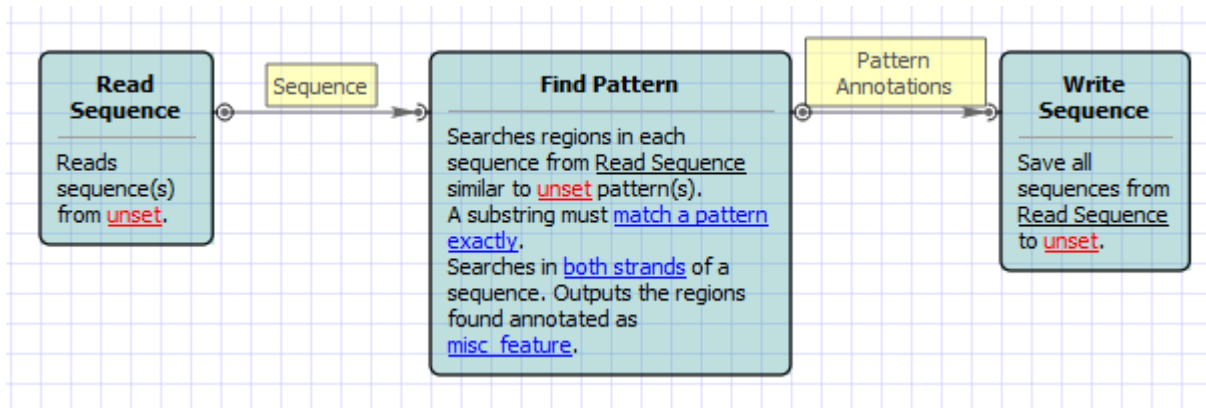


# Find patterns

This simple workflow finds patterns in your sequences and saves them as annotations. You can use the workflow to map primers, regulatory signals, genes, etc. It loads any set of sequences from your files or folders and finds patterns in them. Just specify a dataset for the algorithm in the "Read sequence" element. Patterns are entered in comma-delimited format in the corresponding field of the "Find Pattern" element. Also, you can load patterns from a file. In that case, names of patterns can be saved as names of annotations. Files with patterns can be in any sequence format or in newline-delimited format.



Also, if required, you can change parameters. Use the workflow wizard to guide you through the parameters setup process. The first wizard page will appear when you click on the Show wizard button on the Workflow Designer toolbar:

