PGDSpider version 2.1.1.5 (May 2018)

An automated data conversion tool for connecting population genetics and genomics programs

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Contents

1 Introduction

PGDSpider is a powerful automated data conversion tool for population genetic and genomics programs. It facilitates the data exchange possibilities between programs (Fig. 1) for a vast range of data types (e.g. DNA, RNA, NGS, microsatellite, SNP, RFLP, AFLP, multi-allelic data, allele frequency or genetic distances). Besides the conventional population genetics formats, PGDSpider integrates population genomics data formats commonly used to store and handle next-generation sequencing (NGS) data. Currently, PGDSpider is not meant to convert very large NGS files as it loads into memory the whole input file, whose size may exceed available RAM. However, since PGDSpider allows one to convert specific subsets of these NGS files into any other format, one could use this feature to calculate parameters or statistics for specific regions, and thus perform sliding window analysis over large genomic regions.

PGDSpider uses a newly developed PGD (Population Genetics Data) format as an intermediate step in the conversion process. PGD is a file format designed to store various kinds of population genetics data, including different data types (e.g. DNA sequences, microsatellites, AFLP or SNPs) and ploidy levels. PGD is based on the XML format and is therefore independent of any particular computer system and extensible for future needs. PGDSpider uses PGD to connect population genetics and genomics programs like a spider knits a web.

PGDSpider is written in Java and is therefore platform independent. It is user friendly due to its intuitive graphical user interface. PGDSpider allows the user to store his preferred conversion settings for repeated conversions of similar input formats. A command line version of PGDSpider is also provided, making it possible to embed PGDSpider in data analysis pipelines.

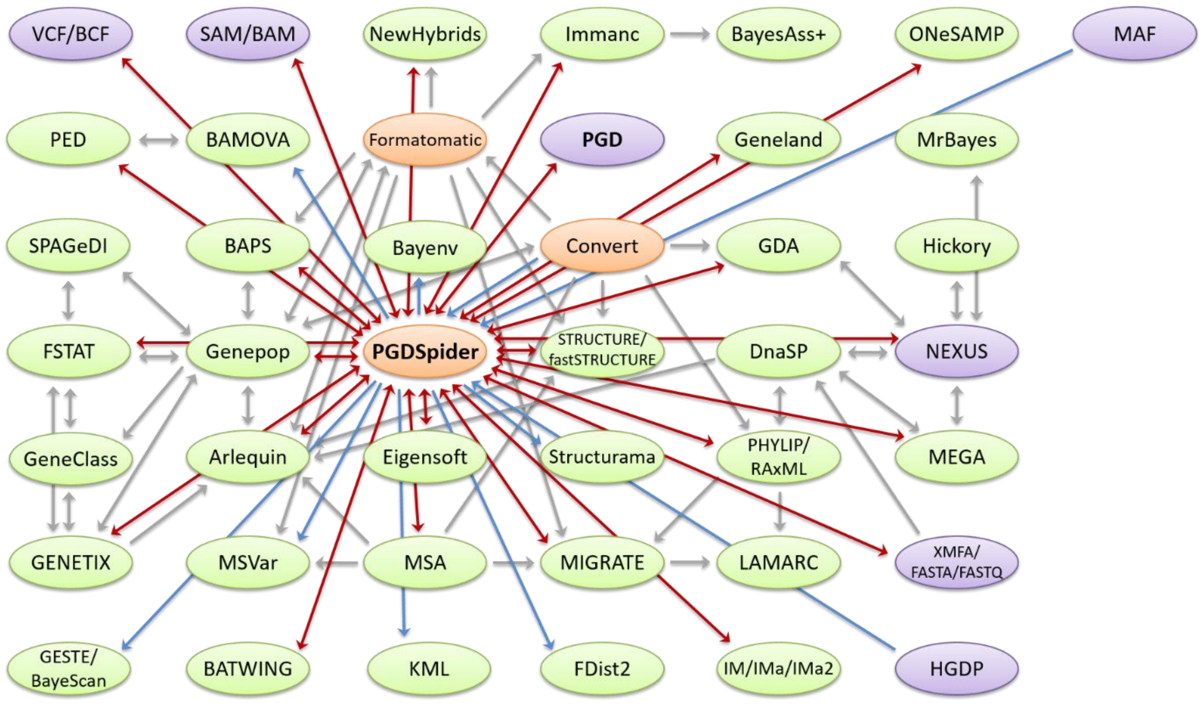


Fig. 1: Connectivity between population genetics programs and format. Red (reading and writing) and blue (reading or writing) arrows indicate direct connections between PGDSpider and other programs. Grey arrows show connections between the programs themselves that are not mediated by PGDSpider. Blue ellipses represent multi-purpose generalist packages and violet ellipses show individual-centred programs. Conversion programs are shown in orange, specialized programs in green and general data formats in red.

2 Formats supported by PGDSpider

PGDSpider is able to parse 33 and to write 36 different file formats:

Data format	Version	References and Links	Input format	Output format
PGD	1.1 (15.02.2016)		x	x
Arlequin	3.5.2 (12.4.2015)	http://cmpg.unibe.ch/software/arlequin35/, http://cmpg.unibe.ch/software/arlequin35/man/arlequin35.pdf, (Excoffier and Lischer, 2010)	x	x
BAM	(17.4.2011)	http://samtools.sourceforge.net, http://samtools.sourceforge.net/SAM1.pdf, (Li, et al., 2009)	x	x
BAMOVA	1.02 (27.9.2011)	http://www.uwyo.edu/buerkle/software/bamova/, (Gompert and Buerkle, 2011; Gompert, et al., 2010)		x
BAPS	6.0 (17.12. 2012)	http://www.helsinki.fi/bsg/software/BAPS/, http://www.helsinki.fi/bsg/software/BAPS/macSnow/BAPS6manual.pdf, (Tang, et al., 2009)	x	x
BATWING	(2003)	http://www.mas.ncl.ac.uk/~nijw/, http://www.mas.ncl.ac.uk/~nijw/batwing/batguide.pdf, (Wilson, et al., 2003)	x	x
Bayenv	2.0 (20.11.2013)	http://gcbias.org/bayenv/ (Coop, et al., 2010; Gunther and Coop, 2013)		x
BCF	(14.5.2011)	http://samtools.sourceforge.net/mpileup.shtml	x	x
CONVERT	1.31 (March 2005)	http://www.agriculture.purdue.edu/fnr/html/faculty/Rhodes/Students%20and%20Staff/glaubitz/software.htm, (Glaubitz, 2004)	x	
EIGENSOFT	5.0.2 (April 2014)	http://www.hsph.harvard.edu/alkes-price/software/ (Patterson, et al., 2006; Price, et al., 2006)	x	x
Extended multi-FASTA (XMFA)		http://www.stats.ox.ac.uk/~didelot/files/xmfa2struct.pdf http://darlinglab.org/mauve/user-guide/files.html	x	x
FASTA		http://en.wikipedia.org/wiki/FASTA_format, http://www.ncbi.nlm.nih.gov/blast/fasta.shtml (Pearson, 1990)	x	x
FASTQ		http://en.wikipedia.org/wiki/FASTQ_format, (Cock, et al., 2010)	x	x
FDist2 (datacal)		http://www.rubic.rdg.ac.uk/~mab/software.html, (Beaumont and Nichols, 1996; Flint, et al., 1999)		x

FSTAT	2.9.3.2 (February 2002)	http://www2.unil.ch/popgen/softwares/fstat.htm, (Goudet, 2001)	x	x
GDA	1.1 (7.1.2002)	http://hydrodictyon.eeb.uconn.edu/people/plewis/software.php, (Lewis, 2001)	x	x
GENELAND	12.4.2011	http://www2.imm.dtu.dk/~gigu/Geneland/ http://www2.imm.dtu.dk/~gigu/Geneland/Geneland-Doc.pdf (Guillot, 2008; Guillot, et al., 2005; Guillot, et al., 2005; Guillot and Santos, 2009; Guillot and Santos, 2010; Guillot, et al., 2008)	x	x
GENEPOP	4.1 (24.3.2011)	http://kimura.univ-montp2.fr/~rousset/Genepop.htm, http://kimura.univ-montp2.fr/~rousset/Genepop.pdf, http://genepop.curtin.edu.au/help_input.html, (Rousset, 2008)	x	x
GENETIX	4.05 (5.5.2004)	http://www.genetix.univ-montp2.fr/genetix/genetix.htm, (Belkhir, 1996-2004)	x	x
GESTE/ BayeScan	GESTE: 2.0/ BayeScan 2.01 (December 2010)	http://www-leca.ujf-grenoble.fr/logiciels.htm http://cmpg.unibe.ch/software/bayescan/index.html GESTE: (Foll and Gaggiotti, 2006) BayeScan: (Fischer, et al., 2011; Foll, et al., 2010; Foll and Gaggiotti, 2008)		x
HGDP	Stanford	http://www.hagsc.org/hgdp/files.html	x	
HGDP-CEPH (Arlequin + log file)	3.0	http://www.cephb.fr/en/hgdp/	x	
Immanc (BayesAss)	5.0 (8.10.1998)	http://www.rannala.org/?page_id=13, http://www.rannala.org/docs/immanc.html, (Rannala and Mountain, 1997) (Wilson and Rannala, 2003)	x	x
IM (IMa)	Updated 17.12.2009	http://genfaculty.rutgers.edu/hey/software, http://lifesci.rutgers.edu/~heylab/ProgramsandData/Programs/IM/Introduction_to_IM_and_IMa_3_5_2007.pdf, (Hey and Nielsen, 2004; Nielsen and Wakeley, 2001), (Hey and Nielsen, 2007)	x	x
IMa2	Updated 26.08.2011	http://genfaculty.rutgers.edu/hey/software#IMa2, http://lifesci.rutgers.edu/~heylab/ProgramsandData/Programs/IMa2/Using_IMa2_8_24_2011.pdf, (Hey, 2010; Hey, 2010)	x	x
KML	2.2	http://code.google.com/intl/de-CH/apis/kml/documentation/kml_tut.html		x
MAF	1.0	https://genome.ucsc.edu/FAQ/FAQformat#format5	x	
MEGA	5 (26.4.2011)	http://www.megasoftware.net/, http://www.megasoftware.net/manual.pdf, (Tamura, et al., 2011)	x	x
MIGRATE	3.2.6	http://popgen.sc.fsu.edu/Migrate/Migrate-n.html,	x	x

	(13.10.2010)	http://popgen.sc.fsu.edu/migratedoc.pdf, (Beerli, 2009)		
MSA	4.05	http://i122server.vu-wien.ac.at/MSA/info.html/MSA_info.html, (Dieringer and Schlotterer, 2003)	x	x
MSVar	0.4.1.b (7.4.1999)	http://www.rubic.rdg.ac.uk/~mab/software.html, (Beaumont, 1999)		x
NewHybrids	1.1 beta (7.4.2003)	http://ib.berkeley.edu/labs/slatkin/eriq/software/software.htm, http://ib.berkeley.edu/labs/slatkin/eriq/software/new_hybs_doc1_1Beta3.pdf (Anderson and Thompson, 2002)	x	x
NEXUS		(Maddison, et al., 1997) → able to read CharSet definitions within a MrBayes block	x	x
ONeSAMP	1.2	http://genomics.jun.alaska.edu/asp/Default.aspx (Tallmon, et al., 2008)	x	x
PED		http://pngu.mgh.harvard.edu/~purcell/plink/data.shtml#ped (Purcell, et al., 2007)	x	x
PHYLIP (RAxML)	3.69 (September 2009)	http://evolution.genetics.washington.edu/phylip/doc/main.html, (Felsenstein, 1989; Felsenstein, 2004)	x	x
SAM	1.4 (17.4.2011)	http://samtools.sourceforge.net, http://samtools.sourceforge.net/SAM1.pdf, (Li, et al., 2009)	x	x
Structurama		http://cteg.berkeley.edu/~structurama/index.html (Huelsenbeck, et al., 2011)		x
STRUCTURE (fastSTRUCTURE)	STRUCTURE 2.3.4 (July 2012)	http://pritchardlab.stanford.edu/structure.html, http://pritchardlab.stanford.edu/structure_software/release_versions/v2.3.4/structure_doc.pdf, http://rajanil.github.io/fastStructure/ STRUCTURE: (Falush, et al., 2003; Falush, et al., 2007; Hubisz, et al., 2009; Pritchard, et al., 2000), fastSTRUCTURE: (Raj, et al., 2014)	x	x
VCF	4.1 (2.8.2012)	http://www.1000genomes.org/wiki/Analysis/Variant%20Call%20Format/vcf-variant-call-format-version-41 → without structural variants (only SNP and INDELs)	x	x

Tab. 1: Data formats supported by PGDSpider including the version number, references and links to webpages and format descriptions, and if the format is supported as input and/or output format.
Note that, PGDSpider is currently not meant to convert large NGS files as it loads into memory the whole input file, which may lead to memory issues. However, PGDSpider allows one to convert specific subsets of these NGS files into any other format, and this approach can be used to perform sliding windows analyses on large NGS files.

3 How to cite PGDSpider and License

Lischer HEL and Excoffier L (2012) PGDSpider: An automated data conversion tool for connecting population genetics and genomics programs. *Bioinformatics* 28: 298-299.

4 System requirements

PGDSpider is written in Java and therefore platform independent, but SUN Java 1.7 RE (or a newer version. At the moment it will not run under Java 9!) has to be installed. Java7 RE can be downloaded under following link: http://www.oracle.com/technetwork/java/javase/downloads/index.html

5 Installing PGDSpider

All necessary links and an installation instruction are also available on http://cmpg.unibe.ch/software/PGDSpider/ or in the readme file.

5.1 Installation Instructions

1st step:

Install the Java7 RE (or a newer version. At the moment it will not run under Java 9!)

- Windows:
  download and install Java7 RE with following link:
  http://www.oracle.com/technetwork/java/javase/downloads/index.html

- Linux:
  - Ubuntu / Debian:
    Execute the following command as root user:
    `"apt-get install openjdk-7-jre"`

  - Other Linux distributions:
    http://www.oracle.com/technetwork/java/javase/downloads/index.html

- Mac:
  Apple Computer supplies their own version of Java. Use the Software Update feature (available on the Apple menu) to check that you have the most up-to-date version of Java for your Mac. Additionally, make sure that Java version 1.7 is set as first preference version. This can be changed under "Applications - Utilities - Java Preferences.app".
  If you have problems with downloading, installing or using Java on Mac, please contact Apple Computer Technical Support.

2nd step:

Download the PGDSpider application from http://cmpg.unibe.ch/software/PGDSpider/ and unzip it on the local drive.

- Execute PGDSpider GUI:
  - Windows: execute the file "`PGDSpider2.exe`" to start the program.
  - Linux: execute the command "`./PGDSpider2.sh`" to start the program.
  - Mac and others: execute the command "`java -Xmx1024m -Xms512m -jar PGDSpider2.jar`" to start the program.
- Execute PGDSpider-cli (command line)
  - Windows: execute the command "`PGDSpider2-cli.exe`"
  - Linux: execute the command "`java -Xmx1024m -Xms512M -jar PGDSpider2-cli.jar`"
  - Mac and others: execute the command "`java -Xmx1024m -Xms512M -jar PGDSpider2-cli.jar`"

5.2 Java Web Start

Additionally we provide the possibility to download and run PGDSpider from the web by the Java Web Start software. Java Web Start provides an easy, one-click activation of PGDSpider and it guarantees that you are always running the latest version.

5.2.1 Launch PGDSpider

Java Web Start is included in the Java Runtime Environment. Have a look at the 1st step of the 5.1 Installation Instructions to get information on how to get Java7 RE (or a newer version).

Launch PGDSpider using Java Web Start from

- Browser:
  Click on the PGDSpider icon on the web page: PGDSpider Web Start
- Java Cache Viewer:
  To launch the PGDSpider Web Start a second time, you do not need to return to the web

page where you first launched it; instead you can launch it from the Java Cache Viewer. To open the Java Cache Viewer execute following command in the console: `javaws -viewer`
To run PGDSpider Web Start, select it and click the Run button or double click the PGDSpider application.

- Desktop:
  You can add a desktop shortcut to the PGDSpider Web Start application. Select the application in the Java Cache Viewer (see above how to open it), then right-click and select "Install Shortcuts" or click the Install button. A shortcut is added to the desktop and you can launch the PGDSpider Web Start application just as you would launch any native application.

5.2.2 Limitations

Starting PGDSpider from Java Web Start it is not possible to change the amount of memory PGDSpider is allowed to use (by default it is set to 1 GB). If you need to change the amount of memory (e.g.: if you have large files to convert), download the PGDSpider application as described in the 2nd step of the 5.1 Installation Instructions.

6 Execute PGDSpider GUI

The graphical user interface of the PGDSpider program is available in four different languages (English, French, German and Italian) and looks like:

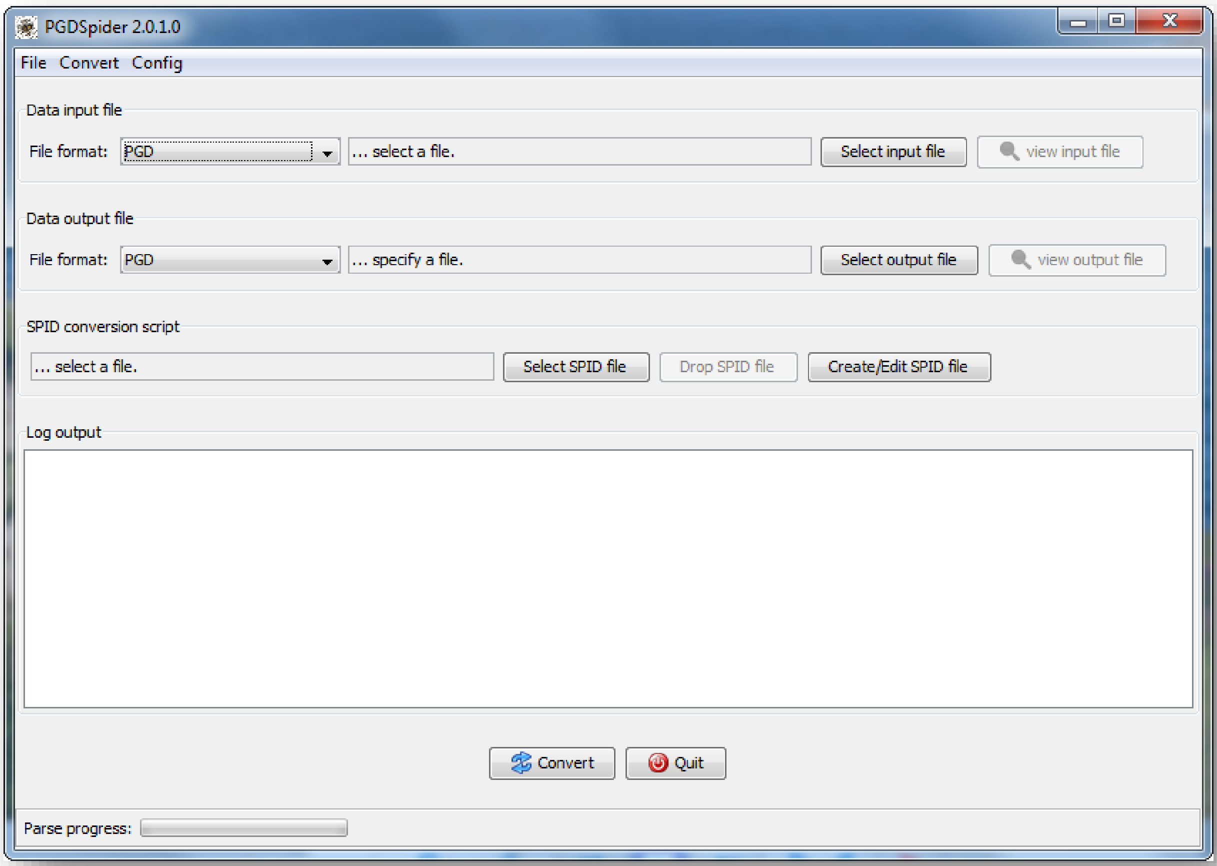


Fig. 2: Screenshot of the English version of the graphical user interface of PGDSpider

Execute PGDSpider GUI:

- Windows: execute the file "`PGDSpider2.exe`" to start the program.
- Linux: execute the command "`./PGDSpider2.sh`" to start the program.
- Mac and others: execute the command
  "`java -Xmx1024m -Xms512M -jar PGDSpider2.jar`"
  to start the program.

6.1 Increase memory

To increase the memory PGDSpider is allowed to use start the program by executing the command "`java -Xmx1024m -Xms512M -jar PGDSpider2.jar`" and adapt the `-Xmx` parameter to your needs (`-Xmx1024m` means: maximum memory of 1’024 MB).

6.2 How to use the PGDSpider GUI

- Select the input file format to be translated:
  First the format of the input file has to be selected. Use the putt down menu (to the left of the text “File format” in the Input File area) to select the input file format.

- Select the input file:
  Click on the button “Select input file” and choose the file to be translated with the specified file format. Note that PGDSpider does not check if the selected file is of the right format.

- View the input file:
  To have a look at the selected input file click on the “view file” button in the Input File area

- Select the output format:
  Choose the desired file format of the output file. To do this select the output file format in the drop down menu to the left of the text “File format” in the Output File area

- Select the output file:
  Click on the button “Select output file” and choose the place where the output file should be saved.

- Select a SPID file:
  Click on the button “Select SPID file” to select a SPID file which contains the answers for the Parser and the Writer Questions.

- Drop SPID file:
  Click on the button “Drop SPID file” to remove the selected SPID file.

- Create/Edit SPID file:
  Click on the button “Create/Edit SPID file” to open a window with the SPID editor to create or edit a SPID file.

- Convert file format:
  To convert the specified input file to the desired output format, press the “Convert” button. If no SPID file was selected a window appear with Parser and Writer questions (SPID editor). When the questions are answered, the user has the possibility to save the answers in a SPID file. Afterwards the answers are applied in the conversion process. A progress bar at the bottom of the graphical user interface shows the progress of the parsing action.
  After conversion, the user should control the output file (mistakes in the input file could lead to mistakes in the output file)!

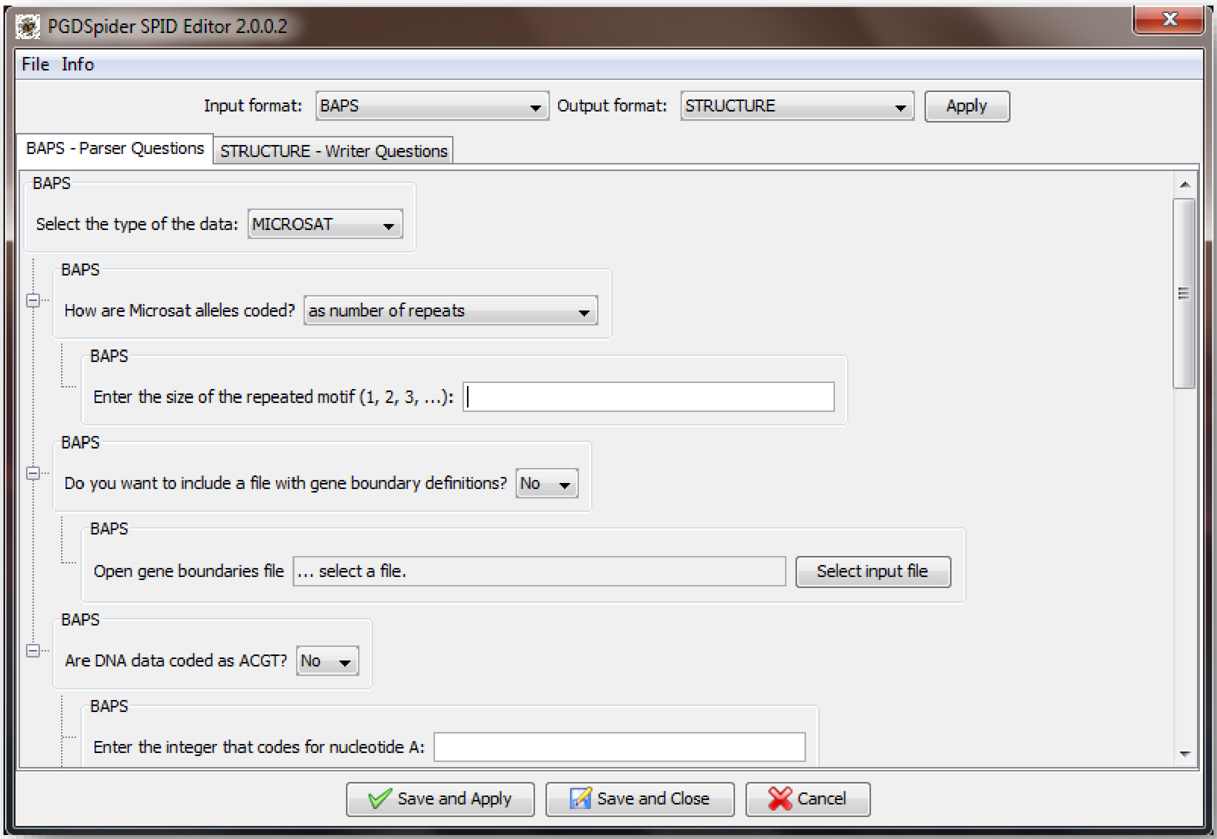
- View the output file:
  If conversion is over, one can have a look at the generated output file if the button “view file” in the Output File area is clicked.

- Create/Edit SPID file:
  Click in the "Convert Menu" on "Create/Edit SPID file" to create a new SPID file or to edit an existing one (selected SPID file in the GUI). A window is opened with the SPID editor, where the user can specify the input and output format and answer the corresponding questions. Afterwards the "SPID file" can be saved and applied (it is inserted in the "SPID conversion script" area in the PGDSpider GUI).

- Quit program:
  To quit the program push the "Quit" button or the red button with the cross in the top right edge of the window

6.3 SPID Editor

The SPID Editor is a tool to answer to the Writer and Parser questions. It also allows one to save these answers in a SPID file, which can then be reused to convert other files with the same format (use the same answers). The SPID Editor can be opened by clicking in the PGDSpider "Convert" menu on "Create/Edit SPID file".



Input format: BAPS
Output format: STRUCTURE

BAPS
Select the type of the data: MICROSAT

BAPS
How are Microsat alleles coded? as number of repeats

BAPS
Enter the size of the repeated motif (1, 2, 3, ...):

BAPS
Do you want to include a file with gene boundary definitions? No

BAPS
Open gene boundaries file ... select a file.

BAPS
Are DNA data coded as ACGT? No

BAPS
Enter the integer that codes for nucleotide A:

Fig. 3: Screenshot of the SPID Editor

6.3.1 How to use the SPID Editor

- Select/ change input format:
  Use the put down menu to the right of the text "Input format to select or change the input format. Afterwards press the "Apply" button to apply the input format (Parser questions will change).

- Select/ change output format:
  Use the put down menu to the right of the text "Output format to select or change the output format. Afterwards press the "Apply" button to apply the output format (Writer questions will change).

- Answer Parser Questions:
  Click on the "Parser Question" tab. Afterwards the Parser questions appearing below the tab can be answered. Some of the questions do not need to be answered in every situation, as they are questions of special cases (all possible questions are listed). For more details have a look at the corresponding data format description part.

- Answer Writer Questions:
  Click on the "Writer Question" tab. Afterwards the Writer questions appearing below the tab can be answered. Some of the questions do not need to be answered in every situation, as they are questions of special cases (all possible questions are listed). For more details have a look at the corresponding data format description part.

- Save and Apply:
  Click on the "Save and Apply" button to save the answers in a SPID file and to apply the answers in the actual conversion process.

- Save and Close:
  Click on the "Save and Apply" button to save the answers in a SPID file and to close the SPID Editor.

- Cancel:
  Click on the "Cancel" button to close the SPID Editor without saving.

6.3.2 SPID file

The SPID file contains the Parser and Writer format and the answers to the corresponding questions. Some of the questions do not need to be answered in every situation, as they are questions of special cases (all possible questions are listed). For more details have a look at the corresponding data format description part. The SPID file is a plain text file encoded with UTF_8 and the ".spid" file extension.

6.4 Menus

6.4.1 PGDSpider

File Menu:

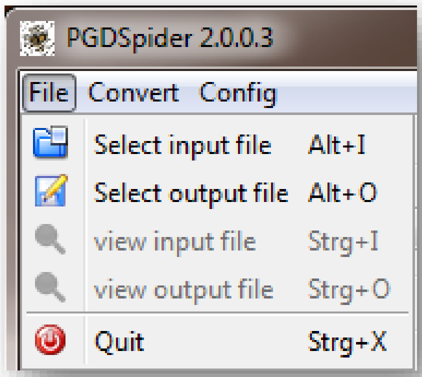


Fig. 4: Screenshot of the file menu

- Select input file: Opens a dialog box to select an input file.
- Select output file: Opens a dialog box to select the place where the output file should be saved.
- View input file: Opens a window with the input file.
- View output file: Opens a window with the output file.
- Quit: Quit the PGDSpider program

Convert Menu:

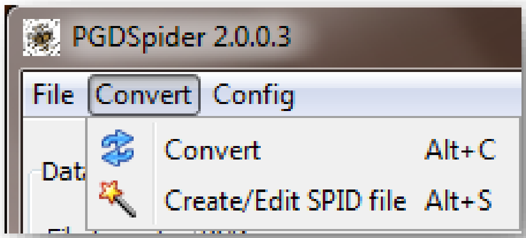


Fig. 5: Screenshot of the convert menu

- Convert: convert the specified input file into the chosen output file format and saves it.
- Create/Edit SPID file: opens a window with the SPID editor to create or edit a SPID file.

Config Menu:

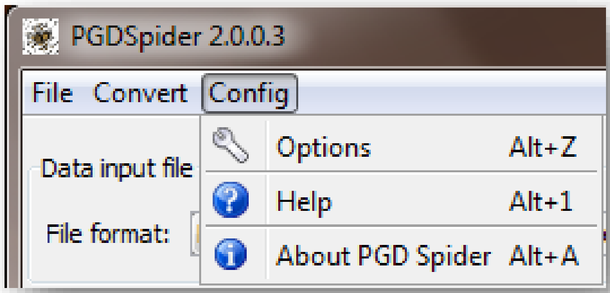
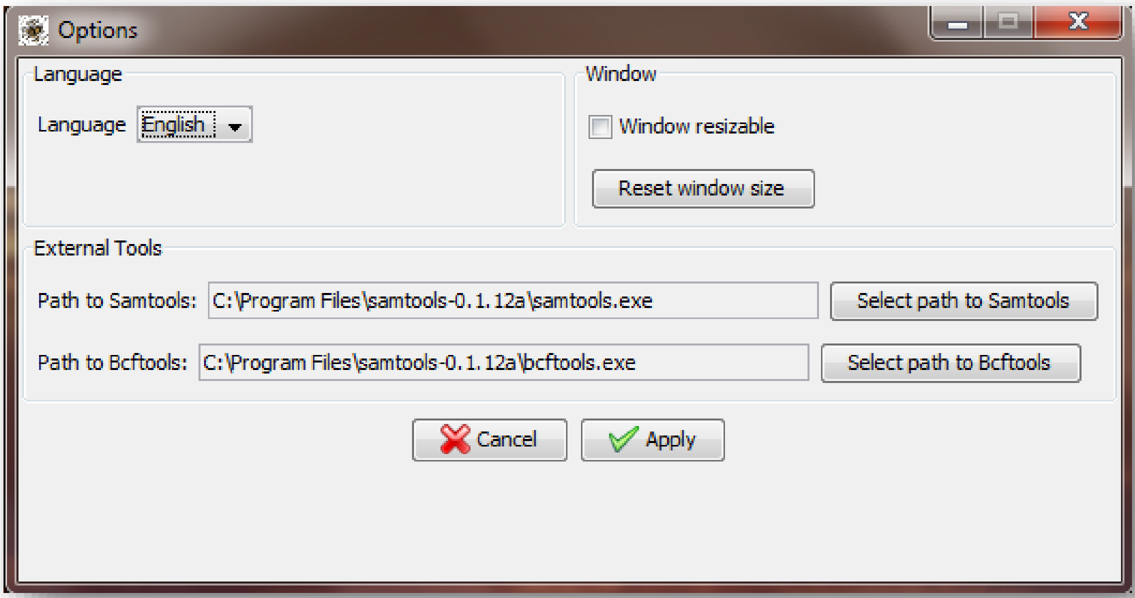


Fig. 6: Screenshot of the config menu

- Options: opens a window with option settings:



Language: English
☐ Window resizable
Path to Samtools: C:\Program Files\samtools-0.1.12a\samtools.exe
Path to Bcftools: C:\Program Files\samtools-0.1.12a\bcftools.exe

Fig. 7: Screenshot of the option window

- Language option:
  In the drop down menu one can select the language of the graphical user interface and the menus. One can choose between four languages: English, French, German and Italian.

- Window option:
  If "Window resizable" box is checked, the PGDSpider window can be resized. In order to reset the window size to the default, press the "Reset window size" button.

- External Tools:
  - Select Path to Samtools:
    Click on the button "Select path to Samtools" and give the path to the samtools.exe program (The Samtools distribution can be downloaded from http://samtools.sourceforge.net). Samtools (version 0.1.12/0.1.06) is needed in the conversion process of the formats SAM, BAM, VCF and BCF.
  - Select Path to Bcftools:
    Click on the button "Select path to Bcftools" and give the path to the bcftools.exe program (The Samtools distribution can be downloaded from http://samtools.sourceforge.net). Bcftools is needed in the conversion process of the formats SAM, BAM, VCF and BCF.

- Cancel/ Apply button:
  Apply or cancel the changed options

- Help: opens a window with a help file
- About PGD Spider: opens a window with short information about the PGDSpider program

6.4.2 SPID Editor

File Menu:

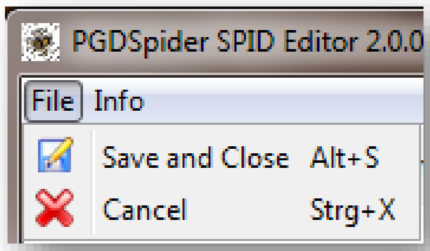


Fig. 8: Screenshot of the file menu in the SPID Editor

- Save and Close: Saves the SPID file and close the SPID Editor.
- Cancel: Cancel the SPID editor without saving.

