

- Curriculum Vitae -

Raphaël Leblois

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Centre de Biologie et Gestion des Populations (CBGP)

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PRESENT POSITION

Sept 2010 – Today **Researcher (CRI)** at the Center for Biology and Management of Populations, National Institute for Agronomical Research (CBGP - INRA), Montpellier, France

EDUCATION & RESEARCH TRAININGS

2006-2010

Assistant Professor (« Maitre de conférence ») at the National Museum of Natural History of Paris (MNHN).

2005-2006

PostDoc (6 months): « *Multilocus genetic analyses and demographic inferences with applications to human populations from Central Asia* » with Pr. Evelyne Heyer et Dr. Renaud Vitalis, Musée de l'Homme - MNHN, Paris, France.

2004-2005

PostDoc, Lavoisier grant (1 year): « *Bottleneck detection and inference of the number of founding individuals from SNPs markers* », with Pr. Montgomery Slatkin, University of California, Berkeley, United-States.

2000-2004

PhD in Integrative Biology (3 ½ years): « *Inference of dispersal parameters from genetic data in subdivided populations* » under the supervision of Dr. François Rousset and Dr. Arnaud Estoup. Montpellier Supagro – University of Montpellier II, France.

1999-2000

MSc in Evolutionary Biology and Ecology, 6 months project: « *Simulation study of the influence of mutational and demographic factors on the inference of demographic parameters from individual microsatellite genotypes* » under the supervision of Dr. François Rousset et Dr. Arnaud Estoup. Montpellier Supagro – University of Montpellier II.

LANGUAGES

FRENCH: MOTHER LANGUAGE

English: Read, written and spoken.

TECHNICAL AND PRACTICAL SKILLS

Statistical and computing tools: population genetic data analyse, advanced programming in C, C++, R and Mathematica (Windows, Linux, Mac).

Molecular techniques: DNA extractions, PCR, microsatellites development and genotyping.

Fieldwork: amphibians/reptiles/insects/trees sampling.

EDITORIAL ACTIVITIES AND SCIENTIFIC EXPERTISE

Referee for *Cladistic*, *Conservation Biology*, *Ecography*, *Ecology Letters*, *Evolutionary Ecology Research*, *Forest Ecology and Management*, *Genetics*, *Human Biology*, *Mitochondrial DNA*, *Molecular Ecology*, and *Molecular Ecology Resources*.

Expertise in theoretical and applied population genetics, conservation genetics, inference of dispersal, modelling in population genetics, coalescent theory.

FUNDING

- **2010-2014: ANR (french national agency for research funding)**, with S. Planes et al., “**IM-MODEL@CORALFISH: An isolation-migration model of the history of coral reef fish communities: theory and data**”. 500 k€
- **2010-2014: ANR**, with C. Denys et al., “**MOHMIE: Modern Human installation in Morocco Influence on the small terrestrial vertebrate biodiversity and its Evolution**”. 809 k€
- **2009-2013: ANR**, with J. -M. Cornuet et al., “**EMILE: Inference methods and software’s for Evolution**”. 372 k€
- **2008-2011: CNRS Amazonia**, with H. Fréville and C. Scotti-Saintagne, “**CLIPS: Past climate change and ecological specialization in tropical species: input from population genetic approaches**”. 100 k€
- **2008-2010: ANR Biodiversity**, with P. Grandcolas et al., “**BioNeoCal: Endemism in New Caledonia: phylogenetic and population study of its emergence**”. 940 k€
- **2007: MNHN - Bonus Qualité Recherche**, R. Leblois : « *Computer station for the development of inference methods from genetic data* ». 4k€
- **2007-2009: MNHN - Bonus Qualité Recherche**, with E. Porcher et al. : « *Using DNA Barcode data to measure phylogenetic biodiversity in plant communities* ». 32k€

MAIN CURRENT RESEARCH PROJECTS

Inference of demographic parameters using importance-sampling algorithms under various demographic models: Isolation by distance, Isolation with migration, Single population with variable size: collaboration with F. Rousset (ISEM, Montpellier), R. Vitalis (CBGP, Montpellier) and C. Reddy Beeravolu (Post-doc ANR, CBGP - EPHE, Montpellier).

