**Laboratoire TIMC - IMAG**  
UMR 5525  
Université Joseph Fourier – CNRS

*Techniques de l’Ingénierie Médicale et de la Complexité - Informatique, Mathématiques et Applications, Grenoble*

---

**RESEARCH PROJECT FOR MASTER STUDENTS**  
Year 2015 – 2016

**Field of the Master:** Bioinformatics, Applied Mathematics, Computer Science, Computational biology  
**Level:** M2  
**Required skills:** computer programming, statistics  
**Duration:** 3 to 6 months  
**Period:** any periods between January and June 2016

<table>
<thead>
<tr>
<th><strong>Title of the research project:</strong></th>
<th>Discovery of epigenetically regulated genomic domains in lung cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Name of the supervisor:</strong></td>
<td>Daniel Jost (<a href="mailto:daniel.jost@imag.fr">daniel.jost@imag.fr</a>)</td>
</tr>
</tbody>
</table>

**Context:** All the cells of a multicellular organism contain the same genetic information but differ by their shapes, their physiologies and their functions. These differences result from specific patterns of gene expression, which largely rely on biochemical tags, the so-called epigenetic marks, that are deposited on top of the genetic information. Failure of preserving the proper epigenetic mark profiles might result in inappropriate gene activity and diseases like cancer. As it becomes more and more clear that epigenetics is central in cancer, a major challenge of cancer computational biology is to analyze how epigenetic deregulation effectively affects gene expression and predicts prognosis. In this project, we propose to address this point by statistically investigate the relation between epigenomic alterations and gene transcription specifically in lung cancer which represent the most common form of cancer in the world today.

**Objectives:** In this internship, the student will have to discover regions that are likely to be under epigenetic control and to characterize statistically their epigenetic signature. The first task will be to identify genes or genomic regions that are significantly over- or under-expressed in the studied cancerous cell lines in comparison to normal cells. The second task will consist in analyzing if the genes or regions identified in the first task exhibit significant changes in their epigenetic landscape. The last task will consist in selecting the regions where changes in transcription are coupled to changes in epigenome. These 3 tasks will involve the manipulation of large datasets, the development of efficient statistical methods to analyze them and the use of advanced statistical modeling. This project will be done in close collaboration with the biologists and doctors (S. Khochbin and E. Brambilla, IAB, Grenoble).

**Expected results:** We expect this work to improve our understanding of the relationship and interdependences between epigenetic marks and gene expression in cancer. The associated molecular investigations have the potential of revealing new drug targets and biomarkers predicting prognosis.