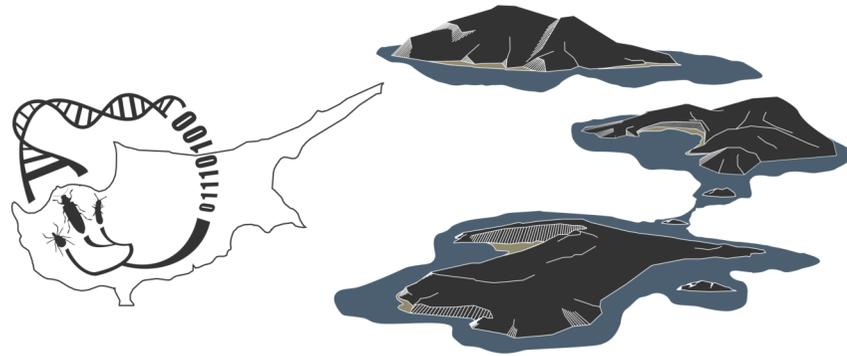


iBioGen: towards a methodological harmonisation in island biodiversity genomics



Anna Papadopoulou
Department of Biological Sciences, University of Cyprus

CIBIO webinar | 8th June 2021



The iBioGen project has received funding from the *European Union's Horizon 2020 research and innovation programme* under grant agreement No 810729.



iBioGen

Twinning for European excellence in Island Biodiversity Genomics



www.ibiogen.eu



- Twinning scheme
- Coordination and support action (CSA)
- Duration: 01/09/2018 - 28/02/2022



The iBioGen project has received funding from the *European Union's Horizon 2020 research and innovation programme* under grant agreement No 810729.



Island **B**iodiversity **G**enomics

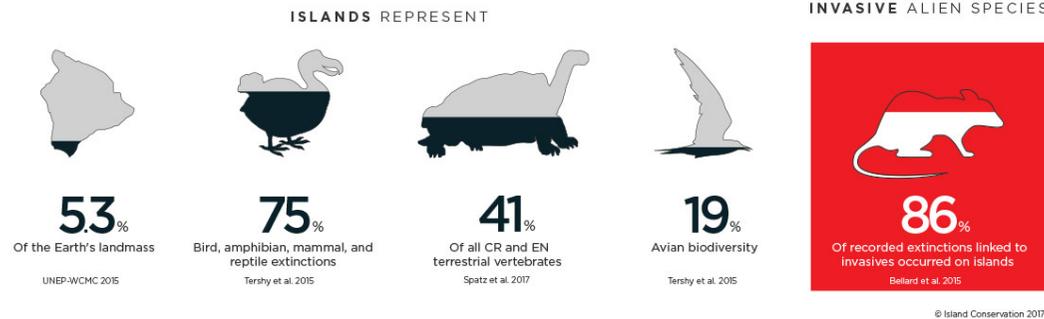


Efficient biodiversity assessment and monitoring



Island biodiversity under threat

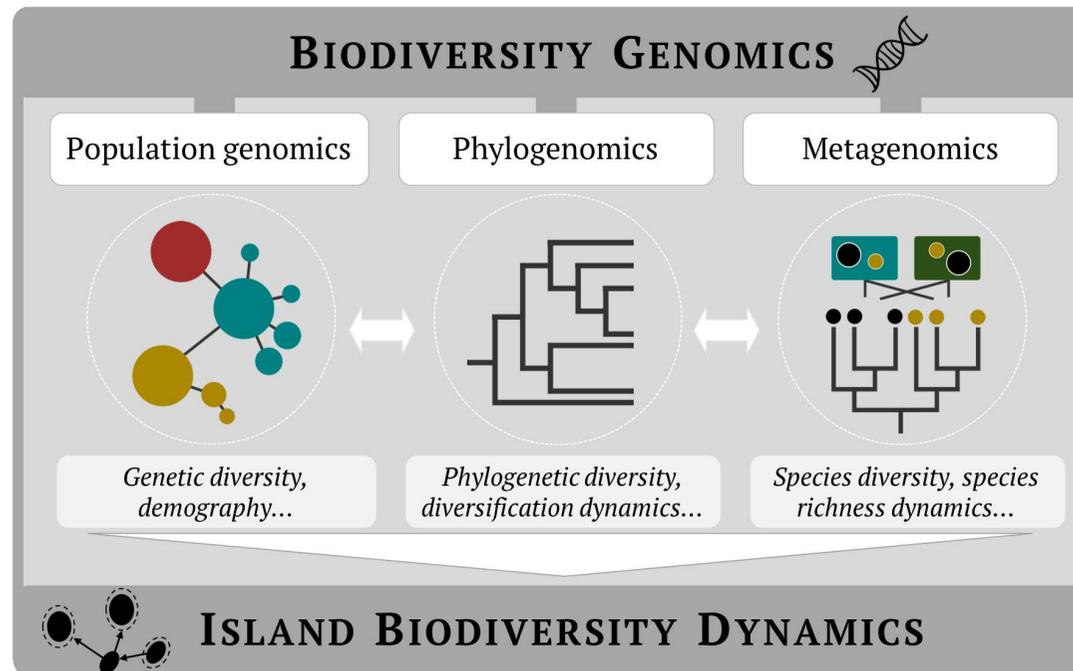
- Invasive alien species
- Climate change
- Habitat destruction (tourism)
- Overexploitation of resources
- Pollution and waste disposal





iBioGen: the field of research

Island **Bio**diversity **Ge**nomics



Towards a synthesis in island biodiversity dynamics



Networking in Biodiversity Genomics

- Better harmonisation of methodologies → improve comparability among datasets
- Better coordination among empirical biologists, bioinformaticians and theoreticians





iBioGen: the partners



Dr. Anna Papadopoulou
University of Cyprus



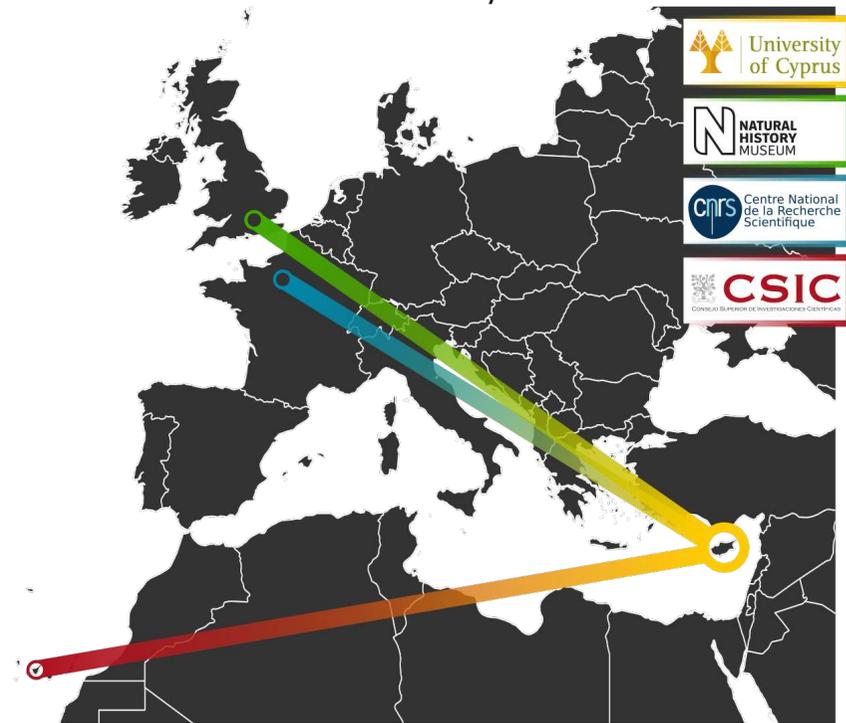
Prof. Alfried P. Vogler
The Natural History Museum, UK



Dr. Hélène Morlon
IBENS-CNRS, France



Dr. Brent Emerson
IPNA-CSIC, Tenerife, Spain





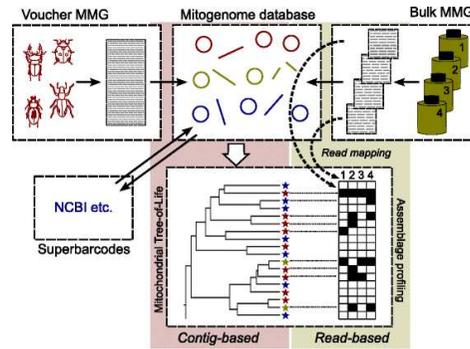
the NHM team: research excellence and training



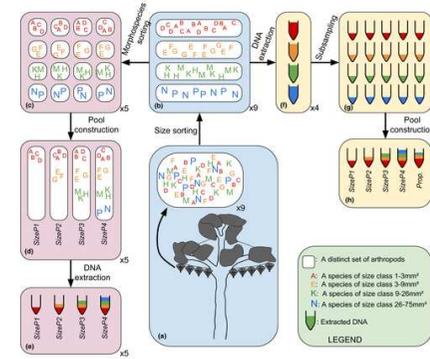
Wet-lab protocols and pipelines for insect metabarcoding and mitochondrial metagenomics



Prof. Alfred P. Vogler



Crampton-Platt et al. (2016) *Gigascience*

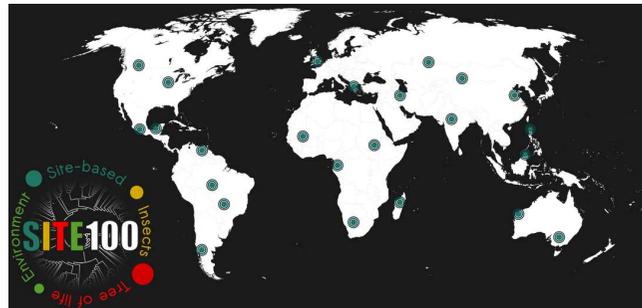


Creedy et al. (2019) *Ecology & Evolution*



Dr. Thomas J. Creedy

Linking site-based with lineage-based biodiversity analyses



www.site100.org



the CSIC team: networking for protocol unification



Standardizing field sampling and sample processing protocols for arthropod biodiversity