Inference of sex-specific dispersal under isolation by distance models using Approximate Bayesian Computations: collaboration with R. Vitalis (CBGP, Montpellier).

PUBLICATIONS

- [34] Gauffre B., S. Mallez, I. Litrico, M.-P. Chapuis, R. Leblois, S. Delaunay, I. Badenhausser. 2015. Effects of landscape structure on the spatial and genetic patterns of a flightless grasshopper (Orthoptera: Acrididae). *Molecular Ecology*, Under review.
- [33] Ferchaud A.-L., R. Eudeline, V. Arnal, M. Cheylan, G. Pottier, R. Leblois and P.-A. Crochet. 2015. Congruent signals of population history but radically different patterns of genetic diversity between mitochondrial and nuclear markers in a mountain lizard. *Molecular Ecology*, under review.
- [32] Vignaud T. M., J. Mourier, J. A. Maynard, R. Leblois, J. Spaet, E. Clua, V. Neglia, S. Planes. 2014. Blacktip reef sharks, *Carcharhinus melanopterus*, have high genetic structure and varying demographic histories in their Indo-Pacific range. *Molecular Ecology*, **23**: 5193-5207. doi : 10.1111/mec.12936.

- [31] Laporte M., R. Leblois, A. Coulon, F. Bonhomme, P. Magnan, P. Berrebi. **2014**. Genetic structure of a vulnerable species, the freshwater blenny (*Salaria fluviatilis*). *Conservation Genetics*, In Press.
- [30] Vignaud T.M., J.A. Maynard, R. Leblois, M.G. Meekan, R. Vazquez-Juarez, D. Ramirez-Macias, S.J. Pierce, D. Rowat, M.L. Berumen, C. Beeravolu, S. Baksay, S. Planes. **2014**. Genetic structure of populations of whale sharks among ocean basins and evidence for their historic rise and recent decline. *Molecular Ecology* **23**: 2590-2601. doi : 10.1111/mec.12754
- [29] Leblois R., P. Pudlo, J. Néron, F. Bertaux, C. Reddy Beeravolu, R. Vitalis, F. Rousset. **2014**. Maximum likelihood inference of population size contractions from microsatellite data. *Molecular Biology and Evolution* **31**: 2805-2823. doi: 10.1093/molbev/msu212
- [28] Cornuet J.-M., P. Pudlo, J. Veyssier, A. Dehne-Garcia, M. Gautier, R. Leblois, J.-M. Marin, A. Estoup. **2014**. DIYABC v2.0: a software to make Approximate Bayesian Computation inferences about population history using Single Nucleotide Polymorphism, DNA sequence and microsatellite data. *Bioinformatics* **30** : 1187-1189. Doi : 10.1093/bioinformatics/btt763
- [27] Lalis A.*, R. Leblois*, E. Lecompte*, C. Denys, J. Ter Meulen, T. Wirth. **2012**. The Impact of Human Conflict on the Genetics of *Mastomys natalensis* and Lassa Virus in West Africa. *PLoS One*, **7** : e37068. doi:10.1371/journal.pone.0037068 * co-first authors.
