The **D**rug-**I**nduced **G**enomic **R**esidual **E**ffect (**DIGRE**) algorithm is developed to predict the compound pair synergistic effect. It ranked first in the NCI DREAM challenge competition of predicting 91 compound pairs from the most synergistic to the most antagonist. *(Nat biotech paper link)*

The DIGRE take three input to do the prediction.

1. **Drug treated gene expression data.**

Gene expression profiles of single compound-treated and negative control-treated cell line sample. Data needs to be log2 transformed.

1. **Dose-response curve data.**

Dose-response curves for viability of cell line you used for gene expression assay. For each compound, two dose-response curve is desired. *(Detail instruction need to be added further)*

1. **Pathway information**

Pathway information is used to estimate drug similarity of effect on upstream and downstream genes.

Currently, the DIGRE algorithm use two pathway information, the KEGG pathway information and self-constructed gene network information. User can specify to use either of them. *(Currently, the gene network only has lymphoma dataset, so it’s better to use KEGG pathway information if your data is generated on other cancer cell lines.)*

By taking the above three input, the DIGRE algorithm will calculate pair synergistic score of all the possible combination of the compound you provided, and their rank from the most synergistic to the most antagonist. Larger score indicates high possibility of the pair to have synergistic effect, and vice versa. *(Notice that this algorithm focus more on predicting the relative rank of your compound pairs not the exact synergistic strength. If you want to do that, maybe you should involve positive control in your experiment. And also the score calculated by two pathway information is not comparable.)*