**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 | 1. Literature  * Journal Club: “High-resolution visualization of H3 variants during replication reveals their controlled recycling” * Read “Enhancer regions show high histone H3.3 turnover that changes during differentiation”  1. Practice ChIP-seq data analysis based on “Biostar” and “Genome-wide mapping of binding sites reveals multiple biological functions of the transcription factor Cst6p in Saccharomyces cerevisiae.” |
| 17th-21st Sept  24th-28th Sept  1st-5th Oct | Familiarize with dataset and softwares. Perform quality control and mapping steps with the yeast genome example. |
| 8th-12th Oct | Quality control and mapping with the human genome. |
| 15th-19th Oct | Normalization (yeast genome) |
| 22nd-26th Oct | Normalization (human genome) |
| 29th-2nd Nov  5th-9th Nov | Peak-calling (both genomes)   * Punctate-source transcription factors * Broad enriched regions from histone marks * Mixed signals |
| 12th-16th Nov | Visualization (both genomes) |
| 19th-23rd Nov | Apply LOLA software |
| 26th-30th Nov | Apply ChromHMM software |
| 3rd-7th Dec | Prepare for presentation and write the report |