Disclaimer: unless otherwise agreed by the Council of UPOV, only documents that have been adopted by the Council of UPOV and that have not been superseded can represent UPOV policies or guidance.

This document has been scanned from a paper copy and may have some discrepancies from the original document.

———

Avertissement: sauf si le Conseil de l'UPOV en décide autrement, seuls les documents adoptés par le Conseil de l'UPOV n'ayant pas été remplacés peuvent représenter les principes ou les orientations de l'UPOV.

Ce document a été numérisé à partir d'une copie papier et peut contenir des différences avec le document original.

———

Allgemeiner Haftungsausschluß: Sofern nicht anders vom Rat der UPOV vereinbart, geben nur Dokumente, die vom Rat der UPOV angenommen und nicht ersetzt wurden, Grundsätze oder eine Anleitung der UPOV wieder.

Dieses Dokument wurde von einer Papierkopie gescannt und könnte Abweichungen vom Originaldokument aufweisen.

———

Descargo de responsabilidad: salvo que el Consejo de la UPOV decida de otro modo, solo se considerarán documentos de políticas u orientaciones de la UPOV los que hayan sido aprobados por el Consejo de la UPOV y no hayan sido reemplazados.

Este documento ha sido escaneado a partir de una copia en papel y puede que existan divergencias en relación con el documento original.

UPOV

BMT/3/6 Add.
ORIGINAL : English
DATE : September 25, 1995

INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS

GENEVA

WORKING GROUP ON BIOCHEMICAL AND MOLECULAR TECHNIQUES AND DNA-PROFILING IN PARTICULAR

Third Session

Wageningen, Netherlands, September 19 to 21, 1995

THE ESTIMATION OF MOLECULAR GENETIC DISTANCES IN MAIZE FOR DUS AND ED PROTOCOLS: OPTIMIZATION OF THE INFORMATION AND NEW APPROACHES OF KINSHIP