- [26] Rousset F., R. Leblois. **2012**. Likelihood-based inferences under a coalescent model of isolation by distance: two-dimensional habitats and confidence intervals. *Molecular Biology and Evolution* **29**: 957-973.
- [25] Perez M., R. Leblois, B. Livoreil, R. Bour, J. Lambourdiere, S. Samadi, M.C. Boisselier. **2012**. Effects of landscape features and demographic history on the genetic structure of *Testudo marginata* populations in the southern Peloponnese and Sardinia. *Biological Journal of the Linnean Society* **105**: 591-606.
- [24] David O., C. Laredo, R. Leblois, B. Shaeffer, N. Vergne. **2012**. Coalescent-based DNA barcoding: multilocus analysis and robustness. *Journal of Computational Biology* **19**: 271-278. (Author list is alphabetical).
- [23] Sagnard F., M. Deu, D. Dembélé, R. Leblois, L. Touré, M. Diakité, C. Calatayud, M. Vaksman, S. Bouchet, Y. Malle, S. Togola, P. Traoré. **2011**. Genetic diversity, structure, gene flow and evolutionary relationships within the *Sorghum bicolor* wild-weedy-crop complex in a western African region. *Theoretical Applied Genetics* **123** : 1231-1246.
- [22] Leblois R*, K. Kuhls*, O. Francois, G. Schöniann, T. Wirth. **2011**. Guns, germs and dogs: On the origin of *Leishmania chagasi*. *Infections, Genetics and Evolution* **188**: 165-179. * co-first authors.
- [21] Girod C., R. Vitalis, R. Leblois, H. Fréville. **2011**. Inferring population decline and expansion from microsatellite data: a simulation-based evaluation of the MSVAR method. *Genetics* **188**: 165-179.
- [20] Morelli G., Y. J. Song, C. J. Mazzoni, M. Eppinger, P. Roumagnac, D. M. Wagner, M. Feldkamp, B. Kusecek, A. J. Vogler, Y. J. Li, Y. J. Cui, N. R. Thomson, T. Jombart, R. Leblois, P. Lichtner, L. Rahalison, J. M. Petersen, F. Balloux, P. Keim, T. Wirth, J. Ravel, R. F. Yang, E. Carniel, M. Achtman. **2010**. *Yersinia pestis* genome sequencing identifies patterns of global phylogenetic diversity. *Nature Genetics* **42**: 1140.
- [19] Verdu P., R. Leblois, A. Froment, S. Thery, S. Bahuchet, F. Rousset, E. Heyer, R. Vitalis. **2010**. Limited dispersal in mobile hunter-gatherer Baka Pygmies. *Biology Letters* **6**: 858-861.
- [18] Nubel U., J. Dordel, K. Kurt, B. Strommenger, H. Westh, S. K. Shukla, H. Zemlickova, R. Leblois, T. Wirth, T. Jombart, F. Balloux, W. Witte. **2010**. A Timescale for Evolution,

