**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 |