

## 1. Coding assignment

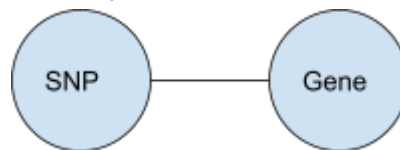
Please prepare a script in R or Python, create or add it to a Github repository and submit the link to the code.

Input: Text file with a list of genetic variants (rs-numbers) (**see other attachment**)

Output: Network in Cytoscape linking variant to gene to pathway

### Steps:

1. Use BioMart to retrieve the associated gene for each of the variants in the file
  - [R](#) and [python](#) have APIs for BioMart
2. Create a network in Cytoscape linking the SNPs to the genes  
(<https://github.com/cytoscape/cytoscape-automation/wiki>)



3. Use the CyTargetLinker app for Cytoscape to add known pathways from WikiPathways in which the genes are involved in (<https://cytargetlinker.github.io/>).
  - WikiPathways linksets available from here:  
<https://cytargetlinker.github.io/pages/linksets/wikipathways>
  - Relevant automation tutorial (in R) can be found here:  
<https://cytargetlinker.github.io/pages/tutorials> (automation tutorial 2)
4. Save an image of the final network and the session.

## 2. Presentation

Please prepare a short presentation (max. 10 minutes) in which you present the code and the results. If you don't manage to finish the complete script, present the steps that you managed and discuss the problems you had.