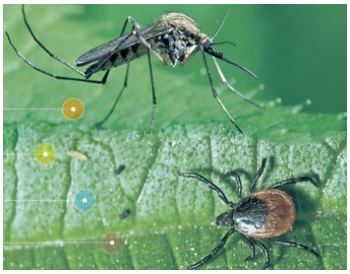
Empirical population genetics training course for beginners

22-25 OCT. 2019
In CEVDI facilities, at Águas de Moura



Background

The biology of natural populations can be studied through direct methods (observation) or indirect methods that use spatiotemporal variation of genetic markers and population genetics tools. Such methods are especially well designed to study small organisms, and particularly parasites and their vectors. Gaining skills on these techniques, through appropriate sampling and the use of relevant genetic markers, should allow improving knowledge on the population biology of targeted organisms. This may be particularly useful in the case of pests, parasites or vectors because results obtained may help building more efficient control strategies.

The learning experiences will allow the trainees to acquire knowledge on the ins and outs of molecular data analyses through population genetics tools, on sampling strategies, marker's selection, and on how to ask the most relevant questions.

Registration:	**Moodle** insaforma+
Deadline:	**September 30**

Overview

I. Notions of molecular biology and formal genetics.

1. DNA.
2. The three domains of life.
3. Mutations.
4. Genetic variation: genotype and phenotype.
5. Genetic variation: Mendel, complex traits, Morgan, recombination and genetic distance.
6. Inbreeding.

II. Population genetics.

1. The population the basic unit in ecology, a demographic notion.
2. The model of Hardy and Weinberg.
3. Hardy-Weinberg when N small, genetic drift.
4. Effective population size: Definitions.
5: More than one locus, linkage disequilibrium.

III. Alterations of Hardy-Weinberg proportions

1. Heterozygote deficits.
2. Heterozygous excesses.
5. Procedures for combining k tests series.
6. Multivariate analyses.
7. Exploration of a hidden structure.

(continue)

Targeted public: Students (Masters or PhD), researchers willing to enlarge their perspectives, or even engineers or bench technicians who feel the need of a better understanding of the ins and outs of their work.

Course language: English

Training officer: Thierry De Meeûs, IRD/CIRAD, UMR 177 INTERTRYP, France (link to CV: http://www.t-de-meeus.fr/cvmeeusGB.pdf)

Organization: Maria Margarida Santos-Silva (coord.), Ana Sofia Santos and Rita Velez.

Course developed under the project PTDC/SAU-PAR/28947/2017 – "The *Ixodes ricinus* group of ticks in the western Mediterranean region and North Africa: new insights into their population genetics and microbiome fauna"

Instituto Nacional de Saúde Doutor Ricardo Jorge

insaforma+

Plataforma de *e-Learning*
http://formamais-insa.min-saude.pt

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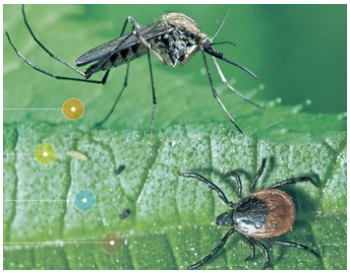

Overview (continued)

IV. Wright's F-statistics.

1. Wright's Island model
2. Inside individuals relative to the sub-population they belong to: FIS.
3. Inside sub-populations relative to the total population: FST.
4. Inside individuals relative to the total population: FIT.
5. Definitions according to heterozygosity: Chesser and Nei.
6. Definitions according to inbreeding: Allele identity probabilities, Weir and Rousset.
7. Summing up.

V. Inferences.

1. Selfing.
2. Dispersal following a Wright's Island model with many Islands and many alleles.
3. Dispersal in a finite Island model (n small), with homoplasy (K small) and local selfing (s).
4. Dispersal in other models of populations, stepping-stone and neighbourhood.
5. Effective population size estimators.
6. Unbiased estimators for Wright's F-statistics.
7. F-statistics for more than three hierarchical levels.
8. F-statistics in clones.

VI. Statistical procedures

1. Definitions.
2. F-statistics confidence intervals (CI): Bootstrap and Jackknife.
3. Significance testing through randomizations.
4. Nested and orthogonal factors.
5. Procedures for combining k tests series.
6. Multivariate analyses.
7. Exploration of a hidden structure.

General information: each attendant must bring a laptop with MS Office, R and R-packages R-commander (Rcmdr) and hierfstat (+other population genetics sofwares). Number of attendants between a minimum of 4 and a maximum of 7.

Timetable: 09h30-13h00 | lunch break | 14h00-17h30. The course extends on 4 days and sums to 24 hours with four 1h30 sessions per day. During sessions, real data sets will be analysed and special theoretical lectures will be undertaken whenever a new parameter or notion is addressed. Each of these can be re-lectured when needed or on the request of attendants.

Registration fee: €300. The payment is made by bank transfer (IBAN **PT50078101120000000404561)**. The transfer receipt must be send to formamais@insa.min-saude.pt till September 30 to confirm the registration.