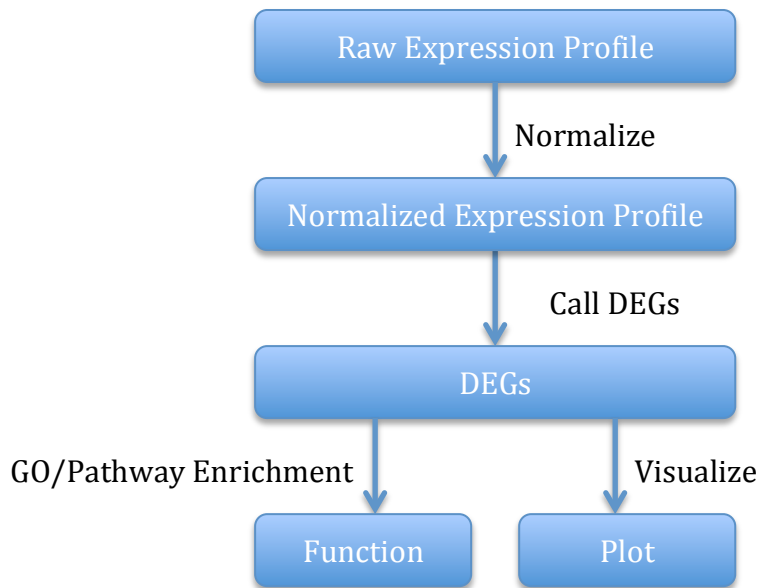


iSeq workflow



① **upload example data**

② **Normalize the data**

③ **Detect differentially expressed genes (DEGs)**

④ **Gene ontology and pathway enrichment analysis**

⑤ **bar-plot heatmap PCA t-SNE Venn-plot**

iSeq: A web-based server for RNA-seq Data Analysis and Visualization

Upload your genes Expression data first!

The screenshot displays the iSeq web interface with the following components:

- Navigation:** Upload, Normalization, DEG calling, Function, Plots, About.
- File Upload:** Sections for "Choose An Expression File of Genes(.csv)" and "Choose a Condition File of Samples(.csv)", with an "Example Data" button highlighted by a blue circle and arrow.
- log10(Expression + 1) Plot:** A bar chart showing expression levels for samples AD_1, AD_0, AD_2, EM_1, EM_0, EM_2, and EM_3.
- Cluster Dendrogram:** A tree diagram showing hierarchical clustering of samples.
- Gene Ontology:** A horizontal bar chart showing enriched GO terms.
- Abhd3 Plot:** A bar chart showing the expression of the Abhd3 gene across conditions.
- PCA:** A scatter plot of PC2 vs PC1 for different samples.
- Gene Expression Heatmap:** A heatmap showing expression levels for all genes across all samples, with a color scale from blue (low) to red (high).