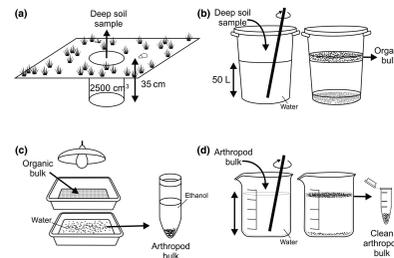
Prof. Brent Emerson



Emerson et al. (2017) *Mol. Ecol. Res.*



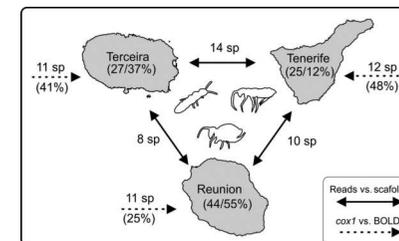
Dr. Paula Arribas



Arribas et al. (2015) *Mol. Ecology*



Dr. Carmelo Andújar



Cicconardi et al. (2017) *Mol. Ecology*



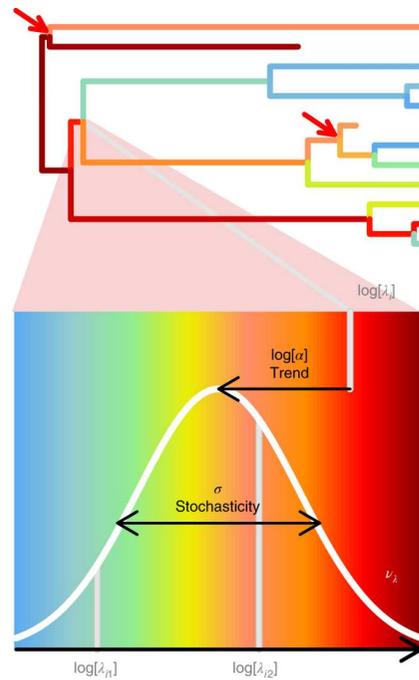
Biodiversity modelling and theory



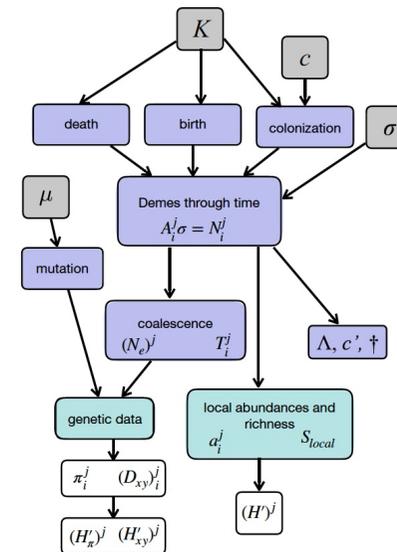
Dr. Hélène Morlon



Dr. Isaac Overcast



Maliet et al. (2019) *Nature Ecology & Evolution*



Overcast et al. (2019) *J. of Biogeography*



the UCY team: promoting Cyprus as model system



University of Cyprus
Department of Biological Sciences

Knowledge transfer and protocol unification across island systems



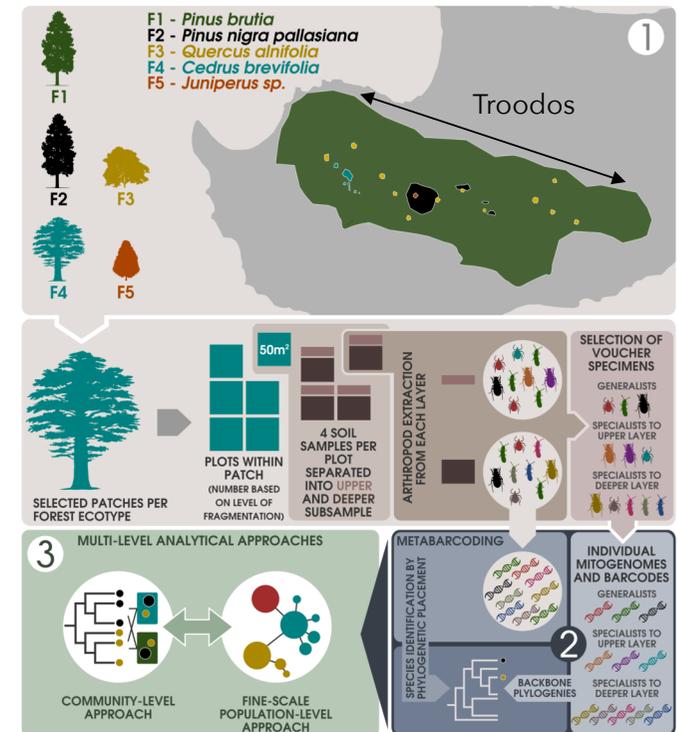
Dr. Anna Papadopoulou



Dr. Víctor Noguerales

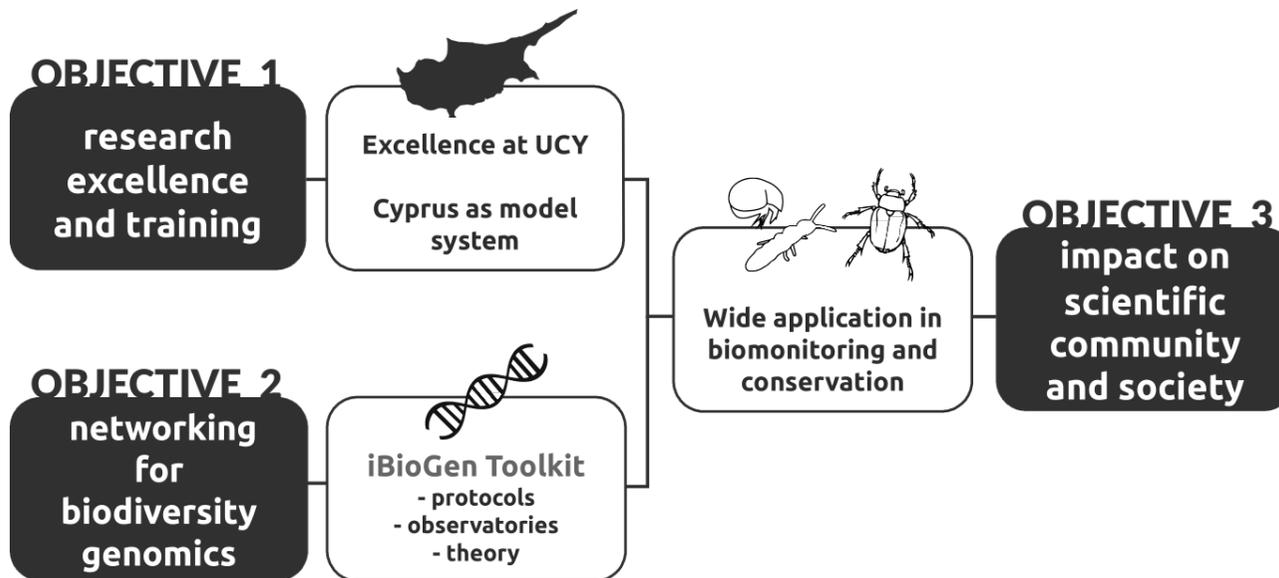


Manolis Meramveliotakis





iBioGen: the objectives



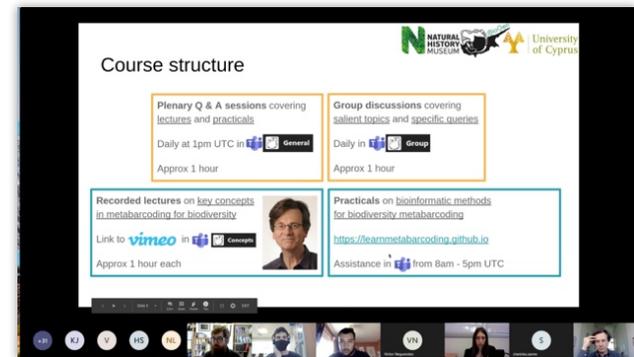


Obj. I Training: workshops on analysis of metabarcoding data

Workshop 1: "Analysis of metagenetic data for macroecology" (Cyprus, Oct. 2019)



Workshop 2: "Theory and practice in metabarcoding for biodiversity" (online, Jan. 2021)





Obj. I Training: workshops on analysis of metabarcoding data

Online resource for self-training on “Bioinformatic Methods for Biodiversity Metabarcoding”

<https://learnmetabarcoding.github.io>



Obj. I Training: enhancing biodiversity genomics in Cyprus

Personalised training of UCY students in field & lab protocols



Staff exchange visits & direct mentoring of UCY staff





Obj. 2 Protocol harmonisation: symposium on Genomic Observatories

Toward harmonisation for metabarcoding data generation in Genomic Observatories



Prof. Vojtech Novotny



Prof. Fredrik Ronquist



Prof. Douglas Yu



Dr. Vasco Elbrecht



Prof. Simon Creer



Prof. Martin Bidartondo



Dr. Kristine Bohmann



Prof. Francesco Ficetola



Dr. Lucie Zinger



Dr. Jeremy deWaard



Dr. Marta Goberna



Dr. Henrik Krehenwinkel



Obj. 2 Protocol harmonisation: symposium on Genomic Observatories

Toward harmonisation for metabarcoding data generation in Genomic Observatories

MOLECULAR ECOLOGY

MEETING REVIEW | [Open Access](#) | [CC](#) | [i](#)

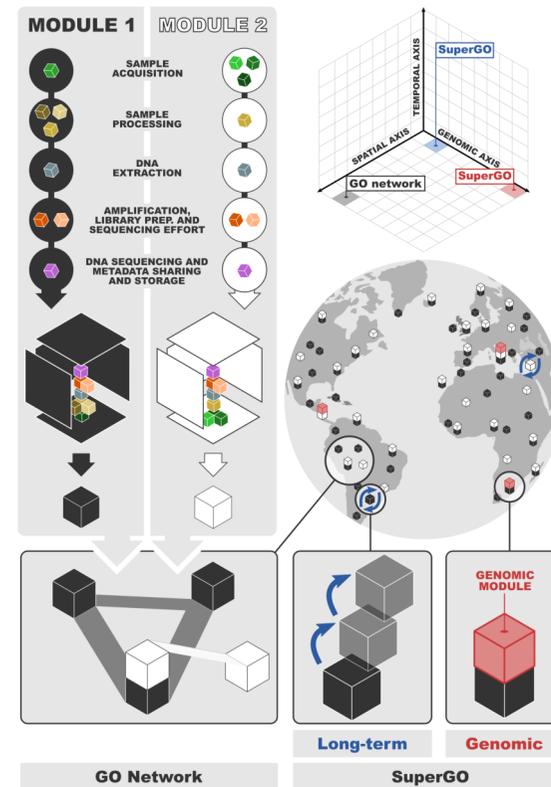
Connecting high-throughput biodiversity inventories: Opportunities for a site-based genomic framework for global integration and synthesis

