Sylvain Foissac, Research Scientist

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RESEARCH STATEMENT

I am interested in **the fundamental mechanisms of life at the molecular scale**, particularly at the genome level. My goal is to understand how the genome is organized, functions, and how its linear and three-dimensional structures regulate gene expression.

To achieve this, **I design, develop, and utilize computational methods and tools to analyze genomics, transcriptomics, and other -omics data**, mostly obtained from high-throughput sequencing experiments. My expertise lies at the interface between various fields, combining molecular biology, bioinformatics, genomics, biostatistics, and computational science. My research focuses on **genome annotation, 3D genomics, and comparative data analysis**.

SUMMARY

- About **20 years of experience in computational biology and omics data analysis**.
- Scientific expertise in structural and functional genomics.
- Publication record of **31 peer-reviewed articles** and 3 book chapters.

EXPERIENCE

- Nov 2012 - present : Research Scientist ("CRCN") at **INRAE** in Toulouse, France.
- Dec 2010 - Oct 2012 : Product Manager at **Integromics, S.L.** in Madrid, Spain.
- Dec 2008 - Dec 2010 : Senior Research Scientist at **Integromics, S.L.** in Madrid, Spain.
- Apr 2008 - Nov 2008 : Data Analyst at **Affymetrix, Inc.** in Santa Clara, California, USA.
- Apr 2005 - Mar 2008 : PostDoctoral researcher at the **CRG** in Barcelona, Catalunya, Spain.

EDUCATION

- 2001-2004 : PhD thesis in Bioinformatics. Toulouse 3 University, France.
- 2000-2001 : Master degree in Bioinformatics. Paris VI & VII University, France.
- 1995-2000 : Bachelor degree in Cellular and Molecular Genetics. Toulouse 3 University, France.

PUBLICATIONS

– Degalez et al (2024). Enriched atlas of lncRNA and protein-coding genes for the GRCg7b chicken assembly and its functional annotation across 47 tissues. **Scientific Reports**. 10.1038/s41598-024-56705-y.
– Neuvial et al (2024). A two-sample tree-based test for hierarchically organized genomic signals. **Journal of the Royal Statistical Society Series C : Applied Statistics**. 10.1093/jrsssc/qlae011.
– Dufour et al (2024). Cell specification and functional interactions in the pig blastocyst inferred from single-cell transcriptomics and uterine fluids proteomics. **Genomics**. 10.1016/j.ygeno.2023.110780.
– Kurylo et al (2023). TAGADA : a scalable pipeline to improve genome annotations with RNA-seq data. **NAR Genomics And Bioinformatics**. 10.1093/nargab/lqad089.
– Hoellinger et al (2023). Enhancer/gene relationships : need for more reliable genome-wide reference sets. **Frontiers in Bioinformatics**. 10.1093/nar/gkx920.
– Jehl et al (2021). RNA-Seq Data for Reliable SNP Detection and Genotype Calling : Interest for Coding Variant Characterization and Cis-Regulation Analysis by Allele-Specific Expression in Livestock Species. **Frontiers in Genetics**. 10.3389/fgene.2021.655707.

– Marti-Marimon et al (2021). Major Reorganization of Chromosome Conformation During Muscle Development in Pig. **Frontiers in Genetics**. 10.3389/fgene.2021.748239.

– Jehl et al (2020). An integrative atlas of chicken long non-coding genes and their annotations across 25 tissues. **Scientific Reports**. 10.1038/s41598-020-77586-x.

– Giuffra et al (2019). Functional Annotation of Animal Genomes (FAANG) : Current Achievements and Roadmap. **Annual Review of Animal Biosciences**. 10.1146/annurev-animal-020518-114913.

– Foissac et al (2019). Multi-species annotation of transcriptome and chromatin structure in domesticated animals. **BMC Biology**. 10.1186/s12915-019-0726-5.

– Fève et al (2017). Identification of a t(3 ;4)(p1.3 ;q1.5) translocation breakpoint in pigs using somatic cell hybrid mapping and high-resolution mate-pair sequencing. **PLoS ONE**. 10.1371/journal.pone.0187617.

– David et al (2017). Genome-wide epigenetic studies in chicken : A review. **Epigenomes**. 10.3390/epigenomes1030020.

– Muret et al (2017). Long noncoding RNA repertoire in chicken liver and adipose tissue. **Genetics Selection Evolution**. 10.1186/s12711-016-0275-0.

– Andersson et al (2015). Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. **Genome Biology**. 10.1186/s13059-015-0622-4.

– Rubio-Peña et al (2015). Modeling of autosomal-dominant retinitis pigmentosa in Caenorhabditis elegans uncovers a nexus between global impaired functioning of certain splicing factors and cell type-specific apoptosis. **RNA**. 10.1261/rna.053397.115.

– Bonnet et al (2013). An overview of gene expression dynamics during early ovarian folliculogenesis : Specificity of follicular compartments and bi-directional dialog. **BMC Genomics**. 10.1186/1471-2164-14-904.

– Djebali et al (2012). Landscape of transcription in human cells. **Nature**. 10.17615/r8aq-6h68.

– Djebali et al (2012). Evidence for transcript networks composed of chimeric rnas in human cells. **PLoS ONE**. 10.1371/journal.pone.0028213.

– The ENCODE Project Consortium (2012). An integrated encyclopedia of DNA elements in the human genome. **Nature**. 10.1038/nature11247.

– Ozsolak et al (2010). Comprehensive polyadenylation site maps in yeast and human reveal pervasive alternative polyadenylation. **Cell**. 10.1016/j.cell.2010.11.020.

– Kapranov et al (2010). New class of gene-termini-associated human RNAs suggests a novel RNA copying mechanism. **Nature**. 10.1038/nature09190.

– Fejes-Toth et al (2009). Post-transcriptional processing generates a diversity of 5'-modified long and short RNAs. **Nature**. 10.1038/nature07759.

– Djebali et al (2008). Efficient targeted transcript discovery via array-based normalization of RACE libraries. **Nature Methods**. 10.1038/nmeth.1216.

– Piqué et al (2008). A Combinatorial Code for CPE-Mediated Translational Control. **Cell**. 10.1016/j.cell.2007.12.038.

– Sammeth et al (2008). A general definition and nomenclature for alternative splicing events. **PLoS Computational Biology**. 10.1371/journal.pcbi.1000147.

– Foissac et al (2008). Genome Annotation in Plants and Fungi : EuGene as a Model Platform. **Current Bioinformatics**. 10.2174/157489308784340702.

– Foissac et al (2007). ASTALAVISTA : dynamic and flexible analysis of alternative splicing events in custom gene datasets. **Nucleic acids research**. 10.1093/nar/gkm311.

– The ENCODE Project Consortium (2007). Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. **Nature**. 10.1038/nature0587.

– Denoeud et al (2007). Prominent use of distal 5' transcription start sites and discovery of a large number of additional exons in ENCODE regions. **Genome Research**. 10.1101/gr.5660607.

– Foissac et al (2005). Integrating alternative splicing detection into gene prediction. **BMC Bioinformatics**. 10.1186/1471-2105-6-25.

– Foissac et al (2003). EUGÈNE'HOM : A generic similarity-based gene finder using multiple homologous sequences. **Nucleic Acids Research**. 10.1093/nar/gkg586.