Software	Description	Publication	Webpage
CERVUS	Summary stats for microsat loci & assigning parents to offspring	http://dx.doi.org/10.1046/j.1365-294x.1998.00374.x	http://www.fieldgenetics.com/pages/aboutCervus_Overview.jsp
GENEPOP	Population genetics summary stats	http://jhered.oxfordjournals.org/content/86/3/248.full.pdf+html	http://genepop.curtin.edu.au
PEDANT	Estimating microsat locus-specific error rates	http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2789690/	http://www.stats.gla.ac.uk/~paulj/pedant.html
FSTAT	Estimating gene diversities and differentiation for codominant markers		http://www2.unil.ch/popgen/softwares/fstat.htm
ARLEQUIN	Population genetics summary stats, AMOVA	http://onlinelibrary.wiley.com/doi/10.1111/j.1755-0998.2010.02847.x/abstract	http://cmpg.unibe.ch/software/arlequin35/
STRUCTURE	Infer distinct genetic populations/clusters	http://www.ncbi.nlm.nih.gov/pubmed/10835412	http://pritchardlab.stanford.edu/structure.html
STRUCTURE HARVESTER	Web-viewer for STRUCTURE results	http://link.springer.com/article/10.1007%2Fs12686-011-9548-7	http://taylor0.biology.ucla.edu/structureHarvester/
CLUMPP	Aligning multiple replicate runs of clustering software	http://bioinformatics.oxfordjournals.org/content/23/14/1801.full	https://web.stanford.edu/group/rosenberglab/clumpp.html
DISTRUCT	Graphical display of results from clustering software	http://onlinelibrary.wiley.com/doi/10.1046/j.1471-8286.2003.00566.x/full	https://web.stanford.edu/group/rosenberglab/distruct.html
SPAGEDI	Spatial genetic structure of individuals or populations.	http://onlinelibrary.wiley.com/doi/10.1046/j.1471-8286.2002.00305.x/full	http://ebe.ulb.ac.be/ebe/SPAGeDi.html
TESS	Spatial population genetics, genome scans for selection	http://onlinelibrary.wiley.com/doi/10.1111/1755-0998.12471/full	http://membres-timc.imag.fr/Olivier.Francois/tess.html
MIGRATE	Estimates effective population size and past migration rates	http://www.pnas.org/content/98/8/4563.full	http://popgen.sc.fsu.edu/Migrate/Migrate-n.html

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MSVAR	Analysing microsat evolution, infer demographic change	http://vbn.aau.dk/ws/files/74875872/The_consequences_Cino_Pertoldi.pdf	https://cran.r-project.org/src/contrib/Archive/MSVAR/
PLINK	Analyse whole genome genotype/phenotype data	http://www.ncbi.nlm.nih.gov/pubmed/17701901	http://pngu.mgh.harvard.edu/~purcell/plink/
POPGENOME	Pop gen stats for large numbers of loci/whole genomes.	https://mbe.oxfordjournals.org/content/early/2014/04/16/molbev.msu136	https://cran.r-project.org/web/packages/PopGenome/index.html
STACKS	Building loci from NGS data, such as RAD-seq	http://www.g3journal.org/content/1/3/171.full	http://catchenlab.life.illinois.edu/stacks/
POPOOLATION	Analysing sequences from samples of pooled individuals	http://bioinformatics.oxfordjournals.org/content/27/24/3435	https://sourceforge.net/p/popoolation/wiki/Main/
SAMTOOLS	SNP calling, viewing, sorting, filtering, interacting with SAM files	http://www.ncbi.nlm.nih.gov/pubmed/19505943	http://www.htslib.org
VCFTOOLS	Interacting with VCF files, filtering, comparing, summarising variant calls	http://bioinformatics.oxfordjournals.org/content/27/15/2156	https://vcftools.github.io/index.html
BAYESCAN	Identify loci under selection	http://www.genetics.org/content/180/2/977.abstract	http://cmpg.unibe.ch/software/BayeScan/
GENABEL	Genome wide association analysis	http://www.ncbi.nlm.nih.gov/pubmed/17384015	http://www.genabel.org
ML-RELATE	Maximum likelihood estimates of relatedness	http://onlinelibrary.wiley.com/doi/10.1111/j.1471-8286.2006.01256.x/abstract	http://www.montana.edu/kalinowski/Software/MLRelate.htm
RELATED	Estimates relatedness from codominant data using 7 methods	http://www.ncbi.nlm.nih.gov/pubmed/25186958	https://frasierlab.wordpress.com/software/
COLONY	Estimates sibship and parentage from multilocus genotype data	http://onlinelibrary.wiley.com/doi/10.1111/j.1755-0998.2009.02787.x/abstract	https://www.zsl.org/science/software/colony
MASTERBAYES	Uses MCMC methods to estimate pedigrees from genotype & phenotype data	http://onlinelibrary.wiley.com/doi/10.1111/j.1365-294X.2006.03050.x/full	https://cran.r-project.org/web/packages/MasterBayes/index.html

Software	**Description**	**Publication**	**Webpage**
TRIMMOMATIC	Trimming tool for Illumina NGS data	http://bioinformatics.oxfordjournals.org/content/early/2014/04/01/bioinformatics.btu170	http://www.usadellab.org/cms/?page=trimmomatic
FASTQC	Visualising quality stats from NGS data		http://www.bioinformatics.babraham.ac.uk/projects/fastqc/
FLASH	Align paired-end reads from NGS data	https://ccb.jhu.edu/software/FLASH/FLASH-reprint.pdf	https://ccb.jhu.edu/software/FLASH/
USEARCH	Searching & clustering algorithms for sequence data	http://www.ncbi.nlm.nih.gov/pubmed/20709691	http://drive5.com/usearch/
MOTHUR	Analysis of metabarcoding data, developed for 16S bacterial community analysis	http://aem.asm.org/content/75/23/7537.short	http://www.mothur.org
QIIME	Analysis of metabarcoding data, developed for microbial community analysis	http://www.nature.com/nmeth/journal/v7/n5/full/nmeth.f.303.html	http://qiime.org
BLAST	Comparing sequences against specific databases		https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastDocs&DOC_TYPE=Download
MEGAN	Visualise taxonomic make-up of metagenetic/metabarcoding sample data	http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1800929/	http://ab.inf.uni-tuebingen.de/software/megan5/
JMHC	Genotyping of MHC amplicon sequencing data	http://www.ncbi.nlm.nih.gov/pubmed/21676201	https://code.google.com/archive/p/jmhc/
BEAST	Inferring phylogenies using Bayesian analysis of molecular data	http://mbe.oxfordjournals.org/content/29/8/1969	http://beast.bio.ed.ac.uk
MRBAYES	Bayesian inference of phylogenetic & evolutionary models	http://bioinformatics.oxfordjournals.org/content/19/12/1572.short	http://mrbayes.sourceforge.net