



GABRIEL RECH, PHD



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[GOOGLE SCHOLAR](#)

SOFT SKILLS

Ability to work independently and as part of a team.

Self-thought and problem solving skills. Used to goal-oriented way of working.

Comfortable supervising people.

Used to communicate and collaborate with people with diverse backgrounds.

Always willing to learn new methods and techniques.

EXPERIENCE

BIOINFORMATICS ANALYST II THE JACKSON LABORATORY FOR GENOMIC MEDICINE FARMINGTON, CONNECTICUT, EEUU.

Aug. 2020 – Present

Analysis of third generation sequencing technologies (PacBio and Oxford Nanopore) data. Structural Variations. Pipeline development and bioinformatic strategies for data analysis and interpretation.

BIOINFORMATICS RESEARCHER INSTITUTE OF EVOLUTIONARY BIOLOGY (CSIC-UPF). BARCELONA, SPAIN.

Sep. 2016 – Aug. 2020

Whole genome sequencing, de-novo assembly and annotation of transposable elements using NGS (Illumina) and third generation sequencing technologies. Transcriptomics. Population genomics.

BIOINFORMATIC TECHNICIAN INSTITUTE OF PREDICTIVE AND PERSONALIZED MEDICINE OF CANCER BARCELONA, SPAIN.

Jan. 2014 – Aug. 2016

Development and maintenance of pipelines for NGS data analysis (WGS, WES, RNA-Seq, I6S amplicons) and expression/methylation arrays. Experimental design, quality control, development of pipelines, data analysis and interpretation.

EDUCATION

PH.D BIOINFORMATICS / 2014

University of Salamanca (Spain)

International Mention, Summa Cum Laude, Ph.D Extraordinary Award.

MSC. AGROBIOTECHNOLOGY / 2011

University of Salamanca (Spain)

DEGREE IN BIOLOGY / 2008

National University of Salta (Argentina)



BIOINFO SKILLS

Administration and advanced command line usage of Unix-based OS. Experience using computer clusters (CPD / HPC) and cloud-based systems (AWS). Experience using containers and workflow management systems (Nextflow, Snakemake). Programming: Python, R, bash, awk. NGS data quality control, de-novo genome assembly. Variant calling. Gene and transposable elements annotation. Comparative Genomics. Methylation and genotyping arrays analysis. Analysis of long read sequencing data (PacBio and Oxford Nanopore). Metagenomics analysis using short and long reads (QIIME2, kraken2). RNA-Seq (smallRNA and mRNA) analysis. Mapping, QC and differential expression. Isoform detection. De novo transcriptome analysis. Phylogenetic reconstruction, molecular evolutionary analysis and population genomics.



RELEVANT COURSES

- Manual Curation of Transposable Element Annotations. INRA, Versailles. Feb 2019.
 - Docker and Singularity. CRG Internal Training. Centre for Genomic Regulation (CRG), Barcelona. Jan 2019.
 - Statistical Programming and Graphics in R Applied to Research. Group CIEF, IMPPC, Badalona. Apr-May 2014.
 - Analysis of Exome-Sequencing Data for Clinical Applications. Centre for Genomic Regulation (CRG), Barcelona. Feb 2014.
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SCIENTIFIC VISITS

- Unité de Recherches en Génomique Info (URGI). Versailles, France. Nov. 2017.
 - Computational Biochemistry Research Group - ETH (Swiss Federal Institute of Technology). Zürich, Switzerland. Sep – Dec 2012.
 - Centre for Bioinformatics and Computational Genetics - University of Adelaide. Adelaide, Australia. Sep – Dec 2011.
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TEACHING AND OUTREACH

- Instructor in the Advanced course in Phylogenomics and Population Genomics. Universitat de Barcelona, July 2019.
- Instructor in the Workshop on “Differential Gene Expression Analysis”. AdaptNET. University of Valencia, Spain, 2017.
- Volunteer PRBB Open Day 2016 and PRBB Biojunior 2017/2018.
- Blog post at [Methods.blog](#), the official blog of Methods in Ecology and Evolution: “[Getting Serious About Transposable Elements](#)”.
- Teaching Assistantship “Bioinformatics and Computational Genomics”. University of Salamanca, Spain, 2010-2014.
- Teaching Assistantship “Microbiology and Genetics”. University of Salamanca, Spain. 2010-2014.
- Teaching Assistantship “Physics”. National University of Salta, Argentina, 2008-2009.
- Teaching Assistantship “Genetics”. National University of Salta, Argentina, 2006-2008.



MAIN PUBLICATIONS SORTED BY TOPIC

Genome-wide NGS, analysis of variants, and transposons, population genomics:

- **Rech et al. 2019.** Stress response, behavior, and development are shaped by transposable element-induced mutations in *Drosophila*. <https://doi.org/10.1371/journal.pgen.1007900>.
- **Mateo et al. 2018.** Genome-wide patterns of local adaptation in Western European *Drosophila melanogaster* natural populations. <https://doi.org/10.1038/s41598-018-34267-0>.
- **Villanueva-Cañas & Rech et al. 2017.** Beyond SNPs: how to detect selection on transposable element insertions. <https://doi.org/10.1111/2041-210X.12781>
- **Rech et al. 2014.** Natural Selection on Coding and Noncoding DNA Sequences Is Associated with Virulence Genes in a Plant Pathogenic Fungus. <https://doi.org/10.1093/gbe/evu192>

Transcriptomics (RNASeq data analysis):

- **Salces-Ortiz et al. 2019.** Transposable elements contribute to the genomic response to insecticides in *Drosophila melanogaster*. <https://doi.org/10.1098/rstb.2019.0341>.
- **Agostini et al. 2018.** Long-lasting primed state in maize plants. Salicylic acid and steroids signaling pathways as leading actors for the early activation of immune responses in silks. <https://doi.org/10.1094/MPMI-07-18-0208-R>

NGS for viral detection:

- **Saludes et al. 2016.** Assessment of the Illumina MiSeq massive parallel sequencing platform for simultaneous analysis of Hepatitis C virus resistance to all direct-acting antivirals combination regimes. <https://doi.org/10.1016/j.jcv.2016.08.028>

Genome assembly and annotation of microorganisms:

- **Rech et al. 2015.** Draft Genome Sequences of *Mycobacterium setense* and the Nonpathogenic Strain *Manresensis*, Isolated in Manresa, Catalonia, Spain. [doi: 10.1128/genomeA.01485-14](https://doi.org/10.1128/genomeA.01485-14).
- **Baroncelli et al. 2014.** Draft Genome Sequence of *Colletotrichum sublineola*, a Destructive Pathogen of Cultivated Sorghum. [doi: 10.1128/genomeA.00540-14](https://doi.org/10.1128/genomeA.00540-14).

Phylogenetic, molecular evolution, plant-pathogen interactions:

- **Vargas et al. 2016.** A fungal effector with host nuclear localization and DNA-binding properties is required for maize anthracnose development. <https://doi.org/10.1094/MPMI-09-15-0209-R>.
- **Rech et al. 2012.** Identification of positive selection in disease response genes within members of the Poaceae. <https://doi.org/10.4161/psb.22362>.
- **O'Connell et al. 2012.** Life-style transitions in plant pathogenic *Colletotrichum* fungi deciphered by genome and transcriptome analyses. <https://doi.org/10.1038/ng.2372>.
- **Vargas et al. 2012.** Plant defense mechanisms are activated during biotrophic and necrotrophic development of *Colletotrichum graminicola* in maize. <https://doi.org/10.1104/pp.111.190397>.

