

MCQTL

Multi-allelic QTL mapping in multi-cross designs

David Delannoy, Rémi Cathelin, Marie-Françoise Jourjon, Jasson Sylvain, Jacques Marcel, Baba Ngom, Brigitte Mangin

INRA, Unité de Biométrie et Intelligence Artificielle, B.P 27, 31326 - Castanet-Tolosan Cedex, France



The aim of MCQTL software package is to perform QTL mapping in multi-cross designs. It allows the analysis of the usual populations derived from inbred lines and can link the families by assuming that the QTL locations are the same in all of them. Moreover, a diallel modelling of the QTL genotypic effect is allowed in multiple related families.

The implemented model is a linear regression model in which the probabilities of QTL genotypes are derived from multiple marker data. A composite interval mapping and an iterative QTL mapping are implemented to deal with multiple QTL models. Marker cofactor selections by forward or backward stepwise method are implemented as well as computation of threshold test values by permutation. MCQTL runs on UNIX operating system.

This work was supported by GENOPLANTE project : "Integrative Tools for Genetics Mapping".

MCQTL functionalities

Cofactor choice	QTL detection method	threshold
Forward method on markers of the whole genome	Composite Interval Mapping	By permutation
By chromosome, backward method on chosen markers	Iterative QTL mapping Automatic method of QTL mapping	

Modeling the kth descendant in AxB cross

$$Y_{A \times B, k} = \mu_{A \times B} + \sum (p_{AA, k}^c \mu_{AA}^c + p_{AB, k}^c \mu_{AB}^c + p_{BB, k}^c \mu_{BB}^c) + (p_{AA, k}^l \mu_{AA}^l + p_{AB, k}^l \mu_{AB}^l + p_{BB, k}^l \mu_{BB}^l) + \epsilon_{A \times B, k}$$

$P_{XY, k}^l$ ← Probability for k of being XY at locus l given marker information

