Fabio ROCHA
Marié, un enfant
28, Quai de la Charente
Paris - France
Tél : +33 07 82 71 55 57
E-mail : fabiorjvieira@gmail.com

Docteur – Informatique

PUBLICATIONS (COMITÉ DE LECTURE)
 *corresponding author, $co-first author

Zhao, X; **Vieira, F. R. J**[*] et al. Probing the Diversity of Polycomb and Trithorax Proteins in Cultured and Environmentally Sampled Microalgae. To appear in *Frontiers in Plant Science-Special Issue Marine epigenetics* **(2020)**.

Sato, S; **Vieira, F. R. J**[$] et al. Genome-enabled phylogenetic and functional reconstruction of an araphid pennate diatom Plagiostriata sp. CCMP470, previously assigned as a radial centric diatom, and its bacterial commensal. To appear in *Nature Scientific Reports* **(2020)**.

Carpenter, E. J; **Vieira, F. R. J**[$] et al. Access to RNA-sequencing data from 1,173 plant_species. The 1000 Plant transcriptomes initiative (1KP). *GigaScience* 8, 10, doi:10.1093/gigascience/giz126, https://github.com/Plant-and-diatom-genomics-IBENS-Paris/Decontamination-pipeline **(2019)**.

Busseni, G; **Vieira, F. R. J**[$] et al. Meta-Omics Reveals Genetic Flexibility of Diatom Nitrogen Transporters in Response to Environmental Changes. *Molecular Biology and Evolution*, msz157, doi:10.1093/molbev/msz157 **(2019**).

Caputi, L; **Vieira, F. R. J**[$] et al. Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. *Global Biogeochemical Cycles* 33, 3, doi:10.1029/2018GB006022 **(2019)**.

Rastogi, A; **Vieira, F. R. J** et al. A genomics approach reveals the global genetic polymorphism, structure, and functional diversity of ten accessions of the marine model diatom Phaeodactylum tricornutum. *The ISME Journal*, doi:10.1038/s41396-019-0528-3 **(2019**).

Kazamia, E; **Vieira, F. R. J** et al. Endocytosis-mediated siderophore uptake as a strategy for Fe acquisition in diatoms. *Science Advances* 4, 5, doi:10.1126/sciadv.aar4536 **(2018)**.

Rastogi, A; **Vieira, F. R. J** et al. Integrative analysis of large scale transcriptome data draws a comprehensive landscape of Phaeodactylum tricornutum genome and evolutionary origin of diatoms. *Nature Scientific Reports* 8, 1, doi:10.1038/s41598-018-23106-x **(2018)**.

Carradec, Q; **Vieira, F. R. J** et al. A global ocean atlas of eukaryotic genes. *Nature Communication* 9, doi:10.1038/s41467-017-02342-1 **(2018)**.

Bernardes, J. S; **Vieira, F. R. J**[$] et al. A multi-objective optimization approach accurately resolves protein domain architectures. *Bioinformatics* 32, 3, doi:10.1093/bioinformatics/btv582, http://www.lcqb.upmc.fr/DAMA/ **(2016)**.

Vieira, F. R. J et al. Scheduling wireless links by vertex multicoloring in the physical interference model. *Computer Networks* 99, doi:10.1016/j.comnet.2016.02.008 **(2016)**.

Bernardes, J. S; **<u>Vieira, F. R. J</u>$** *et al*. Evaluation and improvements of clustering algorithms for detecting remote homologous protein families. ***BMC Bioinformatics*** 16, doi:10.1186/s12859-014-0445-4 **(2014)**.

<u>Vieira, F. R. J</u> *et al*. Local heuristic for the refinement of multi-path routing in wireless mesh networks. ***Computer Networks*** 57, 1, doi:10.1016/j.comnet.2012.09.009 **(2013)**.

<u>Vieira, F. R. J</u> *et al*. Scheduling links for heavy traffic on interfering routes in wireless mesh networks. ***Computer Networks*** 56, 5, doi:10.1016/j.comnet.2012.01.011 **(2012)**.

<u>Vieira, F. R. J</u> *et al*. Optimization of supply diversity for the self-assembly of simple objects in two and three dimensions. ***Natural Computing*** 10, 1, doi:10.1007/s11047-010-9209-x **(2011)**.

