public version	YES		YES	
main change			solving the bug with -ac, adding	
J	categorical covariates and an option		main effect correction for survival	
	to perform a two-stage analysis		data (based on cox model)	
known bugs				
option	command	default	command	default
handle binary trait	binary		binary	0.0.0.0.0.0
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	-р	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	-0	_output.txt	-0	_output.txt
specify model file name	-02	_models.txt		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	е
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	е
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	е
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		-rt RANK_TRANSFORM	no

MBMDR-4.4.1

MBMDR-4.3.3

	MBMDR-4.3.2		MBMDR-4.2.2	
public version	YES		YES	
main change	(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	-0	_output.txt		_output.txt
specify model file name	-02	_models.txt	not available	е
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		е
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	e
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			<ul> <li>-v LONG still crashes, paworkflow does not work</li> </ul>	
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	9	not available	е
handle covariates	not available	(D	not available	Э
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	-0	_output.txt	-0	_output.txt
specify model file name	not available	(I)	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	е
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		е
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

	MBMDR-4.0.1		MBMDR-3.3.1		
public version	YES		NO		
main change	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	е	not available	е	
handle covariates	not available	е	not available	е	
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	-0	_output.txt	-0	_output.txt	
specify model file name	not available	е	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	е	
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	е	
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	е	not available	e	
no rank transform	-rt NONE	no	-rt NONE	no	
rank transform	-rt RANK_TRANSFORM	yes	-rt RANK_TRANSFORM	yes	

