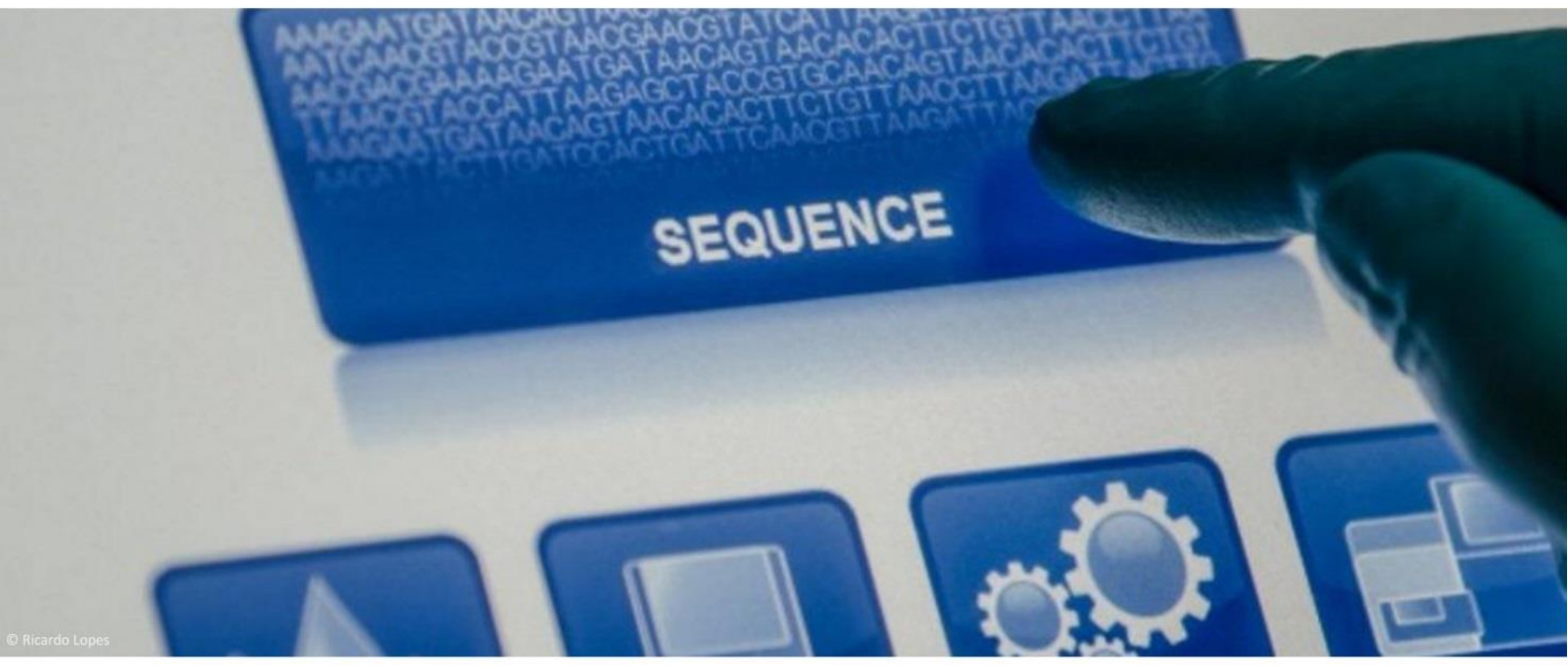
GENOMICS WEEK @ CIBIO-InBIO

June 15-19, 2015 – CIBIO-InBIO, Vairão, Portugal

June 15-17 | **Advanced Course "Genotyping by Sequencing (GBS): principles, approaches and applications"**
June 18-19 | **"Genomics Seminar"**



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ADVANCED COURSE GENOTYPING BY SEQUENCING (GBS): PRINCIPLES, APPROACHES AND APPLICATIONS

June 15-17, 2015 | Room 2 - Vairão Campus

PROGRAMME

Session 1
Monday, June 15 | 9.30 - 12.30
Introduction to Genotyping-by-Sequencing (GBS) part 1: getting the data
In this session, we will introduce the rationale for using GBS approaches. We will describe several commonly used methods for obtaining sequence data, including RAD sequencing, GBS, double-digest (dd) RAD and ddGBS, and explore the advantages and disadvantages of each approach.

Session 2
Monday, June 15 | 14.30 - 17.30
Further into GBS
This session will start off with Sharon Mitchell (Director of the Genomics Diversity Facility at Cornell) discussing troubleshooting, dealing with various different organisms, and future developments in the field including working with degraded DNA. James Beck (Wichita State University, Kansas) will describe his very recent results applying GBS to museum (herbarium) specimens. The remainder of the session will follow on the themes introduced by Drs Mitchell and Beck to provide a detailed assessment of what is and what is not possible with GBS and to highlight further possible developments in the technique in the future.

Session 3
Tuesday, June 16 | 9.30 - 12.00
Introduction to Genotyping-by-Sequencing (GBS) part 2: analysing the data
In this session, we will describe the principles behind data analysis, for systems both with and without reference genomes. For the case of non-genome-enabled species, we will describe the methods used by the UNEAK pipeline, stacks and the aftrRAD software.

Session 4
Tuesday, June 16 | 13.00 - 14.00
In this session, Gabriel Margarido (Universidade de São Paulo) and Katie Hyma (Bioinformatician at the Genomics Diversity Facility at Cornell) will discuss the application of GBS for polyploid organisms.

Session 5
Tuesday, June 16 | 14.00 - 16.00,
Practical session 1: analysis with a reference genome
Taking an example dataset (raw output from the Illumina sequencer), we will work through the steps required to filter the data, align reads to the reference genome, call SNPs/indels, call genotypes and filter the genotype data.

Session 6
Tuesday, June 16 | 16.00 - 17.30
Practical session 2: analysis without a reference genome
Using the same raw dataset as above, we will work through the steps of identifying homologous reads, calling SNPs, calling genotypes and filtering the genotype data, using the UNEAK pipeline, the aftrRAD software, and Perl scripting.

Session 7
Wednesday, June 17 | 9.30 - 12.30
Case study session
This will provide attendees with the opportunity to present their study system, and there will be a whole-group discussion on how the various methods might best be applied to the system in question.

Session 8
Wednesday, June 17 | 14.00 - 17.00
Question and answer session (including Sharon Mitchell and Katie Hyma, Genomics Diversity Facility at *University of Cornell)*
This will be a whole-group discussion that will provide the opportunity to review what has been covered in the workshop and to address any outstanding technical questions.