Bioarchive

Jaouadi, C; **<u>Vieira, F. R. J</u>*** *et al*. DAVI: a tool for protein domain architecture clustering and visualization. http://genome.lcqb.upmc.fr/Domain-Architecture-Viewer **(2020)**.

Kritli, S; **<u>Vieira, F. R. J</u>*** *et al*. 2dSS: a web server for protein secondary structure visualization. http://genome.lcqb.upmc.fr/2dss/, doi:10.1101/649426 **(2019)**.

Soumis

Zhao, X; **<u>Vieira, F. R. J</u>*** *et al*. H3K27me3 natural variation selectively marks genes predicted to be important for differentiation in unicellular algae. New Phytologist, **(2020)**.

Dorrell, R; **<u>Vieira, F. R. J</u>** *et al*. Lineage and habitat-specific evolutionary innovations uncovered in genome sequences of Arctic photosynthetic nanoflagellates. ***Nature Microbiology***, **(2020)**.

Coronado, M; **<u>Vieira, F. R. J</u>*** *et al*. Domain functional analysis of C. pseudotuberculosis strains reveals more variability in strains of biovar equi than ovis. ***Journal of Biomolecular Structure & Dynamics,*** **(2020)**.

<u>Vieira, F. R. J</u> *et al*. An Effective Determination of Centroids improves protein sequence clustering. ***Bioinformatics,*** **(2020)**.

En préparation

Hoguin, A; **<u>Vieira, F. R. J</u>*** *et al*. The diversity of DNA methyltransferases: novel insights from microalgal lineages.

Hoguin, A; **<u>Vieira, F. R. J</u>*** *et al*. Monoallelic expression in single cell organisms, insights from the diatom Phaeodactylum tricornutum.

Shao, Z; **<u>Vieira, F. R. J</u>** *et al*. Characterization of a chitin synthase from the diatom Thalassiosira pseudonana and its influence on cell cycle and photosynthesis.

<u>Vieira, F. R. J</u> *et al*. The top 100 diatom functions most expressed on the ocean.

<u>Vieira, F. R. J</u> *et al*. A new approach to detect small virus in ocean samples.

COMMUNICATIONS ORALES

Artificial intelligence finds its way to biolabs. **Seminaire - Unité Fonctionnalité et Ingénierie des Protéines**, 4/9/2019, Université de Nantes - France.

Diatoms abundance in TARA samples. **Dragon Metagenomic Analysis Platform workshop,** 29 March 2017, King Abdullah University of Science and Technology - Saudi Arabia.

Improving taxonomic assignation in TARA samples. **EuroMarine Open Science Exploration**, 5 September 2017, Porto - Portugal.

Homology detection in TARA sequences. **Le programme Tara Oceans : structuration de la coopération scientifique internationale avec l'Amérique du Sud** (Fonds Français pour l'Environnement Mondial), 4 September 2017, Université de Concepción - Chile.

Most expressed diatom genes in TARA. **MARINE BIOGEOCHEMISTRY: ADVANCING THE LINK BETWEEN OBSERVATIONS, DATA, AND MODELS workshop**, 23 of June 2017, Villefranche-sur-mer - France.

Metabarcoding versus Metagenomic data in TARA. **IBENS section meeting**, 15 of June 2017, Paris - France.

Machine Learning methods in TARA metagenomes. **TARA SNP MEETING**, 4 of April 2016, Naples - Italy.

POSTER

Vieira, F. R. J; BERNARDES, J. S. Greedy cluster, a fast and sensitive method for grouping protein sequences. ***Machine Learning in Systems Biology***, Strasbourg, **(2014)**.

SERVICES INFORMATIQUES

Developpeur Modules Galaxy Ansible
https://github.com/galaxyproject/ansible-galaxy/graphs/contributors
https://github.com/galaxyproject/ansible-galaxy-extras/graphs/contributors
https://github.com/galaxyproject/ansible-galaxy-os/graphs/contributors
https://github.com/fabiorjvieira/ansible-galaxy-instance

Administrateur/Developpeur GitHub Plant-and-diatom-genomics-IBENS-Paris
https://github.com/Plant-and-diatom-genomics-IBENS-Paris

Administrateur/Chercheur Open Science Framework
Ancient DNA https://osf.io/ks7yw
eDAF https://osf.io/964yt

Mendeley Advisor
https://www.mendeley.com/profiles/fabio-vieira6/