option	MBMDR-4.4.1		MBMDR-4.3.3	
	command	default	command	default
public version	YES		YES	
main change	adding on-the-fly correction of categorical covariates and an option to perform a two-stage analysis		solving the bug with -ac, adding main effect correction for survival data (based on cox model)	
known bugs				
handle binary trait	--binary		--binary	
handle continuous trait	--continuous		--continuous	
handle survival trait	--survival		--survival	
handle multiple traits	-at AMOUNT -ct CUR	-at 1 -ct 1	-at AMOUNT -ct CUR	-at 1 -ct 1
handle covariates	-ac AMOUNT	-ac 0	-ac AMOUNT	-ac 0
set result size	-n	1000	-n	1000
set permutation amount	-p	999	-p	999
set random seed	-r	random	-r	random
set minimum group size	-m	10	-m	10
cutoff value for chi-square	-x	0.1	-x	0.1
specify outfile name	-o	_output.txt	-o	_output.txt
specify model file name	-o2	_models.txt	-o2	_models.txt
no multiple testing correction	-mt NONE	no	-mt NONE	no
use MAXT algorithm	-mt MAXT	no	-mt MAXT	no
use MINP algorithm	-mt MINP	no	-mt MINP	no
use RAWP algorithm	-mt RAWP	no	-mt RAWP	no
use STRAT1 algorithm	-mt STRAT1	no	-mt STRAT1	no
use STRAT2 algorithm	-mt STRAT2	no	-mt STRAT2	no
use speedMAXT algorithm	not available		not available	
use gammaMAXT algorithm	-mt gammaMAXT	yes	-mt gammaMAXT	yes
no correction for main effect	-a NONE	no	-a NONE	no
codominant correction	-a CODOMINANT	yes	-a CODOMINANT	yes
additive correction	-a ADDITIVE	no	-a ADDITIVE	no
on-the-fly covariates correction	-rc ONTHEFLY	no	not available	
analyze main effect	-d 1D	no	-d 1D	no
analyze interactions	-d 2D	yes	-d 2D	yes
analyze 3-way interactions	-d 3D	no	-d 3D	no
do not verbose	-v NONE	yes	-v NONE	yes
verbose shortly	-v SHORT	no	-v SHORT	no
verbose with some details	-v MEDIUM	no	-v MEDIUM	no
verbose with a lot of details	-v LONG	no	-v LONG	no
no progress bar	-pb NONE	no	-pb NONE	no
show progress bar	-pb NORMAL	yes	-pb NORMAL	yes
erase markers from a LIST	-e LIST	no	-e LIST	no
erase markers from a FILE	-E FILE	no	-E FILE	no
filter markers from a LIST	-f LIST	no	-f LIST	no
filter from two FILES	-F FILE	no	-F FILE	no
second stage of 2-stage analysis	-s FILE	no	not available	
use MBMDR input format	-if MBMDR	yes	-if MBMDR	yes
use MDR input format	-if MDR	no	-if MDR	no
no rank transform	-rt NONE	yes	-rt NONE	yes
rank transform	-rt RANK_TRANSFORM	no	-rt RANK_TRANSFORM	no

option	MBMDR-4.3.2		MBMDR-4.2.2	
public version	YES		YES	
main change	handle multiple traits, covariates (working with residuals). Return a new file containing the models.		adding the new gammaMAXT algorithm (and parallel workflow) and revising the default options	
known bugs	-ac does not work properly (it does not take account of all subjects)			
option	**command**	**default**	**command**	**default**
handle binary trait	--binary		--binary	
handle continuous trait	--continuous		--continuous	
handle survival trait	--survival		--survival	
handle multiple traits	-at AMOUNT -ct CUR	-at 1 -ct 1	not available	
handle covariates	-ac AMOUNT	-ac 0	not available	
set result size	-n	1000	-n	1000
set permutation amount	-p	999	-p	999
set random seed	-r	random	-r	random
set minimum group size	-m	10	-m	10
cutoff value for chi-square	-x	0.1	-x	0.1
specify outfile name	-o	_output.txt	-o	_output.txt
specify model file name	-o2	_models.txt	not available	
no multiple testing correction	-mt NONE	no	-mt NONE	no
use MAXT algorithm	-mt MAXT	no	-mt MAXT	no
use MINP algorithm	-mt MINP	no	-mt MINP	no
use RAWP algorithm	-mt RAWP	no	-mt RAWP	no
use STRAT1 algorithm	-mt STRAT1	no	-mt STRAT1	no
use STRAT2 algorithm	-mt STRAT2	no	-mt STRAT2	no
use speedMAXT algorithm	not available		not available	
use gammaMAXT algorithm	-mt gammaMAXT	yes	-mt gammaMAXT	yes
no correction for main effect	-a NONE	no	-a NONE	no
codominant correction	-a CODOMINANT	yes	-a CODOMINANT	yes
additive correction	-a ADDITIVE	no	-a ADDITIVE	no
	not available		not available	
analyze main effect	-d 1D	no	-d 1D	no
analyze interactions	-d 2D	yes	-d 2D	yes
analyze 3-way interactions	-d 3D	no	-d 3D	no
do not verbose	-v NONE	yes	-v NONE	yes
verbose shortly	-v SHORT	no	-v SHORT	no
verbose with some details	-v MEDIUM	no	-v MEDIUM	no
verbose with a lot of details	-v LONG	no	-v LONG	no
no progress bar	-pb NONE	no	-pb NONE	no
show progress bar	-pb NORMAL	yes	-pb NORMAL	yes
erase markers from a LIST	-e LIST	no	-e LIST	no
erase markers from a FILE	-E FILE	no	-E FILE	no
filter markers from a LIST	-f LIST	no	-f LIST	no
filter from two FILES	-F FILE	no	-F FILE	no
second stage of 2-stage analysis	not available		not available	
use MBMDR input format	-if MBMDR	yes	-if MBMDR	yes
use MDR input format	-if MDR	no	-if MDR	no
no rank transform	-rt NONE	yes	-rt NONE	yes
rank transform	-rt RANK_TRANSFORM	no	-rt RANK_TRANSFORM	no

	MBMDR-4.1.0		MBMDR-4.0.3	
public version	YES		YES	
main change	solving bugs with the 3D option (with -f or with the parallel workflow) and the -v LONG bug		adding the possibility to combine 3D and speedMAXT, solving the -v bug, allowing MDR format	
known bugs			-v LONG still crashes, parallel workflow does not work for 3D	
option	**command**	**default**	**command**	**default**
handle binary trait	--binary		--binary	
handle continuous trait	--continuous		--continuous	
handle survival trait	--survival		--survival	
handle multiple traits	not available		not available	
handle covariates	not available		not available	
set result size	-n	1000	-n	1000
set permutation amount	-p	999	-p	999
set random seed	-r	random	-r	random
set minimum group size	-m	10	-m	10
cutoff value for chi-square	-x	0.1	-x	0.1
specify outfile name	-o	_output.txt	-o	_output.txt
specify model file name	not available		not available	
no multiple testing correction	-mt NONE	no	-mt NONE	no
use MAXT algorithm	-mt MAXT	yes	-mt MAXT	yes
use MINP algorithm	-mt MINP	no	-mt MINP	no
use RAWP algorithm	-mt RAWP	no	-mt RAWP	no
use STRAT1 algorithm	-mt STRAT1	no	-mt STRAT1	no
use STRAT2 algorithm	-mt STRAT2	no	-mt STRAT2	no
use speedMAXT algorithm	-mt speedMAXT	no	-mt speedMAXT	no
use gammaMAXT algorithm	not available		not available	
no correction for main effect	-a NONE	no	-a NONE	no
codominant correction	-a CODOMINANT	yes	-a CODOMINANT	yes
additive correction	-a ADDITIVE	no	-a ADDITIVE	no
	not available		not available	
analyze main effect	-d 1D	no	-d 1D	no
analyze interactions	-d 2D	yes	-d 2D	yes
analyze 3-way interactions	-d 3D	no	-d 3D	no
do not verbose	-v NONE	yes	-v NONE	yes
verbose shortly	-v SHORT	no	-v SHORT	no
verbose with some details	-v MEDIUM	no	-v MEDIUM	no
verbose with a lot of details	-v LONG	no	-v LONG	bug
no progress bar	-pb NONE	no	-pb NONE	no
show progress bar	-pb NORMAL	yes	-pb NORMAL	yes
erase markers from a LIST	-e LIST	no	-e LIST	no
erase markers from a FILE	-E FILE	no	-E FILE	no
filter markers from a LIST	-f LIST	no	-f LIST	no
filter from two FILES	-F FILE	no	-F FILE	no
second stage of 2-stage analysis	not available		not available	
use MBMDR input format	-if MBMDR	yes	-if MBMDR	yes
use MDR input format	-if MDR	no	-if MDR	no
no rank transform	-rt NONE	no	-rt NONE	no
rank transform	-rt RANK_TRANSFORM	yes	-rt RANK_TRANSFORM	yes

option	MBMDR-4.0.1		MBMDR-3.3.1	
public version	YES		NO	
main change	more flexible code using virtual functions to avoid code duplication		implementation of speedMAXT, renaming options to have an easier manual, progress bar for STRAT1/2	
known bugs	the -v option does not print the right HLO matrices and test-stats			
option	**command**	**default**	**command**	**default**
handle binary trait	--binary		--binary	
handle continuous trait	--continuous		--continuous	
handle survival trait	--survival		--survival	
handle multiple traits	not available		not available	
handle covariates	not available		not available	
set result size	-n	1000	-n	1000
set permutation amount	-p	999	-p	999
set random seed	-r	random	-r	random
set minimum group size	-m	10	-m	10
cutoff value for chi-square	-x	0.1	-x	0.1
specify outfile name	-o	_output.txt	-o	_output.txt
specify model file name	not available		not available	
no multiple testing correction	-mt NONE	no	-mt NONE	no
use MAXT algorithm	-mt MAXT	yes	-mt MAXT	yes
use MINP algorithm	-mt MINP	no	-mt MINP	no
use RAWP algorithm	-mt RAWP	no	-mt RAWP	no
use STRAT1 algorithm	-mt STRAT1	no	-mt STRAT1	no
use STRAT2 algorithm	-mt STRAT2	no	-mt STRAT2	no
use speedMAXT algorithm	-mt speedMAXT	no	-mt speedMAXT	no
use gammaMAXT algorithm	not available		not available	
no correction for main effect	-a NONE	no	-a NONE	no
codominant correction	-a CODOMINANT	yes	-a CODOMINANT	yes
additive correction	-a ADDITIVE	no	-a ADDITIVE	no
	not available		not available	
analyze main effect	-d 1D	no	-d 1D	no
analyze interactions	-d 2D	yes	-d 2D	yes
analyze 3-way interactions	-d 3D	no	-d 3D	no
do not verbose	-v NONE	yes	-v NONE	yes
verbose shortly	-v SHORT	bug	-v SHORT	no
verbose with some details	-v MEDIUM	bug	-v MEDIUM	no
verbose with a lot of details	-v LONG	bug	-v LONG	no
no progress bar	-pb NONE	no	-pb NONE	no
show progress bar	-pb NORMAL	yes	-pb NORMAL	yes
erase markers from a LIST	-e LIST	no	-e LIST	no
erase markers from a FILE	-E FILE	no	-E FILE	no
filter markers from a LIST	-f LIST	no	-f LIST	no
filter from two FILES	-F FILE	no	-F FILE	no
second stage of 2-stage analysis	not available		not available	
use MBMDR input format		yes		yes
use MDR input format	not available		not available	
no rank transform	-rt NONE	no	-rt NONE	no
rank transform	-rt RANK_TRANSFORM	yes	-rt RANK_TRANSFORM	yes

option	MBMDR-3.2.1 command	default	MBMDR-3.1.2 command	default
	MBMDR-3.2.1		MBMDR-3.1.2	
public version	NO		NO	
main change	implementation of STRAT1 and STRAT2		implementation of RAWP, MINP, erase markers from a file and verbose long.	
known bugs				
option	**command**	**default**	**command**	**default**
handle binary trait	--binary		--binary	
handle continuous trait	--continuous		--continuous	
handle survival trait	--survival		--survival	
handle multiple traits	not available		not available	
handle covariates	not available		not available	
set result size	-n	1000	-n	1000
set permutation amount	-p	999	-p	999
set random seed	-r	random	-r	random
set minimum group size	-m	10	-m	10
cutoff value for chi-square	-x	0.1	-x	0.1
specify outfile name	-o	_output.txt	-o	_output.txt
specify model file name	not available		not available	
no multiple testing correction	--no-permut	no	--no-permut	no
use MAXT algorithm	-v MAXT	yes	-v MAXT	yes
use MINP algorithm	-v MINP	no	-v MINP	no
use RAWP algorithm	-v RAWP	no	-v RAWP	no
use STRAT1 algorithm	-v STRAT1	no	not available	
use STRAT2 algorithm	-v STRAT2	no	not available	
use speedMAXT algorithm	not available		not available	
use gammaMAXT algorithm	not available		not available	
no correction for main effect	-a NONE	no	-a NONE	no
codominant correction	-a CODOMINANT	yes	-a CODOMINANT	yes
additive correction	-a ADDITIVE	no	-a ADDITIVE	no
	not available		not available	
analyze main effect	--1D	no	--1D	no
analyze interactions		yes		yes
analyze 3-way interactions	--3D	no	--3D	no
do not verbose		yes		yes
verbose shortly	--verbose-s	no	--verbose-s	no
verbose with some details	--verbose	no	--verbose	no
verbose with a lot of details	--verbose-l	no	--verbose-l	no
no progress bar	--no-progress	no	--no-progress	no
show progress bar		yes		yes
erase markers from a LIST	not available		not available	
erase markers from a FILE	-d FILE	no	-d FILE	no
filter markers from a LIST	-f SNP_NAME	no	-f SNP_NAME	no
filter from two FILES	not available		not available	
second stage of 2-stage analysis	not available		not available	
use MBMDR input format		yes		yes
use MDR input format	not available		not available	
no rank transform	--no-ranking	no	--no-ranking	no
rank transform		yes		yes

option	MBMDR-3.1.0		MBMDR-3.0.3	
public version	YES		YES	
main change	implementation of the progress bar and solving the 3D bug.		implementation of survival and solving the cholesky bug	
known bugs			the --3D option does not work properly	
option	**command**	**default**	**command**	**default**
handle binary trait	--binary		--binary	
handle continuous trait	--continuous		--continuous	
handle survival trait	--survival		--survival	
handle multiple traits	not available		not available	
handle covariates	not available		not available	
set result size	-n	1000	-n	1000
set permutation amount	-p	999	-p	999
set random seed	-r	random	-r	random
