GENOPOLE

POSTOCOTRAL FELLOWSHIP PROGRAMME - GENOPOLE 2020

The post-doctoral fellowship programme of Genopole is a funding scheme launched every year and dedicated to youg researchers who wants to return to France after a PhD or a post-doctoral period spent abroad. In order to facilitate the identification of hosting laboratories and positions offered, proposed research projects are described herein below.

Click here for more information on the academic laboratories located in Genopole Biocluster

Click here for the application file and the eligibility criteria and conditions.

Contact roxane.brachet@genopole.fr

Project descriptions – Academic sector

GENETHON CURE THROUGH INNOVATION | Inserm Institut national de la santé et de la recherche médicale | Université Evry | École Pratique des Hautes Études | integrare UMR 951

Généthon-INTEGRARE, D.A. GROSS team

Post-doctoral position	
Project title	Dissection of T cell responses after rAAV-mediated gene transfer
Typology	Postdoctoral position
Activity area	Immunology – AAV gene therapy
LABORATORY	
Laboratory name	INSERM U951 – INTEGRARE (Integrated genetic approaches for the treatment of rare genetic diseases)
Host institution	Généthon – INSERM - UEVE
Short desciption of the laboratory	The UMR_S951 INTEGRARE unit (https://integrare-umrs951.jimdo.com/), located in Genopole Evry, is integrated in the R&D organization of Genethon, which is a non-profit biotherapy organization funded by the Association Française contre les Myopathies. It is devoted to gene therapy products for rare diseases, ensuring translational development from research up to clinical validation (https://www.genethon.fr/). The present project will be developed under the supervision of Dr. D.A. GROSS in the "Immunology and Liver Diseases" team.
SCIENTIFIC PROJECT/ MISSIONS	
Detailed description	First successes of Adeno-Associated Virus (rAAV)-based gene therapy are now being reported in increasing number of clinical trials for the treatment of monogenic diseases. However, efficacy and broader use of these treatments are limited by deleterious immune responses induced by this viral vectors. The candidate will develop new rAAV vectors to dissect in mouse models the CD8+ T cell responses and tolerance mechanisms at play after gene transfer, with the will to propose functional immunomodulations, as well as new appropriate markers for patient immunomonitoring.

CANDIDATE PROFILE	
Essential skills	Candidates should have a PhD in Immunology and a strong background in cellular immunology, FACS, and molecular biology. Previous experience in translational research in the field of genetic diseases with viral vectors and/or animal models of disease is preferred.
Languages / Required level	English
CONTRACT CONDITIONS	
Type of contract	2 to 3 years position – limited term contract
Starting date	Q4 2020
Salary	According to experience
CONTACT	
A detailed CV with publication list and references should be sent to D.A. GROSS at dagross@genethon.fr	

LAMBE 1 – Juan PELTA team

Post-doctoral positions	
Intitulé du projet scientifique / Project title	**Biosensor platform based on nanopore technology to detect peptide and protein biomarkers at the single molecule level**
Typology	24 months, Post doctoral position in France
Activity area	Biotechnology
LABORATORY	
Laboratory name	LAMBE
Host institution	Evry (Evry University/Paris-Saclay University)
Short desciption of the laboratory	The laboratory works on the structure/reactivity of biomolecules, the interaction of complex molecular assemblies, the reactivity at the interface for the environment and the design of polymer materials. The laboratory challenges are to design, manufacture and characterize new biomimetic nanopores, nanotubes, membranes and supramolecular organization in order to understand the dynamics in confined medium from ions to biomolecules transport. The laboratory develops applications such as ultra-fast-protein sequencing, single virus particle detection and drug delivery using a single molecule level electrical detection method. The LAMBE is also involved in understanding tumor cell mechanical properties.
SCIENTIFIC PROJECT/ MISSIONS	

Detailed description	**Context and objectives** **Biomarker detection in low quantities for disease early diagnosis like cancer remains a challenge**. Analytical methods used in medical analysis require high quantities of biomarkers to be specifically detected in biofluids or cells. Biomedical science ought to address connectivity barriers restricting personalized medicine. Personalized medicine is based on medical biology which purpose is to define the metabolic profile of patients in order to adapt their treatment and minimize secondary effects. These metabolic profiles consist in an ensemble of biomarkers which allow to early diagnose diseases like cancer, establish vital prognostics, but also classify patients as a function of their sensitivity to treatments and ability to metabolize drugs. **The objective is to develop an experimental biosensor platform based on protein, solid-state and/or hybrid nanopore technology, to detect peptide and protein biomarkers at the single molecule level. The final goal of this project is to be able to detect biomarkers from biofluids and a single cell.** We intend to: - Identify and quantify few copies of proteins or peptides known as biomarkers. - Perform nano-enzymology by determining the enzymatic activity from single copies of enzymes.
CANDIDATE PROFILE	
Essential skills	- Backgroung in single molecule technics. - Have a strong desire to work in academia. - Demonstrate a high-level of skill in teamworking, communication, and academic writing. - Previous research experiences in any of the following subjects: single molecule approach, electrophysiology, nanotechnology, bioingenieering, molecular biology. - Previous experience with nanopores or biomarker detection is preferred
Langues /Languages Niveau requis/ Required level	English French (not mendatory)
CONDITIONS D'EMPLOI	
Type de contrat/ Type of contract	Short term contract 2 years
Entrée en fonction/ Starting date	As soon as possible
Rémunération/ Remuneration	130 000 € gross salary charged for 24 months
CONTACT	
Professor Juan Pelta ; juan.pelta@univ-evry.fr Co-funder of DreamPore Start-up, nanopore team leader	