Info Menu:

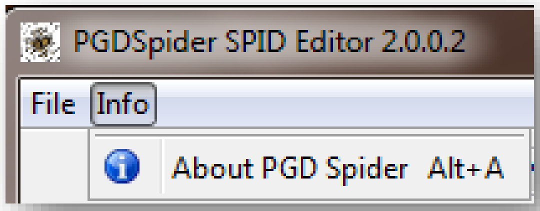


Fig. 9: Screenshot of the info menu in the SPID Editor

- About PGD Spider:
  Opens a window with short information about the PGDSpider program

6.5 Shortcuts

6.5.1 PGDSpider

Menu – Shortcuts:

Shortcut	Action
Alt + F	Open 'File' menu.
Alt + V	Open 'Convert' menu.
Alt + N	Open 'Config' menu.

Tab. 2: Menu shortcuts

Shortcut	Action

File menu – Shortcuts:

Alt + I	Select an existing input file.
Alt + O	Select an output file.
Ctrl + I	View the input file
Ctrl + O	View the output file
Ctrl + X	Quit PGDSpider application.

Tab. 3: File menu shortcuts

Convert menu – Shortcuts:

Shortcut	Action
Alt + C	Convert selected input file.
Alt + S	Create or edit the SPID file.

Tab. 4: Convert menu shortcut

Config menu – Shortcuts:

Shortcut	Action
Alt + Z	Show PGDSpider options panel.
Alt + 1	Show PGDSpider help.
Alt + A	Show some information about PGDSpider.

Tab. 5: Config menu shortcuts

6.5.2 SPID Editor

Menu – Shortcuts:

Shortcut	Action
Alt + F	Open 'File' menu.
Alt + I	Open 'Info' menu.

Tab. 6: Menu shortcuts

File menu – Shortcuts:

Shortcut	Action
Alt + S	Save and Close SPID editor.
Ctrl + X	Cancel SPID editor.

Tab. 7: File menu shortcuts

Info menu – Shortcuts:

Shortcut	Action
Alt + A	Show some information about PGDSpider.

Tab. 8: Info menu shortcuts

6.6 Log Output

The "Log Output" is an area of the graphical user interface which is used to print program messages for the user. These messages consist of 3 types:

- INFO:
  These are normal program messages with the actions the user performed (e.g.: "Opening input file", "convert...", etc.)
- WARN (yellow marked):
  Warning messages are written if something is missing or small error occurs but the program is able to deal with it.
- ERROR (red marked):
  If a severe error occurs during the parsing or writing of a file, the program stops and an error message is written (none or an incomplete output file is written).

7 Execute PGDSpider-cli

Execute PGDSpider-cli (command line)

- Windows: execute the command "`PGDSpider2-cli.exe`"
- Linux: execute the command
  "`java -Xmx1024m -Xms512m -jar PGDSpider2-cli.jar`"
- Mac and others: execute the command
  "`java -Xmx1024m -Xms512m -jar PGDSpider2-cli.jar`"

Increase memory:
To increase the memory PGDSpider is allowed to use start the program by executing the command "`java -Xmx1024m -Xms512M -jar PGDSpider2-cli.jar`" and adapt the `–Xmx` parameter to your needs (`–Xmx1024m` means: maximum memory of 1'024 MB).

Specify samtools/bcftools path:
The path to the samtools/bcftools program can be specified in the "spider.conf.xml" file within the PGDSpider distribution (the file will be automatically generated the first time you run PGDSpider). The samtools distribution can be downloaded from http://samtools.sourceforge.net. Samtools (version 0.1.12/0.1.06)/bcftools are needed in the conversion process of the formats SAM, BAM, VCF and BCF.

The command line version of the PGDSpider program can be executed with the following options (the order does not matter):

- **-? or -h:**
  To show a help text with the different options

- **-inputfile <file>** (mandatory):
  Specify the input file for the conversion process.

- -**inputformat <format>:**
  - Specify the format of the input file. This option is mandatory if the input format is not defined in the answer (SPID) file.
  - Possible input formats are:
    PGD, ARLEQUIN, BAM, BAPS, BATWING, BCF, CONVERT, EIGENSOFT, FASTA, FASTQ, FSTAT, GDA, GENELAND, GENEPOP, GENETIX, HGDP, HGDP_CEPH, IMMANC, IM, IMA2, MAF, MEGA, MIGRATE, MSA, NEWHYBRIDS, NEXUS, ONESAMP, PED, PHYLIP, SAM, STRUCTURE, VCF, XMFA

- **-outputfile <file>** (mandatory):
  Specify the output file for the conversion process.

- **-outputformat <format>:**
  - Specify the format of the output file. This option is mandatory if the output format is not defined in the answer (SPID) file.
  - Possible output formats are:
    PGD, ARLEQUIN, BAM, BAMOVA , BAPS, BATWING, BAYENV, BCF, EIGENSOFT, FASTA, FASTQ, FDIST2, FSTAT, GDA, GENELAND, GENEPOP, GENETIX,GESTE_BAYE_SCAN,

IMMANC, IM, IMA2, KML, MEGA, MIGRATE, MSA, MSVAR, NEWHYBRIDS, NEXUS, ONESAMP, PED, PHYLIP, SAM, STRUCTURAMA, STRUCTURE, VCF, XMFA

- **-spid <file>** (mandatory):
  Specify the SPID file containing the pre-answered conversion questions. The SPID file can be generated with the help of the SPID Editor (see Section 6.2 SPID Editor) integrated in the PGDSpider GUI. Alternatively, a template SPID file is automatically generated if no SPID file is provided. This template SPID file can be used to answer the required conversion questions. Some of the questions do not need to be answered in every situation, as they are questions of special cases (all possible questions are listed). For more details have a look at the corresponding data format description part.

7.1 Examples

- call help:
  `PGDSpider_cli -?` or `PGDSpider_cli -h`

- convert a STRUCTURE file to an Arlequin file:
```
PGDSpider2-cli -inputfile examples\example_Structure.txt
-inputformat STRUCTURE -outputfile examples\output_Arlequin.arp
-outputformat ARLEQUIN -spid examples\Structure_Arlequin.spid
```

- Execute the jar file itself and convert a STRUCTURE file to an Arlequin file:
```
java -Xmx1024m -Xms512m -jar PGDSpider2-cli.jar -inputfile
examples\example_Structure.txt -inputformat STRUCTURE
-outputfile examples\output_Arlequin.arp -outputformat ARLEQUIN
-spid examples\Structure_Arlequin.spid
```

8 Conversion examples

The PGDSpider distribution contains following simple example files (in the “examples” folder) to do some trial format conversion with PGDSpider:

- “example_Arlequin.arp”:
  - Data: DNA, haploid
  - Convert to:
    BAM, BAPS, BCF, FASTA, FDist2, GENELAND, MEGA, MIGRATE, NEXUS, PGD, PHYLIP, SAM, VCF

- “example_Genepop.txt”:
  - Data: Microsat, diploid
  - Convert to:
    Arlequin, BAPS, BATWING, FDist2, FSTAT, GDA, GENELAND, GENETIX, GESTE/BayeScan, Immanc, IM/IMa, MIGRATE, MSA, NewHybrids, MSVar, PGD, STRUCTURE

- “example_MEGA.meg”:
  - Data: DNA, haploid
  - Convert to:
    Arlequin, BAM, BAPS, BCF, FASTA, FDist2, GENELAND, MIGRATE, NEXUS, PGD, PHYLIP, SAM, VCF

- “example_PGD.xml” (can be displayed in a nice way with any browser by using the stylesheet_PGD.xsl):
  - Data: standard (multi-allelic), diploid, with distance matrix
  - Convert to:
    Arlequin, BAPS, FDist2, FSTAT, GDA, GENELAND, GENEPOP, GENETIX, GESTE/BayeScan, Immanc, MIGRATE , NewHybrids

- “example_SAM.sam” and its reference file “example_SAM_references.fasta”:
  - Data: NGS, diploid
  - Convert to:
    Arlequin, BAM, BAPS, BCF, FASTA, FASTQ, FDist2, GENELAND, MEGA, MIGRATE, NEXUS, PGD, PHYLIP, SAM, VCF

- “example_Structure.txt”:
  - Data: Microsat (as number of repeats), diploid (on two consecutive rows), “Phase Information” row is not present, Missing value code = -9, “Locus names” are present, “individual labels” are present, “PopData” column is present, “Recessive Alleles/Inter-Marker Distance” rows are not present.

- Convert to:
  Arlequin, BAPS, BATWING, FDist2, FSTAT, GDA, GENELAND, GENEPOP, GENETIX, GESTE/BayeScan, Immanc, IM/IMa, MIGRATE, MSA, NewHybrids, MSVar, PGD
- The spid file “Structure_Arlequin.spid” can be used for the conversion to the Arlequin format.

9 Reporting bugs and comments

If there are any bugs, send me an e-mail. Please give me a short description of the bug and tell me the input and output file format. If it is possible also attach the input file which caused the problem.

PGDSpider is an on-going project. For any comments or suggestions of further file formats, please send me an e-mail.

e-mail address: heidi.lischer@iee.unibe.ch

10 File format descriptions and PGDSpider questions

In the next sections, a short description of every supported file format is provided. The table below shows the file extensions and handled data types of the different file formats:

		handled data types									
format	**File extension**	**NGS**	**DNA**	**RNA**	**Microsat**	**SNP**	**RFLP**	**AFLP**	**Standard**	**Frequency**	**distance**
Arlequin	.arp		x		x	x	x	x	x	x	
BAM	.bam	x	x	x							
BAMOVA	.txt	x	x	x	x	x	x	x	x		
BAPS	.txt		x		x	x		x	x		
BATWING	.txt				x	x					
Bayenv	.txt					x					
BCF	.bcf	x	x	x		x					
CONVERT	.txt				x	x	x	x	x		
EIGENSOFT	.geno, .ind, .snp, .txt					x					
Extended multi-FASTA (XMFA)	.xmfa	x	x	x							
FASTA	no standard, .fa, .mpfa, .fna, .fsa, .fas, .fasta, .txt	x	x	x		x					
FASTQ	no standard, .fastq, .fq, .txt	x									
FDist2 (datacal)	no standard		x	x	x	x	x	x	x		
FSTAT	.dat				x	x		x	x		
GDA	.nex				x	x	x	x	x		
GENELAND	.txt		x		x	x		x	x		
GENEPOP	.txt				x	x		x	x		
GENETIX	.gtx				x	x	x	x	x		
GESTE / BayeScan	no standard				x	x		x	x		
HGDP	.txt					x					
HGDP-CEPH	.arp		(x)		(x)	x	(x)		(x)	(x)	
Immanc	.inp or .txt				x	x	x	x	x		
IM/IMa/IMa2	.u or .txt		x		x						
KML	.kml										
MAF	.maf or .txt		x	x							
MEGA	.meg		x	x							x
MIGRATE	no standard, .txt		x		x	x		x	x		
MSA	.dat, .txt				x						
NewHybrids	.dat, .txt				x	x		x	x		
MSVar	no standard				x						
NEXUS	.nex		x	x	x	x	x	x	x		
ONeSAMP	.txt				x						

PED	.ped					x					
PGD	.xml	x	x	x	x	x	x	x	x	x	x
PHYLIP	.txt		x	x							x
SAM	.sam	x	x	x							
Structurama	.nex	x	x	x	x	x	x	x	x		
STRUCTURE	no standard				x	x	x	x	x		
fastSTRUCTURE	no standard					x					
VCF	.vcf	x	x	x		x					

Tab. 9: Table of the different file formats and their handled data types and file extensions

10.1 PGD

PGD version 1.1 (15.02.2016)

PGD (Population Genetics Data) is a file format designed to contain population genetics data. The aim of this format is to facilitate the transfer among several population genetics software packages. PGD plays an important role in the new data format converter PGDSpider.

PGD is written in XML and is therefore independent of any particular computer system and extensible for future needs (W3Schools, 2008). The XML structure can easily be processed by computer programs. An additional XSLT style sheet makes it possible to display the data in an understandable and comprehensive way. This XSLT style sheet is delivered within the PGDSpider download (stylesheet_PGD.xsl).

The PGDSpider distribution also includes an XML Schema (PGD_schema.xsd), which defines the structure of the PGD file. The purpose of an XML Schema is to define the legal building blocks of an XML document and the allowable contents (W3Schools, 2008). The provided XML Schema can be used to validate a PGD file.

10.1.1 Data type handled

PGD is able to handle the following data types:

- DNA
- NGS (Next-Generation Sequencing data)
- Microsat (coded as number of repeats!)
- RFLP
- SNP
- AFLP
- Standard
- Frequency (Allele Frequency)
- etc.

10.1.2 PGD format

The PGD format is written in XML (eXtensible Markup Language) and can be created and edited in any text editor (file extension *.xml). An XML document has an ordered, labelled tree structure with following rules:

- An XML declaration needs to be included at the beginning of the file:
  `<?xml version="1.0" encoding="iso-8859-1"?>`
- If a style sheet exists, the name of an XSL style sheet reference must be mentioned with the absolute or relative file path to the style sheet after the declaration:
  `<?xml-stylesheet type="text/xsl" href="stylesheet_PGD.xsl"?>`
- A root element is needed. This element is "the parent" of all other elements and includes all other elements. In the PGD file format the root element is named: `<PGD>`

- All XML elements need to have a start and a closing tag and have to be properly nested
- XML tags are case sensitive
- Attribute values have to be within quotes
- The characters "<" and "&" are strictly illegal within text tags. They can be replaced with the expression "&lt;" (for "<") and "&amp;" (for "&").
- Comments have to be written within "<!--" and "-->":
  ```
  <!-- This is a comment -->
  ```

The PGD file format has a block structure and the information's are saved in a hierarchical way. Therefore the format is very modular and general information can be saved at a higher level than information specific for one individual. This is very convenient because general information's need to written only once.

A short description of the different blocks can be found below:

Root Element:

The root element named "PGD" encapsulates all other elements of the XML file.

Header block:

The header block contains the general information's about the data. The tag is named "header" and can contain an attribute named "title=" that defines the title of the data. The header block has the following sub tags:

- <organism> (optional):
  - Value: String
  - Indicates from which organism the data come from
- <numPop> (mandatory):
  - Value: Integer
  - gives the number of populations listed in the file
- <ploidy> (mandatory):
  - Value: "mixed" or any Integer
  - Specify the ploidy level of the data
  - It contains the value "mixed" if the ploidy level is not the same in every population or individual.
- <missing> (mandatory):
  - Value: Character
  - Character which codes missing values
- <gap> (optional):
  - Value: Character
  - Character which codes gaps

- <gameticPhase> (optional):
  - Value: “known” or “unknown”
  - Define if the gametic Phase of the genotypes is known or not
- <recessiveData> (optional):
  - Value: “no” or “yes”
  - Define if genotypic data present a recessive allele

DataDescription block:

The dataDescription block contains specifications about the different loci. The tag is named “dataDescription” and contains following sub tags:

- <numLoci> (mandatory):
  - Value: Integer
  - Gives the number of loci studied
- <dataType> (mandatory):
  - Value: “mixed”, “DNA”, “NGS”, “Microsat”, “RFLP”, “SNP”, “AFLP”, “Standard”, “Frequency” or etc.
  - Defines the data type of the data
  - It has the value “mixed” if the data contain different data types
- <locus> with attribute “id=” (optional):
  - Describes the different loci contained in the file
  - Could be repeated for multiple times (as many times as there are different loci)
  - The “id” attribute gives the name of the locus

The <locus> tag has following sub tags:

- <locusDataType> (optional):
  - Value: “DNA”, “NGS”, “Microsat”, “RFLP”, “SNP”, “AFLP”, “Standard”, “Frequency” or etc.
  - Only required if the <dataType> tag contains the value “mixed”
  - Defines the data type of the locus
- <locusChromosome> (optional):
  - Value: Integer, “X”, “Y”, “W”, “Z”, “mtDNA” or etc.
  - Gives the chromosome the locus come from
- <locusLocation> (optional):
  - Value: Integer
  - Gives the location/position on a chromosome the locus come from
- <locusGenic> (optional):
  - Value: “coding” or “noncoding”
  - Defines if the locus codes for a gene or not
- <locusLength> (optional):
  - Value: Integer

  - Gives the length of the locus in number of base pairs (for DNA)
- <locusAncestralState> (optional):
  - Value: String
  - Gives the ancestral state of the locus
- <locusLinks> (optional):
  - Value: String
  - Here one can specify internet links (URL) to locus information
- <locusComments> (optional):
  - Value: String
  - Here one can put comments about the locus

Population block:

The population block contains information about the population and their individuals with the data. This block could be repeated for multiple times (as many times as there are different populations in the sample). This block is structured differently if the data are aligned or not, and if the data are of the same data type or not. The tag is named “population” and can contain an attribute named “name=” which defines the name of the population. The population block has the following sub tags:

- <popSize> (mandatory):
  - Value: Integer
  - Defines the number of individuals in the population
- <popGeogCoord> (optional):
  - Value: longitude, latitude
  - Defines the geographic coordinate of the population
- <popLingGroup> (optional):
  - Value: String
  - Defines the linguistic group to which the population belongs
- <popPloidy> (optional):
  - Value: “mixed” or any Integer
  - Only required if the <ploidy> tag in the header block contains the value “mixed”
  - Specify the ploidy level of the data in this population
  - It contains the value “mixed” if the ploidy level is different between different individuals.
- <popLoci> (optional):
  - Value: String, String, ...
  - Only if all individuals in this population have the same loci
  - Defines the names of the loci in the data for this population, separated by comma
  - The loci have to be of the same type
- <ind> with attribute “name=” (mandatory):
  - Defines the different individuals in this population
  - Could be repeated for multiple times (as many as there are different individuals in this population)

  - The “name” attribute gives the name of the individual

The <ind> tag has following sub tags:

- <indGeogCoord> (optional):
  - Value: longitude, latitude
  - Defines the geographic coordination of the individual
- <indLingGroup> (optional):
  - Value: String
  - Defines the linguistic group which the individual belongs to
- <indLoci> (mandatory, if aligned data with different data types)
  - Value: String, String, ...
  - Only if the data are of different data types in this population
  - Defines the loci names of the data with the same data type in this individual separated by “,”
  - The loci must be of the same data type
- <indPloidy> (optional):
  - Value: Integer
  - Only required if the <popPloidy> tag in the population block contains the value “mixed”
  - Specify the ploidy level of the data in this individual
- <indFreq> (optional, but obligatory if “Frequency” data type)
  - Value: Integer
  - Defines the absolute frequency of this genotype in the population
- <data> (mandatory, if non-NGS data):
  - Value: locus data, locus data, ...
  - Can be repeated for multiple times (as many as there are different reads in this individual)
  - Contains the data of one read of each specified locus (same order as the locus names) separated by a comma
- <read> with attribute “id=” (mandatory, if NGS data (Next Generation Sequencing)):
  - Defines the different reads in this individual
  - Could be repeated for multiple times (as many as there are different reads in this individual)

The <read> tag has the following sub tags:

- <start> (mandatory):
  - Value: Integer
  - Defines the starting point of the sequence
- <length> (optional):
  - Value: Integer
  - Gives the length of the sequence
- <data> (mandatory):

  - Value: locus data
  - Contains the data of one read for the specified locus

- <quality> (optional):
  - Value: white space separated Integers
  - Contains the quality scores of the read

Structure block:

The structure block is optional. It contains the information about the genetic structure of the population (grouping). The tag is named “structure” and can contain an attribute named “name=” which defines the name of the structure. The structure block has following sub tags:

- <numGroups> (mandatory):
  - Value: Integer
  - Defines the number of groups of populations
- <group> with attribute “name=” (mandatory):
  - Value: String, String, ...
  - Defines which populations belong to this group. The population names are separated by a comma
  - Could be repeated for multiple times (as many as there are different groups)
  - The “name” attribute is the name of the group

DistanceMatrix block:

The distanceMatrix block is optional. It contains information about the genetic distances between haplotypes. The tag is named “distanceMatrix” and can contain an attribute named “name=” which defines the name of the distance matrix. The distanceMatrix block has following sub tags:

- <matrixSize> (mandatory):
  - Value: Integer
  - Defines the size of the distance matrix
- <matrixLabels> (mandatory):
  - Value: String, String, ...
  - Defines the labels of the distance matrix separated by a comma
- <matrix> (mandatory):
  - Value: Integer (line break) Integer, Integer (line break) ...
  - Gives the genetic distances of each specified individual to each other (same order as in the <matrixLabels> tag
  - Data have to be in the lower triangle with diagonals. Lines are separated by a line break and values by a comma

10.1.3 Schema of the PGD format

Specifications

• Root element:	<PGD>
• Header/loci block:	obligatory and only one per file
• Population block:	obligatory and can exist multiple times
• Structure/ distanceMatrix block:	optional and only one per file

- Microsat data must be coded as number of repeats
- Distance Matrix: lower triangle with diagonals

Block	sub tags			data type		
				Microsat, SNP, AFLP, RFLP, standard	DNA	Freq
header	organism			o	o	o
(attribute: title)	numPop			x	x	x
	ploidy * *(-> mixed / 1 / 2 /...)*			x (a 4)	x (a 4)	x
	missing			x	x	
	gap			o	o	
	gameticPhase *(->known/ unknown)*			o	o	
	recessiveData *(-> no / yes)*			o	o	
dataDescription	numLoci			x	x	
	dataType * *(-> mixed / DNA /NGS / Microsat / SNP / AFLP / RFLP/ Standard / Frequency /...)*			x (a 1)	x (a 1)	X
	locus (attribute: id)	locusDataType *(-> DNA / NGS / Microsat / SNP / AFLP / standard /...)*		a 1	a 1	
		locusChromosome *(->number/ X/ Y/ W/ Z/ mtDNA/ ...)*		o	o	
		locusLocation		o	o	
		locusGenic *(-> coding/ noncoding)*		o	o	
		locusLength		o	o	
		locusAncestralState		o	o	
		locusLinks *(->URL)*		o	o	
		locusComments		o	o	
population	popSize			x	x	x
(attribute: name)	popGeogCoord * *(lon, lat)*			o (a 2)	o (a 2)	o
	popLingGroup *			o (a 3)	o (a 3)	o
	popPloidy * *(-> mixed / 1 / 2 /...)*			a 4	a 4	
	popLoci *(locus name, locus name,...)* -> all locus of same data type			o	o	
	ind (attribute: name)	indGeogCoord *(lon, lat)*		o (a 2)	o (a 2)	
		indLingGroup		o (a 3)	o (a 3)	
		indLoci *(locus name, locus name,...) -> all locus of same data type*		o	o	
		indPloidy *(-> 1 / 2 /...)*		a 4	a 4	
		indFreq *(absolute Freq)*		o	o	x
		data *(locus data, locus data, ...)*		x	x	
		read (attribute: id)	**start**		x	
			length		o	
			data		x	
			quality		o	
structure (o)	numGroups			x	x	x
(attribute: name)	group (attribute: name) *(pop name, pop name, ...)*			x	x	x
distanceMatrix	matrixSize			x	x	x
(attribute: name)	matrixLabels *(name, name,...)*			x	x	x
(o)	matrix *(number (line break) number, number (line break)...)*			x	x	x

Tab. 10: Schema of the PGD file format

Legend:	**Non NGS data**	**NGS data**	x: obligatory
	same data type (loci) for all individuals (genotypes)		o: optional
	different data types (aligned within each locus)		a: alternative to
	* if all populations or individuals are identical for a given tag		

10.1.4 PGD file examples

- Data of two loci with Standard data type from two diploid populations:

```
<?xml version="1.0" encoding="iso-8859-1"?>
<?xml-stylesheet type="text/xsl" href="stylesheet_PGD.xsl"?>

<PGD xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:noNamespaceSchemaLocation="PGD_schema.xsd">
  <header title="Fake HLA data">
    <numPop> 2 </numPop>
    <ploidy> 2 </ploidy>
    <missing> ? </missing>
    <gap> - </gap>
    <gameticPhase> known </gameticPhase>
  </header>

  <dataDescription>
    <numLoci> 2 </numLoci>
    <dataType> Standard </dataType>
    <locus id="loci one">
      <locusChromosome> 3 </locusChromosome>
      <locusLocation> Hs8_23892 </locusLocation>
    </locus>
    <locus id="loci two">
      <locusChromosome> 3 </locusChromosome>
      <locusLocation> Hs8_23992 </locusLocation>
    </locus>
  </dataDescription>

  <population name="A sample of  Algerians">
    <popSize> 2 </popSize>
    <popLoci> loci one, loci two </popLoci>
    <ind name="1">
      <indGeogCoord> 35, 4 </indGeogCoord>
      <indLingGroup> African </indLingGroup>
      <data> 1104, 0200 </data>
      <data> 0700, 0301 </data>
    </ind>
    <ind name="3">
      <indGeogCoord> 36, 4 </indGeogCoord>
      <indLingGroup> Africanic </indLingGroup>
      <data> 0302, 0200 </data>
      <data> 1310, 0402 </data>
    </ind>
  </population>

  <population name="A sample of Bulgarians">
    <popSize>1</popSize>
    <popGeogCoord> 35, 4 </popGeogCoord>
    <popLingGroup> African </popLingGroup>
    <popLoci> loci one, loci two </popLoci>
    <ind name="2">
      <data> 1101, 0301 </data>
      <data> 0700, 0200 </data>
    </ind>
  </population>

  <structure name="My population structure">
    <numGroups> 2 </numGroups>
    <group> A sample of Algerians </group>
    <group> A sample of Bulgarians </group>
  </structure>

  <distanceMatrix name="Faked distance matrix">
    <matrixSize> 3 </matrixSize>
    <matrixLabels> 1, 2, 3</matrixLabels>
    <matrix> 0
             1, 0
             3, 4, 0
    </matrix>
  </distanceMatrix>
</PGD>
```

- Data of two loci with different data types (Standard and DNA) from two diploid populations:

```
<?xml version="1.0" encoding="iso-8859-1"?>
<?xml-stylesheet type="text/xsl" href="stylesheet_PGD.xsl"?>

<PGD xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:noNamespaceSchemaLocation="PGD_schema.xsd">
  <header title="Fake HLA data">
    <numPop> 2 </numPop>
    <ploidy> 1 </ploidy>
    <missing> ? </missing>
    <gap> - </gap>
    <gameticPhase> known </gameticPhase>
  </header>

  <dataDescription>
    <numLoci> 2 </numLoci>
    <dataType> mixed </dataType>
    <locus id="loci one">
      <locusDataType> Standard </locusDataType>
      <locusChromosome> 3 </locusChromosome>
      <locusLocation> Hs8_23892 </locusLocation>
    </locus>
    <locus id="loci two">
      <locusDataType> DNA </locusDataType>
      <locusChromosome> 3 </locusChromosome>
      <locusLocation> Hs8_23992 </locusLocation>
      <locusLength> 29 </locusLength>
    </locus>

 </dataDescription>
  <population name="A sample of Algerians">
    <popSize> 4 </popSize>
    <ind name="1">
      <indLoci> loci one </indLoci>
      <data> 1104 </data>
    </ind>
    <ind name="2">
      <indLoci> loci one </indLoci>
      <data> 0302 </data>
    </ind>
    <ind name="1">
      <indLoci> loci two   </indLoci>
      <data> GACTCTCTACGTAGCATCCGATGACGATA </data>
    </ind>
    <ind name="2">
      <indLoci> loci two </indLoci>
      <data> GACTGTCTGCGTAGCATACGACGACGATA </data>
    </ind>
  </population>

  <population name="A sample of Bulgarians">
    <popSize>2</popSize>
    <ind name="5">
      <indLoci> loci one </indLoci>
      <data> 1103</data>
    </ind>
    <ind name="5">
      <indLoci> loci two </indLoci>
      <data> GCCTGTCTGCGTAGCATAGGATGACGATA </data>
    </ind>
  </population>

  <structure name="My population structure">
    <numGroups> 2 </numGroups>
    <group>A sample of Algerians </group>
    <group>A sample of Bulgarians </group>
  </structure>
</PGD>
```

- NGS data of two loci from two haploid populations:

```
<?xml version="1.0" encoding="iso-8859-1" ?>
<?xml-stylesheet type="text/xsl" href="stylesheet_PGD.xsl"?>

<PGD xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:noNamespaceSchemaLocation="PGD_schema.xsd">
  <header title="faked example data">
    <organism> homo sapiens sapiens </organism>
    <numPop> 2 </numPop>
    <ploidy> 1 </ploidy>
    <missing> ? </missing>
    <gap> - </gap>
  </header>

  <dataDescription>
    <numLoci> 2 </numLoci>
    <dataType> NGS </dataType>
    <locus id="loci one">
      <locusChromosome> 3 </locusChromosome>
      <locusLocation> Hs8_23892 </locusLocation>
      <locusGenic> coding </locusGenic>
      <locusLinks> www.loci.ch/faked_adress/ </locusLinks>
      <locusComments> faked </locusComments>
    </locus>
    <locus id="loci two">
      <locusChromosome> 3 </locusChromosome>
      <locusLocation> Hs8_23992 </locusLocation>
      <locusGenic> noncoding </locusGenic>
    </locus>
  </dataDescription>

  <population name="pop 1">
    <popSize> 2 </popSize>
    <ind name="1">
      <indGeogCoord> 35, 4 </indGeogCoord>
      <indLingGroup> African </indLingGroup>
      <indLoci> loci one </indLoci>
      <indFreq> 10 </indFreq>
      <read>
        <start> 230 </start>
        <length> 70 </length>
        <data> ATTAGCACCCAAAGCTAAGATTCTAATTTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTA </data>
        <quality> IIIIIHHHHHHHHHHBIIIIIIIIIIIIIIIIIIIIIIIIIHHHHHHHHHHHHHHHHHHHHHHHHHHHHA </quality>
      </read>
      <read>
        <start> 240 </start>
        <length>71 </length>
        <data> AAAGCTAAGATTCTAATTTAAACTATTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCCAAGTA    </data>
        <quality> IIIIIHHHHHHHHHHBIIIIIIIIIIIIIIIIIIIIIIIIHHHHHHHHHHHHHHHHHHBBBBHHHHHHA,, </quality>
      </read>
    </ind>

    <ind name="2">
      <indGeogCoord> 36, 4 </indGeogCoord>
      <indLingGroup> Africanic </indLingGroup>
      <indLoi> loci one </indLoci>
      <indFreq> 11 </indFreq>
      <read>
        <start> 273 </start>
        <length> 57 </length>
        <data> TCTTTCATGGGGAAGCAGATTTGGGTACCACCCAAGTATTGACTCACCCATCAACAT </data>
        <quality> IIIIIHHHHHHHHHHBIIIIIIIIIIIIIIIIIIIIIIIIIHHHHHHHHHHHHHHHH </quality>
      </read>
    </ind>
  </population>

  <population name="pop 2">
    <popSize> 1 </popSize>
    <popGeogCoord> 8, 48 </popGeogCoord>
    <popLingGroup> European </popLingGroup>
    <popLocus> loci two </popLocus>
    <ind name="4">
      <read>
        <start> 265 </start>
        <length> 65 </length>
        <data> TTCTCTGTTCTTTCATGGGGAAGCAGATTTGGGTACCACCCAAGTATTGACTCACCCATCAACAT </data>
        <quality> IHHHHHHHHHBIIIIIIIIIIIIIIIIIIIIIIIIIIHHHHHHHHHHHHHHHHHHHHHHHHHHHA </quality>
      </read>
  </population>
</PGD>
```

10.2 ARLEQUIN

ARLEQUIN version 3.5.2 (released 12 April 2015)

ARLEQUIN provide a large set of basic methods and statistical tests, in order to extract information on genetic and demographic features of a collection of population samples. It is able to compute standard genetic diversity indices, to estimate allele and haplotype frequencies, to test departure from linkage equilibrium, departure from selective neutrality and demographic equilibrium, to estimate parameters from past population expansion, and to analyse population subdivision under the AMOVA framework (Excoffier and Lischer, 2010).

10.2.1 Data type handled

ARLEQUIN can handle haploid and diploid data of following data types:

- DNA
- RFLP
- SNP
- Microsatellite
- Standard data
- Allele frequency data

10.2.2 ARLEQUIN format

The input files should have an "*.arp" extension (for ARLEQUIN Project). They are structured into two main sections:

- Profile section (mandatory)
- Data section (mandatory):
    - Haplotype list (optional)
    - Distance matrices (optional)
    - Samples (mandatory)
    - Genetic structure (optional)
    - Mantel tests (optional)

Profile section:

The profile section contains the properties of the data. The beginning is indicated by [Profile].

Specify:

- Title (string within ""): `Title="title xy"`
- Number of samples (integer 1-1000): `NbSamples =3`
- Type of data (DNA, RFLP, MICROSAT, STANDARD, FREQUENCY): `DataType = DNA`
- Haplotypic/genotypic data (0/1): `GenotypicData = 0`

Optionally (default value):

- locus separator (WHITESPACE, TAB, NONE, …): `LocusSeparator = TAB`
- gametic phase known/unknown (1/0): `GameticPhase = 1`
- recessive/ co-dominant allele (1/0): `RecessiveData = 1`
- code for recessive allele (string within "null"): `RecessiveAllel ="xxx"`
- code for missing data (character within "?" or '?'): `MissingData = '$'`
- frequencies as absolute/relative values (ABS/REL): `Frequency = ABS`
- significant digits for haplotype frequency outputs (real number 1e-2 – 1e-7(1e-5)): `FrequencyThreshold = 0.00001`
- convergence criterion for the EM algorithm (real number 1e-7 – 1e-12): `EpsilonValue = 1e-10`

Data section:

The data section contains the raw data to be analysed. The beginning is indicated by [Data]. It contains several subsections:

- Haplotype list (optional):
  One can define a list of haplotypes, which are used for all samples. It is possible to define the list in an external file.
  - intern:

```
[[HaplotypeDefinition]]    #start the section of Haplotype definition
  HaplListName="list1"     #give any name you wish to this list
  HaplList={
   h1  A  T                 #on each line, the name of the haplotype
   h2  G  C                 #is followed by its definition.
   h3  A  G
   h4  A  A
   h5  G  G
  }
```

  - extern:

```
[[HaplotypeDefinition]]     #start the section of Haplotype definition
  HaplListName="list1"      #give any name you wish to this list
  HaplList = EXTERN "hapl_file.hap"
```

- Distance matrix (optional):
  This subsection contains a matrix of genetic distances between haplotypes. It is also possible to define the matrix in an external file.

- intern:

```
[[DistanceMatrix]] #start the distance matrix definition section
  MatrixName= "none" # name of the distance matrix
  MatrixSize= 4 # size = number of lines of the distance matrix
  MatrixData={
    h1 h2 h3 h4 # labels of the distance matrix (identifier of the
    0.00000     # haplotypes)
    2.00000 0.00000
    1.00000 2.00000 0.00000
    1.00000 2.00000 1.00000 0.00000
  }
```

- extern:

```
[[DistanceMatrix]]      #start the distance matrix definition section
   MatrixName= "none"   #name of the distance matrix
   MatrixSize= 4        #size = number of lines of the distance matrix
   MatrixData= EXTERN "mat_file.dis"
```

- Samples (obligatory):
  This subsection defines the haplotypic/genotypic content of the different samples:
  - start of the subsection: `[[Samples]]`
  - name for each sample (string within “ ”): `SampleName = “name xy”`
  - size of sample (integer value): `SampleSize = 732`
  - data itself (list of haplotypes or genotypes and their frequencies, entered with braces “{ }”):

```
[[Samples]]                 #start the samples definition section
  SampleData={
   id1  1   ACGGTGTCGA
   id2  2   ACGGTGTCAG
   id3  8   ACGGTGCCAA
   id4  10  ACAGTGTCAA
   id5  1   GCGGTGTCAA
  }
```

Frequency data:

```
SampleData={
  id1  1
  id2  2
  id3  8
  id4  10
  id5  1
}
```

Haplotypic data: Define for each haplotype its identifier and sample frequency (if no haplotype list has been defined: specify also allelic content of the haplotype)

Genotypic data: for each genotype its identifier, sample frequency and allelic content (on two separate lines) is needed.

```
Id1   2    ACTCGGGTTCGCGCGC        # the first pseudo-haplotype
           ACTCGGGCTCACGCGC        # the second pseudo-haplotype
```

- Genetic structure (only required for AMOVA):
  The genetic structure specifies the hierarchical genetic structure of the samples. It is possible to define groups of populations.
  - start of the subsection: `[[Structure]]`
  - name for the genetic structure (string within " "): `StructureName = "name"`
  - number of groups defined in the structure (int value): `NbGroups = 5`
  - group definitions (list containing the names of the samples belonging to the group, entered within braces "{ }"):

```
NbGroups=2
Group ={
  population1
}
Group ={
  population2
  population3
}
```

- Mantel test settings (optional):
  This subsection specifying some distance matrices. The goal is to compute a correlation between the Ymatrix and X1 or a partial correlation between the Ymatrix, X1 and X2. The Ymatrix can be either a pairwise population FST matrix or a custom matrix entered into the project by the user. X1 (and X2) have to be defined in the project.
  - start of the subsection: `[[Mantel]]`
  - size of the matrices (pos. integer value): `MatrixSize= 5`
  - number of matrices among which we compute the correlations (2/3): `MatrixNumber = 2`
  - matrix that is used as genetic distance ("fst" (→Y=Fst)/ "log_fst" (→Y=log(Fst))/ "slatkinlinearfst" (→Y=Fst/(1-Fst))/ "log_slatkinlinearfst" (→Y=log(Fst/(1-Fst)))/ "nm" (→Y=(1-Fst)/(2 Fst))/ "custom" (→Y= user-specified in the project)): `YMatrix = "fst"`
  - labels that identify the columns of the YMatrix (list containing the names of the label name belonging to the group, entered within braces "{ }"):

```
YMatrixLabels = {
  "Population1 " "Population4" "Population2"
  "Population8" "Population5"
}
```

- keyword that allows to define a matrix with witch the correlation with the YMatrix is computed:

```
DistMatMantel={
  0.00
  3.20 0.00
  0.47 0.76 0.00
  0.00 1.23 0.37 0.00
  0.22 0.37 0.21 0.38 0.00
}
```

- Labels defining the sub-matrix on which the correlation is computed:

```
UsedYMatrixLabels={
  "Population1 "
  "Population5"
  "Population8"
}
```

Example input file:

The following small example is a project file containing four populations. The data type is STANDARD genotypic data with unknown gametic phase:

```
[Profile]
Title="Fake HLA data"
  NbSamples=2
  GenotypicData=1
  GameticPhase=0
  DataType=STANDARD
  LocusSeparator=WHITESPACE
  MissingData='?'
[Data]

[[Samples]]
  SampleName="A sample of 6 Algerians"
  SampleSize=6
  SampleData={
   1 1 1104 0200
       0700 0301
   3 3 0302 0200
       1310 0402
   4 2 0402 0602
       1502 0602
  }
  SampleName="A sample of 11 Bulgarians"
  SampleSize=5
  SampleData={
   1 1 1103 0301
       0301 0200
   2 4 1101 0301
       0700 0200
  }
```

```
[[Structure]]
  StructureName="My population structure"
  NbGroups=2
  Group={
   "A sample of 6 Algerians"
  }
  Group={
   "A sample of 11 Bulgarians"
  }
```

10.2.3 Links and References

Website: http://cmpg.unibe.ch/software/arlequin35/,

Manual: http://cmpg.unibe.ch/software/arlequin35/man/arlequin35.pdf

(Excoffier and Lischer, 2010)

10.2.4 Special PGDSpider input/output questions

- Input: none

- Output:
    - Specify which data type should be included (optional):
      DNA/NGS/SNP/RFLP/MICROSAT/AFLP/STANDARD/FREQUENCY
      If more than one allowed data type exists, one have to select the data type which should be included in the output file (only one data type can be analysed per file).
    - Do you want to convert SNP/DNA to numeric format with 0 representing ancestral state?:
      FALSE/TRUE
      Used in Arlequin to run derived (unfolded) SFS estimations. This is only possible if ancestral state is known!
    - Specify the locus/locus combination which should be written to the output file (optional):
      String
      If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.
    - Specify the DNA locus you want to write to the output file or write "concat" for concatenation:
      String/CONCAT
      In case of a multi-loci DNA data set one has to choose the DNA locus to write to the output file or specify “CONCAT” to concatenate the loci into one sequence (Arlequin cannot handle multi-loci DNA data).

10.3 BAM

BAM (17. April 2011)

BAM is a generic format for storing large nucleotide sequence alignments. It is the binary equivalent to SAM for intensive data processing.

The program SAMtools provide various utilities for manipulating alignments in the BAM/SAM format, including sorting, merging, indexing and generating alignments in a per-position format (Li, et al., 2009).

The conversion process of the format BAM needs the programs Samtools (version 0.1.12/0.1.06) and Bcftools, which can be downloaded from http://samtools.sourceforge.net. The paths to the program files (samtools.exe and bcftools.exe) have to be specified in the "Config" menu under "Options" (see section 5.3.1 PGDSpider menus) or in the "spider.conf.xml" file within the PGDSpider distribution (the file will be automatically generated the first time you run PGDSpider).

Currently, PGDSpider is not meant to convert very large BAM files as it loads into memory the whole file, whose size may exceed available RAM. However, PGDSpider allows one to convert specific subsets of BAM files into any other format. This feature can be used to perform sliding window analysis.

10.3.1 Data type handled

BAM can handle data of following type:

- DNA
- NGS (Next-Generation Sequencing data)

10.3.2 BAM format

BAM is the binary file format of SAM with following file extension: *.bam
For a detailed description of the format see http://samtools.sourceforge.net/SAM1.pdf.

10.3.3 Links and References

Website: http://samtools.sourceforge.net,
Manual: http://samtools.sourceforge.net/SAM1.pdf

(Li, et al., 2009)

10.3.4 Special PGDSpider input/output questions

- Input:
  - Reference file:
    Absolute file path
    Choose the file with the reference sequences
  - Select what should be imported:
    READS/SNP/CONSENSUS
    Defines if all reads, the consensus sequences or only the variant sites (SNP) should be imported
  - Concatenate consensus sequences from different reference data (only works if you choose to import consensus sequences):
    TRUE/FALSE
    Specify if consensus sequences coming from different reference sequences should be concatenated or not
  - What is the ploidy of the data:
    DIPLOID/HAPLOID
    Define if the data are haploid or diploid
  - Only import following regions (optional):
    String (e.g.: chr1:100:5000 or chr1:100:5000 chr2:1:100)
    Defines which regions should be imported. Regions should be defined in following format: refSeqName:start:end, multiple regions: separate it with white spaces

- Output:
  - Save an additional file with reference sequences:
    TRUE/FALSE
    Saves a file with the reference sequences
  - Save reference file:
    Absolute file path
    Choose the path where the reference file should be written
  - Specify which data type should be included (optional):
    NGS/DNA/RNA
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).

10.4 BAMOVA

Bamova version 1.02 (27. September 2011):

Bamova implements a Bayesian Analysis of Molecular Variance and different likelihood models for three different types of molecular data (including two models for high throughput sequence data), as described in detail in Gompert and Buerkle (2011) and Gompert et al. (2010).

10.4.1 Data type handled

Bamova is able to deal with haplotype data including NGS:

10.4.2 Bamova format

All analyses require an input text file that gives the observed counts of each of the haplotypes for each population and locus. The format of this file is identical for the known haplotypes model and NGS-population model:

- Each genetic region begins with a line that gives the genetic region's number
    - "`Marker0`" for the first genetic region, "`Marker1`" for the second, …
    - The numbers should be consecutive and begin with 0.
- Genetic region identification line should be followed by one line of data for each populations.
    - These lines begin with "`Population`"
    - Then give the population number (start with 0 and number populations consecutively)
    - Then the counts of each haplotype, which should come in the same order for each population.
- The NGS-population model requires a second input text file that provides the number of diploid gene copies that were sampled for each population and genetic regions:
    - In the form of a white-space separated matrix:
        - Rows: genetic regions
        - Columns: populations

The haplotype count file for the NGS-individual model is a bit different from the other models:

- Genetic regions are denoted as described above
- Followed by population identifiers
- Then a single line per individual giving the number of reads of each haplotype observed for that individual

Population group file:

- This file should have one row per group that gives the group number and the numbers of the populations in each group

Examples:

- Population model file: A short example with two genetic regions each with five haplotypes sequenced in four populations:

```
Marker0
Population 0 0 30 0 5 5
Population 1 0 10 0 5 5
Population 2 5  0 5 0 0
Population 3 5 10 5 0 0
Marker1
Population 0 2 12 1 1  5
Population 1 4  8 1 5  3
Population 2 7  7 7 1  1
Population 3 5 17 3 4 12
```

- NGS-individual model file: as shown below for three populations and one genetic region:

```
Marker0
Population 0
10 0 0 0 5
10 0 0 0 5
 . . . . .
 . . . . .
10 0 0 0 5
Population 1
10 0 0 0 0
10 0 0 0 5
 . . . . .
 . . . . .
5 0 5 0 0
Population 2
0 0 10 5 0
0 4 10 0 0
 . . . . .
 . . . . .
0 0 10 5 0
```

- Population group file:

```
Group0 0 3
Group1 1 2 4
```

10.4.3 Links and References

- Website: http://www.uwyo.edu/buerkle/software/bamova/
- (Gompert and Buerkle, 2011; Gompert, et al., 2010)

10.4.4 Special PGDSpider input/output questions

- Output:
  - Specify which data type should be included (optional):
    MICROSAT/SNP/AFLP/RFLP/STANDARD/DNA/RNA/NGS
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - Select the format of the NGS model:
    INDIVIDUAL/ POPULATION
    Select if the the NGS model file should be written as individual or population based file (only required if NGS data)
  - NGS number of pooled individuals file:
    Absolute file path
    Choose the file with number of pooled individuals (only required in NGS population based model)
  - Save an additional population group file:
    TRUE/FALSE
    If yes, an additional file with population groups is written
  - Population group file:
    Absolute file path
    Choose the file with the population groups.

10.5 BAPS

BAPS version 6.0(17 December 2012)

BAPS (Bayesian Analysis of Population Structure) is a program for Bayesian inference of the genetic structure in a population. One can cluster molecular data (assign the data to different groups) and perform admixture analysis at the group or at the individual level (Tang, et al., 2009).

10.5.1 Data type handled

BAPS can handle haploid or diploid data of the following data types:

- DNA (also tetraploid data possible)
- SNP (numeric)
- AFLP
- Microsatellite
- Standard (multi-allelic markers)

10.5.2 BAPS format

Clustering of individuals:

The molecular data are assigned to the corresponding individual. The individuals again can be assigned to groups (populations).

- The data file contains a data matrix:
    - columns: loci at which the individuals were observed
    - rows: individuals
    - additional column at the right end of the matrix (last column):
      Each row contains an index of the individual whose alleles are reported. There can be more than one row per individual (e.g. in diploids)
- alleles are indexed with any non-negative integer
- individuals: indices start with 1 for the first individual and end with the value that corresponds to the total number of individuals
- missing alleles: coded by a negative integer (e.g. -999 or -9)
- If the populations of the individuals are known, one can input two additional files:
  The first file contains the names of the populations and the second file contains the indices of the first individual of each sampling populations.

- Example (cluster 5 diploid individuals (two rows per individual). The first individual has alleles 5 and 7 at the first locus and so on. Individuals 1, 2 and 3 were sampled in America and individuals 4 and 5 in Europe):

- data file:

```
5           2           1
7           2           1
5           8           2
3           9           2
2           5           3
-999        5           3
5           -999        4
2           3           4
3           8           5
2           5           5
```

- name file:

```
American
European
```

- Index file:

```
1
4
```

Clustering groups of individuals:

The molecular data are assigned to the corresponding group of individuals. Data of individuals coming from the same group (population) cannot be separated at the individual level.

- The data file contains a data matrix:
  - columns: loci at which the individuals were observed
  - rows: individuals
  - Last column contains the index of the group that is the origin of the alleles on the particular row
- the names of the groups can be given in a separate file

- example (data from four distinct groups)
  - data file:

```
5      2      1
7      2      1
5      8      1
3      9      2
2      5      2
-999   5      3
5      -999   4
2      3      4
3      8      4
2      5      4
```

  - name file:

```
American
European
African
Asian
```

Trained clustering

Find the best clustering for individuals with unknown origin with the help of individuals whose origin is known.

- Not included, because not enough information is available from a PGD file to generate this kind of data file.

Spatial clustering

The spatial clustering is a genetic mixture analysis using a spatial model. The spatial clustering model requires the coordinate data for the clustered units (groups or individuals).

- Uses the same files as: "Clustering of individuals" or "Clustering groups of individuals". But an additional file with coordinate values have to be given:
  The coordinate file contains as many rows as there are individuals (spatial clustering of individual's → sample coordinates of each individual) or groups (spatial clustering of groups → sample coordinates of each group) in the data file.
- Missing geographic coordinates are coded as two consecutive zeros

- Example (individual 1 has the coordinates: 172, 88 and individual 4 has missing geographic coordinates):
  - Data file: see first example
  - Coordinate file:

```
172  88
155  96
180  78
0    0
-18  81
```

Clustering of linked molecular data (nucleotide sequence data)

Clustering of linked molecular data is genetic mixture analysis done either for haploid sequence data, phased diploid/tetraploid sequence data or for linked marker data for which a single allele is recorded per locus.

Haploid data need a single data row per individual, diploid two and tetraploid four rows. There are a numeric and a sequence input format:

- numeric format:
  - replace each nucleotide (A,C,G,T) with a unique positive integer and missing values with a negative integer (e.g.: -999)
  - Individual indices are located after the sequence and separated by a space
  - example: a single data row for individual 110 with sequence AACCG-T could look like this:

```
65 65 67 67 71 -999 84 110
```

- sequence format:
    - Individual Indexes are located after the sequence and separated by a space
    - Gaps and missing nucleotides should be denoted by a dash (-)
    - example (diploid):

```
ATTTGCCTACGTAGCCAATT 1
TTACCGACCTTAAAAACCTT 1
ATTTCCCAAAGGGTTTAAAA 2
TAACCGGACATAGCCAATAA 2
```

- Need to concatenate the sequences from all considered genes into a single one and tell the program about the gene boundaries in a separate file:
    - The number of rows is equal to the number of genes
    - at each row, the integers refer to columns of the data matrix that correspond to the specific gene
    - Additional zeros are used to fill the rows to have an equal number of columns
    - Example ("linkage map" of 3 genes. The first gene corresponds to the columns 1-10 in the data matrix, the second gene to the columns 11-19 and so on):

```
1 2 3 4 5 6 7 8 9 10
11 12 13 14 15 16 17 18 19 0
20 21 22 23 24 25 26 27 0 0
```

10.5.3 Links and References

Website: http://www.helsinki.fi/bsg/software/BAPS/

Manual: http://www.helsinki.fi/bsg/software/BAPS/macSnow/BAPS6manual.pdf

(Tang, et al., 2009)

10.5.4 Special PGDSpider input/output questions

- Input:
    - Select the data type:
      MICROSAT/SNP/AFLP/DNA/STANDARD
      One has to define the type of the data (e.g.: DNA, SNP, AFLP, MICROSAT or STANDARD)
    - How are Microsat alleles coded?
      REPEATS/LENGTH/ARBITARY
      Need to define if the Microsat data are coded as number of repeats, as the length of the PCR fragments or as an arbitrary number.
    - Enter the size of the repeated motif:
      Integer/Integer,Integer, …

Need to define the size of the repeated motif, so that the number of repeats can be calculated (Microsat alleles have to be saved as number of repeats in the PGD format). Same for all loci: enter one number. Different between loci: comma separated list (e.g.: 2,2,3,2)

- Gene boundaries file:
  TRUE/FALSE
  Possibility to add a file with gene boundary definitions
- Gene boundaries file:
  Absolute file path
  Choose file with gene boundaries.
- DNA coded as ACGT:
  TRUE/FALSE
  Need to define the format of the molecular data file (coded as ACGT or as integers)
- Enter the integer that codes for the nucleotide:
  Integer
  Define the integer that codes for a specific nucleotide
- Missing value code:
  String/Integer
  Specify the code for the missing values (e.g.: -9, -999, ?, etc.)
- The last column of the input file contains the index of the individual or group:
  INDIVIDUAL/GROUP
  Select if the last column contains the indices of the individuals (when clustering of individuals) or of the groups (when clustering of groups of individuals)
- Are individuals assigned to populations:
  TRUE/FALSE
  If yes, one can add a file with population names (in individual clustering the index file is also needed)
- Population name file:
  Absolute file path
  Choose the file with the population names.
- Index file:
  Absolute file path
  Choose the file with the indexes
- Include a file with population names:
  TRUE/FALSE
  If yes, one can add a file with population names.
- Population name file:
  Absolute file path
  Choose the file with the population names.
- Include file with coordinates:
  TRUE/FALSE
  Possibility to add a file with geographic coordinates.
- Geographic coordinates file:
  Absolute file path

Choose the file with the geographic coordinates.

- Output:
  - Specify which data type should be included (optional):
    MICROSAT/SNP/AFLP/DNA/NGS/STANDARD
    If more than one allowed data type exists, select the data type which should be included in the output file (only one can be analysed per file).
  - Clustering of individuals or groups of individuals:
    INDIVIDUALS/GROUPS
    Choose between these two options
  - Save additional file with population/group names:
    TRUE/FALSE
    Saves a file with the population/group names
  - Name file:
    Absolute file path
    Choose the path where the name file should be written
  - Index file:
    Absolute file path
    Choose the path where the index file should be written
  - Save additional file with geographic coordinates:
    TRUE/FALSE
    Saves a file with the geographic coordinates of individuals or groups (used for spatial clustering analysis)
  - Coordination file:
    Absolute file path
    Choose the path where the coordination file should be written
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.
  - Specify the DNA locus you want to write to the output file or write "concat" for concatenation:
    String/CONCAT
    In case of a multi-loci DNA data set one has to choose the DNA locus to write to the output file or specify “CONCAT” to concatenate the loci into one sequence (BAPS cannot handle multi-loci DNA data).

10.6 BATWING

BATWING (updated 2003)

BATWING uses multi-locus haplotype data, model (stepwise mutation model, mutation models for unique event polymorphism, standard coalescent model), distribution specifications and a Markov chain Monte Carlo (MCMC) method based on coalescent theory to generate approximate random samples from the posterior distributions of parameters such as mutation rates, effective population sizes and growth rates, and times of population splitting events. It also generates approximate posterior samples of the entire genealogical tree underlying the sample, including the tree height, which corresponds to the time since the most recent common ancestor. BATWING is intended for within-species data, and not between-species data (Wilson, et al., 2003).

10.6.1 Data type handled

BATWING can deal with haploid SNP and Microsatellite data

10.6.2 BATWING format

- The input file contains one line per haplotype, with one or more spaces separating the alleles at distinct loci
- Everything after a # is ignored (the whole line is ignored if # is the first non-space character)
- The UEP (unique event polymorphism) alleles (SNP) which may be coded by any two single alphanumeric characters (e.g. “0” and “1”, or “A” and “T”) comes first in the line, followed by the microsatellite or STR (Short Tandem Repeat) data
- The data are coded by integer values. Microsatellite data are coded as the number of tandem repeats at that locus
- Missing STR data can be specified using −1
- If the data are drawn from several distinct populations:
    - One can store the population assignments in a location file.
    - The rows of the location file should correspond to the rows of the data file
    - Subpopulation are coded by any positive integers
    - missing location information can be specified using −1

- example (these input file specifies 10 STR loci, no UEP (SNP) loci and a sample size of 6 haplotypes):

```
3 3 2 1 7 8 2 3 10 11
5 5 4 7 9 1 2 3 4 3
2 5 1 3 1 5 6 2 4 4
3 3 1 5 7 8 2 3 11 13
5 5 4 7 9 1 2 3 4 3
1 7 6 2 3 3 2 3 2 1
```

Location file:

```
1
1
2
2
3
-1
```

10.6.3 Links and References

Website: http://www.mas.ncl.ac.uk/~nijw/

Manual: http://www.mas.ncl.ac.uk/~nijw/batwing/batguide.pdf

(Wilson, et al., 2003)

10.6.4 Special PGDSpider input/output questions

- Input:
    - Enter how many SNP loci are defined in the data file:
      Integer
      The parser needs to know how many columns of the data file contains SNP data
    - Include a file with locations:
      TRUE/FALSE
      Possibility to add a file with the definition of populations (individuals assigned to populations).
    - Location file:
      Absolute file path
      Choose the file with the population definitions.

- Output:
    - Save an additional file with population definitions:
      TRUE/FALSE
      Allow to save a location file with the population definitions
    - Population file:
      Absolute file path
      Choose the path where the population file should be written
    - Specify the locus/locus combination which should be written to the output file (optional):
      String
      If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.7 Bayenv

Bayenv version 2.0(20 November 2013)

Loci involved in local adaptation can potentially be identified by an unusual correlation between allele frequencies and important ecological variables, or by extreme allele frequency differences between geographic regions. However, such comparisons are complicated by differences in sample sizes and the neutral correlation of allele frequencies across populations due to shared history and gene flow. To overcome these difficulties, they have developed a Bayesian method that estimates the empirical pattern of covariance in allele frequencies between populations from a set of markers, and then uses this as a null model for a test at individual SNPs (Coop, et al., 2010; Gunther and Coop, 2013)

10.7.1 Data type handled

Bayenv can handle data of following type:

- SNP

10.7.2 Bayenv format

SNPSFILE:

- contains the allele counts across populations of each SNP are represented by two lines in the file
    - first line: counts of first allele
    - second line: counts for second allele
- The counts of allele 1 and allele 2 are assumed to sum to the sample size typed at this SNP in this population (i.e. the total sample size excluding missing data)
- Counts are separated by tabs
    - Note that there should be just polymorphic sites in the data set

- Example (allele counts of 2 SNPS in 5 populations):

```
0   0   0   0   2
42  24  16  22  30
2   0   0   1   1
40  24  16  21  31
```

SNPFILE:

- identical as SNPSFILE

SAMPLEFILE:

- file containing the sample sizes per population when the populations have been sequenced as pools (i.e. the number of chromosomes per pool).
- The file contains a single line of tab separated values.
- The sample sizes must be in the same population order that they appeared in the SNPSFILE

- Example:

```
42  24  16  22  32
```

10.7.3 Links and References

Website: http://gcbias.org/bayenv/

(Coop, et al., 2010; Gunther and Coop, 2013)

10.7.4 Special PGDSpider input/output questions

- Output:
  - Save an additional sample file:
    TRUE/FALSE
    Allows to saves a file with the sample sizes
  - Sample file:
    Absolute file path
    Choose the path where the sample file should be written
  - Assign half missing genotypes (one allele missing) as complete missing:
    TRUE/FALSE
    Turn half missing genotypes, where one allele is missing, into complete missing genotypes.
  - Save two additional files with used sample and loci names:
    TRUE/FALSE
  - Sample/loci names file:
    Absolute file path
    Choose the path where the sample name file ("_sample.txt") and loci name file ("_loci.txt") should be written
    The sample name file has following format:

```
Ind_1     pop_1
Ind_2     pop_1
Ind_3     pop_2
Ind_4     pop_2
```

10.8 BCF

BCF (14. May 2011)

BCF, or the binary variant call format, is the binary version of VCF. It keeps the same information in VCF, while much more efficient to process especially for many samples. The relationship between BCF and VCF is similar to that between BAM and SAM.

The conversion process of the format BCF needs the programs Samtools (version 0.1.12/0.1.06) and Bcftools, which can be downloaded from http://samtools.sourceforge.net. The paths to the program files (samtools.exe and bcftools.exe) have to be specified in the “Config” menu under “Options” (see section 5.3.1 PGDSpider menus) or in the “spider.conf.xml” file within the PGDSpider distribution (the file will be automatically generated the first time you run PGDSpider).

Currently, PGDSpider is not meant to convert very large BCF files as it loads into memory the whole file, whose size may exceed available RAM. However, PGDSpider allows one to convert specific subsets of BCF files into any other format. This feature can be used to perform sliding window analysis.

10.8.1 Data type handled

BCF can handle data of following type:

- SNP
- DNA
- UHTS (Ultra High-Throughput Sequencing data)

10.8.2 BCF format

BCF is the binary format of VCF with following file extension: *.bcf

The detailed format description of the BCF format can be found in bcf.tex included in the samtools source code package.

10.8.3 Links and References

Website: http://samtools.sourceforge.net/mpileup.shtml

10.8.4 Special PGDSpider input/output questions

- Input:
  - What is the ploidy of the data:
    HAPLOID/DIPLOID
    Define if the data are haploid or diploid
  - Only import following regions (optional):
    String (e.g.: chr1:100:5000 or chr1:100:5000 chr2:1:100)
    Defines which regions should be imported. Regions should be defined in following format: refSeqName:start:end, multiple regions: separate it with white spaces
  - Take most likely genotype if "PL" or "GL" is given in the genotype field:
    TRUE/FALSE
    If "PL" or "GL" is given in the genotype field, take most likely genotype or take genotype specified in "GT".
  - Minimal phred-scaled quality of SNPs (optional):
    Double
    Output SNPs with phred-scaled quality ("QUAL" field) of at least the specified value
  - Minimal phred-scaled genotype quality (optional):
    Double
    Output genotype as missing if the phred-scale genotype quality is below specified value.
  - Minimal read depth of a position for the sample (optional):
    Integer
    Output genotype as missing if the read depth of a position for the sample is below specified value.
  - Specify individuals you want to output (optional):
    String
    If only a subset of individuals should be output, one could give a list of individual names (comma separated: ind1, ind2, ind4, …)
  - Include non-polymorphic SNPs (optional):
    TRUE/FALSE
    Define if non-polymorphic SNPs should be included.
  - Include a file with population definitions
    TRUE/FALSE
    Possibility to add a file with the definition of populations (individuals assigned to populations).
  - Specify a file with population definitions (optional):
    Absolute file path
    One can specify a file containing the definition of which individual belongs to which population. The population definition file should have following format (names without whitespaces):

```
Ind_1     pop_1
Ind_2     pop_1
Ind_3     pop_2
Ind_4     pop_2
```

- Output:
    - Save an additional file with reference sequences:
      TRUE/FALSE
      Saves a file with the reference sequences
    - Reference file:
      Absolute file path
      Choose the path where the reference file should be written
    - Specify which data type should be included (optional):
      SEQUENCES/SNP
      If the input file contains sequence and SNP data, one has to select which should be included in the output file (only sequence or SNP can be analysed per file).
    - Enter the integer that codes for the nucleotide:
      Integer
      Define the integer that codes for a specific nucleotide

10.9 CONVERT

CONVERT version 1.31 (March 2005)

CONVERT is a user friendly program that facilitates the transfer of co-dominant, diploid genotypic data among commonly used population genetic software packages. CONVERT reads input files in its own “standard” data format and in GENEPOP format. It can convert these formats into the input formats of the following programs: GDA, GENEPOP, ARLEQUIN, POPGENE, MICROSAT, PHYLIP, and STRUCTURE. In addition, CONVERT can produce a summary table of allele frequencies in which private alleles and the sample sizes at each locus are indicated (Glaubitz, 2004).

10.9.1 Data type handled

CONVERT is able to deal with co-dominant, diploid genotypic data of following data type:

- Microsat
- RFLP
- SNP (numeric)
- Standard
- AFLP

10.9.2 CONVERT format

The CONVERT format is defined as follow:

- It is an EXCEL file saved as a tab delimited Text file (*.txt)
- The first line (cell A1) contains a brief description of the data file (title)
- The second line (cell A2) gives the number of populations present in the data file (e.g.: `npops = 2`)
- The third line (cell A3) contains the number of loci (e.g.: `nloci = 7`)
- fourth line: the names of the loci (in order, without spaces, underscores are allowed)
- Each population starts with the line `pop = pop_name`. There must be at least one space between 'pop' and '='. Spaces within population name are not allowed, but an underscores can be used.
- Each individual within a population begins with an individual name. It can be a number, characters like: '/', '=', '?', ':', ';' or ',' are not allowed and there must be no spaces within names.
- After an individual’s name, the diploid genotypes are given:
    - on the same line or wrapped to the next line
    - alleles must be given in numeric form (two alleles for each locus)
    - alleles can be coded as any integer between 1 and 9999
    - Typically the numbers will indicate the size of the allele in base pairs (e.g., for microsats)
    - Missing data are coded as: '?'

- Example:

```
Canucks vs Yanks for the Ice Hockey gold - Salt Lake City 2002
npops = 2
nloci = 4
      SSR01        SSR02        SSR03        SSR04
pop = Canadian_Team
Lemieux      239    245    204    222    169    185    180    206
Sakic        241    247    216    238    195    195    174    198
Fleury       ?      ?      224    224    175    189    160    218
Kariya       229    239    226    240    181    203    182    194
Yzerman      223    239    224    226    191    195    174    180
Lindros      237    245    222    226    179    193    194    222
pop = American_Team

Chelios      235    243    216    226    179    183    172    218
Leetch       235    239    208    216    179    191    198    208
Suter        237    241    222    224    185    197    166    192
Housley      ?      ?      212    228    183    191    184    218
Hatcher      237    241    222    222    173    187    160    198
Amonte       235    245    226    230    181    181    178    192
```

10.9.3 Links and References

Website:
http://www.agriculture.purdue.edu/fnr/html/faculty/Rhodes/Students%20and%20Staff/glaubitz/software.htm

(Glaubitz, 2004)

10.9.4 Special PGDSpider input/output questions

- Input:
  - Select the data type:
    MICROSAT/RFLP/SNP/STANDARD/AFLP
    Allows selecting the type of the data
  - How are Microsat alleles coded:
    REPEATS/LENGTH
    Needs to define if the Microsat data are coded as number of repeats or as length of the PCR fragments
  - Enter the size of the repeated motif:
    Integer/Integer,Integer, …
    Needed to convert the Microsatellite data (length of the PCR fragments) to number of repeat data (PGD can only save number of repeat Microsatellite data). Same for all loci: enter one number. Different between loci: comma separated list (e.g.: 2,2,3,2)

10.10 EIGENSOFT

EIGENSOFT version 5.0.2 (April 2014)

The EIGENSOFT package combines functionality from population genetics methods (Patterson, et al., 2006) and the EIGENSTRAT stratification correction method (Price, et al., 2006). The EIGENSTRAT method uses principal components analysis to explicitly model ancestry differences between cases and controls along continuous axes of variation; the resulting correction is specific to a candidate marker's variation in frequency across ancestral populations, minimizing spurious associations while maximizing power to detect true associations.

10.10.1 Data types handled

EIGENSOFT is able to deal with diploid SNP data.