Addendum prepared by experts from France

Two corrected pages of BMT/3/6

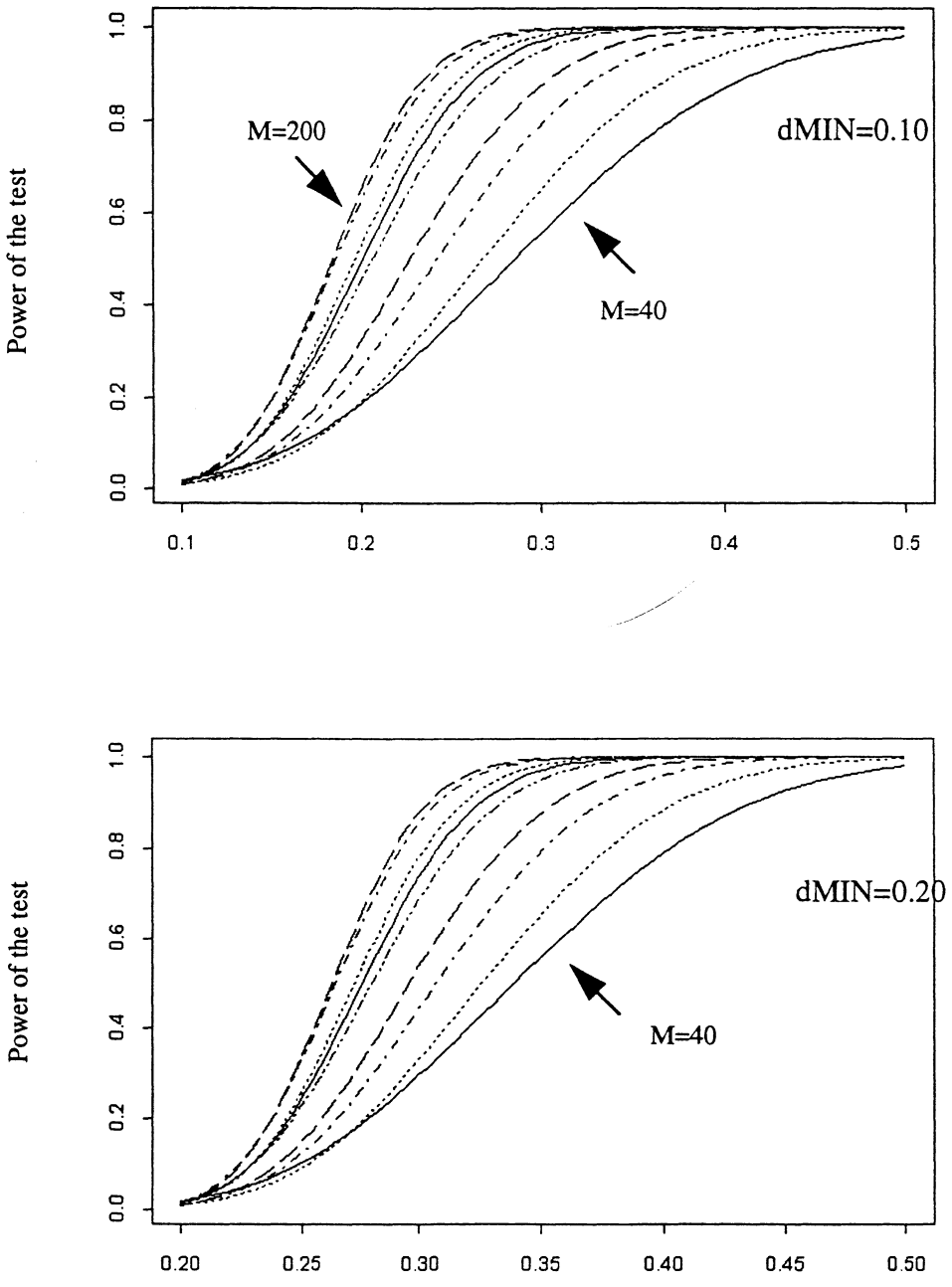


Figure 4 : Power of the test dAB<dMIN at the 2% level for sample sizes ranging from 40 to 200 and for different values of dMIN.

d_{MIN}	α	M	d_T
0.05	0.02	80	0.100
		160	0.087
0.10	0.02	80	0.175
		160	0.150
0.15	0.02	80	0.237
		160	0.212
0.20	0.02	80	0.300
		160	0.269
0.25	0.02	80	0.350
		160	0.319

Table 2 : Value of the effective minimum distance for the test of $H_0: d_{AB} \leq d_{MIN}$ with the Rogers distance.

Collection of Transparencies

The estimation of molecular genetic distances in Maize for DUS and ED protocols

Optimisation of the information and new approaches of kinship

C. Dillmann[1],
A. Charcosset[2],A. Bar-Hen[3],P. Vincourt[6]
B. Goffinet[4], J. S. Smith[5],Y. Dattée[1],
J. Guiard[1]

Research program granted by the French Ministery of Agriculture in the frame of a C.T.P.S action.

DUS = Distinction, Uniformity, Stability

ED = Essential Derivation

DUS = Distinction, Uniformity, Stability

ED = Essential Derivation

During this talk, I will speak about DUS for Distinction, Uniformity, Stability and about ED for Essential Derivation.

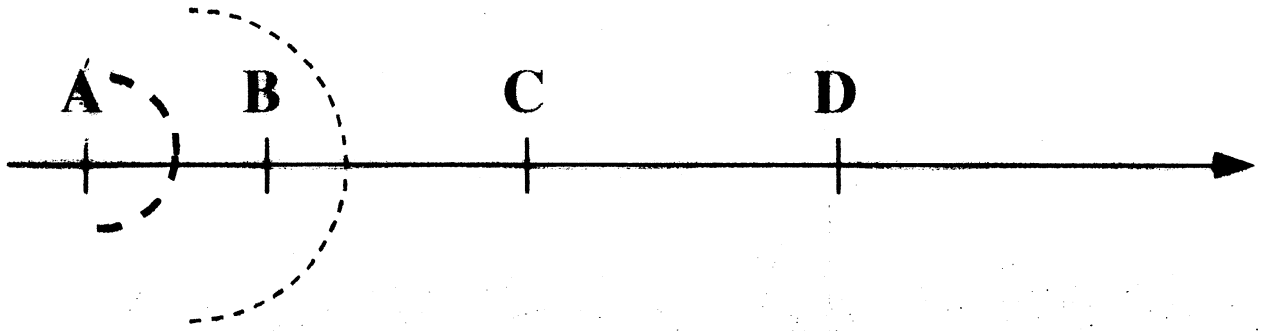
The estimation of genetic distances in Maize for DUS and ED protocols

In Maize, a large number of molecular markers, located on the genetic map, are available.

