

BENOÎT ALIAGA

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KEYWORDS

Evolution, genome, epigenome, G x E interaction, development, cancer and aging.

PROFILE

I am a Ph.D. in biology. I am looking for a postdoc on the stem cells/cancer/aging mechanisms throughout the tree of life. During my studies and my previous works, I developed different skills in genomics, epigenomics, bioinformatics, ecology fields and biostatistics.

EDUCATION

University of Perpignan Via Domitia Ph.D., Epigenetics	Perpignan, France May 2018
University of Perpignan Via Domitia M.Sc., Integrated Biology: Molecules, Population and Sustainable Development	Perpignan, France June 2014
University of Perpignan Via Domitia B.Sc., Biology-Ecology	Perpignan, France June 2011

FELLOWSHIPS

Wellcome Trust Sanger Institute for an advanced course on Single Cell technologies and analysis	2019
National Ph.D. grant for disabled graduate students (French Ministry of Education and Research)	2014-2018

RESEARCH EXPERIENCE

University of Montpellier Montpellier, France
Ingénieur de Recherche with Dr. Antoine Claessens 2019

- Transcriptomic analysis (RNA-seq) on *Plasmodium falciparum* from asymptomatic and symptomatic patients (Malaria).
- DNA replication study with SNS-seq (Short Nascent Strand Sequencing) in *Leishmania major* and *Trypanosoma brucei*. I analyzed the preliminary results (in collaboration with Dr. Yvon Sterkers).

University of Perpignan Via Domitia Perpignan, France
Graduate Student with Dr. David Duval and Prof. Christoph Grunau 2014-2018
Dissertation: Epigenomics comparison of non-model species

- The main aim was to identify several epigenomic patterns in various species living in different environments and throughout evolution.
- I continued my master's work on the development a bioinformatic tool to predict DNA methylation patterns. I validated it with DNA methylation patterns in gene bodies described in very well know species in the literature. We called it Notos.
- Used Notos results to identify the evolution of DNA methylation patterns in gene bodies in a pan-species study.
- Compared the epigenome (ChIP-seq) of two different *Schistosoma mansoni* life cycle stages: miracidia and sporocysts which live in different environments (freshwater for miracidia and intra-molluscan for sporocyst).

- Tested the effect of an epidrug (Trichostatine A) on *Schistosoma mansoni* larvae and observed their plasticity during infestation and development inside their intermediate host *Biomphalaria glabrata*.

University of Perpignan Via Domitia

Perpignan, France

Intern with Prof. Jan Bulla and Prof. Christoph Grunau

2014

Dissertation: Pan-species analysis of DNA methylation with bioinformatic tools

- The objective was to develop a bioinformatic tool (based on CpGo/e ratios) to study DNA methylation patterns in the gene bodies with only the sequences present in databases.
- Used three statistical approaches (Silvermann test, Gaussian and non-Gaussian distributions) to define DNA methylation patterns.

University of Lausanne

Lausanne, Switzerland

Intern with Dr. Pierre Bize

2013

Dissertation: Telomeres length, individual quality and fitness

- The goal of this work was studying the aging plasticity in natural population of bird.
- Extracted DNA from bird blood and measured telomere length by qPCR (3298 samples).
- Searched statistical relations between aging, dispersal, habitat quality, development, life history traits and telomere length.

University of Rennes I

Rennes, France

Intern with Dr. Armel Salmon and Prof. Malika Ainouche

2012

Dissertation: Reconstruction and assembly of ribosomal DNA (45S rDNA) in Spartines polyploidy

- The aim was to validate the 45S rDNA haplotypes present in *Spartina maritima* (Poaceae) and detected by bioinformatic tools for pyrosequencing and Illumina.
- Amplified by PCR the different regions of 45S rDNA containing the previously identified SNPs (Single Nucleotide Polymorphisms) previously which are necessary to differentiate the haplotypes.
- Cloned and sequenced the PCR products.
- Assembled the different sequenced regions and reconstructed the different haplotypes.

University of Perpignan Via Domitia

Perpignan, France

Literature study with Dr. Eric Lasserre

2011

Dissertation: LTR retrotransposons in plants

- The goal of this work was to write a review of LTR retrotransposons in plants (structure, transposition mechanisms, epigenetics, role and impact ...).

SKILLS AND TECHNIQUES

- Epigenetics: ChIPseq, gene positioning
- Bioinformatics: RNA-seq, SNS-seq, Galaxy, HPC, single cell analysis
- Biostatistics: R, JMP
- Molecular Biology: DNA extraction, PCR, qPCR, molecular cloning, Tecan freedom evo, bionalyzer, TrueSeq library, single cell technologies (Smart-seq 2, 10X)
- Parasitology: familiarized with the *Schistosoma mansoni* techniques in a L2 lab and *Plasmodium falciparum* cellular culture in a L3 lab
- Microscopy: optical microscopes
- Microbiology: general techniques
- Programming languages: Bash, HTML5, CSS3, Git, PHP, MySQL and Python
- Text processing softwares: Word, Excel, Powerpoint, LibreOffice and LaTeX
- Languages: French (mother tongue), English (B1 level), French Sign Language (fluent)
- Other: CNRS Geslab software

