Modular analysis of gene expression data with GNU R or Matlab

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ABSTRACT
Summary:
Availability:
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1 INTRODUCTION

What is biclustering. What is the ISA.

2 METHODS

Normalization.
Random and smart seeding.
The ISA iteration.
Merging the modules.
The robustness measure and filtering the modules.
Module trees.

3 R IMPLEMENTATION

Two packages: isa2 does the computation, eisa does everything related to biology.

3.1 Work flow

Two workflows, the simple workflow does everything with default parameters. In the detailed workflow the user has access to every step of the analysis.

3.1.1 The simple work flow

3.1.2 The detailed work flow

3.2 Visualization

Expression plots, GO tree plots, module tree plots, HTML summary generation. ExpressionView.

3.3 Connection to other software

The biclust package.

4 MATLAB IMPLEMENTATION

ACKNOWLEDGEMENT

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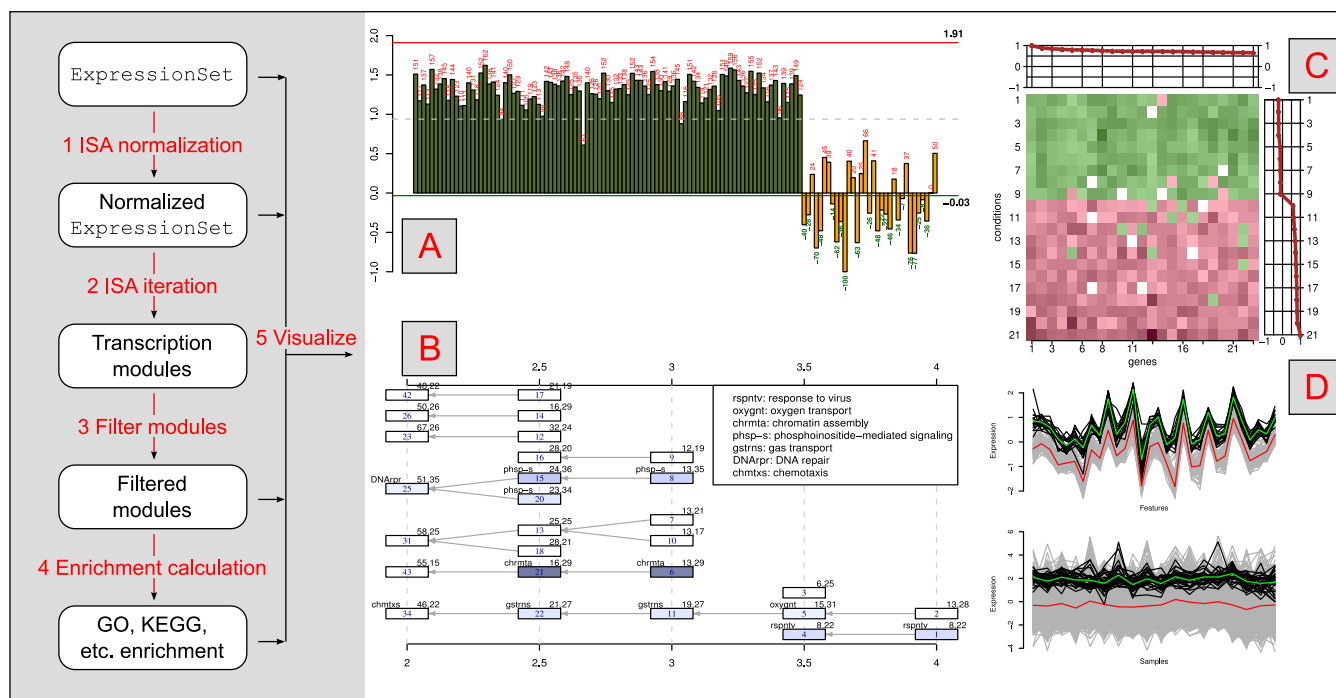
Fig. 1.