LAMBE 2 – MIMEGAG, Regis DANIEL Team

Post-doctoral position

Project title	Structural and bio-interaction properties of peptide-based m i m i c s o f glycosaminoglycans studied by mass spectrometry and hyphenated affinity methods
Typology	Post-doc position
Activity area	Glycosciences, Biochemistry, Analytical & Bioanalytical Chemistry, Biophysics
LABORATORY	
Laboratory name	Laboratoire Analyse et Modélisation pour la Biologie et l'Environnement (LAMBE), CNRS UMR8587
Institution d'accueil/ Host institution	Université Paris-Saclay
Short desciption of the laboratory	The laboratory LAMBE is a CNRS research unit at Université Paris-Saclay University and is member of two Laboratories of Excellence: LaBex CHARM3AT (science of materials for energy, health, environment), and LabEx Lermit (Research on Medication and Innovative Therapeutics). The laboratory has a long-standing research experience in mass spectrometry (MS), in MS- hyphenated techniques and in single molecule-based methods for the characterization of sulfated carbohydrates and GAG-protein interactions. LAMBE hosts a Génopole® labeled mass spectrometry (MS) platform comprising seven mass spectrometers, and hyphenated separative and thermodynamic methods like surface plasmon resonance imaging coupled to mass spectrometry (SPRi-MS) and affinity capillary electrophoresis coupled with ESI-MS.
SCIENTIFIC PROJECT/ MISSIONS	
Detailed description	Glycosaminoglycans (GAGs) are sulfated polysaccharides anchored to a protein core at the outer cell surface where they constitute the proteoglycans assemblies. They mediate cell-cell and cell-matrix interactions involved in a variety of physiological and pathological functions such as in embryonic development, cell growth and differentiation, homeostasis, inflammatory response, tumor growth and microbial infection. Most of these GAG functions rely upon binding to protein effectors such as growth factors and cytokines whose biological activities are in turn regulated by modulating their availability, stability, structure and reactivity. However, the mechanisms of these interactions involving GAGs are still poorly understood, especially the molecular basis governing strength and specificity of the binding to target proteins. Difficulties mainly arise from the high structural diversity and from the isomeric properties of GAGs. To unravel this extraordinary complexity, defined compounds are necessary. Unfortunately, both extraction of pure compounds from natural sources and chemical or enzymatic synthesis of GAG fragments remain difficult. To overcome this difficulty, the project will investigate a new strategy based on the rational design of synthetic GAGs mimics. Upon interactions between proteins and GAGs, the correct space distribution of charges (sulfate, carboxylate) along the GAGs chain is crucial to ensure high affinity and specific interactions. This observation suggests that a feasible strategy could involve a peptide scaffold approach for controlled spatial presentation of charges. The main goals of the project will be the comparative structural and modeling analysis of GAG mimics consisting of synthetic anionic peptides with precisely located negatives charges. Preliminiray results have been obtained with different tetrapeptide motifs mimicking dodecasaccharides, and presenting different charge patterns (carboxylates, sulfonates). Together, this allows for further exploration of the effect of length and charge-pattern recognition on biomolecular interaction properties compared to GAGs oligosaccharides. Interaction of peptide GAGS mimics with targets proteins will be studied by using state-of-art mass spectrometry (MS) methods, especially hyphenated methods like surface plasmon resonance imaging coupled to MALDI TOF mass spectrometry (SPRi-MS) and affinity capillary electrophoresis with ESI-MS. Such developed new mimics molecules are valuable structural tools to decipher the biological roles of GAGs, and are of great therapeutic interest for diseases involving GAGs as biomarkers or as pharmacological targets.

CANDIDATE PROFILE	
Essential skills	Solid background in biochemistry, or chemistry with knowledge in bioanalytical and analytical chemistry and biophysic methods. Experience in glycosciences and/or mass pectrometry will be appreciated. Excellent communication and interpersonal skills □ Excellent time management and organisational skills □ Ability to work independently and within multidisciplinary teams Strong oral & written communication skills
Languages Required level	Englishs (B2) or French (B2)
CONDITIONS D'EMPLOI	
Type de contrat Type of contract	Limited term contract to 2 years
Entrée en fonction Starting date	Sept-2020
Rémunération	Average 3 600 € / month according to experience
CONTACT (name of the scientific supervisor)	
Dr. Régis Daniel Tel : 33 1 69 47 76 41 Email : regis.daniel@univ-evry.fr Web page of the lab group: http://www.lambe.univ-evry.fr/ Laboratoire Analyse et Modélisation pour la Biologie et l'Environnement (LAMBE) CNRS UMR 8587 Université Evry-Val-d'Essonne Bd François Mitterrand 91025 Evry Cedex France	

