A tutorial for metaOmic

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1 Introduction

MetaOmics is a GUI for meta-analysis implemented using R shiny. Current version includes MetaQC for quality control, MetaDE for differential expression analysis, MetaPath for pathway enrichment analysis, MetaClust for sparse clustering analysis, MetaPCA for principal component analysis, MetaKTSP for classification analysis, MetaDCN for differential co-expression network analysis, MetaLA for liquid association analysis.

In this tutorial, we will go through installation and usage step by step using a real example.

The metaOmics suit software is publicly available at `https://github.com/metaOmic/metaOmics`. Individual R packages are also available on GitHub and the url will be introduced in each individual package section.

2 Preliminaries

2.1 Citing MetaOmics

MetaOmics implements many meta-analytic methodology by their authors. Please cite appropriate papers when you use result from MeteOmics suit, by which the authors will receive professional credit for their work.

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