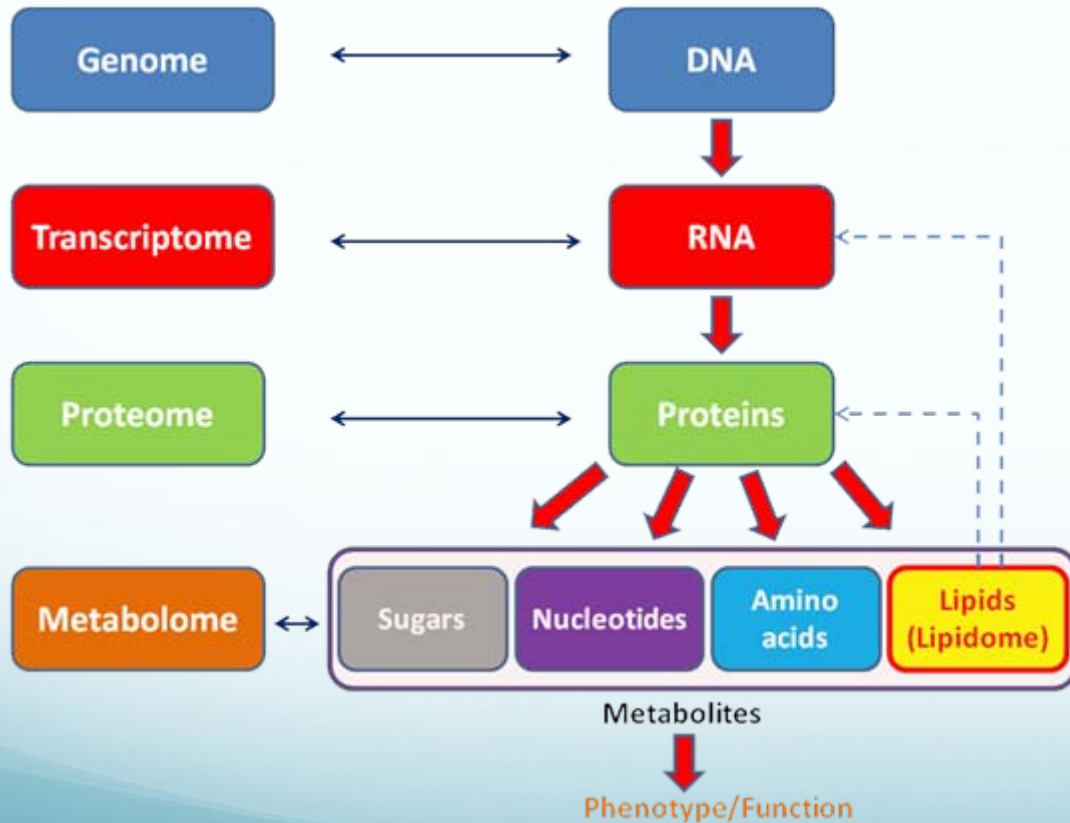


A Gentle Introduction to High Throughput Sequencing Applications and Study Design



Alexander S. Hall
allopatry.com



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Genome sequencing cost as estimated by NHGRI
(September 2001 to April 2014)



Sequences Can Tell Your Story!

Multi-omics of permafrost, active layer and thermokarst bog soil microbiomes

Jenni Hultman^{1†}, Mark P. Waldrop², Rachel Mackelprang^{3,4}, Maude M. David¹, Jack McFarland², Steven J. Blazewicz², Jennifer Harden², Merritt R. Turetsky⁵, A. David McGuire⁶, Manesh B. Shah^{7†}, Nathan C. VerBerkmoes⁷, Lang Ho Lee⁸, Kostas Mavrommatis^{4†} & Janet K. Jansson^{1,4,9,10†}

TECHNICAL REVIEW

Sequencing breakthroughs for genomic ecology and evolutionary biology

MATTHEW E. HUDSON

Department of Crop Sciences, University of Illinois, Urbana, 334 NSRC, 1101 W. Peabody Blvd., IL 61801, USA

Ecological coherence of diversity patterns derived from classical fingerprinting and Next Generation Sequencing techniques

Angélique Gobet,^{1,2*} Antje Boetius^{1,3} and Alban Ramette^{1*}

Environmental monitoring through protist next-generation sequencing metabarcoding: assessing the impact of fish farming on benthic foraminifera communities

JAN PAWLOWSKI,* PHILIPPE ESLING,*† FRANCK LEJZEROWICZ,* TOMAS CEDHAGEN‡ and THOMAS A. WILDINGS§

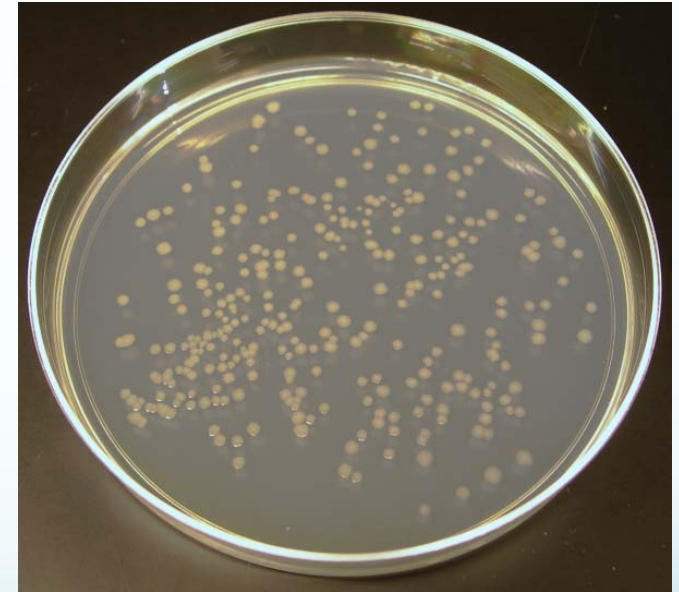
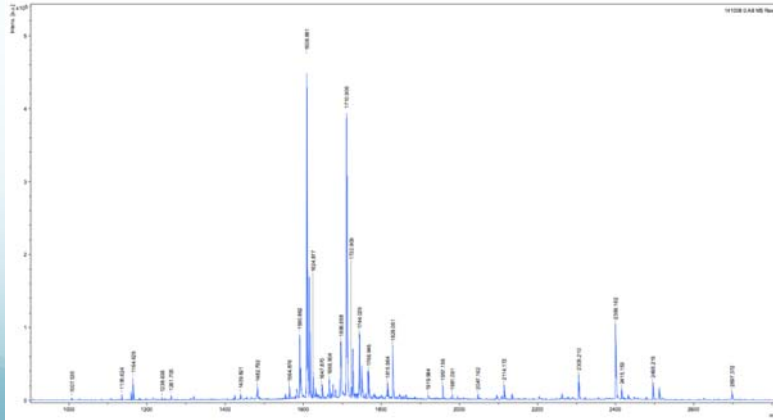
**Department of Genetics and Evolution, University of Geneva, Sciences 3, 30, Quai Ernest Ansermet, CH-1211, Geneva 4, Switzerland, †IRCAM, UMR 9912, Université Pierre et Marie Curie, Paris, France, ‡Department of Biological Sciences, Aquatic Biology, Aarhus University, Aarhus, Denmark, §Ecology Department, SAMS, Scottish Marine Institute, Oban, Argyll, UK*

HTS Applications

- Species richness measurements
- Resequence soil over time points
- Detect hybrid zones
- Indirect alternative to mark-recapture

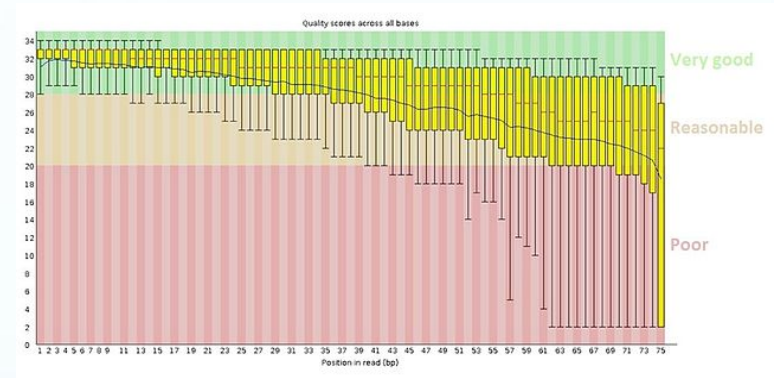
“Omics” Techniques

- Barcoded 16S Sequencing
- Genomic subsampling (RADseq)
- Proteomics (MALDI)

