A novel technique for exposing Arctic ecosystem change

Yinqiu Ji[1], Tea Huotari[2], Tomas Roslin[2,3], Niels Martin Schmidt[4,5], Jiaxin Wang[1], Douglas W. Yu[1,6,7], Otso Ovaskainen[8,9]

Abstract

High-throughput sequencing offers promising tools for the molecular characterization of eukaryotic community structure, but accurate quantification of species abundances remains a key challenge. Mitogenomics uses mitogenomes as easily-assembled 'super-barcodes' for the taxonomic assignment of reads from shotgun-sequenced bulk samples. We introduce simple yet crucial additions to extant mitogenomic approaches. Through these modifications, we achieve high accuracy (R^2>0.95) of intraspecific abundance estimates from community samples of known composition. As a proof of concept, we use community data obtained by this method to resolve ecological signal in 17 years of arthropod samples from the High Arctic. Overall, the method promises cost-efficient and reliable quantification of ecological communities where species complements are known.

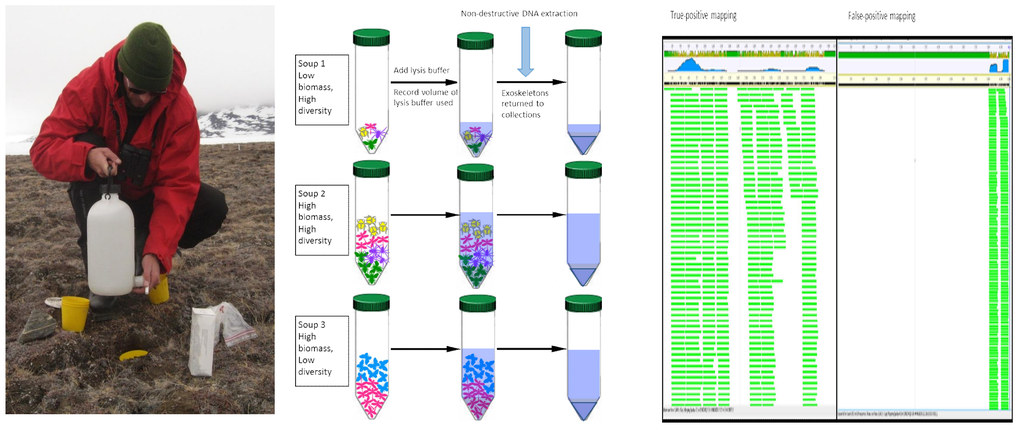
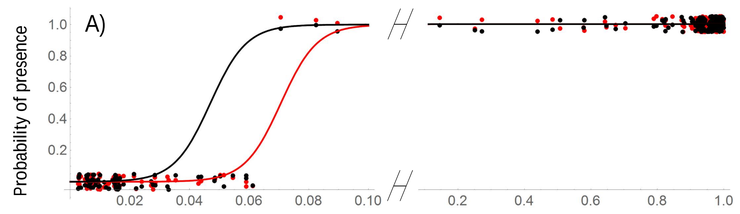


Figure 1. An overview of the challenges offered by bulk samples of DNA from insect communities ("soups", collected in the left-hand part of the fig) between sample extraction (mid part of figure) to final output in terms of sequence reads mapped onto reference mitogenomes (right-hand part of fig). Our approach allows quantification of both species composition and biomass, as illustrated by the three types of samples contrasted in the vertical plane.



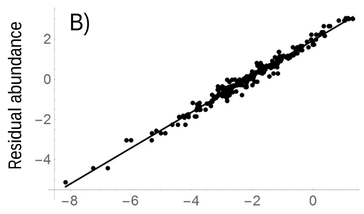


Figure 2. Using mock community data (i.e. DNA blends of known species composition) to parameterize statistical models for converting mitogenome sequence mapping into probabilities of species presence and estimates of DNA abundance. Panel A illustrates a logistic regression model predicting the probability of species presence based on mapping and run identity (the red and black colors). The data points have been jittered vertically to reveal overlapping points. Panel B illustrates linear regressions predicting species abundance (log-transformed amount of DNA in ng) as a function of mapped reads.