Population Expansion, and Spatial Spread of an Emerging Clone of Methicillin-Resistant *Staphylococcus aureus*. *Plos Pathogens* **6**: e1000855.

- [17] Alberto F., P. T. Raimondi, D. C. Reed, N. C. Coelho, R. Leblois, A. Whitmer, E. A. Serrão. **2010**. Habitat continuity and geographic distance predict population genetic differentiation in giant kelp. *Ecology* **91**: 49-56.
- [16] Boisselier-Dubayle M. -C., R. Leblois, M. I. Khodabux, S. Samadi, J. Lambourdière, C. Sarthou. **2010**. Genetic structure of a xerophilous bromeliad in a fragmented habitat and the forest refuge hypothesis: *Pitcairnia geyskeysii* on inselbergs in French Guyana. *Ecography* **33**: 175-184.
- [15] Guillot G., R. Leblois, A. Coulon, A. C. Frantz. **2009**. Statistical methods in spatial genetics. *Molecular Ecology* **18**: 4734-4756.
- [14] Austerlitz F., O. David, B. Schaeffer, K. Bleakley, M. Olteanu, R. Leblois, M. Veuille, C. Laredo. **2009**. Comparing phylogenetic and statistical classification methods for DNA barcoding. *BMC Bioinformatics* **10**: Suppl. 14: S10.
- [13] Leblois, R., A. Estoup, F. Rousset. **2009**. IBDSim: a computer package for coalescent simulations under isolation by distance with temporal and spatial heterogeneities. *Molecular Ecology Resources* **9**: 107–109.
- [12] Frezal L., R. Leblois. **2008**. 4 years of DNA barcoding: current advances and prospects. *Infection, Genetics & Evolution* **8**: 727–736.
- [11] Rousset, F., R. Leblois. **2007**. Likelihood and approximate likelihood analyses of genetic structure in a linear habitat: performance and robustness to model mis-specification. *Molecular Biology and Evolution*. **24**:2730–2745.
- [10] Leblois, R., M. Slatkin. **2007**. Estimating the number of founder lineages from haplotypes of closely linked SNPs. *Molecular Ecology* **16**, 2237-2245.
- [9] Watts P.C., F. Rousset, I.J. Saccheri, R. Leblois, S.J. Kemp, D.J. Thompson. **2007**. Compatibility of genetic and demographic estimates of ‘neighborhood size’ in insect populations: analysis of *Coenagrion mercuriale* (Odonata: Zygoptera) using an improved estimator of genetic divergence. *Molecular Ecology* **16**, 737–751.
- [8] Leblois, R., Estoup, A., Streiff, R. **2006**. Habitat contraction and reduction in population size: Does isolation by distance matter? *Molecular Ecology* **15**, 3601–3615.
- [7] De Iorio M., Griffiths R., Leblois R., Rousset F. **2005**. Stepwise mutation likelihood computation by sequential importance sampling in subdivided population models. *Theoretical Population Biology* **68**: 41-53. (Author list is alphabetical).
- [6] Leblois R., Rousset F., Estoup A. **2004**. Influence of spatial and temporal heterogeneities on the estimation of demographic parameters in a continuous population from microsatellite data. *Genetics* **166**: 1081-1092
- [5] Brouat C., Sennedot F., Audiot P., Leblois R., Rasplus J. -Y. **2003**. Fine-scale genetic structure of two carabid species with contrasted levels of habitat specialization. *Molecular Ecology* **12**: 1731 - 1745.
- [4] Leblois R., Estoup A. 2003. Invited commentary on the article by Wilson IJ, Weale ME, Balding DJ (2003): Inferences from DNA data: population histories, evolutionary processes, and forensic match probabilities, *Journal of the Royal Statistical Society A* **166**: 1-33.
- [3] Leblois R., Estoup A., Rousset F. 2003. Influence of mutational and sampling factors on the estimation of demographic parameters in a continuous population under isolation by distance. *Molecular Biology and Evolution*. **20**: 491-502

[2] Tikel D., Peatkau D., Cortinas N., Leblois R., Moritz C., Estoup A. 2000. Microsatellite loci in the invasive toad species *Bufo marinus*. *Molecular Ecology* **9**: 1927-1929.

[1] Leblois R., Rousset F., Tikel D., Moritz C., Estoup A. 2000. Absence of evidence for isolation by distance in an expanding cane toad (*Bufo marinus*) population: an individual-based analysis of microsatellite genotypes. *Molecular Ecology* **9**: 1905-1909.

PUBLICATIONS IN PREPARATION

Lalis A., R. Leblois, M.-C. Boisselier-Dubayle, C. Denys. Genetic structure and dispersal of *Mastomys* species in Guinea. In prep.

Leblois R., C. Reddy Beeravolu, R. Vitalis, F. Rousset. Importance sampling on Isolation with Migration models. Work in progress.

Vitalis R., R. Leblois. IBDSex : a coalescent-based computer program to simulate sex-specific gene genealogies under isolation by distance. Work in progress.

ACADEMIC PUBLICATIONS

Leblois, R. 2004. Estimation de paramètres de dispersion en populations structurées à partir de données génétiques. Thèse de doctorat de l'Agro-M (ENSA-Montpellier), 233 pp.

Leblois, R. 2000. Etude par simulation de l'influence de facteurs mutationnels et démographiques sur l'estimation de paramètres démographiques à partir de génotypes individuels. Diplôme d'Etudes Approfondies (DEA Biologie de l'Evolution et Ecologie, Agro-M et Université Montpellier II). 30pp.

TEACHING AND STUDENT SUPERVISION

2006-Today: 50h per year of population genetic teaching: population genetic data analysis, inference of demographic parameters, coalescent theory and DNA Barcoding (Master and PhD courses at the University of Montpellier II, MNHN, Ecole Normale Supérieure de Paris, Université Paris VII, EPHE and Université Lille I).