LAMBE 3 – nanoGAG, Régis DANIEL team

Post-doctoral position	
Project title	Single molecule detection and sequencing of bioactive carbohydrates by protein nanopore sensing
Typology	Research, postdoctoral position
Activity area	Glycosciences, Biochemistry, Analytical & Bioanalytical Chemistry, Biophysics
LABORATORY	
Laboratory name	Laboratoire Analyse et Modélisation pour la Biologie et l'Environnement (LAMBE), CNRS UMR8587
Host institution	Université Paris-Saclay
Short desciption of the laboratory	The laboratory LAMBE is a CNRS research unit at Université Paris-Saclay University and is member of two Laboratories of Excellence: LaBex CHARM3AT (science of materials for energy, health, environment), and LabEx Lermit (Research on Medication and Innovative Therapeutics). The laboratory has a long-standing research experience in mass spectrometry (MS), in MS-hyphenated techniques and in single molecule-based methods for the characterization of sulfated carbohydrates and GAG-protein interactions. LAMBE hosts a Génopole® labeled mass spectrometry (MS) platform comprising seven mass spectrometers, and is equiped with several protein nanopore set-ups.

SCIENTIFIC PROJECT/ MISSIONS	
Detailed description	The strong interest for detection and characterization of biomolecules using nanopore sensing is illustrated by the numerous studies concerning nucleic acid and proteins. Single nanopore analysis remains however comparatively much less applied to carbohydrates, especially bioactive polysaccharides like glycosaminoglycans (GAGs). Yet, nanopore-based methods are promising for deciphering information encoded in a linear polymer, and they meet the demand of glycoscience for innovative approaches. In the project, the effect of various sulfated patterns on the nanopre translocation of GAGs-derived sulfatd oligosaccharides will be studied using different protein nanopres showing distinct geometry (aerolysin, a-hemolysin). Specific signatures will be revealed, allowing a major step towards oligosaccharide sequencing at the single molecule. GAGs are biologically active anionic carbohydrates that are among the most challenging biopolymers with regards to their structural analysis and functional assessment. These sulfated polysaccharides are expressed at the cell surface and in the extracellular matrix: they represent a formidable analytical challenge, because of the huge variability of sulfation and the presence of epimers throughout these very large linear anionic polysaccharides. The project herein will produce a powerful leverage effect through combination of the cutting edges MS- and nanopore-based methods, thereby allowing an unprecedented multi-dimensional analytical strategy for GAGs sequencing. A significant outcome of the project will be a first analytical method for the rapid identification of different sulfate patterns in natural GAGs like heparan sulfate (HS) and chondroitin sulfate (CS), leading to a breakthrough in deciphering the HS/CS sulfo code and immediate applicability in pathophysiological research.
CANDIDATE PROFILE	
Essential skills	Solid background in biochemistry, or chemistry with knowledge in bioanalytical and analytical chemistry and biophysic methods. Experience in glycosciences and/or mass pectrometry will be appreciated. Excellent communication and interpersonal skills □ Excellent time management and organisational skills □ Ability to work independently and within multidisciplinary teams Strong oral & written communication skills
Languages	Englishs (B2) or French (B2)
CONDITIONS D'EMPLOI	
Type of contract	Short term contract of 2 years
Starting date	Sept-2020
Remuneration	Up to 3 600 € / month according to experience
CONTACT (name of the scientific supervisor)	
Dr. Régis Daniel Tel : 33 1 69 47 76 41 Email : regis.daniel@univ-evry.fr Web page of the lab group: http://www.lambe.univ-evry.fr/ Laboratoire Analyse et Modélisation pour la Biologie et l'Environnement (LAMBE)	

IBISC 1 – COSMO, Frank DELAPLACE team

POST-DOCOTRAL POSITION	
Project title	Design & Analysis of Cell Reprogramming Patterns
Typology	Posto-dcotoral position

Activity area	Computational Biology, Precision Medicine
LABORATORY	
Laboratory name	IBISC - Informatique Bio-Informatique et Systèmes Complexes
Host institution	Paris-Saclay University, Univ. Evry
Short desciption of the laboratory	IBISC (Informatique, Bio-informatique et Systèmes Complexes – Computer Science, Bio-Informatics and Complex Systems) is a laboratory of Paris-Saclay University. The IBISC laboratory is composed by 4 teams: AROBAS, COSMO, IRA2, and SIAM. Their scientific activities are divided into two scientific axes: ICT & SMART SYSTEM and ICT & LIFE, each focused on a specific application area which is respectively: drone & vehicle, and precision and personalized medicine. More specifically, the ICT & LIFE axis challenges cover a wide spectrum of biological and biomedical issues: data analysis, biological or biomedical signals, biological system modeling, prediction in precision medicine. The research focuses on the development of theoretical frameworks, algorithmic methods and platforms to meet the challengesin personalized medicine.
SCIENTIFIC PROJECT/ MISSIONS	
Detailed description	Cell reprogramming consists in modifying the expression of specific genes to induce a particular cell behavior either naturally or artificially. The theme is at the confluence between essential areas of health: precision medicine, regenerative medicine, and stem cells. Although the progress in cell reprogramming during the last decade, more breakthroughs are required before cellular reprogramming yields the cure for disease routinely. The main issues lie on the discovery of reliable way to trigger reprogramming process to understand exactly how the process works and to design reprogramming patterns. In this undertaking, designing computational framework is critical for this investigation. However, the state of the art reveals a blatant lack of maturity of computer methods. Hence, the project aims at characterizing the principles of cell reprogramming in the objective to design software system for reprogramming design and prediction. Two main characteristics of cell reprogramming guide the study: the action is applied on molecular networks, and the goal is assessed by a cell phenotype change (eg. healthy/sick) induced by a modification of the network. These basic characteristics focus the study on network dynamics where a reprogramming pattern is a sub-network controlling the phenotypic change. The analysis is based on discrete network formalism. The post-doctoral fellow will be involved in the study of properties of the reprogramming patterns. The objective is to design a framework for the inference of cell reprogramming patten comprising: drug target identification, network based etiology and property analysis as robustness.
CANDIDATE PROFILE	

Essential skills	The candidates should have a strong background in computer science with skills in network based formal methods. A background on Boolean network will constitute an asset but it is not mandatory. They should also have a reasonable skill in system biology, more specifically in biological network analysis and a high motivation towards application in precision medicine.
Langues /Languages Niveau requis/ Required level	English: Fluent French: a fair level will be an asset but not mandatory
CONDITIONS D'EMPLOI	
Type de contrat/ Type of contract	Post-doctoral short term contract of 2 years
Entrée en fonction/ Starting date	July – Sept 2020
Rémunération/ Remuneration	Up to 130 000 € gross salary charged
CONTACT	
Franck Delaplace : franck.delaplace@ibisc.univ-evry.fr	

IBISC 2 –AROBAS, Fariza TAHI team

JOB	
Project title	Computational methods for long non-coding RNA prediction and analysis in context of human skin cellular sensibility to cancer radiotherapy
Typology	Post-doctoral position in bioinformatics and computational biology
Activity area	Computational biology; bioinformatics of RNA; structural bioinformatrics; Genomics; personalized medicine; genomic medicine; AI; machine learning; combinatorial algorithmics, big data, high performance computing
LABORATORY	
Laboratory name	IBISC (Informatique, Bioinformatique et Systèmes Complexes) Collaboration with LGRK (Laboratoire de Génomique et Radiobiologie de la Kératinopoïèse) from CEA
Host institution	University of Evry/Paris-Saclay.
Short desciption of the laboratory	IBISC laboratory is one of the laboratories of university of Evry and Paris-Saclay involved in Computational biology and personalized medicine. Various methods of informatics and data sciences (artificial intelligence including machine learning and deep learning), algorithmics, combinatory optimization, formal methods, etc., are developed for genomics and health. The team involved in this project is AROBAS team (Algorithmique, Recherche Opérationnelle, Bioinformatique et Apprentissage Statistique), where research works are led in the field of RNA Bioinformatics.
SCIENTIFIC PROJECT/ MISSIONS	

Detailed description	Non-coding RNAs (ncRNAs) play important roles in different biological processes and their identification is in the heart of many research works. With the advent of next-generation sequencing (NGS) technologies, their identification at a large scale became an important purpose. Bioinformatics plays therefore a critical role. Nowadays, different classes of ncRNAs are known to be involved in gene regulation, and therefore in many diseases such cancer. There are small ncRNAs, with several well-defined classes (according to the structure and function), the most known (and largely studied) being the class of microRNAs. There are also long ncRNAs (lncRNAs), more recently discovered, with no clearly defined classification. The goal of the project is to develop computational methods to predict and classify lncRNAs according to several characteristics, an important one being the 2D and 3D structure. Determinig the structure of an RNA is indeed an important step in the comprehension of its function. For instance, pseudoknots are important motifs of the secondary structure, and their presence (or absence) can helps in determining the function of the RNA. Many tools exist for predicting secondary structure of RNAs, some of them including pseudoknots. However, because the high computational complexity of the algorithms for RNA structure prediction, there are very few tools able to treat, in reasonable times, very long sequences (of several thousands of nucleotides). Especially, predicting RNA structure including all types of pseudoknots in long sequences still an open task. This is limiting, since in RNAseq data, some ncRNAs can be very long, with several thousands of nucleotides. This is the case of the data the team of Michèle Martin from LGRK laboratory has. The team works on human skill cells and studies the causes of the sensibility of these cells to the treatment of cancer by radiotherapy (Martin et al. 2016, Vulin et al. 2018, Fortunel et al. 2019). One of their current main interests is the involvement of the lncRNAs in this sensibility. There are RNAseq data on several patients that show, thanks to a preliminary analysis, the presence of a high number of lncRNAs (of various sizes: mean size of 1500 bp,) until 30 000) up or down regulated. In this project we will have to analyse these data. Important steps of the analysis will be to classify and to predict the structure of these lncRNAs, in order to determine their functions. For this purpose, we will have to develop new algorithms and tools able to predict the structure including all types of pseudoknots of very long RNAs. Parallel algorithms and big data will be used to improve the speed of the developed algorithms. The developed tools will be made available to the international scientific community through our bioinformatics plateform called EvryRNA (http://EvryRNA.ibisc.univ-evry.fr). EvryRNA is a platform labelled by Genopole and is one of the Paris-Saclay University platforms. Many tools we developed and dedicated to RNA prediction are available on the platform, most of them as web servers. There are tools on RNA structure prediction (BiORSEO (Becquey et al. 2020), Biokop (Legendre et al. 2018), Tfold (Engelen and Tahi 2010)), RNA complexes prediction (C-RCPred, RCPred (Legendre et al. 2019)), RNA prediction and classification (CRSOM (Platon etal. 2019), IRSOM (Platon et al. 2018)), microRNA prediction (miRBoost (Tran et al. 2015), miRNAFold (Tempel and Tahi 2012), (Tav et al. 2016)), piRNA prediction (IpiRId (Boucheham et al. 2017), piRPred (Brayet et al. 2014)), etc. **References:**

