Curriculum Vitae

Tristan Bitard-Feildel, PhD

Objective: NVIDIA GPU seeding grant

Bioinformatician, computational scientist

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Professional experience

2017- Research scientist

Institut de Biologie Paris-Seine, Université Pierre et Marie Curie, Paris 6

Laboratory of Computational and Quantitative Biology

Supervisor: Pr. Alessandra Carbone alessandra.carbone@lip6.fr

Projects:

Understanding the protein mutational landscape using protein dynamics simulation

2015- Research Scientist (ongoing)

2017 Institut de minéralogie, de physique des matériaux et de cosmochimie, Université Pierre et Marie Curie, Paris 6 Bioinformatics and Biophysics group

Supervisor: DR2 CNRS. Isabelle Callebaut isabelle.callebaut@impmc.upmc.fr

Projects:

Physico-chemical changes of proteins in the light of their evolutionary history

2013- Research Scientist

2015 Westfälische Wilhelms University (WWU) Münster Evolutionary Bioinformatics Group

Principal Investigator: Pr. PhD. Erich Bornberg-Bauer ebb@uni-muenster.de

Projects:

Evolution and emergence of new domains and new proteins (physico-chemical properties, hypothesis testing, ancestral protein)

Protein domain arrangements changes and their role in functional innovation (transcriptomics, functional annotation)

Software development using protein domain annotation (classification, parallelism, user experience).

2009- PhD thesis

2012 MIG INRA Jouy-en-Josas (Paris area)

Visiting PhD student at KAUST Saudi Arabia (2 months)

Supervisors

Antoine Vigneron, PhD and Jean-François Gibrat, PhD

Project: Development of an *Ab initio* method for protein structure prediction

- Protein dynamics simulation (Molucular Dynamics, Normal Mode Analysis)
- Dynamical properties in link with protein sequence and genomics polymorphism
- Protein sequence coevolution, sequences statistical analyses mapped to protein structure
- Physico-chemical properties of the dark proteome
- Novel genes and domains analyses: physico-chemical properties, mechanisms of emergence and dynamics.
- Automatic classification of unannotated protein domains
- Databases of unannotated domains in Mammals, Dicots and Monocots
- Biomineralization Evolution in cyanobacteria species (Master student supervision)
- Data mining and statistical analysis of large datasets (genomes and transcriptomes)
- Statistical evaluation of methodologies (ROC, AUC, FPR)
- Molecular and phylogenetic analyses of large protein structure and sequence datasets (tree computation, orthology prediction, ancestral reconstruction)
- Protein domain annotation, good knowledge of protein domain databases (Pfam, SUPERFAMILY) and associated functional resources
- Pipeline for gene expression analysis, reads preprocessing, differential expression, de novo transcriptome assembly
- Creation of a collaboration between French and German laboratories
- Coordination and teaching of various BioComputing lectures, students supervision (at PhD, MSc and BSc levels)
- Development of coarse grained modelling of protein structures
- Creation of statistical potentials for the computation of protein energy
- Algorithms for protein folding simulation (Monte Carlo, Replica Sampling, Genetic algorithms)
- Machine learning clustering algorithms (density based, spectral clustering)

Skills

Python numpy, scipy, sklearn, matplotlib	Machine learning (supervised and unsupervised clustering, random forest, SVD), statistical analysis and modeling (HMM, PCA, hypothesis testing), modules for computational biology
R/Bioconductors edgeR, DESeq, ggplot2	Statistical analysis (multidimensional analysis, hypothesis testing), gene expression analyses, data visualization
C/C++/C for CUDA OpenMP, boost	Parallelization, optimization, software development. Strong interest in deep learning application for molecular biology (Tensorflow, Caffee, Torch,)
Molecular Biology (BSc)	Basic Molecular Biology skills: Cell culture, PCR, gel electrophoresis, column chromatography,