Modeling QTL and cofactor effects

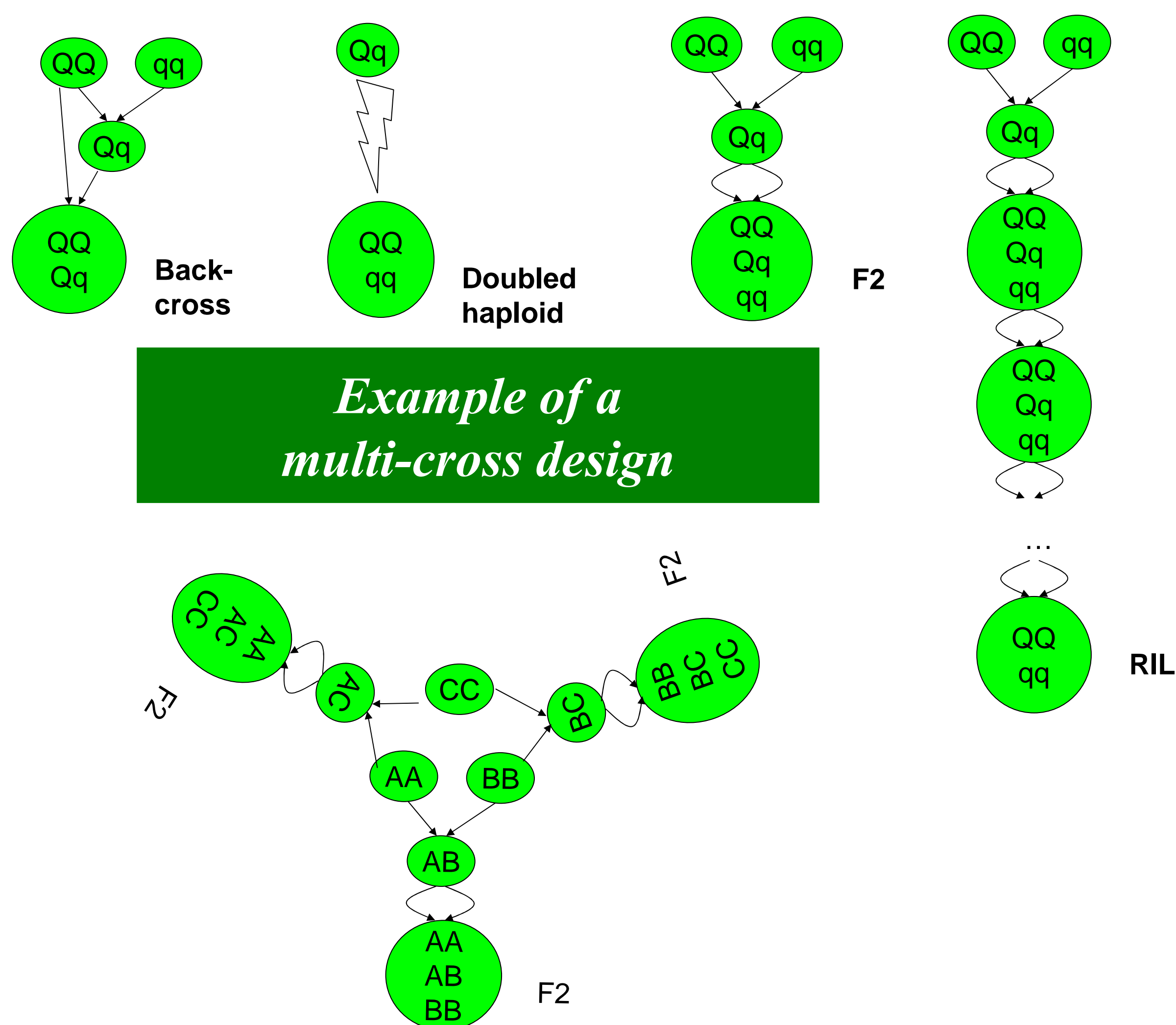
Intra-family additive model

$$\mu_{XY}^l = a_{XY, X}^l + a_{XY, Y}^l$$

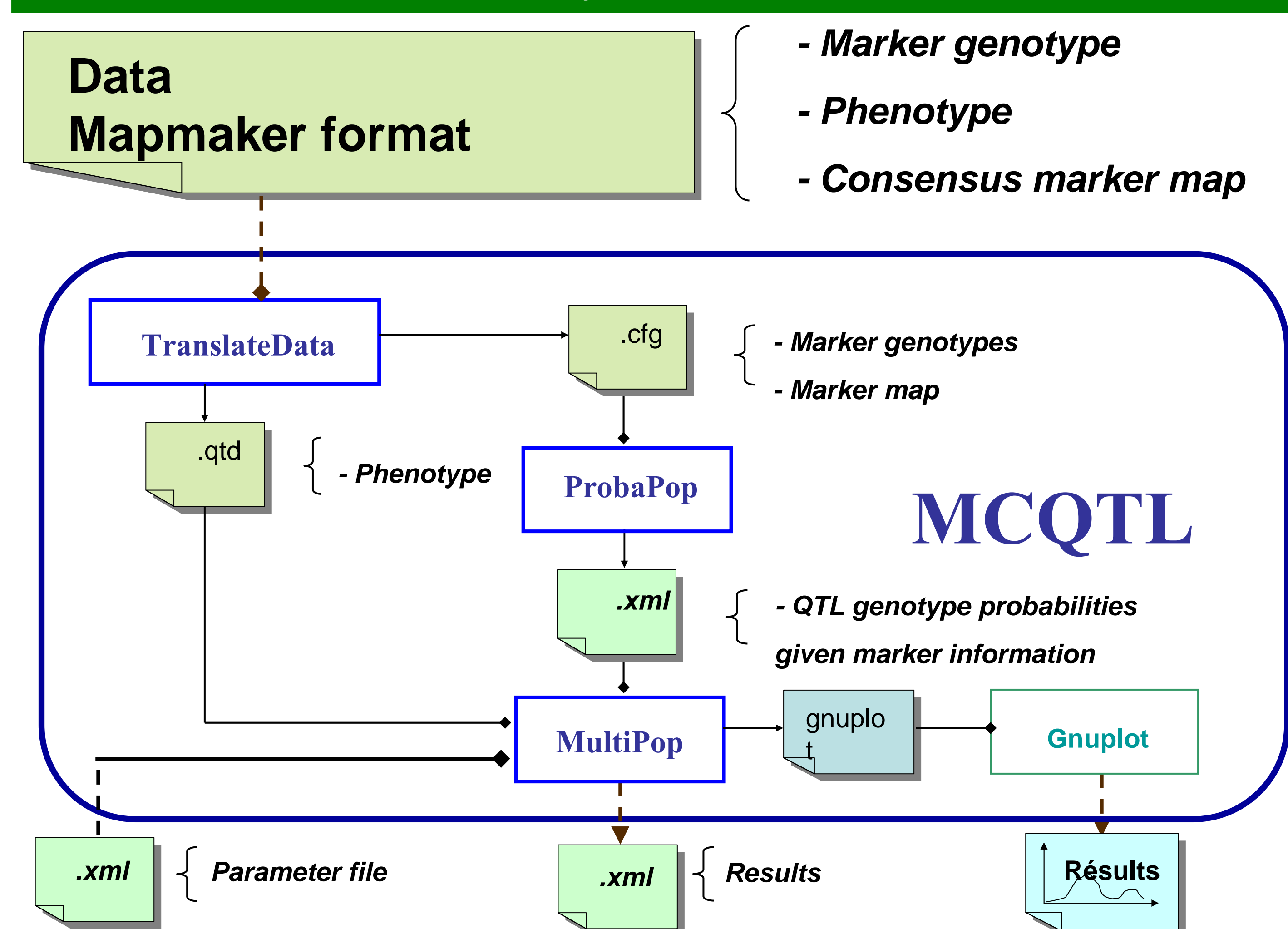
Additive diallel model

$$\mu_{XY}^l = a_X^l + a_Y^l$$

