Adapt this title to indicate what you did

LCG BEII personal work – 2022

Firstname LASTNAME

2022-02-11

## Instructions

* *The report can be written in English, Spannish or French*
* *This template is provided in Rmd and .docx formats.*
* *Whichever environment you use to generate the report (Rstudio, Word, LibreOffice),* ***your final report should be submitted in .docx format****. This enables me to comment it in the margin.*
* *Rename this file to indicate your LASTNAME and Firstname*
* *Adapt the title to your specific study*
* *Indicate your name and mail in the header above*
* *Update the date*
* *Before submitting the report, suppress all the instructions in italics below, including this whole section*

## Introduction

* *size: ~1/2 page*
* *context*
* *general motivation of the analysis*
* *particular questions/approaches addressed in this document*

## Methods

* ~ *1/2 page + all details in supplementary material*
* *indicate the main resources and tools used in your analysis, and what they were used to do*
* *explanation of the main methodological choices*

## Results and discussion

* *~ 2 pages, figures and tables non-included*

## Conclusions and perspectives

* *~ 1/2 page, with summary of the results, some consideration about their relevance, and a perspective (what coul be done next ?)*

## Supplementary material

*An essential issue of scientific activity is tractability (how were the results produced?) and reroducibility (can someone else reproduce the experiment, and get the same results?): the supmat must contain the precise list of all the commands / parameters used to achieve the results.*

### Bioinformatics resources used for this work

*The Table below indicates the bioinformatics resources (tools, databases) used for this analysis.*

| Acronym | Description | URL |
| --- | --- | --- |
| RSAT | Regulatory Sequence Analysis Tools | <http://rsat.eu/> |
| … | …. | … Please complete the table … |

### Data sources

*A complete list of the data sources: provide the original IDs of the datasets (e.g. ReMap URL of your Factor, name of the Factor, cell typoe, ID of your peaks, Jaspar ID, Hocomoco ID, …).*

### Complete list of commands and parameters

*Please indicate here the complete list of tools, commands and parameters used to produce the results. In principle this should enable anyone to reproduce your analysis.*