10.10.2 EIGENSTRAT/ANCESTRYMAP format

EIGENSTRAT genotype format:

- contains 1 line per SNP
- Each line contains 1 character per individual:
    - `0`: zero copies of reference allele
    - `1`: one copy of reference allele
    - `2`: two copies of reference allele
    - `9`: missing data

ANCESTRYMAP genotype format:

- contains 1 line per valid genotype
- There are 3 columns:
    - 1st column: SNP name
    - 2nd column: sample ID
    - 3rd column: number of reference alleles (0 or 1 or 2)
- Missing genotypes are encoded by the absence of an entry in the genotype file

SNP file format:

- contains 1 line per SNP
- There are 6 columns (last 2 optional):
    - 1st column: SNP name
    - 2nd column: chromosome
        - X chromosome is encoded as 23
        - Y as 24
        - mtDNA as 90

        - XY as 91
        - SNPs with illegal chromosome values, such as 0, will be removed
    - 3rd column: genetic position (in Morgans). If unknown: 0.0
    - 4th column: physical position (in bases)
    - Optional 5th and 6th columns: reference and variant alleles. For monomorphic SNPs: the variant allele can be encoded as X (unknown)

INDIV file format:

- contains 1 line per individual
- There are 3 columns:
    - 1st column: sample ID. Length is limited to 39 characters, including the family name if that will be concatenated
    - 2nd column: gender (M or F). If unknown: U for Unknown
    - 3rd column: a label which might refer to Case or Control status, or might be a population group label. If this entry is set to "Ignore", then that individual and all genotype data from that individual will be removed from the data set

Examples:

- EIGENSTRAT genotype file:

```
012
211
001
```

- ANCESTRYMAP genotype file:

```
rs1111              SAMPLE0    0
rs1111              SAMPLE1    1
rs1111              SAMPLE2    2
rs2222              SAMPLE0    2
rs2222              SAMPLE1    1
rs2222              SAMPLE2    1
rs3333              SAMPLE0    0
rs3333              SAMPLE1    0
rs3333              SAMPLE2    1
```

- SNP file:

```
rs1111  11        0.001000          100000 A G
rs2222  11        0.002000          200000 A T
rs3333  11        0.003000          300000 C A
```

- INDIV file:

```
SAMPLE0 F       Case
SAMPLE1 M       Case
SAMPLE2 F    Control
```

10.10.3 Links and References

Website: http://www.hsph.harvard.edu/alkes-price/software/

(Patterson, et al., 2006; Price, et al., 2006)

10.10.4 Special PGDSpider input/output questions

- Input:
    - Select the format of the genotype file:
      EIGENSTRAT/ANCESTRYMAP
      Specify if the format of the genotype file is EIGENSTRAT or ANCESTRYMAP
    - INDIV file:
      Absolute file path
      Choose the file with the sample information
    - SNP file:
      Absolute file path
      Choose the file with the SNP information

- Output:
    - SNP data are already in binary format:
      TRUE/FALSE
      SNP data are encoded in binary format (number of reference alleles: 0, 1 or 2 reference alleles)
    - Select the format of the genotype file:
      EIGENSTRAT/ANCESTRYMAP
      Specify if the genotype file should be written in EIGENSTRAT or ANCESTRYMAP format
    - Save INDIV file:
      Absolute file path
      Choose the path where the INDIV file should be written
    - Save SNP file:
      Absolute file path
      Choose the path where the SNP file should be written
    - Specify the locus/locus combination which should be written to the output file (optional):
      String
      If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.11 FASTA

FASTA format is a text based format for representing either nucleic acid sequences or peptide sequences, in which base pairs or amino acids are represented using single-letter codes. Sequence names and comments can also be included before the sequences (Pearson, 1990).

10.11.1 Data type handled

The FASTA format can contain nucleic acid or peptide sequences.

10.11.2 FASTA format

- FASTA has no standard file extension. The following extensions are often used: .fa, .mpfa, .fna, .fsa, .fas or .fasta
- The FASTA format begins with a single line description, followed by lines of sequence data. It is recommended that all lines of text be shorter than 80 characters.
- The sequence ends if another line starting with a ”>” appears (this indicates the start of another sequence)

- The header line is arranged as follows:
    - It begins with a ”>”
    - The following word following is the identifier and/or name of the sequence (optional)
    - The rest of the line is the description (optional)
    - There should be no space between the ”>” and the first letter of the identifier
    - The header line may contain more than one header separated by a ^A (Control-A) character
    - Possible sequence identifiers: Many different sequence databases use standardized headers, which helps to automatically extract information from the header:

GenBank	`“gi”|gi-number|”gb”|accession|locus`
EMBL Data Library	`“gi”|gi-number|”emb”|accession|locus`
DDBJ, DNA Database of Japan	`“gi”|gi-number|”dbj”|accession|locus`
General database identifier	`“gnl”|database|identifier`
“simply”	`identifier`

    - Population definition in header line:
      String after “population:” until the first space is parsed as population name
      e.g.: `>sample1 population:pop1 gene:HMA4`

- Sequence representation:

- The sequences comes after the header line and comments
- each line of a sequence should have fewer than 80 characters
- Sequences may be protein sequences or nucleic acid sequences
- Sequences can contain gaps or alignment characters
- Sequences are expected to be represented in the standard IUB/IUPAC amino acid and nucleic acid codes, with these exceptions: lower-case letters are accepted and are mapped into upper-case, a single hyphen or dash can be used to represent a gap character and in amino acid sequences: U and * are acceptable letters
- Numerical digits are not allowed but are used in some databases to indicate the position in the sequence

- simple example of a cytochrome b protein sequence:

```
>gi|5524211|gb|AAD44166.1| cytochrome b [Elephas maximus maximus]
LCLYTHIGRNIYYGSYLYSETWNTGIMLLLITMATAFMGYVLPWGQMSFWGATVITNLFSAIPYIGTNLV
EWIWGGFSVDKATLNRFFAFHFILPFTMVALAGVHLTFLHETGSNNPLGLTSDSDKIPFHPYYTIKDFLG
LLILILLLLLLALLSPDMLGDPDNHMPADPLNTPLHIKPEWYFLFAYAILRSVPNKLGGVLALFLSIVIL
GLMPFLHTSKHRSMMLRPLSQALFWTLTMDLLTLTWIGSQPVEYPYTIIGQMASILYFSIILAFLPIAGX
IENY
```

10.11.3 Links

Wikipedia: http://en.wikipedia.org/wiki/FASTA_format

NCBI's FASTA format description: http://www.ncbi.nlm.nih.gov/blast/fasta.shtml

10.11.4 Special PGDSpider input/output questions

- Input:
    - Select the data type:
      DNA/RNA/SNP_haploid/SNP_diploid
      Allows the user to specify if the data are sequence or SNP data. Diploid SNP data can be encoded with IUPAC ambiguity codes.

- Output:
    - Specify which data type should be included (optional):
      DNA/RNA/NGS/SNP
      If there is more than one allowed data type, one has to select the data type that should be included in the output file (only one data type can be analysed per file).
    - If numeric SNP data: Enter the integer that codes for the nucleotide:
      Integer
      Define the integer that codes for a specific nucleotide

- Save sequences on a single line:
  TRUE/FALSE
  Saves sequence on a single line (do not break sequences to several lines)
- Specify the locus/locus combination which should be written to the output file (optional):
  String
  If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file. Type “All loci” if you want to write all loci to the FASTA file.
- Specify the DNA locus you want to write to the output file, write "concat" for concatenation or "separate" to separate the loci:
  String/CONCAT/SEPARATE
  In case of a multi-loci DNA data set one has to choose the DNA locus to write to the output file, specify “CONCAT” to concatenate the loci into one sequence or specify “SEPARATE” to write each loci separately.
- Save haploid sequences
  TRUE/FALSE
  Saves haploid sequences (consensus sequence with ambiguity codes is taken if ploidy is higher)

10.12 Extended multi-FASTA (XMFA)

The extended multi-FASTA (XMFA) format is an extension of the FASTA format, that can include aligned sequence data from several different genomic regions.

10.12.1 Data type handled

The XMFA format can contain nucleic acid sequences.

10.12.2 XMFA format

- XMFA files are made of blocks of aligned sequences
- Each block is a multi-FASTA file followed by the = symbol
- Header line:
    - Starts with: >seq_id:start:end [+/-] comments
    - Seq_id: unique identifier for the isolate
    - Start and end: indicates were the block is located on the genome of the isolate
    - [+/-]: indicates on which DNA strand the sequence is found

- Example with 3 isolates and 2 blocks:

```
> ST1:11-20 +
ACGTACGTAC
> ST2:11-20 +
ACGTAAATAC
> ST3:535-544 +
ACGTAC-TAA
=
> ST1:21-25 +
ACGTA
> ST2:21-25 +
ACGTT
> ST3:5733-5737 -
ACGTA
=
```

10.12.3 Links

http://www.stats.ox.ac.uk/~didelot/files/xmfa2struct.pdf

http://darlinglab.org/mauve/user-guide/files.html

10.12.4 Special PGDSpider input/output questions

- Input: none

- Output:
    - Specify which data type should be included (optional):
      DNA/RNA/NGS
      If there is more than one allowed data type, one has to select the data type that should be included in the output file (only one data type can be analysed per file).
    - Save sequences on a single line:
      TRUE/FALSE
      Saves sequence on a single line (do not break sequences to several lines)

10.13 FASTQ

FASTQ format is a text-based format for storing both a biological sequence (usually nucleotide sequence) and its corresponding quality scores. Both the sequence letter and quality score are encoded with a single ASCII character. It was originally developed at the Wellcome Trust Sanger Institute to bundle a FASTA sequence and its quality data, but has recently become the de facto standard for storing the output of high throughput sequencing instruments (Cock, et al., 2010).

10.13.1 Data type handled

The FASTQ format contains sequences and their quality scores.

10.13.2 FASTQ format

- FASTQ has no standard file extension. The following extensions are often used: .fastq, .fq or .txt
- A FASTQ file normally uses four lines per sequence:
    - Line 1: begins with a '@' character and is followed by a sequence identifier and an optional description (like a FASTA title line)
    - Line 2: is the raw sequence letters (IUPAC ambiguity codes: ACTGNURYSWKMBDHV)
    - Line 3: begins with a '+' character and is optionally followed by the same sequence identifier (and any description).
    - Line 4: encodes the quality values for the sequence in Line 2 and must contain the same number of symbols as letters in the sequence.
- The original Sanger FASTQ files also allowed the sequence and quality strings to be wrapped (split over multiple lines), but this is generally discouraged as it can make parsing complicated due to the unfortunate choice of ”@” and ”+” as markers (these characters can also occur in the quality string).

- simple example of a fastq file:

```
@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
+
!''*((((***+))%%%++)(%%%%).1***-+*''))**55CCF>>>>>>CCCCCCC65
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=36
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACC
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=36
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9IC
```

10.13.3 Links

Wikipedia: http://en.wikipedia.org/wiki/FASTQ_format

(Cock, et al., 2010)

10.13.4 Special PGDSpider input/output questions

- Input:
  - Select the quality score encoding:
    33/64
    Allows the user to specify how the quality scores are encoded (Phred Score + 33 or Phred Score +64)

- Output:
  - Specify the locus/locus combination which should be written to the output file (optional):
    String/ALL
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file. Type "ALL" if you want to write all loci to the FASTQ file.

10.14 FDist2

FDist2 is a program to detect loci that might be under selection in samples drawn from structured populations (Beaumont and Nichols, 1996; Flint, et al., 1999).

10.14.1 Data type handled

FDist2 can handle Microsat, DNA and Standard (multi-allelic marker) data

10.14.2 FDist2 format

The datacal program (in the FDist2 distribution) can read the following input file:

- In the first line, a 1 or 0 indicate the format of the data matrix: alleles by rows (1) or populations by rows (0).
- The second line gives the number of populations
- Third line: number of loci
- Fourth line: number of alleles at locus 1
- Then the matrix of data at locus 1 follows either with each row corresponding to the same allele or to the same population
- The number of alleles at locus 2 is listed followed by the next data matrix, etc.
- The data matrices can also contain populations for which a locus was not genotyped, these missing data should be indicated by zero entries

- Example:

```
0
5
2

3
4 76 0
45 115 0
109 11 0          Locus 1
120 0 0
0 0 0

3
4 23 53
0 38 122
0 72 48           Locus 2
0 57 63
0 0 0
```

10.14.3 Links and References

Website: http://www.rubic.rdg.ac.uk/~mab/software.html

(Beaumont and Nichols, 1996; Flint, et al., 1999)

10.14.4 Special PGDSpider input/output questions

- Output:
  - Specify which data type should be included (optional):
    DNA/RNA/MICROSAT/SNP/RFLP/AFLP/STANDARD
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).

10.15 FSTAT

FSTAT version 2.9.3.2 (February 2002)

FSTAT estimates and tests gene diversities and differentiation statistics from codominant genetic markers. It computes both Nei and Weir & Cockerham families of estimators of gene diversities and F-statistics, and tests them using randomization methods. Jackknife and bootstrap confidence intervals are also provided (Goudet, 2001).

10.15.1 Data type handled

FSTAT can handle Microsatellite and standard (multi-allelic marker) data

10.15.2 FSTAT format

- FSTAT files have the extension *.dat
- The total number of individuals in the data set needs to be less than 20'000
- The first line contains 4 numbers separated by any number of spaces:
    - The number of samples, np (‹=200)
    - The number of loci, nl (‹=100)
    - The highest number used to label an allele, nu (‹=999)
    - And a 1 if the code for alleles is a one digit number (1-9), a 2 if the code for alleles is a 2 digit number (01-99) or a 3 if the code for alleles is a 3 digit number (001-999)
- The first line is followed by nl (number of loci) lines, each containing the name of a locus, in the order they will appear in the rest of the file
- The line nl+2 contains a series of numbers like: `1 0102 0103 0101 0203 0 0303`
    - The first number identifies the sample to which the individual belongs
    - The second number is the genotype of the individual at the first locus
    - And the third number is the genotype at the second locus and so on
- Missing genotypes are encoded with zeros (0001 or 0100 are not valid formats, because both alleles at a locus have to be known, otherwise the genotype is considered as missing)
- No empty lines are needed between samples
- The number of spaces between genotypes can be anything
- The numbering of the samples need not be sequential
- Samples need not to be ordered
- nu needs to be equal to the largest code given to an allele (even if there are less than nu alleles)

- example (code for alleles is a two digit number):

```
3  5  4  2
loc-1
loc-2
loc-3
loc-4
loc-5
1       0404 0403 0403 0303 0404
1       0404 0404 0403 0303 0404
1       0404 0404 0403 0403 0404
2       0404 0404 0303 0302 0404
2       0404 0303 0404 0403 0404
2       0404 0403 0404 0403 0404
3       0404 0404 0404 0403 0404
3       0404 0404 0404 0404 0404
3       0404 0404 0403 0201 0404
```

- To label the populations an additional label file can be given:
  - It is a text file with the extension *.lab and contains the names (labels) of the populations
  - Each line should contain the name (label) of one sample
  - The samples should appear in the same order as in the *.dat file
  - The labels can be of any length but they will be truncated to six characters in the output files
  - example:

```
Stade de France
Twickenham
Arms Park
```

10.15.3 Links and References

Website: http://www2.unil.ch/popgen/softwares/fstat.htm

(Goudet, 2001)

10.15.4 Special PGDSpider input/output questions

- Input:
  - Include file with labels:
    TRUE/FALSE
    Possibility to add a file with labels (name the populations)
  - Label file:
    Absolute file path
    Choose the file with the labels

  - Select the data type:
    MICROSAT/SNP/AFLP/STANDARD
    Needs to specify the type of the data
  - How are the Microsat alleles coded:
    REPEATS/LENGTH/ARBITARY
    Need to define if the Microsat data are coded as number of repeats, as length of the PCR fragments or as an arbitrary number.
  - Enter the size of the repeated motif:
    Integer/Integer,Integer, …
    Information needed to convert the Microsatellite data (length of the PCR fragments) to number of repeat data (PGD can only save number of repeat Microsatellite data). Same for all loci: enter one number. Different between loci: comma separated list (e.g.: 2,2,3,2)

- Output:
  - Safe additional file with labels:
    TRUE/FALSE
    Allows saving an additional file with the population names
  - Save label file:
    Absolute file path
    Choose the path where the label file should be written
  - Specify which data type should be included (optional):
    MICROSAT/STANDARD/SNP/AFLP/DNA
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.16 GDA

GDA version 1.1 (7. January 2002)

GDA allows one to compute linkage and Hardy-Weinberg disequilibrium, some genetic distances, and provides method-of-moments estimators for hierarchical F-statistics (Lewis, 2001).

10.16.1 Data type handled

GDA deals with Microsatellite, RFLP, AFLP, SNP and Standard (multi-allelic marker) data

10.16.2 GDA format

GDA uses the NEXUS format (also have a look at the NEXUS file format description) and allows the definition of a GDADATA block:

If a token (a word or a name) begins with a single or double quote character, then every character until the next, matching quote character will be treated as a single token. This is useful for putting blank spaces inside population or locus labels. The commands are not case-sensitive, except in the matrix command (allele named A is treated as being distinct form a). The following commands exist:

- begin
- dimensions:
    - number of populations: `npops=2`
    - number of loci: `nloci=5`
- format:
    - `tokens / notokens`
    - `labels / nolables`
    - `interleaved`
    - `haploid`
    - `missing = ?`
    - `separator=/`
    - `datapoint=standard`
- locusallelelabels (optional):
    - contains the loci names
    - allele names can be provided
    - loci will be numbered beginning with 1 if this command is absent
- matrix:
    - end of the data for one population is signed by either a comma or the semicolon indicating the end of the matrix command
- end

Haploid data can be described in two ways: First, if all loci are haploid one can include the keyword “haploid” in the format command. And second, if a mixture of haploid and diploid data exists one can use the command “hapset” to specify which loci are haploid.

Examples:

- diploid data:

```
#nexus
begin gdadata; [comments are surrounded by square brackets]
  dimensions npops=2 nloci=3;
  format missing=? seperator=/;
  locusallelelabels
    1 'pgi 1',
    2 'pgi 2',
    3 adh / slow fast
  ;
  matrix
    Embudo:
      indiv_1 A/A 100/100 slow/fast
      indiv_2 A/A 75 / 90 slow/slow
      indiv_3 A/a 75/100  fast/Slow
      indiv_4 A/A 100/100 fast/fast,
    Black_Mesa:
      1 a/a 110/100 fast/slow
      2 a/A  75/100 slow/slow
      3 a/a 100/100 fast/fast
  ;
end;
```

- haploid data:

```
#nexus
begin gdadata;
        dimensions nloci=5 npops=2;
        format haploid tokens missing=? datapoint=standard;
        locusallelelabels
                1 locus_1 [ / 1 2 3 4],
                2 locus_2 [ / 1 2 3 4],
                3 locus_3 [ / 1 2 3 4],
                4 locus_4 [ / 1 2 3 4],
                5 locus_5 [ / 1 2 3 4];
        matrix
        Pop_1: _1_  4 3 3 3 4
               _2_  4 4 3 3 4
               _3_  4 4 3 3 4
               _4_  4 4 ? 3 4
               _5_  4 4 2 4 4,
        Pop_2: _1_  4 4 2 2 4
               _2_  4 3 4 3 4
               _3_  4 4 3 3 4
               _4_  4 4 4 4 4
               _5_  4 3 4 4 4
;
end;
```

- mixed haploid/diploid data:

```
#NEXUS
[Note: first 2 loci are diploid and last 3 are haploid]
begin gdadata;
  dimensions nloci=5 npops=6;
  format tokens labels missing=? datapoint=standard;
  hapset 3-5;
  locusallelelabels
    1 'dip 1',
    2 'dip 2',
    3 'hap 1',
    4 'hap 2',
    5 'hap 3'
  ;
  matrix
    Pop1:
      indiv1 4/4 4/3 3 3 4
      indiv2 4/4 4/4 3 3 4
      ...
```

10.16.3 Links and References

Website: http://hydrodictyon.eeb.uconn.edu/people/plewis/software.php

(Lewis, 2001)

10.16.4 Special PGDSpider input/output questions

- Input:
  - Select the data type:
    MICROSAT/RFLP/AFLP/SNP/STANDARD
    Needs to specify the type of the data
  - How are Microsat alleles coded:
    REPEATS/LENGTH
    Needs to define if the Microsat data are coded as number of repeats or as length of the PCR fragments
  - Enter the size of the repeated motif:
    Integer/Integer,Integer, …
    Information needed to convert the Microsatellite data (length of the PCR fragments) to number of repeat data (PGD can only save number of repeat Microsatellite data). Same for all loci: enter one number. Different between loci: comma separated list (e.g.: 2,2,3,2)

- Output:
  - Specify which data type should be included (optional):
    MICROSAT/SNP/RFLP/AFLP/STANDARD/DNA
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.17 GENELAND

GENELAND (12. April 2011)

GENELAND is a computer program whose main goal is to process individual multilocus genetic data to detect population structure, i.e sub-populations at (or close to) Hardy-Weinberg and linkage equilibrium. Although the concept of population refers here to genetic structure only, it is often realistic to assume that populations are spatially organised. Toward this aim, GENELAND is based on a spatially explicit model that can make use of both geographic and genetic informations to estimate the number of populations in a dataset and delineate their spatial organisation. Important areas of application include landscape genetics, conservation genetics, human genetics and epidemiology (Guillot, 2008; Guillot, et al., 2005; Guillot, et al., 2005; Guillot and Santos, 2009; Guillot and Santos, 2010; Guillot, et al., 2008).

GENELAND is released as an add-on to the free statistical program R and is currently available for Linux, Mac-OS and Windows. It includes a fully clickable user interface requiring no particular knowledge of R.

10.17.1 Data type handled

GENELAND handles Microsatellite, SNP, AFLP, Standard (multi-allelic markers) and DNA data types.

10.17.2 GENELAND format

- Genotypes file: contains the genotypes of n haploid or diploid individuals at L co-dominant markers
- Coordinates file (optional): contains the spatial coordinates representative of each individual.

Genotypes file

Assuming that you have data for n individuals genotyped at L loci, the data must be arranged in:

- a plain ascii file
- without any extra invisible characters (like in MS-Word .doc files)
- with one line per individual
- each allele must be coded by an integer
- the number of digits of each field is arbitrary and can vary across loci
- extra header lines are not allowed
- missing data are allowed and can be coded by any arbitrary character string (e.g. 000, 00, NA or -999). By default, it is assumed that missing data are coded as NA.
- for haploid organisms with L loci, the genotype file must have L columns.

Diploid data:

Codominant data (SNP or Microsat):

- one line and 2x L columns per individual
- Example (2 individuals with 10 loci, missing data are coded as 000):

```
198 000 358 362 141 141 179 000 208 224 243 243 278 284 86 88 120 124 238 244
200 202 000 358 141 141 183 183 218 224 237 243 276 278 88 88 120 124 240 244
```

Dominant data (AFLP):

- one line and L columns per individual
- absence/presence of the allele is coded as 0/1
- Example (2 individuals with 10 loci, missing data are coded as 000):

```
0 1 1 1 0 1 0 0 0
1 0 0 1 1 0 0 1 000
```

Haploid data:

- for Microsat, SNP or mtDNA data
- one line and L columns per individual
- Example (2 individuals with 10 loci, missing data are coded as 000):

```
198 000 358 362 141 141 179 000 208 224
200 202 000 358 141 141 183 183 218 224
```

Coordinates file

- one line per individual and two columns (x-axis and y-axis coordinate)
- the units do not matter
- coordinates are planar coordinates such as UTM coordinates. Coordinates given as spherical coordinates will be interpreted as planar coordinates.
- extra header lines are not allowed
- missing data are not allowed. If some coordinates are missing, you can either substitute an estimated value or do the analysis without spatial coordinates at all using the non-spatial model.
- Example (2 individuals):

```
25.6 745.2
54.1 827.8
```

10.17.3 Links and References

Website: http://www2.imm.dtu.dk/~gigu/Geneland/,

Manual: http://www2.imm.dtu.dk/~gigu/Geneland/Geneland-Doc.pdf

(Guillot, 2008; Guillot, et al., 2005; Guillot, et al., 2005; Guillot and Santos, 2009; Guillot and Santos, 2010; Guillot, et al., 2008)

10.17.4 Special PGDSpider input/output questions

- Input:
  - Select the data type:
    MICROSAT/SNP/AFLP/STANDARD/DNA
    One has to define the type of the data (e.g.: SNP, AFLP, Microsat , Standard or DNA)
  - How are Microsat alleles coded?
    REPEATS/LENGTH/ARBITARY
    Need to define if the Microsat data are coded as number of repeats, as the length of the PCR fragments or as an arbitrary number.
  - Enter the size of the repeated motif:
    Integer/Integer,Integer, …
    Need to define the size of the repeated motif, so that the number of repeats can be calculated (Microsat alleles have to be saved as number of repeats in the PGD format). Same for all loci: enter one number. Different between loci: comma separated list (e.g.: 2,2,3,2).
  - Enter the integer that codes for the nucleotide:
    Integer
    Define the integer that codes for a specific nucleotide
  - Missing value code:
    String/Integer
    Specify the code for the missing values (e.g.: 000,00, NA, -999, etc.)
  - Include file with coordinates:
    TRUE/FALSE
    Possibility to add a file with geographic coordinates
  - Coordinate file:
    Absolute file path
    Choose the file with the coordinates

- Output:
  - Save additional file with geographic coordinates:
    TRUE/FALSE
    Saves a file with the geographic coordinates of individuals or groups (used for spatial clustering analysis)
  - Save coordination file
    Absolute file path
    Choose the path where the coordination file should be written

- Specify which data type should be included (optional):
  MICROSAT/SNP/AFLP/STANDARD/DNA/NGS
  If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
- Specify the locus/locus combination which should be written to the output file (optional):
  String
  If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.
- Specify the DNA locus you want to write to the output:
  String/CONCAT
  In case of a multi-loci DNA data set one has to choose the DNA locus to write to the output file or specify "CONCAT" to concatenate the loci into one sequence (GENELAND cannot handle multi-loci DNA data).

10.18 GENEPOP

GENEPOP version 4.1 (24. March 2011)

GENEPOP allows one to compute exact tests for Hardy-Weinberg equilibrium, for population differentiation and for genotypic disequilibrium among pairs of loci. It also computes estimations of F-statistics, null allele frequencies, allele size based statistics for microsatellites, etc. It performs analyses of isolation by distance from pairwise comparisons of individuals or population samples, including confidence intervals for “neighbourhood size” (Raymond and Rousset, 1995). This format is also used by many other population genetics programs (BAPS, FSTAT, ARLEQUIN, GENETIX, etc).

10.18.1 Data type handled

GENEPOP handles haploid and diploid data of Microsatellite and Standard (multi-allelic markers) data type.

10.18.2 GENEPOP format

- GENEPOP accepts input file names either with the extension *.txt or without any extension, but the input files have to be ASCII text files
- The first line can contain anything. It can be used to store information about the data
- The locus names may be given next, one per line or on the same line but separated by commas
- Then the population sample indicator “Pop” follows (capitalization does not matter). Each sample from a different geographical origin is declared by a line with a pop statement.
- Information for the first individual:
    - `ind#001 fem ,0101 0202 0000 0410`
    - Here “ind#001 fem” is an identifier. It is possible to use any character (except a comma!). The last identifier of every sub-population is used as the sample name in the output files. The comma between the identifier and the list of genotypes is required.
    - “0101” indicates that this individual is homozygous for the 01 allele at the first locus.
    - The third locus (0000) contains missing data
    - At the fourth locus, the genotype is 0410, which indicates the presence of alleles 04 and 10.
    - Alleles are numbered from 01 to 99 or 001 to 999 if needed. 2-digits and 3-digits coding of alleles can be intermixed (among loci, not within loci).
    - Haploid and diploid data can be intermixed. (6-digits genotypes are recognized as 3-digits diploid genotypes; 4-digits genotypes are recognized as 2-digits diploid genotypes; 2- and 3-digits genotypes are recognized as haploid genotypes. The same coding should be used consistently within each locus (for haplo-diploid data haploid data should be coded as diploid data with one unknown allele).)
    - Genotypes can extend on more than one line

- Each additional individual information starts on a new line, and may extend over several lines (but it is not allowed to start a new line in the middle of a locus genotype)
- Additional samples begin with a "Pop" statement on a new line
- There is no constraint on the number of blanks separating the various fields, but blank lines at the end of the file are not allowed
- Missing data should be indicated with 00 (or 000 for 3-digits coding) and not with blanks
- The number of locus names should correspond to the number of genotypes in each individual

- Example:

```
Title line: "Grape populations in southern France"
ADH Locus 1
ADH #2
ADH three
Pop
Grange des Peres , 0201 003003 01
Grange des Peres , 0202 003001 01
Grange des Peres , 0102 004001 01
Grange des Peres , 0103 002002 01
Grange des Peres , 0203 002004 01
POP
Tertre Roteboeuf , 0102 002002 01
Tertre Roteboeuf , 0102 002001 01
Tertre Roteboeuf , 0201 002003 01
Tertre Roteboeuf , 0201 003003 01
Tertre Roteboeuf , 0101 002001 01
Pop
, 0000 002001 01
, 0200 002001 01
, 0010 002001
01
last pop, 0101 002001 02
```

10.18.3 Links and References

Website: http://kimura.univ-montp2.fr/~rousset/Genepop.htm,

Manual: http://kimura.univ-montp2.fr/~rousset/Genepop.pdf

Input file: http://genepop.curtin.edu.au/help_input.html

(Rousset, 2008)

10.18.4 Special PGDSpider input/output questions

- Input:
  - Select the data type:
    MICROSAT/SNP/AFLP/STANDARD
    One has to define the type of the data (e.g.: SNP, AFLP, MICROSAT or STANDARD)

- How are the Microsat alleles coded:
  REPEATS/LENGTH/ARBITARY
  Need to define if the Microsat data are coded as number of repeats, as length of the PCR fragments, or as an arbitrary number
- Enter the size of the repeated motif:
  Integer/Integer,Integer, …
  Information needed to convert the Microsatellite data (length of the PCR fragments) into number of repeat data (PGD can only save number of repeat Microsatellite data). Same for all loci: enter one number. Different between loci: comma separated. list (e.g.: 2,2,3,2)

- Output:
  - Specify which data type should be included (optional):
    MICROSAT/STANDARD/SNP/AFLP/DNA
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.19 GENETIX

GENETIX version 4.05 (5. May 2004)

This set of programs computes several basic parameters of population genetics such as Nei's D and H, Wright's F-statistics and linkage disequilibrium D. For each of them, the distribution of the parameter values under the null hypothesis (for instance Hardy-Weinberg equilibrium for Fstats) is generated by the appropriate resampling scheme of the relevant objects (e.g. alleles between individuals in the case of Fis) using permutations. The permutation-based statistical inference procedures implemented in GENETIX represent an alternative to bootstrapping and jack-knifing, or to exact probability tests when available (Raymond and Rousset, 1995). In addition, an adaptation of Mantel's test for the correlation between distance matrices is available. A correspondence analysis program adapted to handle individual diploid genotypes, with tridimensional graphics, is also implemented (Belkhir, 1996-2004).

10.19.1 Data type handled

GENETIX deals with following diploid data types:

- Microsat
- RFLP
- AFLP
- SNP (numeric)
- Standard

10.19.2 GENETIX format

- The GENETIX file format has the extension *.gtx and must be an ASCII file
- The text separators can be blanks, tabulators, or other characters that need to be specified
- The first line contains the number of loci
- Second line: the number of populations
- Third line: the name of the first locus with maximal 5 characters length
- Fourth line: the number of alleles followed by a list of alleles coded with 3 numbers
- Fifth line: name of second locus
- …
- n. line: name of the first population (only 15 characters are taken)
- n+1. line: number of samples (individuals)
- n+2. line: identifier of the individual with a length of 10 characters followed by its genotype (The loci have the same order as in the list above (6 numbers per locus, because data have to be diploid)
- …
- m. line: name of the second population
- etc.

- Genotypes are coded with 6 numbers. The first 3 numbers stands for the first allele and the rest of the numbers for the second allele. The smaller allele has to come first!
- Haploid data have to be coded as homozygous diploids
- Missing values are coded as 000000. If one allele is unknown then the whole genotype must be coded as missing

- example:

```
4
2
aat1
1 120
aat2
3 100 132 146
adh
2 100 123
est1
4 100 107 110 115
Population "i"
3
i001       120120 132132 100100 107110
i002       120120 132132 100100 107110
i003       120120 100132 100100 110110
Population "j"
2
j001      120120 132132 100100 107107
j002      120120 132132 100123 107107
```

10.19.3 Links and References

Website: http://www.genetix.univ-montp2.fr/genetix/genetix.htm

(Belkhir, 1996-2004)

10.19.4 Special PGDSpider input/output questions

- Input:
  - Select the data type:
    MICROSAT/AFLP/RFLP/SNP/STANDARD
    Allows specifying the type of the data
  - How are Microsat alleles coded:
    REPEATS/LENGTH
    Need to define if the Microsat data are coded as number of repeats or as length of the PCR fragments
  - Enter the size of the repeated motif:
    Integer/Integer,Integer, …
    Needed to convert the Microsatellite data (length of the PCR fragments) to number of repeat data (PGD can only save number of repeat Microsatellite data). Same for all loci: enter one number. Different between loci: comma separated list (e.g.: 2,2,3,2).

- Output:
    - Specify which data type should be included (optional):
      MICROSAT/AFLP/RFLP/SNP/STANDARD/DNA
      If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
    - Specify the locus/locus combination which should be written to the output file (optional):
      String
      If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.20 GESTE / BayeScan

BayeScan version 2.01 (December 2010)**:**
This program identifies candidate loci under natural selection. It's applicable to both, dominant and codominant data.

GESTE version 2.0:
"GEnetic STructure inference based on genetic and Environmental data" is a Bayesian method to evaluate the effect that biotic and abiotic environmental factors (geographic distance, language, temperature, altitude, local population sizes, etc.) have on the genetic structure of populations. It can also be used to study spatial population processes, such as range expansions, by simply introducing longitude and latitude as the explanatory variables.
GESTE estimates FST values for each local population and relates them to environmental factors using a generalized linear model. The method requires genetic data from codominant markers (e.g. allozymes, microsatellites, or SNPs) and environmental data specific to each local population. The software is written in C++ and integrates a tool to draw posterior density functions (histogram, running mean, traces, etc.) and to estimate parameters from them (mean, mode, variance, HPDI etc.).

10.20.1 Data type handled

GESTE / BayeScan is able to deal with following data types:

- AFLP
- SNP
- Microsatellites
- Allozymes

10.20.2 GESTE / BayeScan format

- The program recognizes keywords in […].
- The number of loci (keyword: [loci]) and populations (keyword: [populaitons]) must be indicated before the main data.
- For each population (keyword: [pop]), there is one line per locus numbered from 1 to the number of loci.
- Population must be numbered from 1 to the number of populations.
- Then there is the number of alleles measured for this population at this locus (50 individuals make 100 alleles for diploids) and the number of possible alleles found at this locus (for all populations).
- After, there is the corresponding allele count. This part must sum to the number of alleles measured.
- Number of individuals can be different at every locus (missing data).
- Comments can be written between sections.

- There is no particular file extension needed.

- Example:

```
[loci]=5

[populations]=2

[pop]=1
  1  100   7   34    0   4   0  13  20  29
  2  100   7    3   26   2   8  56   2   3
  3  100   7   46    0  17   1  10  25   1
  4  100   7    4    7   2  52  23  12   0
  5  100   7   23  28    0   1   2   38   8

[pop]=2
  1  100   7   11   6  17   2   8  36  20
  2  100   7    8   6   3  26  36   9  12
  3  100   7   11   7  35  13  26   8   0
  4  100   7   14   2   0  24  36  24   0
  5  100   7   20   6  19  36   6  10   3
```

10.20.3 Links and References

GESTE:

- Website: http://www-leca.ujf-grenoble.fr/logiciels.htm
- (Foll and Gaggiotti, 2006)

BayeScan:

- Website: http://cmpg.unibe.ch/software/bayescan/index.html
- (Fischer, et al., 2011; Foll, et al., 2010; Foll and Gaggiotti, 2008)

10.20.4 Special PGDSpider input/output questions

- Output:
  - Specify which data type should be included (optional):
    MICROSAT/SNP/AFLP/STANDARD/DNA
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).