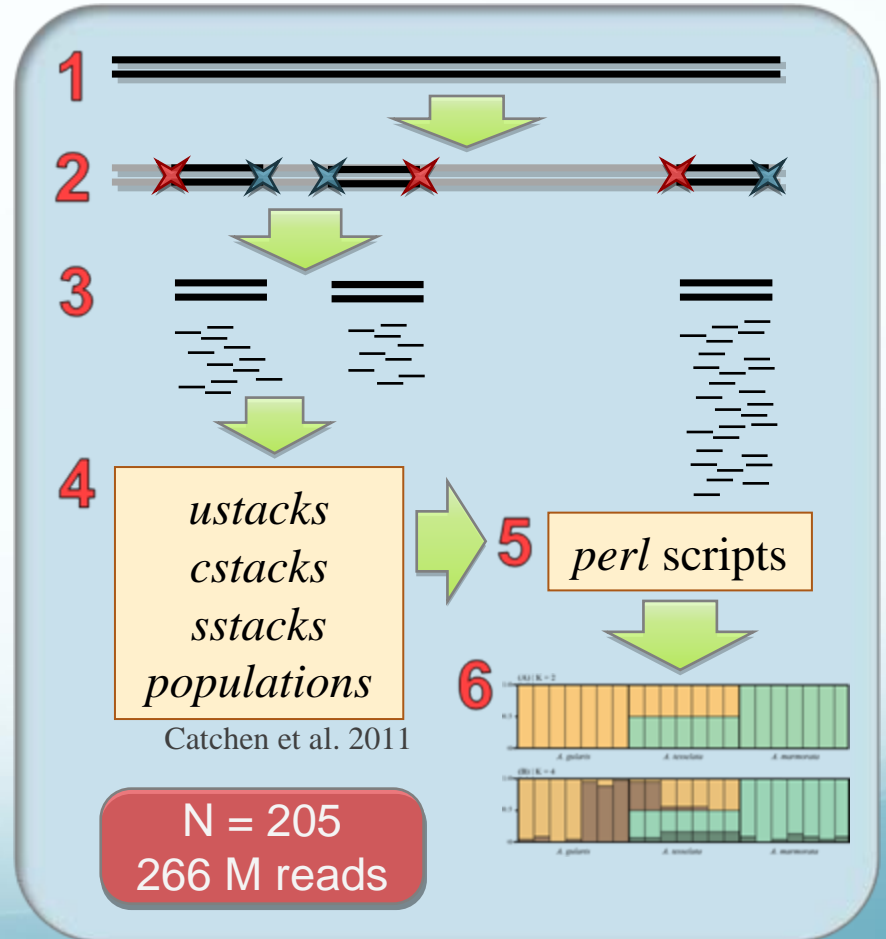
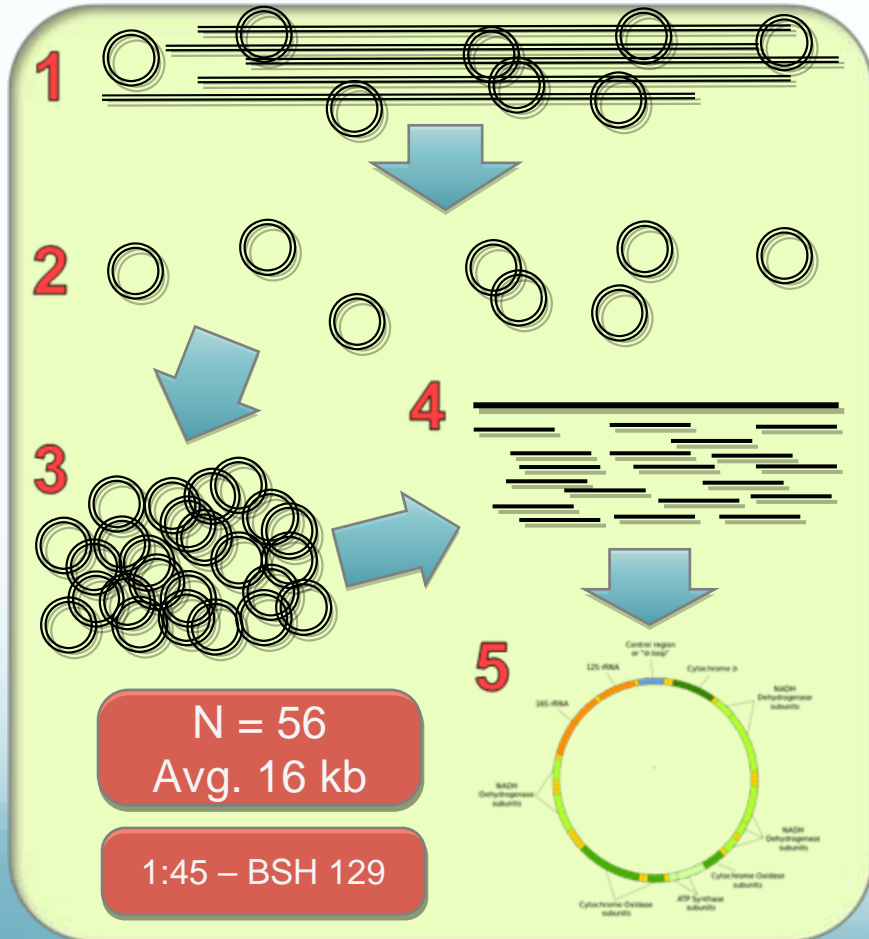