Paula Arribas [✉](#), Carmelo Andújar, Martín I. Bidartondo, Kristine Bohmann, Éric Coissac, Simon Creer, Jeremy R. deWaard, Vasco Elbrecht, Gentile F. Ficetola, Marta Goberna, Susan Kennedy, Henrik Krehenwinkel, Florian Leese, Vojtech Novotny, Fredrik Ronquist, Douglas W. Yu, Lucie Zinger, Thomas J. Creedy, Emmanouil Meramveliotakis, Víctor Nogueras, Isaac Overcast, Hélène Morlon, Alfred P. Vogler, Anna Papadopoulou, Brent C. Emerson ... [See fewer authors](#) ^

First published: 12 January 2021 | <https://doi.org/10.1111/mec.15797>



Symposium in Cyprus (November 2019)



Arribas et al. (2021) *Molecular Ecology*



Obj. 2 Protocol harmonisation: working group

Working group on protocol harmonisation for two modules:

- a) Soil biodiversity
- b) Terrestrial Arthropods



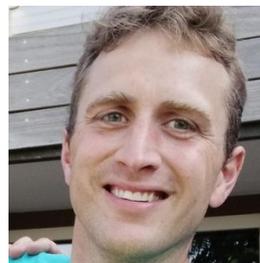
Prof. Vojtech Novotny



Dr. Vasco Elbrecht



Dr. Kristine Bohmann



Dr. Stefan Geisen



Prof. Evan Economo



Dr. Lucie Zinger



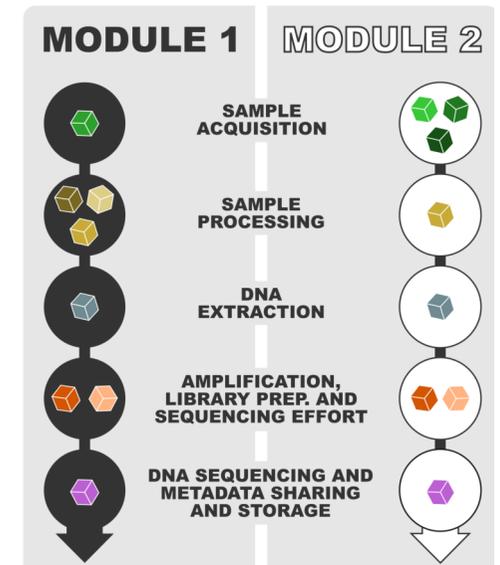
Dr. Jeremy deWaard



Dr. Marta Goberna



Dr. Henrik Krehenwinkel



Working group (November, 2020)



Obj. 2 Protocol harmonisation: bioinformatic pipelines

Reviewing and comparing bioinformatic pipelines for COI metabarcoding

DOWNLOAD PDF 314 VIEWS

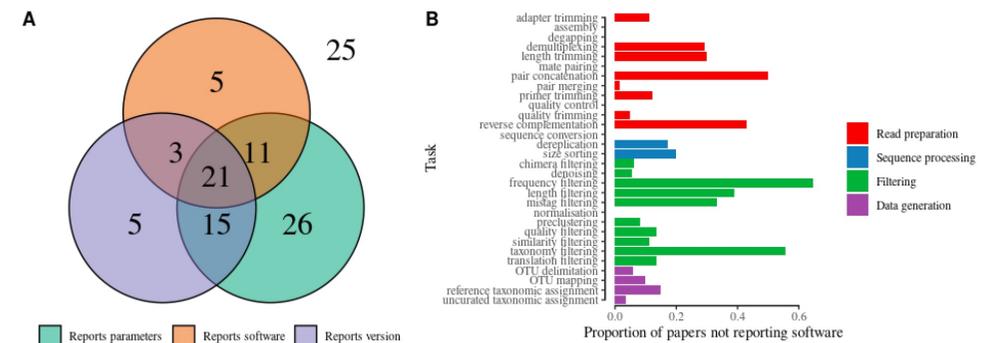
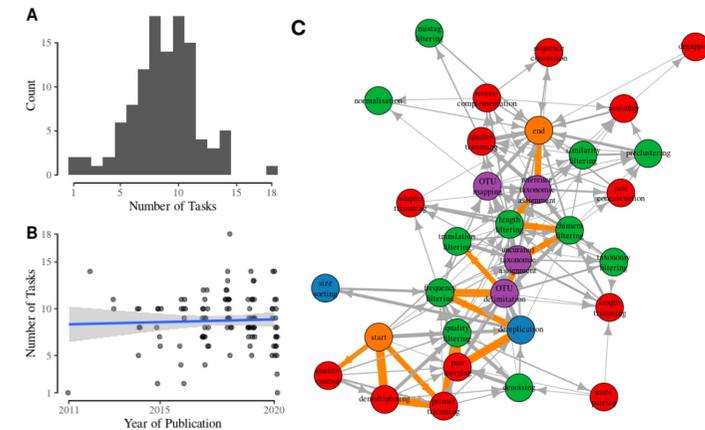
Coming of age for COI metabarcoding of whole organism community DNA: towards bioinformatic harmonisation

ANIMAL COMMUNITIES | BIOINFORMATICS | COI BARCODE | COMMUNITY ECOLOGY
HIGH-THROUGHPUT SEQUENCING | METABARCODING

Thomas Creedy, Carmelo Andujar, Emmanouil Meramveliotakis, Victor Noguerales, Isaac Overcast, Anna Papadopoulou, H  l  ne Morlon, Alfried Vogler, Brent Emerson, Paula Arribas

- high heterogeneity across pipelines
- serious underreporting of tasks, software and parameters
- limited adaptation to the nature of the COI fragment

Creedy et al. (under review in *Molecular Ecology Resources*)
DOI: 10.22541/au.162141276.61766048/v1





Obj. 2 Protocol harmonisation: bioinformatic pipelines

development of bioinformatic tools for metazoan mtDNA metabarcoding: **metaMATE**

MOLECULAR ECOLOGY RESOURCES

FROM THE COVER

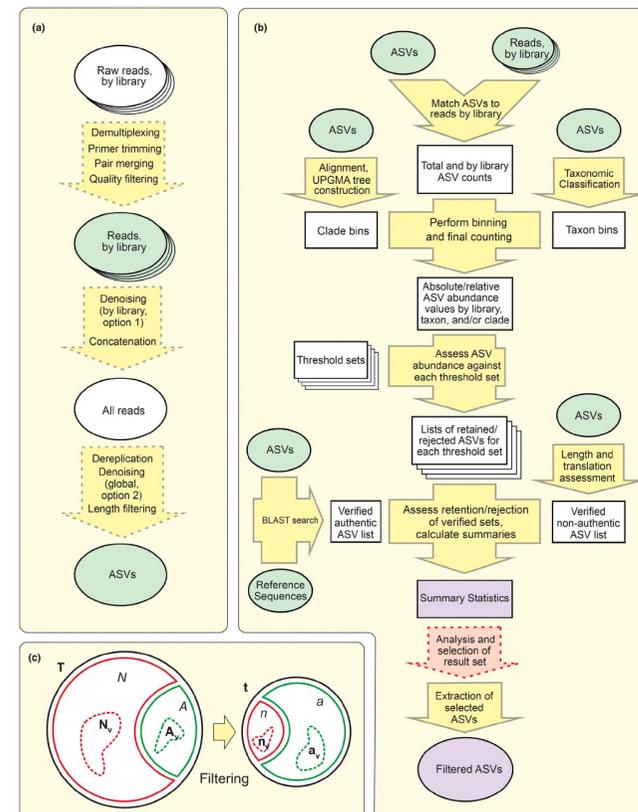
Validated removal of nuclear pseudogenes and sequencing artefacts from mitochondrial metabarcode data

Carmelo Andújar ✉, Thomas J. Creedy, Paula Arribas, Heriberto López, Antonia Salces-Castellano, Antonio José Pérez-Delgado, Alfried P. Vogler, Brent C. Emerson ... [See fewer authors](#) ^

First published: 27 January 2021 | <https://doi.org/10.1111/1755-0998.13337> | Citations: 2

Andujar, Creedy *et al.* (2021) *Mol. Ecol. Resources*

github.com/tjcreedy/metamate





Obj. 2 Networking for theoretical synthesis

Synthesizing ecological and evolutionary theory for community-wide genetic data

Prof. Rampal Etienne
University of Groningen,
Netherlands



Dr. Isabel Sanmarín
Real Jardín Botánico,
Spain



Dr. Claire Jacquet
University of Zurich,
Switzerland



Prof. Amaury Lambert
Sorbonne Université,
France



Megan Ruffley
University of Idaho, USA



Dr. Guillaume Achaz
MNHN, France



Dr. Flora Jay
Université Paris-Sud
France



Dr. Robin Aguilée
Université Toulouse
III Paul Sabatier



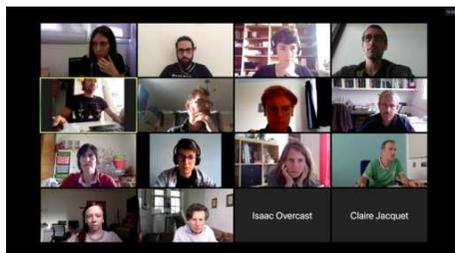


Obj. 2 Networking for theoretical synthesis

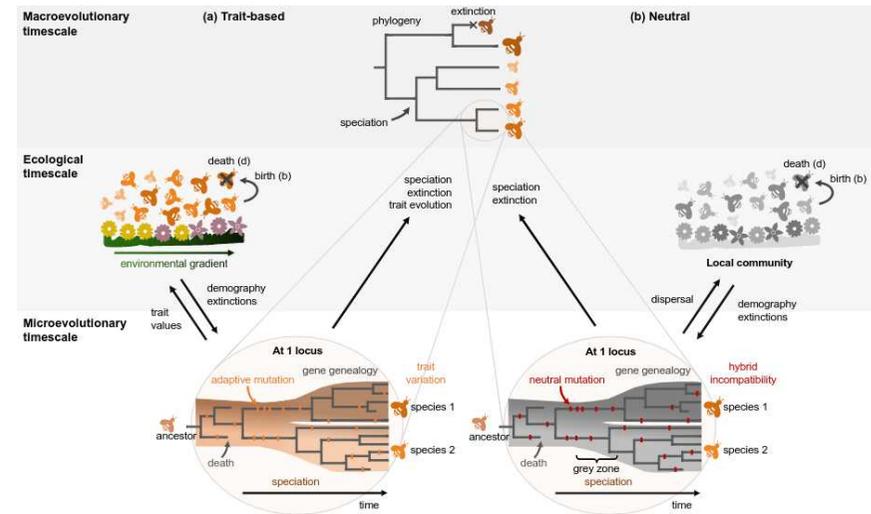
Synthesizing ecological and evolutionary theory for community-wide genetic data



Symposium (La Réunion, July 2019)



Working group (June, 2020)



Overcast *et al.* (*in prep*) Genetic Theory of Island Biogeography: Inferring Processes from Multi-Dimensional Community-Scale Data



Obj. 3 Impact on society

Interaction with stakeholders and dissemination to the broader public

8,700,000 species exist on planet Earth

We have described about 1,300,000 species, while up to 7,400,000 are still unknown to us.

