the legs and have a cup of tea in the Lounge</b>			
<b>Location</b>	<b>America Hall</b>	<b>Europe Hall</b>	<b>Asia Hall</b>	<b>Africa Hall</b>
<b>16:00</b>	<b>Parallel 2a: Ecosystem change and predictability in a changing world</b>	<b>Parallel 2b: Spatial Ecology</b>	<b>Parallel 2c: Genomics of Conservation Ecology</b>	<b>Parallel 2d: A new era in Microbial Ecology</b>
	<i>Conveners:</i> 1. Elisa Benincà (University of Amsterdam) 2. Vasilis Dakos (Wageningen University)	<i>Conveners:</i> 1. Ellen Weermaan (University of Groningen) 2. Maarten Eppinga (Utrecht University)	<i>Conveners:</i> 1. Cees Musters (Leiden University) 2. Krijn Trimbos (Leiden University) 3. Klaas Vrieling (Leiden University)	<i>Conveners:</i> 1. Laura Villanueva (Royal Netherlands Institute for Sea Research) 2. Suzanne Haaijer (Radboud University)
<b>16:00</b>	Ecosystem change and predictability in a changing world: what do plankton dynamics tell us? (Elisa Benincà and Vasilis Dakos, University of Amsterdam / Wageningen University)	Interspecific facilitation and critical transitions in ecosystems (Christian Smit, University of Groningen)	Conservation genomics: the science of plentiful scarcity (Joop Ouborg, Radboud University)	Can the Microbial Ecology Blackbox be cracked open? (Laura Villanueva, Royal Netherlands Institute for Sea Research)
<b>16:20</b>	Slow recovery from local disturbances: an early-warning signal for regime shifts? (Ingrid van de Leemput, Wageningen University)	Alternate mechanisms for spatial self-organization in mussel beds (Quan-Xing Liu, University of Groningen / Netherlands Institute of Ecology)	Genomic characterization of inbreeding depression in thermal resistance (Corneel Vermeulen, University of Groningen)	IS-pro: fully automated analysis of the human intestinal microbiota (Dries Budding, VU University Medical Center)
<b>16:40</b>	Nuisance foam events and <i>Phaeocystis globosa</i> blooms in Dutch coastal waters analyzed with fuzzy logic (Anouk Blauw, University of Amsterdam)	Scale-dependent effects of an ecosystem engineer determine the spatial distribution of bivalves in an intertidal ecosystem (Serena Donadi, University of Groningen)	The use of genetics for lion conservation (Laura Bertola, Leiden University)	Influence of soil structure and matric potential on microbial interactions (A. Wolf, Netherlands Institute of Ecology)
<b>17:00</b>	Break			

## Parallel Session 2 Continued

<b>17:10</b>	The (in)stability of salt marshes in a changing environment; the effects of enhanced sea-level rise (Elske Koppenaar, University of Groningen)	Spatial processes, temporal variability and ecosystem functioning in salt-marshes (Jim van Belzen, Netherlands Institute of Ecology)	Assessing effective size, dispersal and origin of amphibian populations (Pim Arntzen, Netherlands Centre for Biodiversity)	Dinitrogen gas production by marine anammox bacteria (Wouter Maalcke, Radboud University)
<b>17:30</b>	Phenology drives mutualistic network structure and diversity (Francisco Encinas-Viso, University of Groningen)	Priority effects in community assembly and repercussions for conservation (Joachim Mergeay, Research Institute for Nature Conservation (INBO) / Katholieke Universiteit Leuven)	Genetic structure of the Dutch and global Black-tailed Godwit breeding population (Krijn Trimbos, Leiden University)	Interactions amongst marine archaeal and bacterial nitrifiers and anammox bacteria under oxygen limitation in a lab-scaled model system (Jia Yan, Radboud University)
<b>17:50</b>	Synergistic effects of nutrient loading and temperature warming on an experimental phytoplankton community: implications for stoichiometry (Lisette Senerpont Domis, Netherlands Institute of Ecology)	Landscape asymmetry and agro-ecosystems and resilience (Dirk van Apeldoorn, Wageningen University)	Poplar community genetics: identifying genomic regions associated with insect and rust damage in a segregating Populus family (René Smulders, Wageningen UR)	Anaerobic methane oxidation coupled to denitrification – a new link in carbon and nitrogen cycles (Katharina Ettwig, Radboud University)
<b>18:10</b>	Drinks in the Lounge and from <b>18:30</b> onwards dinner in the restaurant			
<b>19:30</b>	Poster sessions / Coffee			
<b>Europe Hall</b>				
<b>21:00</b>	<b><u>Evening Programme:</u></b> <i>Evolution Bites: evolution and ecology of venomous snakes (Freek Vonk, Sylvius Lab, IBL, Leiden University)</i>			

## Wednesday 9 February

<b>07:30</b>	Breakfast in the restaurant			
<b>08:00</b>	Registration for those coming on Day 2 only			
	<b>America Hall</b>	<b>Europe Hall</b>	<b>Asia Hall</b>	<b>Africa Hall</b>
<b>8:30</b>	<b>Parallel 3a: Plant ecophysiology - Surviving in a heterogeneous world</b>	<b>Parallel 3b: Movement ecology of plants and animals: similarities and differences</b>	<b>Parallel 3c: From water to land; ecology across borders</b>	<b>Parallel 3d: Free Session</b>
	<i>Conveners:</i> 1. Eric Visser (Radboud University) 2. Liesje Mommer (Wageningen University)	<i>Conveners:</i> 1. Merel Soons (Utrecht University) 2. Silke Bauer (Netherlands Institute of Ecology)	<i>Conveners:</i> 1. Judith Sameel (Netherlands Institute of Ecology) 2. Liesbeth Bakker (Netherlands Institute of Ecology)	<i>Conveners:</i> 1. Wolf Mooij (Netherlands Institute of Ecology)
<b>8:30</b>	Within-species changes in traits between the native and introduced range of alien plants: a global scale comparison (Alejandro Ordonez, University of Groningen)	Movement ecology of plants and animals: Similarities and differences (Silke Bauer, Netherlands Institute of Ecology)	Plant growing from water to land: disentangling the factors that impede terrestrialization in fens. (Judith Sarneel, Netherlands Institute of Ecology)	Importance of olfactory cues from host larvae and cowpea flowers in the host foraging by <i>Apanteles taragamae</i> Viereck, a larval parasitoid of the cowpea pod borer <i>Maruca vitrata</i> Fabricius (Elie Dannon, Wageningen University)
<b>8:50</b>	Overwhelming root overproduction of <i>Plantago lanceolata</i> leads to unproportional above and belowground responses to competition (Francisco Padilla, Radboud University)	Lévy walks evolve through feedback between movement strategies and environmental complexity (Monique de Jager, Netherlands Institute of Ecology)	Major shifts in trophic structure along a salt marsh succession: a stable isotope approach (Maarten Schrama, University of Groningen)	Restricted recruitment of forest herb layer plants in post-agricultural forests: can tree species help? (Arno Thomaes, Research Institute for Nature and Forest (INBO), Belgium)
<b>9:10</b>	Species-specific soil biota cause overyielding in diverse plant communities (Marloes Hendriks, Radboud University)	Resource aggregation and density have direct and interactive effects on search performance of Lévy, correlated random and nested random walks (Tom Huisman, Wageningen University)	Impact of waterlevel and management on the establishment of plant species in a peatland (Wout Opdekamp, University of Antwerp)	Tree species identity drives responses of dipteran communities to tree and herb diversity (Elke Vockenhuber, University of Göttingen)
<b>9:30</b>	Break			
<b>9:40</b>	The ecological relevance of auxin regulated shade avoidance response to neighbour proximity signals (Diederik Keuskamp, Utrecht University)	Modelling dispersal of wetland plant seeds by wind and water (Hester Soomers, Utrecht University)	Interacting effects of sulphate pollution in the surface water and eutrophication of the bank on vegetation development in fens: a mesocosm experiment (Jeroen Geurts, Radboud University)	Turning northern peatlands upside down: disentangling microclimate and substrate quality effects on vertical distribution of collembola. (Eva Krab, Vrije Universiteit)
<b>10:00</b>	Regulation of branching in plants competing for light (Jochem Evers, Wageningen University)	Spring migration timing of arctic-breeding geese (Andrea Kölzsch, Netherlands Institute of Ecology)	Biodiversity in small farmland ponds: multigroup congruency and associations with land use practices at multiple spatial scales. (Steven Declerck, Netherlands Institute of Ecology)	Direct and indirect impacts of hemiparasitic plants on community structure and biogeochemical cycling in semi-natural grasslands (Andreas Demey, Ghent University)
<b>10:20</b>	Competition for light compromises pathogen defense (Mieke de Wit, Utrecht University)	Using species' life-history traits to design restoration measures for fragmented habitats (Toos van Noordwijk, Radboud Universiteit)	Vertebrate herbivores: drivers of alternative stable or transient states? Comparing lakes and boreal forests (Bert Hidding, Université Laval)	Genotype x temperature interactions support the maintenance of clonal diversity in diatom blooms (Alena Gsell, Netherlands Institute of Ecology)
<b>10:40</b>	Coffee in the lounge			

Europe Hall				
Plenary 2: "Ecological effects of disease"				
11:00	1. <b>Coinfection, host susceptibility and survival in natural populations</b> (Mike Begon, University of Liverpool)			
11.45	2. <b>Emergence of infectious agents in foodwebs and ecosystems</b> (Hans Heesterbeek, Utrecht University)			
12:30	Lunch in the restaurant			
13:30	Poster Session Day 2 / Coffee			
	America Hall	Europe Hall	Asia Hall	Africa Hall
15:00	<b>Parallel 4a: Multitrophic interactions and Food webs</b>	<b>Parallel 4b: Species Distribution Modelling</b>	<b>Parallel 4c: Eco-toxicology and Chemical Stress Ecology</b>	<b>Parallel 4d: Free Session</b>
	<i>Conveners:</i> 1. Peter de Ruiter (Wageningen University) 2. Sanne de Visser (University of Groningen)	<i>Conveners:</i> 1. Thomas Groen (ITC) 2. Sabrina Carvalho (ITC/Netherlands Institute of Ecology) 3. Henjo de Knegt (Wageningen University)	<i>Conveners:</i> 1. Mazhar Iqbal Zafar (Wageningen University) 2. Nika Galic (Wageningen University) 3. Jacqueline Augusiak (Wageningen University)	<i>Conveners:</i> 1. Nicole van Dam (Radboud University)
15:00	Robustness analyses of the Serengeti food web: theoretical versus realistic extinction scenarios (Sanne de Visser, University of Groningen)	Species distribution modelling: objectives, challenges and terminology (Thomas Groen, University of Twente)	Linking ECO and ECOTOX; signposting research development (Wim Admiraal, University of Amsterdam)	C4 photosynthetic subtypes phylogeny or functional ecology? a review and evaluation from isotopic evidence (Elmar Veenendaal, Wageningen University)
15:20	Food-safety trade-off on intertidal flats (Ellen Weerman, University of Groningen)	From herbarium collections to patterns of biodiversity, endemicity and phytogeography - A Bornean case study (Niels Raes, NCB Naturalis, Leiden University)	Ecological impacts of time-variable exposure regimes of the fungicide Azoxystrobin on the zooplankton community of outdoor microcosms. (Mazhar Iqbal Zafar, Wageningen University)	The use and misuse of multivariate statistics based on ordination diagrams in ecology (Patrick Kabouw, Netherlands Institute of Ecology)
15:40	The evolution and coexistence of generalist and specialist herbivores under between-plant competition. (Ellen van Velzen, University of Groningen)	Modelling habitat preference, species richness and abundance of alien macrocrustaceans in surface waters in Flanders (Belgium) (Pieter Boets, Ghent University)	Exposure to perfluorooctane sulfonic acid (PFOS) adversely affects the life-history of damselflies (Luc De Bruyn, INBO, Belgium / University of Antwerp)	Idiosyncrasy in ecology (Gera Hol, Netherlands Institute of Ecology)
16:00	Break			
16:10	Population dynamics of a phytoflagellate eating its toxic competitor (Susanne Wilken, Netherlands Institute of Ecology / University of Amsterdam)	Enhancing coarse-resolution species atlas data using an expert system (Aidin Niamir, University of Twente)	Multi-generation exposure of the non-biting midge <i>Chironomus riparius</i> to three model toxicants (Marino Marinkovic, University of Amsterdam)	Resource limitation and interspecific competition constrain reproduction in an endangered finch (Erica van Rooij, Macquarie University, Australia)
16:30	The temporal dynamics of interaction networks: the role of resource switching, adaptive morphological traits and diversification (Jofre Carnicer, University of Groningen)	Discovering traits that explain species-environment relationships: a Generalized linear mixed model approach (Tahira Jamil, Wageningen University)	Toxicity and accumulation of the cyanobacterial neurotoxin $\beta$ -N-methylamino-L-alanine (BMAA) in <i>Daphnia magna</i> . (Els Faassen, Wageningen University)	The impact of climate change on oystercatchers (Bruno Ens, SOVON/ Netherlands Institute of Ecology)
16:50	Lovely ladybirds under attack: does the exotic species win? (Lidwien Raak-van den Berg, Wageningen University)	Using the assembly theory to make more robust predictions of vegetation distribution in a changing climate (Bob Douma, Vrije Universiteit)	Oxidative Stress: Lessons Learned From A Nanotoxicology Perspective (Sourav Bhattacharjee, Wageningen University)	Are earthworms good or bad for the soil greenhouse gas balance? A review (Ingrid Lubbers, Wageningen University)

	<b>Europe Hall</b>
<b>17:20</b>	Closing Session (Hans de Kroon) <ul style="list-style-type: none"><li>• Awards ceremony<ul style="list-style-type: none"><li>◦ Best PhD research paper Award (Member of the Evaluation Committee)</li><li>◦ Best Poster Award (Roland Bobbink)</li></ul></li><li>• Synthesis (Louise Vet)</li></ul>
	<b>Lounge</b>
<b>18:00</b>	Fare-well drinks and Dinner
<b>19:30</b>	Travel Home (Shuttle available between Conference Centre and Station)

# **Session 1**

## **1a: Innovative understanding of biodiversity and ecosystem functioning**

**Conveners:** Joana Salles (University of Groningen)  
Britas Klemens Eriksson (University of Groningen)

### **1. Integrating complexity into BEF research**

Helmut Hillebrand and Carl-von-Ossietzky  
University Oldenburg, Oldenburg-Wilhemshaven, Germany

### **2. Plant diversity and composition as driver of ecosystem multi-functionality in grassland ecosystems**

Gerlinde De Deyn, Nick Ostle and Richard Bardgett  
Netherlands Institute of Ecology

In this study we show how plant species richness, composition and soil fertility impact on carbon (C) and nitrogen (N) pools in vegetation, soil microbes and bulk soil and on C and N losses from soil through leaching and respiration. We hypothesised that species richness would promote C and N pools in vegetation and would reduce C and N losses from soil. We tested this in grassland communities grown in low or high fertility soil and composed of 1, 2, 3 and 6 species of 1, 2 or 3 functional groups using a pool of 6 species and 3 functional groups (legumes, forbs and C3 grasses). The amount of C and N stored in vegetation (aboveground and belowground) and soil microbes increased with larger plant species and functional group richness and with soil fertility. Greater plant species richness also reduced the loss of water and dissolved N via soil leaching, but also the abundance of specific species significantly affected N loss: increasing or decreasing it depending on species identity. The amount of C and N stored in soil at the end of the experiment differed between plant communities and was not related to the richness of plant species or functional groups but specifically due to the presence (*T. repens*) or abundance (*L. corniculatus*) of legume species. Our findings that different key plant species promote C and N storage in vegetation and soil, and the suppression of soil leaching indicate that the maintenance of plant diversity is important to sustain the multiple functions grasslands provide. Plant diversity and composition as driver of ecosystem multi-functionality in grassland ecosystems

### **3. Unexpected consequences of diversity loss**

Andrea S. Downing, Egbert H. van Nes, Wolf M. Mooij and Marten Scheffer  
Wageningen University

Research has widely revealed that diversity loss is detrimental, mainly because simple systems tend to be more prone to invasions as well as less constant and reliable in terms of general properties – such as total biomass, overall structure and functioning – than diverse systems. While global diversity is rapidly declining, it is still unsure what the effect on ecosystems will be and whether the system may undergo critical transitions in response to this loss of species. We here show in a simple model that diversity decline may in some cases lead to a collapse of an ecosystem. We use Lake Victoria as an example where all species of a community exert a negative control back on the introduced predator: Nile perch. When diversity is high, the predator cannot invade. However, as species are lost, the system slowly loses resilience until it reaches a threshold beyond which remaining diversity suddenly collapses and the invader dominates. Our model yields alternative stable states and thus hysteresis, indicating that the system will not recover with a simple species reintroduction. Our theoretical findings can be related to collapses seen in real systems. We conclude that diversity loss may uncover strong processes previously masked by the higher resilience of diverse states and thus shape the dynamics of the resulting simple system. Species losses from diverse mature communities may often be both very sudden and irreversible, especially when these communities exert a feedback on their environment.

### **4. Consequences of species loss for the ability of communities to recover from a simulated heat wave**

Karin M. de Boer, Helen Moor, Birte Matthiessen and Britas Klemens Eriksson  
University of Groningen

We studied the importance of community structure on the recovery of biomass production after a heat wave in spatially heterogeneous meta-communities of marine benthic diatoms of the Baltic Sea. We specifically tested how subdominant species may contribute to resilience after the heat treatment. The experimental meta-community consisted of 10 naturally occurring species. We manipulated community structure by creating four different communities: 1) all 10 species, 2) the dominant producer removed, 3) the most heat-resistant species removed and 4) both the dominant producer and the most heat-resistant species removed.



When the dominant producer was removed two other species increased to dominate the community. These communities showed better recovery after the heat wave than the communities with the dominant producer present, but the total biomass production was lower.

Our results show that the communities without a dominant producer were more resilient to a simulated heat wave by maintaining community functioning while undergoing change. This ability to resist changes and regenerate significant functions could be addressed to a shift in dominant species that was more heat tolerant, but less productive.

## **5. Recovery from eutrophication in times of global change: interactive drivers of phylogenetic and functional plankton diversity**

Francesco Pomati, Blake Matthews, Jukka Jokela, Andrea Schildknecht and [Bas W. Ibelings](#)  
Netherlands Institute of Ecology

Long-term studies on rates and direction of changes in biodiversity help us understand and predict the impact of interactive anthropogenic stressors on ecosystems. Here we report the combined effects of re-oligotrophication and climate warming on taxonomic and functional accrual of plankton diversity in a peri-alpine lake, spanning a period of more than three decades. The ecosystem became increasingly characterized by enhanced temporal stability of lake descriptors like temperature, pH or conductivity, combined with stronger temporal fluctuations in the availability of plankton resources, nutrients and light. Climate warming resulted in enhanced water-column stability of the lake, so that resource gradients steepened, and spatial heterogeneity increased. The increased stability of the physical lake structure allowed for a re-distribution of phytoplankton in more defined vertical layers, contributing to the potential for co-existence and community-diversity. Strong biodiversity accrual was observed at two trophic levels simultaneously. Slopes of the species-time relationships were comparable for phyto- and zooplankton richness and similar at all different lake depths. Recovery of functional diversity, however, lagged behind, indicating that restoration of ecosystem functioning required more time than recovery of species richness. The biodiversity accrual was matched by an increasing tendency for related species or functional groups to co-occur, signaling an increasing role of habitat filtering. Much of the change we observed over time was non-linear, and statistically significant regime-shifts in environmental conditions and plankton diversity were detected. These regime shifts were synchronized in time, in response to changes in the regional climate. Our study provides new and relevant insights in how interactive effects of decreased nutrient loading and climate warming changed variations in lake conditions and plankton resources, allowing for restoration of phylogenetic and functional plankton diversity in times of global change.

