

## Data

For RNA-seq studies, MetaOmics allows input of both raw count data and continuous data (e.g. FPKM/RPKM/TPM). For MetaDE and MetaPath modules, the count data is recommended for better statistical power and accuracy. For the other modules, the meta-analysis methods will require continuous data input.

Download GEO dataset (optional)

(1) Choosing/Upload Expression Data

(2) Upload Clinical Data

## Preprocessing

(3) Annotate / Impute / Replicate

## Saving Study

Type of Data

microarray

Study Name:

some study

save single study

## some study Summary

[1] "No file uploaded"

## Expression Data Preview

## Clinical Data Preview