Every year we discover 15,000 to 20,000 species, while at the same time up to 400,000 of species known or unknown to us go extinct.

HIDDEN HEROES AND WHERE TO FIND THEM

Hidden biodiversity is those species we do not know they exist, but are still active parts of our ecosystems.

Despite being tiny or hidden in unreachable places, they keep our forests standing, shape the lands we cultivate and recycle the building blocks of life.

Species that are found only in one place on Earth, one called endemic.

Islands, like Cyprus, harbour a high percentage of endemic species. This is why they are considered biodiversity hotspots.

EXPLORING HIDDEN BIODIVERSITY THE UNKNOWN INHABITANTS OF OUR WORLD

What hides in plain sight in the forest? What hides in the soil we step on? Turn the page to explore!

IBIOGEN TEAM
at the UNIVERSITY OF CYPRUS

Logos for partners: iBioGen, CIFS, NIS, etc.

With tiny sizes, comes great responsibility

Digging through the soil you can find hundreds of organisms. Earthworms moving around and ants building their nests, beetles of all sizes and shapes. They aggregate that you need all of that. Even thousands of microorganisms, like bacteria and fungi, live unseen though most of them invisible to the human eye. What are they doing there?

DECOMPOSERS
Decomposers, such as beetles, and many bacteria and other organic matter, and convert it into very fine substances. Then bacteria break them down completely, enriching the soil, nutrients and making plants grow.

POLLINATORS
Insect pollinators, like bees, butterflies or moths, are responsible for the reproduction of the majority of flowering plants.

SOIL ENGINEERS
Soil engineers, such as ants and earthworms, help to mix the soil layers, providing food for organisms hidden deeper in the soil. They also increase soil porosity and capacity to hold water, nutrients and oxygen, creating a healthy underground environment for plants to grow.

SYMBIOTIC MICROORGANISMS
Symbiotic nitrogen fixing bacteria and mycorrhizal fungi colonize the roots of their host plant and play a crucial role in the plant's nutrition.

How to find a needle in a haystack

How can we find all these elusive organisms? Each of the 8.7 million species on Earth carries a unique DNA fingerprint or "DNA barcode". We can identify species from the DNA they carry in their cells or the DNA they shed in the environment.

DNA MOLECULAR FINGERPRINT

If we extract DNA from a soil sample used for a tree, we will get a "DNA soup" of all the fungi, beetles, insects or worms associated with this tree. By reading all the DNA barcodes found in the "soup" and comparing them to databases we can identify previously known species or discover new ones. Similarly, if we extract DNA from a flower we can identify DNA traces of the insects that pollinate it. That is how DNA helps us to discover the unknown inhabitants of Earth and their role in the ecosystems.



TEDEd
Lessons Worth Sharing

ibioGen
@ibioGen_project

The project iBioGen has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 810728

372 following 206 Followers

Retweeted
@ibioGen_project · Oct 18
Join our FREE online workshop on "Theory and practice in metabarcoding for biodiversity!"
7-13th January 2021
Instructors: Prof. Alfred P. Vogler, Dr Thomas J. Creedy
Applications until 20th November
metagenomics.eu

ibioGen
Using DNA to discover the hidden biodiversity. Funded by the European Union's Horizon 2020 research and innovation programme.

POSTS

A grid of six images showing various insects: a dragonfly, a grasshopper, a butterfly, a spider, and other small organisms.

@iBioGen_project

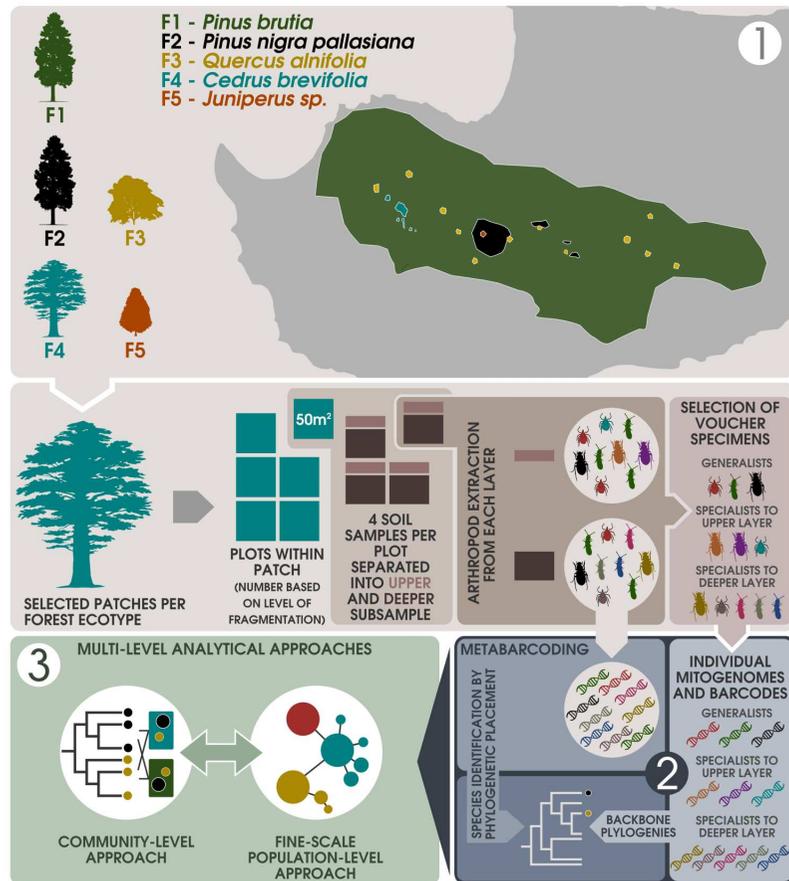


Cyprus montane forests as a case study

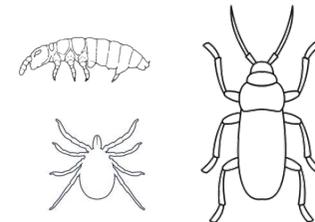
DNA metabarcoding of soil microarthropod assemblages across a mosaic of montane forests



Dr. Víctor Noguerales



- Isolated mountain range
- Understudied fauna
- Topographic complexity
- Environmental heterogeneity
- Habitat fragmentation