## **6. MECOMECON: Methanotrophic diversity and gene expression as a Controlling factor of global Methane Consumption**

[Sascha Krause](#), Marion Meima-Franke and Paul Bodelier  
Netherlands Institute of Ecology

Microorganisms form a major part of the Earth's biomass and biodiversity and have a crucial role in biogeochemistry and ecosystem functioning. However, in on-going debates about biodiversity loss, global change and conservations issues they have hardly been considered. It has always been assumed that microbial communities are being highly redundant and omnipresent and therefore inextinguishable, but microbial communities can display habitat preference, are not universally distributed and can be sensitive to environmental disturbance. In the European collaborative Project MECOMECON the general hypothesis is addressed that microbial diversity and gene expression is linked to important ecosystem services and therefore cannot be ignored in nature conservation and management issues. Aerobic methane consumption by methane oxidizing bacteria (MOB) is used as a model system thereby reducing the complexity, linking function to identity and catalyzing an important ecosystem service. Our group focuses on methanotrophic diversity and activity in abandoned peat meadows in particular the effect of rewetting. In the Netherlands formerly agricultural land will be converted into natural wetlands by raising the water table and reducing the agriculture. This process will lead to more emission of CH<sub>4</sub> which is strongly dependent on oxidation by MOB which in turn may be affected by processes associated with the changing biogeochemistry. The work is carried out in two areas, each containing a restored site where the water table has already been raised and a reference site. The areas differ in agricultural management, their restoration history and soil type. CH<sub>4</sub> oxidation kinetics and clone libraries have already been analyzed to characterize the initial methanotrophic diversity and activity. An additional 454 *pmoA*-tag pyrosequencing is in preparation. From here MOB are being isolated and characterized in terms of phylogeny, methane oxidation kinetics and response to disturbances. In a second step with the isolates, random mixtures will be established to manipulate compositional as well as functional diversity of these artificial communities. By manipulating in a controlled way the diversity we want to assess the link between diversity and methane consumption and whether diversity plays a role in resilience of methanotrophic communities to disturbance. The obtained data will be used to test and calibrate a modeling framework that explicitly incorporates microbes into process models. This model will be used to facilitate the prediction of the effects of rewetting of peat meadows on methane consumption in these ecosystems using methanotrophic traits as input.

## **1b: Element cycles in aquatic systems under global change**

**Conveners:** Sarian Kosten (Wageningen University)  
Dick van Oevelen (Netherlands Institute of Ecology)

### **1. Influence of warming and macrophyte presence on lake denitrification across climatic regions**

Annelies J. Veraart, Sarian Kosten, Gissell Lacerot and Jeroen J.M. de Klein  
Wageningen University

In temperate lakes and streams, denitrification rates may greatly increase with rising temperature. However, in subtropical lakes, where temperatures are higher throughout the year, these rates are probably limited by available resources rather than temperature. As macrophyte presence may change with global warming, and macrophytes influence denitrification rates, we studied the combined effects of warming and macrophyte presence. We used a warmed chamber method to test the response of denitrification to warming in six temperate and four subtropical lakes. Denitrification rates were measured in situ in denitrification chambers using the <sup>15</sup>N isotope pairing technique. The water temperature in half of the denitrification chambers was increased to three degrees above ambient. Denitrification rates were mainly determined by nutrient concentrations in the lake water. In the temperate lakes, denitrification rates were higher in the warmed than in the ambient chambers. In most of these lakes, the effect of warming was strongest when macrophytes were present. In the subtropical lakes, warming had no effect on denitrification rates, but denitrification rates were highest when macrophytes were present. As denitrification rates in the temperate and subtropical lakes responded differently to warming, our results show that the outcome of local climate change experiments cannot be extrapolated to other climatic regions.

### **2. Setting critical values for nutrient loading in ditches with an ecological model**

Jeroen de Klein, Jan Janse and Annelies Veraart  
Wageningen University

The Water Framework Directive demands good ecological status of all surface waters. For ditches and (small) lowland streams the good status is described as a clear water state, dominated by a diverse submerged macrophyte community. In many urban and agricultural regions most surface waters do not comply with this condition, due to high nutrient loads and intensive management practices. Subsequent deteriorated ecological states are: single species dominance (e.g. *Elodea*), floating plant dominance (e.g. *Lemna*) or even dominance by filamentous algae. The transitions of vegetation structure are not gradual but occur often suddenly at certain critical nutrient conditions. To study this the ecological model PC-Ditch was developed (Janse, 1998), that was calibrated with datasets of experimental ditches. In a preceding study critical values for nutrients were derived (Van Liere, Janse & Arts, 2007). The ditch research project PLONS (2007-2011) revealed new insights in the effect of nutrient loading and management practices on vegetation structure, but importantly also vice versa. Complex feedbacks occur in contrasting vegetation types, regulated by dissolved oxygen content, temperature, light etc. These conditions, in turn, affect nutrient processes and availability both in the water column and the sediment. An important result is that small temperature increase will boost denitrification in ditches rates disproportionately (Veraart, submitted). Also it may be expected that internal phosphorus release will increase with increasing temperature.

In this study we present results of simulations with a combination of the PC-ditch model and a dynamic hydrological flow model (Duflow). This coupling enables taking into account the effect of macrophytes on flow properties and subsequent residence times. The objective is to study changes in critical values of phosphorus and nitrogen loading, in the light projected temperature rise due to climate change.

### **3. Aquatic herbivores as a regulating factor of methane emission in the land-water transition zone of shallow lakes.**

Paul.L.E. Bodelier, Bas J.J Dingemans and Elisabeth S. Bakker  
Netherlands Institute of Ecology

Wetlands are significant sources of atmospheric methane. Methane produced by microbes enters roots and escapes to the atmosphere through the shoots of emergent as well as submerse wetland plants. Herbivorous birds graze on macrophytes, but their effect on methane emission remains unknown. We hypothesized that grazing on shoots of wetland plants can modulate methane emission from wetlands. Diffusive methane emission was monitored inside and outside bird-exlosures, using static flux chambers placed over whole vegetation and over single shoots. Both methods showed significantly higher methane release from grazed reeds. Surface-based diffusive methane emission from grazed plots was up to 5 times higher compared to exclosures. In case of grazing on submerse macrophytes the opposite effect was found, emitting more methane from non-grazed plots. Modulation of methane emission by animal-plant-microbe interactions deserves further attention considering the increasing bird populations and changes in wetland vegetation as a consequence of changing land use and climate change.

#### **4. Hypoxia in a changing world**

Lorenz Meire, Karline Soetaert and Filip Meysman  
Netherlands Institute of Ecology

Nowadays hypoxia is becoming a worldwide important phenomenon. The occurrence of hypoxia in coastal and marine ecosystems has increased exponentially since 1960s. This has some severe consequences on ecosystem functioning. First of all O<sub>2</sub> plays a crucial role in the biogeochemical cycles. Depletion of O<sub>2</sub> leads to the use of other electron acceptors changing the energy flow in the sediment. Therefore hypoxia affects the degradation rate of organic material, the production of reduced substances like sulphides and changes the nutrient fluxes from the sediments. As oxygen is also essential for all aerobic life, hypoxia leads to a loss of habitat of many bottom-dwelling fishes and benthic fauna, compression of habitat for pelagic fishes, direct mortality and altered migration. Since the occurrence and strength of hypoxia depends on climatic drivers, it is expected that climate change will have a profound impact on hypoxia. We have developed a one dimensional mechanistic model to examine the effect of climate change and other environmental problems like eutrophication on hypoxia. The model comprises all reactions affecting the oxygen concentration in the benthic and pelagic compartments and is developed and calibrated using data from the Dutch oyster grounds (Dutch North Sea). This approach allows us to study the net effect of changing temperature, storm frequency, nutrient loadings, run off, wind patterns on hypoxia.

#### **5. C:N:P ratios of individual bacteria: an explanation for enhanced regeneration of P relative to carbon from marine sediments?**

Anne K. Steenbergh, P.L.E. Bodelier, M. Haldal, C.P. Slomp and H.J. Laanbroek  
Netherlands Institute of Ecology

Sediments overlain by anoxic bottom waters have been shown to release more P to the water column than oxic sediments. An increased availability of P in the water column can lead to an increase in primary production with an accompanying higher sedimentation flux of organic matter. As a result of the higher oxygen demand for the remineralization of this organic matter, higher benthic P fluxes under anoxic conditions can sustain a positive feedback loop that leads to an increase in the extent of anoxia in aquatic systems. On short timescales, the higher P flux from anoxic sediments can be explained by release of P from iron-bound P and polyphosphates, but the mechanism responsible for long term higher P fluxes remains largely unclear.

As bacteria play a key role in the mineralization of organic matter in marine sediments, the stoichiometry of microbial biomass is of crucial importance in determining the release of carbon and nutrients from the sediment. However, little is known about the elemental composition of benthic bacteria because direct measurements of bacterial C:N:P ratios are generally hampered by the low abundance of bacteria compared to other sediment particles.

In this study, we used X-ray Micro-Analysis (XRMA) to directly measure C:N:P ratios of individual sediment bacteria. Sediments from the Baltic Sea in which the microbial activity was limited by carbon availability were incubated in slurries under oxic or anoxic conditions and with or without the addition of C, N, and P.

While bacterial C:N ratios were on average 6.4:1, and thus close to the Redfield ratio for marine organic matter, bacterial C:P ratios were significantly higher at 400:1. We postulate that the low P content of benthic bacteria relative to carbon explains the enhanced regeneration of P during organic matter mineralization observed in marine sediments. This enhanced regeneration of P, in combination with a proposed lower retention of P in anoxic sediments, helps to explain the higher P fluxes from sediments overlain by anoxic bottom waters.

#### **6. Stoichiometric effects of food on growth and movement decisions in zooplankton: implications for competitive ability**

Tibor Bukovinszky  
Netherlands Institute of Ecology

Changing nutrient loads of freshwater ecosystems have consequences for species composition and nutrient cycling. It is therefore important to understand how changes in mineral limitation affect growth, reproduction and competitive ability of consumers. On poor quality food, herbivores may increase ingestion rates, where the extent of such compensation may depend on physiological and behavioural differences between species. However, few studies have focused on how different zooplankton species respond to varying nutrient contents at different quantities of available food. Here we compared relative somatic growth rates and body elemental composition of three *Daphnia* species/clones on algal food (*Scenedesmus obliquus*) that was poor or rich in phosphorus. Under ad libitum food quantities, phosphorus enrichment of food affected relative growth rates, egg production and body nutrient composition of zooplankton in different ways. At different food quantities, phosphorus enrichment had different effects on growth rates, and this depended on the species studied. Changes in elemental composition of zooplankton reflected the role of carbon and nutrients

in covering costs of nutrient assimilation and metabolic processes. The ability of animals to move long a gradient of resource quality may alleviate the effects of suboptimal food conditions. Using a novel behavioral bioassay, we studied whether decisions in *Daphnia* to leave local patches of food are influenced by 1) the presence/absence and 2) the nutrient content of algal food. We discuss the effects of varying food quality on growth and food selection behaviour in *Daphnia* and possible implications for competitive ability.

## **1c: Interface between ecology and paleo-ecology**

**Conveners:** Henry Hooghiemstra (University of Amsterdam)  
Gert-Jan Reichart (Utrecht University)

### **1. Climate forcing due to optimization of maximal leaf conductance in subtropical vegetation under rising CO<sub>2</sub>**

Hugo J. de Boer, Emmy I. Lammertsma, Friederike Wagner-Cremer, Stefan C. Dekker, Martin J. Wassen and David L. Dilcher  
Utrecht University

New data series are presented that show consistent and significant reduction in maximum stomatal conductance ( $g_{smax}$ ) of ~34% (+/- 12%) in nine common Florida C3 species over the 100 ppm CO<sub>2</sub> increase of the past century. Despite species specific strategies in adaptation of stomatal densities and geometries, all species display highly similar reductions of  $g_{smax}$  in response to rising CO<sub>2</sub>. Based on the similarity in observed CO<sub>2</sub> responses, we hypothesise that all species reduce  $g_{smax}$  in order to optimize carbon gain under the constraint of a physiological cost of water loss. Based on the optimization hypothesis, we develop and validate a model to simulate structural stomatal adaptation from photosynthesis and diffusion of CO<sub>2</sub> and water vapor through stomata. Our model reproduces the observed stomatal adaptations for each species observed and predicts that adaptation will continue beyond double today's CO<sub>2</sub> concentration of 780 ppm. We suggest that the on-going response of  $g_{smax}$  to CO<sub>2</sub> is eventually limited by species specific limits to phenotypic plasticity. Based on species specific strategies to adapt stomatal densities and geometries we predict that that angiosperms reach their CO<sub>2</sub> response limits on average at 740 ppm, and conifers on average at 1250 ppm, roughly reflecting the ambient CO<sub>2</sub> under which these lineages evolved. Upscaled to canopy level and including response limits, our simulations predict that doubling present CO<sub>2</sub> will decrease the annual transpiration flux of subtropical vegetation in Florida by approximately 60 W.m<sup>-2</sup>. We conclude that stomatal adaptations to rising CO<sub>2</sub> are currently altering the hydrological cycle and climate in Florida and will continue to do so throughout this century. Furthermore, the on-going rise in CO<sub>2</sub> might give competitive advantage to plant lineages with higher CO<sub>2</sub> response limits and thereby allow a shift of existing vegetation composition favouring plant lineages tied to an earlier time.

### **2. How will peat bogs respond to climate change? Results of combined palaeo-ecological, experimental and model research**

Monique M.P.D. Heijmans, A. Breeuwer, M. van der Linden, B. van Geel and F. Berendse  
Wageningen University

Peat bogs are important and interesting ecosystems for research on the impacts of climate change. 1) Peat-forming bogs serve as significant long-term sinks for atmospheric carbon dioxide. 2) The peat forms an archive of bog responses to past climatic changes. We studied the effects of climate warming and increased nitrogen deposition on species composition and carbon sequestration in bogs. Our approach was a combination of a palaeo-ecological reconstruction of changes in bog ecosystems during the past 400 years, experiments to determine potential responses of bog vegetation to climatic changes, and a simulation model to analyze the long-term vegetation and carbon dynamics of bog ecosystems in relation to global change. All three subprojects used four bog sites along a north-south transect from northern Sweden to eastern Germany.

All three approaches showed shifts in bog plant species composition with climatic changes. Both climate warming and increased nitrogen deposition favor vascular plants over peat mosses. This resulted in a significant expansion of ericoid plant species in bog mesocosms that were transplanted to more southern sites. With respect to carbon accumulation there was less agreement among the three approaches. The peat core data showed that carbon sequestration rate was largest in the most southern site. In contrast, model results suggest that future climate warming decreases carbon accumulation, particularly at high nitrogen deposition sites, although carbon accumulation may still increase at cool, low nitrogen deposition sites. The simulated negative trends in long-term carbon sequestration rates were related to strong vascular plant expansion at the cost of peat mosses. In short, the combination of three approaches showed us that observed patterns of carbon sequestration in the past are no guarantee for the future and that vegetation changes should be taken into account when analyzing long-term effects of global change in peatlands.

### **3. Non-pollen palynomorphs: towards more complete ecological information in Quaternary studies**

Bas van Geel  
University of Amsterdam

In pollen preparations other microfossils of various origin are often preserved. Quaternary deposits have been studied palynologically at the University of Amsterdam for more than 40 years. The analysis of pollen and macrofossils was combined with the study of all 'extra' microfossils (non-pollen

palynomorphs: NPP). The aim was to discern still unexplored fossils, and this strategy resulted in an increase in the number of palaeoenvironmental indicators. Among the extra fossils are spores of fungi, remains of algae, and cyanobacteria. Several hundred 'Types' have now been distinguished. The identification of the fossils was attempted with the aid of literature and by consulting colleagues in invertebrate zoology, phycology, mycology and plant anatomy. Among the NPP there are still some taxa which are not properly identified, but some of them nevertheless can be used as palaeoenvironmental indicators. In these cases, the ecological information is inferred from the co-occurrence (curve matching) with identified taxa (e.g., pollen, seeds). Most fungal and algal taxa and cyanobacteria have a very long geological history, and therefore some of the NPP-studies are also valuable for palynologists specialised in the analysis of pre-Quaternary deposits. The value of the analysis of NPP will be shown by presenting some examples, from cyanobacteria in lake sediments to coprophilous fungi in frozen mammoth dung.

#### **4. Identification and distribution of intact polar branched glycerol dialkyl glycerol tetraether lipids in a Swedish peat bog**

Francien Peterse, Ellen C. Hopmans, W. Irene C. Rijpstra, Anchélique Mets, Stefan Schouten and Jaap S. Sinninghe Damsté

Royal Netherlands Institute for Sea Research

Branched glycerol dialkyl glycerol tetraethers (GDGT) are membrane lipids of supposedly anaerobic bacteria that occur ubiquitously in soils worldwide and have, with the introduction of the MBT/CBT proxy of Weijers et al. (2007), formed the basis of several paleoclimatic studies. Although the exact bacteria that are producing branched GDGTs are as yet unknown, *Acidobacteria* have been suggested as possible source organism.

Until recently, it was also unknown how these GDGTs occur in the cell membrane, i.e. as intact polar lipids (IPLs). Liu et al. (2010) identified two IPL-branched GDGTs with glycosidic headgroups in a German peat bog. To investigate the occurrence of these and other IPLs, we investigated the extracts of a Swedish peat bog. In addition to the previously reported glycosidic IPL branched GDGTs, we also identified IPL-branched GDGTs with a phospho-containing headgroup. Based on the thus far identified IPL branched GDGTs, we developed an HPLC- Selected Reaction Monitoring (SRM)-MS assay to examine changes in headgroup distribution throughout a depth profile of the Swedish peat bog, and subsequently compared these trends with quantified IPL-derived branched GDGT core lipids.

Branched GDGTs with glycosidic headgroups were more abundant above the water table than below, whereas branched GDGTs with phospho-containing headgroups show the opposite trend. This suggests that branched GDGTs are primarily produced in the anoxic part of the peat, since phospholipids are more sensitive to degradation than glycolipids, and thus serve as a better marker for *in situ* production. This is supported by the absolute amounts of IPL-derived branched GDGTs, which also show this increase below the water table. The high concentration of branched GDGTs in the anoxic part of the peat implies that they are indeed most likely produced by anaerobic bacteria. Our SRM method now allows the tracing of IPL-branched GDGTs in natural environments and, through comparison with bacterial gene abundances, should lead to better constraints on the exact source of the orphan branched GDGTs.

#### **5. Differences in cyclopentane distribution amongst intact polar tetraether lipids: implications for the $TEX_{86}$ paleothermometer**

Sabine K. Lenggger, Ellen C. Hopmans, Gert-Jan Reichart, Jaap S. Sinninghe Damsté and Stefan Schouten

Royal Netherlands Institute for Sea Research

The  $TEX_{86}$  is a widely used paleotemperature proxy which relies on the fact that the number of cyclopentane moieties in thaumarchaeal membrane lipids (glycerol dibiphytanyl glycerol tetraether lipids, GDGTs) are related to temperature. In living Archaea, these lipids are present as intact polar lipids (IPL) with sugar- and/or phosphate-containing groups attached to the core lipids (CL). From intact polar lipid analysis of cultures, it has been observed that GDGTs containing different numbers of cyclopentane moieties are not equally distributed amongst the various headgroups. In this study we analyzed Arabian Sea sediments from different water depths and bottom water oxygen concentrations. As previously observed in cultures, GDGT-2 and -3 (numbers indicate the number of cyclopentane moieties) are predominantly associated with glycolipids, while GDGT-1 is associated predominantly with a phosphoglycolipid. Thus, the  $TEX_{86}$ -values generated by GDGTs derived from glycolipids are substantially higher than those generated from the phospholipid derived GDGTs, though the  $TEX_{86}$  of total IPL-derived GDGTs is approaching the value of the CL-GDGTs. Our results suggest that differences in preservation potential between phosphoglycolipids and the diglycolipids will lead to changes in  $TEX_{86}$  in IPL derived GDGTs with progressing degradation. Therefore, differences in  $TEX_{86}$  between IPL-derived and CL-GDGTs are not necessarily indicating differences in origin between the two. The culture results suggest there may be a consistent distribution of GDGTs amongst headgroups, maybe ultimately defining the  $TEX_{86}$ . Cultivation studies performed at different

temperatures will shed more light on the determining factors for the GDGT distributions within the different IPLs.