The estimation of genetic distances in Maize for DUS and ED protocols

After a brief introduction, I would like to discuss the interest and the consequences of taking the genetic map into account, and apply it to the elaboration of new genetic distances. One specific for the ED approach, and one specific for the DUS approach.

Introduction



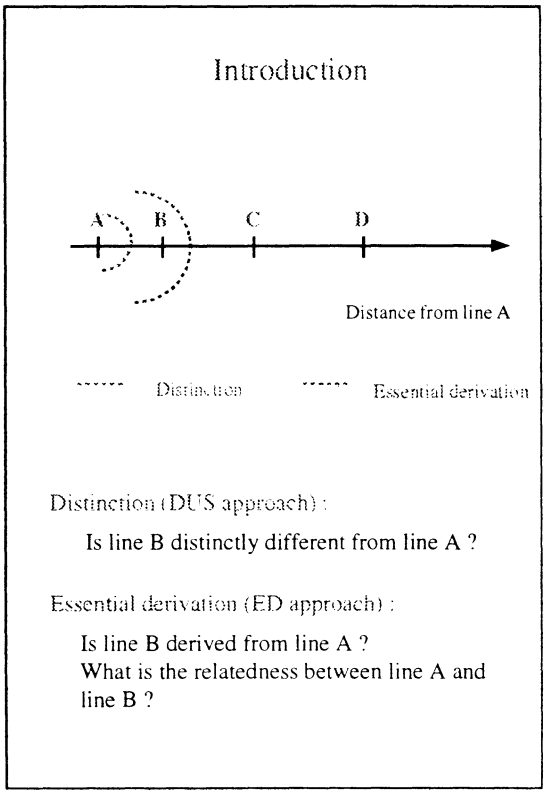
– – – Distinction ------ Essential derivation

Distinction (DUS approach) :

Is line B distinctly different from line A ?

Essential derivation (ED approach) :

Is line B derived from line A ?
What is the relatedness between line A and line B ?



In Maize, both the DUS and ED approaches apply the comparison of two inbred lines, like line A and line B on the diagram. In the DUS approach, the question to answer is " Is line B distinctly different from line A ? " while in the ED approach, the question to answer is " Is line B derived from line A ? " or " What is the relatedness between lines A and B ? ". Both questions may be answered by computing a genetic distance between the two lines.

Introduction
The Rogers distance

L loci over the whole genome

M markers randomly sampled among the L loci

A and B = the two inbred lines to be compared

For each marker locus :

$d_{AB}^{m} = 0$ A and B identical at locus *m*

$d_{AB}^{m} = 1$ A and B are different at locus *m*

The Rogers distance
=
% of loci which differ between lines A and B among the M markers

Introduction
Statistical properties of the Rogers distance

They are a consequence of the following hypothesis :

markers are randomly sampled throughout the genome

=

no correlation between distances at marker loci

Introduction
Statistical properties of the Rogers distance

They are a consequence of the following hypothesis :

