

scRNA-seq
expression data

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graph TD; A(scRNA-seq expression data) --> B[Data preprocessing with normalization and gene selection]; B --> C[Cell sampling]; C --> D[GEP detection with WSSMFA]; D --> E[Gene Regulatory network construction with TRRUST];
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The diagram illustrates a five-step pipeline for constructing a gene regulatory network from scRNA-seq data. It begins with 'scRNA-seq expression data' in a blue rounded rectangle. This is followed by four rectangular blocks: 'Data preprocessing with normalization and gene selection' (yellow), 'Cell sampling' (teal), 'GEP detection with WSSMFA' (green), and 'Gene Regulatory network construction with TRRUST' (purple). Each step is connected to the next by a downward-pointing arrow. The steps are also labeled with letters A, B, C, and D on the left side of the flow.

A Data preprocessing with normalization
and gene selection

B Cell sampling

C GEP detection with WSSMFA

D Gene Regulatory network
construction with TRRUST