## **6. Evidences for silicic acid leakage to South East Australia during interglacials and MIS 3**

Raquel A. Lopes dos Santos, Daniel Wilkins, Patrick De Deckker and Stefan Schouten

Royal Netherlands Institute for Sea Research

Stable carbon isotope minima in planktonic foraminifera during deglaciations has been suggested as an isotopical signal of  $^{13}\text{C}$ -depleted  $\text{CO}_2$  from upwelled deep Southern Ocean waters in southern hemisphere mid-lower latitudes. Here, we investigated the occurrence and impact of this upwelling in the Murray Canyons area (Southeast Australia – SEA). We analyzed the  $\delta^{13}\text{C}$  of *G. bulloides* from a core from this area and compared it to the diol index record of the same core, as a proxy for upwelling. We show that although Southern Ocean waters containing  $^{13}\text{C}$ -depleted  $\text{CO}_2$  upwelled in SEA during deglaciations they did not lead to enhanced productivity. In contrast, *Proboscia* diatoms, an algae present in early upwelling, bloomed at SEA only during interglacials and Marine Isotope Stage 3. This late productive upwelling in SEA is associated with a strong decrease in diatom production in Southern Ocean, suggesting that at these times silicic acid could leak from Southern Ocean to SEA stimulating diatom productivity in lower latitudes. Previous studies linked silicic acid leakage to glacial periods, but our results suggest it had a wider distribution during glacial-interglacial cycles, controlled not only by the concentration of silicic acid in Southern Ocean waters but also by the intensity of the water masses transporting this nutrient.

## **1d: Ecology regarding genetically modified organisms**

**Conveners:** Patrick Kabouw (Netherlands Institute of Ecology)  
Emilia Hannula (Netherlands Institute of Ecology)  
Martine Kos (Wageningen University)

### **1. Quantitative aspects of field studies of risk assessment of GM plants**

Joe N. Perry

Rothamsted Research, United Kingdom.

I discuss several quantitative aspects of the risk assessment of genetically-modified (GM) plants. Starting with risk assessment for food/feed safety, I discuss attempts to quantify the principle of substantial equivalence and to formalise the associated tests. The concept of equivalence testing has its roots in the biopharmaceutical literature. Equivalence tests will be used to supplement the traditional difference tests. These new tests will be employed in future field trials to assess the composition of GM plants. They differ from previous trials because they include reference varieties which are used to set equivalence limits required by the equivalence tests. I discuss the implications of these tests for risks to consumer and producer in the context of statistical power.

Equivalence testing also features in new guidance for the environmental risk assessment of GM plants, although not in this case employing reference varieties. Instead, equivalence limits will be set directly, using limits of concern that relate closely to environmental harm and protection goals.

Finally, I describe work to build a mathematical model to analyse the exposure of non-target Lepidoptera to Bt pollen from maize MON810. For the first time, bioassays in the laboratory that relate mortality to dose are combined with field measurements of maize pollen that relate dose to distance from Bt fields to obtain a simple relationship between mortality and distance. The resulting relationship is useful to supplement estimates of mortality rates in situations where field observations may be challenging.

### **2. The baseline across soils: transformation of plant-borne organic matter**

Agnieszka Szturc-Koetsier and Heike Schmitt

Utrecht University

A reliable risk assessment of possible adverse effects of genetically modified organisms in soils depends on knowledge of the basic variations in soil functions and microbial diversity of the soils. Such a "normal operating range" (baseline) can be used to understand the relevance of potential changes induced into the soils (e.g. by genetically modified plants or other stresses). The baseline should include the most descriptive biotic and abiotic soil characteristics. As part of a larger research initiative to define the soil baseline, our focus is on the transformation of carbon substrates (plant material) by soil microorganisms. Our hypothesis is that microbial functional diversity determines the respiration activity of soil and that both parameters might vary between different soils. Therefore we investigate the possible link between the structure of active microbial community and the variability in soil functioning (carbon degradation).

We measured soil respiration kinetics to investigate carbon transformation by microbial communities. A stable isotope probing (SIP) approach was used for studying the diversity of the active bacterial degraders.

In our research we studied 8 representative Dutch agricultural soils. Soil samples were taken 4 times during the year, during several growing seasons.

As a model substrate for root exudates <sup>13</sup>C-labeled arginine was used and the respiration was measured in time. Curve fitting was used to compare respiration kinetics. Total soil DNA was extracted and after separation <sup>13</sup>C DNA was used to determine total bacterial diversity of the arginine degraders by terminal restriction fragment length polymorphism (T-RFLP).

In all investigated soils we observed similar profiles of the arginine degrading bacterial communities, despite different soils characteristics. Three dominant species were found and there were the same for all analyzed soils.

Respiration kinetics showed that the activity of arginine transformation was slightly different within soils. However, there was no consistent influence of the soil type or season.

Only few bacterial species, which were identical between differing soils, were responsible for the substrate degradation. Small differences in respiration kinetics can be explained by a relatively low microbial diversity of the arginine degraders in the investigated soils. The results suggest that the observed species are indicator species responsible for the arginine degradation.



### 3. Quantifying stochastic introgression risks with hazard rates

Atiyo Ghosh

Leiden University

Introgression is the permanent incorporation of genes from one population into another. It is of particular concern with the advent of genetically modified crops, since genetically modified genes might introgress into wild populations with adverse consequences. For example, a gene conferring some fitness advantage (e.g. herbicide resistance) might produce a so-called superweed in a wild population which would outcompete indigenous plants, consequently damaging biodiversity. Furthermore, there are several random components in introgression (e.g. weather patterns, offspring distributions, competition with wild plants) that must be taken into account. This talk outlines a novel approach in measuring introgression risks using a quantity called the hazard rate.

### 4. How non-native plants affect natural ecosystems

Thomas van Hengstum, Gerard Oostermeijer and Peter van Tienderen

University of Amsterdam

One aspect of Environmental Risk Assessments (ERA) of transgenic crops involves the introduction of the transgene in natural environments through outcrossing with a wild relative or through the establishment of feral populations. The potential chain of events that follows an invasion may lead to the disappearance of other, competing species and quantitative and qualitative changes in the functional diversity of the ecosystem. We focus on the potential changes in insect assemblages and herbivore damage patterns associated with the expansion of the plants: Do specific herbivores increase to levels beyond the baseline, and do they increase the attack on native plants by spillover to adjacent native vegetation?

In order to simulate a crop escape into natural habitat we introduced 12 plots of (i) Prickly lettuce (*Lactuca serriola*) and 12 plots of (ii) Oilseed rape (*Brassica napus*), as well as 12 control plots. Around each of those plots we placed two native indicator species, namely *Tragopogon pratensis* and *Diplotaxis tenuifolia*. Using various insect sampling methods, including insect suction sampling, we were able to characterize the insect assemblages of each plot type.

We found higher airborne herbivore abundance around *B. napus* plots compared to control and *L. serriola* plots. Furthermore, a higher abundance of ground dwelling herbivores was found around both *B. napus* and *L. serriola* compared to the control plots. Leaf damage by herbivores on indicator plants did not differ between the plot types.

The local introduction of a non-native species into natural ecosystems does indeed alter local insect assemblages. We are currently investigating how those changes affect herbivory patterns, pollinator interactions and the reproductive success of native plants.

### 5. Introgression of crop (trans-)genes into wild relatives: Environment specific effects in *Lactuca*.

Yorike Hartman, B. Uwimana, D.A.P. Hooftman and P.H. van Tienderen

University of Amsterdam

The fate of a transgene after outcrossing to wild relatives depends on its effect on plant fitness but also on the effects of neighboring crop genes. Genome regions with negative effects on the fitness of hybrid plants are less likely to become introgressed into the genome of related species including inserted transgenes (Stewart *et al.* 2003). In our studies, we focus on the identification of crop genomic regions under selection after hybridization with a wild relative. We use Recombinant Inbred Lines (RILs) from a cross between (non-GM) *Lactuca sativa* cv. Salinas (Lettuce) and wild *L. serriola*. We perform QTL-analysis with a 1107 marker genetic map, spanning 1,254 cM with nine linkage groups (adapted from Argyris *et al.* 2005).

Specifically, our work concerns two main questions:

- i. What are the fitness effects of genes inherited from the crop in greenhouse and field?
- ii. Can small-scale contained experiments with transgenes be used to assess potential ecological consequences?

Through a combination of greenhouse and field studies we identified a wide variety of QTLs for fitness in different life stages from germination up to seed output in the adult stage. Only traits with a high heritability, such as days until first flower, provide a good overlap between greenhouse-based and field-based QTLs. This suggests that small-scale contained greenhouse experiments on lower heritability traits are not suitable to assess potential ecological consequences of transgene escape into wild relatives.

We identified genomic hotspots where many traits overlap. Depending on the trait, a crop genomic background may have positive as well as negative fitness effects. This implies that the outcome of hybridization could be rather unpredictable and environment dependent. Hence gene inserts could be better avoided there. To assess the impact of all QTLs together on the fitness of hybrids, models are being developed that use the empirical data as input.

## **6. Comparison of the whole-genome response to perturbations and its ecological applications.**

Benyamin Houshyani

Wageningen University

The whole-genome profiling approaches such as micro-array analysis and metabolites fingerprinting are being widely used for an unbiased global screening of the genome and to unravel the genome plasticity and variation due to all kinds of perturbations. Multivariate analysis of these profiles is subsequently used to reduce the dimensionality of the data to a number of principle components (PCs) that explain the maximum variation. This is followed by visualization of the data structure, statements about clustering of the samples and interpretations related to the response to the studied perturbation. However, due to limitations in our imagination and visualization power these statements about clustering are usually based on just two or rarely three PCs. Hence, some of the additional components that contain relevant biological variation and important for understanding the relationship between samples, are excluded from the analysis. Furthermore, even if there is visual separation between clusters of samples, quantification of the distances between clusters in a hyperplane would greatly help in interpreting the biological relevance of clustering of samples and the distance between these clusters.

In this presentation, a metric for the distance between groups of biological replicates in a hyperplane such as a PCA scores plot is introduced. Furthermore, we denote some of its potential applications in ecology and molecular biology.

## **Session 2**

### **2a: Ecosystem change and predictability in a changing world**

**Conveners:** Elisa Beninca (University of Amsterdam)  
Vasileios Dakos (Wageningen University)

#### **1. Ecosystem change and predictability in a changing world: what do plankton dynamics tell us?**

Elisa Beninca and Vasilis Dakos

University of Amsterdam / Wageningen University

In the last century there has been a recurring debate in ecology about the importance of different factors affecting the predictability of ecosystem dynamics. In particular, the relative impact of biotic versus abiotic factors in controlling population fluctuations has been debated. Here, using plankton as an example, we discuss how the delicate interplay between species interactions and environmental forcing play a major role in predicting the dynamics of species communities

#### **2. Slow recovery from local disturbances: an early-warning signal for regime shifts?**

Ingrid A. van de Leemput, Vasilis Dakos, Marten Scheffer and Egbert H. van Nes

Wageningen University

Theoretical studies suggest that slow recovery from perturbation experiments can be used as an indication that a system is approaching a regime shift. The idea behind such experiments is that a system recovers slower when it is close to a tipping point. In practice, however, applying a disturbance to the whole system can be unrealistic. Therefore, it would be good if the response to a local disturbance could also provide insight into the resilience of a system as a whole. Here, we use a spatially-explicit model to quantify the recovery of such local disturbances and to test whether this could be used as an indicator for the resilience of the system at a larger scale. We suggest that a decreasing recovery rate of local disturbances may be used as an early warning signal for systemic collapse. Although removing a local patch in a large-scale system may theoretically trigger a global collapse, we suggest that monitoring the recovery rate of natural local disturbances like hurricanes in coral reefs or fires in forests may help to indicate an upcoming catastrophe.

#### **3. Nuisance foam events and *Phaeocystis globosa* blooms in Dutch coastal waters analyzed with fuzzy logic**

Anouk N. Blauw, F.J. Los, J. Huisman and L. Peperzak

University of Amsterdam

*Phaeocystis globosa* is a nuisance algal species because it can cause foam on beaches which are associated with coastal blooms. Models of *Phaeocystis* have considered its bloom dynamics, but not the foam formation. The process of foam formation is poorly understood which limits the suitability of traditional deterministic model approaches. We therefore applied fuzzy logic to simulate observed *Phaeocystis* bloom dynamics in coastal waters of the North Sea and foam formation on adjacent beaches. *Phaeocystis* bloom initiation is estimated to occur when the mean mixed layer daily irradiance exceeds circa 25 to 35  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ . Peak bloom intensity was higher at monitoring stations with higher nutrient availability, although bloom termination did not coincide with nutrient depletion. Foam events occurred on Dutch beaches during and following *Phaeocystis* blooms, when the wind direction was landward. Over the period 2003-2007, 90% of observed foam events were correctly predicted by the model, however, there were many false positives. The fuzzy logic approach proved helpful in screening and adjusting hypotheses on the dynamics of *Phaeocystis* and associated foam events. The resulting model communicates current understanding of foam formation, enhances the predictability of these events, and provides a basis for more detailed modelling efforts.

#### **4. The (in)stability of salt marshes in a changing environment; the effects of enhanced sea-level rise**

Elske C. Koppenaar, J.P. Bakker, K.S. Dijkema, H.F. van Dobben and S. Temmerman

University of Groningen

There are many global climatic changes going on and predicted that will affect many ecosystems in the world. One of the predicted changes is an enhanced sea-level rise. Salt marshes are regularly inundated by the sea and therefore they will be affected by the predicted enhanced sea-level rise. On Ameland, a back barrier island in the north of the Netherlands, there is soil subsidence since 1986 because of gas extraction. Since the actual soil subsidence is up to about 30 cm on the salt marsh and the effects of soil subsidence (increased flooding) is the same as enhanced sea-level rise it is a perfect study area to monitor how salt marshes will react. It was expected that the vegetation would show regression. However, results so far show that the vegetation is more stable than expected. Other mechanisms like sedimentation and properties of an established plant community may

contribute to this stability. The aim in this talk is to identify underlying mechanisms that drive the succession of the salt marsh that can account for the extent of this stability.

## **5. Phenology drives mutualistic network structure and diversity**

Francisco Encinas-Viso, Tomas Revilla, David Alonso and Rampal S. Etienne  
University of Groningen

Mutualistic interactions are ubiquitous in nature and have been suggested to even represent the backbone of ecological communities. Several network properties have been identified that play a pivotal role in determining the stability and complexity and the interplay between them are nestedness and asymmetry. However, the mechanisms that give rise to those network properties are still unclear. Phenology in particular seems important, as it shapes the topology of mutualistic interaction networks. But, the effects of species phenologies on the dynamics, stability and coexistence of mutualistic networks, to our knowledge, have scarcely been studied. Here, we study these effects with a general mathematical population dynamics model of mutualistic and competitive interactions where the strength of these interactions depends on the species temporal overlap resulting from their phenologies. We find that the shape of the distribution of phenologies (i.e. the variation of starting and final dates distribution, measured by their variance) simultaneously determines stability, coexistence and network structural properties of mutualistic communities: phenology distributions that maximize mutualistic interactions and minimize intra-guild competitive interactions generate speciose, highly nested and poorly connected with weak asymmetric interaction strengths and low resilience. Furthermore, we find that increases in the season length (SL) increase the stability, resilience and diversity of the communities. This study highlights the fragility of real mutualistic communities living in short SL (e.g. Arctic environments) to drastic environmental changes because of their low resilience. Finally, we argue that phenology not only drives mutualistic interactions networks, but also affects stability and diversity of other ecological networks, especially in communities living under high environmental seasonality.

## **6. Synergistic effects of nutrient loading and temperature warming on an experimental phytoplankton community: implications for stoichiometry**

Lisette Senerpont Domis  
Netherlands Institute of Ecology

The impact of climate change on biological systems is already apparent through changes in the phenology and the distribution of individual species. However, other stressors of ecosystem functioning, such as habitat fragmentation, eutrophication and pollution may act in concert with climate change. Possible non-additive impacts of these multiple 'stressors' make it difficult to predict effects based on single-stressor studies. Earlier studies suggest that nutrient loading and climate warming may have non-additive synergistic effects on lake ecosystems. To obtain a more mechanistic understanding of the combined effect of nutrient loading and temperature warming on the planktonic food web base, we exposed experimental phytoplankton communities to different nutrient loading and temperature warming scenarios using a full-factorial design. At first glance, the combined effects of nutrient loading and temperature warming on phytoplankton biomass seem to be additive, implying that these multiple drivers target different community properties. However, logistic growth model analysis showed that despite these seemingly additive effects, both temperature warming and nutrient loading affect the same aspect of the phytoplankton community, i.e. carrying capacity. A likely mechanism behind the effect of temperature warming on phytoplankton carrying capacity is a more efficient use of nutrients at warmer temperatures, resulting in higher carbon-nutrient ratios. This mechanism is backed-up by our results on seston carbon-nutrient ratios, which showed non-additive synergistic effects of nutrient loading and temperature warming on carbon-nutrient ratios. At higher temperatures, nutrient content of our experimental phytoplankton community decreases as indicated by higher carbon-nutrient ratios of the seston. By lowering the stoichiometric food quality of the planktonic food web base, this interaction between nutrient loading and temperature warming can potentially lead to stoichiometric bottlenecks in aquatic food webs, even more so under low nutrient supply.

## **2b: Spatial Ecology**

**Conveners:** Ellen Weerman (University of Groningen)  
Maarten Eppinga (Utrecht University)

### **1. Interspecific facilitation and critical transitions in ecosystems**

Christian Smit

University of Groningen

The spatial organization of ecosystems importantly reflects their 'state' or 'healthiness'. For example, recent studies performed in arid ecosystems indicate that increased patchiness of the vegetation – i.e. a drop in number and size of vegetated patches with increased environmental stress – is a possible warning signal prior to a critical transition from a vegetated to a non-vegetated state (desertification). Similar results come from observational and modelling studies of various ecosystems (e.g. peatlands, savannas, intertidal mudflats, coral reefs) indicating the importance of spatial structure for ecosystem functioning. As of now, experimental studies that aim to test model predictions or unravel the underlying mechanisms behind observations are relatively scarce. Such studies are presently highly needed to improve our understanding of how spatial structure influences ecosystem functioning. In this talk I will discuss planned experimentations on the important role of species interactions – in particular facilitation – for spatial organization in ecosystems. Furthermore, I will bring together two important ecological theories that have been so far developed separately: the stress gradient hypothesis and critical transitions in ecosystems.

### **2. Alternate mechanisms for spatial self-organization in mussel beds**

Quan-Xing Liu, Ellen Weerman, Peter Herman, Han Olf and Johan van de Koppel

University of Groningen / Netherlands Institute of Ecology

Theoretical models predict that spatial self-organization may affect the functioning of ecosystems. Whether and how these emergent effects depend on alternate formulations of the underlying mechanisms is an often ignored question. Here, we compare three models of regular spatial pattern formation in mussel beds that have different mechanistic descriptions for facilitative interactions between mussels. The first mechanism involves a higher mussel persistence at higher density, which is the basis of prior studies on pattern formation in mussels. The second mechanism assumes that mussels feed more efficiently on top of mussel-generated hummocks, for which we present new evidence. Model simulations point out that the alternate model formulations produce very similar types of spatial patterns in mussel beds. Yet, they predict a strikingly contrasting effect of these spatial patterns on ecosystem functioning, in terms of productivity and resilience. The first model, where high mussel densities reduce mussel loss rates, patterns are predicted to strongly increase productivity and decrease the recovery time of the bed following a disturbance. When pattern formation is generated by the increased feeding efficiency on hummocks, only minor emergent effects of pattern formation, on ecosystem functioning are predicted. Our results provide a cautionary warning when interpreting model of spatial self-organization for their emergent of spatial patterning, highlight the importance to test alternate explanatory mechanisms, both in theoretical and empirical studies.

### **3. Scale-dependent effects of an ecosystem engineer determine the spatial distribution of bivalves in an intertidal ecosystem**

Serena Donadi, Tjisse van der Heide, Els van der Zee, Johan Eklöf, Johan van de Koppel and

Britas Klemens Eriksson

University of Groningen

Increasing evidence shows that scale-dependent biotic interactions mediated by ecosystem engineering species structure associated communities and promote landscape complexity of many ecosystems. Here we tested the hypothesis that contrasting scale-dependent effects of *Mytilus edulis* (blue mussel), a dominant intertidal ecosystem engineer in the Wadden Sea, might explain increased abundances of the burrowing bivalve *Cerastoderma edule* (cockle) at intermediate distances from mussel aggregations. A field survey within and around a 150x100m mussel bed showed a peak in cockle densities at 100m towards the coast-side (behind) of the mussels, while cockle abundances in the study area were otherwise negligible. Next, field experiments showed higher survival of young cockles and increased spatfall behind the bed compared to a control area. Contrastingly, growth was significantly decreased behind the mussels. Field measurements suggested that the peak in cockle numbers resulted from a scale-dependent interaction between 1) settlement facilitation, caused by reduction of hydrodynamics, and 2) inhibition of growth caused by algal depletion and deteriorated sediment conditions. Our results indicate that reef-forming ecosystem engineers can have large effects on the community structure through multiple scale-dependent biotic interactions that encompass long distances. Understanding these spatial, cross-habitat interactions is essential for effective conservation and restoration of intertidal communities, such as the Wadden sea.