2007-Today: co-organisation, with R. Vitalis, of one week course for PhD students: "Data analyses in population genetics" (European Master MEME, University Montpellier II).

2006-2010: co-organisation, with R. Vitalis and E. Heyer, of one week course for Master students (Ecole Doctorale ParisVI-ParisVII-MNHN): "Molecular population genetics and coalescent theory"

2012 : Master students : Timothée Bonnet (University of Montpellier II, Supagro) "Modeling of Mitochondrial and nuclear introgression in a secondary contact zone" (co-sup. P.-A. Crochet, F. Rousset)

and Julie Landes (University of Montpellier II) "Différentiation allochronique chez la processionnaire du pin : apport des marqueurs neutres pour bâtir des scénarios évolutifs " (co-sup. C. Kerdelhué)

2011-Today : Postdoc : Champak Reedy Beravolu "Importance sampling on sequence data : inference under an isolation with migration model"

and Aude Lalis " MOHMIE: Modern Human installation in Morocco Influence on the small terrestrial vertebrate biodiversity and its Evolution "

2009: Master student from Paris Polytechnic School: François Bertaux “Inference of population demographic history: detection of past changes in population sizes”

2008: Master student from Paris Polytechnic School: J. Néron “Inference of population demographic history: detection of past changes in population sizes”

2007-2008: co-supervision of an “Assistant Lecturer” (ATER) from EPHE: L. Frezal “Using multiple genes for DNA Barcoding in Drosophila” (with M. Veuille)

2007: Master students : Sandrine Bérot (MNHN): “Inference of divergence times and migration rates using importance sampling algorithms” (co-sup. R. Vitalis)

and Camille Made (MNHN): “Sex-biased dispersal inferences using Approximate Bayesian Computations” (co-sup. R. Vitalis)

COLLECTIVE AND ADMINISTRATIVE ACTIVITIES

2011-Today: Scientific manager of the CBGP computer cluster (132 nodes, CBGP technical platform).

2008-2010: Internal seminar organisations for the department “systematic and evolution” , MNHN.

2008-2010: Internal seminar organisations at the “Origine, Structure and Evolution of biodiversity” lab (OSEB, MNHN, UMR 7205).

2008-2010: Scientific manager of the Museum computer cluster (76 nodes, MNHN, UMS 2700).

2006-2010: participation to the DNA Barcoding initiative to develop DNA barcoding in France.

2006-Today: members of various PhD supervision committees: Anne-Laure Ferchaud (EPHE, Montpellier 2008, 2010), Christophe Girod (MNHN Paris, 2008, 2009), Camille Roux (Université Lille I, 2008), Romain Nattier (MNHN Paris, 2008, 2009), Erhan Yalcindag (Université Montpellier II, 2009), Stéphanie Wagner (INRA Bordeaux – Munich University, 2011), Axelle Bouiges (EPHE-MNHN, 2011).

2006: member of the organizing committee for the international meeting “DNA sampling: Strategy & Design” at the MNHN (March 15th-16th 2007)

2001-2002: Weekly seminar organisations at the “environment and genetics” lab (ISEM – UMR 5554).

ORAL COMMUNICATIONS AND SEMINARS

Invited Communication :

June 2013 :

Summer Research School "Software and Statistical methods for population genetics", (Aussois, France) : “The Migraine project : A user- friendly software for likelihood-based inferences of spatial structure and demographic history from genetic data”, Leblois R., C. Beeravolu Reddy, F. Rousset.

February 2009 :

4th international symposium on Leishmania (Lucknow, India) : “Guns, Germs and Dogs: on the origin of Leishmania chagasi”, T. Wirth, R. Leblois, K. Kuhls and G. Schönian.

September 2007 :

International "Conservation genetics Symposium" at the American Museum of Natural History in New York City, USA : : « "Why isolation by distance is a realistic model for spatial population genetics" » R. Leblois.

November 2006 :

International Workshop on „Advances in molecular evolutionary ecology: statistical tools to unravel evolutionary processes in natural populations“ (Munich, Germany) : : « Inference of demographic parameters : isolation by distance, maximum likelihood and bayesian approaches » R. Leblois. 2*3 hours seminar.