main change implementation of STRAT STRAT2  known bugs  option command handle binary traitbinary handle continuous traitcontinuous handle survival traitsurvival handle multiple traits not available set result size -n set permutation amount -p set random seed -r set minimum group size -m cutoff value for chi-square -x specify outfile name -o specify model file name not available no multiple testing correctionno-permut use MAXT algorithm -v MAXT use MINP algorithm -v MAXT use STRAT1 algorithm -v STRAT1 use STRAT2 algorithm -v STRAT1 use STRAT2 algorithm -v STRAT1 use speedMAXT algorithm -v STRAT1 use speedMAXT algorithm not available no correction for main effect -a NONE codominant correction -a CODOMINANT additive correction -a CODOMINANT additive correction -a ADDITIVE not available analyze main effect1D analyze interactions analyze 3-way interactions do not verbose	1000 999 random 10 0.1 output.txt no yes no no no no	implementation of RAW erase markers from a fill verbose long.  commandbinarycontinuoussurvival not available not available -n -p -r -m -x -o not available -no-permut -v MAXT -v MINP -v RAWP not available not available	default  ee 1000 999 random 10 0.1 _output.txt ee no yes no no
known bugs  option  handle binary trait handle continuous trait handle survival trait handle survival trait handle covariates handle covariates set result size set permutation amount set random seed result file name cutoff value for chi-square specify model file name no multiple testing correction use MAXT algorithm use MINP algorithm use STRAT1 algorithm use STRAT1 algorithm use STRAT1 algorithm use speedMAXT algorithm use gammaMAXT algorithm use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect analyze main effect analyze interactions analyze 3-way interactionscontinuousbinarybinarybinarybinarybinarybinarybinarybinarybinarybinarybinarybinarybinarybinarycontinuoussurvivalsurviv	default  1000 999 random 10 0.1 _output.txt  no yes no no no	commandbinarycontinuoussurvival  not available not available -n -p -r -m -x -o  not availableno-permut -v MAXT -v MINP -v RAWP	default  ee 1000 999 random 10 0.1 _output.txt ee no yes no no
Andle binary trait handle continuous trait handle survival trait handle survival trait handle multiple traits handle covariates set result size set permutation amount set minimum group size cutoff value for chi-square specify model file name no multiple testing correction use MAXT algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect analyze main effect analyze interactions analyze 3-way interactionssurvivalcontinuouscontinuouscontinuouscontinuouscontinuouscontinuouscontinuoussurvivalcontinuouscontinuouscontinuouscontinuoussurvivalcontinuousconti	1000 999 random 10 0.1 output.txt  no yes no no no	binarycontinuoussurvival not available not available -n -p -r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP	e 1000 999 random 10 0.1 _output.txt e no yes no no
handle binary trait handle continuous trait handle survival trait handle survival trait handle multiple traits handle covariates handle covariates set result size set result size set permutation amount set random seed rset minimum group size cutoff value for chi-square specify outfile name no multiple testing correction use MAXT algorithm use MINP algorithm use STRAT1 algorithm use STRAT2 algorithm use STRAT2 algorithm use gammaMAXT algorithm use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect1D analyze main effect analyze interactions analyze 3-way interactionssurvivalcontinuouscontinuoussurvivalcontinuoussurvivalsurvi	1000 999 random 10 0.1 output.txt  no yes no no no	binarycontinuoussurvival not available not available -n -p -r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP	e 1000 999 random 10 0.1 _output.txt e no yes no no
handle binary trait handle continuous trait handle survival trait handle survival trait handle multiple traits handle covariates handle covariates set result size set result size set permutation amount set random seed rset minimum group size cutoff value for chi-square specify outfile name no multiple testing correction use MAXT algorithm use MINP algorithm use STRAT1 algorithm use STRAT2 algorithm use STRAT2 algorithm use gammaMAXT algorithm use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect1D analyze main effect analyze interactions analyze 3-way interactionssurvivalcontinuouscontinuoussurvivalcontinuoussurvivalsurvi	1000 999 random 10 0.1 output.txt  no yes no no no	binarycontinuoussurvival not available not available -n -p -r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP	e 1000 999 random 10 0.1 _output.txt e no yes no no
handle continuous trait handle survival trait handle multiple traits handle covariates handle covariates handle covariates set result size set permutation amount set random seed result five and available set random seed set minimum group size cutoff value for chi-square specify outfile name specify model file name no multiple testing correction use MAXT algorithm use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use speedMAXT algorithm use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect analyze main effect1D analyze interactions analyze 3-way interactions3D	999 random 10 0.1 _output.txt  no yes no no no	continuoussurvival not available not available -n -p -r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP	1000 999 random 10 0.1 _output.txt e no yes no no
handle multiple traits handle covariates set result size set permutation amount set random seed set minimum group size cutoff value for chi-square specify outfile name no multiple testing correction use MAXT algorithm use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use gammaMAXT algorithm use gammaMAXT algorithm use gammaMAXT algorithm use gammaMAXT algorithm and tavailable no correction for main effect codominant correction additive correction analyze main effect analyze interactions analyze 3-way interactions 3D	999 random 10 0.1 _output.txt  no yes no no no	not available not available -n -p -r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP not available	1000 999 random 10 0.1 _output.txt e no yes no no
handle covariates set result size set permutation amount set random seed result size set minimum group size cutoff value for chi-square specify outfile name specify model file name no multiple testing correction use MAXT algorithm use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use STRAT2 algorithm use gammaMAXT algorithm use gammaMAXT algorithm no correction for main effect codominant correction analyze main effect analyze interactions analyze 3-way interactions  A	999 random 10 0.1 _output.txt  no yes no no no	not available -n -p -r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP	1000 999 random 10 0.1 _output.txt e no yes no no
handle covariates set result size set permutation amount set random seed result size set minimum group size cutoff value for chi-square specify outfile name rout specify model file name no multiple testing correction use MAXT algorithm use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use STRAT2 algorithm use gammaMAXT algorithm not available rout available	999 random 10 0.1 _output.txt  no yes no no no	-n -p -r -r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP not available	1000 999 random 10 0.1 _output.txt e no yes no no