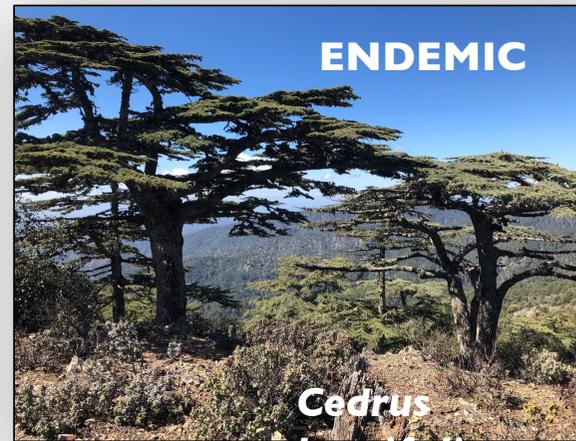


Cyprus montane forests as a case study

CYPRUS MONTANE FOREST TYPES



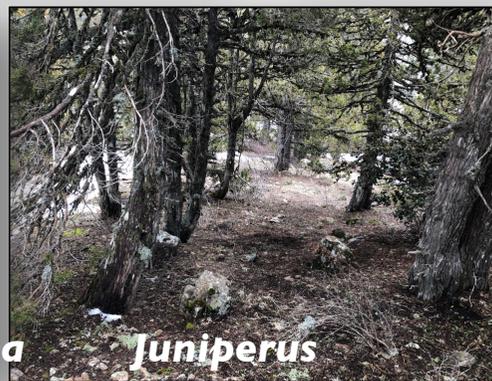
*Quercus
alnifolia*



*Cedrus
brevifolia*



Pinus brutia



*Juniperus
foetidissima*

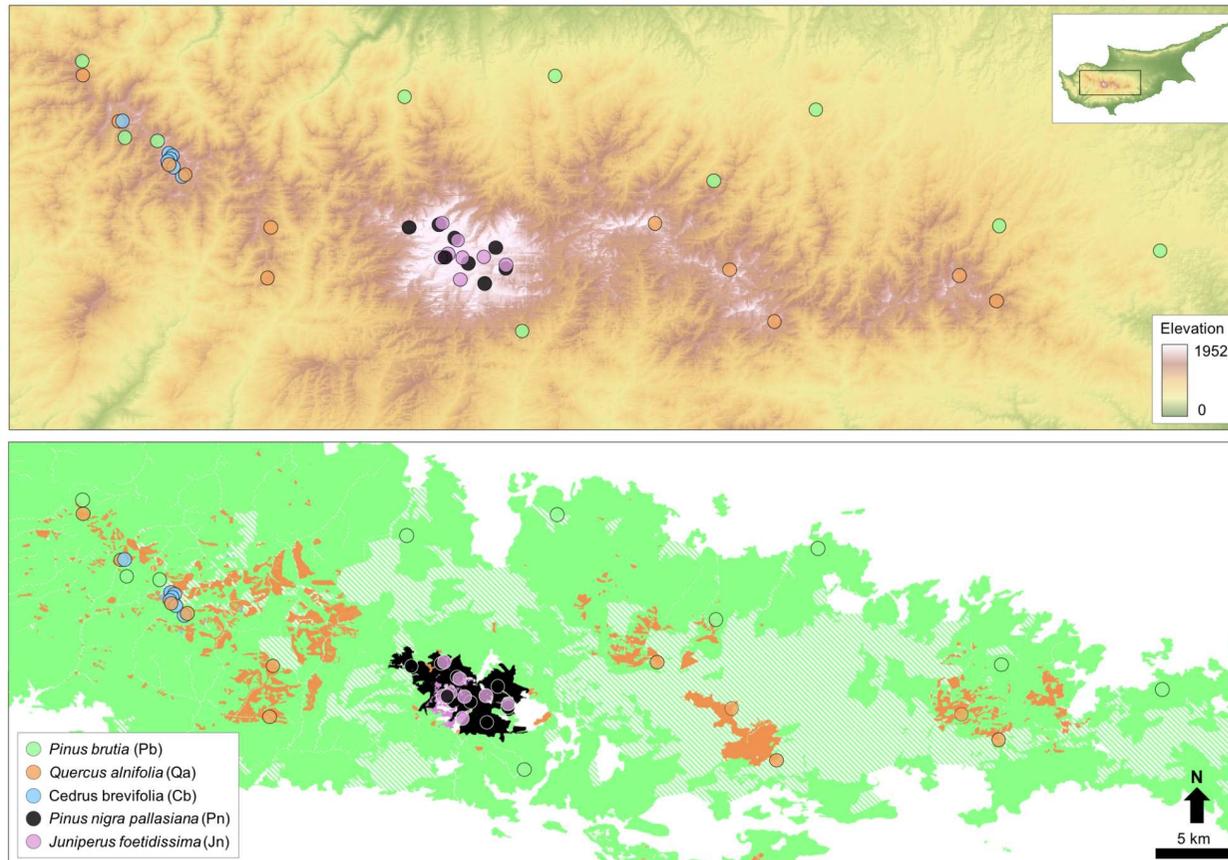


Pinus nigra



Cyprus montane forests as a case study

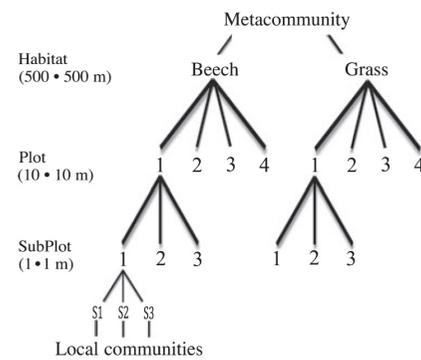
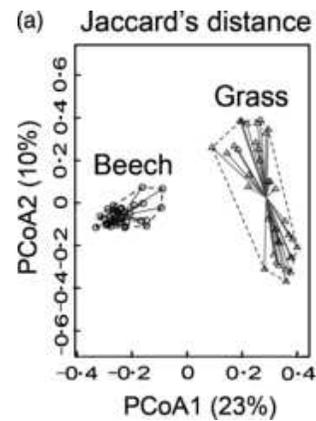
FOREST HABITAT DISTRIBUTION



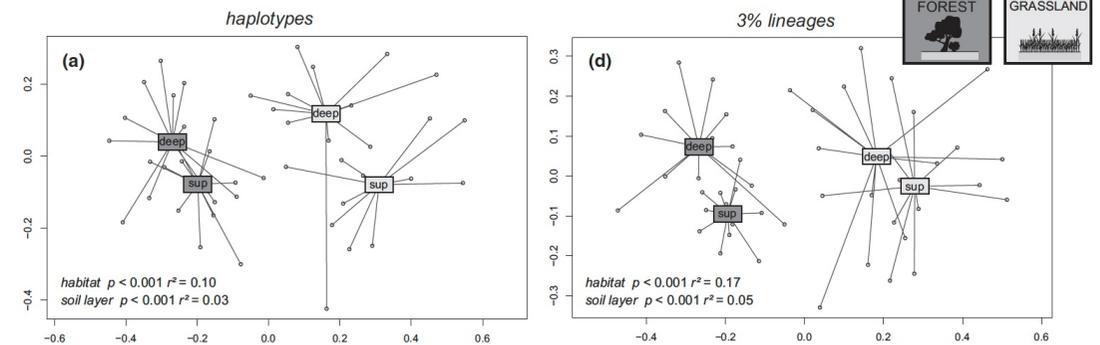


Case study: questions

Question 1: Previous studies on soil microarthropods show that forests vs. grasslands harbor largely different metacommunities. Does **forest type** also impose a **habitat filtering** effect?



Caruso *et al.* (2012) *Journal of Animal Ecology*



Arribas *et al.* (2021) *Molecular Ecology*



Case study: questions

Question 2: What is the relative contribution of **spatial vs. environmental** processes as drivers of **within-habitat** metacommunity structure?

Received: 25 June 2018 | Revised: 15 November 2018 | Accepted: 22 November 2018
DOI: 10.1111/jbi.13501



RESEARCH PAPER

WILEY **Journal of Biogeography**

Oribatid mites show how climate and latitudinal gradients in organic matter can drive large-scale biodiversity patterns of soil communities

Tancredi Caruso¹ | Ina Schaefer² | Frank Monson³ | Aidan M. Keith⁴

Received: 30 March 2020 | Revised: 27 July 2020 | Accepted: 31 July 2020
DOI: 10.1111/mec.15591



FROM THE COVER

MOLECULAR ECOLOGY WILEY

The limited spatial scale of dispersal in soil arthropods revealed with whole-community haplotype-level metabarcoding

Paula Arribas^{1,2,3} | Carmelo Andújar^{1,2,3} | Antonia Salces-Castellano¹ | Brent C. Emerson¹ | Alfred P. Vogler^{2,3}

Morphology-based studies emphasize environmental filtering, while metabarcoding studies emphasize dispersal limitation.

- taxonomic resolution?
- scale-dependency?
- context-dependency?



Case study: questions

Question 3: Focusing on the highly fragmented endemic *Quercus alnifolia* habitat, does **habitat connectivity** play an important role in metacommunity structure?

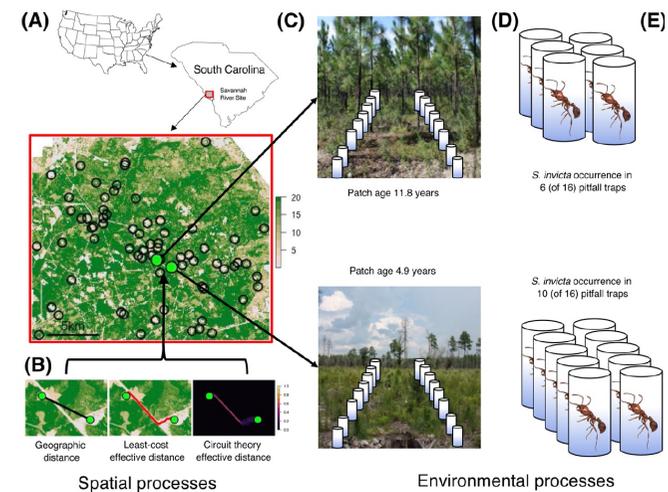
Landscape Ecol
<https://doi.org/10.1007/s10980-021-01203-z>



RESEARCH ARTICLE

Accounting for connectivity alters the apparent roles of spatial and environmental processes on metacommunity assembly

Julian Resasco · Robert J. Fletcher Jr



Resasco & Fletcher (2021) *Landscape Ecology*



Case study: questions

Question 4: Do we obtain equivalent α and β diversity patterns when using **ASVs** vs. **OTUs**?

OPEN

The ISME Journal (2017) 11, 2639–2643
www.nature.com/ismej

PERSPECTIVE

Exact sequence variants should replace operational taxonomic units in marker-gene data analysis

Benjamin J Callahan¹, Paul J McMurdie² and Susan P Holmes³

¹Department of Population Health and Pathobiology, NC State University, Raleigh NC, USA; ²Whole Biome Inc, San Francisco CA, USA and ³Department of Statistics, Stanford University, Stanford CA, USA

frontiers
in Ecology and Evolution

REVIEW
published: 11 August 2020
doi: 10.3389/fevo.2020.00248



Putting COI Metabarcoding in Context: The Utility of Exact Sequence Variants (ESVs) in Biodiversity Analysis

Teresita M. Porter and Mehrdad Hajibabaei*

Centre for Biodiversity Genomics and Department of Integrative Biology, University of Guelph, Guelph, ON, Canada

Joos et al. BMC Genomics (2020) 21:733
https://doi.org/10.1186/s12864-020-07126-4

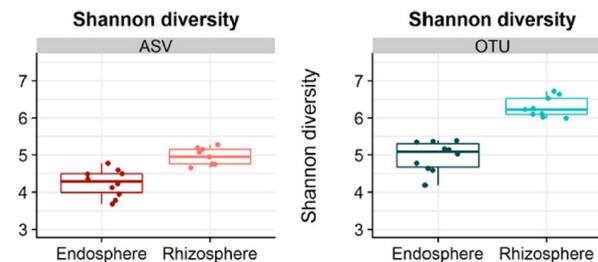
BMC Genomics

RESEARCH ARTICLE

Open Access

Daring to be differential: metabarcoding analysis of soil and plant-related microbial communities using amplicon sequence variants and operational taxonomical units

Lisa Joos^{1,2†}, Stien Beirinckx^{1,3,4†}, Annelies Haegeman¹, Jane Debode¹, Bart Vandecasteele¹, Steve Baeyen¹, Sofie Goormachtig^{3,4}, Lieven Clement² and Caroline De Tender^{1,2*}



ASVs can now be reliably recovered and offer:

