



## Education

- 2005 **Habilitation à Diriger des Recherches**, Univ. Montpellier, France.  
*Algorithms for sequence analysis in bioinformatics*
- 1993–1996 **PhD in Computer Science**, Univ. Lille, France.  
*Compression and genetic sequence analysis*
- 1992–1993 **Master in Computer Science**, Univ. Lille, Lille, Fr.

## Experience

- 2008–present **Research director**, CNRS, LIRMM, Montpellier.  
o Head of the ATGC Montpellier Bioinformatic platform (2016-)  
o Head of Institute of Computational Biology (2015-2018);  
o Head of CNRS research network (GdR) Molecular Bioinformatics (2010-2015);
- 1999–2007 **Research fellow**, CNRS, LIRMM, Montpellier.  
o Head of the Dpt of Computer Science (2007-2010)  
o Launch of “Next Generation Sequencing” activity on ATGC Bioinformatic platform (2007)
- 1996–1999 **Postdoctoral fellow**, German Cancer Research Center (DKFZ), Heidelberg, Germany.  
Fast algorithms for similarity search – Transcriptomics

## Project leadership (> 2008)

- 2017-2020 **Flagship “Gene expression Modelling” Labex NUMEV - 250 KE** 5 research units
- 2016-2018 **3GenSeq “Long read error correction” Inst. Français de Bioinformatique - 90 KE**
- 2012-2018 **“Next Gen. Sequencing & algorithms” Inst. of Computational Biology - 200 KE**
- 2014-2017 **“Translation” Fondation Recherche Médicale (FRM) - 150 KE** Co-head J. Pannequin
- 2013-2014 **“Assembling the reference genome of a marine algae” Labex NUMEV - 40 KE** with Arago lab
- 2012-2016 **“Big Data: SeqPheHD++”, MASTODONS CNRS - 370 KE** 5 research units
- 2012-2016 **“RNA-seq” workpackage, PIA France Génomique - 150 KE** Co-head D. Gautheret
- 2008-2012 **“Comparison of complete genomes” ANR blanche - 150 KE** with 3 INRA research units

## Group & supervision

### Current

- PhD students **S. Relier** (2017-20), Translation - cs A. David; **N. Romaschenko** (2018-21) Metagenomics - cs F. Pardi  
Postdocs **G. Scholz** (2018-20), Metagenomics; **J. Ripoll** (2019-20), Translation GEM project

### Past

- PhD students S. Pulicani (2018), B. Cazaux (2016), N. Philippe (2011), R. Uricaru (2010), S. Leclercq (2007), F. Nicolas (2005), S. Bérard (2003), J.-S. Varré (2000)
- Engineers J. Veyssier (2017-18), A. Makrini (2014-16), V. Maillol (2012-14), F. Lethiec (2003-05)
- Postdocs D. Paulet (2014-18), R. Canovas (2015-17), M. Hébrard (2012-13), A. Mancheron (2007-09)

## Editorial boards & Program committees (PC)

- Journals NAR Bioinformatics & Genomics (Oxford Univ. Press); BMC Bioinformatics (BioMedCentral)  
PC Chair ECCB European Conference on Computational Biology 2014 (area chair); JOBIM 2009 (co-chair I. Rusu)

### Main PC memberships in Computer Science (CS) and Bioinformatics

CS SOFSEM 2020; SPIRE 2017; CPM 2017; DICTAP 2011; STACS 2008;

Bioinformatics Workshop on Algorithms in Bioinformatics WABI 2018, 2019, 2020;  
ECCB European Conference on Computational Biology: 2003, 2008, 2012, 2014, 2016  
RECOMB-SEQ 2016; RECOMB Comparative Genomics: 2010, 2013

## Conference and workshop organisation

- Workshop **Data Structures in Bioinformatics**, creation & org., Montpellier 2014, Bielefeld Germany, 2016  
Colloquium **Indexing for scientific Big Data**, Paris 2014 (125 participants)  
Symposium **Bioinformatics**, National network (GdR), Paris 2013, Paris 2015 (80-120 p.)  
Colloquium **Bioinformatics for High Throughput Sequencing**, creation & org., Paris 2010 (250 p.), Paris, 2011 (380 p.)

## Teaching and training

### Summer - winter

#### Schools

- Big data, open data  
Univ. Strasbourg 2018
- EMBO Pasteur,  
Tunis 2014
- EPIT Oléron 2014
- NOVA, Sweden, 2012

### University course

#### Master, Licence

- Montpellier
- Text Algorithms
- Bioinformatics
- Licence, Lille
- Database
- Computer networks

### Bioinformatics training sessions at ATGC platform

- for Next Gen. Sequencing, 2015-2020
- Linux and Python for bioinformatics, 2017-2020

## Selected publications

- [1] The Computational Pan-Genomics Consortium. Computational pan-genomics: status, promises and challenges. *Briefings in Bioinformatics*, 19(1):118–135, 2018.
- [2] Damien Paulet, Alexandre David, and Eric Rivals. Ribo-seq enlightens codon usage bias. *DNA Research*, 24(3):303–210, 2017.
- [3] Jasmijn A. Baaijens, Amal Zine El Aabidine, Eric Rivals, and Alexander Schönthuth. De novo assembly of viral quasispecies using overlap graphs. *Genome Research*, 27(5):835–848, 2017.
- [4] Leena Salmela and Eric Rivals. LORDEC: accurate and efficient long read error correction. *Bioinformatics*, 30(24):3506–3514, 2014. doi:10.1093/bioinformatics/btu538.
- [5] Nicolas Philippe, Mikael Salson, Thérèse Commes, and Eric Rivals. CRAC: an integrated approach to the analysis of RNA-seq reads. *Genome Biology*, 14(3):R30, 2013.

## Web links

Lists  
(clickable)

[Google Scholar](#) – [Scopus](#) – [PubMed](#) – ORCID – [ID](#) – [dblp](#)