

This table is restricted to tools that deduce workflows logically from declarative statements about dependencies, and ignores tools & libraries aimed at building pipelines explicitly (including web shells such as Galaxy, or workflow engines like CWL)													
To update, please contact: Ian Holmes <ihholmes+biomake@gmail.com>													
Chris Mungall <cmungall+biomake@gmail.com>													
Latest version of this table: https://docs.google.com/spreadsheets/d/1EPyilhXoTC8BGK8SG4eUG7yCkOhR_SndYz22005dq3Y/edit?usp=sharing													
Earlier version of this table: https://biowiki.org/wiki/index.php/Make_Comparison													
See also: https://github.com/common-workflow-language/common-workflow-language/wiki/Existing-Workflow-systems													
<i>Tool</i>	<i>URL</i>		<i>Implementation language</i>	<i>MD5/hash tests for file staleness?</i>	<i>Functional language extensions (e.g. for filename manipulation)?</i>	<i>Logic programming extension language (e.g. ontology integration)?</i>	<i>Multiple wildcards per rule?</i>	<i>Multi-threaded parallelism?</i>	<i>SGE (Sun Grid Engine) compatible?</i>	<i>PBS (Portable Batch System) compatible?</i>	<i>SLURM (Simple Linux Utility for Resource Management) compatible?</i>	<i>GNU Makefile syntax compatible?</i>	
GNU make	https://www.gnu.org/software/make/		C	no	yes	no	no	yes	no	no	no	yes	
Biomake	http://biomake.org/		Prolog	yes	yes	yes	yes	yes	yes	yes	yes	yes	
Erlang make	http://erlang.org/doc/man/make.html		Erlang	no	no	no	no	yes	no	no	no	no	
omake	http://omake.metapri.org/index.html		C	yes	yes	yes	no	yes	no	no	no	no	
makepp	http://makepp.sourceforge.net/		Perl	yes	yes	yes	no	yes	no	no	no	yes	
snakemake	https://snakemake.readthedocs.io/en/stable/		Python	no	yes	yes	yes	yes	yes	yes	yes	no	
qmake	http://gridscheduler.sourceforge.net/htmlman/		C	no	yes	no	no	yes	yes	no	no	yes	
distmake	http://distmake.sourceforge.net/pmwiki/pmwiki.php		C	no	yes	no	no	yes	yes	no	no	yes	