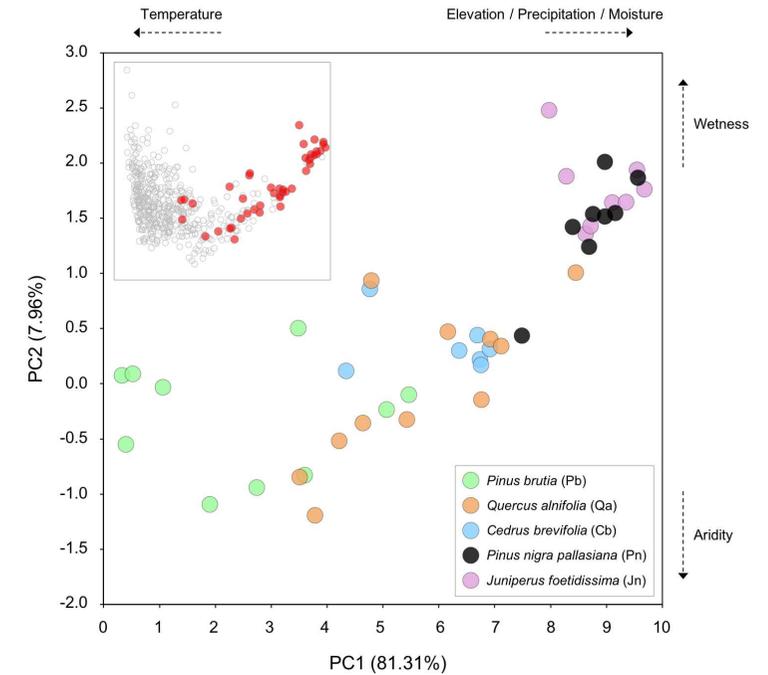
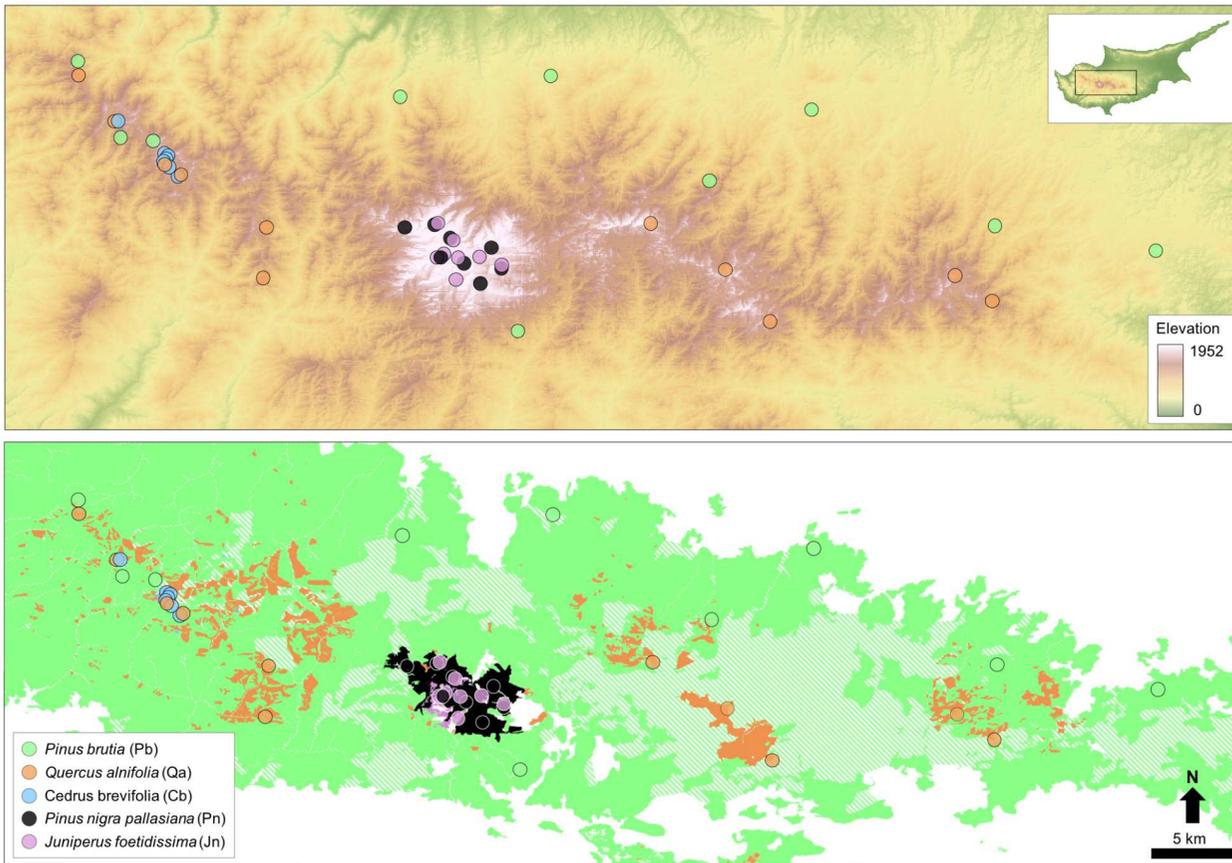
- Intrinsic biological significance
- Higher resolution
- Reproducibility
- Comparability among studies
- Equivalent diversity estimates (?)

Should they replace OTUs?



Case study: methods

FOREST HABITAT DISTRIBUTION & SAMPLING POINTS



Variables	Code	Data source ^{(1) (2) (3)}	PC1	PC2
Elevation	ALT	NASA STRM	0.981	0.020
Annual mean temperature	BIO1	WorldClim	-0.989	-0.021
Maximum temperature of warmest month	BIO5	WorldClim	-0.883	0.032
Minimum temperature of coldest month	BIO6	WorldClim	-0.955	-0.078
Annual precipitation	BIO12	WorldClim	0.984	-0.010
Precipitation of wettest quarter	BIO16	WorldClim	0.968	-0.042
Precipitation of driest quarter	BIO17	WorldClim	0.952	0.079
Climatic moisture index	CMI	ENVIREM	0.990	0.025
Thornthwaite aridity index	TAI	ENVIREM	-0.649	-0.430
Topographic wetness index	TWE	ENVIREM	-0.538	0.772
Explained variance (%)			81.312	7.965



Case study: methods

soil sampling and extraction for soil arthropods

SOIL SAMPLE COLLECTING



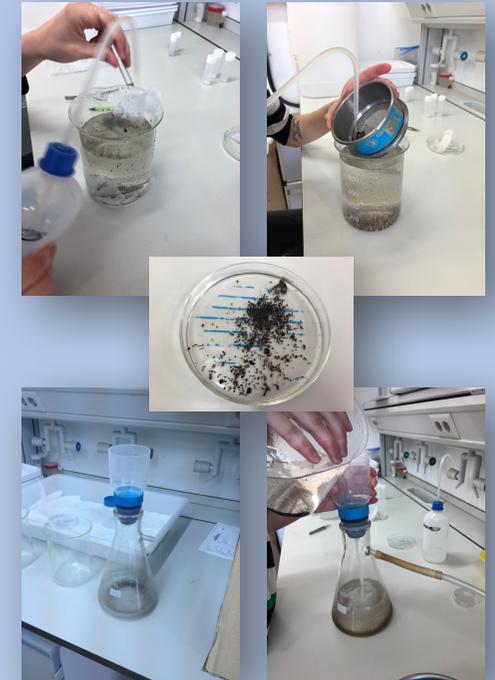
FLOTATION I



BERLESE



FLOTATION II



Flotation-Berlese-Flotation protocol (Arribas et al., 2016, *Methods in Ecology and Evolution*)



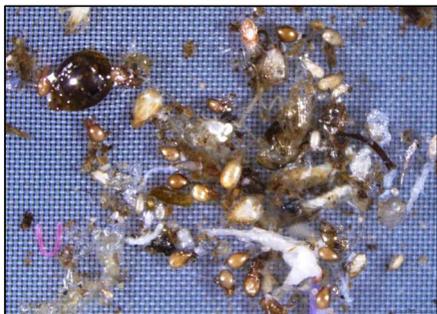
Case study: methods

88 bulk samples → Illumina MiSeq
418bp of Folmer's COI barcode region

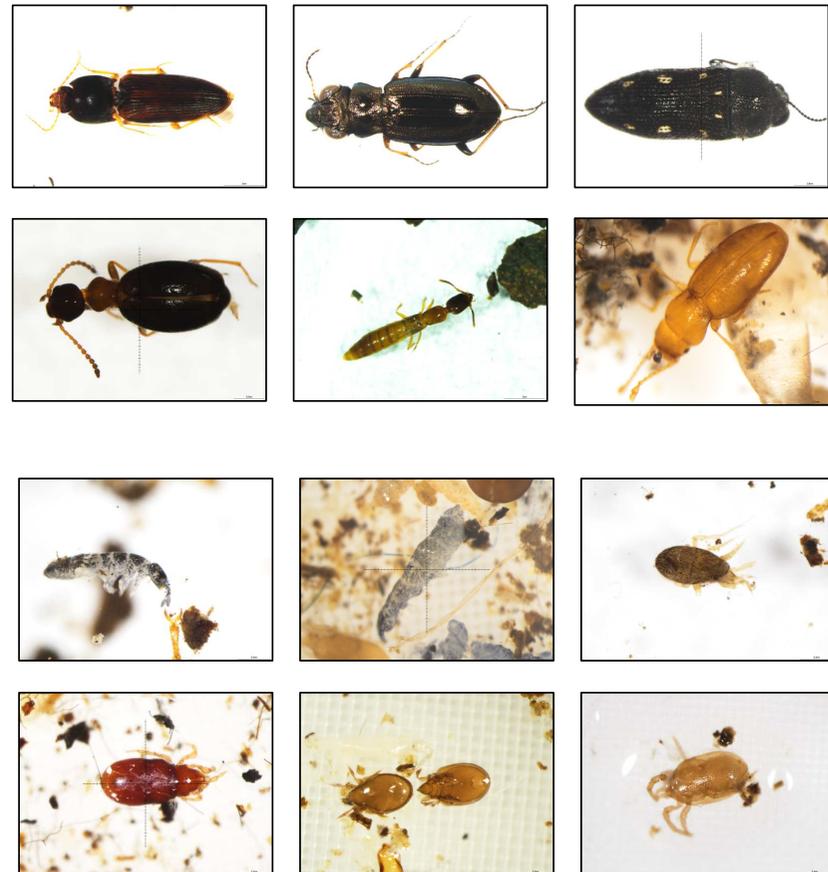
Coleoptera



Acari &
Collembola



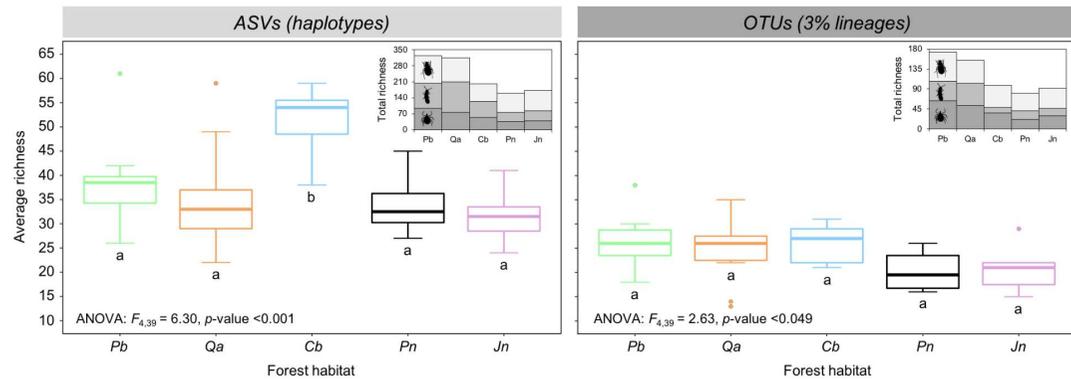
344 voucher specimens → Sanger
Folmer's COI barcode region (658bp)