Available type of families



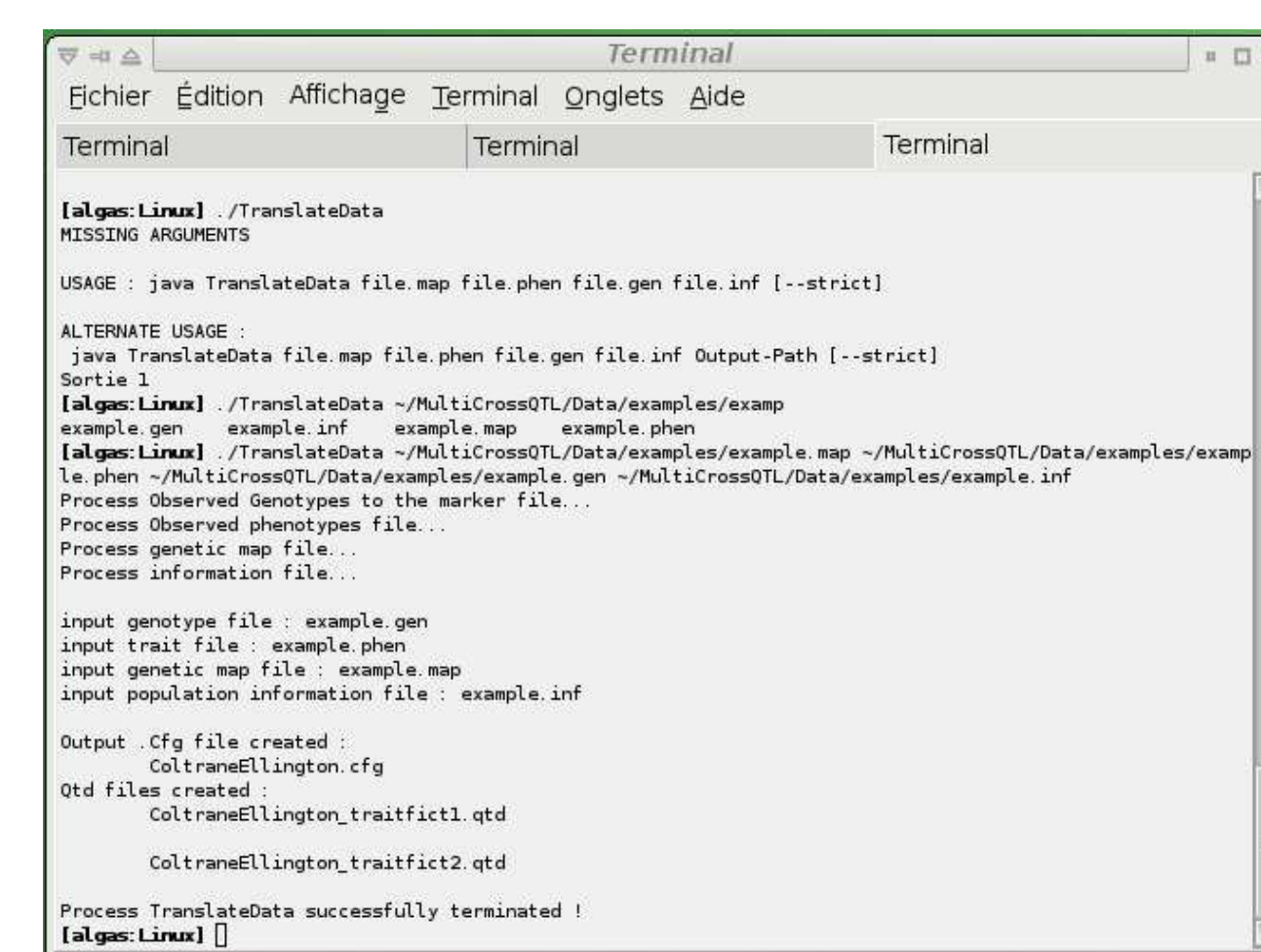
MCQTL software architecture



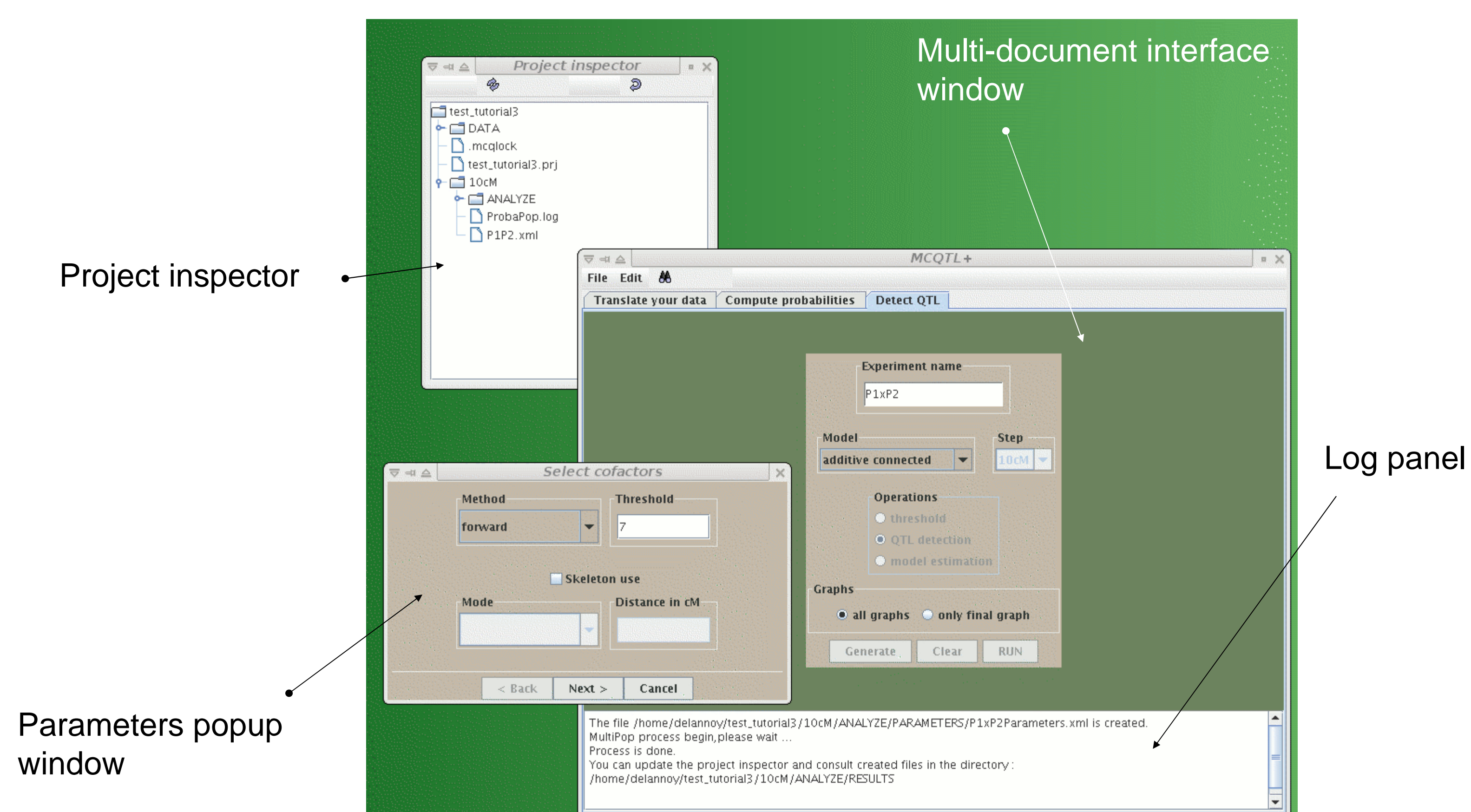
Running MCQTL

Two different ways

- Command line application
- Java graphical user interface



MCQTL graphical user interface



Jourjon M.F., Jasson S., Marcel J., Ngom B., Mangin B. (2004)
MCQTL: multi-allelic QTL mapping in multi-cross design
Bioinformatics, 21, 128-130

mangin@toulouse.inra.fr
www.genoplante.com