#### **4. Spatial processes, temporal variability and ecosystem functioning in salt-marshes**

Jim van Belzen, Johan van de Koppel, Daphne van der Wal, Peter Herman and Tjeerd Bouma  
Netherlands Institute of Ecology

Many coastal ecosystems show large temporal fluctuation in presence and extant. In these rugged environments, ecosystem engineering species play an important role actively influencing currents, waves and sedimentation processes. However, the same processes that shape those intertidal habitats can, on the long run, lead to instabilities putting large scale collapses into effect. Consequently, spatial and temporal variability can profoundly affect ecosystem functioning due to autogenic processes. Therefore, it is essential to consider and be able to estimate this variability in order to refine predictions of ecosystem-level responses to changing conditions. The temporal variability in salt-marsh extent is an interesting example. On a time scale from decades to centuries these ecosystems can go through cycles of development by sediment accretion, and retreat by large scale lateral erosion. This temporal variability in marsh area can have large consequences for their ability to attenuate waves and floods, and, therefore, it is of particular value to estimate this temporal variability. We show that, to be able to infer larger scale spatiotemporal dynamics, it is crucial to understand the spatial feedback processes leading to disturbance and recovery of salt-marshes. The spatial and temporal scales over which those spatial processes act, set by the local hydrodynamic conditions, lead to markedly different ecosystem dynamics. Furthermore, we demonstrate that the spatial vegetation structure can inform on the local conditions influencing disturbance and recovery of the salt-marsh. Power-laws in the vegetation patches are strongly related to local currents, and deviations point to size-dependent recovery of pioneer vegetation due to wave exposure. Consequently, temporal variability in the extent of salt-marshes, and, thereby, its ecosystem functioning, can potentially be estimated.

#### **5. Priority effects in community assembly and repercussions for conservation**

Joachim Mergeay, Steven Declerck and Luc De Meester  
Research Institute for Nature Conservation (INBO) / Katholieke Universiteit Leuven

The way we practice nature restoration is typically founded on restoration of environmental conditions, and the reliance on natural processes such as dispersal for this restoration to happen. There is a general consensus that also we need to restore processes of dispersal to be successful in the short term, or either be very patient. Nevertheless, other processes may interfere, as a result of which dispersal potential is not translated into realized dispersal and establishment, because the window of opportunity for successful colonization may be strongly narrowed due to biotic interactions. Here we present such a very potent process, namely that of priority. Due to priority effects, genotypes or species with overlapping niches can pre-empt resources (space, light, nutrients, food, ...) at the detriment of competing genotypes or species. The first founders to colonize a habitat can grow and multiply and thereby reduce essential resources below a sustainable level for later colonists, thus exerting a potentially long-lasting priority effect. Using a zooplankton model, we present a series of empirical, experimental and simulation studies to infer the role of priority effects in community assembly. We show 1) that priority effects can be important at both the genotypic and species level, 2) that even inferior competitors can outcompete superior species when exerting a priority effect, 3) that priority effects are not merely transient lags in responses to change but can be long-lasting, and 4) that local genetic adaptation of founders can strongly enhance priority effects and thereby affect community structure. We discuss the implications of this phenomenon for practical nature conservation and restoration.

#### **6. Landscape asymmetry and agro-ecosystems and resilience**

Dirk van Apeldoorn  
Wageningen University

In agricultural landscapes, patterns with distinct characteristics can be observed. These patterns reflect drivers at different spatial and temporal scales that create a non-random spatio-temporal variability of landscape characteristics. Patterns of soil organic matter (SOM) are for example controlled by both pedological and climatic factors as well as historic and current land use. The observed patterns linked to their generating processes can be referred to as the landscape asymmetry of SOM. In this presentation we first identify and evaluate landscape asymmetry of SOM in an agricultural landscape in the Netherlands. Subsequently we infer implications of landscape asymmetry for agro-ecosystem functioning and resilience. We modeled SOM dynamics of grassland soils to identify dominant long-term drivers and combined and analyzed land use history and landscape characteristics to explain the spatial variability of SOM contents. Sensitivity analyses show that the dominant parameter for attainable SOM content is the mineralization rate of SOM. Results furthermore indicate, that SOM content is related to temporal variability in land use and to spatial variability of groundwater hydrology and soil texture. Since SOM affects physical, chemical and biological soil properties, differences in SOM contents shape farm management. High SOM contents for example made it possible for some farmers to reduce fertilizer input. Ignorance of SOM landscape asymmetry, however, might result in cascading events across scales threatening the resilience of region as whole.

## **2c: Genomics of Conservation Ecology**

**Conveners:** Cees Musters (Leiden University)  
Krijn Trimbos (Leiden University)  
Klaas Vrieling (Leiden University)

### **1. Conservation genomics: the science of plentiful scarcity**

Joop Ouborg

Radboud University

Over the past twenty years conservation genetics has progressed from being mainly a theory-based field of population biology to a full-grown empirical discipline. Technological developments in molecular genetics have led to extensive use of neutral molecular markers such as microsatellites in conservation biology. This has allowed assessment of the impact of genetic drift on genetic variation, of the level of inbreeding within populations, and of the amount of gene flow between or within populations. Recent developments in genomic techniques, including next generation sequencing, whole genome scans and gene-expression pattern analysis, have made it possible to step up from a limited number of neutral markers to genome-wide estimates of functional genetic variation. These developments stimulate the transition of conservation genetics to conservation genomics.

Conservation genomics is necessary for studying functional genomic variation as function of drift and inbreeding, for studying the mechanisms that relate low genetic variation to low fitness, for integrating environmental and genetic approaches to conservation biology, and for developing modern, fast monitoring tools.

### **2. Genomic characterization of inbreeding depression in thermal resistance**

Corneel Vermeulen

University of Groningen

Inbreeding depression is a phenomenon of major relevance for conservation biology. Although the population genetic principles of inbreeding depression are well known, the functional genomic basis remains poorly characterised. At the moment, knowledge of the mechanistic causes of inbreeding depression and the molecular properties of genes that give rise to or modulate its deleterious effects is lacking. This warrants the detailed study of genetic loci giving rise to inbreeding depression. Since the complex and polygenic nature of general inbreeding depression makes this a formidable task, we focus on one aspect, conditional lethals in the fruitfly model system (*Drosophila melanogaster*). Highly inbred lines harboring conditionally expressed lethals display large and reproducible inbreeding effects at restrictive thermal conditions, but are otherwise easy to culture and handle. We use genomic, transcriptomic and proteomic approaches to characterise the inbreeding event and identify the lethal alleles. This will ultimately allow us to assess whether similar inbreeding effects consistently map to the same genome regions and whether genetic variation at these regions is associated with variation in thermal tolerance in outbred populations.

### **3. The use of genetics for lion conservation**

Laura Bertola

Leiden University

The recent advances in sequencing and genotyping techniques have opened new possibilities for molecular research in non-model organisms, like the lion. Genetic parameters giving insight into the geographic pattern of genetic variation within the species can therefore be included when setting up management strategies for conservation purposes.

Based on mtDNA from lions throughout their complete geographic range, we found a distinction between lions from West and Central Africa and lions from southern and East Africa. The West and Central African lions are more closely related to the Asiatic lions than to the southern and East African lions. This can be explained by a Pleistocene extinction and subsequent recolonization of Western Africa from refugia in the Middle East. This recent colonisation of West and Central Africa is also reflected by the fact that the West and Central African clade shows relatively little genetic diversity and is therefore thought to be an evolutionary young clade. In the view of these results and the generally small population size in West and Central Africa, we also hypothesize that within population diversity in West and Central Africa is more limited, compared to southern and East Africa, which may result in a higher risk of inbreeding depression. Currently, West and Central African lion populations are regionally threatened by habitat degradation, prey depletion, retaliatory killing and hunting.

For genotyping and phylogenetic purposes we plan to use Single Nucleotide Polymorphisms (SNPs) developed with next generation sequencing. The results of these techniques will provide answers about kinship, genetic differentiation and risk of inbreeding depression at the population level and about (sub)speciation and evolutionary history on the species level. Understanding the geographic pattern of genetic diversity is key to developing conservation strategies, both for in situ management as well as for breeding of captive stocks. Both for monitoring extinction risks of wild populations and

for zoo based captive breeding programmes, abundant genome wide estimators of genetic diversity at the individual level are of paramount importance and can be considered a major advance in conservation genetics.

#### **4. Assessing effective size, dispersal and origin of amphibian populations**

Pim Arntzen

Netherlands Centre for Biodiversity

Molecular genetic techniques are gradually being integrated into mainstream conservation research. My own work on European amphibians is focused on the assessment of amphibian dispersal as a function of the landscape. Direct field ecological approaches are tedious at best. I aim to show that genetic techniques are a straightforward alternative to assess patterns of dispersal with, as a by-product, information on the effective size and demographic history of populations. Data on dispersal and size can also be used to distinguish between natural and introduced populations.

#### **5. Genetic structure of the Dutch and global Black-tailed Godwit breeding population**

Krijn Trimbos

Leiden University

With 40% of the European Black-tailed Godwit population breeding in The Netherlands, this country harbours internationally significant numbers of this species. However, ongoing agricultural intensification has resulted in the fragmentation of the population and drastic population declines since 1967. Although, Black-tailed Godwit habitat is becoming ever more fragmented and habitat quality decreasing, this species shows high breeding site fidelity and some degree of natal philopatry. It was shown that 90% of the adult breeding birds returned within 700 m of the previous nest site. Natal philopatry was demonstrated to be high as well, with 75% of the birds returning within 18 km of their previous hatching site. With such limited dispersal in a fragmenting landscape, breeding areas could become isolated from each other. This might affect population dynamics, resulting in a metapopulation structure including source-sinks dynamics and isolation by distance. Here we describe gene flow indirectly by investigating genetic diversity and differentiation on a national scale covering breeding areas of the Dutch and global Black-tailed Godwit breeding population. Additionally, the population genetic structure of the Black-tailed Godwit breeding sites was assessed through genetic diversity, genetic differentiation and isolation by distance analysis.

#### **6. Poplar community genetics: identifying genomic regions associated with insect and rust damage in a segregating Populus family**

Marinus J.M. (René) Smulders, Jennifer DeWoody, Maud Viger, Gail Taylor, Katalin Tuba and Ferenc Lakatos

Wageningen UR

Forest trees are often keystone species, associated with large number of plant, animal, and fungal species. Genetic variation in leaf physical and chemical properties of forest trees is predicted to influence the extent of these community interactions, e.g. through palatability to herbivores. In order to identify genomic regions associated with susceptibility to insect and rust damage, parents and the progeny of a mapping population of poplars (*Populus trichocarpa* X *P. deltoides*, POP1) was analysed for seven types of leaf damage, namely due to chewers, skeletonisers, leaf miners, leaf galls, leaf rollers, sap suckers, and rust infection. Trees were scored in early (June) and late (August) summer, with greater levels of damage observed later in the season. Damage levels were highly variable between progeny trees, with little correlation between types of damage on individual trees. Damage levels were treated as quantitative traits in a QTL mapping approach. For the June data, one QTL was identified for skeletonisers and one for leaf miners. For the August data, between two and four QTLs were identified for each damage type, except for galls and leaf rollers, for which no QTLs were identified. Different QTLs were identified for skeletonisers and leaf miners for the June and August data, indicating potential facultative defence mechanisms being induced later in the season. Alternatively, the underlying insect species may have been different between these two time points. For the August data, QTLs for chewing and leaf mining damage types co-located in a single position, indicating this genomic region may contain genes related to damage or defence. A single QTL explained between 2.9% and 9.2% of the variance in the trait assessed. The distribution of QTL across the genome indicates the insect community may react to a large amount of genetic variation in this offspring of a species cross. These QTLs will be the basis of a bioinformatics study to identify potential chemical mechanisms underlying the variation in insect and rust damage in this hybrid population.



## **2d: A new era in Microbial Ecology**

**Conveners:** Laura Villanueva (Royal Netherlands Institute for Sea Research)  
Suzanne Haaijer (Radboud University)

### **1. Can the Microbial Ecology Blackbox be cracked open?**

Laura Villanueva

Royal Netherlands Institute for Sea Research

Microbial ecology is said to be driven (but also limited) by techniques. The field has come a long way over the past decade with respect to 'who is there?' and 'what are they doing?'. Although recent studies are using combined methodological approaches to unravel both diversity and physiology, the coupling between identity, function and dynamics of microbial communities remains the weakest point.

Microbial ecology is facing two big challenges: (1) Lack of conceptual and theoretical approaches that restrict our ability to predict the behavior of microbial communities and, (2) how to deal with sequencing datasets. The application and testing of ecological theory concepts in microbial ecology will allow the classification, interpretation and prediction of microbial ecosystems. However, quantitative information on the links between structure and activity is urgently needed. In addition, large-scale sequencing programs have resulted in a regression back to treating microbial communities as black boxes. To overcome this limitation, microbial ecologists should merge traditional methodologies with cutting edge omic approaches (return to the basics to move forward) and also perform functional verification of genes by physiological methods under controlled conditions.

Can the microbial ecology blackbox be cracked open? It will be only possible by further development and combination of existing approaches and by interdisciplinary research. The link between understanding and predicting a microbial ecosystem is the key in the new age of microbial ecology.

### **2. IS-pro: fully automated analysis of the human intestinal microbiota**

Dries E. Budding, M.E. Grasman, A.A. van Bodegraven and P.H.M. Savelkoul

VU University Medical Center

The human large intestine is one of the most densely populated microbial ecosystems on earth, with bacterial cell counts of up to  $10^{11}$  / gram luminal content. An especially intriguing feature of this ecosystem is its commensalism with the human host. It has been shown that the intestinal microbiota is strictly species specific, implying that host and microbiota have co-evolved for a long time. The relatively recent adoption of a modern 'westernized' lifestyle, coincides with a dramatic increase in a number of previously rare diseases, including inflammatory bowel disease, asthma, diabetes mellitus, rheumatoid arthritis, multiple sclerosis and others. Many of these diseases have now been shown to be characterized by an altered intestinal microbiota.

Analysis of the exact nature of the often complex changes in the intestinal microbiota may greatly enhance our understanding of the etiology of these diseases. Moreover, as these changes are often disease specific, analysis of fecal microbiota may be used as a non-invasive diagnostic tool. Currently however, the techniques employed for these analyses are typically expensive, laborious or both. This has restricted research in this field to small patient numbers and has prohibited implementation of microbiota analysis in clinical diagnostics.

Here we present IS-pro: an inexpensive and fast method for high-throughput analysis of the human intestinal microbiota which has been fully validated in silico, in vitro and in vivo in human samples [1]. The method combines species identification by 16S-23S interspace (IS) length with phylum identification by colour labelling of primers. The entire process of IS-pro consists of a single PCR followed by fragment analysis by capillary gel electrophoresis and automated analysis of digital profiles. For the automated analysis we developed a web-based software tool that first calibrates profiles and identifies peaks and then translates profiles into a list of bacterial species by means of a large library of IS sequence data that we built. An internal amplification control consisting of multiple DNA fragments of varying lengths is used for quality control of the PCR process over the entire range of fragment lengths. IS-pro is currently optimized for the human intestinal microbiota, but may easily be adapted for use in other microbial communities.

### **3. Influence of soil structure and matric potential on microbial interactions**

Alexandra B. Wolf, M. Vos and G.A. Kowalchuk

Netherlands Institute of Ecology

Soil is an extremely heterogeneous environment containing a mosaic of microhabitats, even at the very fine scale. Whether organisms inhabiting distinct microhabitats in soil can interact depends on how well these habitats are connected. In this study, we sought to examine how the connectivity between microhabitats can affect bacterial interactions.

We conducted a series of microcosm experiments introducing competing bacterial strains into artificial soils in which the connectivity was varied by the geometry of the pores and the matric potential. Results show that the competing strains could not coexist in an unstructured environment, yet could co-exist in a spatially structured environment, suggesting that isolation at the small-scale can affect the establishment and maintenance of soil-borne bacterial communities.

#### **4. Dinitrogen gas production by marine anammox bacteria**

Wouter Maalcke, Jia Yan, Wim Geerts, Marcel M.M. Kuypers, Susannah Tringe, Stephanie Malfatti, Jaap S. Sinninghe Damsté, Mike S.M. Jetten and Boran Kartal  
Radboud University

The earth's atmosphere is primarily composed of nitrogen (N<sub>2</sub>), an element essential to all life. One of the major biological sources of N<sub>2</sub> is anaerobic ammonium oxidizing (anammox) bacteria. These bacteria have been shown to be ubiquitous in oxygen minimum zones of many seas and oceans and they are responsible for a massive loss of fixed nitrogen. So far, the only anammox bacterium detected in the marine environment is a Planctomycete belonging to the genus *Scalindua*. A representative of this genus was successfully enriched after incubating a marine sediment sample in a continuous bioreactor with artificial sea water containing nitrite and ammonium. The enrichment culture has enabled detailed studies on the microbial and molecular basis of N<sub>2</sub> production by marine anammox bacteria. To assess the physiological versatility of *Scalindua*, several batch experiments and new cultures were started at different environmentally relevant conditions with respect to carbon, temperature and oxygen. DNA, RNA, lipids and proteins were extracted from the biomass and analyzed. High throughput 454 sequencing was employed to assemble the genome of the dominant anammox bacterium from the enrichment culture. Analysis of the genome and comparison to the transcriptome of the model anammox organism, *Kuenenia stuttgartiensis*, revealed that the most of the important anammox genes were also encoded by the enriched *Scalindua* species. Expression of these genes was confirmed by sequencing of total RNA via illumina technology and by analysis of total proteins via liquid chromatography coupled to tandem mass spectrometry. Analysis of the acquired data showed high expression of the genes involved in the central catabolism and carbon fixation. Isolation and characterization of the major nitrogen converting proteins of marine anammox bacteria have started.

#### **5. Interactions amongst marine archaeal and bacterial nitrifiers and anammox bacteria under oxygen limitation in a lab-scaled model system**

Jia Yan, Huub J.M. Op den Camp, Laura van Niftrik, David Stahl, Martin Könnecke, Darci Rush, Jaap S. S Damsté, Mike S.M. Jetten, Yong Y. Hu and Suzanne C.M. Haaijer  
Radboud University

Anaerobic ammonia oxidation is a newly discovered process, which may play an important role in the marine nitrogen cycle. In marine oxygen minimum zones (OMZs), the nitrite required for anammox bacteria needs to be provided by either partial nitrification (aerobic ammonia oxidation) or via partial denitrification (nitrate reduction). Since aerobic ammonia-oxidizing archaea (AOA) are highly abundant and co-exist with anammox bacteria in marine OMZs, it is possible that AOA rather than marine ammonia-oxidizing bacteria (AOB) may provide nitrite to marine anammox bacteria. In addition, AOA and AOB may have to compete for their substrates ammonium and oxygen. The present study explored the possibility of cooperation between marine anammox bacteria and nitrifiers as well as the competition between AOA and AOB under oxygen limitation and varying ammonium concentrations in a lab-scale model system.

A bioreactor containing marine anammox bacteria was supplemented with AOA (*Nitrosopumilus maritimus*) cells. Oxygen was carefully introduced to ensure growth of both the introduced and indigenous nitrifiers as well as oxygen limited conditions. A stable culture of AOA, AOB and anammox bacteria was established. Changes in activities of the different functional groups (AOA, AOB and anammox bacteria) were monitored by batch incubations and oxygen respiration measurements. Changes in the community composition were monitored by real-time qPCR of functional genes. Furthermore total RNA was extracted, reverse transcribed and the cDNA sequenced by Illumina technology. The culture was further characterized with respect to lipid content and cellular ultrastructure. Due to rapid oxygen consumption by AOA and AOB, anammox activity was not inhibited by the introduction of oxygen. Induced expression of ammonium uptake genes was observed for all community members which may be accounted for by the increased competition for ammonium under oxygen limitation. A C18[3] ladderane fatty acid became highly dominant in the *Scalindua* anammox bacteria-dominated culture, which was never observed before and may be caused by oxygen exposure. When the residual ammonium concentration was relatively high (more than 300  $\mu$ M), *amoA* gene copy numbers of indigenous AOB increased and were higher than those of the AOA, but as soon as the residual ammonium concentration decreased (less than 30  $\mu$ M), the *amoA* copy numbers of AOA increased. The community composition of the culture then remained quite stable with almost equal numbers of AOA and AOB *amoA* copy numbers. This observation was further confirmed by sequencing mRNA and inhibition activity analyses. As far as we know, this study

is the first direct proof that AOA can provide nitrite to anammox, and this AOA-associated CANON (Completely Autotrophic Nitrogen Removal Over Nitrite) system might be a new candidate in future treatment of polluted marine waters.

