

# Christophe Djemiel

*Ph.D. student in bioinformatics*

## Current research interests

I joined the plant fiber team to better understand the key steps in microbial ecology of complex samples, from collect, sample preparation to data analysis and interpretation. I was able to draw upon my different skills molecular biology and bioinformatics. I will defend my Ph.D. thesis in March 2017 and I'm looking for a postdoctoral position in the continuity of my thesis in meta-omics.

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## Education and diplomas

- 2013 - Present **Preparation of a Ph.D. thesis in bioinformatics**, UGSF laboratory, University of Lille 1 (Fr).
- 2013 **Master's degree in computer science**, with high honors, University of Bordeaux (Fr).
- 2011 **Bachelor's degree in Biology**, University of Bordeaux (Fr).
- 2009 **2-year technical college degree**, St. Louis High School (Bordeaux - Fr).
- 2007 **French HS diploma in Science major**, Montesquieu High School (Bordeaux - Fr).

## Professional experiences

- 2013 - Present **Ph.D. thesis in bioinformatics**  
*'Future project' 'StructuratIoN de la filière Fibres techniques d'Origine végétale pour usages matériaux' (SINFONI)*  
**Dynamics of bacterial and fungal communities during the dew-retting of flax by meta-omics approaches**  
Advisors: Dr Sébastien Grec and Pr Simon Hawkins (UMR 8576 - CNRS - UGSF, Lille 1 - Fr).
  - Preparation of samples from field experimental design to Illumina sequencing.
  - Re-design universal reverse primer of V3-V4 rRNA gene subregion for plant-associated bacteria studies.
  - Development of various methods to remove rRNA or enrich to mRNA from plant-associated microbiome for metatranscriptomic studies.
  - Implementation of pipelines and statistical analysis for microbial diversity.
  - Looking for microbial and CAZymes markers.
- 2013 (6 months) **Master's internship**  
**Development of metagenomic pipelines for classify and clustering 16S rRNA gene sequences**  
Advisor: Jérôme Mariette, Software engineer (INRA - Genotoul, Toulouse - Fr).
  - Development of pipelines (Roche 454 and Illumina Miseq platform) with **Jflow** API based on Makeflow and Weaver and be integrated in NGSpipelines and **NG6** environment.
  - Implementation Perl script to convert taxonomy file from **mothur** to hierarchical **Krona**.
  - Implementaion of jQuery plugin for comparing lists with Venn Diagrams: **jvenn**.
- 2011 - 2012 **International Genetically Engineered Machine competition (iGEM)**  
**Pseudo-bacterial eye**  
Advisors: Dr Denis Depuy (molecular biology) and Dr Marie Beurton-Aimar (computer science).
  - Involvement in setting up of the first team of Bordeaux and mangement for the second participation.
  - Responsible for modeling and simulation of complex existing regulatory mechanisms in prokaryotes in eukaryotic organisms. Development of a wiki website for your project.
  - Participation of oral and poster communication in Amsterdam, 5th - 7th October 2012, we won a bronze medal.
- 2008 - 2009 (4 months) **BTS internship**  
**Functional analysis of cell cycle genes regulator and endocycle from tomato**  
Advisors: Pr Michel Hernould (UMR 1332 Biologie du Fruit et Pathologie - INRA / University of Bordeaux - Fr) and Dr Elodie Mathieu-Rivet (Glyco-MEV, University of Rouen - Fr).
  - Constructing various expression vectors of cell cycle genes for a transitoire approach by biolistic method and for a stable approach by *Agrobacterium tumefaciens*.
  - Development of plasmid manager tool (VBA langage) called 'Plasmidator' on my free time.

## Teaching

Generally, I supervised a group of about 30 students for the practical work. I was in charge the elaboration of quick quiz at beginning of lessons, the evaluation of scientific experiments and the correction of drawings. For the 'Initiation of computer science' course for a Next Generation Sequencing workshop for 15 M.Sc. students, I developed a lesson (duration 6h) with practical work.

- 2015/2016 **Practical work in cellular biology**, 1st year of Bachelor degree, 45h.  
**Practical work in plant biology**, 1st year of Bachelor degree, 16h.  
**Teaching assistant**, Initiation of computer science by Python language MsC in Biotechnology, 4h.
- 2014/2015 **Practical work in plant biology**, 1st year of Bachelor degree, 58h.  
**Teaching assistant**, Initiation of computer science by Python language MsC in Biotechnology, 6h.
- 2013/2014 **Practical work in plant biology**, 1st year of Bachelor degree, 64h.

