**UPDATED PROJECT IN MOLECULAR LIFE SCIENCES: PROJECT PLAN**

During this project, our aim is to acquire an extensive background on current state-of-the-art computational tools and pipelines for the analysis and interpretation of ChIP-seq data. Also, we would like to be able to understand nucleosome dynamics based on ChIP-seq. We are going to reproduce time-ChIP analysis to assess histone H3.3 turnover genome-wide during differentiation of mouse ESCs (Aimee, 2016).

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| **WEEK** | **TASK** |
| 3rd-7th Sept  10th-14th Sept | * Literature * Practice ChIP-seq data analysis based on “Biostar” and one yeast genome project |
| 17th-21st Sept  24th-28th Sept  1st-5th Oct | * Familiarize with dataset and softwares. * Quality control with the yeast genome example. * Mapping with the yeast genome example |
| 8th-12th Oct | * Quality control with the human genome. * Mapping with the human genome |
| 15th-26th Oct | \* Exam preparation |
| 28th-31th Oct | * Normalization with the yeast genome |
| 1st-3rd Nov | * Normalization with the human genome |
| 29th-2nd Nov  5th-9th Nov | * Peak-calling with both genomes   + Punctate-source transcription factors   + Broad enriched regions from histone marks   + Mixed signals |
| 12th-16th Nov | * Visualization with both genomes |
| 19th-23rd Nov | * Enrichment analysis with LOLA |
| 26th-30th Nov | * Chromatin-state discovery and genome annotation with ChromHMM |
| 3rd-7th Dec | * Final presentation and report |