10.21 HGDP

Scientists at Stanford University have collaborated on a large study to understand genetic diversity in human populations. They analyzed genomic DNA from 1,043 individuals from around the world, determining their genotypes at more than 650,000 SNP loci, with the Illumina BeadStation technology. Genomic DNA samples from these fully-consenting individuals were collected by the Human Genome Diversity Project (HGDP), in a collaboration with the Centre Etude Polymorphism Humain (CEPH) in Paris.

The HGDP-CEPH Human Genome Diversity Cell Line Panel is a widely used resource for studies of human genetic variation (Cann, et al., 2002).The DNA samples in the HGDP panel are publicly available for studies of genetic variation, and they now form the basis for a sizeable body of human genetics research (Cavalli-Sforza, 2005).

10.21.1 Data type handled

HGDP data consist of genome wide SNPs

10.21.2 Stanford HGDP format

Main file:

- Tab-delimited (matrix format)
- First line: Sample names
- Columns: genotypes for 1043 samples
- Rows: 660918 markers
- Missing values: -
- Example:

```
             HGDP00448   HGDP00479    HGDP00985   HGDP01094   HGDP00982
MitoA10045G  AA          AA           AA          AA          AA
MitoA10551G  AA          AA           AA          AA          AA
MitoA13106G  GG          GG           GG          GG          GG
rs10000543   CC          CC           TC          CC          CC
```

Map file (marker information):

- Tab-delimited list of 660918 markers
- First column: marker names
- Second column: chromosome
- Third column: coordinates
- Example:

```
MitoA10045G   M   10045
MitoA10551G   M   10551
MitoA13106G   M   13106
rs10000543    4   30979886
```

10.21.3 Links

Website: http://www.hagsc.org/hgdp/files.html

10.21.4 Special PGDSpider input/output questions

- Input:
    - Include a file with marker information (map file):
      TRUE/FALSE
      If yes, one can add a file with marker information.
    - Specify the map file (marker information):
      Absolute file path
      Choose the file with the marker information.
    - Include a file with population definitions:
      TRUE/FALSE
      If yes, one can add a file with marker information.
    - Specify a file with population definitions (optional):
      Absolute file path
      One can specify a file containing the definition of which individual belongs to which population. The population definition file should have following format (names without whitespaces):

```
Ind_1      pop_1
Ind_2      pop_1
Ind_3      pop_2
Ind_4      pop_2
```

10.22 HGDP-CEPH

The HGDP-CEPH Human Genome Diversity Cell Line Panel is a widely used resource for studies of human genetic variation. The HGDP-CEPH Human Genome Diversity Cell Line Panel (henceforth the "HGDP panel") is a collection of 1064 DNA samples from individuals distributed around the world (Cann, et al., 2002).The DNA samples in the HGDP panel are publicly available for studies of genetic variation, and they now form the basis for a sizeable body of human genetics research (Cavalli-Sforza, 2005).

The HGDP Database is designed to receive and store the polymorphic marker genotypes generated by users of the DNAs of the HGDP-CEPH Diversity Panel. The data are accessible publically via a web interface (database V2.0 only) and/or as flat files. In addition to genotypes, the database includes information on the geographic and population origin, and on the gender of each of the participating volunteers, who are identified by code numbers only (HGDP identifiers).

10.22.1 HGDP-CEPH export formats

The HGDP data can be exported into two different formats: The LINKAGE-like and the ARLEQUIN format (see the ARLEQUIN format description) with an additional log file. The PGDSpider can only read in the ARLEQUIN format with the additional log file.

The log file looks like the following example:

```
#HGDP database V2.0 ; 2008/04/09 12:04:24
#Dump format : Arlequin ; Filename : 20080409_120424_report.log
#Selected populations : Karitiana, Surui, Colombians, Maya, Pima, Cambodians
identifier   dbsnp_id     chrom  physical_pos MAF_Europe   HetZ_Europe
rs6696404    rs6696404    1      3015090       0.0268       0.0537
rs760567     rs760567     1      3023622       0.1946       0.2819
rs2993491    rs2993491    1      3034767       0.2349       0.2953
rs2817172    rs2817172    1      3064676       0.3926       0.4631
```

10.22.2 Links

Website: http://www.cephb.fr/en/hgdp/

10.22.3 Special PGDSpider input/output questions

- Input:
  - Select log file:
    Absolute file path
    Choose the log file.

10.23 Immanc and BayesAss

Immanc version 5.0 (8 October 1998)

Detecting Immigrants Using Multilocus Genotypes (Rannala and Mountain, 1997).

BayesAss+ version 1.3 (4 May 2005)

Bayesian Estimation of Recent Migration Rates Using Multilocus Genotypes (Wilson and Rannala, 2003).

10.23.1 Data type handled

Immanc/ BayesAss can handle diploid data of following data types:

- microsatellites
- RFLPs
- SNPs
- Standard
- allozymes

10.23.2 Immanc format

- The Immanc file should have the suffix of *.inp or *.txt
- The Columns can be separated by any whitespace
- Missing genotypes should be represented by 0, 00, or 000
- Blanks are not allowed
- The first column contains the individual labels
- The second column contains the population labels
- The third column contains the locus labels
- The remaining 2 columns contain the alleles at each locus that make up a genotype
- Spaces within names are not allowed
- Each individual has a row entry for every locus
- The order of the alleles determines the haplotype phase (this information is not currently used and so the ordering is arbitrary)
- The setup for the data file should be:

```
Individual1     population1     locus1     allele1     allele2
Individual2     population1     locus1     allele1     allele2
```

- Example (data for 15 individuals from two populations, genotyped for two loci)

```
ind1    pop1    locA    194     198
ind2    pop1    locA    198     198
ind3    pop1    locA    192     198
ind4    pop2    locA    184     194
ind5    pop2    locA    190     194
ind6    pop2    locA    184     194
ind7    pop2    locA    192     194
ind8    pop2    locA    184     194
ind1    pop1    locB    158     162
ind2    pop1    locB    148     162
ind3    pop1    locB    150     158
ind5    pop2    locB    150     162
ind6    pop2    locB    158     162
ind7    pop2    locB    152     156
ind8    pop2    locB    156     158
```

10.23.3 Links and References

Website: http://www.rannala.org/?page_id=13

Manual: http://www.rannala.org/docs/immanc.html

(Rannala and Mountain, 1997)

(Wilson and Rannala, 2003).

10.23.4 Special PGDSpider input/output questions

- Input:
    - Select the data type:
      MICROSAT/SNP/RFLP/AFLP/STANDARD
      Allows specifying the type of the data
    - How are Microsat alleles coded:
      REPEATS/LENGTH/ARBITARY
      Need to define if the Microsat data are coded as number of repeats, as length of the PCR fragments or as an arbitrary number
    - Enter the size of the repeated motif:
      Integer/Integer,Integer, …
      Needed to convert the Microsatellite data (length of the PCR fragments) to number of repeat data (PGD can only save number of repeat Microsatellite data). Same for all loci: enter one number. Different between loci: comma separated list (e.g.: 2,2,3,2).

- Output:
  - Specify which data type should be included (optional):
    MICROSAT/SNP/RFLP/AFLP/STANDARD/DNA
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.24 IM/IMa

IM/IMa (17. December 2009)

IM is a program estimating the parameters of an isolation model with migration from haplotype data drawn from two closely related species or populations. A relatively large numbers of loci can be studied simultaneously, and different mutation models can be used. IM estimates the divergence time and the migrations having occurred in the ancestry of two populations, which might have grown exponentially since they split (Hey and Nielsen, 2004; Nielsen and Wakeley, 2001).

IMa allows log likelihood ratio tests of nested demographic models to be performed. IMa is faster and better than IM (i.e. by virtue of providing access to the joint posterior density function), and it can be used for most (but not all) of the situations and options that IM can be used for (Hey and Nielsen, 2007).

10.24.1 Data type handled

IM can handle DNA and Microsatellite (STR) data.

10.24.2 IM/IMa format

- line 1 contains arbitrary text, usually explaining the content of the file
- After line 1, comments can be included to provide explanatory information. Each line of comment must begin with a '#'.
- Line 2 (or line after comments): two population names, for populations 1 and 2 respectively, separated by one or more spaces
- Line 3: the number of loci in the data set (integer)
- Line 4: basic information for locus 1. This line contains at least five items separated by one or more spaces
  1. The locus name (no spaces within the name)
  2. The sample size for population 1 (n1)
  3. The sample size for population 2 (n2)
  4. The length of the sequence
  5. A letter indicating the mutation model
     - I: Infinite Sites (IS) model (Kimura, 1969). Under this model every mutation that has occurred in the history of a sample of sequences occurs at a different place in a DNA sequence.
     - H: Hasegawa-Kishino-Yano (HKY) model (Hasegawa, et al., 1985) was applied to the Isolation with Migration model by Palsboll et al. (Palsboll, et al., 2004). It is a general model that allows for multiple substitution, with different rates of transitions and transversions as well as unequal frequencies of the four nucleotides.
     - S: Stepwise Mutation Model (SMM) (Kimura and Ohta, 1978). This model can be applied to allelic variation in which each mutation causes an allele to increase or decrease by one step on whatever scale the alleles are being measured.

        - J: joint SSM and IS model. This model is named HapSTR
        - If this letter is not included on this line, the default is IS. If SSM (S) or HapSTR (J), the letter is followed immediately (no spaces) by the number of linked STR markers within the locus.
    6. Inheritance scalar (e.g.: 1 for autosome, 0.75 for X-linked, 0.25 for Y-linked or mtDNA)
    7. The mutation rate per year for the locus (not per base pair). This can be left blank, but is needed for estimating parameters on demographic scales. If there are multiple STRs in the locus then there can be multiple mutation rates on this line separated by spaces. If the locus is a HapSTR, then the first mutation rate given applies to the sequence portion of the locus with subsequent values corresponding to STR markers included in the locus.
    8. If the mutation rate is given, it can be followed by a range of mutation rates that can be used (with ranges for other loci in the analysis) to set priors on the ratios of mutation rate scalars. The range is entered with open parentheses, the lowest value, a comma, the highest value, and closed parentheses (e.g. '(0.00001, 0.00004)'. The range must bracket the rate. For a locus with multiple mutation rates, and multiple ranges, each range follows its corresponding mutation rate immediately on line.
- Line 5: data for first gene copy from population 1:
    - The first 10 spaces are devoted to the sample name.
    - The sequence or allele length (for SSM model) begins in column 11 of the file. The sequence for a given sample is given all on one line without gaps
    - For SSM or HapSTR data, the allele length assumes a step size of 1. This means that data from STRs that are multiples of lengths greater than 1 must be converted to counts of the number of base repeats.
    - If the data is for an SSM model locus and there are multiple STRs, then there will be one integer on each line for each STR, separated by a space.
    - If the locus is HapSTR (joint IS and SSM) then the STR data is given on the line, beginning at column 11, followed by the sequence data.
    - For SSM data, as for other types of data, only one gene copy is represented on each line of the data file. Diploid genotype data must be broken up and listed, with one data line for each gene copy.
- Line 6 through line (n1+n2 +4): the remainder of the data for locus 1. Each line contains the data for one sample. The data for population 1 samples are given in lines 5 through line (n1 + 4). The data for population 2 begins on line (n1+5) and proceeds to line (n1+n2+4).
- Additional lines for additional loci: If there is more than one locus, then the data for locus 2 begins on line (n1+n2+5) with a line similar to line 4 presenting the basic information for locus 2. The sample names and sample sizes for locus 2 and the inheritance scalars and mutation model for locus 2 does not need to be the same as for locus 1
- The last line should end with a newline so that the file ends on a blank line

- **Example** (a tiny three locus data set. The mutation rate per year is known and specified for locus 1, but not for loci 2 and 3)

```
Example data for IM
# im test data
population1 population2
3
locus1 1 1 13 I 1 0.0000000008 (0.0000000001, 0.0000000015)
pop1_1    ACTACTGTCATGA
pop2_1    AGTACTATCACGA
hapstrexample 2 1 4 J2 0.75
pop1_1    13 34 GTAC
pop1_2    12 35 GTAT
pop2_1    12 37 GTAT
strexample 2 2 1 S1 1 0.00001 (0.000001, 0.00005)
strpop11a 23
strpop11b 26
strpop21a 25
strpop21b 31
```

10.24.3 Links and References

Website: http://genfaculty.rutgers.edu/hey/software

Manual: http://lifesci.rutgers.edu/~heylab/ProgramsandData/Programs/IM/Using_IM_3_5_2007.pdf

(Hey and Nielsen, 2004; Nielsen and Wakeley, 2001)

(Hey and Nielsen, 2007)

10.24.4 Special PGDSpider input/output questions

- Input:
  - Keep loci independent:
    TRUE/FALSE
    Specify if you like to keep loci independent (separate) or not

- Output:
  - Select first population:
    String
    Need to define the first population, because only two populations can be included
  - Select second population:
    String
    Need to define the second population, because only two populations can be included
  - Are the loci linked:
    TRUE/FALSE
    Need to define if the specified loci are linked or not
  - Select the inheritance scalar of the loci:
    1/0.75/0.25
    Need to give the inheritance scalar of the specified loci. One can choose between 1 (autosome), 0.75 (X-linked) and 0.25 (Y-linked or mtDNA)

10.25 IMa2

IMa2 (26. September 2011)

The program implements a method for generating posterior probabilities for complex demographic population genetic models. IMa2 works similarly to the older IMa program, with some important additions. IMa2 can handle data and implement a model for multiple populations (for numbers of sampled populations between one and ten) – not just two populations (as was the case with the original IM and IMa programs).

10.25.1 Data type handled

IMa2 can handle DNA and Microsatellite (STR) data.

10.25.2 IMa2 format

The format for data files for IMa2 is very similar to that for IM and IMa. The differences are that IMa2 requires two extra lines, one for the number of populations and one for the population tree string.

- Line 1 contains arbitrary text, usually explaining the content of the file
- After line 1, comments can be included to provide explanatory information. Each line of comment must begin with a '#'.
- Line 2 (or line after comments): number of populations (npops)
- Line 3: population names in order, separated by one or more spaces. This order also corresponds to the order in which the populations are numbered in the population tree and the order in which the data occur for each locus.
- Line 4: the population string in modified Newick format. The string contains information on the topology of the tree for the sampled populations and information on the ordering of the internal nodes in time. These internal nodes correspond to ancestral populations. The ancestral populations are numbered beginning with npops for the most recent ancestral population and proceeds up to 2×(npops-1) for the ancestor of all the sampled populations. Sampled populations in the string are represented by their respective number. Ancestral populations are represented by a colon, i.e. ':', followed by their ancestral population number.
    - If there is only a single population then the tree string is simply: 0.
    - If there are two populations then the tree string is: (0,1):2
- Line 5: the number of loci in the data set (integer)
- Line 6: basic information for locus 1. This line contains at least five items separated by one or more spaces
    1. The locus name (no spaces within the name)
    2. The sample size for each population for that locus. These numbers do not need to be the same for different loci. If a population is not represented at this locus, a zero is used for that population
    3. The length of the sequence

4. A letter indicating the mutation model
    - I: Infinite Sites (IS) model (Kimura, 1969). Under this model every mutation that has occurred in the history of a sample of sequences occurs at a different place in a DNA sequence.
    - H: Hasegawa-Kishino-Yano (HKY) model (Hasegawa, et al., 1985) was applied to the Isolation with Migration model by Palsboll et al. (Palsboll, et al., 2004). It is a general model that allows for multiple substitutions, with different rates of transitions and transversions as well as unequal frequencies of the four nucleotides.
    - S: Stepwise Mutation Model (SMM) (Kimura and Ohta, 1978). This model can be applied to allelic variation in which each mutation causes an allele to increase or decrease by one step on whatever scale the alleles are being measured.
    - J: joint SSM and IS model. This model is named HapSTR
    - If this letter is not included on this line, the default is IS. If SSM (S) or HapSTR (J), the letter is followed immediately (no spaces) by the number of linked STR markers within the locus.
5. Inheritance scalar (e.g.: 1 for autosome, 0.75 for X-linked, 0.25 for Y-linked or mtDNA)
6. The mutation rate per year for the locus (not per base pair). This can be left blank, but is needed for estimating parameters on demographic scales. If there are multiple STRs in the locus then there can be multiple mutation rates on this line separated by spaces. If the locus is a HapSTR, then the first mutation rate given applies to the sequence portion of the locus with subsequent values corresponding to STR markers included in the locus.
7. If the mutation rate is given, it can be followed by a range of mutation rates that can be used (with ranges for other loci in the analysis) to set priors on the ratios of mutation rate scalars. The range is entered with open parentheses, the lowest value, a comma, the highest value, and closed parentheses (e.g. '(0.00001, 0.00004)'. The range must bracket the rate. For a locus with multiple mutation rates, and multiple ranges, each range follows its corresponding mutation rate immediately on line.

- Line 7: data for first gene copy from population 1:
    - The first 10 spaces are devoted to the sample name.
    - The sequence or allele length (for SSM model) begins in column 11 of the file. The sequence for a given sample is given all on one line without gaps
    - For SSM or HapSTR data, the allele length assumes a step size of 1. This means that data from STRs that are multiples of lengths greater than 1 must be converted to counts of the number of base repeats. Any number less than 5 causes the program to stop with an error.
    - If the data is for an SSM model locus and there are multiple STRs, then there will be one integer on each line for each STR, separated by a space.
    - If the locus is HapSTR (joint IS and SSM) then the STR data is given on the line, beginning at column 11, followed by the sequence data.
    - For SSM data, as for other types of data, only one gene copy is represented on each line of the data file. Diploid genotype data must be broken up and listed, with one data line for each gene copy.

- Line 8 through line: the remainder of the data for locus 1. Each line contains the data for one sample. The data for locus 1 for population 1 immediately follow those for population 0, and so on
- Additional lines for additional loci: If there is more than one locus, then the data for locus 2 begins on line (n1+n2+5) with a line similar to line 4 presenting the basic information for locus 2. The sample names and sample sizes for locus 2 and the inheritance scalars and mutation model for locus 2 does not need to be the same as for locus 1
- The last line should end with a newline so that the file ends on a blank line

- **Example** (a tiny three locus data set. The mutation rate per year is known and specified for locus 1, but not for loci 2 and 3)

```
Example data  for IMa
# example data set
3
pop0 pop1 pop2
((0,1):3,2):4
3
locus1 1 1 2 13 I 0.25 0.0000000008
pop0_1    ACTACTGTCATGA
pop1_1    AGTACTATCACGA
pop2_1    AGTACTATCACGA
pop2_2    AGTACTATCATGA
hapstrexample 2 1 0 4 J1 0.75
pop1_1    13 GTAC
pop1_2    12 GTAT
pop2_1    12 GTAT
strexample 2 2 2 1 S3 1  0.00001  0.000015 0.00008
strpop01a 23 12 9
strpop01b 26 10 11
strpop11a 25 10 9
strpop11b 31 11 9
strpop21a 26 12 11
strpop21b 26 13 12
```

10.25.3 Links and References

Website: http://genfaculty.rutgers.edu/hey/software#IMa2

Manual:
http://lifesci.rutgers.edu/~heylab/ProgramsandData/Programs/IMa2/Using_IMa2_8_24_2011.pdf

(Hey, 2010; Hey, 2010)

10.25.4 Special PGDSpider input/output questions

- Input:
  - Keep loci independent:
    TRUE/FALSE
    Specify if you like to keep loci independent (separate) or not

- Output:
    - Enter the population tree string (modified Newick format with population names):
      String
      Need to specify the population tree string (see the input format section for a description). The population names should be given as a string and not as integers (to avoid mistakes).
    - Are the loci linked:
      TRUE/FALSE
      Need to define if the specified loci are linked or not
    - Select the inheritance scalar of the loci:
      1/0.75/0.25
      Need to give the inheritance scalar of the specified loci. One can choose between 1 (autosome), 0.75 (X-linked) and 0.25 (Y-linked or mtDNA)

10.26 KML

KML version 2.2

KML is a file format used to display geographic data in an Earth browser such as Google Earth, Google Maps, and Google Maps for mobile. KML uses a tag-based structure with nested elements and attributes and is based on the XML standard (Google, 2009).

10.26.1 Data type handled

KML is able to handle geographic data (coordinates).

10.26.2 KML format

A Placemark is one of the most commonly used features in Google Earth. It marks a position on the Earth's surface, using a yellow pushpin as the icon. The simplest Placemark includes only a <Point> element, which specifies the location of the Placemark. One can specify a name and a custom icon for the Placemark, and one can also add other geometry elements to it. There exist three different types of placemark: simple, floating, and extruded.

The structure of a KML file breaks down as follows:

- An XML header: This is line 1 in every KML file. No spaces or other characters can appear before this line: `<?xml version=”1.0” encoding=”UTF-8”?>`
- A KML namespace declaration and root element. This is line 2 in every KML 2.2 file: `<kml xmlns=http://www.opengis.net/kml/2.2>`
- A element named “Document” which surrounds all other elements
- A Style element:
    - “id” attribute giving the name of the style
    - “IconStyle” element containing the “Icon” element, which contains the “href” element with the URL to the icon picture
- A Placemark element that contains the following elements:
    - “name” element used as the label for the Placemark
    - “styleUrl” element giving the name of the used style
    - “description” element containing a description that appears in the “balloon” attached to the Placemark
    - “Point” element that contains the “coordinates” element specifying the position of the Placemark on the Earth's surface (longitude, latitude, and optional altitude)

Example:

```
<?xml version="1.0" encoding="UTF-8"?>
<kml xmlns="http://www.opengis.net/kml/2.2">
  <Document>

    <Style id="blue">
      <IconStyle>
        <Icon>
          <href>http://maps.google.com/mapfiles/ms/icons/blue.png</href>
        </Icon>
      </IconStyle>
    </Style>

    <Placemark>
      <name>IconStyle.kml</name>
      <styleUrl>#blue</styleUrl>
      <Point>
        <coordinates>-122.36868,37.831145,0</coordinates>
      </Point>
    </Placemark>

    <Style id="blue-dot">
      <IconStyle>
        <Icon>
          <href>http://maps.google.com/mapfiles/ms/icons/blue-dot.png</href>
        </Icon>
      </IconStyle>
    </Style>

    <Placemark>
      <name>IconStyle.kml</name>
      <styleUrl>#blue-dot</styleUrl>
      <Point>
        <coordinates>-123.36868,37.831145,0</coordinates>
      </Point>
    </Placemark>

  </Document>
</kml>
```

10.26.3 Links and References

Website: http://code.google.com/intl/de-CH/apis/kml/documentation/kml_tut.html

10.26.4 Special PGDSpider input/output questions

- Output: none

10.27 MAF

MAF version 1

The multiple alignment format stores a series of multiple alignments in a format that is easy to parse and relatively easy to read. This format stores multiple alignments at the DNA level between entire genomes.

10.27.1 Data type handled

MAF is able to handle DNA data type

10.27.2 MAF format

General structure:

- The MAF files have the extension *.maf and are ASCII text files
- It is line orientated
- Each multiple alignment ends with a blank line
- Each sequence in alignment is on a single line (no length limit)
- Words in a line are delimited by any white space
- Comment lines starts with #
- Lines with meta-data starts with ##
- File is divided into paragraphs that terminate in a blank line.
- The first word of a line indicates its type
- Alignments:
    - Each multiple alignment is in a separate paragraph
    - begins with an “a” line
    - contains an “s” line for each sequence
    - optional lines:
        - “i” line: information about what is in the aligned species
        - “e” line: information about the size of the gap between the alignments that span the current block
        - “q” line: indicating the quality of each aligned base for the species

Custom Tracks:

- First line must be a “track” line that contains a name=value pair specifying the track name: `track name=sample`
- Optional specifications:
    - description="Sample Track": Gives a long name for the track
    - frames=multiz28wayFrames: Tells the browser which table to grab the gene frames from
    - mafDot=on: Use dots instead of bases when bases are identical
    - visibility=dense|pack|full: Sets the default visibility mode for this track

  - speciesOrder="hg18 panTro2": White-space separated list specifying the order in which the sequences in the maf should be displayed

Header line:

- begins with ##maf, followed by white-space separated variable=value pairs (no whitespace surrounding "="):
  `##maf version=1 scoring=tba.v8`
- current variables:
  - version: required, currently set to 1
  - scoring (optional): a name for the scoring scheme used for the alignments:
    - bit: corresponds to blast bit values
    - blastz: blastz scoring scheme
    - probability: some score normalized between 0 and 1
- usually followed by a comment line (starts with #) that describes the parameters that were used to run the alignment program

Alignment block lines:

- lines starting with "a", followed by name=value pairs: `a score=23262.0`
- there are no required name=value pairs
- current variables:
  - score (optional): floating point score
  - pass (optional): positive integer value, defines which pass the alignment came from

- lines starting with "s": a sequence within an alignment block:
```
s hg16.chr7    27707221 13 + 158545518 gcagctgaaaaca
s panTro1.chr6 28869787 13 + 161576975 gcagctgaaaaca
s baboon         249182 13 +   4622798 gcagctgaaaaca
s mm4.chr6     53310102 13 + 151104725 ACAGCTGAAAATA
```
- They have the following fields:
  - src: name of one of the source sequences for the alignment. For sequences that are resident in a browser assembly, the form 'database.chromosome' allows automatic creation of links to other assemblies.
  - start: start of the aligning region in the source sequence. This is a zero-based number. If the strand field is '-' then this is the start relative to the reverse-complemented source sequence.
  - size: size of the aligning region in the source sequence. This number is equal to the number of non-dash characters in the alignment text field below
  - strand: either '+' or '-'. If '-', then the alignment is to the reverse-complemented source
  - srcSize: size of the entire source sequence, not just the parts involved in the alignment
  - text: nucleotides (or amino acids) in the alignment and any insertions (dashes) as well

- lines starting with “I”: information about what’s happening before and after this block in the aligning species:

```
s hg16.chr7    27707221 13 + 158545518 gcagctgaaaaca
s panTro1.chr6 28869787 13 + 161576975 gcagctgaaaaca
i panTro1.chr6 N 0 C 0
s baboon         249182 13 +   4622798 gcagctgaaaaca
i baboon       I 234 n 19
```

- contains information about the context of the sequence line immediately preceding them
- contains following fields:
    - src: name of the source sequence for the alignment. Should be the same as the 's' line immediately above this line.
    - leftStatus: A character that specifies the relationship between the sequence in this block and the sequence that appears in the previous block.
    - leftCount: Usually the number of bases in the aligning species between the start of this alignment and the end of the previous one.
    - rightStatus: A character that specifies the relationship between the sequence in this block and the sequence that appears in the subsequent block:
        - C: the sequence before or after is contiguous with this block.
        - I: there are bases between the bases in this block and the one before or after it.
        - N: this is the first sequence from this src chrom or scaffold.
        - N: this is the first sequence from this src chrom or scaffold but it is bridged by another alignment from a different chrom or scaffold.
        - M: there is missing data before or after this block (Ns in the sequence).
        - T: the sequence in this block has been used before in a previous block (likely a tandem duplication)
    - rightCount: Usually the number of bases in the aligning species between the end of this alignment and the start of the next one.

- lines starting with “e”: information about empty parts of the alignment block:

```
s hg16.chr7    27707221 13 + 158545518 gcagctgaaaaca
e mm4.chr6     53310102 13 + 151104725 I
```

- indicate that there isn't aligning DNA for a species
- following fields are defined by position:
    - src: The name of one of the source sequences for the alignment.
    - start: The start of the non-aligning region in the source sequence. This is a zero-based number. If the strand field is '-' then this is the start relative to the reverse-complemented source sequence.
    - size: The size in base pairs of the non-aligning region in the source sequence.
    - strand: Either '+' or '-'. If '-', then the alignment is to the reverse-complemented source.
    - srcSize: The size of the entire source sequence, not just the parts involved in the alignment. alignment and any insertions (dashes) as well.
    - status: A character that specifies the relationship between the non-aligning sequence in this block and the sequence that appears in the previous and subsequent blocks:

- C: the sequence before and after is contiguous implying that this region was either deleted in the source or inserted in the reference sequence. The browser draws a single line or a '-' in base mode in these blocks.
- I: there are non-aligning bases in the source species between chained alignment blocks before and after this block. The browser shows a double line or '=' in base mode.
- M: there are non-aligning bases in the source and more than 90% of them are Ns in the source. The browser shows a pale yellow bar.
- n: there are non-aligning bases in the source and the next aligning block starts in a new chromosome or scaffold that is bridged by a chain between still other blocks. The browser shows either a single line or a double line based on how many bases are in the gap between the bridging alignments.

- lines starting with “q”: information about the quality of each base for the species:

```
s hg18.chr1                  32741 26 + 247249719 TTTTTGAAAAACAAACAACAAGTTGG
s panTro2.chrUn            9697231 26 +  58616431 TTTTTGAAAAACAAACAACAAGTTGG
q panTro2.chrUn                                   99999999999999999999999999
s dasNov1.scaffold_179265     1474  7 +      4584 TT----------AAGCA---------
q dasNov1.scaffold_179265                         99----------32239---------
```

- compressed version of the actual raw quality data with a single character of 0-9 or F (finished sequence). Calculated as follows:
  `MAF quality value = min( floor(actual quality value/5), 9 )`
- following fields are defined:
  - src: The name of the source sequence for the alignment. Should be the same as the 's' line immediately preceding this line.
  - value: MAF quality value corresponding to the aligning nucleotide acid in the preceding 's' line. Insertions (dashes) in the preceding 's' line are represented by dashes in the 'q' line as well.

- Example (with 3 alignment blocks):

```
track name=euArc visibility=pack
##maf version=1 scoring=tba.v8
# tba.v8 (((human chimp) baboon) (mouse rat))

a score=23262.0
s hg18.chr7    27578828 38 + 158545518 AAA-GGGAATGTTAACCAAATGA---ATTGTCTCTTACGGTG
s panTro1.chr6 28741140 38 + 161576975 AAA-GGGAATGTTAACCAAATGA---ATTGTCTCTTACGGTG
s baboon         116834 38 +   4622798 AAA-GGGAATGTTAACCAAATGA---GTTGTCTCTTATGGTG
s mm4.chr6     53215344 38 + 151104725 -AATGGGAATGTTAAGCAAACGA---ATTGTCTCTCAGTGTG
s rn3.chr4     81344243 40 + 187371129 -AA-GGGGATGCTAAGCCAATGAGTTGTTGTCTCTCAATGTG

a score=5062.0
s hg18.chr7    27699739 6 + 158545518 TAAAGA
s panTro1.chr6 28862317 6 + 161576975 TAAAGA
s baboon         241163 6 +   4622798 TAAAGA
s mm4.chr6     53303881 6 + 151104725 TAAAGA
s rn3.chr4     81444246 6 + 187371129 taagga

a score=6636.0
s hg18.chr7    27707221 13 + 158545518 gcagctgaaaaca
s panTro1.chr6 28869787 13 + 161576975 gcagctgaaaaca
s baboon         249182 13 +   4622798 gcagctgaaaaca
s mm4.chr6     53310102 13 + 151104725 ACAGCTGAAAATA#Chicken
```

10.27.3 Links and References

Website: https://genome.ucsc.edu/FAQ/FAQformat#format5

10.27.4 Special PGDSpider input questions

- Input: none

10.28 MEGA

MEGA version 5 (26. April 2011)

MEGA is an integrated tool for conducting automatic or manual sequence alignment, inferring phylogenetic trees, mining web-based databases, estimating rates of molecular evolution, and testing evolutionary hypotheses (Tamura, et al., 2007).

10.28.1 Data type handled

MEGA is able to handle following data types:

- DNA
- RNA
- nucleotide
- distance
- protein sequences

10.28.2 MEGA format

- The MEGA files have the extension *.meg and are ASCII text files
- The first line need to contain the keyword #MEGA
- The second line of the data file may contain a description of the data. The Title statement is written according to a set of rules:
    - always begins with `!Title` and ends with a semicolon (“;”)
    - do not occupy more than one line of text
    - a semicolon inside the statement is not allowed
    - example:

```
#mega
!Title This is an example title;
```

- The third line contains the description statement:
    - Gives detailed information on the data file
    - always begins with `!Description` and ends with a semicolon (“;”)
    - may occupy multiple lines
    - a semicolon inside the statement is not allowed
    - example:

```
#mega
!Title This is an example title;
!Description This is detailed information the data file;
```

- The format statement includes the information on the data type present in the file and some of its attributes:
  - written after the Title and the Description statement
  - contains one or more command statements. This command statements contain a predefined command, followed by an equal sign and a valid setting keyword (`command=keyword`).
- Comments can be anywhere in the data file, can span multiple lines, are enclosed in square brackets ([and]) and can be nested
- Keyword can be written in any combination of lower- and uppercase letters
- Taxa Names:
  - Every label must be written on a new line, and a '#' sign must precede the label
  - There are no restrictions on the length of the labels
  - The labels are not required to be unique (although identical labels may result in ambiguities and should be avoided)
  - Labels must start with alphanumeric characters (0-9, a-z, and A-Z) or a special character: `-`, `+` or `.`
  - After the first character, taxa labels may contain the following additional special characters: `_`, `*`, `:`, `( )`, `|`, `\`, `/`
  - For multiple word labels, an underscore can be used to represent a blank space

Sequence Input Data:

- Need to consist of two or more aligned sequences of equal length
- Sequences are written in the IUPAC single-letter code in any combination of upper- and lowercase letters
- Spaces and tabs are ignored
- Generally used special symbols : "." for identical sites, "-" for alignment gaps and "?" for missing data
- Keywords for the Format Statement:

Command	**Setting**	**Remark**	**Example**
DataType	DNA, RNA, nucleotide, protein		DataType=DNA
NSeqs	integer	Number of sequences	NSeqs=85
NTaxa	integer	Synonymous with NSeqs	NTaxa=85
NSites	integer	Number of nucleotides	Nsites=4592
Property	Exon, Intron, Coding, Noncoding, and End	Specifies whether a domain is protein coding. Exon and Coding are synonymous, as are Intron and Noncoding. End specifies that the domain with the given name ends at this point	Property=cyt_b
Indel	single character	dash (-) to identify insertion/deletions	Indel = -

Identical	single character	use period (.) to show identity with the first sequence	Identical = .
MatchChar	single character	Synonymous with the identical keyword	MatchChar = .
Missing	single character	use question mark (?) to indicate missing data	Missing = ?
CodeTable	A name	This instruction gives the name of the code table for the protein coding domains of the data	CodeTable = Standard

Tab. 11: table with the keywords of the format statement

- Defining Genes and Domains:

Attributes of different sites (and groups of sites, termed domains) are specified within the data "on the spot" rather than in an attributes block before or after the actual data.

