



*Development, optimisation and validation of molecular tools
for assessment of biodiversity in forest trees*
**European Union DGXII Biotechnology FW IV Research
Programme**
Molecular Tools for Biodiversity



Software for Marker Analysis

Final Compendium of the Research Project

Software for inheritance analysis

CoTrix

HAPLOGEN

DIPLOGEN

AFLP® Image Analysis Software

Software for modelling of genetic processes

Eco-Gene

METAPOPOP

Software for assessing genetic variation

GSED

Software tools

GeneKonv

CoTrix- software for inheritance analysis

Developed by: Bernd Degen

*Institut für Forstgenetik und Forstpflanzenzüchtung, Bundesforschungsanstalt für Forst- und
Holzwirtschaft, Grosshansdorf, Germany*

Present address: INRA, Station de Recherches Forestières, Kourou, Guyane Française



CoTrix Version 3.0 for Windows NT V.4.0 and Windows 95

CoTrix is an interactive user-friendly computer programme for analysis of complex DNA banding patterns. The windows programme was developed for the following tasks:

- Band adjustment for experimentally caused migration differences in pherogrammes
- Transformation of banding patterns into 1/0 matrix
- Inheritance analysis => search for codominant (dominant) inherited DNA- fragments
- Calculation of distances (Tanimoto) between individual banding patterns

Technical information

CoTrix V. 3.0 is written in Visual Basic V. 5.0 (Professional Edition) and has been compiled as 32 bit versions for the operating system Windows 95/98 and Windows NT.

Necessary hard- and software:

- For sufficient computing speed: PC Pentium 90 MHz and higher
- 8 MB RAM => for big data sets (32 - 64 MB RAM)
- VGA
- WINDOWS 95/98, WINDOWS NT 4.0
- Mouse
- Colour monitor
- Printer (colour or black white)

[Top] [Download CoTrix at <http://kourou.cirad.fr/genetique/software.html>]

HAPLOGEN- *software for inheritance analysis*

Developed by: Elizabeth Gillet

Institut für Forstgenetik und Forstpflanzenzüchtung, Universität Göttingen, Göttingen, Germany

The computer program HAPLOGEN performs qualitative inheritance analysis of zymograms and DNA electropherograms observed in haploid gametophytes. Input consists of the banding patterns, encoded as lists of 0's and 1's, of a genetically closed sample of gametophytes, i.e., the sample contains all possible banding patterns that can result as interlocus combinations of the alleles in the sample. Although genetic closure can only be judged after completion of inheritance analysis, certain sampling strategies increase the chances for genetic closure. DIPLOGEN systematically generate all hypotheses for the mode of inheritance of these patterns that conform to qualitative rules for the genetic interpretation of single bands. These rules follow from the concept of "transmission homology" (Gillet, *Silvae Genetica* 45, 8-16, 1996).

[Top] [Download HAPLOGEN at <http://www.uni-forst.gwdg.de/forst/fg/index.htm>]

DIPLOGEN - *software for inheritance analysis*

Developed by: Elizabeth Gillet

Institut für Forstgenetik und Forstpflanzenzüchtung, Universität Göttingen, Göttingen, Germany

The computer program DIPLOGEN performs qualitative inheritance analysis of zymograms and DNA electropherograms observed in diploid individuals. Input consists of the banding patterns, encoded as lists of 0's and 1's, of a genetically closed sample of diploid individuals, i.e., the sample contains all possible banding patterns that can result as interlocus combinations of the alleles in the sample. Although genetic closure can only be judged after completion of inheritance analysis, certain sampling strategies increase the chances for genetic closure. DIPLOGEN systematically generate all hypotheses for the mode of inheritance of these patterns that conform to qualitative rules for the genetic interpretation of single bands. These rules follow from the concept of "transmission homology" (Gillet, *Silvae Genetica* 45, 8-16, 1996).

[Top] [Download DIPLOGEN at <http://www.uni-forst.gwdg.de/forst/fg/index.htm>]

AFLP® Image Analysis Software- *software for inheritance analysis*

Johan Peleman, Keygene n.v., Wageningen, The Netherlands

The AFLP® Image Analysis Software is developed for the possibility to analyze AFLP® patterns co-dominantly. Therefore a lot of effort has been put into the characterization of the bands with respect to the exact size, exact intensity and shape. A combination of semi-automatic lane tracking and good quality gels will enable you to do so with the co-dominant package. Automation in lane alignment and automation in the positioning of markers allows a fast, efficient, reliable and accurate analysis, which is currently not met by other packages. Samples extending one image can be jointly analyzed as well.

Whereas many other available software packages will help you to analyze fingerprint images, they are not able to deal with the many data generated by AFLP® fingerprinting in a reliable and efficient way. The AFLP® Image Analysis Software is developed for this purpose and utilizes information intrinsic in an AFLP® pattern for reliable analyses. Reliable co-dominant scoring has not been proven by other packages yet.

The currently available package allows dominant scoring (presence/absence of bands). This package can be upgraded with the co-dominant module for the determination of hetero- and homozygosity (available early in the year 2000).

