

**USING BARCODE DATA IN STUDIES OF MOLECULAR  
AND EVOLUTIONARY DYNAMICS**

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The Banbury Center, Cold Spring Harbor Laboratory, 28-31 October 2007

Organized By: David E. Schindel, Smithsonian Institution,  
Mark Blaxter, University of Edinburgh,  
Paul Gilna, University of California, San Diego,  
Richard G. Harrison, Cornell University,  
David M. Rand, Brown University,  
Michel Veuille, Museum d'Histoire Naturelle

**PROGRAM**

**Sunday, 28 October**

Afternoon Arrival at Robertson House, Banbury Center, for registration and room assignment

6:00 pm Reception at Robertson House

7:30 pm Dinner at Robertson House

Jesse H. Ausubel, Rockefeller University, New York:  
Historical background to Banbury 3.

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**Monday, 29 October**

7:00-8:15 am Breakfast at Robertson House

8:35-8:45 am Jan A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York:  
Introductory remarks

8:35-12:15 pm **SESSION 1: Overview of Barcode Data**  
Chair:

8:45-9:05 am David E. Schindel, Smithsonian Institution, Washington, D.C.:  
Linking barcoded data to multiple users.

9:05-9:15 am Discussion

- 9:15-9:35 am Robert Hanner, University of Guelph, Ontario, Canada:  
BARCODE data standard and trace analysis.
- 9:35-9:45 am Discussion
- 9:45-10:05 am Sujeevan Ratnasingham, University of Guelph, Ontario, Canada:  
The Barcode Life Data Systems: An informatics platform for the biodiversity  
informatics community.
- 10:05-10:15 am Discussion
- 10:15-10:45 am Break
- 10:45-11:05 am Mehrdad Hajibabaei, University of Guelph, Ontario, Canada:  
Minimalist barcode sequences.
- 11:05-11:15 am Discussion
- 11:15-12:15 pm General Discussion
- 12:30 pm Luncheon at Robertson House
- 2:00-6:00 pm **SESSION 2: Species Boundaries, Speciation Processes and Models.**  
Chair: Richard G. Harrison, Cornell University, Ithaca, New York
- 2:00-2:20 pm Richard G. Harrison, Cornell University, Ithaca, New York:  
Multi-locus approaches to defining species boundaries.
- 2:20-2:30 pm Discussion
- 2:30-2:50 pm Mark Blaxter, University of Edinburgh, United Kingdom:  
Defining and constructing MOTUs.
- 2:50-3:00 pm Discussion
- 3:00-3:20 pm Mark Stoeckle, Rockefeller University, New York:  
Iterative taxonomy-DNA barcoding cycle provides insights into species limits in  
birds.
- 3:20-3:30 pm Discussion
- 3:30-4:00 pm Break
- 4:00-4:20 pm Jody Hey, Rutgers University, Piscataway, New Jersey:  
Population assignment likelihoods in a phylogenetic and demographic model.
- 4:20-4:30 pm Discussion
- 4:30-4:50 pm Axel Meyer, University of Konstanz, Germany:  
Sharing of mitochondrial DNA haplotypes in cichlid fishes.
- 4:50-5:00 pm Discussion

- 5:00-6:00 pm General Discussion
- 6:15 pm Reception at Robertson House
- 7:00 pm Dinner of Robertson House
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## **Tuesday, 30 October**

- 7:00-8:15 am Breakfast at Robertson House
- 8:30-12:30 pm **SESSION 3: Phylogeography, Community Evolutions, and The Use of Barcodes For Multi-Species Studies**  
Chair: Michel Veuille, Museum d'Histoire Naturelle, Paris, France:
- 8:30-8:50 am Michel Veuille, Museum d'Histoire Naturelle, Paris, France:  
Can we extend intraspecific population genetics to community population genetics?
- 8:50-9:00 am Discussion
- 9:00-9:20 am Robert DeSalle, American Museum of Natural History, New York:  
Utilizing DNAS barcodes in biodiversity studies: some practical and philosophical issues.
- 9:20-9:30 am Discussion
- 9:30-9:50 am Eldredge Bermingham, Smithsonian Tropical Research Institute, Balboa, Republic of Panama:  
Phylogeography of Caribbean birds
- 9:50-10:00 am Discussion
- 10:00-10:30 am Break
- 10:30-10:50 am Graham Stone, University of Edinburgh, United Kingdom:  
Beyond the barcode: setting our sites on reconstructing community evolution.
- 10:50-11:00 am Discussion
- 11:00-11:20 am L. Lacey Knowles, University of Michigan, Ann Arbor:  
(Field: Statistical Phylogeography)
- 11:20-11:30 am Discussion
- 11:30-12:30 pm General Discussion
- 12:45 pm Luncheon at Robertson House
- 2:00-5:30 pm **SESSION 4: Selection On and Variation In Mitochondrial DNA Sequences**  
Chair: David M. Rand, Brown University, Providence, Rhode Island

- 2:00-2:20 pm David M. Rand, Brown University, Providence, Rhode Island:  
Barcodes and selection of mtDNA.
- 2:20-2:30 pm Discussion
- 2:30-2:50 pm Tim Barraclough, Imperial College London, Ascot, United Kingdom:  
Patterns of divergent selection from combined barcode and phenotypic data.
- 2:50-3:00 pm Discussion
- 3:00-3:20 pm Rasmus Nielsen, University of Copenhagen, Denmark:  
Statistical approaches for DNA barcoding.
- 3:20-3:30 pm Discussion
- 3:30-4:00 pm Break
- 4:00-4:20 pm Graham Wallis, University of Otago, Dunedin, New Zealand:  
Beyond the bar: roles for a million COI sequences in studies of molecular  
adaptation.
- 4:20-4:30 pm Discussion
- 4:30-5:30 pm General Discussion
- 6:00 pm Reception at Robertson House
- 7:00 pm Dinner at Robertson House
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### Wednesday, 31 October

- 7:15-8:45 am Breakfast at Robertson House
- 9:00-10:00 am **SESSION 5: Visualization of Large Sequence Datasets**  
Chair: Paul Gilna, California Institute for Telecommunications & Information  
Technology
- 9:00-9:20 am Paul Gilna, California Institute for Telecommunications & Information  
Technology, San Diego:  
CAMERA data and their visualization.
- 9:20-9:30 am Discussion
- 9:30-9:50 am Mehrdad Hajibabaei, University of Guelph, Ontario, Canada:  
Visualizing barcode data.
- 9:50-10:00 am Discussion
- 10:00-10:30 am Break

10:30-12:00 pm **SESSION 6: Final Discussion of Conclusions, Recommendation and Action Items**

Chair: David E. Schindel, Smithsonian Institution, Washington, D.C.

12:15 pm Luncheon at Robertson House

Afternoon departure