Command	**Setting**	**Remark**	**Example**
Domain	A name	defines a domain with the given name	Domain=first_exon
Gene	A name	defines a gene with the given name	Gene=cytb
Property	Exon, Intron, Coding, Noncoding, and End	specifies the protein-coding attribute for a domain	Property=cytb
CodonStart	A number	specifies the site where the next 1st-codon position will be found in a protein-coding domain	CodonStart=2

Tab. 12: table with the keywords of the attributes of the different sites

- Defining Groups:
  - Assign different taxa to groups in a sequence as well as to distance data files.
  - The name of the group is written in a set of curly brackets ({ }) following the taxa name. The group name can be attached to the taxa name using an underscore or just can be appended.
  - There should be no spaces between the taxa name and the group name
- Labelling Individual Sites:
  - The individual sites in nucleotide or amino acid data can be labelled to construct non-contiguous sets of sites.
  - Each site can be associated with only one label
  - A label can be a letter or a number.

- Example:

```
!Gene=FirstGene Domain=Exon1 Property=Coding;
#Human_{Mammal} ATGGTTTCTAGTCAGGTCACCATGATAGGTCTCAAT
#Mouse_{Mammal} ATGGTTTCTAGTCAGGTCACCATGATAGGTCCCAAT
#Chicken_(Waterston, et al.)
ATGGTTTCTAGTCAGCTCACCATGATAGGTCTCAAT

!Gene=SecondGene Domain=Intron Property=Noncoding;
#Human ATTCCCAGGGAATTCCCGGGGGGTTTAAGGCCCCTTTAAAGAAAGAT
#Mouse GTAGCGCGCGTCGTCAGAGCTCCCAAGGGTAGCAGTCACAGAAAGAT
```

Distance Input Data

- Must be a lower-left or an upper-right triangular matrix
- After writing the #mega, !Title, !Description and !Format commands (some of which are optional), one need to write all the taxa names
- Taxa names are followed by the distance matrix
- Keywords for Format Statement are:

Command	**Setting**	**Remark**	**Example**
DataType	Distance	Specifies that the distance data is in the file	DataType=distance
NSeqs	integer	Number of sequences	NSeqs=85
NTaxa	integer	Same as NSeqs	NTaxa=85
DataFormat	Lowerleft, upperright	Specifies whether the data is in lower left triangular matrix or the upper right triangular matrix	DataFormat=lowerleft

Tab. 13: table with the keywords of the format statement

- Defining Groups: see above
- Example:

```
#mega
!Title: Concatenated Files;
!Format DataType=Distance
DataFormat=LowerLeft NTaxa=6;

#Rodent
#Primate
#Lagomorpha
#Artiodactyla
#Carnivora
#Perissodactyla

0.514
0.535 0.436
0.530 0.388 0.418
0.521 0.353 0.417 0.345
0.500 0.331 0.402 0.327 0.349
```

10.28.3 Links and References

Website: http://www.megasoftware.net/

Manual: http://www.megasoftware.net/manual.pdf

(Tamura, et al., 2011)

10.28.4 Special PGDSpider input/output questions

- Input:
  - Select the data type:
    DNA/RNA/DISTANCE
    Allows specifying the type of the data
  - Keep loci independent:
    TRUE/FALSE
    Specify if you like to keep loci independent (separate) or not

- Output:
  - Select the kind of data to print:
    SEQUENCE/DISTANCE
    Need to define to write a file with sequence data or distance matrix
  - Specify which data type should be included (optional):
    DNA/RNA/NGS/DISTANCE/SNP
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - If numeric SNP data: Enter the integer that codes for the nucleotide:
    Integer
    Define the integer that codes for a specific nucleotide

10.29 MIGRATE

MIGRATE version 3.2.6 (13. October 2010)

MIGRATE estimates effective population sizes and past migration rates between populations, assuming a migration matrix model with asymmetric migration rates and different subpopulation sizes. It uses a coalescent theory approach taking into account the history of mutations and the uncertainty of the genealogy. The estimation of the parameter values are done under either a Maximum likelihood or a Bayesian inference framework. The output can contain estimates of all migration rates and all population sizes, assuming constant mutation rates among loci or a gamma distributed mutation rate among loci; profile likelihood tables, percentiles, likelihood-ratio tests, and simple plots of the log-likelihood surfaces for all populations and all loci (Beerli, 2006; Beerli, 2008; Beerli, 2009; Beerli and Felsenstein, 1999; Beerli and Felsenstein, 2001).

10.29.1 Data type handled

MIGRATE can deal with following data types:

- DNA sequence
- SNP
- Microsatellite
- Standard (Electrophoretic marker)

10.29.2 MIGRATE format

Some syntax specifications:

- < token >: the token is obligatory
- [token]: optional
- {token}: obligatory for some
- < token1|token2 >: choose one of the token kind of data
- <individual1 10-10>: means that this token needs to be 10 characters long
- The characters for any word token can normally include special characters, punctuation, and blanks (e.g.:`Ind1 02 @` is legal)

Enzyme electrophoretic data or microsatellite data would look like this:

```
<Number of populations> <number of loci> {delimiter between alleles} [project title 0-79]
<Number of individuals> <title for population 0-79>
<Individual 1 10-10> <data>
<Individual 2 10-10> <data>
....
<Number of individuals> <title for population 0-79>
<Individuum 1 10-10> <data>
<Individuum 2 10-10> <data>
....
```

Enzyme electrophoretic data (infinite allele model):

- The project title is optional
- The individual name is by default 10 characters long
- The “data token” contains the genotypes
- Missing data are coded by ”?”
- One can use multi-character coding when using a delimiter

Microsatellite data:

- The project title is optional
- The individual name is by default 10 characters long
- The third argument on the first line has to be a delimiter character (e.g.: ”.”)
- The data contain the genotypes
- Homozygote individual needs to be coded as e.g.: 6.6 (”.” is the delimiter)
- Missing data are symbolized by ”?’”
- Each individual must have two alleles, which are coded as number of repeats or as fragment length (in this case an extra line with repeat numbers is needed: second line, starting with `#M`)

Sequences data:

- The individual name is followed by the base sequence of that species
- Blanks will be ignored and characters can be either upper or lower case
- characters constitute the IUPAC (IUB) nucleic acid code plus some slight extensions

Non-interleaved data:

```
<Number of populations> <number of loci> [project title 0-79]
<number of sites for locus1> <number of sites for locus 2> ...
<Number of individuals locus1> <#ind locus 2> ... <#ind loc n> <title for population 0-79>
<Individuum 1 10-10> <data locus 1>
<Individuum 2 10-10> <data locus 1>
....
<Individuum 1 10-10> <data locus 2>
<Individuum 2 10-10> <data locus 2>
....
<Number of individuals> <#ind locus 2> ... <#ind loc n> <title for population 0-79>
<Individuum 1 10-10> <data locus 1>
<Individuum 2 10-10> <data locus 1>
....
```

Interleaved data (not anymore supported by MIGRATE):

```
<Number of populations> <number of loci> [project title 0-79]
<number of sites for locus1> <number of sites for locus 2> ...
<Number of individuals locus1> <#ind locus 2> ... <#ind loc n> <title for population 0-79>
<Individual 1 10-10> <data locus 1 part 1>
<Individuum 2 10-10> <data locus 1 part 1>
....
<data ind1 locus 1 part 2>
<data ind2 locus 1 part 2>
....
<Individual 1 10-10> <data locus 2 part 1>
....
<data ind1 locus 2 part 2>
....
```

SNP data:

- The individual name is followed by the base sequence of that species
- Blanks will be ignored and characters can be either upper or lower case
- characters constitute the IUPAC (IUB) nucleic acid code plus some slight extensions
- two different formats: Nucleotide and HapMap

Nucleotide format:

- Same format as sequence data, except that first line starts with an `N`
- Linked SNP: more than one site on one line
- Unlinked SNP: one site per line

```
N <Number of populations> <number of loci> [project title 0-79]
<number of sites for locus1> <number of sites for locus 2> ...
<Number of individuals locus1> <#ind locus 2> ... <#ind loc n> <title for population 0-79>
<Individuum 1 10-10> <data locus 1>
<Individuum 2 10-10> <data locus 1>
....
<Individuum 1 10-10> <data locus 2>
<Individuum 2 10-10> <data locus 2>
....
<Number of individuals> <#ind locus 2> ... <#ind loc n> <title for population 0-79>
<Individuum 1 10-10> <data locus 1>
<Individuum 2 10-10> <data locus 1>
....
```

HapMap format:

- assumes that each SNP is biallelic
- <allele> contains the nucleotide
- <number> contains the number of individuals with the specific allele
- <total> is the sum of both numbers

```
H <Number of populations> <number of loci> [project title 0-79]
<Any Number> <title for population 0-79>
<Position on chr locus1> <TAB><allele><TAB><number><TAB><allele><TAB><number><TAB><total>
<Position on chr locus2> <TAB><allele><TAB><number><TAB><allele><TAB><number><TAB><total>
....
<Position on chr locus1> <TAB><allele><TAB><number><TAB><allele><TAB><number><TAB><total>
<Position on chr locus2> <TAB><allele><TAB><number><TAB><allele><TAB><number><TAB><total>
....
```

Examples:

- Enzyme electrophoretic data
    - 2 populations and 11 loci and with 2 or 1 individuals per population:

```
2 11 Migration rates between two Turkish frog populations
2 Akcapinar (between Marmaris and Adana)
PB1058    ee bb ab bb bb aa aa bb ?? cc ab
PB1059    ee bb ab bb bb aa aa bb bb cc aa
1 Ezine (between Selcuk and Dardanelles)
PB16843   ee bb ab bb aa aa aa cc bb cc aa
```

    - Same data but with / as separator:

```
2 11 / Migration rates between two Turkish frog populations
2 Akcapinar (between Marmaris and Adana)
PB1058    e/e b/b a/b b/b b/b a/a a/a b/b ?/? c/c Rs/Rf
PB1059    e/e b/b a/b b/b b/b a/a a/a b/b b/b c/c Rs/Rs
1 Ezine (between Selcuk and Dardanelles)
PB16843   e/e b/b a/b b/b a/a a/a a/a c/c b/b c/c Rs/Rs
```

- Microsatellite data:
    - Encoded as repeat numbers:

```
2 3 . Rana lessonae: Seeruecken versus Tal
2   Riedtli near Guendelhart-Hoerhausen
0         42.45 37.31 18.18
0         42.45 37.33 18.16
1   Tal near Steckborn
1         43.46 33.? 18.18
```

    - Encoded as fragment length:

```
2 3 . Rana lessonae: Seeruecken versus Tal
#M 2 2 3
2   Riedtli near Guendelhart-Hoerhausen
0         84.90 74.62 54.54
0         84.90 74.66 54.48
1   Tal near Steckborn
1         86.92 66.? 54.54
```

- Sequence data:
  - not interleaved (2 population with 2 loci):

```
   2 2 Make believe data set using simulated data (2 loci)
50 46
2 2   pop1
eis        ACACCCAACACGGCCCGCGGACAGGGGCTCGAGGGATCACTGACTGGCAC
zwo        ACACAAAACACGGCCCGCGGACAGGGGCTCGAGGGGTCACTGAGTGGCAC
eis        ACGCGGCGCGCGAACGAAGACCAAATCTTCTTGATCCCCAAGTGTC
zwo        ACGCGGCGCGAGAACGAAGACCAAATCTTCTTGATCCCCAAGTGTC
2   pop2
vier       CAGCGCGCGTATCGCCCCATGTGGTTCGGCCAAAGAATGGTAGAGCGGAG
fuef       CAGCGCGAGTCTCGCCCCATGGGGTTAGGCCAAATAATGTTAGAGCGGCA
vier       TCGACTAGATCTGCAGCACATACGAGGGTCATGCGTCCCAGATGTG
fuef       TCGACTAGATATGCAGCAAATACGAGGGGCATGCGTCCCAGATGTG
```

  - interleaved (2 populations with 2 loci, not anymore supported by MIGRATE):

```
   2 2 Make believe data set using simulated data (2 loci,interleaved)
50 46
2 1   pop1
zwo        ACACAAAACACGGCCCGCGGACA
drue       ATACCCAGCACGGCCGGCGGACA
           GGGGCTCGAGGGATCACTGACTGGCAC
           GGGGCTCGAGGGGTCACTGAGTGGCAC
           GGGGCTCGAGGGAGCACTGAGTGGAAC
zwo        ACGCGGCGCGAGAACGAAGACCA
           AATCTTCTTGATCCCCAAGTGTC
           AATCTTCTTGATCCCCAAGTGTC
2 2 pop2
vier       CAGCGCGCGTATCGCCCCATGTGGTTCGGCCAAAGAATG
fuef       CAGCGCGAGTCTCGCCCCATGGGGTTAGGCCAAATAATG
           GTAGAGCGGAG
  TTAGAGCGGCA
           TCGACTAGATCTG CAGCACATAC
           TCGACTAGATATG CAGCAAATAC
  GAGGGTCATGCGTCCCAGATGTG
  GAGGGGCATGCGTCCCAGATGTG
```

- SNP data:
  - Nucleotide format (2 populations and 2 loci):

```
N 2 2 Make believe data set using simulated data (2 loci)
1 4
3 3 pop1
ind1       A
ind2       A
ind3       A
ind1       ACAC
ind2       ACAC
ind3       ACGC
2 pop2
ind4       C
ind5       C
ind4       TGGA
ind5       TCGA
```

- HapMap format:

```
H 2 2 Make believe data set using simulated data (2 loci)
3 pop1
1    A 3 C 0 3
1000 A 3 T 0 3
1010 C 3 G 0 3
1011 A 2 G 1 3
1015 C 3 A 0 3
2 pop2
1    A 0 C 2 2
1000 A 0 T 2 2
1010 C 1 G 1 2
1011 A 0 G 2 2
1015 C 0 A 2 2
```

10.29.3 Links and References

Website: http://popgen.sc.fsu.edu/Migrate/Migrate-n.html

Manual: http://popgen.scs.fsu.edu/migratedoc.pdf

(Beerli, 2009)

10.29.4 Special PGDSpider input/output questions

- Input:
  - Select the data type:
    MICROSAT/STANDARD/SEQUENCE/SNP/AFLP
    Need to define if the data file contains Microsatellite, Standard, Sequence or SNP data.
  - Are the data interleaved? :
    TRUE/FALSE
    Define if the data in the file are interleaved (use more than one line) or not.

- Output:
  - Specify which data type should be included (optional):
    DNA/RNA/NGS/SNP/MICROSAT/AFLP/STANDARD
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - Are the loci linked:
    TRUE/FALSE
    Need to define if the SNP loci are linked or not
  - If numeric SNP data: Enter the integer that codes for the nucleotide:
    Integer
    Define the integer that codes for a specific nucleotide

- Specify the locus/locus combination which should be written to the output file (optional):
  String
  If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.30 MSA

MSA version 4.05

MSA is a universal, platform independent, data analysis tool. It was designed to handle large microsatellite data sets. Microsatellite analyzer calculates the standard suite of descriptive statistics and provides input files for other software packages (Dieringer and Schlotterer, 2003).

10.30.1 Data type handled

MSA can only handle Microsatellite data

10.30.2 MSA format

The input files can be generated using a spreadsheet software (such as Excel), where the data are arranged either as one column per locus or as two columns per locus. The input file has to be saved as "tab delimited text" file.

The MSA input files should follow these rules:

- The microsatellites data should be coded as the PCR product size
- Missing data are indicated by either an empty cell or a negative value (not '0')
- For compatibility with PHYLIP the population labels are limited to 8 characters
- cell A1 contains a 1 or a 2, whether the data are arranged in the one column (1) or two column (2) format
- The first column encloses the names of the populations (no empty cell is allowed)
- The second column specifies whether the data are inbred (h) or outbred (d). The same allele needs to be entered twice when only a single allele was detected (empty cells are thought to be missing data).
- The third column allows one to group populations. In the absence of grouping give the same number to all populations. Only consecutive group numbers are allowed, but groups are assigned without any constraints in order.
- The first two rows give information about each locus:
    - First row specifies the repeat type (1, 2, 3, etc). This is used to compute the number of repeats out of the PCR product size.
    - Second row indicates the length of the sequence flanking the microsatellite (in bp). This row can be empty.
- The third row contains the name of the microsatellite locus. In the two-column format, MSA allows two different names for the same locus (each entered in one cell)

- **Example:**

```
2                    2             2             2             2
              113           81            112           159
              1770   X13444 1818   X65444 1774   X66788 1772   X65644
Pop1   d      1      140    140                  147    159
Pop1   d      1      134    134                  147    151    184    186
Pop1   d      1      134    134    104    106    147    147    186    178
Pop2   d      1      134    136    104    100    159    153    186    172
Pop2   d      1      134    140    104    104    151    143    184    178
Pop2   d      1      134    134    104    104    147    151    186    188
Pop2   d      1      134    134                  147    141    184    178
Pop3   h      2                    104    104
Pop3   h      2      134    134    104    104    149    149    186    178
Pop3   d      2      134    134                  147    147    184    186
Pop3   h      2                    104    98
Pop3   d      2                    104    106                  186    178
```

10.30.3 Links and References

Website: http://i122server.vu-wien.ac.at/MSA/info.html/MSA_info.html

(Dieringer and Schlotterer, 2003)

10.30.4 Special PGDSpider input/output questions

- Input: none

- Output:
  - Enter the size of the repeated motif:
    Integer/Integer,Integer, …
    This is needed to convert the Microsatellite data (PGD saves it as number of repeats) to the length of the PCR fragments (MSA can only save Microsatellite data as the length of the PCR fragment). If it is the same for all loci just enter one number else one has to enter a number for each locus separated by a comma.
  - Are data inbred (h) or outbred (d):
    h/d
    Need to define if the data are in- or outbred
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.31 MSVar

MSVar version 0.4.1.b (7. April 1999)

This program is designed to help the user to explore the most probable demographic and genealogical histories consistent with a sample of chromosomes typed at one or more loci. It relies on Markov Chain Monte Carlo (MCMC) simulation (Beaumont, 1999).

10.31.1 Data type handled

MSVar can only handle Microsatellite data.

10.31.2 MSVar format

- The first row contains the number of loci
- Second row: number of alleles (allelic classes) at the first locus
- Third row: counts of chromosomes with the same length (same number of repeats)
- Fourth row: the number of repeats corresponding to counts above
- Fifth row: number of alleles at next locus
- Etc.

- **Example:**

```
4
2
28 20
0 7
2
11 29
0 3
3
12 14 6
0   1 2
2
50 6
0 2
anything you want down here
```

10.31.3 Links and References

Website: http://www.rubic.rdg.ac.uk/~mab/software.html

(Beaumont, 1999)

10.31.4 Special PGDSpider input/output questions

- Output:
    - Do you want to combine all populations? :
      TRUE/FALSE
      Need to define if the MSVar file includes one population or a combination of all populations (all individuals of the different populations in one population)
    - Select the population you want to include:
      String
      Need to choose the population which should be included.
    - Specify the locus/locus combination which should be written to the output file (optional):
      String
      If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.32 NewHybrids

NewHybrids version 1.1 beta (7. April 2003)

NewHybrids is a program for computing the posterior distribution that individuals in a sample fall into different hybrid categories (Anderson and Thompson, 2002).

10.32.1 Data type handled

NewHybrids handles diploid Microsatellite, AFLP and Standard (multi-allelic markers) data types.

10.32.2 NewHybrids format

- whitespace (spaces and or tabs) separated text file *.txt/*.dat
- first line: `NumIndivs` number of individuals
- second line: `NumLoci` number of loci
- third line: `Digits` number of digits used to denote a particular allele
- fourth line: `Format Lumped` (genotype at a single locus is given by a single number) or `NonLumped`
- next lines: `LocusNames` names of all loci separated by whitespace
- next lines: genotype data
- first character: number of the individual (numbering must be serially)
- next characters: genotypes (all on same line or on different lines)
- `Lumped` format: two alleles are encoded as one number, `Digits` specify how many digits are used to represent each locus
- `NonLumped` format: alleles at each locus are given by a consecutive pair of numbers that are white space separated
- Missing data: `Lumped:` encoded as `0, NonLumped:` encoded as `-1` (each allele at the missing locus must have a `-1`)

AFLP data:

- `LumpedLumped` format
- `+` band is present
- `−` band is absent
- `0` missing data
- data types can be mixed

Example

- `Lumped` data file:

```
NumIndivs 2
NumLoci 6
Digits 1
Format Lumped
LocusNames sAAT1 sAAT2 sAAT3 ADA1 ADA2 ADH
1 11 11 11 0 11 32
2 21 11 21 11 11 12
```

- `NonLumped` data file:

```
NumIndivs 2
NumLoci 6
Digits 1
Format NonLumped
LocusNames sAAT1 sAAT2 sAAT3 ADA1 ADA2 ADH
1 123 143 -1 -1 144 144 120 122 157 158 144 144
2 135 135 134 140 144 144 120 122 161 161 144 144
```

- AFLP data file (4 Microsat loci, 5 AFLP loci):

```
NumIndivs 2
NumLoci 9
Digits 1
Format Lumped
LocusNames m1 m2 m3 m4 A1 A2 A3 A4 A5
1 11 12 13 11 + + + - +
2 22 33 11 22 - - 0 - -
3 12 13 13 11 + - - - +
```

10.32.3 Links and References

Website: http://ib.berkeley.edu/labs/slatkin/eriq/software/software.htm,

Manual: http://ib.berkeley.edu/labs/slatkin/eriq/software/new_hybs_doc1_1Beta3.pdf

(Anderson and Thompson, 2002)

10.32.4 Special PGDSpider input/output questions

- Input:
  - Select the data type:
    MICROSAT/AFLP/STANDARD/SNP/MICROSAT & AFLP/STANDARD & AFLP/SNP & AFLP
    One has to define the type of the data (e.g.: Microsat, AFLP or Standard)
  - How are Microsat alleles coded?
    REPEATS/LENGTH/ARBITARY

Need to define if the Microsat data are coded as number of repeats, as the length of the PCR fragments or as an arbitrary number.

  - Enter the size of the repeated motif:
    Integer/Integer,Integer, …
    Need to define the size of the repeated motif, so that the number of repeats can be calculated (Microsat alleles have to be saved as number of repeats in the PGD format). Same for all loci: enter one number. Different between loci: comma separated list (e.g.: 2,2,3,2).

- Output:
  - Specify which data type should be included (optional):
    MICROSAT/AFLP/STANDARD/SNP/MICROSAT & AFLP/STANDARD & AFLP/SNP & AFLP/DNA
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).

10.33 NEXUS

NEXUS is a file format designed to contain systematic data. The goals of the format are to allow future expansion, to include diverse kinds of information, to be independent of particular computer operating systems, and to be easily processed by a program (Maddison, et al., 1997).

10.33.1 NEXUS format

NEXUS files are free-format, which means that the entire file could conceivably consist of a single, long line of text. It does not matter where the line is broken (as long as you don't split up a keyword or the name of a locus, allele or population), nor does it matter if one space or a dozen spaces are used to separate the individual words (tokens) in the file. Tokens may be casually defined as sequences of characters separated by whitespace (e.g., spaces, carriage returns, line feeds, tabs, etc.)

NEXUS files are for the most part not case-sensitive by default. A big exception is in the matrix command, where (by default) an allele named A is treated as being distinct from a.

The NEXUS files are built as follows:

- Comments can be added by enclosing text within brackets: `[comment]`
- The file has to start with: `#NEXUS`
- The tokens in a NEXUS file are organized into commands, which are in turn organized into blocks.
  - Commands: the first token in the command is the command name, which is followed by a series of tokens and whitespace; the command is terminated by a semicolon: `command-name token token . . . ;`
  - Blocks: series of commands, beginning with a BEGIN command and ending with an END command:

```
BEGIN block-name;
 command-name token . . . ;
 command-name token . . . ;
 ...
END;
```

The most used public blocks are:

(Tokens within [ ] are optional, within { | | } are mutually exclusive and underlined tokens are the default):

- TAXA:
  TAXA block defines the taxa and gives them names. The block also establishes the order (numbering) of the taxa. Taxa consist of the entities whose attributes might be recorded in characters block.

```
BEGIN TAXA;
 DIMENSIONS NTAX=number-of-taxa;
 TAXLABELS taxon-name [taxon-name ...] ;
END;
```

- CHARACTERS:
  This block contains the information about discrete and continuous data, including that for morphological structure and molecular sequences. Polymorphism and frequency data can be accommodated. Names can be given to the characters and their states.

```
BEGIN CHARACTERS;
 DIMENSIONS [NEWTAXA NTAX=number-of-taxa] NCHAR=number-of-characters;
 [FORMAT
  [DATATYPE={STANDARD|DNA|RNA|NUCLEOTIDE|PROTEIN|CONTINUOUS}
  [RESPECTCASE]                                  default: A and a is the same
  [MISSING=symbol]                               default: ?
  [GAP=symbol]
  [SYMBOLS=”symbol [symbol...]”]
  [EQUATE=”symbol=entry [symbol=entry]”]
  [MATCHCHAR=symbol]
  [[No]LABELS]
  [TRANSPOSE]
  [INTERLEAVE]
  [ITEMS=([MIN][MAX][MEDIAN][AVERAGE][VARIANCE][STCERROR][SAMPLESIZE][STATES])]
  [STATESFORMAT={STATESPRESENT|INDIVIDUALS|COUNT|FREQUENCY}]
  [[No]TOKENS]
 ;]
 [ELIMINATE character-set;]
 [TAXLABELS taxon-name [taxon-name...];]
 [CARSTATELABELS character-number [charact-name] [/state-name [state-name..]]
  [, character-number [character-name] [/state-name [state-name...]] ...]
 ;]
 [CHARLABELS character-name [character-name...];]
 [STATELABELS character-number [character-name] [/state-name [state-name...]]
  [, character-number [character-name] [/state-name [state-name...]]  ...]
 ;]
 MATRIX data-matrix;
END;
```

  - example:

```
BEGIN CHARACTERS;
 DIMENSION NCHAR=3;
 CHARSTATELABELS 1 hair/absent present, 2 color/red blue,
                 3 size/small big;
 FORMAT TOKENS;
 MATRIX
  taxon_1 absent red big
  taxon_2 absent blue small
  taxon_3 present blue small;
END;
```

- UNALIGNED:
  similar to a CHARACTERS block, but contains unaligned molecular sequence data.

```
BEGIN UNALIGNED;
 [DIMENSIONS NEWTAXA NTAX=number-of-taxa;]
 [FORMAT
  [DATATYPE={STANDARD|DNA|RNA|NUCLEOTIDE|PROTEIN}]
  [RESPECTCASE]
  [MISSING=symbol]
  [SYMPOLS=”symbol [symbol...]”]
  [EQUATE=”symbol=entry [symbol=entry...]”]
  [[No]LABELS]
 ;]
 [TAXLABELS taxon-name [taxon-name...];]
 MATRIX data-matrix;
END;
```

- DISTANCES:
  This block contains distance matrices

```
BEGIN DISTANCES;
 [DIMENSIONS [NEWTAXA] NTAX=number-of-taxa NCHAR=number-of-characters;]
 [FORMAT
  [TRIANGLE={LOWER|UPPER|BOTH}]
  [[NO]DIAGONAL]
  [[NO]LABELS]
  [MISSING=symbol]
  [INTERLEAVE]
 ;]
 [TAXLABELS taxon-name [taxon-name...];]
 [MATRIX distance-matirx;
END;
```

  - example:

```
BEGIN DISTANCES;
 FORMAT TRIANGLE=UPPER;
 MATRIX
  taxon_1 0.0 1.0 2.0
  taxon_2     0.0 3.0
  taxon_3         0.0;
END;
```

- DATA:
  DATA is a CHARACTERS block that includes not only the definition of characters but also the definition of taxa (this block is not recommended).
  - example:

```
BEGIN DATA;
 DIMENSIONS NTAX=5 NCHAR=20;
 FORMAT DATATYPE=DNA GAP=-;
 MATRIX
  taxon-1 A-CTAGGACTA---GATCAA
  taxon-2 A-CCAGGACTAGCGGATCAA
  taxon-3 A-CCAGGACTA---GATCAA
  taxon-4 AGCCAGGACTA---GTTCAA
  taxon-5 ATC-AGGACTA---GATCAA;
END;
```

- SETS:
  This block contains descriptions of collections of objects. These objects include characters, taxa, trees, states, and kinds of changes. In addition, partitions of characters, taxa, and trees can be formed.

```
BEGIN SETS;
 [CHARSET charstet_name [({STANDARD|VECTOR})]=character-set;]
 [STATESET stateset-name [({STANDARD|VECTOR})]=state-set;]
 [CHANGESET changeset-name=state-set<->state-set [state-set<->state-set...];]
 [TAXSET taxset-name [({STANDARD|VECTOR})]=taxon-set;]
 [TREESET treeset-name [({STANDARD|VECTOR})]=tree-set;]
 [CHARPARTITION partition-name [([{[NO]TOKENS}] [{STANDARD|VECTOR}])]
  =subset-name:character-set [, subset-name:character-set...];]
 [TAXPARTITION partition-name [([{[NO]TOKENS}] [{STANDARD|VECTOR}])]
  =subset-name:taxon-set [, subset-name:taxon-set...];]
 [TREEPARTITION partition-name [([{[NO]TOKENS}] [{STANDARD|VECTOR}])]
  =subset-name:tree-set [, subset-name:tree-set...];]
END;
```

- ASSUMPTIONS:
  contains assumptions about the data. These can include assignment of weights to various characters, specification of the nature of character changes, exclusion of particular characters, and designation of ancestral states.

```
BEGIN ASSUMPTIONS;
 [OPTIONS [DEFTYPE=type-name]
  [POLYTCOUNT={MINSTEPS|MAXSTEPS}]
  [GAPMODE={MISSING|NEWSTATE}];]
 [USERTYPE type-name[({STEPMATRIX|CSTREE})]=USERTYPE-description;]
 [TYPESET [*] typeset-name [({STANDARD|VECTOR})]=TYPESET-definition;]
 [WTSET [*] stset-name [({STANDARD|VECTOR} {TOKENS|NOTOKENS})]=WTSET-
   definition;]
 [EXSET [*] exset-name [({STANDARD|VECTOR})]=character-set;]
 [ANCSTATES [*] ancstates-name [({STANDARD|VECTOR} {TOKENS|NOTOKENS})]
   =ANCSTATES-definition;]
END;
```

- CODONS:
  contains information about the genetic code, the regions of DNA and RNA sequences that are protein coding, and the location of triplets coding for amino acids in nucleotide sequences.

```
BEGIN CODONS;
 [CODONPOSSET [*] name [({STANDARD|VECTOR})]=
  N: character-set,
  1: character-set,
  2: character-set,
  3: character-set;]
 [GENETICCODE code-name
  [([CODEORDER=123|other] [NUCORDER=TCAG|other] [[NO]TOKENS]
     [EXTENSIONS="symbols-list"])]
    =genetic code description];]
 [CODESET [*] codeset-name {(CHARACTERS|UNALIGNED|TAXA)}
    =code-name:character-set or taxon-set [,code-name:character-set or
taxon-
     set...];]
END;
```

- TREES:
  stores information about trees.

```
BEGIN TREES;
 [TRANSLATE arbitrary-token-used-in-tree-description valid-taxon-name
  [, arbitrary-token-used-in-tree-description valid-taxon-name. . . ] ;]
 [TREE [*] tree-name= tree-specification;]
END;
```

- NOTES:
  allows attachment of additional information (text, pictures, etc.) to various objects (trees, taxa, characters, etc.) in the file.

```
BEGIN NOTES;
 [TEXT [TAXON=taxon-set] [CARACTER=character-set] [STATE=state-set]
   [TREE=tree-set]
  SOURCE={INLINE|FILE|RESOURCE}TEXT=text-or-source-description:]
 [PICTURE [TAXON=taxon-set] [CARACTER=character-set] [STATE=state-set]
   [TREE=tree-set]
  [FORMAT=[PICT|TIFF|EPS|JPEG|GIF}] [ENCODE={NONE|UUENCODE|BINHEX}]
  [SOURCE={INLINE|FILE|RESOURCE}PICTURE=picture-or-source-descriptior;]
END;
```

- The order of blocks is predetermined for some pairs of blocks but not others (most programs will require a CHARACTERS or DATA block to precede the ASSUMPTIONS block so that the characters will be defined)
- Names should be unique (no duplicate names), must be single words (no spaces) and cannot consist entirely of digits.

Example:

```
#NEXUS
BEGIN TAXA;
      Dimensions NTax=4;
      TaxLabels fish frog snake mouse;
END;

BEGIN CHARACTERS;
      Dimensions NChar=20;
      Format DataType=DNA;
      Matrix
        fish   ACATA GAGGG TACCT CTAAG
        frog   ACATA GAGGG TACCT CTAAG
        snake  ACATA GAGGG TACCT CTAAG
        mouse  ACATA GAGGG TACCT CTAAG
END;

BEGIN TREES;
      Tree best=(fish, (frog, (snake, mouse)));
END;
```

10.33.2 References

Maddison, D. R., D. L. Swofford, et al. (1997). "Nexus: An extensible file format for systematic information." Systematic Biology **46**(4): 590-621.

10.33.3 Special PGDSpider input/output questions

PGDSpider is also able to read the CharSet definitions within a MrBayes block.

- Input:
  - Do you want to include the sequence not specified within the TaxSet in the SET block? :
    TRUE/FALSE
    If one or more sequences are not specified within the TaxSet in the SET block, one need to specify if these sequences should be included (they are put all together in one population without a name) or not.