## **6. Anaerobic methane oxidation coupled to denitrification – a new link in carbon and nitrogen cycles**

Katharina F. Ettwig, Dorien Kool and Mike S.M. Jetten  
Radboud University

A major sink for methane, the second most important greenhouse gas, is its oxidation by micro-organisms. Methane is one of the least reactive organic molecules and due to the high activation energy required for its oxidation, only oxygen was thought to be a sufficiently strong electron acceptor. Therefore, anaerobic methane sinks have long remained unrecognized.

In recent years we have demonstrated that anaerobic methane oxidation can be coupled to the reduction of nitrite. Bacterial enrichment cultures carrying out this process could be obtained from several Dutch freshwater wetlands receiving high N-input. All cultures were dominated by bacteria of the uncultivated NC10 phylum. To obtain mechanistic insight into their pathway of methane oxidation, metagenomic analyses together with isotope labeling studies were conducted. They revealed that these bacteria, tentatively named '*Candidatus* Methylomirabilis oxyfera', oxidize methane by a unique biochemical mechanism: in the absence of extracellular oxygen, they produce their own oxygen from the reduction of nitrite, which is then used to drive the canonical aerobic enzyme pathway of methane oxidation to CO<sub>2</sub>.

The discovery of this new process may have important implication for our understanding of both the carbon and nitrogen cycle. *M. oxyfera*-like bacteria have been demonstrated to be present in diverse eutrophic freshwater systems, but little is known about estuarine and marine ecosystems, and their quantitative contribution to carbon and nitrogen cycling in the environment. We will present the current state of research and future perspectives on anaerobic methane oxidation coupled to denitrification.

## **Session 3**

### **3a: Plant Ecophysiology - Surviving in a heterogeneous world**

**Conveners:** Eric Visser (Radboud University)  
Liesje Mommer (Wageningen University)

#### **1. Within-species changes in traits between the native and introduced range of alien plants: a global scale comparison**

Alejandro Ordonez and Han Olff  
University of Groningen

Invasion biology has searched extensively for traits that predict invasiveness, mostly assuming that species express the same traits in their native and alien range. This trait conservatism assumption needs critical evaluation if we aim to predict which introduced species might become invasive. Using a global database of three key plant functional traits (specific leaf area, maximum possible canopy height and individual seed weight) we evaluated this assumption across maximally 162 different species. We show that plant traits are generally not different between the naturalized and the invasive range of the same species. This trait conservatism was consistent after controlling for environmental conditions, the phylogenetic relation between analyzed clades and when viewed in multidimensional trait space. We suggest that the observed trait conservatism originates from core ecological, physiological and genetic constraints. Our conclusions are important for the prediction and understanding of biological invasions from species traits across large numbers of species.

#### **2. Overwhelming root overproduction of *Plantago lanceolata* leads to unproportional above and belowground responses to competition**

Francisco M. Padilla, Liesje Mommer, Hannie de Caluwe, Annemiek E. Smit-Tiekstra, Cornelis A.M. Wagemaker and Hans de Kroon  
Radboud University

Plant species coexist in diverse communities in close vicinity, most frequently competing for essential soil nutrients. The consequences of this interspecific competition have traditionally been observed aboveground, but to date it is still unclear how aboveground responses are mirrored belowground. Here we report on a competition experiment carried out with one grass (*Festuca rubra*) and one dicot (*Plantago lanceolata*) with a belowground focus. We used the latest molecular technique to unravel species abundances in mixed root samples and looked at root growth patterns through minirhizotron tubes. We found a strong belowground response to interspecific when compared to intraspecific competition that was not foreseen nor proportional aboveground; 80% more root biomass was produced in mixtures than expected from monocultures, mostly driven by an overwhelming overproduction of roots of *P. lanceolata*, while no effects were found aboveground. Such root overproduction was detected immediately after plantation, and remained steady over 15 months until harvest. Species-specific root recognition processes seem to explain such an immediate increase in root investments of *P. lanceolata* rather than nutritional cues or soil biota. Overall, unveiling the link between root recognition processes and root overproduction may improve our knowledge on carbon budgets, plant community functioning and competition in biodiversity studies. Proper tools for quantifying root species abundances in biodiversity studies are becoming available, and their application is encouraged.

#### **3. Species-specific soil biota cause overyielding in diverse plant communities**

Marloes Hendriks, Liesje Mommer, Wim H. van der Putten and Hans de Kroon  
Radboud University

Plants growing in diverse plant communities produce more biomass than when growing in monocultures. It is suggested that this so-called overyielding can be caused by belowground niche differentiation. However, recent research of Mommer et al (2010) does not find too much evidence for this hypothesis. There are several alternative mechanisms that also can explain root overyielding, e.g. root responses due to species-specific nutrient depletion, plant-soil feedback caused by species-specific microbial communities or root exudates. The aim of my study is to investigate the mechanisms that cause overyielding in diverse plant communities. Therefore, we performed a plant-soil feedback experiment with four species on conditioned soil. In the second, the actual feedback phase of the experiment five different communities were grown (four monocultures and a 4 spp mixture) on the four monoculture soils and its 1:1:1:1 soil mixture. Also half of the soil was sterilized, resulting in a full-factorial design with five different plantings, five different soil types and two sterilization levels.

Our results suggest that overyielding in diverse plant communities is caused by interactions with species-specific soil biota. Competitive hierarchies were changed by the presence of specific soil biota. Competitive hierarchies were far less different among the five sterile soils, despite difference in their soil nutrient availability. We conclude that soil biota are important drivers for biodiversity and species coexistence in grasslands.

#### **4. The ecological relevance of auxin regulated shade avoidance response to neighbour proximity signals**

Diederik H. Keuskamp, Rens Vaessen, Laurentius A.C.J. Voesenek and Ronald Pierik  
Utrecht University

Plants grow in dense vegetations at the risk of being out-competed by neighbours. In order to increase their competitive power plants display adaptive responses such as rapid shoot elongation (shade avoidance) to consolidate light capture. These responses are induced upon detection of proximate neighbours through perception of the reduced ratio between red (R) and far-red (FR) light that is typical for dense vegetations. The plant hormone auxin is a central regulator of plant development and plasticity, but so far it was unknown how auxin transport is controlled to regulate shade avoidance responses. Here, we show that low R:FR detection changes the cellular location of the PIN-FORMED 3 protein, a regulator of auxin efflux, in Arabidopsis seedlings. As a result, auxin levels in the elongating hypocotyls are increased under low R:FR. Seedlings of the *pin3-3* mutant lack this low R:FR-induced increase of endogenous auxin in the hypocotyl and accordingly have no elongation response to low R:FR.

The adaptive significance of PIN3-mediated control of shade avoidance fitness is shown in plant competition studies. It was found that *pin3-3* mutants are out-competed by wild-type neighbours who suppress fitness of *pin3-3* by 40%. Interestingly, *pin3-3* had a delayed shade avoidance response compared to Col-0 in dense stands. These results do not only give convincing data on the ecological significance of the shade avoidance response of rosette plant species. The data also shows that timing of the response is evident to compete successfully against neighbouring plants.

#### **5. Regulation of branching in plants competing for light**

Jochem B. Evers, A.R. van der Krol and J. Vos  
Wageningen University

Shoot branching is a key determinant of overall aboveground plant form. During plant development, the number of branches formed strongly influences the amount of light absorbed by the plant, and thus the plant's competitive strength in terms of light capture in relation to neighbouring plants. Shoot branching is regulated by multiple internal factors which are modulated by different environmental signals.

A key environmental signal in the context of a plant population is a low red / far-red intensity ratio (R:FR) of the light reflected by neighbouring plants. Low R:FR results in suppression of branching in favour of elongation growth, which is a key aspect of shade avoidance. Shade avoidance enables plants to anticipate future competition by preventing being shaded, rather than to react to prevailing shade conditions. A low R:FR is indicative of surrounding vegetation, since red light is mainly absorbed by green plant parts, in contrast to far-red light which is mainly scattered.

Internally, shoot branching is regulated by a finely tuned plant hormone network, with key roles for the hormones auxin, cytokinin and strigolactone. The interactions within this network are modified by environmental cues such as R:FR which is perceived by specific photoreceptors. Combined, internal and external signals enable regulation of branch formation under environmental conditions of competitive growth.

The different aspects of shoot branching control (from R:FR via photoreceptors and hormonal regulation to plant form), act at different levels of biological organization (organ, whole plant, plant community). We show how these aspects can be integrated in one modelling approach. The methodology proposed here explicitly considers spatial 3D plant development, allowing it to incorporate the effects of plant structure on light environment and *vice versa*. In combination with dedicated experiments, this modelling tool can be used to analyse the response of plants to (imminent) competition, simulate the competitive advantage of shade avoidance for plants of different architecture, and predict plant form in various light environments. Examples will be shown for wheat (*Triticum aestivum*) and Arabidopsis (*Arabidopsis thaliana*).

#### **6. Competition for light compromises pathogen defense**

Mieke de Wit, Gabino Sanchez-Perez, Laurentius A.C.J. Voesenek and Ronald Pierik  
Utrecht University

Growth in high densities changes the light environment of plants, but also increases the risk of pathogen attack as plants in close proximity facilitate plant-plant infection and the enclosed atmosphere of a canopy forms a microclimate favorable for pathogens. How plants cope with having to compete for light and fend off a pathogen at the same time remains largely unknown.

Through physiological responses and gene expression studies in Arabidopsis thaliana we aim to gain insight into how well plants are able to respond to these two stresses simultaneously. We show that shade avoidance induction through light signals suppresses different defense pathways. Genome-wide gene expression studies are providing further insight into the mechanisms behind the interaction between shade avoidance and pathogen defense.

### **3b: Movement ecology of plants and animals: similarities and differences**

**Conveners:** Merel Soons (Utrecht University)  
Silke Bauer (Netherlands Institute of Ecology)

#### **1. Movement ecology of plants and animals: Similarities and differences**

Silke Bauer and Merel Soons  
Netherlands Institute of Ecology

Since the earliest times, humans have studied how organisms move. Naturalists and scientists have investigated plant and animal invasions, animal migrations, natal and breeding dispersal and foraging behavior. But until recently a common framework for the study of movement was lacking. In 2008, Nathan and colleagues introduced a generalized approach to the study of movement, the 'Movement ecology paradigm' (Nathan et al, PNAS, 2008). They proposed to analyze all movements considering the internal state of the organism (why move?), its motion (how to move?) and navigation abilities (when and where to move?), in relation to the external factors affecting these aspects of movement. Here, we take a closer look at the three stages of movement - departure, travelling, and settlement - from a Movement ecological perspective and identify important similarities between plants and animals. These organism groups are now usually studied separately by different researchers (plant or animal ecologists), while we may learn a lot from methods and techniques used by our colleagues!

As a case study, we discuss one question in greater detail - namely how organisms time departure. Specifically, we identify the cues, i.e. the internal and external information, that organisms use for an optimal departure 'decision' and compare them among various plant and animal groups. Although a variety of cues has been found, surprising similarities exist between the diverse organisms. Once the cues are known, we can also make predictions on their reliability under global changes and thus, the threat organisms may face to experience the consequences of mistiming.

#### **2. Lévy walks evolve through feedback between movement strategies and environmental complexity**

Monique de Jager  
Netherlands Institute of Ecology

Because adopting an efficient movement strategy is of importance for animals to increase their fitness, movement strategies should, from an evolutionary perspective, reflect the environment in which they are used. However, the fact that movement strategies also shape the environment is little acknowledged. Here, we show how the interaction between individual behavior and self-organized pattern formation can explain the evolution of Lévy walks. With experiments, we show that the movement type of mussels is best described by a Lévy walk. By means of models, we provide the explanation that employing movement strategies leads to pattern formation, which determines the fitness of these movement strategies and consequently leads to the evolution of Lévy walks. Our results exemplify that feedback between movement strategies and environmental structure can explain the emergence of spatial patterns via individual selection.

#### **3. Resource aggregation and density have direct and interactive effects on search performance of Lévy, correlated random and nested random walks**

Tom Huisman  
Wageningen University

An important topic in movement ecology is to determine which movement strategy optimizes search efficiency. So far, the performance of several random walks has been analysed in varying resource densities, but a systematic analysis of the effect of variation in the degree of resource aggregation is lacking. To address this we simulated searches by three random search strategies, namely correlated random, nested random and Lévy walks.

Firstly, our results show that resource density, resource aggregation as well as the interaction between density and aggregation determine the search performance of the random walks. Random distributions favour higher directionality, and increased aggregation more extended local searches. In random or nearly random distributions the optimal random strategy for animals is to use a correlated random walk. As resource aggregation increases, the optimal random search strategy becomes a Lévy walk, and at highest resource aggregation levels a nested random walk becomes optimal.

Secondly, the simulations show that random searches employed by animals each have their own region of optimality. This provides an explanation for the variety of observed movement patterns. The contradicting evidence for species 'doing the Lévy walk' may be explained by the fact that the optimality of Lévy walks is limited to specific levels of density and aggregation. Furthermore, the fact that many species seem to be employing correlated random walks is explained since they are, despite their inefficiency in highly aggregated distributions, actually optimal across a range of aggregation, depending on density. Similarly evidence indicating that species use nested or multi-scaled searches may mean that their resources are more highly aggregated or at very low densities.

We conclude that in order to formulate optimal strategies as basic hypothesis for movement patterns in nature it is necessary to include both aggregation and density in the analysis. Furthermore the interactive effect of aggregation and density necessitates knowledge on movement behaviour and resource density and aggregation in order to understand or the effects of habitat changes.

#### **4. Modelling dispersal of wetland plant seeds by wind and water**

Hester Soomers, D. Karssenbergh, M.B. Soons, P.A. Verweij, J.T.A. Verhoeven and M.J. Wassen  
Utrecht University

Over the last decades, landscape modification has led to habitat fragmentation for many species. Therefore, knowledge on mechanisms that determine the dispersal range of plant seeds is of vital importance for determining promising ways to restore biodiversity.

In wetlands, surface water is an important vector for dispersal. In Western Europe, drainage ditches are ubiquitous in former wetlands that are reclaimed and now used as farmland. The banks of these ditches serve as refuges for many wetland plant species. As these species produce highly buoyant seeds, drainage ditches may also function as dispersal corridors between isolated fen nature reserves. Because of the relatively low rate of flow in ditches, the results of studies on hydrochory (i.e. dispersal by surface water) in rivers cannot be extrapolated to drainage ditches. Apart from hydrochory, also anemochory (i.e. dispersal by wind) plays a role in dispersing seeds of wetland species. Until now, no models exist in which both dispersal mechanisms are included.

We developed a coupled spatial anemochory-hydrochory model for reclaimed wetlands with drainage ditches. Terminal velocity experiments and seed release and retrace experiments were performed to parameterise the model. With this model, we assess the relative importance of wind and water as dispersal vectors for four wetland plant species differing in seed characteristics, and for different landscape configurations. Results give insight into dispersal ranges of wetland plant seeds, the relative contribution of wind and water to these ranges and seed exchange between habitat patches.

#### **5. Spring migration timing of arctic-breeding geese**

Andrea Kölzsch, Rien E. van Wijk, Helmut Kruckenberg, Barwolt S. Ebbinge, Gerhard J.D.M. Müskens, Henk P. van der Jeugd, Klaus-Michael Exo, Marc Naguib, Johan van de Koppel and Bart A. Nolet  
Netherlands Institute of Ecology

Geese breeding in the high arctic have a very tight schedule at their breeding sites. Therefore, arriving at the right time and in good condition in spring is essential. Several studies indicate that herbivores, like geese, follow the flush of plant growth during spring migration in order to acquire the most nutrient-rich plants on the way. Unlike previous work, we tested this so-called green wave hypothesis at the level of the individual animal using GPS data of Western Palearctic greater white-fronted geese (*Anser albifrons albifrons*). Furthermore, we compared their habitat preferences for spring stopover sites with those of barnacle geese (*Branta leucopsis*), which have earlier been shown to follow the green wave.

Using 13 complete spring migration tracks, we related the dates of arrival at each stopover site to cumulative temperature (Growing Degree Days, GDD), snow cover, photoperiod accumulation and latitude. We found that geese arrived at spring stopovers at the peak of GDD jerk (i.e. temperature acceleration), an index of the very start of spring growth, with breeders seen to track the GDD jerk maxima more closely than non-breeders.

Barnacle geese also seem to follow the green wave and use wintering and breeding grounds that widely overlap with those of white-fronted geese. However, they greatly differ in their spring migration movement strategy. Comparing the GPS tracks of the white-fronted geese with 11 spring migration GPS tracks of barnacle geese, we show that differences in foraging preferences relate to the routes and stopover selection of the two species.

#### **6. Using species' life-history traits to design restoration measures for fragmented habitats**

Toos van Noordwijk  
Radboud University

Many natural habitats have become increasingly small and isolated. Research confirms that habitat isolation is currently one of the main threats to characteristic plant and animal species in many of these habitats. To be able to design effective measures to tackle this threat it is important to understand the dispersal mechanisms of different taxonomic groups and their limitations. Studying life-history traits related to locomotion and dispersal behaviour both at the individual and the population level gives insight in the ability of species to (re-) colonise sites. Comparing these mechanisms within and between taxonomic groups highlights the importance of spatial scale. Chalk grasslands in the Netherlands are taken as a case study to demonstrate how the analysis of species traits can be used to design effective restoration measures to counter dispersal bottlenecks for different taxonomic groups.

### **3c: From water to land; ecology across borders**

**Conveners:** Judith Sameel (Netherlands Institute of Ecology)  
Liesbeth Bakker (Netherlands Institute of Ecology)

#### **1. Plant growing from water to land: disentangling the factors that impede terrestrialization in fens.**

Judith Sameel, M.B. Soons, J.J.M. Geurts, B. Beltman and J.T.A. Verhoeven  
Netherlands Institute of Ecology

The natural succession in fens, in which plants growing on the bank colonize the open water, is called terrestrialization. In Dutch fens, this process is hampered by multiple causes, of which some may be more important than others. We performed a large-scale field study on 62 fen ponds, to investigate the relative importance of 1) the deterioration of water and peat quality, 2) habitat fragmentation and 3) changes in biotic interactions (i.e. with the invasive muskrat and the declining keystone species *Stratiotes aloides*). *Phragmites* and *Typha* most frequently colonized the ponds over large distances. A factor analysis showed that regional differences influence both the expansion into open water (colonization) and the species richness of the bank. Plants expanded further into open water and banks were more species-rich in areas with older ponds and lower muskrat densities. Colonization was also related to local factors, most importantly water turbidity and depth. Whenever the water was clear, colonization was higher in shallow ponds and in deep ponds if *Stratiotes* was present. Species richness of the bank was negatively correlated to nutrient availability of the bank soil and positively to hydrological isolation, which decreased sulphate concentrations. Dispersal limitations seemed to be overruled by habitat limitations as colonization often failed even though propagule sources were present or connectivity was high.

This study shows that the colonization process is influenced by the quality of both water and land, and restoration should aim at increasing the quality of both, e.g. sod cutting & hydrological isolation

#### **2. Major shifts in trophic structure along a salt marsh succession: a stable isotope approach**

Maarten Schrama  
University of Groningen

Food web ecology primarily focuses at finding generalities within food webs. Only recently it was argued that spatial and temporal variation should be explicitly taken into account when studying food web dynamics. In this talk I focus on how some key properties of a terrestrial food web change over successional time, explicitly taking into account the links with the marine food web.

It was hypothesized that 1) over succession, the terrestrial food web becomes more independent of the marine web. From a relatively open system, it will become more of a closed system in which nutrients are recycled locally and 2) Different energy channels in the food web show different dynamics over succession. Over succession, detritivores are sustained by a number of different food sources whereas the herbivore channel is fuelled by a different basal resource.

