



UNIVERSITÀ DEGLI STUDI DI MILANO

DIPARTIMENTO DI SCIENZE AGRARIE
E AMBIENTALI - PRODUZIONE,
TERRITORIO, AGROENERGIA



DIPARTIMENTO DI BIOLOGIA
E BIOTECNOLOGIE
CHARLES DARWIN

SAPIENZA
UNIVERSITÀ DI ROMA



Università degli Studi di Pavia

Summer School *Introduction to RAD-seq Data Analysis* *Second edition*

Summer school content

RAD (Restriction site Associated DNA) sequencing is boasting genome-scale analyses in non-model organisms, also from species without available genomic resources. RADseq techniques have been used for SNP discovery and genotyping, genotype-phenotype association mapping, linkage mapping, QTL analysis, analyses of hybridization and gene flow, and, in general, in population genetics. More recently, RADseq data has also been used to address problems in phylogeographic and phylogenetic studies taking advantage of linked SNPs in “mini-contigs” obtained from paired end sequencing. RADseq is a flexible and cost-effective method for population-level genome-wide analyses on both model and non-model organisms.

The summer school will:

- i) introduce the participants to the basic Unix/BASH environment necessary for handling and analyzing genomic dataset; Day 1 – half day
- ii) provide an overview of the different RADseq approaches (e.g., single-digest, double-digest, 2b-RAD, etc.); Day 1 – half day
- iii) give a comparative presentation of the available bioinformatic pipelines for processing RADseq (e.g., Stacks, dDocent, PyRad, etc.); Day 2 – half day
- iv) offer hands-on tutorials for the use of Stacks, the most used bioinformatics tool for analyzing different types of RADseq data: topics of the tutorials will include processing the raw data, assembling the sequences *de novo* and with a reference genome, SNP calling, calculating basic population genetic statistics and natural selection inference from the assembled data, and exporting the RAD data for downstream analyses; Day 2 – half day + Day 3 – whole day
- v) show the participants how to employ RADseq data in standard and novel phylogenetic, phylogeographic and population genetics applications (e.g. phylogenetic tree reconstruction, population structure analysis, demographic inference, gene flow and introgression analysis, etc.) through hands-on analyses of small datasets; Day 4 and Day 5 – whole day

Course directors

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Teaching language: English

Who should apply: Advanced Undergrads, Ph.D. students, post-docs and faculty. Participation will be limited to 25 people allowing efficient instruction with hands-on computer exercises during the course.

When: Como, October 2-7, 2017 (40 hours)

Instructors: Emiliano Trucchi, Matteo Montagna, Alessio De Biase, Davide Sassera.

Other international instructors will be contacted in order to cover specific topics.