- Output:
  - Specify which data type should be included (optional):
    DNA/RNA/NGS/MICROSAT/SNP/RFLP/AFLP/STANDARD
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - Do you want to convert SNPs into binary format?
    TRUE/FALSE
    Converts SNP data into binary format (e.g. for SNAPP)

- Specify the locus/locus combination which should be written to the output file (optional):
  String
  If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.34 ONeSAMP

ONeSAMP version 1.2

ONeSAMP is an effective population size (Ne) estimator that requires a single sample of microsatellite data from a single population. ONeSAMP uses summary statistics calculated from the data in an approximate Bayesian framework to infer the effective size of the population that generated those data (Tallmon, et al., 2008). The user must provide a series of inputs in order to parameterize the simulations that are used to infer Ne.

10.34.1 Data type handled

ONeSAMP handles diploid Microsatellite data.

10.34.2 ONeSAMP format

- Make sure to remove all tabs and make your file space delimited
- The first line is ignored. It can be used to store information about the data
- The locus names are given next, one per line. The repeat motif of each locus is given after the locus name. Keep a space after the "," and before the repeat motif for each locus.
- Then the population sample indicator "Pop" follows (not "POP"). Note that ONeSAMP is designed to estimate Ne for a single population.
- Information for the first individual:
    - First an individual identifier, followed by a comma and a space
    - Then the data are given for each locus separated by spaces (3 digits for each allele, the two alleles of each loci are concatenated)
    - Numbers should correspond to microsatellite length
    - missing data are encoded as "000000"
- Each additional individual information starts on a new line
- The number of locus names should correspond to the number of genotypes in each individual
- Text after the individuals and loci is ignored

- **Example:**

```
The text on the first line is ignored by OneSamp software
1, 2
2, 2
3, 2
4, 2
10, 3
Pop
1, 202206  192212  192190  186198  100106
2, 000000  210190  190190  186186  103106
3, 198196  188188  196190  186186  106100
4, 208198  000000  194196  192190  100106
5, 194198  198186  196190  190190  106106
6, 196206  192192  196190  192192  103100
7, 196194  192192  196192  186196  103106
8, 198194  212192  196196  192190  100103
9, 200190  192186  196190  192196  103106
```

10.34.3 Links and References

Website: http://genomics.jun.alaska.edu/asp/Default.aspx

Input file: http://genomics.jun.alaska.edu/asp/sample.txt

(Tallmon, et al., 2008)

10.34.4 Special PGDSpider input/output questions

- Input: none

- Output:
  - Enter the size of the repeated motif:
    Integer/Integer,Integer, …
    This is needed to convert the Microsatellite data (PGD saves it as number of repeats) to the length of the PCR fragments (ONeSAMP can only save Microsatellite data as the length of the PCR fragment). If it is the same for all loci just enter one number else one has to enter a number for each locus separated by a comma.
  - Select the wished population (optional):
    String
    Need to define a population which should be written to the output file, because only one population can be included
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.35 PED

The PED file format refers to the widely-used format for linkage pedigree data and used as input for the program PLINK. PLINK is a free, open-source whole genome association analysis toolset, designed to perform a range of basic, large-scale analyses in a computationally efficient manner (Purcell, et al., 2007).

10.35.1 Data types handled

PED is able to deal with diploid SNP data.

10.35.2 PED format

- whitespace (spaces and or tabs) separated text file *.ped
- each line correspond to one individual
- following first 6 columns are mandatory (The IDs are alphanumberic):
  - `Family ID`
  - `Individual ID`
  - `Paternal ID`
  - `Maternal ID`
  - `Sex` (1=male; 2=female; any other character=unknown)
  - `Phenotype` (only 1 phenotype! The phenotype can be either a quantitative trait or an affection status column: PLINK will automatically detect which type (i.e. based on whether a value other than 0, 1, 2 or the missing genotype code is observed))
- Comments: line starts with `#`
- Affection status, by default, should be coded:
  - -9 missing
  - 0 missing
  - 1 unaffected
  - 2 affected
- column 7 onwards: Genotypes
  - any character (e.g.: 1,2,3,4 or A,C,G,T or anything else)
  - missing genotype: `0`
  - All markers must be biallelic (diploid). Either both alleles should be missing or neither. Haploid data: encode them as diploid homozygote. Two alleles are shown after each other.

If specially specified following columns can be missing:

- `Family ID`
- `Individual ID`
- `Paternal ID` and `Maternal ID`
- `Sex`
- `Phenotype`

MAP files

- Each line of the MAP file describes a single marker and must contain exactly 4 columns:
    - chromosome (1-22, X, Y, MT or 0 if unplaced)
    - rs# or snp identifier
    - Genetic distance (morgans) (missing: 0)
    - Base-pair position (bp units) (Base-pair positions are expected to correspond to positive integers within the range of typical human chromosome sizes)
- The MAP file must contain as many markers as are in the PED file.
- The markers in the PED file do not need to be in genomic order, but the order MAP file should align with the order of the PED file markers).

Example

- PED files:

```
FAM001  1  0 0  1  2  A A  G G  A C
FAM001  2  0 0  1  2  A A  A G  0 0
```

```
1 1 0 0 1   1   A A   A A   A A   A A   A A
2 1 0 0 1   1   A C   A C   A C   A C   A C
3 1 0 0 2   1   A A   A A   A A   A A   A A
4 1 0 0 2   1   A C   A C   A C   A C   A C
```

- MAP files:

```
rs123456  0  1234555
rs234567  0  1237793
rs224534  0  -1237697
rs233556  0  1337456
```

```
1    snp1   0   1000
X    snp2   0   1000
Y    snp3   0   1000
XY   snp4   0   1000
MT   snp5   0   1000
```

10.35.3 Links and References

Website: http://pngu.mgh.harvard.edu/~purcell/plink/data.shtml#ped

(Purcell, et al., 2007)

10.35.4 Special PGDSpider input/output questions

- Input:
    - Include MAP file with loci information:

TRUE/FALSE
Possibility to add a file with loci information
  - MAP file:
    Absolute file path
    Choose the file with the loci information
  - Is the "Family ID" column absent in the input file:
    TRUE/FALSE
    Specify if the Family IDs are absent or not
  - Is the "Individual ID" column absent in the input file:
    TRUE/FALSE
    Specify if the Individual IDs are absent or not
  - Is the "Parental ID" and the "Maternal ID" columns absent in the input file:
    TRUE/FALSE
    Specify if the Paternal IDs and the Maternal IDs are absent or not
  - Is the "Sex" column absent in the input file:
    TRUE/FALSE
    Specify if the Sexes are absent or not
  - Is the "Phenotype" column absent in the input file:
    TRUE/FALSE
    Specify if the Phenotypes are absent or not
  - Group individuals into populations according to "Family ID" or "Phenotype":
    FAMILY/PHENOTYPE
    Specify if the individuals should be grouped into populations according to Famaly ID items or Phenotype items. Individuals are grouped into one population if the items are not available

- Output:
  - Save additional file with loci information:
    TRUE/FALSE
    Saves a MAP file with loci information
  - Save MAP file:
    Absolute file path
    Choose the path where the MAP file should be written
  - Replacement character for allele encoded as 0:
    Character
    Specify the character which should encode for allele 0 (0 encodes for missing data in PED)
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.36 PHYLIP

PHYLIP version 3.69 (September 2009)

PHYLIP, the Phylogeny Inference Package, is a package of programs for inferring phylogenies (evolutionary trees). It can infer phylogenies by parsimony, compatibility, distance matrix methods, and likelihood. It can also compute consensus trees, compute distances between trees, draw trees, resample data sets by bootstrapping or jackknifing, edit trees, and compute distance matrices (Felsenstein, 1989; Felsenstein, 2004).

10.36.1 Data types handled

PHYLIP is able to deal with following data types:

- nucleotide sequences
- protein sequences
- gene frequencies
- restriction sites
- restriction fragments
- distances
- discrete characters
- continuous characters

10.36.2 PHYLIP format

For most of the PHYLIP programs, information comes from a series of input files, and ends up in a series of output files.

Nucleotide sequences data:

- The first line contains the number of species and the number of characters. These are in free format, separated by blanks.
- The next lines include information for each species: First, the species name has to be 10 characters long (it can include blanks and punctuation marks), followed by the data for that species (the data have to start at the 11th character of the line!). The name should be on the same line as the first character of the data.
  In the relaxed PHYLIP format (e.g. for RAxML) the species names could be of any length and are separated from the data by a whitespace.
  RAxML allows the specification of a partition file (e.g. to separate DNA sequence from different loci):

  ```
  DNA, p1=1-30
  DNA, p2=31-60
  ```

  (p1 and p2 are just arbitrarily chosen names for the partition)

- The conventions for interleaved data are different between the molecular sequence programs and the others. The molecular sequence programs can take the data in “aligned” or “interleaved” format:
    - In the interleaved format DNA sequences can be specified on several lines. It is important that the sequence length in each group is the same for all species. The sequences might look like this:

```
    2   39
Archaeopt CGATGCTTAC CGCCGATGCT
HesperorniCGTTACTCGT TGTCGTTACT

TACCGCCGAT GCTTACCGC
CGTTGTCGTT ACTCGTTGT
```

    - In the sequential format the character data can run on a new line at any time. Thus, it is legal to have:

```
Archaeopt 001100
1101
```

      or even:

```
Archaeopt
0011001101
```

- Blanks and digits within sequences are allowed to make them easier to read

- **Example:**

```
   6   13
Archaeopt CGATGCTTAC CGC
HesperorniCGTTACTCGT TGT
BaluchitheTAATGTTAAT TGT
B. virginiTAATGTTCGT TGT
BrontosaurCAAAACCCAT CAT
B.subtilisGGCAGCCAAT CAC
```

- Example relaxed PHYLIP format:

```
   6   13
Archaeopt CGATGCTTAC CGC
Hesperorni CGTTACTCGT TGT
Baluchithea TAATGTTAAT TGT
B.virgini TAATGTTCGT TGT
Brontosaurus CAAAACCCAT CAT
B.subtilis GGCAGCCAAT CAC
```

Distance Matrix

- The first line of these input files must contain the number of species
- Then the species data follow, starting with a species name:
  - species names have to be ten characters long
  - Then a set of distances to all the other species follows for each species (the distance matrix can be upper- or lower-triangular or square). The distances can continue to a new line.
- **Examples:**
  - A square matrix:

```
     5
Alpha      0.000 1.000 2.000 3.000 3.000
Beta       1.000 0.000 2.000 3.000 3.000
Gamma      2.000 2.000 0.000 3.000 3.000
Delta      3.000 3.000 0.000 0.000 1.000
Epsilon    3.000 3.000 3.000 1.000 0.000
```

  - A lower-triangular input matrix with distances continuing to new lines as needed:

```
   14
Mouse
Bovine      1.7043
Lemur       2.0235  1.1901
Tarsier     2.1378  1.3287  1.2905
Squir Monk  1.5232  1.2423  1.3199
1.7878
Jpn Macaq   1.8261  1.2508  1.3887
1.3137  1.0642
```

10.36.3 Links and References

Website: http://evolution.genetics.washington.edu/phylip/doc/main.html

(Felsenstein, 1989; Felsenstein, 2004)

10.36.4 Special PGDSpider input/output questions

- Input:
  - What type of data is listed in the PHYLIP file:
    SEQUENCE/DISTANCE
    Need to define if the file contains molecular sequence data or distance matrix data
  - Specify the format of the data:
    SIMPLE/INTERLEAVED/SEQUENTIAL
    Need to define if the data are simple (on one row), interleaved or sequential
  - Is it a relaxed PHYLIP format (e.g. from RAxML):
    TRUE/FALSE

Need to define if the data is stored as relaxed PHYLIP format (needed for program RAxML). The relaxed forma separates the species names and species data by a white space.

- Load an additional file with sequence partitions separating loci:
  TRUE/FALSE
  Load a file with sequence partitions
- Load partition file:
  Absolute file path
  Choose the path where the partition file is stored
- Specify the format of the distance matrix:
  LOWER/BOTH/UPPER_DIAGONAL/UPPER_NO_DIAGONAL
  Need to define if the distance matrix is of the format lower-triangular, square matrix (both), upper-triangular (with diagonals) or upper-triangular (without diagonals).

- Output:
  - Select the kind of file you want to write:
    SEQUENCE/DISTANCE
    Need to define if a molecular sequence data file or a distance matrix data file should be written to the output file.
  - Save relaxed PHYLIP format (e.g. for RAxML):
    TRUE/FALSE
    Need to define if the data should be stored in a relaxed PHYLIP format (needed for program RAxML). The relaxed forma separates the species names and species data by a white space.
  - Save an additional file with sequence partitions separating loci (may be used within RAxML):
    TRUE/FALSE
    Saves a file with sequence partitions
  - Save partition file:
    Absolute file path
    Choose the path where the partition file should be written
  - Specify which data type should be included (optional):
    DNA/RNA/NGS/SNP
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - If numeric SNP data: Enter the integer that codes for the nucleotide:
    Integer
    Define the integer that codes for a specific nucleotide
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

- Specify the DNA locus you want to write to the output file or write "concat" for concatenation:
  String/CONCAT
  In case of a multi-loci DNA data set one has to choose the DNA locus to write to the output file or specify “CONCAT” to concatenate the loci into one sequence (PHYLIP cannot handle multi-loci DNA data).

10.37 SAM

SAM version 1.4 (17. April 2011)

SAM (Sequence Alignment/Map) format is a generic format for storing large nucleotide sequence alignments.SAM aims to be a format that:

- Is flexible enough to store all the alignment information generated by various alignment programs;
- Is simple enough to be easily generated by alignment programs or converted from existing alignment formats;
- Is compact in file size;
- Allows most of operations on the alignment to work on a stream without loading the whole alignment into memory;
- Allows the file to be indexed by genomic position to efficiently retrieve all reads aligning to a locus.

The program SAMtools provide various utilities for manipulating alignments in the SAM format, including sorting, merging, indexing and generating alignments in a per-position format (Li, et al., 2009).

The conversion process of the format SAM needs the programs Samtools (version 0.1.12/0.1.06) and Bcftools, which can be downloaded from http://samtools.sourceforge.net. The paths to the program files (samtools.exe and bcftools.exe) have to be specified in the “Config” menu under “Options” (see section 5.3.1 PGDSpider menus) or in the “spider.conf.xml” file within the PGDSpider distribution (the file will be automatically generated the first time you run PGDSpider).

Currently, PGDSpider is not meant to convert very large SAM files as it loads into memory the whole file, whose size may exceed available RAM. However, PGDSpider allows one to convert specific subsets of SAM files into any other format. This feature can be used to perform sliding window analysis.

10.37.1 Data type handled

SAM can handle data of following type:

- DNA
- UHTS (Ultra High-Throughput Sequencing data)

10.37.2 SAM format

SAM is a tab-delimited text format with following file extension: *.sam
It consist of a header and a alignment section.

Header section:

- Optional, but recommended
- Each header line begins with a “@”, followed by a two-letter record type code

- The following table gives the defined record types and and tags (* required when record type is present)

Type	**Tag**	**Description**
HD (header)	VN*	File format version
	SO	Sort order (unsorted/queryname/coordinate)
	GO	Group order (none/query/reference)
SQ (sequence dictionary)	SN*	Sequence name
	LN*	Sequence length
	AS	Genome assembly identifier
	M5	MD5 checksum of the sequence in the uppercase
	UR	URI of the sequence
	SP	species
RG (read group)	ID*	Unique read group identifier
	CN	Name of the sequencing center producing the read
	SM	Sample
	LB	Library
	DS	Description
	PU	Platform unit
	PI	Predicted median insert size
	DT	Date the run was produced
	PL	Platform/technology used to produce the reads
PG (Program)	ID*	Program name
	PN	Program name
	VN	Program version
	CL	Command line
	PP	Previous PG-ID
CO (comment)		One-line text comments

Alignment Section

The format of each field in a line is:

- QNAME and FLAG are required for all alignments
- SEQ and QUAL can be absent and represented as a * (if QUAL is present, it must have the same length as SEQ)
- Optional fields: all optional fields follow the format TAG:TYPE:VALUE (for more details http://samtools.sourceforge.net/SAM1.pdf)
    - TAG: two-character string. Each TAG can only appear once in one alignment line
    - TYPE: single case sensitive letter which defines the format of VALUE
    - Example: RG:Z:MarCHGS13

Field	Regular expression	Range	Description
QNAME	`[!-?A-~]f1,255g`		Query pair name if paired; or query name if unpaired (unique!)
FLAG	`[0-9]+`	[0,216-1]	bitwise FLAG (0: forward read, 16: reverse read)
RNAME	`[!-()+-<>-~][!-~]*`		Reference sequence name (If SQ is present in the header, RNAME and MRNM must appear in an SQ header record)
POS	`[0-9]+`	[0,229-1]	1-based leftmost position/coordinate of the clipped sequence
MAPQ	`[0-9]+`	[0,28-1]	Mapping quality (phred-scaled posterior probability that the mapping position of this read is incorrect), mapping quality is not available: 255
CIGAR	`([0-9]+[MIDNSHPX=])+`		extendend CIGAR string
RNEXT	`=|[!-()+-<>-~][!-~]*`		Ref. name of the mate/next fragment, '=' if the same as RNAME, '*' if pairing information is not available
PNEXT	`[0-9]+`	[0,229-1]	Position of the mate/next fragment, '0' if pairing information is not available
TLEN	`-?[0-9]+`	[-229,229]	observed Tempplate LENgth, '0' if pairing information is not available
SEQ	`[A-Za-z=.]+`		fragment sequence, '=' for a match to the reference, n/N/. for ambiguity
QUAL	`[!-~]+`	[0,93]	base quality, ASCII-33 gives the Phred base quality
TAG	`[A-Z][A-Z0-9]`		two-character tag, optional
TYPE	`[AifZH]`		casesensitive single letter which defines the format of VALUE (e.g.: RG for read group), optional
VALUE	`[^\t\n\r]+`		match TYPE, optional

CICAR format:

- CIGAR string is a comprised of series of operation length plus the operation:
- Example: `43M1I14M1D10M`
  43 bases which matches/mismatches to the reference sequence, followed by 1 insertion, followed by 14 matches/mismatches, followed by 1 deletion, followed by 10 matches/mismatches

op	Description
M	Alignment match (sequence match or mismatch)
I	Insertion to reference
D	Deletion from reference
N	Skipped region from reference
S	Soft clip on the read (clipped sequence present in <seq>)
H	Hard clip on the read (clipped sequence not present in <seq>)
P	Padding
=	sequence match
X	sequence mismatch

- Sum of lengths of the M/I/S/=/X operations ought to equals the length of SEQ

Example:

```
@HD     VN:1.0
@SQ     SN:chr20 LN:62435964
@RG     ID:L1 PU:SC_1_10 LB:SC_1 SM:NA12891
@RG     ID:L2 PU:SC_2_12 LB:SC_2 SM:NA12891
read_28833_29006_6945   99   chr20   28833   20   10M1D25M   =   28993  195
AGCTTAGCTAGCTACCTATATCTTGGTCTTGGCCG   <<<<<<<<<<<<<<<<<<<<<:<9/,&,22;;<<<
read_28701_28881_323b   147  chr20   28834   30   35M        =   28701  -168
ACCTATATCTTGGCCTTGGCCGATGCGGCCTTGCA   <<<<<;<<<<7;:<<<6;<<<<<<<<<<<<7<<<<
```

10.37.3 Links and References

Website: http://samtools.sourceforge.net,
Manual: http://samtools.sourceforge.net/SAM1.pdf

(Li, et al., 2009)

10.37.4 Special PGDSpider input/output questions

- Input:
    - Reference file:
      Absolute file path
      Choose the file with the reference sequences
    - Select what should be imported:
      READS/SNP/CONSENSUS
      Defines if all reads, the consensus sequences or only the variant sites (SNP) should be imported
    - Concatenate consensus sequences from different reference data (only works if you choose to import consensus sequences):
      TRUE/FALSE
      Specify if consensus sequences coming from different reference sequences should be concatenated or not
    - What is the ploidy of the data:
      DIPLOID/HAPLOID
      Define if the data are haploid or diploid
    - Only import following regions (optional):
      String (e.g.: chr1:100:5000 or chr1:100:5000 chr2:1:100)
      Defines which regions should be imported. Regions should be defined in following format: refSeqName:start:end, multiple regions: separate it with white spaces

- Output:
    - Save an additional file with reference sequences:
      TRUE/FALSE
      Saves a file with the reference sequences
    - Save reference file:
      Absolute file path
      Choose the path where the reference file should be written
    - Specify which data type should be included (optional):
      NGS/DNA/RNA
      If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).

10.39 Structurama

Structurama is a program for inferring population structure from genetic data. The program assumes that the sampled loci are in linkage equilibrium and that the allele frequencies for each population are drawn from a Dirichlet probability distribution.

10.39.1 Data type handled

Structurama is able to handle diploid or haploid data.

10.39.2 Structurama format

- Structurama has a unique, NEXUS-like, file format.
- Tabs should not be included in the file
- The data are entered in a data block
    - block starts with "begin data;"
    - ends with "end;"
- The data block contains your observations, which are assumed to be alleles at different loci. Alleles are encoded with arbitrarily lables:
    - Diploid: "(1,2)" (homozygous: "(1,1)")
    - Haploid: "(1)"
- Missing alleles: enter a question mark "?"
- Comments are contained in between square brackets (e.g., "[This is a comment.]")

- Example:

```
begin data;
  dimensions nind=3 nloci=4;
  info
  Larry ( 1 , 1 ) ( 0 , 3 ) ( 8 , 8 ) ( 7 , 2 ) ,
  Moe   ( 1 , 1 ) ( 3 , 3 ) ( 8 , 8 ) ( 7 , 7 ) ,
  Curly ( 1 , 2 ) ( 0 , 0 ) ( 8 , ? ) ( 7 , 8 )
  ;
end;
```

10.39.3 References

Website: http://cteg.berkeley.edu/~structurama/index.html
Manual: http://cteg.berkeley.edu/~structurama/manual.html

(Huelsenbeck, et al., 2011)

10.39.4 Special PGDSpider input/output questions

- Output:
  - Specify which data type should be included (optional):
    DNA/RNA/NGS/MICROSAT/SNP/RFLP/AFLP/STANDARD
    If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
  - Specify the locus/locus combination which should be written to the output file (optional):
    String
    If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.40 STRUCTURE (fastSTRUCTURE)

STRUCTURE version 2.3.4 (July 2012)

The program STRUCTURE implements a model-based clustering method for inferring population structure using genotype data consisting of unlinked markers. It includes inferring the presence of distinct populations, assigning individuals to populations, studying hybrid zones, identifying migrants and admixed individuals, and estimating population allele frequencies in situations where many individuals are migrants or admixed (Falush, et al., 2003; Falush, et al., 2007; Pritchard, et al., 2000).

fastSTRUCTURE

fastStructure is an algorithm for inferring population structure from large SNP genotype data. It is based on a variational Bayesian framework for posterior inference and is written in Python2.x (Raj, et al., 2014).

10.40.1 Data type handled

STRUCTURE can handle haploid and diploid data of following type:

- SNP (numeric)
- Microsatellites
- RFLP
- AFLP

fastSTRUCTURE can only handle diploid SNP data

10.40.2 STRUCTURE format

The STRUCTURE data file is arranged as a matrix, in which the data for individuals are in rows, and the loci are in columns. For a diploid organism, data for each individual can be stored either on 2 consecutive rows, where each locus is in one column, or alternatively on one row, where each locus is in two consecutive columns.

The rows contain the:

- Marker Names (Optional; string):
  The first row can contain a list of identifiers for each of the markers (loci) in the data set.
- Recessive Alleles (Data with dominant markers only; integer):
  SNPs or microsatellites data sets would generally not include this line. This row indicates which allele (if any) is recessive at each locus.
- Inter-Marker Distances (Optional; real numbers):
  The next row is a set of inter-marker distances, for use with linked loci. These should be genetic distances (e.g., centiMorgans). The markers must be in map order within linkage groups. When consecutive markers are from different linkage groups (e.g.: different

chromosomes), these should be indicated by the value -1. A value -1 is also assigned to the first marker. All other distances should be non-negative.

- Phase Information (Optional; diploid data only; real number in the range [0,1]):
  This is for use with the linkage model only. A single row of probabilities that appears after the genotype data for each individual. There are two alternative representations for the phase information:
  - The two rows of data for an individual are assumed to correspond to the paternal and maternal contributions. The phase line indicates the probability that the ordering is correct at the current marker (set MARKOVPHASE=0) respectively.
  - the phase line indicates the probability that the phase of one allele relative to the previous allele is correct (set MARKOVPHASE=1)
- Individual/Genotype data (Required):
  Data for each sampled individual are arranged into one or more rows.

Each row of individual data contains the following elements (columns):

1. Label (Optional; string):
   A string of integers or characters used to name each individual in the sample.
2. PopData (Optional; integer):
   An integer designating a user-defined population from which the individual was obtained
3. PopFlag (Optional; 0 or 1):
   A Boolean flag which indicates whether to use (1) or not (0) use the PopData when learning samples are used. These are samples whose origin is unknown, but they are classified with the help of individuals whose origin is known.
4. LocData (Optional; integer):
   An integer designating a user-defined sampling location
5. Phenotype (Optional; integer):
   An integer designates the value of a phenotype of interest for each individual.
6. Extra Columns (Optional; string):
   It maybe convenient for users to include additional data in the input file which are ignored by the program. These go here, and maybe strings of integers or characters.
7. Genotype Data (Required; integer):
   Each allele at a given locus should be coded by a unique integer (e.g. microsatellite repeats score).

- Missing data should be indicated by a number that is not present anywhere else in the data (often -9 by convention).

- **Example:**

```
             loc_a  loc_b  loc_c  loc_d  loc_e
George   1   -9     145     66     0      92
George   1   -9     -9      64     0      94
Paula    1   106    142     68     1      92
Paula    1   106    148     64     0      94
Matthew  2   110    145     -9     0      92
Matthew  2   110    148     66     1      -9
Bob      2   108    142     64     1      94
Bob      2   -9     142     -9     0      94
```

10.40.3 fastSTRUCTURE format

fastSTRUCTURE expects a more specific STRUCTURE format:

- rows correspond to samples (e.g.: no row with marker names)
- only diploid data are handled and two rows per sample are expected
- columns correspond to SNPs
- first 6 columns of the file are ignored (including IDs, metadata,…)
- only handles bi-allelic loci
- two alleles at each locus can be encoded as desired
- missing data should be encoded as "-9"

- **Example:**

```
George   1   1   0   0   extraCol   -9     145     66     0     92
George   1   1   0   0   extraCol   -9     -9      64     0     94
Paula    1   1   0   0   extraCol   106    142     68     1     92
Paula    1   1   0   0   extraCol   106    148     64     0     94
Matthew  2   1   0   0   extraCol   110    145     -9     0     92
Matthew  2   1   0   0   extraCol   110    148     66     1     -9
Bob      2   1   0   0   extraCol   108    142     64     1     94
Bob      2   1   0   0   extraCol   -9     142     -9     0     94
```

10.40.4 Links and References

STRUCTURE:

Website: http://pritchardlab.stanford.edu/structure.html
Manual: http://pritchardlab.stanford.edu/structure_software/release_versions/v2.3.4/structure_doc.pdf

(Falush, et al., 2003; Falush, et al., 2007; Hubisz, et al., 2009; Pritchard, et al., 2000)

fastSTRUCTURE:

Website: http://rajanil.github.io/fastStructure/

(Raj, et al., 2014)

10.40.5 Special PGDSpider input/output questions

- Input:
  - What is the ploidy of the data:
    HAPLOID/DIPLOID_ONE_ROW/DIPLOID_TWO_ROWS
    Must be defined if the data are haploid, diploid (on one row), diploid (on two rows)
  - "Phase information" row present:
    TRUE/FALSE
    Specify if a phase information row is present or not

- What is the missing value code:
  Integer
  Enter the symbol coding for missing values, e.g.: -9, -999, etc.
- Select the data type:
  MICROSAT/RFLP/SNP/AFLP
  Define if the data are Microsatellite, RFLP, SNP or AFLP data
- How are Microsat alleles coded:
  REPEATS/LENGTH/ARBITARY
  Define if the Microsat data are coded as number of repeats, as length of the PCR fragments or as an arbitrary number
- Enter the size of the repeated motif:
  Integer/Integer,Integer, …
  Needed to convert the Microsatellite data (length of the PCR fragments) to number of repeat data (PGD can only save number of repeat Microsat data). Same for all loci: enter one number. Different between loci: comma separated list (e.g.: 2,2,3,2)
- Are marker (locus) names included:
  TRUE/FALSE
  Specify if locus names are included or not
- Enter number of markers (loci) listed in the input file:
  Integer
  If loci names are not present, define the number of loci.
- Are individual names (labels) included in the input file:
  TRUE/FALSE
  Specify if individual names are included or not
- Is the "PopData" column (population identifier) present in the input file:
  TRUE/FALSE
  Specify if the population identifiers are present or not
- Are the "Recessive Alleles" row and/ or the "Inter-Marker Distance" row present in the input file:
  NONE/ RECESSIVE/MARKERDIST/*BOTH*
  Define if both, only the recessive alleles, only the inter-marker distance or none of the two rows are present

- Output:
  - Save more specific fastSTRUCTURE format:
    TRUE/FALSE
    Need to define if data should be stored in the more specific fastSTRUCTURE format (needed for the program fastSTRUCTURE). See above for a short description of the format.
  - Do you want to include inter-marker distances:
    TRUE/FALSE
    If loci are linked and locations are known it is possible to add an additional line containing the distances between loci.

- Specify which data type should be included (optional):
  MICROSAT/SNP/AFLP/RFLP/STANDARD/DNA
  If there is more than one allowed data type, one has to select the data type which should be included in the output file (only one data type can be analysed per file).
- Specify the locus/locus combination which should be written to the output file (optional):
  String
  If several locus or locus combinations exists (PGD format is able to store several locus or locus combinations), one has to specify the locus or locus combination which should be included in the output file.

10.41 VCF

VCF version 4.1 (2. August 2012) without structural variants (only SNP and INDELs)

VCF (Variant Call Format) format stores structural variant data.

The conversion process of the format VCF needs the programs Samtools (version 0.1.12/0.1.06) and Bcftools, which can be downloaded from http://samtools.sourceforge.net. The paths to the program files (samtools.exe and bcftools.exe) have to be specified in the "Config" menu under "Options" (see section 5.3.1 PGDSpider menus) or in the "spider.conf.xml" file within the PGDSpider distribution (the file will be automatically generated the first time you run PGDSpider).

Currently, PGDSpider is not meant to convert very large VCF files as it loads into memory the whole file, whose size may exceed available RAM. However, PGDSpider allows one to convert specific subsets of VCF files into any other format. This feature can be used to perform sliding window analysis.

10.41.1 Data type handled

VCF can handle data of following type:

- SNP
- DNA
- UHTS (Ultra High-Throughput Sequencing data)

10.41.2 VCF format

VCF is a tab-delimited text format with following file extension: *.vcf

The format contains meta-information lines, a header line, and data lines which contain information about a position in the genome.

Meta-information lines

- begins with `##`
- must be key=value pairs
- 'fileformat' (mandatory):
  - VCF format version
  - e.g.: `##fileformat=VCFv4.1`
- 'INFO':
  - `##INFO=<Flag_ID>,<Number_of_Values>,<Value_Type>,<Description>`
  - `<Number_of_Values>`: Integer that describes the number of values that can be included in the INFO field (values varies, unknown or unbounded: -1)

  - `<Value_Types>`: Integer, Float, Character, String and Flag. The 'Flag' type indicates that the INFO field does not contain a Value entry, and hence `<Number_of_Values>` should be 0 in that case.
- 'FILTER':
  - Filters that have been applied to the data
  - `##FILTER=<FILTER_ID>,<Description>`
- 'FORMAT':
  - `##FORMAT=<FORMAT_ID>,<Number_of_Values>,<Value_Type>, <Description>`
  - `<Value_Types>`: Integer, Float, Character, and String.

Header line

- tab delimited
- names the 8 fixed, mandatory columns:
  1. #CHROM
  2. POS
  3. ID
  4. REF
  5. ALT
  6. QUAL
  7. FILTER
  8. INFO
- If genotype data is present:
  9. FORMAT column header
  10. an arbitrary number of sample ids

Data line

Fixed fields:

- tab-delimited
- missing values: "."
- 8 fixed fields per record:
  1. CHROM chromosome:
     - an identifier from the reference genome.
     - Alphanumeric String, required
  2. POS position:
     - The reference position (1st base having position 1).
     - Positions are sorted numerically, in increasing order, within each reference sequence.
     - Integer, required

3. ID:
   - A unique identifier. If this is a dbSNP variant: use the rs number.
   - Alphanumeric String, Missing value: ”.”
4. REF reference base:
   - One of A, C, G, T, N. Bases should be in uppercase.
   - Multiple bases are permitted. The value in the POS field refers to the position of the first base in the String.
   - For InDels, the reference String must include the base before the event (which must be reflected in the POS field).
   - String, required
5. ALT:
   - Comma separated list of alternate non-reference alleles.
   - Options are A, C, G, T, Dn (for delete n bases starting with the base at POS), I<seq> (where <seq> is a list of ACGT bases to be inserted just after the base at POS).
   - If there are no alternative alleles, then period character should be used.
   - Bases should be in uppercase.
   - Alphanumeric String, Missing value: ”.”
6. QUAL:
   - Phred-scaled quality scores for the assertion made in ALT.
   - If ALT is ”.” (no variant) then this is -10log_10 p(variant) and if ALT is not ”.” this is -10log_10 p(no variant).
   - High QUAL scores indicate high confidence calls.
   - Although traditionally people use integer phred scores, this field is permitted to be a floating point so to enable higher resolution for low confidence calls if desired.
   - Numeric, Missing Value: -1
7. FILTER filter:
   - PASS if this position has passed all filters
   - If site not passed all filters, a semicolon-separated list of codes for filters that fail.
   - Alphanumeric String, Missing Value: ”.”
8. INFO additional information:
   - Alphanumeric String, Missing Value: ”.”
   - Encoded as a semicolon-separated series of short keys with optional values in the format: <key>=<data>[,data]. The subfields could be e.g.:
     - AA: ancestral allele
     - AC: allele count in genotypes, for each ALT allele, in the same order as listed
     - AF: allele frequency for each ALT allele in the same order as listed: use this when estimated from primary data, not called genotypes
     - AN: total number of alleles in called genotypes
     - BQ: RMS base quality at this position
     - CIGAR: cigar string describing how to align an alternate allele to the reference allele
     - DB: dbSNP membership
     - DP: combined depth across samples, e.g. D=154
     - END: end position of the variant described in this record

        - H2: membership in hapmap2
        - H3: membership in hapmap3
        - MQ: RMS mapping quality, e.g. MQ=52
        - MQ0: Number of MAPQ == 0 reads covering this record
        - NS: Number of samples with data
        - SB: strand bias at this position
        - SOMATIC: indicates that the record is a somatic mutation, for cancer genomics
        - VALIDATED: validated by follow-up experiments
        - 1000G: membership in 1000 Genomes
        - etc. The exact format of each INFO subfield should be specified in the meta-information.
    - It is not necessary to list all the properties that a site does NOT have, by e.g. H2=0.