markers are randomly sampled throughout the genome

=

no correlation between distances at marker loci

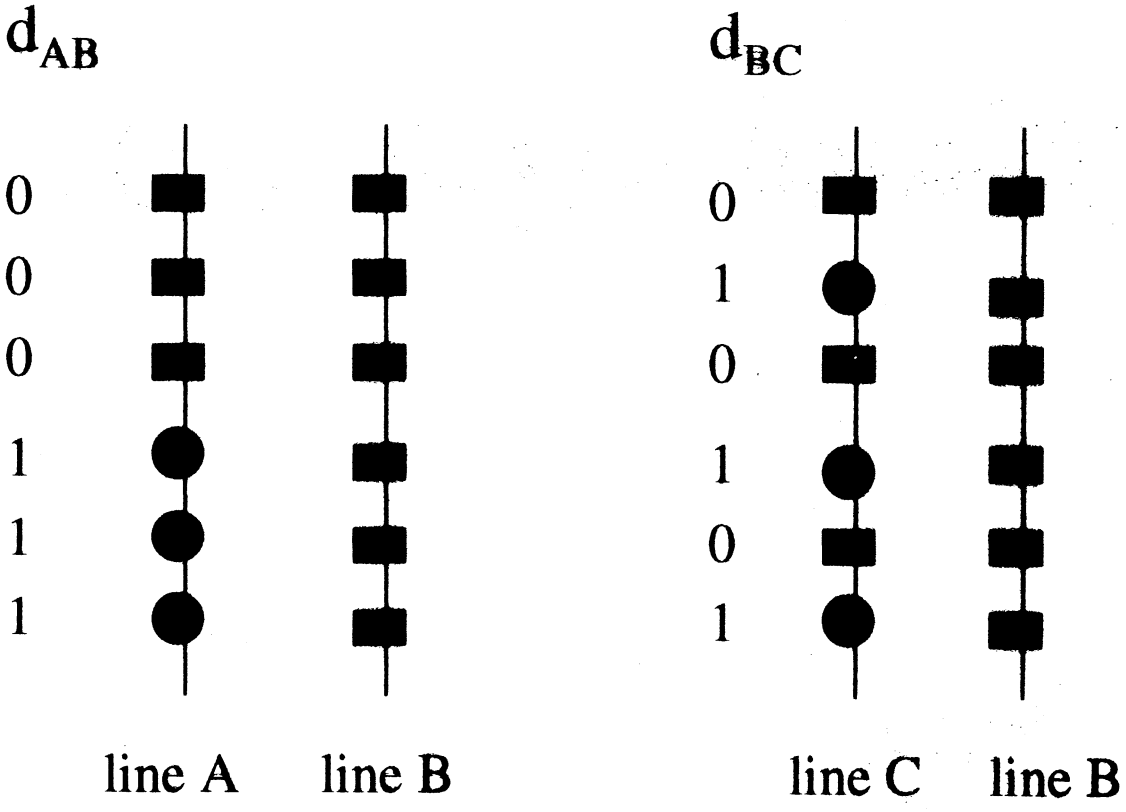
I would just like to recall here that those statistical properties are a consequence of the hypothesis that the markers are sampled at random throughout the genome - In this case, there is no correlation between distances at marker loci or, in other words, the distance between two lines at one locus is independent on the distance between the two lines at another locus, whatever the distance between the loci -

The estimation of genetic distances in Maize for DUS and ED protocols

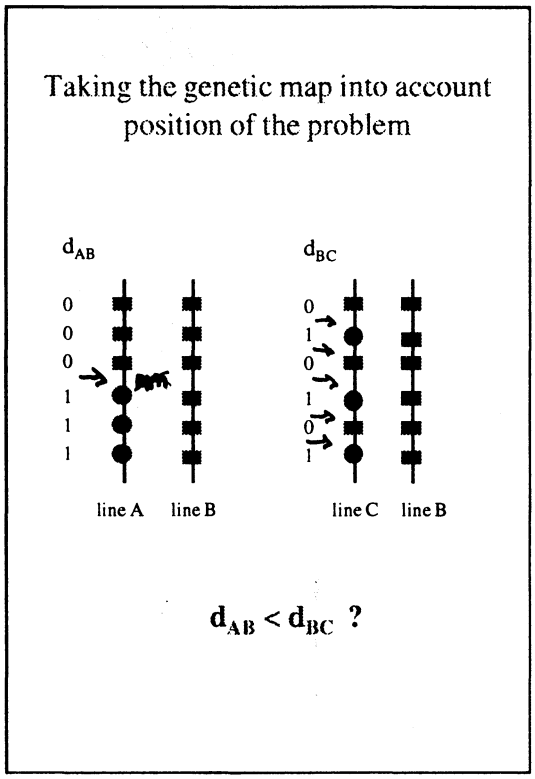
The estimation of genetic distances in Maize for DUS and ED protocols

However, we've seen yesterday that a genetic map is available in more and more species like maize, tomato or maritime pine. In such species, once a set of markers has been chosen, it is often used repeatedly in different comparisons. Moreover, the genome coverage is not allways perfect. For those reasons, and for other ones that I will detail now, it may be interesting to consider the genetic map as fixed and to reason conditionally to that given genetic map.