Case study: methods

Step	Software and version
Primer removal	CUTADAPT v.2.10
Merging	PEAR v.0.9.11
Quality filtering	VSEARCH v.2.9.1
Dereplication I	VSEARCH v.2.9.1
Length filtering	VSEARCH v.2.9.1
Denoising	VSEARCH v.2.9.1
Chimera filtering	VSEARCH v.2.9.1
Dereplication II	VSEARCH v.2.9.1
BLAST search	NCBI-BLAST v.2.8.1
Community table generation	VSEARCH v.2.9.1
Read-abundance filtering	METAMATE v.0.1b18

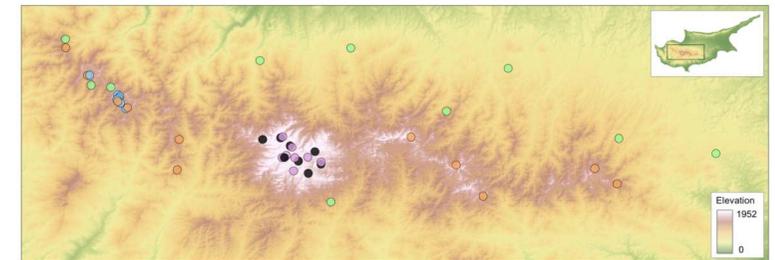
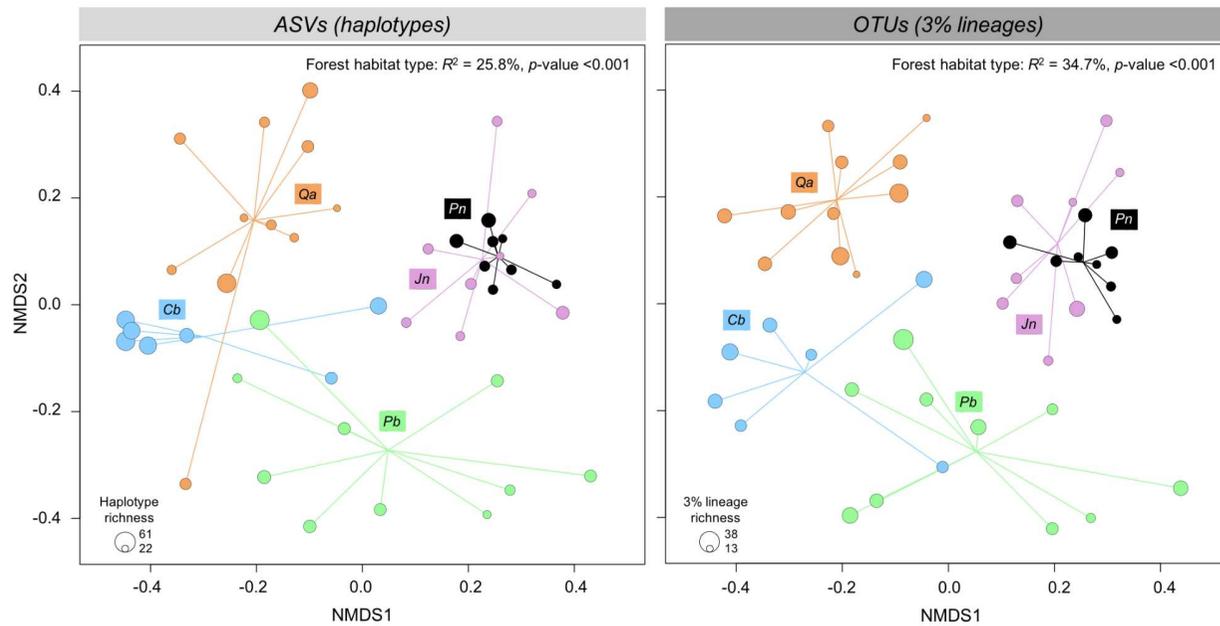


Total ASVs: 907
Total OTUs: 386



Case study: results

Question 1: strong habitat filtering imposed by forest type (but less for two highland forest types)

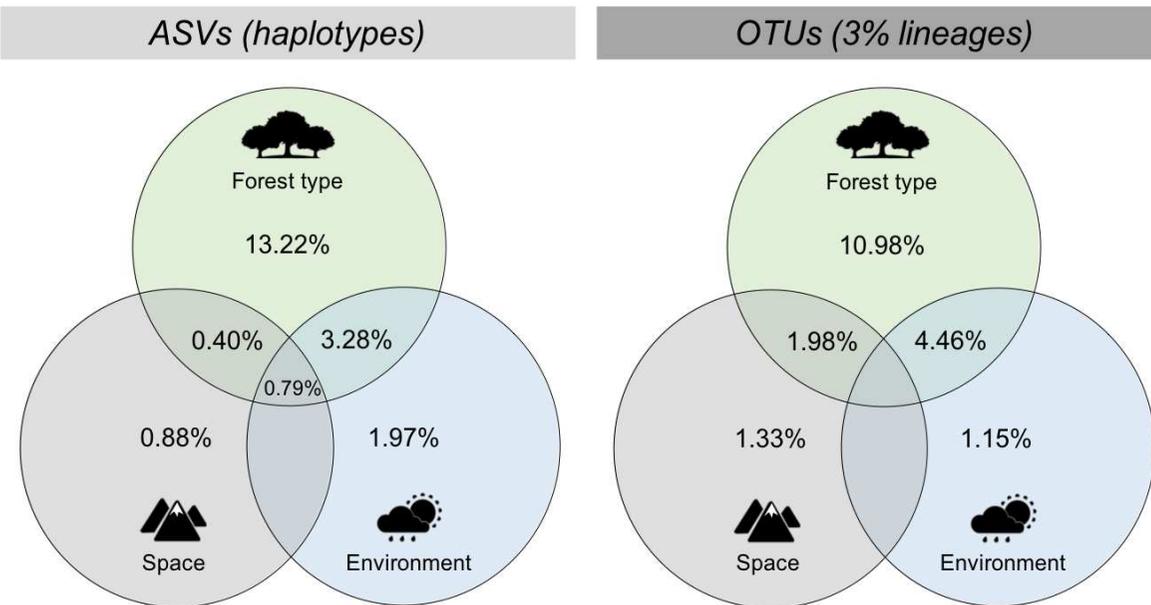


Non-metric multidimensional scaling ordination of sampling sites according to community dissimilarity



Case study: results

Question 1: forest type is the most important explanatory variable of the variance in community composition



Variance partitioning conducted on the best-fit dbRDA models



Case study: results

Question 2: At within-habitat scale, in most cases environmental variation plays a more important role than spatial distances

Dataset	ASVs (haplotypes)				OTUs (3% lineages)			
	Predictors	F	p-value	R ² _{ADJ}	Predictors	F	p-value	R ² _{ADJ}
<i>Pinus brutia</i> (Pb)	ENV _{PC1}	4.808	0.048	0.024	ENV _{PC1}	1.650	0.003	0.067
<i>Quercus alnifolia</i> (Qa)	ENV _{PC1}	1.618	0.002	0.058	SPA _{PCNM1}	2.892	0.002	0.231
					SPA _{PCNM2}	1.850	0.007	
<i>Cedrus brevifolia</i> (Cb)	ENV _{PC1}	4.808	0.041	0.388	ENV _{PC1}	3.602	0.006	0.420
					ENV _{PC2}	2.014	0.024	
<i>P. nigra</i> (Pn) + <i>J. foetidissima</i> (Jn)	ENV _{PC1}	1.459	0.047	0.030	ENV _{PC1}	1.687	0.026	0.092
					SPA _{PCNM3}	1.755	0.018	

distance-based redundancy analyses (dbRDA) on community composition (Simpson dissimilarity index, β_{SIM})

- o taxonomic resolution → same between two studies (all field, lab, bioinformatic methods same)
 - o scale-dependency → for some habitats, same sampling scale between two studies
 - o context-dependency → steeper elevation and environmental gradients in our study



Received: 30 March 2020 | Revised: 27 July 2020 | Accepted: 31 July 2020

DOI: 10.1111/mec.15591

FROM THE COVER

MOLECULAR ECOLOGY WILEY

The limited spatial scale of dispersal in soil arthropods revealed with whole-community haplotype-level metabarcoding

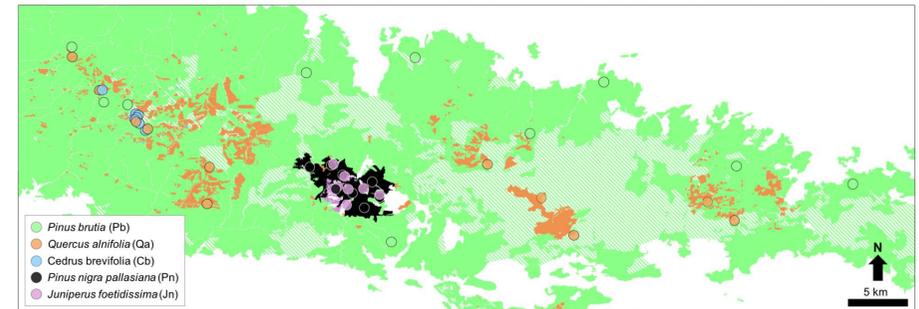
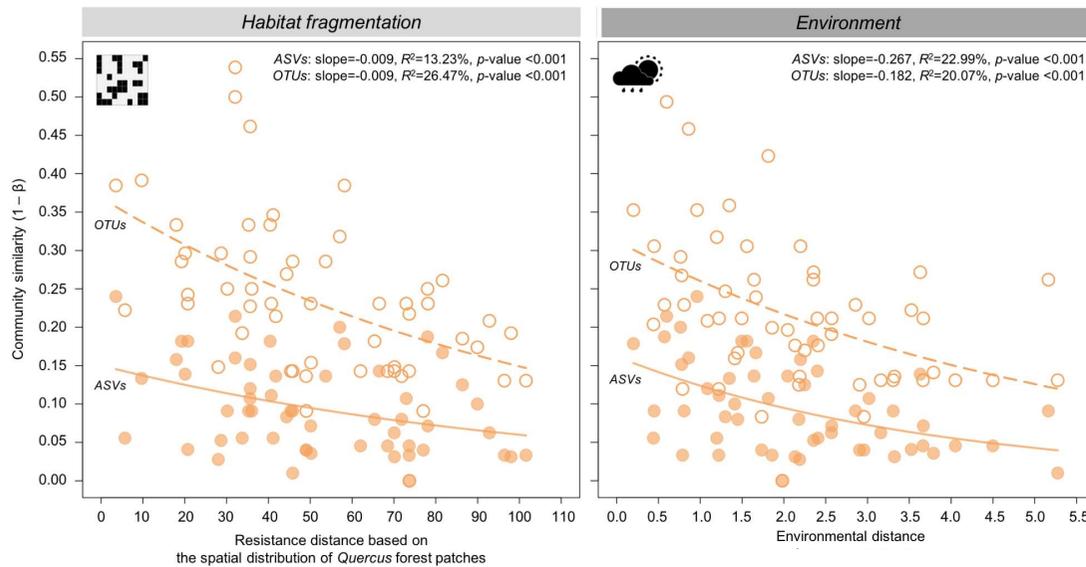
Paula Arribas^{1,2,3} | Carmelo Andújar^{1,2,3} | Antonia Salces-Castellano¹ | Brent C. Emerson¹ | Alfred P. Vogler^{2,3}

