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Here you can find all the code required to produce the results reported in the main text and supplementary material of the article "On the effects of the modularity of gene regulatory networks on phenotypic variability and its association with robustness", authored by us. All scripts are written in C++ and R. The programs require the GSL numeric library for C++ (`https://www.gnu.org/software/gsl/`). Therefore, compilation using `g++` requires including the flags `-lgsl -lgslcblas`.

Our codes saves the data that we generate in a specific directory structure that we provide here.

1 libs/

This directory contains libraries with functions that our scripts require. Compilation of most of our code requires linking with some of the libraries in this directory.

2 premuestra/

This directory contains the programs required to build large samples of networks. The `muestrario/` directory is used to store the networks; the `hist/` directory is used to store data related to the sample; and the `pars/` directory is required to save the parameters used to build the sample. The `premuestra_*.cc` files provide the code required to build the networks. Hereafter, if the term "set1" is in the name of a file, the networks on that file sustain the target GAPs. On the contrary, if the term "2m" is in the name of a file, the networks on that file sustain the alternative target GAPs. The `*.R` files are required to plot graphs of properties of the sample.

3 robustez_miope/

This directory contains the programs required to study the association between the modularity and the robustness of a network. Moreover, the programs in this directory allow us to study the GAPs produced by the single-mutants of a network. The name of the subdirectories within this directory refers to the experiments performed within each subdirectory. The `access_phen/` subdirectory contains the programs required to study the GAPs of the single-mutants of a network. The `miope/` subdirectory provides the programs required to perform the directed evolution of a network to increase their robustness or modularity. The `robustez/` subdirectory provides the programs required to study the correlation between the modularity

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and robustness of a network. Within each directory the `muestra_*.cc` files contain the code required to move already sampled networks (in the `premuestra` directory) into the appropriate location.

Within the `access_phen/` subdirectory, the `1mut_access_phen*.cc` files are required to build the GAPs of the single-mutants of a network and analyze their characteristics. These files use the `access_phen/` directory to export their results. Within the `miope/` subdirectory, the `miope_mod_all_*.cc` files provides the code that is used to evolve a network under selection for greater modularity. On the other hand, the `miope_rob_all_*.cc` files provides the code required to evolve a network under selection for greater robustness. The files export their resulting data into the `miope_mod/` directory or into the `miope_rob/` subdirectory depending on the criteria used to select the networks during their evolution: modularity or robustness respectively. Within the `robustez/` subdirectory, the `rob_dist_1mut_multic_*.cc` files contain the code required to assess the correlation between the modularity of a network and its modularity. The files export their results into the `rob/` directory. Within each subdirectory the `*.R` files contain the code required to graph the results produced by each experiment.

4   modab

This directory contains tools that allow us to analyze the effect of modularity in the phenotypic variability of networks under the effect of the accumulation of multiple mutations. The `muestra_2inter_70_*.cc` files contain code required to build networks sets with high and with low modularity using the sample in the `premuestra` directory. These files export the selected set of networks to the `modab/premuestra/` subdirectory. The file `mult_carp_*.cc` contains the code to prepare the aforementioned set of networks for the following analyses. The `distbtnw_multrep_transph_*.cc` files provide the code required to analyze the effect of modularity in the phenotypic variability of a network under the accumulation of multiple mutations. The `*.R` files are used to graph the results produced by the latter programs.