set permutation amount  set random seed -r  set minimum group size -m  cutoff value for chi-square -y  specify outfile name -o  specify model file name no multiple testing correction use MAXT algorithm -v MAXT  use MINP algorithm -v RAWP use STRAT1 algorithm -v STRAT1  use STRAT2 algorithm -v STRAT1  use speedMAXT algorithm -v STRAT2  use speedMAXT algorithm not available analyze main effect -a NONE -a CODOMINANT -a ADDITIVE  analyze interactions analyze 3-way interactions3D	999 random 10 0.1 _output.txt  no yes no no no	-p -r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP not available	999 random 10 0.1 _output.txt e no yes no no
set random seed -r set minimum group size -m cutoff value for chi-square -x specify outfile name -o specify model file name not available no multiple testing correctionno-permut use MAXT algorithm -v MAXT use MINP algorithm -v MINP use RAWP algorithm -v STRAT1 use STRAT1 algorithm -v STRAT1 use STRAT2 algorithm -v STRAT2 use speedMAXT algorithm not available use gammaMAXT algorithm not available codominant correction -a CODOMINANT additive correction -a ADDITIVE  analyze main effect1D analyze interactions analyze 3-way interactions3D	random 10 0.1 _output.txt  no _yes _no _no _no _no	-r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP not available	random 10 0.1 _output.txt e no yes no no
set random seed set minimum group size cutoff value for chi-square specify outfile name specify model file name no multiple testing correction use MAXT algorithm use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use speedMAXT algorithm use speedMAXT algorithm or orrection for main effect codominant correction additive correction analyze main effect analyze interactions analyze 3-way interactions	10 0.1 _output.txt  no _yes _no _no _no _no	-r -m -x -o not availableno-permut -v MAXT -v MINP -v RAWP not available	10 0.1 _output.txt e no yes no no
cutoff value for chi-square  specify outfile name  specify model file name  no multiple testing correction  use MAXT algorithm  use MINP algorithm  use RAWP algorithm  use STRAT1 algorithm  use STRAT2 algorithm  use speedMAXT algorithm  use speedMAXT algorithm  not available  analyze main effect  analyze interactions  analyze 3-way interactions  - o  not available  - not available  - x  - x  - x  - x  - x  - x  - x  -	0.1 _output.txt  no yes no no no	-x -o not availableno-permut -v MAXT -v MINP -v RAWP not available	0.1 _output.txt e no yes no no
specify outfile name specify model file name no multiple testing correction use MAXT algorithm use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use speedMAXT algorithm use speedMAXT algorithm not available use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect1D analyze interactions analyze 3-way interactions	no yes no no no	-o not availableno-permut -v MAXT -v MINP -v RAWP not available	_output.txt e no yes no no
specify outfile name specify model file name no multiple testing correction use MAXT algorithm use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use speedMAXT algorithm use speedMAXT algorithm not available use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect1D analyze interactions analyze 3-way interactions	no yes no no	not availableno-permut -v MAXT -v MINP -v RAWP not available	no yes no no
specify model file name no multiple testing correction use MAXT algorithm use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use speedMAXT algorithm use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect analyze interactions analyze 3-way interactionsno-permutv MINPv RAWPv STRAT1v STRAT2 use speedMAXT algorithm not availablea NONEa NONEa CODOMINANTa ADDITIVE	no yes no no	no-permut -v MAXT -v MINP -v RAWP not available	no yes no no
no multiple testing correction  use MAXT algorithm  use MINP algorithm  use RAWP algorithm  use STRAT1 algorithm  use STRAT2 algorithm  use speedMAXT algorithm  use gammaMAXT algorithm  no correction for main effect  codominant correction  additive correction  analyze main effect  analyze interactions  analyze 3-way interactions  v MAXT  v MINP  v RAWP  v STRAT1  v STRAT2  v STRAT2  v STRAT2  v STRAT2  v STRAT2  a NONE  a NONE  a CODOMINANT  a ADDITIVE  1D  analyze main effect  1D  analyze main effect  3D	yes no no no	-v MAXT -v MINP -v RAWP not available	yes no no
use MAXT algorithm use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use speedMAXT algorithm use gammaMAXT algorithm not available no correction for main effect codominant correction additive correction analyze main effect1D analyze interactions analyze 3-way interactions V MAXT V MINP	no no no	-v MAXT -v MINP -v RAWP not available	no no
use MINP algorithm use RAWP algorithm use STRAT1 algorithm use STRAT2 algorithm use speedMAXT algorithm use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect1D analyze interactions analyze 3-way interactions>	no no no	-v RAWP not available	no no
use RAWP algorithm -v RAWP use STRAT1 algorithm -v STRAT1 use STRAT2 algorithm -v STRAT2 use speedMAXT algorithm not available use gammaMAXT algorithm not available no correction for main effect -a NONE codominant correction -a CODOMINANT additive correction -a ADDITIVE  not available analyze main effect1D analyze interactions analyze 3-way interactions3D	no	not available	
use STRAT1 algorithm -v STRAT1 use STRAT2 algorithm -v STRAT2 use speedMAXT algorithm not available use gammaMAXT algorithm not available no correction for main effect -a NONE codominant correction -a CODOMINANT additive correction -a ADDITIVE not available analyze main effect1D analyze interactions analyze 3-way interactions3D		not available	e
use STRAT2 algorithm use speedMAXT algorithm use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect analyze interactions analyze 3-way interactions -v STRAT2 not available -a NONE -a CODOMINANT -a ADDITIVE not available1D1D3D	no		
use speedMAXT algorithm use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect analyze interactions analyze 3-way interactions - ot available - a NONE - a CODOMINANT - a ADDITIVE - not available 1D - analyze interactions 3D		not available	
use gammaMAXT algorithm no correction for main effect codominant correction additive correction analyze main effect analyze interactions analyze 3-way interactions -a NONE -a CODOMINANT -a ADDITIVE not available1D1D		not available	
no correction for main effect  codominant correction  additive correction  analyze main effect  analyze interactions  analyze 3-way interactions  -a NONE  -a CODOMINANT  -a ADDITIVE  not available 1D  analyze interactions 3D		not available	
additive correction -a ADDITIVE not available analyze main effect1D analyze interactions analyze 3-way interactions3D	no	-a NONE	no
not available analyze main effect1D analyze interactions analyze 3-way interactions3D	yes	-a CODOMINANT	yes
analyze main effect1D analyze interactions analyze 3-way interactions3D	no	-a ADDITIVE	no
analyze interactions analyze 3-way interactions3D	not available not avai		е
analyze 3-way interactions3D	no	1D	no
, ,	yes		yes
do not verbose	no	3D	no
	yes		yes
verbose shortlyverbose-s	no	verbose-s	no
verbose with some detailsverbose	no	verbose	no
verbose with a lot of detailsverbose-l	no	verbose-l	no
no progress barno-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	e
second stage of 2-stage analysis not available		not available	e
use MBMDR input format			yes
use MDR input format not available	yes	not available	-
no rank transformno-ranking	yes	noc available	no
rank transform	yes	no-ranking	110