Genotype fields:

- If genotype information is present, then the same types of data must be present for all samples.
- First a FORMAT field is given specifying the data types and order.
- This is followed by one field per sample, with the colon-separated data in this field corresponding to the types specified in the format.
- The first subfield must always be the genotype (GT)

- There are several common, reserved keywords, which are defined as follows:
    - GT genotype (mandatory):
        - encoded as alleles values separated by ”/” or “|”
        - e.g.: The allele values are 0 for the reference allele (what is in the reference sequence), 1 for the first allele listed in ALT, 2 for the second allele list in ALT and so on. For diploid calls examples could be 0/1 or 1|0 etc.
        - For haploid calls (Y, male X, mitochondrion) only one allele value should be given.
        - missing allele: ”.” (e.g.: ./. for a diploid).
        - The meanings of the separators are:
          “/”': genotype unphased
          “|”': genotype phased.
    - DP:
        - read depth at this position for this sample
        - Integer, Missing value: -1
    - FT:
        - sample genotype filter indicating if this genotype was “called” (similar in concept to the FILTER record for the entire CHROM/POS)
        - PASS: indicate that all filters have been passed
        - a semi-colon separated list of codes for filters that fail
        - ”.”: indicate that filters have not been applied.

        - These values should be described in the meta-information in the same way as FILTERs
        - Alphanumeric String, Missing value: ”.”
    - GL genotype likelihoods:
        - Comma separated log10-scaled likelihoods for all possible genotypes given the set of alleles defined in the REF and ALT fields.
        - If A is the allele in REF and B,C,... are the alleles as ordered in ALT, the ordering of genotypes for the likelihoods is given by: F(j/k) = (k*(k+1)/2)+j e.g.: for biallelic sites the ordering is: AA,AB,BB;
          for triallelic sites the ordering is: AA,AB,BB,AC,BC,CC
    - GLE:
        - Genotype likelihoods of heterogenous ploidy
    - PL:
        - Phred-scaled genotype likelihoods rounded to the closest integer
        - Ordering like in GL
    - GP:
        - Phred-scaled genotype posterior probabilities
    - GQ genotype quality:
        - encoded as a phred quality (genotype call is wrong)
        - max quality 99
        - Integer, Missing value: -1
    - HQ haplotype qualities:
        - two phred qualities comma separated
        - Integer, Missing value: -1 for each quality. e.g. ”-1,-1”
    - PS phase set:
        - Non-negative 32-bit integer
    - PQ phasing quality:
        - Phred-scaled probability that alleles are ordered incorrectly in a heterozygote
    - EC:
        - Comma separated list of expected alternate allele counts for each alternate allele in the same order as listed in the ALT field
    - MQ:
        - RMS mapping quality
    - Additional Genotype fields can be defined in the meta-information

Example:

```
##fileformat=VCFv4.0
##fileDate=20090805
##source=myImputationProgramV3.1
##reference=1000GenomesPilot-NCBI36
##phasing=partial
##INFO=<ID=NS,Number=1,Type=Integer,Description="Number of Samples With Data">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Total Depth">
##INFO=<ID=AF,Number=.,Type=Float,Description="Allele Frequency">
##INFO=<ID=AA,Number=1,Type=String,Description="Ancestral Allele">
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP membership, build 129">
##INFO=<ID=H2,Number=0,Type=Flag,Description="HapMap2 membership">
##FILTER=<ID=q10,Description="Quality below 10">
##FILTER=<ID=s50,Description="Less than 50% of samples have data">
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=HQ,Number=2,Type=Integer,Description="Haplotype Quality">
#CHROM POS      ID         REF  ALT      QUAL FILTER  INFO
      FORMAT             NA00001            NA00002                NA00003
20     14370    rs6054257  G    A        29   PASS    NS=3;DP=14;AF=0.5;DB;H2
      GT:GQ:DP:HQ        0|0:48:1:51,51     1|0:48:8:51,51         1/1:43:5:.,.
20     17330    .          T    A        3    q10     NS=3;DP=11;AF=0.017
      GT:GQ:DP:HQ        0|0:49:3:58,50     0|1:3:5:65,3           0/0:41:3
20     1110696  rs6040355  A    G,T      67   PASS    NS=2;DP=10;AF=0.333,0.667;AA=T;DB
      GT:GQ:DP:HQ        1|2:21:6:23,27     2|1:2:0:18,2           2/2:35:4
20     1230237  .          T    .        47   PASS    NS=3;DP=13;AA=T
      GT:GQ:DP:HQ        0|0:54:7:56,60     0|0:48:4:51,51         0/0:61:2
20     1234567  microsat1  GTCT G,GTACT  50   PASS    NS=3;DP=9;AA=G
      GT:GQ:DP           0/1:35:4           0/2:17:2               1/1:40:3
```

10.41.3 Links and References

Website: http://www.1000genomes.org/wiki/Analysis/Variant%20Call%20Format/vcf-variant-call-format-version-41

10.41.4 Special PGDSpider input/output questions

- Input:
  - What is the ploidy of the data:
    DIPLOID/HAPLOID
    Define if the data are haploid or diploid
  - Only import following regions (optional):
    String (e.g.: chr1:100:5000 or chr1:100:5000 chr2:1:100)
    Defines which regions should be imported. Regions should be defined in following format: refSeqName:start:end, multiple regions: separate it with white spaces
  - Take most likely genotype if "PL" or "GL" is given in the genotype field:
    TRUE/FALSE
    If "PL" or "GL" is given in the genotype field, take most likely genotype or take genotype specified in "GT".
  - Minimal phred-scaled quality of SNPs (optional):

Double
Output SNPs with phred-scaled quality ("QUAL" field) of at least the specified value
- Minimal phred-scaled genotype quality (optional):
  Double
  Output genotype as missing if the phred-scale genotype quality is below specified value.
- Minimal read depth of a position for the sample (optional):
  Integer
  Output genotype as missing if the read depth of a position for the sample is below specified value.

- Specify individuals you want to output (optional):
  String
  If only a subset of individuals should be output, one could give a list of individual names (comma separated: ind1, ind2, ind4, …)
- Include non-polymorphic SNPs (optional):
  TRUE/FALSE
  Define if non-polymorphic SNPs should be included.
- Include a file with population definitions
  TRUE/FALSE
  Possibility to add a file with the definition of populations (individuals assigned to populations).
- Specify a file with population definitions (optional):
  Absolute file path
  One can specify a file containing the definition of which individual belongs to which population. The population definition file should have following format (names without whitespaces):

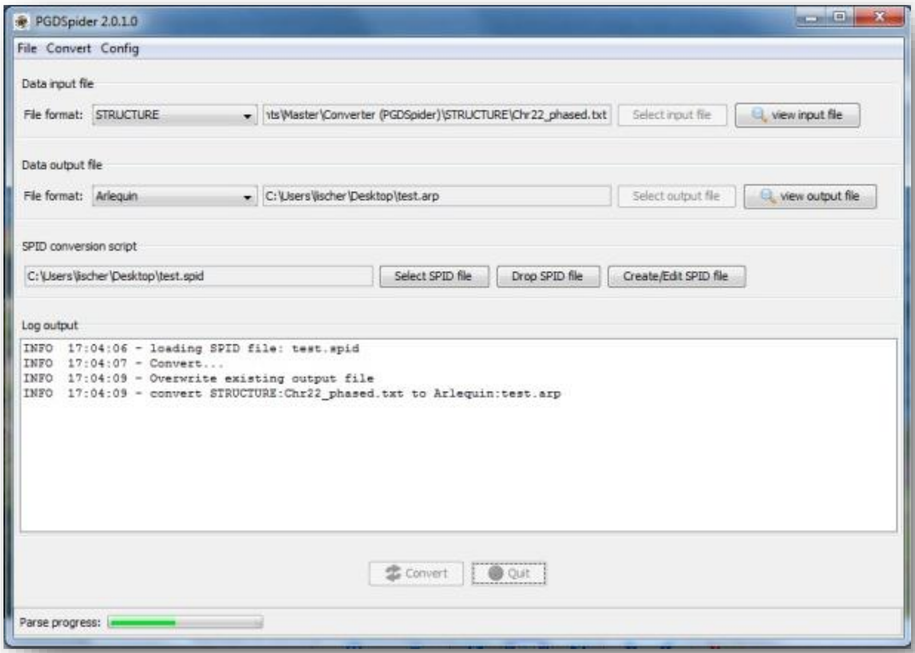
```
Ind_1      pop_1
Ind_2      pop_1
Ind_3      pop_2
Ind_4      pop_2
```

- Output:
  - Save an additional file with reference sequences:
    TRUE/FALSE
    Saves a file with the reference sequences
  - Save reference file:
    Absolute file path
    Choose the path where the reference file should be written
  - Specify which data type should be included (optional):
    SEQUENCES/SNP
    If the input file contains sequence and SNP data, one has to select which should be included in the output file (only sequence or SNP can be analysed per file).

- Enter the integer that codes for the nucleotide:
  Integer
  Define the integer that codes for a specific nucleotide

11 PGDSpider Screenshots

- PGDSpider while it is converting. At the bottom of the GUI the progress of the parser can be seen in the progress bar and during the writing process a waiting symbol appears:



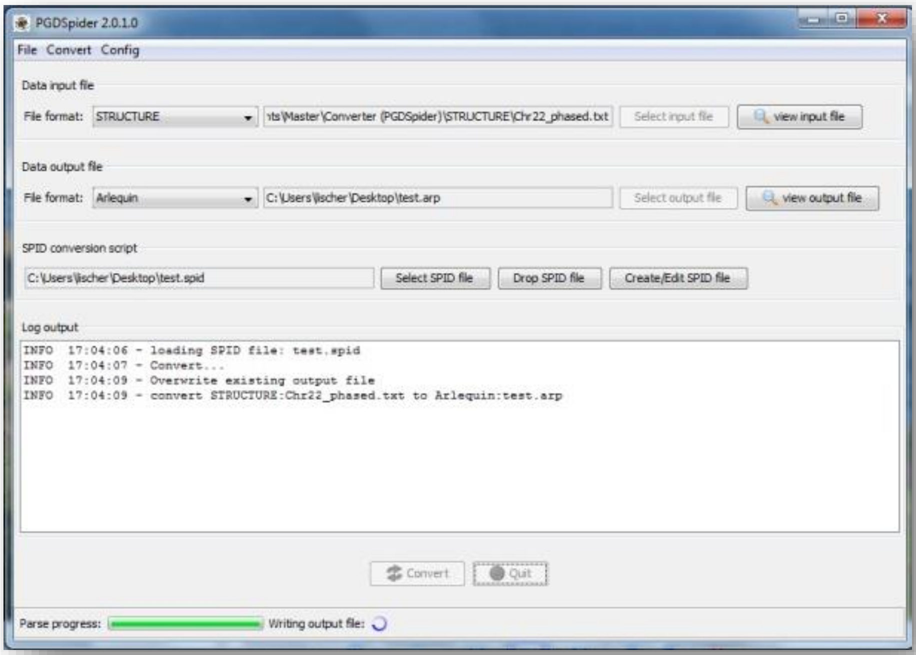
File format: STRUCTURE \ts\Master\Converter (PGDSpider)\STRUCTURE\Chr22_phased.txt

File format: Arlequin C:\Users\lischer\Desktop\test.arp

C:\Users\lischer\Desktop\test.spid

```
INFO  17:04:06 - loading SPID file: test.spid
INFO  17:04:07 - Convert...
INFO  17:04:09 - Overwrite existing output file
INFO  17:04:09 - convert STRUCTURE:Chr22_phased.txt to Arlequin:test.arp
```

Fig. 10: Screenshot of the PGDSpider GUI during conversion. The parser progress is visible at the bottom left.



File format: STRUCTURE \ts\Master\Converter (PGDSpider)\STRUCTURE\Chr22_phased.txt

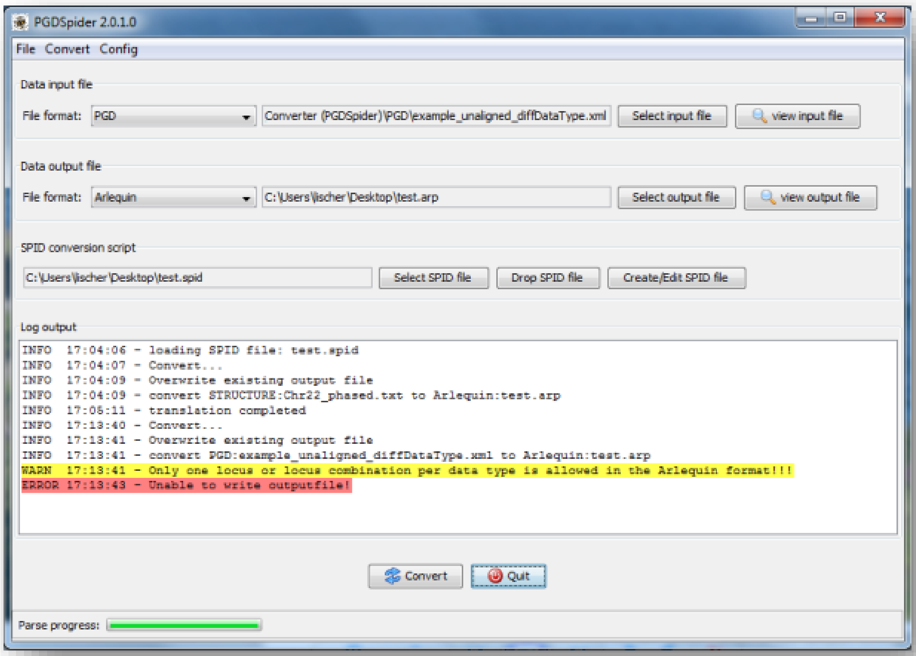
File format: Arlequin C:\Users\lischer\Desktop\test.arp

C:\Users\lischer\Desktop\test.spid

```
INFO  17:04:06 - loading SPID file: test.spid
INFO  17:04:07 - Convert...
INFO  17:04:09 - Overwrite existing output file
INFO  17:04:09 - convert STRUCTURE:Chr22_phased.txt to Arlequin:test.arp
```

Fig. 11: Screenshot of the PGDSpider GUI during conversion. The writing of the output file is shown by awaiting symbol

- PGDSpider GUI with “WARNING” and “ERROR” messages in the “Log Output”:



Data input file

File format: PGD

Converter (PGDSpider)\PGD\example_unaligned_diffDataType.xml

Data output file

File format: Arlequin

C:\Users\lischer\Desktop\test.arp

SPID conversion script

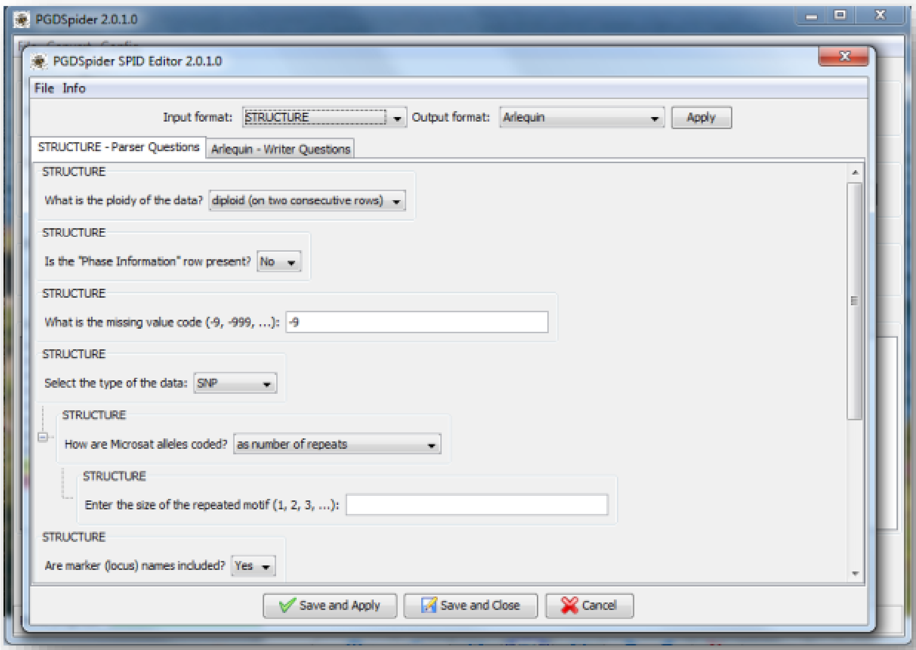
C:\Users\lischer\Desktop\test.spid

Log output

```
INFO  17:04:06 - loading SPID file: test.spid
INFO  17:04:07 - Convert...
INFO  17:04:09 - Overwrite existing output file
INFO  17:04:09 - convert STRUCTURE:Chr22_phased.txt to Arlequin:test.arp
INFO  17:06:11 - translation completed
INFO  17:13:40 - Convert...
INFO  17:13:41 - Overwrite existing output file
INFO  17:13:41 - convert PGD:example_unaligned_diffDataType.xml to Arlequin:test.arp
WARN  17:13:41 - Only one locus or locus combination per data type is allowed in the Arlequin format!!!
ERROR 17:13:43 - Unable to write outputfile!
```

Fig. 12: Screenshot of the PGDSpider GUI with WARNING and ERROR messages within the log output

- PGDSpider GUI during conversion with the SPID Editor containing questions concerning a file format:


PGDSpider 2.0.1.0
PGDSpider SPID Editor 2.0.1.0
File Info
Apply
STRUCTURE - Parser Questions
Arlequin - Writer Questions
Save and Apply
Save and Close
Cancel

Input format: STRUCTURE   Output format: Arlequin

STRUCTURE

What is the ploidy of the data? diploid (on two consecutive rows)

STRUCTURE

Is the "Phase Information" row present? No

STRUCTURE

What is the missing value code (-9, -999, ...): -9

STRUCTURE

Select the type of the data: SNP

STRUCTURE

How are Microsat alleles coded? as number of repeats

STRUCTURE

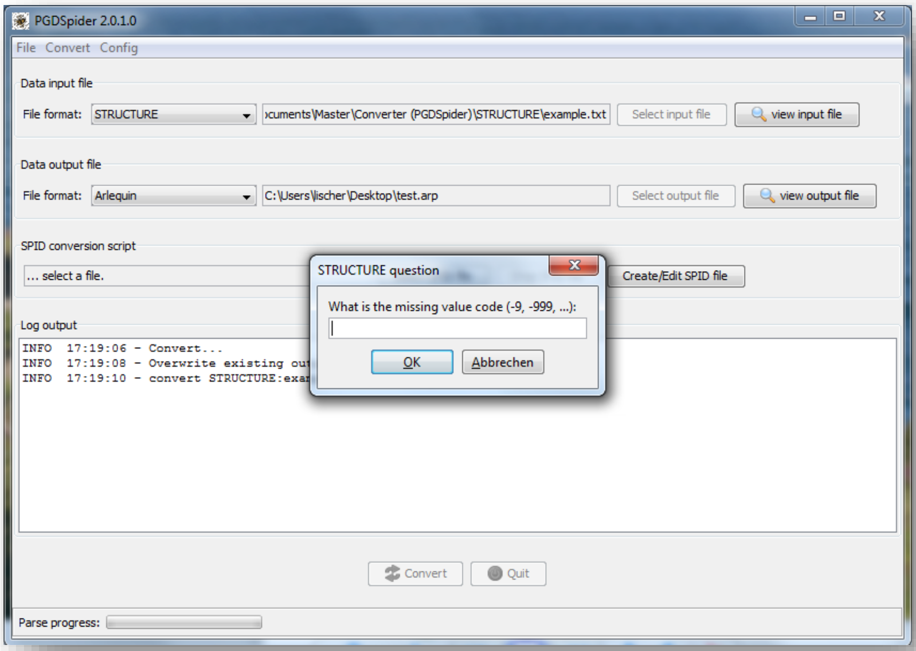
Enter the size of the repeated motif (1, 2, 3, ...):

STRUCTURE

Are marker (locus) names included? Yes

Fig. 13: Screenshot of the SPID Editor with STRUCTURE Parser Questions.

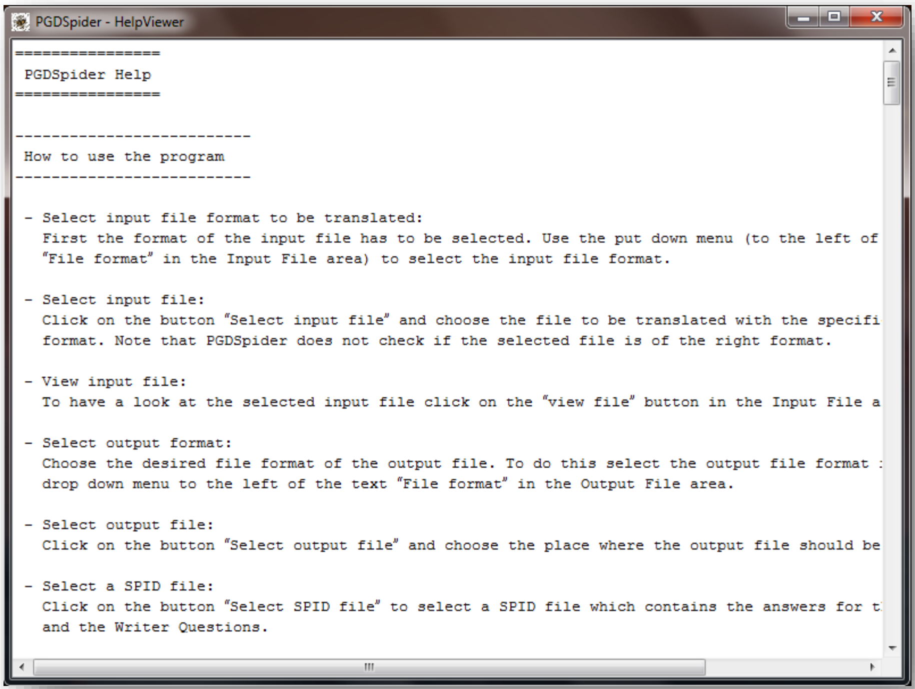
- PGDSpider GUI during conversion with a question concerning a file format:



```
INFO  17:19:06 - Convert...
INFO  17:19:08 - Overwrite existing out
INFO  17:19:10 - convert STRUCTURE:exam
```

Fig. 14: Screenshot of the PGDSpider GUI with a question concerning the STRUCTURE file format

- English help file, found in the PGDSpider GUI “Info” menu under “Help”:



```
================
 PGDSpider Help
================

--------------------------
 How to use the program
--------------------------

 - Select input file format to be translated:
   First the format of the input file has to be selected. Use the put down menu (to the left of
   "File format" in the Input File area) to select the input file format.

 - Select input file:
   Click on the button "Select input file" and choose the file to be translated with the specifi
   format. Note that PGDSpider does not check if the selected file is of the right format.

 - View input file:
   To have a look at the selected input file click on the "view file" button in the Input File a

 - Select output format:
   Choose the desired file format of the output file. To do this select the output file format :
   drop down menu to the left of the text "File format" in the Output File area.

 - Select output file:
   Click on the button "Select output file" and choose the place where the output file should be

 - Select a SPID file:
   Click on the button "Select SPID file" to select a SPID file which contains the answers for t
   and the Writer Questions.
```

Fig. 15: Screenshot of the English help file.

- PGDSpider graphical user interfaces in different languages:

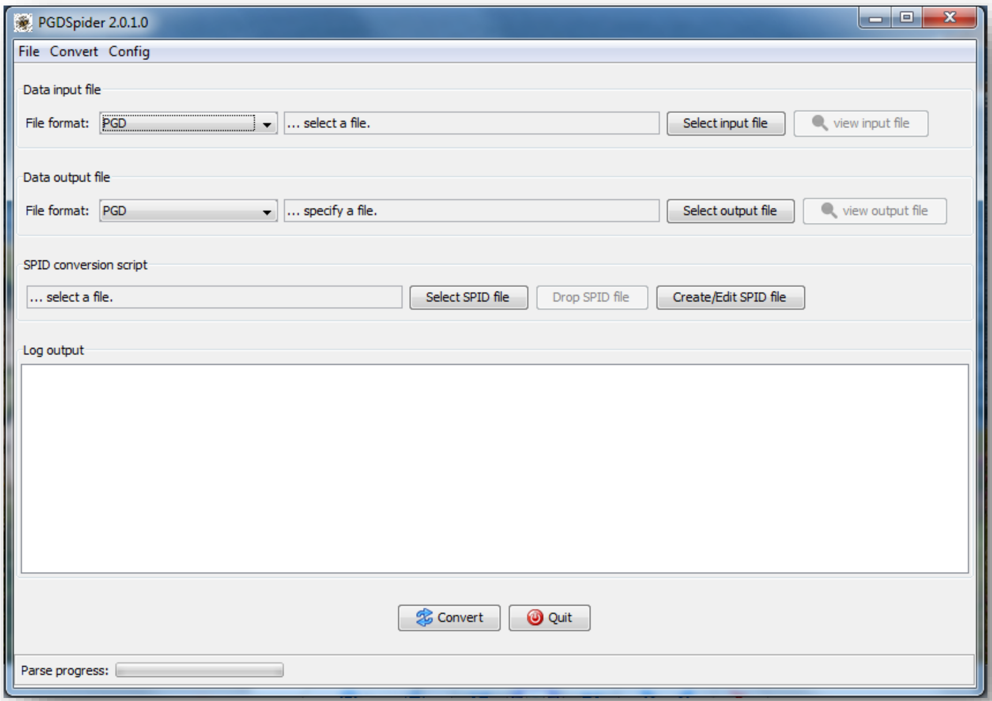
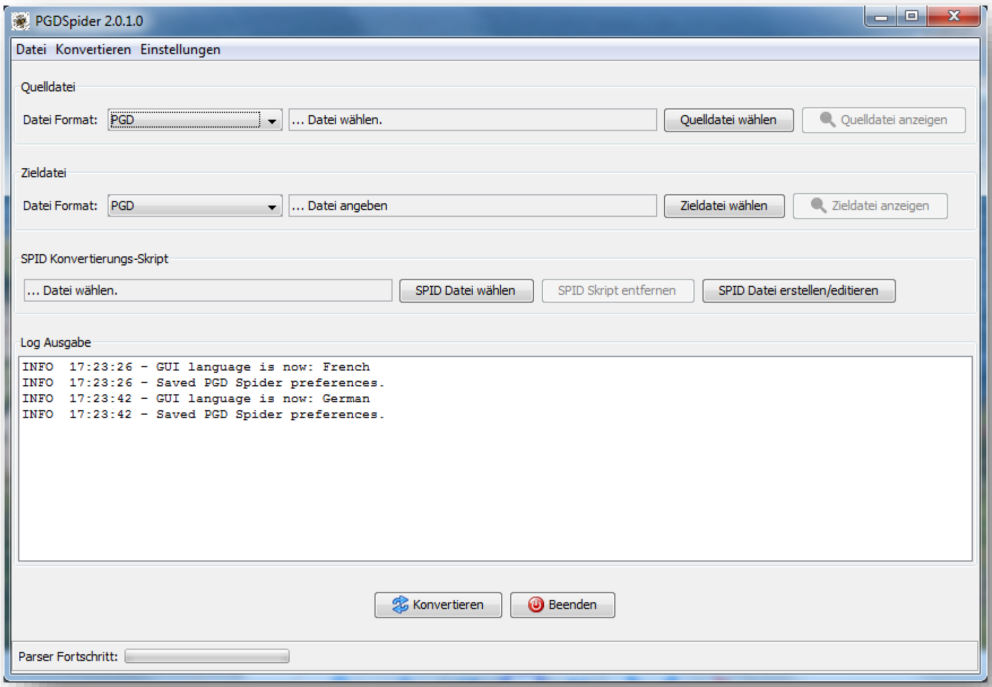
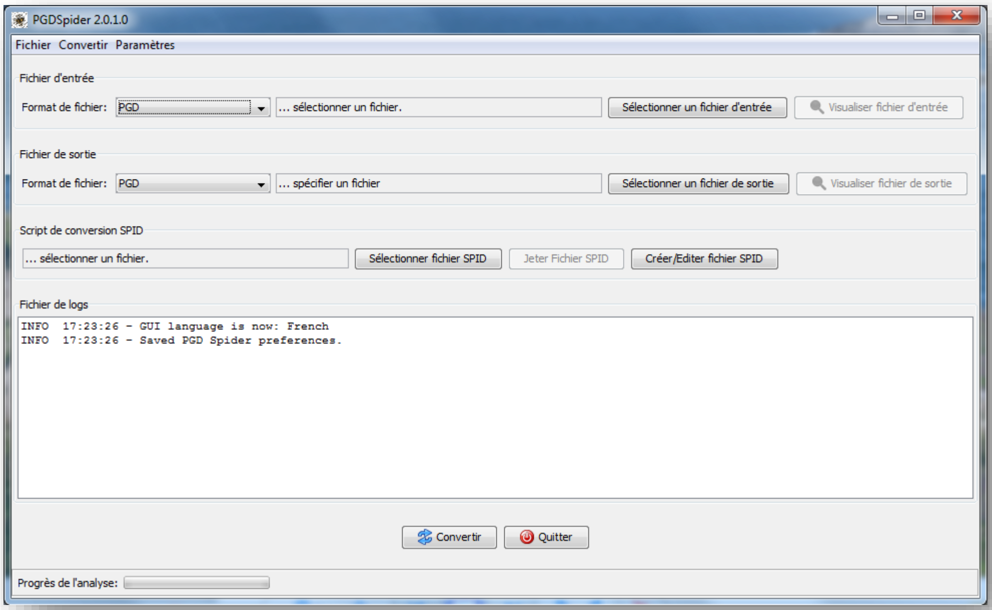


Fig. 16: English version of the PGDSpider GUI



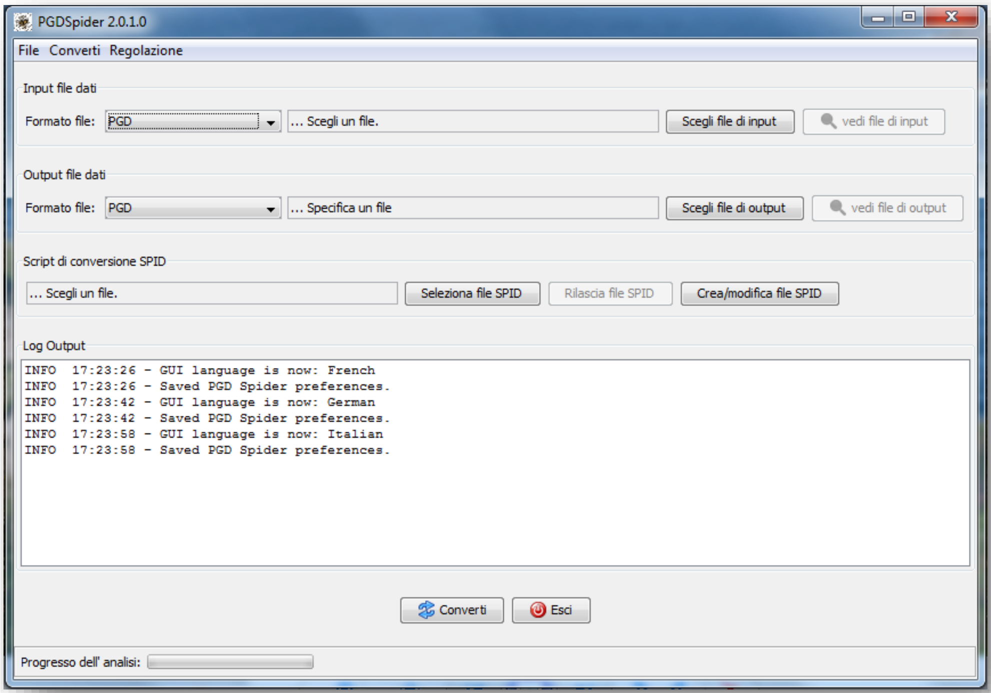
```
INFO  17:23:26 - GUI language is now: French
INFO  17:23:26 - Saved PGD Spider preferences.
INFO  17:23:42 - GUI language is now: German
INFO  17:23:42 - Saved PGD Spider preferences.
```

Fig. 17: German version of the PGDSpider GUI


PGDSpider 2.0.1.0
Fichier Convertir Paramètres
Fichier d'entrée
Format de fichier: PGD
... sélectionner un fichier.
Sélectionner un fichier d'entrée
Visualiser fichier d'entrée
Fichier de sortie
Format de fichier: PGD
... spécifier un fichier
Sélectionner un fichier de sortie
Visualiser fichier de sortie
Script de conversion SPID
... sélectionner un fichier.
Sélectionner fichier SPID
Jeter Fichier SPID
Créer/Editer fichier SPID
Fichier de logs
Convertir
Quitter
Progrès de l'analyse:

```
INFO  17:23:26 - GUI language is now: French
INFO  17:23:26 - Saved PGD Spider preferences.
```

Fig. 18: French version of the PGDSpider GUI



```
INFO  17:23:26 - GUI language is now: French
INFO  17:23:26 - Saved PGD Spider preferences.
INFO  17:23:42 - GUI language is now: German
INFO  17:23:42 - Saved PGD Spider preferences.
INFO  17:23:58 - GUI language is now: Italian
INFO  17:23:58 - Saved PGD Spider preferences.
```

Fig. 19: Italian version of the PGDSpider GUI

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