

Tool	GWAtoolbox	Metal	GWAMA	Mantel	Meta	*ABEL	plink	snpStats
Website	http://www.eurac.edu/GWAtoolbox.html	http://genome.sph.umich.edu/wiki/METAL_Documentation	http://www.well.ox.ac.uk/gwama/	http://debakker.med.harvard.edu/resources.html	http://www.stats.ox.ac.uk/%7Ejsliu/meta.html	http://www.genabel.org	http://pngu.mgh.harvard.edu/~purcell/plink/	http://www.bioconductor.org/packages/release/bioc/html/snpStats.html
Main purpose	QC of data to be included in a GWA meta-analysis.	Meta analysis of whole genome association data.	Meta analysis of whole genome association data.	Meta analysis of whole genome association data.	Meta analysis of whole genome association data.	Analysis of individual level data and meta-analysis of whole genome association data.	Analysis of individual level data and meta-analysis of whole genome association data.	Analysis of individual level data and meta-analysis of whole genome association data.
Programming language	R, C++	C++	C++	Perl, R	C++, Perl	R, C++	C++	R, C++
Multi-platform	Windows, Mac, Linux	Windows, Linux	Linux	Linux	Linux	Windows, Mac, Linux	Windows, Mac, Linux	Windows, Mac, Linux
Parrallel processing	Yes	No	No	parts	parts	No	No	No
Flexible input format (e.g. column headers can be re-assigned)	Yes, Metal based	Yes	No	No, but script helps with this task	No	No	No	No, but can be done in R
Report format	HTML, csv	Text log file	Text log file	Text log file	Text log file	Text log file	Text log file	Text log file
File-format checks								
Check the consistency of column names with meta analysis guidelines.	+	~	~ §	~	~ ‡	-	-	-
Check if the minimal required information for the meta-analysis is present.	+	~	~ §	~	~ ‡	-	-	-
Check if data are in a format that can be analyzed (numeric, character, factor).	+	~	~	~	~	~	+	~
Check if all SNP identification numbers are unique.	+	+	-	+	-	+	+	+
Check if alleles are coded in letters/numbers as expected.	+	~	~	+	~	-	+	+
Check if missing values are coded in a consistent way.	+	~	~	~	-	-	~	-
Check if the field separator is as expected.	+	~	~	~	~	~	~	-
Check if strand information is present and unequivocal.	+	~	~	~	-	-	-	-
Check if the number of chromosomes and chromosome coding are as expected.	+	~	~	~	-	-	+	-
Quality check at the individual study level								
Assess the presence of unexpected values for the key items required for the meta-analysis (e.g.: negative p-values or negative standard errors)	+	~	~	~	-	~	~	~
Assess p-value inflation and analyze p-value distribution.	+	~	~	~	~	+	+	~
Assess the distribution of main summary statistics, including the effect estimates, their standard errors, and genotype imputation quality.	+	-	-	-/~	-	-	~	~
Between-study consistency check								
Compare the distribution of summary statistics between studies to detect studies that are sistematically different from the others	+	-	-	-	-	-	-	~

Legend

- not supported
- ~ basic support
- + fully supported

Notes

- § only GWAMA specific names are supported
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