Our results show that our focal food web is externally driven in early succession and becomes progressively independent of marine input towards late succession. Over succession,  $\delta C^{13}$  levels of detritivores and carnivores show strong decreases where plants and herbivores show no change. Also  $\delta N^{15}$  levels are high in early succession indicating high trophic material being deposited in these stages. Both results indicate that the early successional stages are fuelled by high trophic marine material while late successional stages rely on internal recycling for nutrients. We conclude by saying that studying a successional sequence provides an entirely different view on food web dynamics as it illustrates the intertwined character of an early successional food web, progressively changing into a self-sustained system where all trophic groups obtain their resources from a local environment. We suggest that the general patterns from our findings represents a general pattern for succession of food webs in terrestrial systems.

#### **3. Impact of waterlevel and management on the establishment of plant species in a peatland**

Wout Opdekamp  
University of Antwerp

We analysed the relative importance of waterlogging, light stress induced by canopy and temporal relief of the latter on seedling establishment in a mesocosm experiment (80 containers, 1m<sup>2</sup>) with 35 species, which occur frequently in floodplains of temperate Europe and represent the whole moisture gradient from mesic meadows to reedbeds and swamps. We interpret the results in terms of functional traits of seedlings. There was no establishment at low light levels. Temporal relief of light stress through mowing enabled very limited recruitment, this in contrast to high establishment rates in full light.

Under full light, waterlogging did not hamper recruitment but lowered biomass and decreased competition between seedlings. Establishment in non-waterlogged – full light conditions depended on



seedling size and traits related to germination success and rate. The poor performance of typical wetlands species regarding these traits explains their exclusion from the oxic treatment.

During the second and third year of the experiment the link between species composition and seedling traits remained high, stressing the importance of the seedling establishment phase in determining vegetation composition in floodplains.

#### **4. Interacting effects of sulphate pollution in the surface water and eutrophication of the bank on vegetation development in fens: a mesocosm experiment**

Jeroen J.M. Geurts, J.M. Sarneel, B.J.C. Willers, J.G.M. Roelofs, J.T.A. Verhoeven, L.P.M. Lamers  
Radboud University

In recent decades, both increased agricultural fertilization and the use of polluted river water to compensate for water shortage have, directly or indirectly, led to a higher nutrient availability, sulphate pollution and formation of potentially toxic compounds. As a result, many characteristic plant species have disappeared and outcompeted by a few fast-growing species, leading to a strong decrease in biodiversity, vegetation development and terrestrialization. Therefore, we investigated the effects of sulphate pollution and eutrophication of the bank or the surface water in outdoor fen mesocosms using aquatic and semi-aquatic macrophytes with different growth strategies.

Fertilization led to higher nutrient concentrations, litter production and decomposition, whereas sulphate addition to the surface water increased alkalinity and concentrations of sulphide, sulphate and humic acids in both the water and the peat bank. In the long term, nutrient concentrations became also highest in the sulphate treatments. Biomass production of aquatic and semi-aquatic macrophytes was higher after fertilization, and colonization of the water by semi-aquatic macrophytes increased. Sulphate pollution led to toxic sulphide levels, which reduced both biomass production and colonization considerably. However, macrophytes in the fertilized treatments were less vulnerable to sulphide toxicity.

This mesocosm experiment clearly shows that competition between species, vegetation succession and terrestrialization are not only influenced by nutrient availability, but also by sulphate pollution, which strongly interacts with the level of eutrophication. It is, therefore, important for the restoration of biodiversity and terrestrialization in fens that not only nutrient loads, but also sulphate pollution will be reduced.

#### **5. Biodiversity in small farmland ponds: multigroup congruency and associations with land use practices at multiple spatial scales**

Steven Declerck  
Netherlands Institute of Ecology

Intensive agricultural land use may have serious adverse effects on the ecological integrity and biodiversity of freshwater ponds. Land use can affect pond biodiversity through a variety of mechanisms at both local and regional scales. Furthermore, the magnitude and nature of the effects may strongly vary among different types of aquatic organisms. We will present the results of a large scale field survey and evaluate the effects of land use on 12 different groups of pond organisms. Our results indicate that local crop land and forest affect the ecological quality of ponds as well as the community composition of at least four organism groups. We were not able to demonstrate any large scale effects of crop land and forest on pond ecological quality. Our analyses, nevertheless, provide evidence for strong large scale land use effects on the community structure of at least six organism groups. We infer from our results that the preponderance of such large scale land use effects is most probably generated by effects on regional species composition which then feed back to local pond communities through metacommunity dynamics.

#### **6. Vertebrate herbivores: drivers of alternative stable or transient states? Comparing lakes and boreal forests**

Bert Hidding  
Université Laval, Canada

The idea that communities or ecosystems may exhibit two alternative equilibria at a given set of abiotic conditions finds application in a variety of ecosystems, most notably shallow lakes. Lakes may switch between vegetated clear water and turbid water devoid of aquatic plants. Avian herbivores have been proposed to be possible drivers of shifts between these states.

In forest ecology, research has focussed on ungulate herbivores as possible drivers of shifts in ecosystems. Herbivory in boreal forests may lead to dominance of browse resistant graminoids that can inhibit the establishment of woody species, whereas a forest canopy may inhibit the establishment of graminoids.

Although boreal forests and shallow lakes exhibit vastly different dynamics, one important question is the same. Are these different ecosystem states really stable or are they a temporary (transient) result of herbivore disturbance? Here, I discuss this question using experimental results from both shallow aquatic systems and the boreal forest.

### **3d: Free Session**

**Convener:** Claudius van de Vijver (Wageningen University)

#### **1. Importance of olfactory cues from host larvae and cowpea flowers in the host foraging by *Apanteles taragamae* Viereck, a larval parasitoid of the cowpea pod borer *Maruca vitrata* Fabricius**

Elie A. Dannon, Manuele Tamò, Arnold van Huis and Marcel Dicke  
Wageningen University / International Institute of Tropical Agriculture

The parasitoid wasp *Apanteles taragamae* is a promising candidate for the biological control of the legume pod borer *Maruca vitrata*. The effects of volatiles from cowpea and peabush flowers, and *M. vitrata* larvae on the host selection behaviour of *A. taragamae* were investigated under laboratory conditions using a Y-tube olfactometer. Female wasps were given a choice between several odour sources including (1) uninfested, (2) *Maruca vitrata*-infested, and (3) mechanically damaged cowpea flowers, as well as (4) stem portions of peabush plants carrying leaves and flowers, and (5) *M. vitrata* larvae. The parasitoid displayed a preference for volatiles from host-damaged flowers. It strongly discriminated between *M. vitrata*-induced floral volatiles and uninfested or mechanically damaged flowers. Female wasps were not attracted to uninfested cowpea flowers, but this behaviour changed when they got an odour experience. The attraction of *A. taragamae* to uninfested peabush leaves and flowers may be a reflection of a genetic trait related to searching in peabush fields. This study also showed the importance of olfactory cues from host larvae in the host selection process of the parasitoid.

#### **2. Restricted recruitment of forest herb layer plants in post-agricultural forests: can tree species help?**

Arno Thomaes, A. De Schrijver and K. Verheyen  
Research Institute for Nature and Forest (INBO), Belgium

In western Europe the ancient forest has diminished dramatically. Restoration of natural forests is limited due to unsuccessful colonization and recruitment of ancient woodland plant species. Colonizing plants are confronted with a strongly modified environment due to historic fertilisation and changing conditions during the afforestation process.

We hypothesized that colonisation chances of ancient woodland species could be optimised by selecting the right tree species. The tree species planted can be considered as an ecosystem engineer affecting environmental factors of importance for the herb layer like light, litter layer and soil. We explored a chronosequence study of first generation Oak (*Quercus robur*) and Poplar (*Populus x euramericana*) forests in post-agricultural forests on acidification sensitive soils.

Our chronosequence study revealed a declining soil-pH true time under Oak compared to a stable soil-pH under Poplar. Plant available phosphor declines over time but is also dependent of pH.

Many of the indicator species for Poplar are associated with the *Arrhenaterion*, while Oak didn't have any indicator species. Only a few forest species were nearly significantly associated with one of the trees, where *Hedera helix*, *Stachys sylvatica*, *Adoxa moschatellina* are found to have some association with Poplar and *Athyrium filix-femina* with Oak.

The cover of the understory is affected by the tree species and age. Under poplar a highly abundant herb layer is found further depending on the presence of a shrub layer. Under the oaks the understory is out shaded very soon after planting and restores only slowly after 20y. Furthermore herb layer cover and Ellenberg value for light is influenced by isolation of the studied forest indicating that the ecological niche of the herb layer remains unfilled in dark isolated forest. Number of forest species are mainly influenced by time since afforestation, only forest edge species are linked to Poplar forests while the cover of ancient and true forest species is higher under Oak.

We conclude that tree species clearly affects the herb layer restoration of forest habitat where light and soil pH seem to be driving environmental factors for forest ecosystem restoration on acidification-sensitive soils.

#### **3. Tree species identity drives responses of dipteran communities to tree and herb diversity**

Elke Vockenhuber, Teja Tschardt and Christoph Scherber  
University of Göttingen

Plant diversity can strongly influence the diversity of associated insect communities. In contrast to grasslands, little is known about this relationship in forest ecosystems. Both herb and tree layer diversity potentially affect insect diversity by changing resource heterogeneity or structural complexity of the habitat. However, not only plant diversity, but also plant cover might be an important driver of insect diversity.

Here we investigate how Dipteran species richness and abundance change along tree and herb diversity gradients in forest stands of the Hainich National Park (Thuringia, Germany), one of the

largest continuous stretches of broad-leaved deciduous forest in Central Europe. Diptera form an ecologically diverse and highly abundant insect taxon that is often overlooked in biodiversity studies. We combined pan traps and suction sampling to estimate Dipteran species richness and abundance.

We found that both tree and herb diversity influenced Dipteran abundance, with herb layer diversity showing a more pronounced effect. However, the direction of the relationship depended on the dominant tree species: In forest stands dominated by *Tilia* spp., tree and herb layer diversity had a positive effect on Dipteran abundance, whereas the effect was negative in stands dominated by *Fagus sylvatica*. In contrast, Dipteran family richness did not respond to tree or herb layer diversity. Herb cover had a consistently positive effect on both Dipteran family richness and abundance. Abundance of the dominant Dipteran taxon Empidoidea was affected by herb layer diversity only.

Our results indicate that plant diversity, particularly of the herb layer, does influence abundance patterns of Diptera; however, plant cover, a measure of biomass, appears to play a much greater role in driving Dipteran species richness and abundance. Also, species identity of dominant tree species has to be taken into account when studying relationships between plant diversity and insect communities in forests.

#### **4. Turning northern peatlands upside down: disentangling microclimate and substrate quality effects on vertical distribution of collembola.**

Eva Krab

Vrije Universiteit

Although direct contributions of soil invertebrates to carbon turnover are modest, they have a disproportionately large indirect impact through their control over the activity of microbial decomposers. Shifts in soil invertebrate species distribution might have a substantial effect on the decomposition process because their functional role depends on the species' vertical position in soils. Gradients in microclimate and substrate quality and structure largely determine the vertical position of soil invertebrates. Because of the possible impact of climate change on soil invertebrate distribution, and consequently on decomposition, it is important to know the relative contributions of microclimate and substrate quality to the vertical distribution patterns of soil invertebrates.

We studied this for springtails (Collembola) as a keystone group in cool and cold biomes, by turning peat cores in a subarctic blanket bog upside down, thereby reversing the substrate quality gradient and leaving temperature and moisture gradients intact.

Two opposing groups of springtail species could be distinguished with respect to their abundance responses along the vertical gradient: (i) species that remain associated with the stratum they were originally found in ('stayers') and (ii) species that re-establish the original stratification pattern, by remigration either to the top or deeper layers, irrespective of any substrate quality change ('movers'). Within the 'mover' response pattern, the direction of their migration in response to microclimate changes seemed to coincide with their ecomorphological traits. Our results not only demonstrate that springtail species differ in their responses to change in climate or substrate quality; they also suggest that interspecific faunal trait variation may provide a useful tool to predict animal responses to climatic changes.

#### **5. Direct and indirect impacts of hemiparasitic plants on community structure and biogeochemical cycling in semi-natural grasslands**

Andreas Demey, E. Ameloot, P. Boeckx, M. Hermy and K. Verheyen

Ghent University

Parasitic angiosperms are represented in the majority of ecosystems worldwide and are most characteristic for disturbed areas such as grasslands. In contrast to holoparasites, hemiparasites only partially depend on their hosts for the supply of carbon compounds, nutrients and water. Parasitic plants may affect population dynamics, community structure and plant diversity, and therefore can be considered keystone species or ecosystem engineers. Two main mechanisms can be distinguished: (1) direct 'parasite effects' on the host community and (2) indirect 'litter effects' through the redistribution of nutrients in the ecosystem. (1) Hemiparasitic infection directly reduces host and total aboveground biomass production. If a host preference exists for dominant graminoids, hemiparasitic infection can alter the competitive balance in favour of forbs. This reduced competition may in turn increase species richness and accelerate the restoration of species-rich grasslands. (2) Most hemiparasites shed their leaves or die of early in the season and produce high quality litter that mineralizes faster. This can enhance nutrient cycling and could indirectly reduce species richness when higher nutrient availability favours competitive species. We hypothesize that (1) direct, structural effects will dominate in more nutrient-rich grasslands and (2) that indirect, biogeochemical effects will dominate in more nutrient-poor grasslands. Here we study the response of aboveground biomass to a weeding treatment. Furthermore, we determine biomass and nitrogen (N) stocks for two hemiparasites of contrasting semi-natural grassland types and evaluate in this context the importance (quantity and quality) of hemiparasite litter.

## **6. Genotype x temperature interactions support the maintenance of clonal diversity in diatom blooms**

Alena Gsell

Netherlands Institute of Ecology

Marine and freshwater phytoplankton populations often show large clonal diversity and distinct biogeographical distributions, which may seem surprising given a seemingly ubiquitous dispersal. Fluctuating selection in heterogeneous environments is a leading explanation for maintenance of genetic diversity. Reaction norms experiments showing genotype by environment (GxE) interactions have been used to demonstrate how a variable environment may boost diversity. So far however, mostly genotypes of spatial or temporal distant origins have been tested to explore local adaptation. In contrast, we report here a large genetic diversity of the diatom *Asterionella formosa* from a population in a solitary, isolated lake. GxE interactions of clonal genotypes originating from a single diatom springbloom water-sample were demonstrated experimentally. Non parallel, even crossing thermal reaction norms were found for *Asterionella* growth-rate as measure of inclusive fitness and several morphological characteristics across an environmentally relevant range of temperatures. Significant GxE interactions for clones inhabiting a diurnally and seasonally variable environment indicate that no genotype can outperform all others at all times or places. A trait based ranking order of genotypes could not be predicted from one temperature to another. This suggests that GxE interactions contribute to the maintenance of diversity in isolated populations of clonally reproducing microorganisms.

## **Session 4**

### **4a: Multitrophic interactions and Food webs**

**Conveners:** Peter de Ruiter (Wageningen University)  
Sanne de Visser (University of Groningen)

#### **1. Robustness analyses of the Serengeti food web: theoretical versus realistic extinction scenarios**

Sanne de Visser, Bernd P. Freyermann and Han Olff  
University of Groningen

Human overexploitation and land-use changes affect species composition, diversity and ecosystem functioning. Theoretical studies model how network properties change under human-induced, non-random species loss, using extinction sequences based on body size or connectance. However, we lack data on realistic species-loss sequences in threatened, real-world food webs to parameterize these models.

Using the size-structured topological food web of one of the most pristine terrestrial ecosystems in the world, the Serengeti (Tanzania), we study the topological changes in this food web that result from the simulated IUCN-based species-loss sequence representing current realistic species vulnerability to human disturbances in and around this savanna ecosystem. We then compare the realistic extinction scenario with theoretical-based extinction scenarios and perform an analysis of robustness of this savanna food web. Unlike theoretically modelled linear species deletion sequences, the realistic extinction scenario causes poor-connected species to be lost first, while more highly connected species become lost as human impact progresses. The robustness analysis shows that the Serengeti food web is highly sensitive to the decreasing connectance deletion scenario.

#### **2. Food-safety trade-off on intertidal flats**

Ellen Weerman  
University of Groningen

Bivalve species of intertidal flats occur along a gradient of inundation time, which makes them face a trade-off for food and safety. Near the salt marsh up-shore, inundation time is low and increases from there towards the deeper gullies, which are permanently submerged. Along this spatial gradient of inundation time bivalves feed by filtering the pelagic algae from the overlaying water column. Bivalves can only feed while submerged, therefore their food availability increases towards the gully. However, this high food availability has also disadvantages since bivalves can be easily eaten by predators, like crustaceans and flatfish, during high water. Conversely, shore birds can enter the intertidal flat and feed on bivalves during low water. This results in a trade-off for bivalves for food and safety along a spatial gradient of inundation time. We investigated this trade-off by analyzing a longterm dataset of predator abundances. In addition we carried out a field experiment on the tidal flats of Schiermonnikoog. In these experiments we tested the interactive role of predation and inundation time on cockle (*Cerastoderma edulis*) abundances. Since each predator prefers a different size of cockle we transplanted both juvenile (<5mm) and adult (>30mm) cockles in separate patches to test the effect of predation and inundation time. Analysis of these experiments showed that the interactive effects of predation and inundation time affected cockle densities. The combined results from the longterm dataset analysis and our field experiment suggest that a food-safety trade off in bivalves is likely to have caused a spatial gradient shift in bivalve abundances on the intertidal flats.

#### **3. The evolution and coexistence of generalist and specialist herbivores under between-plant competition.**

Ellen van Velzen  
University of Groningen

Consumer-resource (predator-prey, herbivore-plant) models have been used extensively to study the evolution and coexistence of generalist and specialist consumers on  $n$  resources. However, current consumer-resource models do not take into account competition between resources. We adapted a standard two-plant model, and used a combination of simulations and Adaptive Dynamics to study the evolution of herbivores under between-plant competition. Competition was included in the model by giving the system a fixed total pool of nutrients, over which plants compete for growth – a more realistic replacement for the more conventional logistic growth function. We find a total of seven different outcomes, depending on the strength of the herbivore trade-off. Four of these have not been found in previous models, and are a result of the more complex interactions between ecological dynamics and herbivore evolution in our model.

#### **4. Population dynamics of a phytoflagellate eating its toxic competitor**

Susanne Wilken, Suzanne Naus-Wiezer, Ellen Van Donk and Jef Huisman  
Netherlands Institute of Ecology / University of Amsterdam

We investigated a nitrogen limited food web consisting of the mixotrophic flagellate *Ochromonas* sp. preying on the toxic cyanobacterium *Microcystis aeruginosa*. Because the mixotroph cannot use nitrate directly, the system resembles an ordinary predator prey system when nitrate is the only nitrogen source present. When ammonium is offered instead the mixotroph is also competing for dissolved nitrogen with its prey and therefore acts as an intraguild predator. The population dynamics of these two food web structures were compared in chemostat experiments at three levels of enrichment. We furthermore investigated the role of the toxic microcystins produced by *M. aeruginosa* in the interaction of these two organisms in batch experiments.

The mixotroph profited most from the presence of ammonium at low nitrogen concentrations using ammonium and the prey as substitutable nitrogen sources. However, it did not reduce its prey to lower densities for high levels of enrichment as expected from intraguild predation theory. We suggest an induced defense in *M. aeruginosa* to explain this deviation from theoretical expectations. Since the mixotroph showed very similar functional and numerical responses on the microcystin-producing strain *M. aeruginosa* PCC7806 and its microcystin-deficient mutant and grazing by the flagellate did not induce an increased microcystin production in *M. aeruginosa*, a possible induced defense would most likely be caused by peptides other than microcystins.

