Adapt this title to indicate what you did

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## 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

* list of the resources and tools
* explanation of the main methodological choices

## Results

~ 2 pages, figures and tables non-included

## Conclusions/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

### Data sources

A complete list of the data sources: provide the original IDs of the datasets (e.g. Gene Expression Omnibus GSE or GSM IDs, ArrayExpress IDs).

### 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 ... |

### Complete list of commands and parameters