

<b>Discipline</b>	<i>Genetics</i>
<b>Title of the course</b>	<i>Quantitative and Population Genetics and Evolution</i>
<b>Code</b>	
<b>Duration</b> <b>Date start</b> <b>Date end</b>	<i>6 ECTS</i> <i>September</i> <i>December</i>
<b>Course coordinator and contact details</b>	<i>Valérie SCHURDI-LEVRAUD</i> <i>valerie.schurdi-levraud@u-bordeaux.fr</i>
<b>Other contact person</b>	<i>Pierre-François BERT</i> <i>pierre-françois.bert@ u-bordeaux.fr</i>
<b>Secretary</b>	<i>Florence Lartigaut</i> <i>Florence.lartigaut@u-bordeaux.fr</i>
<b>Mode of delivery</b>	<i>in-class face-to-face, seminars, flipped classroom (24 hours)</i> <i>Data and in silico study, work on dataset (22 hours)</i> <i>Professional seminars (6 hours)</i>
<b>Level</b>	<i>Master</i>
<b>ECTScredit points</b>	<i>52 h in-class</i> <i>128h personal work including distance-based, personal project preparation</i>
<b>Language</b>	<i>English</i>
<b>Description<sup>1</sup></b>	<i>Students will be able to</i> – <i>calculate and explain genetic diversity estimates, alleles frequency</i> - <i>integrate theoretical and practical knowledge in detecting loci involved in quantitative traits</i> – <i>integrate advanced statistics, bioinformatics, highthrough-put phenotyping and genome data</i>  <i>A project will be conducted on a dataset integrating population diversity analysis and population structure, linkage disequilibrium estimation and association genetics to detect loci involved quantitative traits in crops.</i> <i>Focus will be put on dataset work.</i> <i>Work on dataset will be co-coordinated with statistics and R teaching.</i>
<b>Content</b>	- <i>Population genetics and genetic diversity</i> - <i>Haplotype structure</i> - <i>Domestication and genetic consequences</i> - <i>Linkage disequilibrium</i> - <i>Genetic variance, estimating variance components, heritability</i> - <i>Genetic correlations</i>

	<ul style="list-style-type: none"> <li>- Association genetics, genomic selection</li> <li>- induced diversity TILLinG, natural diversity ecoTILLinG</li> <li>- Linking genetics, genomics and bioinformatics : from fine-mapping to gene cloning; genotyping by sequencing</li> </ul>
<b>Methods</b>	Lectures, seminars, project containing data study
<b>Assessment procedures</b>	<p>Assessment will be done by :</p> <ul style="list-style-type: none"> <li>- summative assessment</li> <li>- essay and group presentation of personal project</li> </ul> <p>Quality of the proposal, quality of the report and quality of presentation will be taken into account.</p> <ul style="list-style-type: none"> <li>- Data study and presentation</li> </ul>
<b>Prerequisites</b>	<ul style="list-style-type: none"> <li>- First year of Master in Biological science</li> <li>- Basis Statistics and R, basis genetics and genomics</li> </ul>
<b>Other information</b>	

*Please note that the number of places available may be limited for certain classes.*