HTS Considerations

- Data management (lots of space!)
- Data problems:
 - Ascertainment bias
 - Sequencing errors (reverse reads)
 - Uneven coverage
- Genotype calling vs genotype likelihoods
- Clever controls

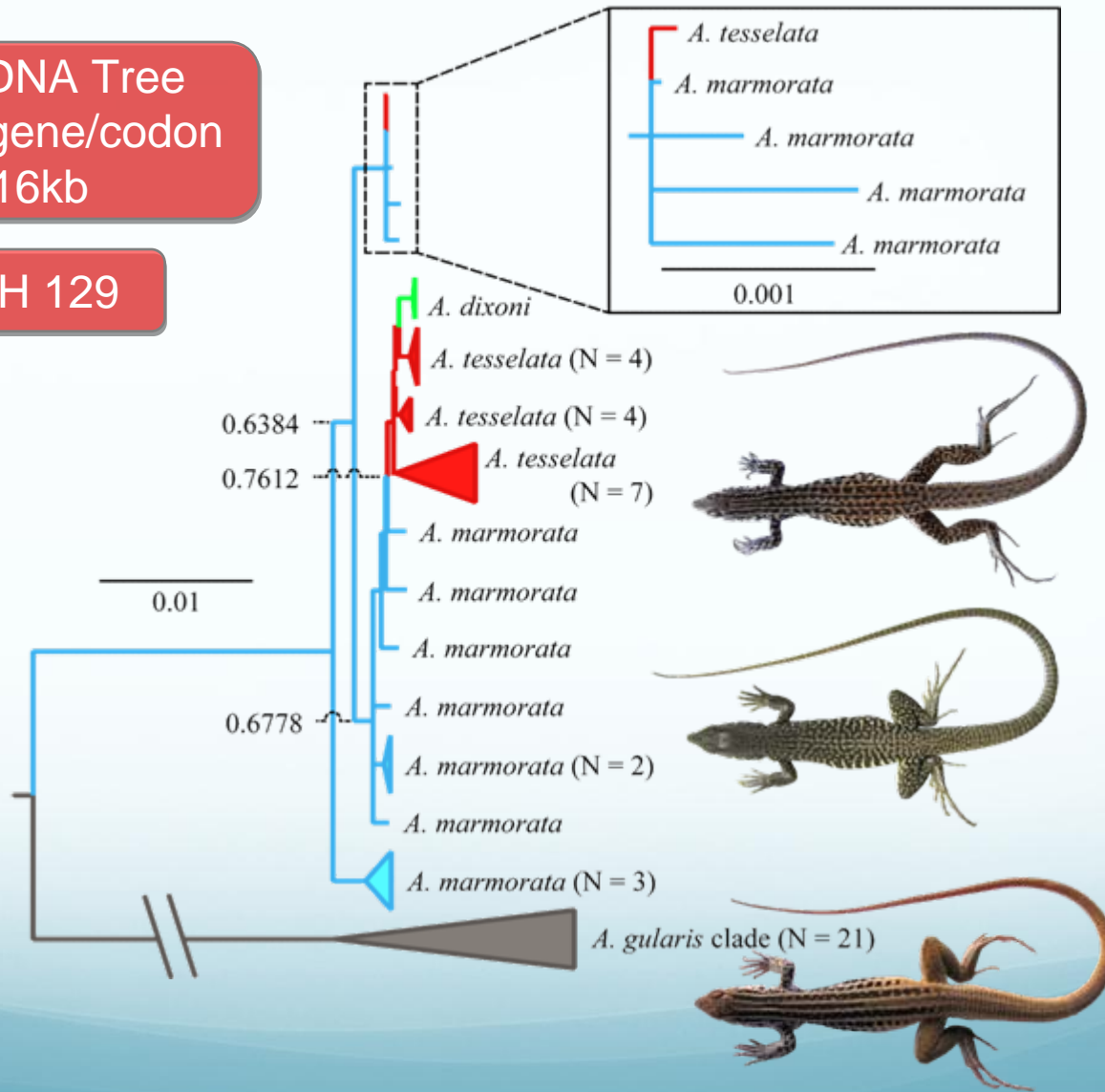


Entire Mitochondria and ddRADseq



Bayesian mtDNA Tree
Partitioned by gene/codon
N=42, ~16kb

1:45 – BSH 129



HTS Resources

- [Peterson et al. 2012](#) – ddRADseq method
- [Genohub](#) – Online NGS experiment creator
- [CoreGenomics](#) – Nice blog outlining NGS advances/critiques
- [Stacks](#) – Software for calling genotypes from NGS data
- [adegenet](#) – R package for genetic data exploration



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- Fujita Lab



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- Graduate Student Senate
- UTA Biology
- MKF Startup Funds



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