#### **5. The temporal dynamics of interaction networks: the role of resource switching, adaptive morphological traits and diversification**

Jofre Carnicer, Pedro Jordano, Peter Abrams and Carlos J. Melián  
University of Groningen

Ecological networks patterns are influenced by a diverse array of ecological processes that operate at different temporal scales. Here we analyzed if the coupled effect of local abundance variation, seasonally phenotypic plastic responses and species evolutionary adaptations might act in concert to shape network patterns. We studied the temporal variation in three interaction properties of bird species (number of interactions per species, interaction strength and asymmetry) in a temporal sequence of 28 plant-frugivore interaction networks spanning two years in a Mediterranean scrub community. Three main hypotheses dealing with the temporal variation of networks properties were tested, examining the effects of abundance, switching behaviour between alternative resources and morphological traits in determining consumer interaction patterns. Our results demonstrate that temporal variation in consumer interaction patterns is explained by short-term variation in resource and bird abundances and seasonal dietary switches between alternative resources (fleshy fruits and insects). Moreover, differences in beak morphology are associated with differences in switching behaviour between resources, suggesting an important role of foraging adaptations in determining network patterns. We argue that beak shape adaptations might determine generalist and specialist feeding behaviours and thus the positions of consumer species within the network. In line with these results, theoretical models show that behavioral switching between two alternative resources can enhance species coexistence and increase adaptive trait diversification (beak shape). Finally, we provide a preliminary framework to interpret phylogenetic signal in plant-animal networks. Indeed, we show that the strength of the phylogenetic signal in networks depends on the relative importance of abundance, behavioural and morphological variables. We show that these variables strongly differ in their phylogenetic conservatism. Consequently, we suggest that moderate and significant phylogenetic effects should be commonly observed in networks.

#### **6. Lovely ladybirds under attack: does the exotic species win?**

Lidwien Raak-van den Berg and Marieke de Lange  
Wageningen University

The multi-coloured Asian ladybird (*Harmonia axyridis*), an invasive species from Asia, has been very successful in establishing populations in the Europe. Following its establishment, population densities of native coccinellids have decreased. Most ladybird species exhibit intra guild predation (IGP) when the preferred food source (aphids) is scarce. Laboratory experiments have shown that *H. axyridis* often outcompetes native species. Is this also the case when studied under more natural circumstances, when escape mechanisms can be used?

In a semi-field setup the interaction between 4<sup>th</sup> instar larvae of 3 ladybird species was tested (*H. axyridis*, *Coccinella septempunctata*, *Adalia bipunctata*) on 2-year old lime trees (*Tilia platyphyllos*). Two experiments were performed to answer the following questions: 1) How often do two larvae come into contact? 2) What happens when they make contact? 3) Which species wins the interaction?

In the first experiment two larvae were positioned on two different leaves of one tree. During 3 hours the position of each larva in the tree was observed, and when contact was made, the outcome of the interaction was observed. The second experiment was performed on one leaf of the tree, two larvae

were positioned on the same leaf and continuous observations were made on the behaviour of both larvae during max. 1000 seconds.

Results of exp. 1 show that larvae are rarely present on the same leaf. When the larvae are directly placed on the same leaf (exp. 2) the number of replicates in which the larvae come into contact ranges from 23 % for the combination *C. septempunctata* – *A. bipunctata* to 42 % for the combination *H. axyridis* - *H.axyridis*. The three species differ in their behaviour. *C. septempunctata* is most prone to drop from the leaf. When contact was made, *H. axyridis* most often started an attack, and most often this attack resulted in predation. In response to contact, escape behaviour could be either by dropping from the leave, or running away. Interestingly, *A. bipunctata* managed to escape from predation several times after being attacked by *H. axyridis*.

Our results show that under more natural conditions, contacts are less frequently observed than in laboratory experiments. When contact is made between two larvae, the exotic species *H. axyridis* shows more aggressive behaviour and most often continues to predate the other larva. This strong IGP behaviour is one of the explanations of the successful invasion of this exotic species in the Netherlands.

#### **4b: Species Distribution Modelling**

**Conveners:** Thomas Groen (University of Twente)  
Sabrina Carvalho (University of Twente /Netherlands Institute of Ecology)  
Henjo de Knegt (Wageningen University)

##### **1. Species distribution modelling: objectives, challenges and terminology**

Thomas Groen

University of Twente

Species distribution models (SDMs) are numerical tools that relate species abundance to environmental variables. As such, they are used to gain ecological insights and to predict distributions across landscapes, making SDMs applicable for conservation planning. Recent developments in GPS and other technologies enable detailed tracking of organisms concurrently with acquisition of landscape data from satellite systems at ever-increasing spatial-temporal resolutions. This requires the integration of statistics, geo-information, remote-sensing and ecology for SDMs to be valuable. In this introductory talk, I will highlight the general objectives of SDMs, as well as some key methodological challenges that remain. Furthermore, I will give an overview of the used terminology, as different disciplines use different terms so that there are many synonyms.

##### **2. From herbarium collections to patterns of biodiversity, endemism and phylogeography - A Bornean case study**

Niels Raes, Emiel van Loon, Ferry Slik, Hans ter Steege, Marco Roos and Pieter Baas  
NCB Naturalis / Leiden University

Although it is widely recognized that Borneo harbours one of the world's most important biodiversity hotspots, the spatial patterns of botanical richness, endemism, the 'centres of endemism', and Borneo's floristic regions, have largely been based on informal expert opinion until now. Recent digitization of the botanical collections of Borneo, housed at the NCB Naturalis, has provided us with a database that allowed a quantitative, spatial analysis of the components of botanical diversity of Borneo.

We developed species distribution models (SDMs) for species treated in 'Flora Malesiana' and represented by at least five unique records. The 2273 SDMs were statistically tested against a null-model, resulting in 1439 significant models (63.3%), covering 8577 grid cells (5 arc-minute resolution ~ 100 km<sup>2</sup>) of Borneo. The 1439 significant SDMs were combined to generate patterns of botanical richness and endemism. We constructed a presence/absence matrix, which was analysed with a hierarchical cluster analysis. The resulting cluster dendrogram was pruned using indicator species analysis (ISA) and partitioned into eleven floristic regions.

The highest botanical richness was predicted for northern and north-western Borneo. The northern Crocker Mountains range with Mount Kinabalu and the mountains of central East Kalimantan are predicted to have the highest endemism values. Together with the southern Müller Mountains, the east side of the Meratus Mountains, and the Sangkulirang peninsula these are predicted 'centres of endemism'. The cluster analysis revealed that the Bornean lowland rain forest, currently recognized one WWF ecoregion, should in fact be divided in at least four (and possibly six) different floristic regions; the lowlands of (i) Sabah and Sarawak, (ii) East Kalimantan, (iii) southern Borneo, and (iv) the 'Wet hill forest of Sarawak'.

Overlaying the patterns of biodiversity, endemism, and floristic regions with the Global Land Cover 2000 reveals Borneo's remaining forests covering 64% of its surface.

##### **3. Modelling habitat preference, species richness and abundance of alien macrocrustaceans in surface waters in Flanders (Belgium)**

Pieter Boets, Koen Lock and Peter L.M. Goethals  
Ghent University

The introduction and spread of invasive species is a worldwide phenomenon causing global ecological and economic damage. Among the invaders, alien macrocrustaceans are known to be very successful and to colonise new habitats rapidly. A combination of several factors such as shipping, interconnection of waterways, prevailing physical-chemical and habitat conditions as well as species characteristics determine the success of these alien species. Data about different fresh and brackish waters gathered by the Flemish Environment Agency (VMM) were used to build data-driven models predicting the preferred habitat, the abundance and the species richness of alien macro-Crustacea in surface waters in Flanders. Different techniques such as regression and classification trees in combination with several optimisation methods were used to construct the models. The analysis pointed out that conductivity and shipping in combination with the chemical water quality were the major factors determining the presence or absence of alien macrocrustaceans. Alien macrocrustaceans were present under brackish waters conditions or in fresh waters with intensive ship traffic and low levels of organic pollution. The alien species richness increased with improving water quality and when there was a lot of ship traffic. Especially in brackish waters, alien



macrocrustaceans reached high abundances. In fresh water the abundance of alien species was positively influenced by low levels of nutrients. Brackish water conditions in combination with high levels of ship traffic seemed to be very favourable for alien macrocrustaceans to establish and to reproduce. Stronger regulations regarding ballast water control and the trade in alien species, especially in estuarine regions, can help to prevent further introductions.

#### **4. Enhancing coarse-resolution species atlas data using an expert system**

Aidin Niamir, Andrew Skidmore, Bert Toxopeus, Antonio-Román Munoz Gallego and Raimundo Real

University of Twente

Noticeable amount of knowledge, either in the form of literature or expert's opinion, are often available in local scales, whereas it have not been addressed adequately in species distribution modelling (SDM). In this presentation, incorporation of existing knowledge into the SDM is outlined by enhancing the sampling scheme from coarse resolution atlas to yield more accurate predication in a finer resolution.

Coarse-resolution distribution map of Bonelli's Eagle (*Aquila faciaata*) in southern Spain was obtained from the Atlas of breeding birds. Bayesian Theorem was used to generate an "expert-enhanced" sampling scheme based on existing knowledge in the literature and local ornithologists. Maximum entropy approach was then employed to predict distribution maps using two treatments: control, where models were calibrated with conventional random sampling point data from the coarse-resolution atlas, and enhanced, where species sampling points were weighted by the result of the expert system. Four categories of environmental explanatory variables, topographic, bioclimatic, biologic, and anthropogenic were served into the modelling core. Independent breeding territories were used to evaluate the predictive performance of models.

#### **5. Discovering traits that explain species-environment relationships: a Generalized linear mixed model approach**

Tahira Jamil, Wim A. Ozinga and Cajo J.F. ter Braak

Wageningen University

Quantification of the effect of plant traits on the assembly of plant communities is challenging from a statistical point of view. Typical data in community ecology used to be arranged in two data tables, a table recording the occurrence and abundance of numerous species in sites and a table recording the values of numerous environmental variables on the sites. More recently a third table is added, that of values and states of numerous traits of the species. A key question is how multi-species occurrence can be explained by characteristics of both the species and the environment. This problem has been addressed by a novel Generalized linear mixed model (GLMM) approach.

We used GLMM to model and identify which species traits and habitat characteristics best explain the distribution of species and which traits are significantly correlated with habitat characteristics. GLMM accounts for pseudo-replication by including sites as random factor and heteroscedastic variance by including species as random factor. It is observed that use of functional traits significantly improved the performance of existing models. A numerical simulation was used to evaluate the testing procedure.

Open problems are how GLMM will work with large numbers of environmental variables (each one giving a variance component) and large numbers of traits. Convergence can also be an issue.

#### **6. Using the assembly theory to make more robust predictions of vegetation distribution in a changing climate**

Bob Douma, J.P.M. Witte, R. Aerts and P.M. van Bodegom

Vrije Universiteit

Predicting vegetation distribution in a changing climate requires reliable habitat distribution models (HDM). Current HDMs are often criticized due to their correlative nature of species distribution with environmental drivers and their lack of causality. Furthermore, these models cannot make a link to ecosystem services and functional diversity. Therefore, several studies propose to include more functionality in these models, for example by adopting the assembly theory framework. The assembly theory states that species are selected by their traits and that only these species can be part of the community that pass the environment filter.

The assembly theory is so far not put to work in a full vegetation model, and here we test if and to what extent the assembly theory framework can be used to make HDMs more mechanistic. This was done by predicting a set of four plant traits (stem density and indicator values for moisture, nutrients and acidity) from four environmental drivers (disturbance, moisture supply, nutrient supply and acidity). These traits are then used to predict the probability of occurrence of 15 vegetation types, covering the spectrum of vegetation types across the Netherlands. We tested this model on 263 plots in the Netherlands.

Our results show that the model performance was good at a landscape level, but was fair at the site level. Model performance was mainly affected by the degree of uncertainty in the environment-trait relationships and the number of vegetation types distinguished.

This study is the first attempt to explicitly use the assembly theory in HDMs. The inclusion of traits in a vegetation model allows quantifying the role of habitat filtering in explaining biodiversity patterns. Furthermore, the inclusion of a functional coupling between environment and vegetation types make it possible to quantify the sources of uncertainty in community assembly, which hitherto could not be separated. Finally, the use of traits allows potential links with, and feedbacks to ecosystem services and biochemical cycling.

#### **4c: Chemical Stress Ecology**

**Conveners:** Mazhar Iqbal Zafar (Wageningen University)  
Nika Galic (Wageningen University)  
Jacqueline Augusiak (Wageningen University)

##### **1. Linking ECO and ECOTOX; signposting research development**

Wim Admiraal

University of Amsterdam

The release of man-made compounds has affected the environment in various ways often with effects on the persistence of species and communities. To understand the chain of effects –from the molecular level of the pollutant, to the individual biological target and the spatially defined ecological change- ecotoxicology has incorporated sub-disciplines such as environmental and geo-chemistry, expertise in (human) toxicology and ecology. Requests for a stronger input of ecology were heard for decades, and recently the field ecotoxicology has also been re-labeled as stress ecology or chemical stress ecology. Yet a partnership with the ecological sciences was apparently difficult, even when the prognostic research on ‘ecological risk assessment’ and diagnostic ecological field studies with ‘effect directed analysis’ seem to provide natural interfaces.

Four developing research lines will be sketched to help sharing the concepts and methods of ecologists and ecotoxicologists. The levels of biological integration will be used again for guidance. Firstly, the adaptive response of biological species to chemical and physical stressors is entering a new era through the advent of genomics. Toxicants and natural agents provide complementary test cases. Secondly, man-made toxicants and natural toxins have both highly diverse modes of action and it is inviting to study these with a shared chemical/toxicological/ecological methodologies. Thirdly, studies on interactions of diversity and function in communities are often curiosity driven, but chemically compromised communities provide excellent test cases for ecological theory. At the highest integration level –landscapes or catchments- essential advance is possible through the use of epidemiological methods. It is argued that these emerging research lines are inviting and urgent for new research consortia.

##### **2. Ecological impacts of time-variable exposure regimes of the fungicide Azoxystrobin on the zooplankton community of outdoor microcosms.**

Mazhar Iqbal Zafar, J. Dick M. Belgers, Rene P.A. van Wijngaarden, Gertie H.P. Arts, Ivo Roessink, Theo C.M. Brock and Paul J. van den Brink  
Wageningen University

The risks of pesticides to aquatic ecosystems are often assessed by performing cosm experiments evaluating a particular exposure regime (e.g. 1 pulse Applikation), Not necessarily corresponding with the exposure part of risk assessment (e.g. multiple applications). This mismatch is one of the biggest challenges in contemporary ecological risk assessment. The aim of the present study is to compare the effects of a chronic exposure with the effects of a peak exposure and a multiple peak scenario with an identical Area Under the Curve. For this, microcosms (water volume approx. 1270 L) were established using sediment of fine clay having communities typical of macrophyte-dominated freshwater ecosystems. Azoxystrobin is a systemic and strobilurin fungicide that currently is used on a number of agronomic and horticultural crops worldwide. Azoxystrobin was introduced into outdoor- microcosms using four different regimes; (1) A single Application of 31 µg a.s./L, ( 2) four applications of 16 µg a.s./L, with a time interval of 10 days and (3 and 4) a continuous exposure of 10 and 33 µg a.s./L for 42 days. Treatment levels of 1 and 4-pulse were based on 42d-Time Weighted Average (TWA) of 15 µg a.s./L which fall between the chronic 10 & 33 µg/L treatments. The Multivariate analyses of the zooplankton data set, reveals small variation in the pre-treatment period and large concentration-dependent differences with the control after start of the treatment. Effects are first observed for the single Application and the chronic 33 µg/L treatment followed by the 4 Application and 10 µg/L treatment. Taxa belonging to Copepoda (*Nauplii*, *Cyclopoida* and *Calanoida*) and Cladocera (*Daphnia longispina*) are the most responsive zooplankton species observed. Rotifera are indicated to have increased due to azoxystrobin exposure as a result of indirect effects. By the end of the experimental period, PRC shows the same effects magnitude for the pulsed treatment regimes, which are placed in between the chronic treatment regimes. This indicates that for long-term effects the TWA could be more important for most zooplankton species than the peak concentration.

##### **3. Exposure to perfluorooctane sulfonic acid (PFOS) adversely affects the life-history of damselflies**

Luc De Bruyn, Jessica Bots, Tom Snijkers, Bert Van den Branden and Hans Van Gossum  
Research Institute for Nature and Forest (INBO), Belgium / University of Antwerp

Perfluorooctane sulfonic acid (PFOS) is a persistent and ubiquitous environmental contaminant that has been detected in organisms worldwide. We evaluated whether long-time exposure to PFOS affects egg development, hatching, larval development, survival, metamorphosis and body mass of

*Enallagma cyathigerum* (Insecta: Odonata). Eggs and larvae were exposed to five concentrations ranging from 0 to 10 000 mg/L. Our results show reduced egg hatching success, slower larval development, greater larval mortality, and decreased metamorphosis success with increasing PFOS concentration. PFOS had no effect on egg developmental time and hatching or on mass of adults. Eggs were the least sensitive stage (NOEC  $\frac{1}{4}$  10 000 mg/L). Larval NOEC values were 1000 times smaller (10 mg/L). Successful metamorphosis was the most sensitive response trait studied (NOEC < 10 mg/L). The NOEC value suggests that *E. cyathigerum* is amongst the most sensitive freshwater organisms tested. NOEC for metamorphosis is less than 10-times greater than the ordinary reported environmental concentrations in freshwater, but is more than 200-times smaller than the greatest concentrations measured after accidental releases.

#### **4. Multi-generation exposure of the non-biting midge *Chironomus riparius* to three model toxicants**

Marino Marinkovic, K. de Bruijn, M. Asselman, M.J. Jonker, M.H.S. Kraak and W. Admiraal  
University of Amsterdam

In polluted ecosystems some species disappear, while others are able to maintain viable populations. Chironomids are particularly successful in persisting in extremely polluted environments, but the mechanism allowing them to survive in such hostile environments remains still unclear. The aim of the present study was therefore to investigate how *Chironomus riparius* copes with prolonged exposure to pollution. To this purpose a multi-generation experiment was performed in which *C. riparius* populations were exposed for nine consecutive generations to sublethal concentrations of three model toxicants, i.e. the essential metal copper, the non-essential metal cadmium and the organometal tributyltin. For each compound two exposure scenarios were designed, one where the concentration remained constant and one where after the 6<sup>th</sup> generation the exposure concentration was drastically increased for three more generations. Total emergence and delay in emergence were monitored during each generation for all populations. To assess if adaptation had taken place, 14-day toxicity tests were conducted with the corresponding toxicant after the 6<sup>th</sup> and 9<sup>th</sup> generation. We observed that all exposed populations were equally affected by the toxicants and that even when the exposure concentrations were increased after the 6<sup>th</sup> generation, the populations persisted and more overly showed a rapid recovery. Indications for increased tolerance were found in the 14-day toxicity tests for the cadmium and copper exposed populations, but not for the tributyltin exposed population. We conclude that *C. riparius* has the ability to withstand strong selection pressure of different toxicants without immediate extinction or adaptation and that due to its phenotypic plasticity it can persist in highly polluted environments.

#### **5. Toxicity and accumulation of the cyanobacterial neurotoxin $\beta$ -N-methylamino-L-alanine (BMAA) in *Daphnia magna*.**

Els Faassen, Justine van Eenennaam, Maria Garcia Altares Perez and Miquel Lurling  
Wageningen University

The neurotoxin  $\beta$ -N-methylamino-L-alanine (BMAA) is produced by cyanobacteria and has been linked to the neurodegenerative diseases Alzheimer's disease, Parkinson's dementia complex and amyotrophic lateral sclerosis. BMAA can bioaccumulate in terrestrial and aquatic food chains. We determined the effects of BMAA on the grazer *Daphnia magna*, a key species in the aquatic food web. BMAA was not acutely lethal to *D. magna* ( $LC_{50-48h} > 10\ 000\ \mu\text{g L}^{-1}$ ), but reduced mobility ( $IC_{50-48h} 40\ \mu\text{g L}^{-1}$ ). Chronic exposure to  $100\ \mu\text{g L}^{-1}$  raised age at first reproduction, decreased clutch size and decreased population growth rates. Moreover, BMAA had transgenerational effects: it reduced population growth rates of non-exposed offspring of exposed females. Animals that had been kept in either food-free medium or were fed the green alga *Scenedemus obliquus* with BMAA accumulated BMAA in their tissue. The highest measured bioconcentration factors were 275 in adult *D. magna* and 3821 in their neonates. This bioconcentration of the neurotoxic BMAA in *D. magna* suggests that these animals may be an important vector of BMAA in the pelagic food web.