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## Achievements

### Articles in international peer-reviewed scientific journals

Citations: 40, H-index:1 based on Google Scholar (July 2016)

- 2016 [3] **Microbial diversity during dew-retting flax**  
C. Djemiel, S. Grec, B. Chabbert and S. Hawkins, ISME Journal, *in progress*
- [2] **Microbial of retting hemp**  
A. Day, C. Djemiel, B. Kurek, B. Chabbert and I. Mangin, Short review AMB, *submitted*
- 2014 [1] **jvenn: an interactive Venn diagram viewer.**  
P. Bardou, J. Mariette, F. Escudié, C. Djemiel and C. Klopp. BMC Bioinformatics

### International conference with proceedings

- 2016 [5] **Tracking dynamics of flax reeting by evolution in stem architecture, call wall structure, and biological activities**, Lignobiotech, Madrid (Sp), Speaker: Bernard Kurek (UMR A614 - INRA - FARE, Reims -Fr), 20 minutes
- [4] **Phenotyping microbial diversity during flax dew-retting by using targeted-metagenomics**, Cost meeting, University of Copenhagen (Dk), 15 minutes

### National conference with proceedings

- 2016 [3] **Microbial diversity of retting - From cultured to uncultured genome sequences**  
Multihemp workshop, University of Lille 1 (Fr), 15 minutes
- 2015 [2] **Dynamics of bacterial and fungal communities during the dew-retting of flax**  
Transatlantic Flax Research meeting, University of Lille 1 (Fr), 20 minutes

### Seminar and oral communications without proceedings

- 2014 [1] **Study of cell wall degrading during the dew-retting of flax by targeted-metagenomics**  
UGSF seminar, University of Lille 1 (Fr), 45 minutes in french

### Posters

- 2016 [7] **Study of microbial diversity and plant cell wall-degrading enzymes during flax dew-retting by using targeted-metagenomics and metatranscriptomics**, ISME, Montréal (Ca), 3 minutes
- [6] **Study of microbial diversity and plant cell wall-degrading enzymes during flax dew-retting by using targeted-metagenomics**, JOBIM, Lyon (Fr)
- [5] **Characterization of microbial diversity and plant cell wall-degrading enzymes during flax dew-retting by using targeted-metagenomics, metatranscriptomics and biochemistry**, Cell Wall Meeting, Chania (Gr)
- [4] **Meta-omics for a better understanding of the early stages of flax fiber extraction during retting**, Polytech seminar, Lille (Fr)
- 2014 [3] **Study of cell wall degrading during the dew-retting of flax by targeted-metagenomics**  
Réseau Français des Parois, Amiens (Fr), in french
- [2] **"Like looking for a needle in a flax stack"**, Bioinformatics for Environmental Genomics workshop, Lyon (Fr)
- 2013 [1] **Integrated next generation sequencing storage and processing environment**, JOBIM, Toulouse (Fr)

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## Computer skills

<b>Operating system</b>	<b>IDE, collaboration</b>
GNU/Linux, macOS	Eclipse, SVN, github
<b>OOP</b>	<b>Web</b>
Python, Java	HTML5/CSS3, jQuery, PHP
<b>Programming languages</b>	<b>Database</b>
Perl, Shell, LISP, Hoc	MySQL, PostgreSQL
<b>Office software</b>	
LaTeX, Beamer, LibreOffice, Adobe Illustrator	

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## Data analysis

<b>Workflow management system</b>
Jflow
<b>Diversity tools</b>
Mothur, PIPTIS, Picrust, LEfSe, Oligotyping
<b>Statistical</b>
Diversity measures, structure and membership composition comparisons
<b>Visualization tools</b>
Highcharts, Krona, jvenn

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## Biology

<b>Methodology</b>
Set up experimental design (sampling, storage)
<b>Molecular technics</b>
RNA/DNA extraction/purification, quantification by picogreen using lightCycler instrument, normalization by epMotion system, PCR, cloning.

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## Referees

**Pr Simon Hawkins**  
*My Ph.D. advisor*  
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**Dr Sébastien Grec**  
*My Ph.D. advisor*  
Plant Fiber Team  
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**Jérôme Mariette (Software Engineer)**  
*My M.Sc. internship advisor*  
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