

Multimic data analysis

TASK 1: File `nci60.Rdata` contains miRNA, mRNA and protein data of melanoma, leukemia and CNS disease. Data are encapsulated in a list where each components stands for a given omic data (NOTE: features are in rows and samples in columns). Data corresponds to cells lines from the NCI-60 panel available at TCGA project. 21 cell lines are providing information about 537 miRNAs, 12,895 gene expression and 7,016 proteins. We are interested in obtaining omic profiles to characterize those diseases. NOTE: The vector `cancer` is a factor variable indicating the type of cancer of each sample.

- Load data into R.
- Perform a separate PCA of each omic data and give the top-10 features more associated with each tumor.
- Perform multi coinertia analysis and provide the top-10 features (they can be proteins, miRNA or genes) associated with each tumor.
- Perform penalized canonical correlation analysis and provide the significant features associated with each tumor
- Compare both results

TASK 2 (optional): The file `MR_data.txt` contains data for 200 SNPs. For each SNP the columns provides the effect size estimate (beta), its standard error (se) and corresponding P-value (pval) for three different quantitative traits (A,B,C) and for one disease (D). Let us imagine that the three traits could be lipids, cholesterol and blood preassure and the disease could be heart disease. All 4 effect sizes are given with respect to the same allele of the SNP.

Read the vignette of the package `MendelianRandomization` availabe at https://cran.r-project.org/web/packages/MendelianRandomization/vignettes/Vignette_MR.pdf and:

- Plot the effect sizes of each trait against the corresponding effect sizes of D. Can you infer something about possible causal relationship between traits and D? Consider also how correlated the effects on the traits are.
- Do standard Mendelian randomization analysis between each trait and D by looking at the SNPs that only affect one trait but not the other two. What can you infer about possible causal relationships from this?