Convert alignments to ClustalW

This workflow converts multiple alignment file(s) of any format to ClustalW document(s). If source file is a sequence format (e.g. FASTA), all contained sequences are added to the result alignment. Yet no real alignment is performed, this particular workflow illustrates pure data format conversion. To get this workflow working, you only need to select "Alignment Reader" task, so its' parameters appear in Property Inspector panel, and specify source

file(s) at "URL" field. Launch the workflow with pressing Ctrl+R shortcut.

After running the workflow, target clustal file will appear in the same folder as the source file, with the same name but different extension (".aln").

If several input files were selected, several clustal files will be generated accordingly.

You can override the target file location by editing "URL" parameter of "Write ClustalW" task.

Read alignment ⊙	Multiple sequence alignment	Write ClustalW
		Save all MSAs
Reads		from Read
MSA(s)		alignment to
from unset.		unset.

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:

