

Master 2 internship

Development of bioinformatic tools for an innovative RNA-seq based approach dedicated to rRNA epigenetic: the RiboMETH-seq

Internship supervisor and Host laboratory

« Nuclear domains and pathologies » team



Team leader: Jean-Jacques Diaz

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<http://www.crcl.fr/107-Domaines-nucleaires-et-pathologies.crcl.aspx?language=fr-FR>

Bioinformatic Plateform – Gilles Thomas



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<http://www.synergielyoncancer.fr/nos-realisations/la-plateforme-de-bioinformatique>

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Project description

Ribosomal RNA (rRNA) is the first identified non-coding RNA (ncRNA) and one of the most abundant. rRNA belongs to a ncRNA class that exhibit enzymatic catalytic activity making the ribosome a ribozyme specifically dedicated to protein synthesis. While it has been considered for 40 years as a neutral actor of gene expression, it recently emerged that rRNA activity is finely regulated by chemical modifications. We and others reported that alteration of rRNA chemical modifications plays unexpected roles in regulating gene expression at translational level and during tumorigenesis. In particular, our team reported for the first time that alteration of rRNA 2'-O-ribose methylation (2'-O-Me) impairs translation of mRNAs encoding oncogenes and tumor suppressor (Marcel et al. Cancer Cell 2013, Eroles et al, PNAS 2017). Development of OMIC technologies dedicated to analyse rRNA 2'-O-Me using a RNA-seq based approach has recently emerged. Among them, the RiboMETH-seq approach allows to analyse 2'-O-Me at the 106 rRNA methylation sites in a single run (Birkedal et al, Angew Chem Int Ed Engl 2015; Marchand et al, NAR 2016). In collaboration with Prof. Y. Motorin, we have contributed in transferring the RiboMETH-seq technology from yeast to human (Eroles et al, PNAS 2017).

Bioinformatic tools

We have already developed a bioinformatics analysis pipeline (based on a R-package) that, given as input a RiboMETHSeq data set, provides quality controls, methylation scores and results of statistical analysis. At the moment, we mainly focused on human data, but we also have RiboMETHseq data from mice. The project is at the interface of bioinformatics and biology. The aim of the internship is

- (1) to analyse data from human and mouse samples using the existing pipeline
- (2) to pool the results in a statistically valid fashion by performing meta-analyses
- (3) to improve the pipeline by adding new functionalities and new visualization methods
- (4) to include new functions specific to the analysis of mouse data.

According to the advancement of the project, the student will develop an interactive interface of data analysis that can easily be used by non-bioinformaticians.

Candidate profile

We are looking for a motivated Master 2 student with a strong interest in bioinformatics data analysis. The candidate should ideally have a substantial background in bioinformatics/biostatistics, computer science or other relevant disciplines, as well as experience with at least one programming language (ideally R) and with bash scripting. Knowledge in high throughput sequencing analysis and/or biology would be a plus. Teamwork skills as well as the ability to work independently are essential.

Grant

The current grant will be applied for the duration of this internship (January to June 2019).

How to apply

Interested applicants should send their CV and a brief motivation letter explaining how the project fits their skills and interests to virginie.marcel@lyon.unicancer.fr

Selected publications

Erales J, Marchand V, Panthu B, Gillot S, Belin S, Ghayad SE, Garcia M, Laforêts F, Marcel V, Baudin-Baillieu A, Bertin P, Coute Y, Adrait A, Meyer M, Therizols G, Yusupov M, Namy O, Ohlmann T, Motorin I, Catez F and Diaz JJ. Evidence for rRNA 2'-O-methylation plasticity: control of intrinsic translational capabilities of human ribosomes. **PNAS** (2017) vol 114(49):12934-12939.

Marcel V*, Ghayad SE*, Belin S*, Therizols G, Morel AP, Solano-González E, Vendrell JA, Hacot S, Mertani HC, Albaret MA, Bourdon JC, Jordan L, Thompson A, Tafer Y, Cong R, Bouvet P, Saurin JC, Catez F, Prats AC, Puisieux A and Diaz JJ. p53 acts as a safeguard of translational control by regulating Fibrillar and rRNA methylation in cancer. **Cancer Cell** (2013) vol 24(3), 318–330.