	- Becquey L., Angel E., Tahi F., BiORSEO: A bi-objective method to predict RNA secondary structures with pseudoknots using RNA 3D modules. Bioinformatics, 2020 btz962. - Boucheham A, Sommard V, Zehraoui F, Boualem A, Batouche M, Bendahmane A, Israeli D, Tahi F. IpiRId: Integrative approach for piRNA prediction using genomic and epigenomic data. PLoS One. 12(6) :e0179787. PLoS One. Jun 16 ;12(6) :e0179787. 2017. -J Brayet, F. Zehraoui, L. Jeanson-Leh, D. Israeli and F. Tahi. Towards a piRNA prediction using multiple kernel fusion and support vector machine. *Bioinformatics*, 30(17):i364-70, 2014. -S. Engelen, F. Tahi. Tfold: ecient in silico prediction of non-coding RNA secondary structures. *Nucleic Acids Res*. 38(1): 2453-66, 2010. - Fortunel NO, Chadli L, Coutier J, Lemaître G, Auvré F, Domingues S, Bouissou-Cadio E, Vaigot P, Cavallero S, Deleuze JF, Roméo PH, and Martin MT. KLF4 inhibition promotes expansion of adult human epidermal precursors and embryonic stem-cell-derived keratinocytes. Nature Biomed Eng, 2019, Dec;3(12): 985-997. doi:10.1038/s41551-019-0464-6. - Legendre, A., E. Angel, and F. Tahi. RCPred: RNA Complex Prediction as a constrained maximum weight clique problem. BMC Bioinformatics, 2019 Mar 29;20(Suppl 3):128. - Legendre A, Angel E, Tahi F. Bi-objective integer programming for RNA secondary structure prediction with pseudoknots. BMC Bioinformatics. Jan 15;19(1) :13. **2018**. - MT Martin, A Vulin, JH Hendry. Human epidermal stem cells: role in skin reactions and carcinogenesis from radiation. Mutation Research, 2016, 770, 349-368. doi: 10.1016/j.mrrev.2016.08.004. - Ludovic Platon, Farida Zehraoui, Abdelhafid Bendahmane, Fariza Tahi. IRSOM, a reliable identifier of ncRNAs based on supervised self-organizing maps with rejection. Bioinformatics, Volume 34, Issue 17, 1 September **2018**, Pages i620 ?i628. -Ludovic Platon. Algorithms for ab intio and large scale prediction and classification of ncRNAs. PhD Thesis. https://hal.archives-ouvertes.fr/tel-02495582 - C. Tav, S. Tempel, L. Poligny, Tahi F. miRNAFold : a web server for fast miRNA precursor prediction in genomes. Nucleic Acids Res. Jul 8 ;44(W1) :W181-4. **2016**. -S. Tempel, Tahi F. A fast ab-initio method for predicting miRNA precursors in genomes. *Nucleic Acids Res*. 40(11): e80, 2012. - VD Tran, S. Tempel, B. Zerath, F. Zehraoui, Tahi F. miRBoost : Boosting support vector machines for microRNA precursor classification. RNA. A Vol. 21, No. 5, **2015**. - A Vulin, M Sedkaoui, S Moratille, N Sevenet, P Soularue, O Rigaud, L Guibbal, J Dulong, P Jeggo, JF Deleuze, J Lamartine and MT Martin. Severe PATCHED1 deficiency in cancer-prone Gorlin patient cells results in intrinsic radiosensitivity. Int J Radiat Oncol Biol Phys.2018,1;102(2):417-425.doi: 10.1016/j.ijrobp.2018.05.057.
CANDIDATE PROFILE	
Essential skills	Backgroud in informatics and computational biology (bioinformatics). Candidates having some experiences in structural bioinformatics will be preferred.
Languages	English
CONTRACT CONDITIONS	
Type of contract	Limited term contract of 24 months

Starting date	Before June 2020
Remuneration	Up to 130 000 € gross salary charged for 24 months (average 3000 € net / month)
Other	
CONTACT (name of the scientific supervisor)	
Fariza TAHI, Professor fariza.tahi@univ-evry.fr Collaboration: Michèle Martin, CEA, iRCM, Laboratory of Genomics and Radiobiology of Keratiniopoiesis michele.martin@cea.fr Nicolas Fortunel, CEA; iRCM, LGRK; nicolas.fortunel@cea.fr	

