



Genome Wide Association Studies

Vincent Segura

► To cite this version:

Vincent Segura. Genome Wide Association Studies. Sustainable Forest Management Research Institute, formed by Forest Research Centre (Next-generation sequencing for beginners: applications to population genetics, forest health and tree breeding), 2013. hal-02809467

HAL Id: hal-02809467

<https://hal.inrae.fr/hal-02809467>

Submitted on 6 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Summer School

Next-generation sequencing for beginners: applications to population genetics, forest health and tree breeding

Dates: June 17-19th.

Venue: University Residence “Reyes Católicos”, in Valladolid (<http://en.wikipedia.org/wiki/Valladolid>).

Description: This course is intended to give a brief introduction to new sequencing technologies (the so-called Next-Generation Sequencing or NGS) and their applications in forest research. The *first part of the course* will provide a general overview on the steps followed by a typical NGS project, covering the following topics:

FASTQ format and sequence quality (Phred score and fastqc software)

A simple pipeline: BWA + Samtools

Visualization: IGV

Identifying SNPs: Samtools

Annotating SNPs: ensembl vep.pl

Identifying structural variants

RNAseq: tophat + cufflinks

De novo assembly: SGA

The *second part of the course* will be focused on applications of NGS to taxonomy, population genetics and breeding, including talks on adaptation to environmental changes, genomic selection and analysis of environmental samples. A hands-on workshop on genome-wide genetic association (GWAS) will take place on the afternoon of the second day. Finally, a second workshop on forest health (pathology) and application of molecular tools to plant disease diagnosis will be developed on the last day of the course.

Accommodation: Students are recommended to take a room University Residence “Reyes Católicos” (34.38 € per night for a single room and 47.31 € per night for a double room, breakfast included).

Organizers: Sustainable Forest Management Research Institute, formed by Forest Research Centre, INIA and University of Valladolid.

Teachers:

Miguel Pérez-Enciso, Universitat Autònoma de Barcelona (Bioinformatics).

Juan José Robledo-Arnuncio, Forest Research Centre, INIA (Population Genetics).

Santiago C. González-Martínez, Forest Research Centre, INIA (Genomic Selection).

Marta Goberna, CEBAS-CSIC, Murcia (Environmental Samples).

Vincent Segura, UR 588 AGPF, INRA Orléans (GWAS).

Speakers for the forest pathology workshop to be confirmed.

Pre-registration: Please, write an email to Elena Hidalgo (ehidalgo@pvs.uva.es) and/or Santiago C. González-Martínez (santiago.c.gonzalez.martinez@gmail.com), indicating your name, organization and (briefly) the reasons why you would like to attend the course.