Arribas et al. (2021) identified greater role of spatial distances



Case study: results

Question 3: Habitat connectivity (resistance distances) and environmental distances jointly drive community dissimilarity in the highly fragmented *Quercus alnifolia* habitat



ASVs (haplotypes)						OTUs (3% lineages)					
Predictors	Coefficient	t	p-value	R^2	R_i^2	Predictors	Coefficient	t	p-value	R^2	R_i^2
<u>Explanatory terms</u>						<u>Explanatory terms</u>					
FRA _{IBR}	0.078	2.745	0.014	0.112	0.013	FRA _{IBR}	0.246	4.434	0.003	0.246	0.020
ENV _{PC1-2}	0.106	3.889	0.000	0.210	0.013	ENV _{PC1-2}	0.172	3.464	0.005	0.158	0.020
<u>Rejected terms</u>						<u>Discarded terms</u>					
SPA _{TWD}		-0.209	0.839			SPA _{TWD}		0.442	0.654		
TRI _{IBR}		1.911	0.272			TRI _{IBR}		0.569	0.704		
NULL _{IBR}		-1.843	0.257			NULL _{IBR}		-0.250	0.827		

Multiple matrix regression with randomization (MRR) analyses on community composition



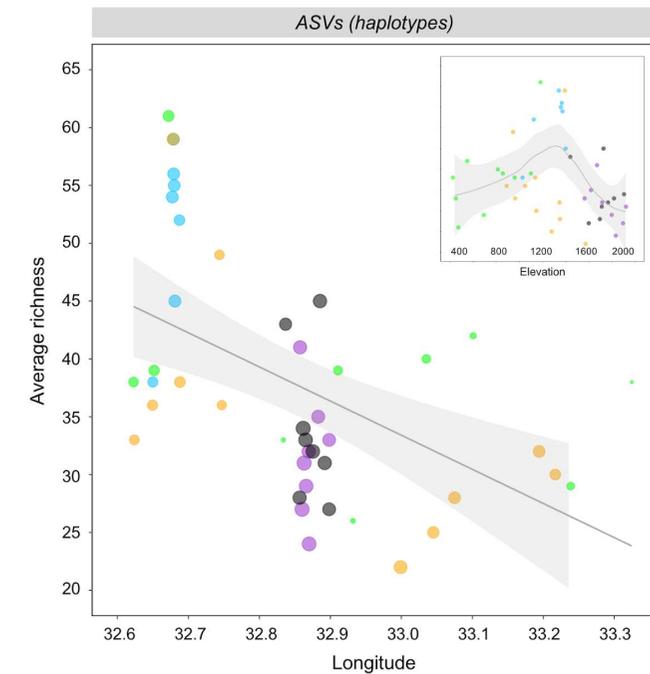
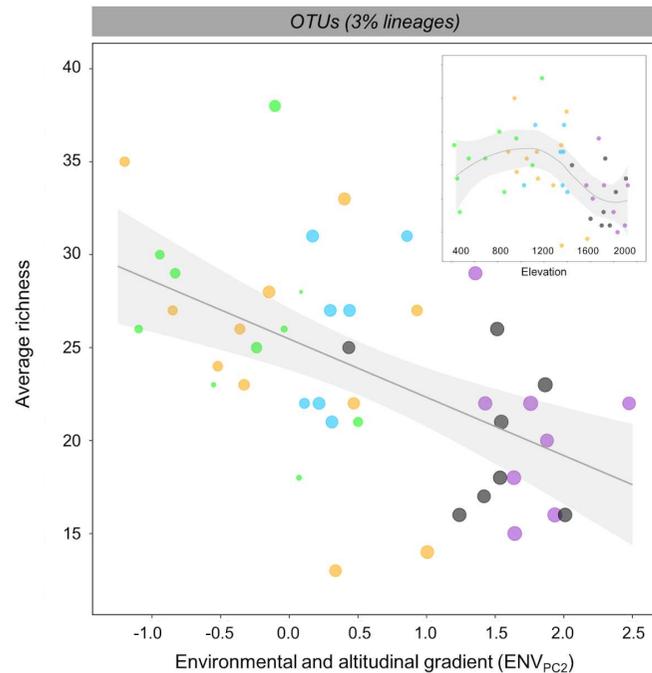
Case study: results

Question 4: similar beta diversity patterns between **ASVs** vs. **OTUs**, but different alpha

OTU richness: environmental/altitudinal gradient

vs.

ASV richness: longitudinal gradient



→ Coincides with lower genetic diversity of forest trees towards the East (Eliades et al., 2011; 2018)



Case study: general conclusions

- DNA metabarcoding provides great opportunities to assess the drivers of metacommunity structure across unexplored fractions of biodiversity
- Implementation of harmonised field, lab and bioinformatics protocols increases comparability among datasets and enables to distinguish methodological biases from context-dependency
- Complementarity of ASVs and OTUs , side-by-side comparisons can help to detect processes that produce uncoupled patterns between the two levels of diversity



Case study: next steps

Intra-OTU genetic diversity

Ecology, 102(1), 2021, e03224
© 2020 by the Ecological Society of America

Freshwater zooplankton metapopulations and metacommunities respond differently to environmental and spatial variation

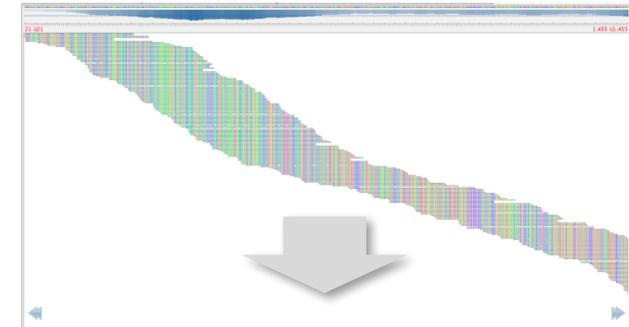
GILLIAN K. MARTIN ^{1,4}, BEATRIX E. BEISNER, ¹ FRÉDÉRIC J. J. CHAIN, ² MELANIA E. CRISTESCU, ³ PAUL A. DEL GIORGIO, ¹ AND ALISON M. DERRY ¹

¹Department of Biological Sciences, Groupe de Recherche Interuniversitaire en Limnologie (GRIL), University of Québec at Montreal, Québec H2X 3Y7 Canada

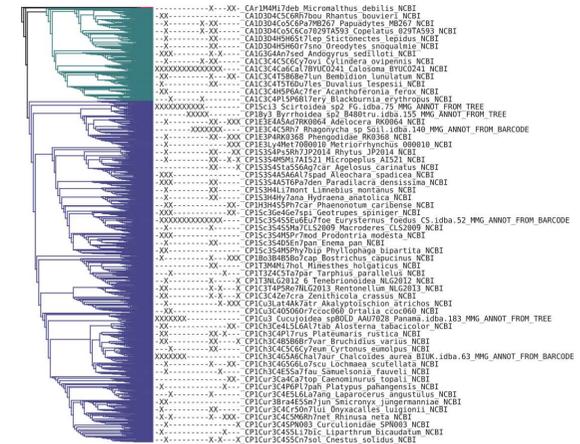
²Department of Biological Science, University of Massachusetts Lowell, Massachusetts 01854 USA

³Department of Biology, Groupe de Recherche Interuniversitaire en Limnologie (GRIL), McGill University, Québec H3A 1B1 Canada

Shotgun sequencing Mitogenome assembly



Phylogenies



Estimating intraspecific genetic diversity from community DNA metabarcoding data

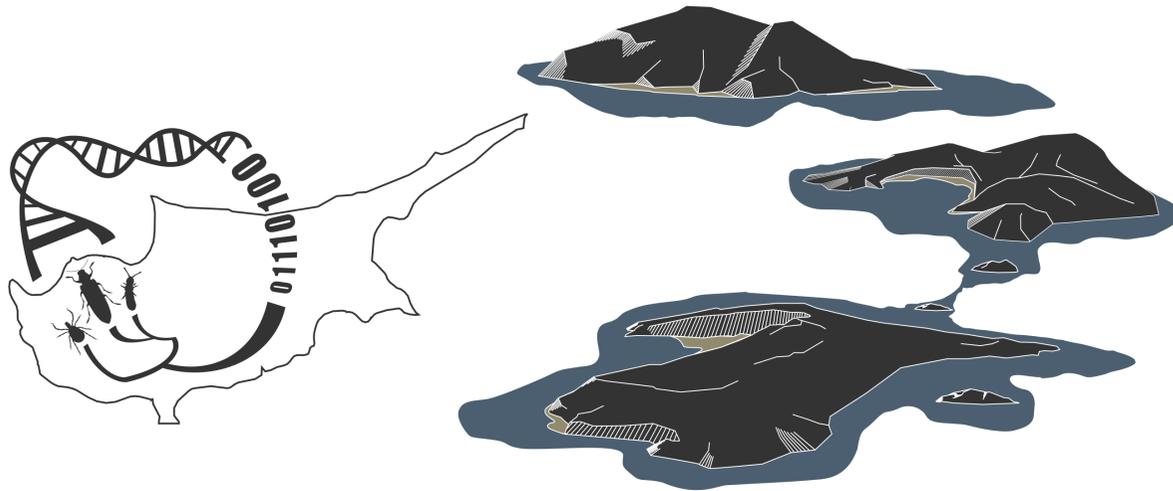
Vasco Elbrecht^{1,2}, Ecatarina Edith Vamos¹, Dirk Steinke² and Florian Leese^{1,3}

¹Aquatic Ecosystem Research, University of Duisburg-Essen, Essen, North Rhine-Westphalia, Germany

²Centre for Biodiversity Genomics, University of Guelph, Guelph, ON, Canada

³Centre for Water and Environmental Research (ZWU) Essen, University of Duisburg-Essen, Essen, North Rhine-Westphalia, Germany

Thank you! Any questions?



The iBioGen project has received funding from the *European Union's Horizon 2020 research and innovation programme* under grant agreement No 810729.