CNRGH – Béatrice SEGURENS team

POST-DOCTORAL POSITION	
Intitulé du projet scientifique	Studies of the intestinal microbiome in human pathologies
Typology	
Activity area	human genetics, NGS, metagenomic, microbiology, bioinformatic, bioanalyse
LABORATORY	
Laboratory name	CNRGH (National Research Center for Human Genomics)
Host institution	Institute of Biology Francois Jacob, direction of fondamental research of CEA (Commissariat for Atomic Energy and Alternative Energies) ,located in Evry
Short desciption of the laboratory	The CNRGH is the French national research center that can answer scientific and medical questions requiring high throughput sequencing and genotyping needs through the development and implementation of innovative and integrated technologies. The organization of CNRGH makes it possible to optimize research in genetics and genomics of human diseases, by creating the indispensable links between the constitution of cohorts (DNA samples), the identification of causal genes, the study of the transcriptome, epigenome and microbiomes as well as host microbiota-genome interactions.
PROJET SCIENTIFIQUE/ SCIENTIFIC PROJECT/ MISSIONS	

Detailed description	The CNRGH Functional Genomics Laboratory is made up of five research teams including the team of Metagenomics Research. The mission of this team is to develop a specialized expertise in the characterization of microbial ecosystems associated with pathologies and in the understanding of their mechanism from a functional point of view. Recruiting a bioinformatician will allow the team to benefit from efficient bioinformatic analysis methods, and thus make the most of each of these new approaches. The candidate who will be recruited will have the mission to test and select the best performing bioinformatics tools for the analysis of massive data from high throughput sequencing, produced by CNRGH's Functional Genomics in Metagenomics laboratory. **The candidate** will be in charge of testing bioinformatic tools dedicated to the analysis of bacterial metagenome data of various kinds (16S, Whole Genome Sequencing, metatranscriptomic). Its role will be to implement these tools within bioinformatics pipelines and then manage their maintenance. The recruited person will also play a key role in performing bioinformatic analyzes of the data generated by the laboratory. It will propose innovative analysis strategies and will lead to the development of new bioinformatic analysis tools (improvement of existing tools or new developments).Finally, the recruited person will participate in the bioinformatics training of the students and post-docs of the team, as well as researchers from the laboratory who wish to use the analysis tools put in place to exploit their data.
CANDIDATE PROFILE	
Essential skills	PhD Graduated in biology and especially microbiology , essential bioinformatics Training in biology and recognized experience in genomics and metagenomics applied to the microorganisms. NGS and bioinformatic analysis of high throughput sequencing data. Participate in the development and optimization of the metagenomic methodologies required for the exploitation of biological material.
Languages	French - English
CONTRACT CONDITIONS	
Type of contract	Short temr contract of 2 years
Starting date	Sept 2020
Gross salary	Up to 3600 € / month according to experience
CONTACT	
Béatrice Segurens, PhD, HDR CEA- CNRGH 2, rue Gaston Crémieux 91057 Evry Cedex, France Tel: +33160878471 E-mail: segurens@cng.fr	

CNRGH 2 – Vincent MEYER Team

POST-DOCTORAL POSITION	
Project title	Methodological Development for long-fragments sequencing technologies.
Typology	Post-Doctoral position
Activity area	Human genetics, NGS, bioinformatics
LABORATORY	
Laboratory name	CNRGH (National Research Center for Human Genomics)
Host institution	Institute of Biology Francois Jacob, direction of fondamental research of the CEA (Commissariat for Atomic Energy and Alternative Energies) ,located in Evry
Short desciption of the laboratory	The CNRGH is the French national research center that can answer scientific and medical questions requiring high throughput sequencing and genotyping needs through the development and implementation of innovative and integrated technologies. The organization of CNRGH makes it possible to optimize research in genetics and genomics of human diseases, by creating the indispensable links between the constitution of cohorts (DNA samples), the identification of causal genes, the study of the transcriptome, epigenome and microbiomes as well as host microbiota-genome interactions.
SCIENTIFIC PROJECT/ MISSIONS	
Detailed description	The « long-reads » sequencing technologies are currently rising as a major technological transition bringing new insights on the structural organizations of the Genome and its products. In this context, algorithms for RNA/DNA "de novo" assembly and structural variation detection will be evaluated with HPC and GPU environments. This work will evaluate and set strategies to establish bioinformatics methods for : - Structural variants detection - RNA transcript analysis - Diploid "de novo" assemblies using orthogonal technologies. In addition, this project will be completed by data integration to support the interpretation of structural variation impact, notably in intergenic regions. The CNRGH has access to the latest long-fragment sequencing technologies (10X, Bionano, Nanopore/Prométhion, PacBio) and data from and for methodological developments. This project will be set in the HPC environments of the TGCC/CCRT to ensure the computing ressources and bioinformatics software environment.
CANDIDATE PROFILE	

Essential skills	PhD Graduated in bioinformatics Recognized experience in genomics. NGS and bioinformatic analysis of high throughput sequencing data.
Languages Required level	French - English
CONDITIONS D'EMPLOI	
Type de contrat/ Type of contract	Short term contract of 2 years
Entrée en fonction/ Starting date	Sept 2020
Salary	Uo to 3600 € gross salary according to experience
CONTACT	
Vincent MEYER, PhD CEA- CNRGH 2, rue Gaston Crémieux 91057 Evry Cedex, France Tel: +33160872592 E-mail: vmeyer@cng.fr	

