The pre-requisite is GSL (https://www.gnu.org/software/gsl/). Please report any bugs to Peng Jiang (peng.jiang.software@gmail.com). For further detail and citation, please refer to our paper:
"**Inference of genes associated with targeted cancer therapy resistance**".

interaction_regression:
This program test interaction effects between all input features and target features. For example, in pharmacological screen data, the response is drug inhibition values across cancer cell lines. The input features are composed of gene expression and somatic mutation profiles of all human genes across screened cancer cell lines. For each targeted therapy drug, the target feature is its annotated drug target gene. Our program will test the interaction significance between all other gene features and drug target gene feature through multivariate linear regression.

Usage: interaction_regression -x Feature -y Response -o Output
Example: get into folder "data" first, then type:
interaction_regression -x CCLE.features.sample -y CCLE.drug.sample -t drug.target.sample -b CCLE.adherent -o CCLE.sample.output

Feature:
Input feature matrix. The column names represent features names, and row names represent data point names (cell line names). As an example, please see "data/CCLE.features.sample".

Response:
Input response matrix. Each column represents one response vector. Missing values are allowed as "NA". Each row represents a data point (cell line). As an example, please see "data/CCLE.drug.sample".
Note: The row names between "Feature" and "Response" do not have to be same. Our program will automatically align common row names together.

Output:

For each response vector, three types of information will be included in output, including “t-value”, “p-value” and “fdr”. The t-value is defined as coefficient/stderr . The p-value is calculated from t-value using the student t-test. Benjamini-Hochberg procedure is used to convert p-values to FDR (false discovery rate).

Optional parameters:

Flag	**Parameter**	**Default**	**Comment**
-t	Target annotation	Empty: the name of response is the same as feature.	Target gene annotation for each drug. As an example: “data/drug.target.sample”.
-b	background matrix	Empty.	Background covariates to be corrected in regression. For example, the growth status of cell lines (adherent or suspension) strongly correlates with inhibition efficiency. You can remove its impact by adding background matrix (“data/CCLE.adherent”).
-v	Verbose 1: yes, 0: no	0	Output detail progress.
For the options below, default values are highly suggested.			
-p	Partial regression 1: yes, 0: no	0	Whether exclude the interaction term to fit partial model: Y = a X + b P + d
-r1 -r2	Combination ratios between interaction and base covariates.	1	Overall t-value will be calculated as: (r1 * b + r2 * c)/stderr(r1 * b + r2 * c) Model: Y = a X + b P + c XP + d