ORGANIZATION & LEADERSHIP EXPERIENCE

II Joint Congress on Evolutionary Biology (volunteer)	2018
Models in Ecology and Evolution seminar (scientific committee)	2018
Member of the IHPE (Interaction Host Pathogen and Environment) lab group communication	2015-2018
Yearly participation in science popularization days	2011-2018
University of Perpignan PhD student congress (scientific committee)	2015
Vice-President of a local association for deaf and hearing-impaired people (APIDA 66)	2011-2019
APIDA 66 Member of the Board of Directors	2008-2019

TEACHING

Population genetics, bioinformatics and biostatistics (ParaFrap PhD South program)	2019
Introduction to microbiology (practical works for 1st year undergraduates)	2015-2016
Animal physiology (practical works for 2nd year undergraduates)	2015-2016

PROFESSIONAL ASSOCIATIONS

- Member of the European Society for Evolutionary Biology (ESEB)
- Member of the Société Française de BioInformatique (SFBI)
- Member of the Jeunes BioInformaticiens de France (JeBIF)

PUBLICATIONS

Aliaga B., Bulla I., Mouahid G., Duval D., Grunau C. (2018) The universality of gene body DNA methylation. *Scientific Reports*.

Roquis D., Taudt A., Geyer K. K., Padalino G., Hoffmann K. F., Holroyd N., Berriman M., **Aliaga B.**, Chaparro C., Grunau., Augusto R. (2018) Histone methylation changes are essential for life cycle progression in the human parasite *Schistosoma mansoni*. *PLOS Pathogens*.

Bulla I., **Aliaga B.**, Lacal V., Bulla J., Grunau C., Chaparro C. (2018) Notos - a Galaxy tool to analyze CpN observed expected ratios for inferring DNA methylation types. *BMC Bioinformatics*.

Fneich S., Theron A., Cosseau C., Rognon A., **Aliaga B.**, Buard J., Duval., Aranciabia N., Boissier J., Roquis D., Mitta G., Grunau C. (2016) Epigenetic origin of adaptative phenotypic variants in the human blood-fluke *Schistosoma mansoni*. *Epigenetics & Chromatin*.

Boutte J., **Aliaga B.**, Lima O., Ferreira de Carvalho J., Aïnouche A., Macas J., Rousseau-Gueutin M., Coriton O., Aïnouche M., Salmon A. (2016) Haplotype detection from next generation sequencing in high ploidy-level species: 45S rDNA genes copies in the hexaploid *Spartina maritima*. *G3: Genes, Genomes, Genetics*.

CONFERENCE PRESENTATIONS

B. Aliaga, I. Bulla, V. Lacal, J. Bulla, D. Duval, C. Grunau, C. Chaparro*. Predicting DNA methylation by means of CpGo/e ratios in the case of a pan-species study. CEMEB Workshop Epigenetics in Ecology and Evolution, April 4th 2016, Montpellier, France. * presented by Chaparro in my absence

B. Aliaga, D. Duval, C. Grunau. How to correlate the prediction of DNA methylation with experimental data: a statistical approach. Brainstorming Workshop: Epigenetics & Mathematics, October 28th-31th 2015, Berlin, Germany.

B. Aliaga, D. Duval, K. Brehm, C. Grunau. Genome-wide comparison of chromatin structure changes in infective forms of parasitic flatworms. Interaction Micro-organismes Hôtes (IMH), November 19th 2014, Montpellier, France.

POSTER PRESENTATIONS

B. Aliaga, I. Bulla, G. Mouahid, D. Duval, C. Grunau. DNA methylation prediction in the gene body by means of CpGo/e ratios in a eukaryotic pan-species study. II Joint Congress on Evolutionary Biology, August 19th-22th 2018, Montpellier, France.

B. Aliaga, I. Bulla, V. Lacal, D. Duval, J. Bulla, C. Chaparro, C. Grunau. Predicting DNA methylation by means of CpGo/e ratios in the case of a pan-species study. Journées Ouvertes de Biologie, Informatique & Mathématiques (JOBIM), June 28th-30th 2016, Lyon, France.

B. Aliaga, V. Lacal, I. Bulla, D. Duval, J. Bulla, C. Grunau. A pan-species study of DNA methylation patterns by means of distributions of CpG o/e ratios. European Society for Evolutionary Biology (ESEB), August 10th-14th 2015, Lausanne, Switzerland.

J. Boutte, **B. Aliaga**, J. Ferreira de Carvalho, O. Lima, S. Coudouel, D. Naquin, P. Wincker, J. Poulain, C. Da Silva, M. Aïnouche and A. Salmon. Automatized detection of duplicated copies from NGS data: application to 45S rDNA and coding genes in hexaploid *Spartina* species (Poaceae). International Conference on Polyploidy, Hybridization, and Biodiversity (ICPHB), May 7th-10th 2012, Průhonice, Czech Republic.