LBEPS, Claire THOMAS-JUNIUS

Post-doctoral position	
Project title	Epigenetic and muscle adaptations to exercise
Typology	Post-doctoral position
Activity area	Cellular and molecular biology
LABORATORY	
Laboratory name	Laboratory of Exercie Biology for Performance and Health (LBEPS)
Host institution	Mixed Research Unit : University of Evry and Institute of Biomedical Research of Armed Forces
Short description of the laboratory	The LBEPS is a new joint research unit specializing in exercise physiology. The research work carried out within this joint research unit deals with responses and adaptations to exercise as well as different recovery strategies. Several integrated physiology approaches from humans in motion to cellular and molecular approaches will make it possible to combine a better understanding of individual response mechanisms while maintaining a concern for transfer to field counselling. This work will be carried out in healthy humans in ordinary conditions or in extreme conditions of fatigue or environment (hot, cold, hypoxia), or when they are affected by metabolic disorders such as diabetes.
SCIENTIFIC PROJECT/ MISSIONS	

Detailed description	As part of the opening of the new Research Unit of the Evry Val d'Essonne University - Institute of Biomedical Research of Armed Forces (France) on 1 January 2020, the Laboratory of Exercie Biology for Performance and Health is applying for the recruitment of a Post-doc researcher specialised in epigenetics and having a good knowledge of muscle energy metabolism.The scientific project of this lab is focused on two main areas to identify factors that modulate the metabolic response to training (age and muscle maturation, diabetes, climatic environment) and factors that increase vulnerability to fatigue (sleep deprivation and climatic constraints) The recruited researcher will benefit from all the laboratory's existing and future research themes and protocols in order to bring an epigenetic approach to explore the role played by these modulations in the greater or lesser effectiveness of a training program or tolerance to climatic constraints and sleep deprivation. It is well established that the metabolic benefits of exercise are achieved through transcriptional changes at the tissue level, primarily skeletal muscle, liver or adipose tissue. In addition, the transcriptional response to a stressor is largely influenced by the epigenetic status of the organism or tissue. Until now, most of the studies in this area has been in the field of oncology and the response of tumour cells to different chemotherapies. In addition, the ability of the muscle to secrete a number of circulating factors (myokins) that exert an effect at a distance is now clearly recognized. More recently, the excretion during exercise of extracellular vesicles containing microRNAs in particular has been described and constitutes another hypothesis of the modality of action of muscle contraction on the modulation of transcriptional regulation at a distance. Therefore, it seems reasonable to believe that metabolic constraints such as the hyperglycemic environment of diabetes, or those generated by exercise (cellular energy deficiency, acidosis, etc.) or a nutritional recovery strategy may interfere with methylation or acetylation processes involved in epigenetic modulation. In the case of type 2 diabetes, hypermethylation of PGC-1α has been described in the muscle, for example, which may limit the transcriptional cascade induced by PGC-1α in response to training, particularly on mitochondrial adaptations or glucose transporters. More recently, the inactivation of deacetylase histones in relation to exercise-induced AMPK activity has been shown to be a determinant of GLUT-4 expression modulation mediating the beneficial effects of exercise on carbohydrate metabolism. Some of these beneficial effects could be transmitted to offspring when exercise is performed by pregnant females, limiting the incidence of type 2 diabetes in newborns. As a corollary, fasting exercise or periodization strategies of carbohydrate intakes, capable of enhancing AMPK activation, could create an epigenetic status favourable to training response in low-responder individuals. A number of studies have studied the modulation of the SIRT-1 activity with the exercise without any concrete applications being deduced from it. Similarly, beta-hydroxybutyrate, one of the ketone bodies mainly produced in situations of fasting and prolonged exercise, could be an epigenetic regulator of interest, particularly through a histone deacetylase function still under discussion depending on the cell type considered. Similarly, metabolic and inflammatory alterations induced by environments such as hypoxia or heat are possible epigenetic modulators that can modify tissue and systemic responses to training. For example, the combination of an inflammatory condition with tissue hypoxia may have been identified as a factor limiting muscle mass gain in response to strength training in patients with chronic obstructive pulmonary disease. However, sleep deprivation currently appears to be a factor capable of generating low-grade inflammation. Furthermore, exercise also