For more information contact <http://www.keygene-products.com>

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Eco-Gene- *software for modelling genetic processes*

Developed by: Bernd Degen

Institut für Forstgenetik und Forstpflanzenzüchtung, Bundesforschungsanstalt für Forst- und Holzwirtschaft, Grosshansdorf, Germany

Present address: INRA Station de Recherches Forestières, Kourou cedex, Guyane Française



Eco-Gene

For a comprehensive evaluation of human influences on the genetic system, the simulation model Eco-Gene was developed. The model combines population genetic and population dynamic processes with forest growth models. The dynamics of genetic structures (single locus and multilocus genotypes up to 200 loci) can be simulated. Spatial and temporal genetic dynamics with respect to several population genetic processes are included in the model. Overlapping or separated generations can be created and different modes of mating systems can be implemented. The model can be run with empirical and fictitious input data. The simulated genetic structures can be directly analysed with established genetic analysis programmes.

Eco-Gene has been developed with the following general **tasks**:

1. Analysing complex population genetic interactions for better understanding of complexity
2. Testing of hypotheses on the genetic system of tree populations
3. Analysing the effects of human influence on the genetic system of tree populations
4. Deriving of recommendations for sustainable management of genetic resources

Technical information

Eco-Gene is written in Visual Basic V. 4.0 and Visual Basic V.5.0 (Professional Edition) and has been compiled as 16 and 32 bit versions for the operating system Microsoft Windows 3.1., Windows 95/98 and Windows NT.

Necessary hard- and software:

- For sufficient computing speed: PC Pentium 133 MHz and higher
- 8 MB RAM => for big data sets (32 - 64 MB RAM)
- VGA
- WINDOWS 95/98, WINDOWS NT 4.0, WINDOWS 3.11
- Mouse
- Colour monitor
- Printer (colour or black white)

[Top] [Download Eco-Gene at <http://kourou.cirad.fr/genetique/software.html>]

METAPOP - *software for simulation of the evolution of diversity*

Developed by: Antoine Kremer, Stephanie Mariette

INRA, Laboratoire de Génétique et d'Amélioration des Arbres Forestiers, Pierroton, France

The evolution of diversity is simulated within a set of populations exchanging genes and

undergoing various evolutionary scenarios.

[Top] Not yet available for downloading

GSED - software for assessing genetic variation

Developed by: Elizabeth Gillet

Institut für Forstgenetik und Forstpflanzenzüchtung, Universität Göttingen, Göttingen, Germany

The computer program GSED ("Genetic Structures from Electrophoresis Data") characterizes genetic structures in population genetic investigations by calculating measures of genetic variation. It is based on a conceptually and mathematically unified system of data analysis.

Measures are calculated for the following genetic structures, input as single- or multilocus absolute frequency distributions:

Single locus frequencies	Allele frequencies among maternal contributions*
	Allele frequencies among paternal contributions*
	Allele frequencies
	Genotype frequencies
Multilocus frequencies	Haplotype frequencies among maternal contributions*
	Haplotype frequencies among paternal contributions*
	Haplotype frequencies
	Genotype frequencies
* (If the gametic sex of the alleles at each locus is specified)	

Measures calculated by GSED:

Analysis of allelic, haplotype and genotype structures

Measures of variation within samples

- Diversity v
- Total population differentiation δ_T
- Evenness e

Measures of variation between samples

- Genetic distance d_0
- Subpopulation differentiation D_j and δ
- Test of homogeneity

Analysis of genotypic structure

- Heterozygosity, single locus and multilocus
- Test of Hardy-Weinberg structure and heterozygosity
- Test of product structure

Analysis of the gene pool

Measures of variation within samples

- Diversity v of the gene pool
- Diversity v_{gam} of the hypothetical gametic output
- Total population differentiation δ_T of the gene pool

Measures of variation between populations

- Distance d_0 between gene pools
- Differentiation D_j and δ of subdivided gene pools

[Top] [Download GSED at <http://www.uni-forst.gwdg.de/forst/fg/index.htm>]

GeneKonv- software tool

Developed by: Ingo Hohmann and Ronald Bialozyt

Institut für Forstgenetik und Forstpflanzenzüchtung, Bundesforschungsanstalt für Forst- und Holzwirtschaft, Grosshansdorf, Germany

GeneKonv is a software tool allowing conversion between the formats of input data files for several common genetic data analysis programs, including BIOSYS, POPGENE, and GSED.

[Top] [Download GeneKonv at <http://www.rrz.uni-hamburg.de/OekoGenetik/welcome.htm>]

Which DNA Marker for Which Purpose? Final Compendium of the Research Project **Development, optimisation and validation of molecular tools for assessment of biodiversity in forest trees** in the European Union DGXII Biotechnology FW IV Research Programme **Molecular Tools for Biodiversity**. Gillet, E.M. (ed.). 1999. URL <http://webdoc.sub.gwdg.de/ebook/y/1999/whichmarker/index.htm>

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