set minimum group size	-m	10	-m	10
cutoff value for chi-square	-x	0.1	-x	0.1
specify outfile name	-o	_output.txt	-o	_output.txt
specify model file name	not available		not available	
no multiple testing correction	--no-permut	no	--no-permut	no
use MAXT algorithm		yes		yes
use MINP algorithm	not available		not available	
use RAWP algorithm	not available		not available	
use STRAT1 algorithm	not available		not available	
use STRAT2 algorithm	not available		not available	
use speedMAXT algorithm	not available		not available	
use gammaMAXT algorithm	not available		not available	
no correction for main effect	-a NONE	no	-a NONE	no
codominant correction	-a CODOMINANT	yes	-a CODOMINANT	yes
additive correction	-a ADDITIVE	no	-a ADDITIVE	no
	not available		not available	
analyze main effect	--1D	no	--1D	no
analyze interactions		yes		yes
analyze 3-way interactions	--3D	no	--3D	bug
do not verbose		yes		yes
verbose shortly	--verbose-s	no	--verbose-s	no
verbose with some details	--verbose	no	--verbose	no
verbose with a lot of details	--verbose-l	no	--verbose-l	no
no progress bar	--no-progress	no	not available	
show progress bar		yes	not available	
erase markers from a LIST	not available		not available	
erase markers from a FILE	-d FILE	no	-d FILE	no
filter markers from a LIST	-f SNP_NAME	no	-f SNP_NAME	no
filter from two FILES	not available		not available	
second stage of 2-stage analysis	not available		not available	
use MBMDR input format		yes		yes
use MDR input format	not available		not available	
no rank transform	--no-ranking	no	--no-ranking	no
rank transform		yes		yes

option	MBMDR-3.0.2 command	default	MBMDR-2.7.5 command	default
public version	YES		YES	
main change	implementation of command-line help, more flexible and faster code		last and most stable version 2 implementation, about 1.5 times slower than MBMDR-3.0.2	
known bugs	bug with the cholesky decomposition		was also containing --h-vs-l and --hlo-ranking options given up later	
option	**command**	**default**	**command**	**default**
handle binary trait	--binary		--binary	
handle continuous trait	--continuous		--continuous	
handle survival trait	not available		--survival	
handle multiple traits	not available		--multiple-trait -t INT	
handle covariates	not available		not available	
set result size	-n	1000	-n	1000
set permutation amount	-p	999	-p	999
set random seed	-r	random	-r	random
set minimum group size	-m	10	-m	10
cutoff value for chi-square	-x	0.1	-x	0.1
specify outfile name	-o	_output.txt	-o	_output.txt
specify model file name	not available		not available	
no multiple testing correction	--no-permut	no	not available	
use MAXT algorithm		yes	--maxT --one-cell-approach --two-te	
use MINP algorithm	not available		--minP --one-cell-approach --two-tes	
use RAWP algorithm	not available		--margP --one-cell-approach --two-t	
use STRAT1 algorithm	not available		not available	
use STRAT2 algorithm	not available		not available	
use speedMAXT algorithm	not available		not available	
use gammaMAXT algorithm	not available		not available	
no correction for main effect	-a NONE	no		yes
codominant correction	-a CODOMINANT	yes	--adjust-codominant	no
additive correction	-a ADDITIVE	no	--adjust-additive	no
	not available		not available	
analyze main effect	--1D	no	-d 1	no
analyze interactions		yes	-d 2	yes
analyze 3-way interactions	not available		-d 3	no
do not verbose		yes		yes
verbose shortly	--verbose-s	no	recompile	
verbose with some details	--verbose	no	--verbose	no
verbose with a lot of details	--verbose-l	no	recompile	
no progress bar	not available		not available	
show progress bar	not available		not available	
erase markers from a LIST	not available		not available	
erase markers from a FILE	-d FILE	no	not available	
filter markers from a LIST	-f SNP_NAME	no	-f LIST	no
filter from two FILES	not available		not available	
second stage of 2-stage analysis	not available		not available	
use MBMDR input format		yes		yes
use MDR input format	not available		not available	
no rank transform	--no-ranking	no	not available	
rank transform		yes	not available	