	influences the inflammatory response, in particular by regulating caspase activity associated with apoptosis, neutrophil function or the miRNA profile of circulating monocytes. It is therefore conceivable that situations such as sleep deprivation/extension or exposure to extreme climatic environments, known as modulators of inflammation and metabolism, may affect the response to training by braking or lifting an epigenetic brake. Nevertheless, to date, knowledge of these epigenetic modulations induced by acute or repeated exercise remains largely to be clarified, particularly in view of the variability that exists depending on the tissues (circulating blood, muscle, adipose tissue, etc.), but also according to the type of exercise practiced (endurance, strength, high intensity), the metabolic state fasting, post prandial, hyperglycemia) and the degree of maturation (child, adolescent, adult). Furthermore, our knowledge of the acute effects of sleep deprivation and the implementation of adaptive responses to constraining climatic environments (hot, cold, hypoxia) leads us to believe that these factors are conditions that can modulate the epigenetic status of individuals. Thus we formulate the hypothesis that the well-chosen combination of these different constraints could modify the transcriptional responses to training and the level of response of athletes or diabetic patients with the long-term prospect of improving it or even removing certain obstacles in individuals with poor responsiveness. We are convinced that this knowledge will make it possible to better understand the epigenetic modulators involved in the training response and to adapt its nature and conditions of implementation according to populations in order to optimize its effectiveness. Our future laboratory will offer an innovative field of application to a researcher competent in epigenetics allowing a true individualization of the prescription of physical activity in diabetic patients and the optimization of training for the performance of athletes.
CANDIDATE PROFILE	
Essential skills	The applicant will have a strong background in exercise physiology and biology. Experiences in experimental cellular and molecular biology and biological system analysis will be favorable.
Languages Required level	English level B2
Divers/ Other	Open-minded
CONTRACT CONDITIONS	
Type of contract	Short temr contract of 2 years
Starting date	
Remuneration	Up to 3600 € gross salary per month, according to experience
CONTACT (name of the scientific supervisor)	
Claire Thomas-Junius claire.thomas@univ-evry.fr Alexandra Malgoyre a.malgoyre@yahoo.fr	

Project descriptions – Private sector (Start'up and SMEs)

TRAASER, Ralph Eckenberg

Post-doctoral position	
Project title	Genomic and medical data integration for diagnostic help
Typology	Data scientist
Activity area	Healthcare digital solutions
LABORATORY	
Laboratory name	Traaser digital integration department
Institution d'accueil/ Host institution	Traaser SAS
Short description of the laboratory	Traaser is a start-up specialized in the development of healthcare digital solutions with a strong background in genomics. Our mission is to enable the practitionners to access to genomics and the patients to benefit from personalized medicine.
SCIENTIFIC PROJECT/ MISSIONS	
Detailed description	The project involves the following aspects: - The definition of data models to represent a knowledge domain related to genetic diseases, phenotypes, variants of medical interest, etc. - The integration of biomedical data sources to feed the data models. - The definition of data treatments that exploit the integrated data to infer new knowledge. Particular emphasis will be given to documentation, testing and validation of the works following the application of norm ISO 62304.
CANDIDATE PROFILE	
Compétences requises/ Essential skills	Manipulation of data, of machine learning approaches, biostatistics. Writing skills. Autonomy, rigor.
Langues /Languages Niveau requis/ Required level	English: Fluent French: Fair
Divers/ Other	Mastering a programmation language would be a plus.
CONTRACT CONDITIONS	
Type de contrat/ Type of contract	CDD
Entrée en fonction/ Starting date	End Q1 2020
Rémunération/ Remuneration	65 000 € / year (gross salary charged)
CONTACT	
Ralph Eckenberg, CSO Traaser ralph.eckenberg@traaser.com	

STRUCTURYS

LE POSTE/ JOB	
Intitulé du projet scientifique / Project title	Research and optimization of a new antibiofilm surface treatment
Typologie du poste / Typology	Research engineer / Post doc
Secteur d'activité/ Activity area	Material sciences, Materials chemistry, Nanotechnology, Biotechnology
LE LABORATOIRE/ LABORATORY	
Nom du laboratoire d'accueil/ Laboratory name	Structurys biotech
Institution d'accueil/ Host institution	Structurys biotech - Genopole
Présentation du laboratoire/ Short desciption of the laboratory	Structurys is a young start up developping an innovative technology to treat industrial surfaces to confer anti-biofilm properties. Incubated within the Genopole, 1st French biocluster, we have access to a wide range of mutalized equipment.
PROJET SCIENTIFIQUE/ SCIENTIFIC PROJECT/ MISSIONS	
Description détaillée du projet / Detailed description	Multiple materials are being investigated (stainless and black steel, polymers) The technology relies on 2 major aspects : - Micro and nanoscale structuration of the surface - Chemical functionnalization (by deposition or grafting) We are looking for a post doctoral candidate to explore, developp and optimize our technology and more specifically : 1) Find and develop new micro and nanoscale geometries to prevent micro-organisms to attach to the surface of interest 2) Find and developp new candidates for functionnalization and assess their attachement to the surfaces, their ability to repell micro-organisms along with their interaction with the surrounding environment specific to its application 3) Find an optimal combination of the two previous parts compatible with the industry

PROFIL DU CANDIDAT RECHERCHÉ/ CANDIDATE PROFILE	
Compétences requises/ Essential skills	- Handling tools and techniques to develop : a) a specific polymeric architecture b) functionnalized surfaces with chemical substances - Choose polymer and methods to answer a complex set of specifications ; - Design, perform and optimize caracterization studies of the materials ; - Design and optimize materials to meet a given function ; - Ability to explore transversal fields of research (biology, biomimetism) Operationnal - Redact repports or technical documentation - Elaborate a scientific method - Teamworking - Inform about advances and delay of the missions - Suggest plans to cope with changes in the timing
Langues /Languages Niveau requis/ Required level	Fluent in French and/or Fluent in English
Divers/ Other	
CONDITIONS D'EMPLOI	
Type de contrat/ Type of contract	CDD-OD
Entrée en fonction/ Starting date	September 2020
Rémunération/ Remuneration	46 - 51 k€
Divers/ Other	
CONTACT	

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