December 2003 :

2nd International Congress on DNA Polymorphisms in Human Populations (Paris, France): « Inference of demographic parameters under isolation by distance: what can we do now? » R. Leblois, M. De Iorio, R. Griffiths, A. Estoup and F. Rousset.

Other communications :

August 2013 :

The 11th International Mammalogical Congress, 2013, Belfast, Ireland: “ Nuclear genetic structure of the bank vole (*Myodes glareolus*) in Fennoscandia with an emphasis on the mitochondrial contact zones ” Pisano, J., Leblois R., Charbonnel, N., Henttonen H., Olsson G., Galan M. & Michaux, J.

August 2013 :

Congress of the European Society for Evolutionary Biology (Lisbon, Portugal): “Incipient allochronic speciation in the pine processionary moth: molecular analysis of a divergent population”, J. Landes, C. Burban, M. Gautier, H. Santos, M. Branco, R. Leblois, & C. Kerdelhué.

June 2013 :

Summer Research School "Software and Statistical methods for population genetics", (Aussois, France) : “Demographic inference from genetic data : consideration of an epidemiological model and a combination of different types of markers”, R. leblois, P. Pudlo, C. Beeravolu Reddy, F. Rousset. (POSTER)

May 2013 :

Congress « Mathematical and Computational Evolutionary Biology 2013» (St Martin de Londres, France) : “Demographic inference from genetic data : consideration of an epidemiological model and a combination of different types of markers ”, R. leblois, P. Pudlo, C. Beeravolu Reddy, F. Rousset. (POSTER)

March 2013 :

Congress « EDENext 2013» (Bellaterra, Spain): “Nuclear genetic structure of the bank vole (*Myodes glareolus*) in Fennoscandia with an emphasis on the mitochondrial contact zones – Preliminary results ” Pisano J., Leblois R., Henttonen H., Galan M., Charbonnel N., Lundkvist A.K., Olsson G., & Michaux J.R.

June 2012 :

Congress « Mathematical and Computational Evolutionary Biology 2012» (St Martin de Londres, France): “Maximum likelihood inference comparing sequence and allelic markers in a population of variable size: an Importance Sampling approach”, C. Beeravolu Reddy, F. Rousset, P. Pudlo et R. Leblois. (POSTER)

June 2012 :

Congress « Mathematical and Computational Evolutionary Biology 2012» (St Martin de Londres, France): “Empirical likelihood for Bayesian inference in population genetics”, P. Pudlo, K. Mengersen , R. Leblois et C. Robert.

June 2012 :

Congress « Mathematical and Computational Evolutionary Biology 2012» (St Martin de Londres, France): “Likelihood-based inference under spatial structure and demographic changes: the Migraine project”, R. Leblois et F. Rousset.

May 2012 :

Congress « MEDINSECT3 » (Hammamet, Tunisia): “Allochronic differentiation of a pine processionary moth population in Portugal: evolutionary scenario based on neutral markers”, C. Burban, H. Santos, J. Landes, R. Leblois, M.-R. Paiva, M. Branco et C. Kerdelhué.

May 2010 :

38th Congress of the Canadian Statistical Society (Québec, Canada): “Likelihood-based inference of dispersal rates from patterns of genetic diversity ». Rousset F. & Leblois R.

June 2010 :

Congrès « Frugivores and seed dispersal » (Montpellier, France): “Past demographic history of *Astrocarium sciophilum* : Chloroplast genetic structure and restricted seed dispersal”, C. Girod, R. Leblois, B. Riera, H. Fréville. (POSTER)

June 2010 :

Congress « Statistiques du Sud » (Mèze, France): “Inference of demographic parameters from genetic data using importance sampling algorithm on coalescent histories”, R. Leblois & F. Rousset.

October 2009 :

Annual meeting of the research group (GDR 1928) « population genetics and evolutionary genomics » (Institut Pasteur, Paris): “Data analyses for DNA Barcodes”, F. Austerlitz, O. David, B. Schaeffer, K. Bleakley, M. Olteanu, R. Leblois, M. Veuille et C. Laredo.

