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WORKSHOP

Saturday, 26 February 2011, 16.00 – 18.00

"Species delimitation using nuclear sequence markers: a practical training in software tools used to resolve heterozygous chromatograms without cloning"

Jean-François Flot

Most nuclear sequence markers variable enough to distinguish closely related species also exhibit intra-specific variations that make them difficult to sequence in heterozygotes. Sequencing cloned PCR products is not a very satisfactory solution since it requires lots of time and money and since its results are often confounded by PCR-generated artifacts. This workshop will provide a hands-on training in using two computer programs (Champuru and SeqPHASE) that allow complete determination of allelic sequences of nuclear markers from direct sequencing, without cloning; both programs are freely available online (<http://www.mnhn.fr/jfflot/>). Training datasets will be provided during the workshop, but participants may also bring their own chromatograms if they wish.

Useful readings:

Flot J-F, Tillier A, Samadi S, Tillier S (2006) Phase determination from direct sequencing of length-variable DNA regions. *Molecular Ecology Notes* 6:627-630
Flot J-F (2007) Champuru 1.0: a computer software for unraveling mixtures of two DNA sequences of unequal lengths. *Molecular Ecology Notes* 7:974-977
Flot J-F (2010) SeqPHASE: a web tool for interconverting PHASE input/output files and FASTA sequence alignments. *Molecular Ecology Resources* 10:162-166