#### **6. Oxidative Stress: Lessons Learned From A Nanotoxicology Perspective**

Sourav Bhattacharjee, Antonius T.M. Marcelis, Han Zuilhof, Ivonne M.C.M. Rietjens and Gerrit M. Alink  
Wageningen University

Oxidative stress had been a key point of discussion/ debate in many nanotoxicology research. Confusion lurches on how oxidative stress is involved in toxicity of nanomaterials. Many argue, oxidative stress is the principle mechanism of the cytotoxicity of nanomaterials. Nanoparticles being immensely surface reactive, induces the production of intracellular reactive oxygen species (ROS) which in turn causes the major damage to the cells. Hence, oxidative stress is (more) a mechanism for cytotoxicity of nanoparticles. However, few recent research articles point towards a different facet of the topic. These articles report that nanoparticles, especially those carrying a positive surface charge, disrupts the normal mitochondrial activity not only by disturbing the normal mitochondrial membrane potential ( $\Psi_m$ ) but inhibits the ongoing electron transport chain (ETC). As a result, ROS

starts getting produced intracellularly which further can result in oxidative stress. In other words, oxidative stress is not a mechanism but rather an effect of mitochondrial interactions with nanoparticles. This talk would like to shed light on this interesting confusion regarding the role of oxidative stress in cytotoxicity of nanomaterials taking into confidence of our own research data. An honest effort would be made trying to inculcate the data available and bridge the gap of understanding this confusing topic...from retrospection to introspection.

#### **4d: Free Session**

**Convener:** Nicole van Dam (Radboud University)

##### **1. C4 photosynthetic subtypes phylogeny or functional ecology? a review and evaluation from isotopic evidence**

Elmar Veenendaal

Wageningen University

It is more than thirty years ago that Ellis et al (1980) first reported in the South African journal of Science that the geographical distribution of C4 photosynthetic subtypes in Southern Africa is related to climate and influences  $^{13}\text{C}$  isotopic ratios. Isotopic ratios are of interest for studies that determine global carbon budgets & productivity, as indicators of past climate change and in trophic level studies. Over time it has been realised that biochemical pathway of a species cannot be separated from growth habit and phylogenetic origin. Recent Investigations into ecophysiological traits in screening experiments have shown differences in plant allocation for different C4 subtypes but no differences in intrinsic or whole plant water use efficiency therefore downplaying the role of leaf physiology. However experimental greenhouse studies mostly have difficulty in mimicking outside climatic conditions, in particular related to atmospheric drying. In this paper we re-examine a field data set from grass species in within Okavango Delta in relation, to phylogeny growth form and life history and study and  $^{18}\text{O}$  isotope ratios. We focus on the question whether the isotope discrimination reflects habitat alone or may be used to indicate differences in leaf physiology between different photosynthetic sub-types in relation to clade origin.

##### **2. The use and misuse of multivariate statistics based on ordination diagrams in ecology**

Patrick Kabouw, Koen Verhoeven and Arjen Biere

Netherlands Institute of Ecology

Multivariate statistics based on ordination (MVS), such as principal component analysis, are powerful tools to simultaneously analyze multiple variables and to uncover structure in complex datasets that would be tedious to analyze using "traditional" statistics. These characteristic and the availability of MVS in statistical packages has ensured a rapid success of MVS in ecology which is reflected by the number of publications which use a form of MVS. However, MVS are not suitable to analyze all datasets generated in ecological sciences. A recent review of ecological literature shows that improper use of MVS in ecology is a common phenomenon. This might be due to the wealth of choices in MVS that are available combined with inadequate training of scientists using MVS. Whatever the reason, improper use might result in misinterpreting ordination diagrams and thus ecological patterns. In the first part of the presentation we will highlight some of these frequently encountered problems when using MVS models and the resulting misinterpretation that could occur. In the second part, besides creating awareness of the problems and constraints, we will present easy to use alternatives and improvements which we will test on simulated datasets. Following the simple guidelines provided in this presentation can improve the accuracy of MVS analysis.

##### **3. Idiosyncrasy in ecology**

Gera Hol, Katrin Meyer and Wim van der Putten

Netherlands Institute of Ecology

The word idiosyncrasy is increasing strongly in ecological papers over the last years. To verify whether idiosyncrasy is more than just a word, we evaluated the different usages of idiosyncrasy in four major ecological areas, i.e. biodiversity-ecosystem functioning, succession, biological invasions, and biogeography. In biogeography idiosyncrasy is used most consistently for outliers, while in the other areas idiosyncrasy represents a variety of results, including random scatter and non-additive effects. Our aim is to show the multifaceted idiosyncrasy in ecology and to discuss approaches to study idiosyncrasies. The value of idiosyncrasy lies in the evolutionary and ecological potential of individuals or species that differ disproportionately from the average. They can occupy new niches or act as stepping stones for rapid evolution during and after extreme events. Then, observations of idiosyncratic responses open up avenues for further investigation into the causes and consequences of these disproportionate responses.

##### **4. Resource limitation and interspecific competition constrain reproduction in an endangered finch**

Erica van Rooij, James Brazill-Boast, Sarah Pryke and Simon Griffith

Macquarie University, Australia

Gouldian Finch (*Erythrura gouldiae*) populations have been declining over several decades and the species is now registered as endangered, occurring in only a small part of its former range. Changes in their habitat caused by altered fire regimes and increased grazing pressures in combination with their limited diet are thought to have contributed to the decline. Meanwhile an ecologically very similar and sympatric grass-finch the Long-tailed Finch (*Poephila acuticauda*) is doing fine. We aim to

get more insight in the decline of the Gouldian finch through comparing aspects of the breeding ecology of both species and competition between them. Therefore, over three breeding seasons (2008 – 2010), the breeding ecology of populations of wild Gouldian and Long-tailed Finches was studied in the savanna woodlands of the Kimberley, the northernmost region of Western Australia. The length of the breeding seasons differed markedly between the two species, with Gouldian Finches only able to breed during the period when competition over nest sites and food was high, while Long-tailed Finches, sustained by a broader diet, had another opportunity to breed after that period. Our findings also demonstrate that these species differed in nesting preferences with Gouldian finches being limited by the availability and quality of nest-sites in the environment and interference competition by the more dominant and more abundant long-tailed finch constrains reproductive success in the Gouldian finch.

## **5. The impact of climate change on oystercatchers**

Bruno Ens, Martijn van de Pol, Kees Oosterbeek and Joost Tinbergen  
SOVON / Netherlands Institute of Ecology

Studying how climate change impacts a shorebird population requires a very long study period, especially if the impact includes changes in the frequency of rare and catastrophic events. We have succeeded in following a breeding population of individually colourmarked oystercatchers since 1983. Two catastrophic events impact oystercatchers: severe winters and occasional flooding during the breeding season. Severe winters cause mass mortality among wintering oystercatchers, so the fact that the frequency with which severe winters occur has decreased is positive for oystercatchers. However, in our study area, the density of ragworm is generally high following a severe winter and since this is an important food species during the breeding season, reproductive success is often high following severe winters. From this point of view, a decrease in the frequency of severe winters must be considered as negative for the oystercatchers. Model simulations indicate that the net effect of a decrease in winter severity is nonetheless positive. Another climate-related catastrophic problem is the risk of flooding during the breeding season, causing high losses of eggs and chicks. This risk has increased throughout the entire Wadden Sea during the last 40 years. Extrapolation of the trend suggests that reproductive output will not suffice to compensate for mortality in the future.

## **6. Are earthworms good or bad for the soil greenhouse gas balance? A review**

Ingrid Lubbers, Lijbert Brussaard and Jan Willem van Groenigen  
Wageningen University

The soils of the world are an important source of all three major greenhouse gases (GHG's). Terrestrial ecosystems have contributed as much as half of the anthropogenic carbon dioxide (CO<sub>2</sub>) emission over the past two centuries; soils are by far the dominant source of nitrous oxide (N<sub>2</sub>O) emissions; and wetlands and landfills dominate global methane (CH<sub>4</sub>) fluxes. Yet, soils can also be a sink for these three GHG's through carbon sequestration, biological reduction of N<sub>2</sub>O, and methanotrophy. The GHG balance of the soil is therefore dependant on soil management.

Nowadays a rising demand for food and energy to support the growing world population results both in land use change as well as land use conversion from conventional tillage to reduced- or no-tillage systems. This raises the question to what degree soil ecosystem engineers such as earthworms can affect the soil GHG balance. It has been suggested that earthworms can stabilize fresh organic C in soil organic matter. Furthermore, several studies have reported effects of earthworms on emissions of N<sub>2</sub>O or CH<sub>4</sub>. Here we review the available literature covering the effects of earthworm activity on the soil GHG balance, and identify knowledge gaps that need to be addressed.

With regard to C, many studies suggest earthworm-induced C stabilization in soil organic matter. However, measurements were almost exclusively indirect (measuring new C in supposedly more stable soil fractions), had a very short duration (less than 4 months), or earthworm effects were confounded by other effects (e.g. tillage). For N<sub>2</sub>O, a growing body of literature indicates that earthworm activity can significantly increase N<sub>2</sub>O emissions. This was, however, mostly measured under controlled conditions and only when a food source was added to the system. Few studies discussed the earthworm effect on CH<sub>4</sub> emission; both positive and negative effects have been reported, but CH<sub>4</sub> emissions appear to be mainly measured in landfills and contaminated soils.

We conclude that available data on the effect of earthworms on the GHG balance of the soil are fragmentary and it has not been conclusively proven that earthworms increase soil organic matter stocks. The most important scientific challenges appear to be (i) direct measurement of C stabilization over longer time periods; (ii) field-based studies on N<sub>2</sub>O effects; and (iii) integral studies measuring all three GHG's simultaneously. Options to fill these knowledge gaps will be discussed.

# Poster Titles

The poster exhibition is arranged according to the titles of the parallel sessions and can be found in the main hall and on the way to the various locations where the parallel sessions are held.

There are two posters sessions, the first on Tuesday evening (8 February) and the second Wednesday afternoon (9 February). Poster session will not deal with the titles of parallel sessions held on that day. Rather, the set-up of the two poster sessions is as follows. All posters have been given a number. During the first poster session (Tuesday evening 8 February) all even numbered posters can be visited and all odd numbered posters during the second poster session (Wednesday afternoon 9 February). This implies that owners of even-numbered posters are present at their poster during the first session and owners of the odd-numbered posters during the second session.

Below you can find a list of posters titles that have been submitted on registration. Please note this list may not be complete and that posters may not be listed but will be exhibited. Note that, although the parallel session Farmland Ecology has been cancelled, the poster session remains.

## Parallel Session 1a: Innovative understanding of biodiversity and ecosystem functioning

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Thijs Janzen	University of Groningen	Biodiversity and biogeography: adaptive radiation in the African rift lakes
2	Michele de Cássia Pereira e Silva	University of Groningen	Abundance, diversity and functional role of ammonia oxidizing communities across Dutch soils
3	Elke Vockenhuber	University of Göttingen	Tree species identity drives responses of Dipteran communities to tree and herb layer diversity

## Parallel Session 1b: Element cycles in aquatic systems under global change

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Willem van Colen	KU Leuven	Consequences of the increasing N:P ratio on the eutrophication of shallow lakes.



### Parallel Session 1c: Interface between ecology and paleo-ecology

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Melike Balk	Utrecht University	Oxidation of Water to Hydrogen Peroxide at the Rock-Water Interface
2	Artem Budishev	Vrije Universiteit, Amsterdam	Increased greenhouse gas emission from thaw ponds in Siberian arctic tundra on continuous permafrost.
3	Ellen Decaestecker	KU Leuven	Transient dynamics in a long-term perspective of a Daphnia-parasite coevolution
4	Wouter Feldmeijer	Vrije Universiteit, Amsterdam	Reconstructing seasonality using Mg/Ca palaeothermometry: a multi species, single specimen approach
5	Alexandra Hincke	Utrecht University	Plants in a low-CO <sub>2</sub> world: validation of botanical and organic geochemical proxies for the Pleistocene
6	Nina Keul	Alfred Wegener Institute (AWI), Germany	Vesicle Dynamics In Foraminifera
7	Anna de Kluijver	Netherlands Institute of Ecology	Carbon fluxes in plankton food webs in Chinese lake systems based on stable isotopes and biomarkers
8	Gerald Langer	Alfred Wegener Institute (AWI), Germany	Mg and Sr banding in the shell of the benthic foraminifer Ammonia tepida revealed by NanoSIMS
9	Ake Nauta	Wageningen University	The effect of climate warming on the arctic ecosystem: The response of soil and vegetation to enhanced seasonal thawing of permafrost in the Siberian tundra
10	Lennart Nooijer	Utrecht University	Foraminiferal Mg/Ca from a sediment trap series in the Arabian Sea: improving temperature reconstructions

### Parallel Session 1d: Ecology regarding genetically modified organisms

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Emilia Hannula	Netherlands Institute of Ecology	Tracking carbon flow in the potato rhizosphere to fungal communities using stable isotope probing
2	Agnieszka Szturc-Koetsier	Utrecht University	Baseline across soils: transformation of plant-borne organic matter

### Parallel Session 2a: Ecosystem change and predictability in a changing world

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Santiago Alvarez-Fernandez	IMARES-Wageningen UR	Plankton regime shift in the North Sea around 2000
2	Koert van Geffen	Wageningen University	Shining light on darkness - the ecosystem consequences of artificial night lighting
3	Amanda Lloyd	IMARES-Wageningen UR	Mussel carrying capacity and dynamic ecosystem models.
4	Tine Meekers	KU Leuven	Effects of habitat fragmentation on the reproductive success of the nectar-producing orchid <i>Gymnadenia conopsea</i> and the nectarless <i>Orchis mascula</i> .
5	Mieke Titulaer	Netherlands Institute of Ecology	The effect of artificial light on flora and fauna in the Netherlands.

### Parallel Session 2b: Spatial Ecology

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Jim van Belzen	Netherlands Institute of Ecology	Chess at the mud flat: disturbance and recovery at salt-marsh pioneer zones
2	Monique de Jager	Netherlands Institute of Ecology	Cooperation in mussel beds
3	Quang-Xing Liu	Netherlands Institute of Ecology	Patterns in mussels beds: Does the prettiest pattern survive best?
4	Agnieszka Malinowska	Wageningen University	Adaptations of landscape to weather extremes
5	Joost Tinbergen	University of Groningen	Reproductive effort affects spatial distribution in Great Tits
6	Els van der Zee	Royal Netherlands Institute for Sea Research	Spatial habitat modification by reef builders cascades through multiple trophic levels

### Parallel Session 2d: A new era in Microbial Ecology

	Name Main Author	University/Institute	Title
1	Rozelin Aydin	Wageningen University	Identity and ecophysiology of bacteria producing gdgt membrane lipids
2	Marlies Coopman	KU Leuven	Microcystis aeruginosa and its cyanophages
3	Armando Dias	University of Sao Paulo	Effect of ammonium input on microbial populations related to ammonium oxidation in mangrove sediments
4	Suzanne de Haaijer	Radboud University Nijmegen	Marine nitrifiers: ecophysiology and interactions
5	Rashid Nazir	University of Groningen	Prevalent migration via fungal hyphae through different soils: an ecological attribute of a cosmopolitan bacterium <i>Bukholderia terrae</i>
6	Derya Ozuolmez	Wageningen University	Microbial interactions in marine anoxic sediments: Competition or teamwork?
7	Max Rudnick	Netherlands Institute of Ecology	The ecological importance of bacterial mycophagy (feeding on fungi) by <i>Collimonas</i> in soil
8	Olaf Tyc	Netherlands Institute of Ecology	The possible biological cost of broad-spectrum antibiotic production for the soil isolate <i>P. fluorescens</i> Pf0-1
9	Diana Vasquez Cardena	Netherlands Institute of Ecology	Reoxidation and chemoautotrophy in coastal sediment ecosystems: rates, regulation and microbial players
10	Baoli Zhu	Radboud University Nijmegen	Enrichment of nitrite-dependent methane oxidizers from an acidic peatland

### Parallel Session 3a: Plant ecophysiology - Surviving in a heterogeneous world

	Name Main Author	University/Institute	Title
1	Melis Akman	University of Amsterdam	Submergence tolerance in Brassicaceae
2	Bruno Cachapa Bailarote	KU Leuven	Has high mycorrhizal specificity contributed to the strong decline of <i>Anacamptis morio</i> in Belgium?
3	Roel Heirman	HAS Den Bosch	Spatial and seasonal chemistry variation in <i>Jacobaea Vulgaris</i>
4	Anne Immers	Netherlands Institute of Ecology	The effects of iron addition on the growth of macrophytes
5	Diederik Keuskamp	Utrecht University	PIN-driven Auxin Regulation of Shade Avoidance
6	Sofie Meeus	KU Leuven	Impact of morph bias on genetic diversity of the partially self-incompatible forest herb <i>Pulmonaria officinalis</i>

### Parallel Session 3b: Movement ecology of plants and animals: similarities and differences

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Rob Fraaije	Utrecht University	Colonization of riparian vegetation at restored lowland streams
2	Annemarie Garssen	Utrecht University	Effects of climate change on colonization and biodiversity of riparian plant communities
3	Andrea Kölzsch	Netherlands Institute of Ecology	Spring migration timing of arctic-breeding geese

### Parallel Session 3c: From water to land; ecology across borders

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Karlijn Brouns	Utrecht University	effect of ground and surface water salinisation on peat decomposition
2	Floris Vanderhaeghe	Research Institute for Nature and Forest (INBO), Belgium	Experimental impact of ammonium, carbon dioxide and water levels on amphibious softwater plant communities

### Parallel Session 3d: Farmland Ecology

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Karst Broelsma	Wageningen University	Plant induced effects on the soil microbial activity, using the MicroResp system
2	Steve Crittenden	Wageningen University	Can reduced tillage and field margins improve soil water dynamics through stimulation of earthworms?
3	William van Dijk	Wageningen University	Benchmarking biodiversity performance of farmers
4	Gera Hol	Netherlands Institute of Ecology	Competition and plant-soil feedback
5	Marije Kuiper	Wageningen University	Local and landscape effects on field margin biodiversity
6	Hanneke Wiggers	Wageningen University	Extensively managed grassland field margins and biodiversity

### Parallel Session 4a: Multitrophic interactions and Food webs

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Hedwig Ens	University of Amsterdam	Tasty Natives and Nasty Exotics? <i>On the track of differences in invertebrate communities on exotic and native plants</i>
2	Wimke Fokkema	University of Groningen	Hybrid interaction networks: unravelling the interplay of herbivory, seed dispersal and pollination in a tropical savanna
3	Taiadjana Fortuna	Netherlands Institute of Ecology	Tritrophic approach to plant preference between an exotic and a native plant
4	Olga Kostenko	Netherlands Institute of Ecology	Disentangling the effects of host plant quality and plant community characteristics on insect community on ragwort ( <i>Jacobaea vulgaris</i> L.)
5	Jeroen van Leeuwen	Wageningen University	Food webs during soil transformations
6	Wesley Tack	Ghent University	The relationship between forest rodents and immature ticks

### Parallel Session 4b: Species Distribution Modelling

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Claudia Pittiglio	Twente University	Identifying transit corridors for elephant from a process-based approach and long-term datasets
2	Claudia Pittiglio	Twente University	A common dominant scale emerges from images of diverse satellite platforms using the wavelet transform

### Parallel Session 4c: Eco-toxicology and Chemical Stress Ecology

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Andreas Focks	Wageningen University	Mechanistic modelling of the effect of the antibiotic sulfadiazine on nitrification in agricultural soils.
2	Nika Galic	Wageningen University	Recovery of aquatic invertebrates after pesticide stress
3	Mazhar Iqbal Zafar	Wageningen University	Ecological impacts of time-variable exposure regimes of the fungicide Azoxytobin on freshwater invertebrate communities in outdoor microcosms

### Parallel Session 4d: Free session

	<b>Name Main Author</b>	<b>University/Institute</b>	<b>Title</b>
1	Koen De Hert	KU Leuven	Patterns of hybridization between diploid and derived allotetraploid species of <i>Dactylorhiza</i> (orchidaceae) co-occurring in Belgium
2	Bas Dingemans	Utrecht University	Soil warming and fertilization effects on recalcitrant litter decomposition
3	Kenny Helsen	KU Leuven	Plant secondary succession in a fragmented landscape
4	Seline Meijer	University of Dublin	The effects of land-use change on arthropod richness and abundance in the Azores
5	Stefanie Nolte	University of Groningen	Differences between cattle and horse grazing-management: Impacts on <i>Aster tripolium</i> as the key species in salt-marsh communities
6	Lidwien Raak-van den Berg	Wageningen University	Hibernation and spring reproduction of <i>Harmonia axyridis</i> in the Netherlands
7	Marjolein de Rijk	Wageningen University	How to test mosquito repellents