October 2009 :

Lab seminar « genetic and evolution of plant populations » (Université de Lille, France): “Detection and quantification of past demographic changes using the coalescent : test and comparison of different methods”, R. Leblois, C. Girod, R. Vitalis, H. Fréville et F. Rousset.

May 2009 :

Molecular Evolution seminar (Ecole Normale Supérieure, Paris, France): « Likelihood estimation for genetic data under the coalescent » R. Leblois.

June 2008 :

SMBE congress (Barcelona, Spain) : « Inference of demographic parameters using importance sampling on coalescence history » R. Leblois et F. Rousset (POSTER).

April 2008 :

Dispersion day (École Nationale du Génie Rural des Eaux et des Forêts, Paris, France) : « Demographic inferences under isolation by distance: Why some methods are more robust than others? » R. Leblois et F. Rousset.

January 2008 :

Internal seminar (Muséum National d’Histoire Naturelle, Paris, France) : « The DNA Barcode Project : potentialities and limits » R. Leblois.

September 2007 :

2de International Barcode Conference, Taipei (Taïwan): " Comparing phylogenetic and statistical classification methods for DNA barcoding" F. Austerlitz, O. David, B. Schaeffer, K. Bleakley, M. Olteanu, R. Leblois, M. Veuille, C. Laredo.

May 2007 :

International EMBO Workshop on “Molecular Biodiversity and DNA Barcode” in Rome (Italy): " What is the molecular signature of speciation events ?" M. Veuille & R. Leblois

May 2006 :

Internal seminar of Ethno-Genetics (Muséum National d'Histoire Naturelle, Paris, France) :
« Estimating the number of founder lineages from haplotypes of closely linked SNPs » R. Leblois and M. Slatkin.

January 2006 :

Internal seminar of conservation biology (Muséum National d'Histoire Naturelle, Paris, France) : « Habitat contraction and reduction in population size: Does isolation by distance matter? » R. Leblois, A. Estoup and R. Streiff.

March 2005 :

Museum of Vertebrate Zoology Annual Retreat (University of California, Berkeley, USA) : “Inference of demographic parameters from genetic data : Why some methods are more robust than others?” R. Leblois.

January 2005 :

Bay Area Conservation Biology Symposium (UC Stanford, CA, USA) : “Habitat contraction and reduction in population size: Does isolation by distance matter? **R. Leblois**, A. Estoup and R. Streiff.

April 2004 :

Internal seminar at the Zoology Department (Cambridge, UK) : “Inference of demographic parameters from genetic data : Where are we now?” **R. Leblois**..

August 2003 :

ESEB Congress (Leeds, UK) : “Maximum likelihood inference of demographic parameters from microsatellites data : precision and robustness of a new algorithm.” **R. Leblois**, M. De Iorio, F. Rousset and R.C. Griffiths.

October 2002 :

researcher training “introduction to population genetics : theory and applications” organized by the National Institute of Agronomical Research (INRA Montpellier, France) : “the use of the coalescence theory for demographic parameter inference from genetic data” **R. Leblois**.

December 2001 :

“Gene flow Day” organized by the INRA (Montpellier, France) : “Use of the coalescence for the estimation of gene flow between populations” **R. Leblois**.

September 2001 :

“Coalescence Day” organized by the INRA (Montpellier, France) : “maximum likelihood estimation of demographic parameters”, **R. Leblois**.

August 2001 :

ESEB congress (Aarhus, Denmark) : « Analyses of isolation by distance: (Why) are some methods more robust than others? » F. Rousset, **R. Leblois**.

August 2001 :

23rd Petit Pois Dérivé, Reunion of the French Genetic and Population Biology Group, (Orsay, France) : « Simulation study of the effects of mutational and demographic factors on the estimation of demographic parameters from individual genotypes » **R. Leblois**.

May 1999 :

Byron-Bay Population Genetics Meeting (Byron Bay, Australie) : « demographic parameters inference from genetic data under isolation by distance models » R. Leblois and A. Estoup.