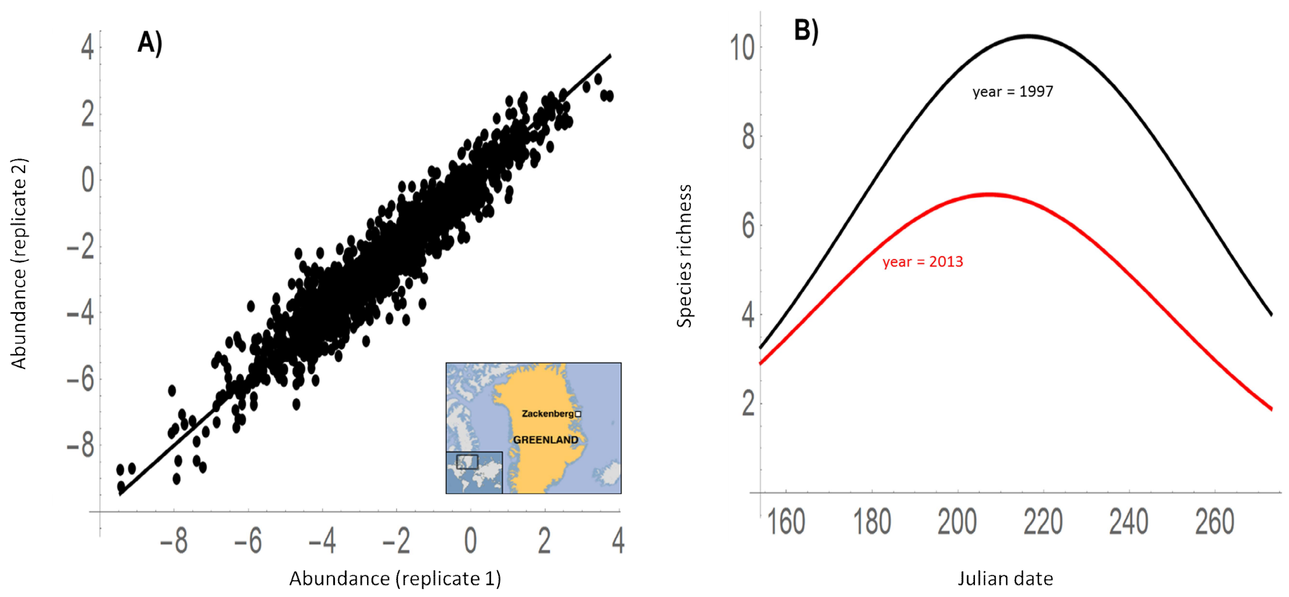


Figure 3 . Results from real arthropod samples (A, B) from Zackenberg, Northeast Greenland, from 1997 and 2013, collected with yellow pitfall traps (C) and processed using the mitogenomic pipeline outlined in Fig. 1. Panel A examines the technical validity of the data by comparing run-corrected abundance estimates for species scored in replicated sequencing rounds. Panel B shows the species richness for the first year of the study (1997, black line) and the last year of the study (2013, red line), predicted by a Poisson regression model fitted to the data. As can be seen from (A), our method offers highly repeatable estimates, and as can be seen from (B), it reveals ecological signal present in the data, demonstrated by an advance in phenology in this high-arctic community (note shift in peak species richness towards an earlier date).

[1] State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, 650223, China

[2] Spatial Foodweb Ecology Group, Department of Agricultural Sciences, University of Helsinki, P.O. Box 27, FI-00014 Helsinki, Finland

[3] Spatial Foodweb Ecology Group, Department of Ecology, Swedish Univ. of Agricultural Sciences, Box 7044, SE-750 07 Uppsala, Sweden

[4] Arctic Research Centre, Aarhus University, DK-8000, Aarhus, Denmark

[5] Department of Bioscience, Aarhus University, DK-4000, Roskilde, Denmark

[6] School of Biological Sciences, University of East Anglia, Norwich Research Park, Norwich, Norfolk, NR47TJ UK

[7] Center for Excellence in Animal Evolution and Genetics, Chinese Academy of Sciences, Kunming Yunnan, 650223 China

[8] Organismal and Evolutionary Biology Research Programme, University of Helsinki, P.O. Box 65, FI-00014, Helsinki, Finland

[9] Centre for Biodiversity Dynamics, Department of Biology, Norwegian University of Science and Technology, N-7491, Trondheim, Norway

SUOMEN AKATEMIA

Ella ja Georg Ehrnroothin säätiö