GUI			command prompt		
		Example		**Example**	**Comment**
	Inputfile	mydatafile		**./famhap18 mydatafile auto <options>**	
GENERAL OPTIONS					
Missings	Required callrate per individual/family (%)	90	u,u60,u70,u80, u90,u95,u99,u100	u90	// u (no callrate required) is the default
Sex	female		female		
	male		male		
	female cases		femalecase		// when combined with at test: female cases vs all controls
	male cases		malecase		
Estimation mode	iterative		it		// use for long haplotypes
	iterative twosides		itt		// even more precise than "it"
	dp		dp		// frequencies according to disease status
	reverse order		ro		
Selected SNPs	selected markers	1-5;22-23	"numbers"	1 2 3 4 5 22 23	
	region starts	1;22	region "numbers"	region 1 2 3 4 5 region 22 23	// simultaneous analysis of unlinked regions. Combine with hapcc!
Quantitative	quantitative		q		// combine with htr!
Print options	enhanced		P		
	detailed		PP		

Further options	entropy	entropy		// a generalized LD measure
	proxies	proxies	proxies 1 2 3 4	// here, the order matters: do not write 1 2 3 4 proxies. If you write 1 2 proxies 3 4, only 1 2 are used do determine 3 and 4
PRODUCE NEW DATAFILES				
	haploview format	haploview		
	windowsize	maxloc	maxloc 5	// produces new data sets in a sliding window fashion
IDENTIFICATION OF GENOTYPING ERRORS				
	Search genotyping errors	ed		
	minloc	minloc	minloc 3	// min length of haplotypes
	maxloc	maxloc	maxloc 10	// max length of haplotypes
	maxhap	maxhap	maxhap 50	// max number of haplotypes
	quotient	quotient	quotient 10000	// improvement of likelihood
ASSOCIATION ANALYSIS				
	Single-marker (cc)	singlecc		// all standard tests. Try large input files!
Single-marker-analysis	TDT (fam)	tdt		// all standard tests. Try large input files!
Likelihood-Ratio-Test	Omnibus (default)	lrtest		

	SIMULATION	SIMULATIONS	SIMULATIONS 100000	
	1 DF	oneDF		// single haplotype tests
Association analysis with weighted haplotype explanation lists (MC-method)				
Case-control	Ominbus Statistic	hapcc		**// standard option for haplotype analysis of cc data**
	Max Statistic	hapccmax		
	HTR	htr		// haplotype trend regression, also for quantitative phenotypes
	Diplotypic Analysis	dipcc		
	Rare Variants Test	diversityhap		// finds excess of rare haplotypes in cases
	sibvssib	sibvssib		// advanced users option. Please read the documentation!
	paired	paired		// advanced users option. Please read the documentation!
	impute	impute		// choose if you want imputed genotypes
Families	Omnibus Statistic	haptdt		**// standard option for haplotype analysis of family data (robust against population stratification)**
	Max Statistic	haptdtmax		
	Imprinting	PAT		//paternal asysmmetry test for imprinting
	Imprinting Max Statistic	PATmax		
	Maternal Transmissions	haptdt imppat		
	Paternal Transmissions	haptdt impat		

	SIMULATIONS		SIMULATIONS	SIMULATIONS 100000	// the smaller the P-value, the more you need
	alpha		alpha	alpha 0.05	// use to save computer storage, combine also with it
	nonoise		nonoise		// ignore rare haplotypes for test
	secondon		secondon		// improved accuracy in computation of gloabl P values
Multiple combinations	multiple combinations		allcombi		// all marker combinations
	maxmarker		maxmarker	maxmarker 2	// all 2-marker combinations
	sliding window		slidingwindow		
	window		window		
	max regions		maxregions		// use in combination with "region"
	STRATIFICATION MARKERS	9;11	strat	strat 9 strat 11 12	// marker 12 is tested conditional on markers 9 and 11
Analysis of imputed SNP	Analysis of imputed SNP with useful markers	15	fimpute	fimpute 15	// marker 15 is imputed using all markers that are typed for training and study sample (quick, conservative pre-test)
	Analysis of imputed SNP with all markers	15	fimpute with_all_markers	3 4 5 fimpute 15 with_all_markers	// marker 15 is imputed using all selected markers (here 3 4 5), even if they are not typed in the study sample (not recommended)
	required genotype prediction score	0.50	gpsbench	gpsbench 0.50	// required accuracy of imputed genotype

OPEN OUTPUT

main output	*.out
Mendel errors (fam)	*_MENDELERRORS.txt
recombinations (fam)	*_families_with_recos.txt
haplotypes	*_H0_HAPLOTYPES.txt
haplotype frequencies	*_FREQ.txt
LD measures	*_LDmeasuresALL.xt
tagging marker	*_TAG.txt
single marker results (cc)	*_SINGLEMARKER.txt
single marker results (fam)	*_SINGLEMARKER_FAM.txt
transmissions (fam)	*_TNT_Tables.txt
show all my P values	*_Pvalues.txt
contingency tables (cc)	*_Contingency_tables.txt
generalized r^2	*_PROXIES.txt
	*_H0_HAPLOTYPESinrow.txt

// Haplotypes per family unit in a different format, can't be opened from GUI