MBMDR-3.2.1

MBMDR-3.1.2

	MBMDR-3.1.0		MBMDR-3.0.3	
public version	YES		YES	
main change			implementation of survival and solving the cholesky bug	
known bugs			the3D option does no 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 availabl	
handle covariates	not available		not availabl	
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	-0	_output.txt		_output.txt
specify model file name	not available	е	not available	
no multiple testing correction	no-permut	no	no-permut	no
use MAXT algorithm		yes		yes
use MINP algorithm	not available		not availabl	
use RAWP algorithm	not available		not availabl	
use STRAT1 algorithm	not available		not availabl	
use STRAT2 algorithm	not available		not availabl	
use speedMAXT algorithm	not available		not available	
use gammaMAXT algorithm	not available	е	not availabl	e
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	е	not availabl	e
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 availabl	
show progress bar		yes	not availabl	
erase markers from a LIST	not available		not availabl	e
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 availabl	
second stage of 2-stage analysis	not available		not availabl	
use MBMDR input format		yes		yes
use MDR input format	not available		not availabl	
no rank transform	no-ranking	no	no-ranking	no
rank transform		yes		yes

	MBMDR-3.0.2		MBMDR-2.7.5	
public version	YES		YES	
main change			last and most stable version 2	
main change	help, more flexible and		implementation, about 1.5 times slower than MBMDR-3.0.2	
known bugs	decomposition		was also containingh hlo-ranking options give	
option	command	default	command	default
handle binary trait	binary		binary	
handle continuous trait	continuous		continuous	
handle survival trait	not available	е	survival	
handle multiple traits	not available	е	multiple-trait -t INT	
handle covariates	not available	е	not availabl	е
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	-0	_output.txt	-0	_output.txt
specify model file name	not available	е	not availabl	e
no multiple testing correction	no-permut	no	not available	
use MAXT algorithm		yes	maxTone-cell-approachtwo-	
use MINP algorithm	not available	е	minPone-cell-approachtwo-t	
use RAWP algorithm	not available	е	margPone-cell-approachtwo-	
use STRAT1 algorithm	not available not available		е	
use STRAT2 algorithm	not available not available		е	
use speedMAXT algorithm	not available		not available	
use gammaMAXT algorithm	not available	not available not available		е
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	е	not availabl	е
analyze main effect	1D	no	-d 1	no
analyze interactions		yes	-d 2	yes
analyze 3-way interactions	not available	е	-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 avail		not availabl	
erase markers from a LIST	not available		not available	
erase markers from a FILE	-d FILE	no	not availabl	e
filter markers from a LIST	-f SNP_NAME	no	-f LIST	no
filter from two FILES	not available	e	not availabl	e
second stage of 2-stage analysis	not available	е	not availabl	e
use MBMDR input format		yes		yes
use MDR input format	not available	e	not availabl	e
no rank transform	no-ranking	no	not availabl	
rank transform		yes	not availabl	e