Taking the genetic map into account position of the problem

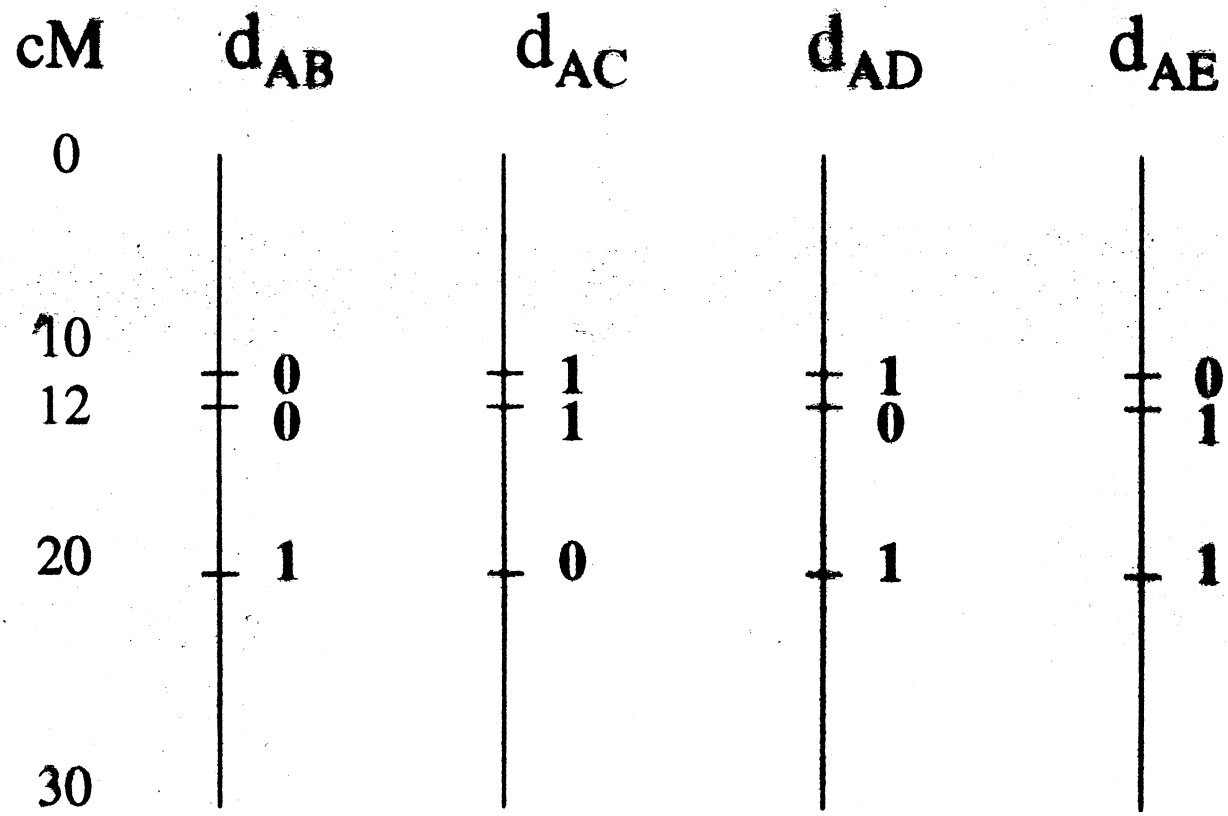


$$d_{AB} < d_{BC} \ ?$$



Suppose, for example, that we have six markers, all situated on the same chromosome and that we want to compare line A and line B on this diagram. At each marker locus, there are two alleles, the green boxes and the red circles. line A and B differ here by three markers out of six, and so do lines B and C. However, if we consider the differences in terms of recombination events, one recombination event is sufficient to give line A from an hybrid between line B and another line,

Taking the genetic map into account position of the problem



	d_{AB}	d_{AC}	d_{AD}	d_{AE}
Rogers	0.33	0.66	0.66	0.66
Wished	0.5	0.5	>0.66	<0.66

Taking the genetic map into account

Position of the problem

Conditionally to a given genetic map,

If lines A and B are related, distances at marker loci are no more independent,

Therefore, finding the "best" estimator of the genetic distance

=

estimating the covariances between distances at marker loci.

The estimation of genetic distances in Maize for DUS and ED protocols

Taking the genetic map into account :

Covariances between distances at marker loci

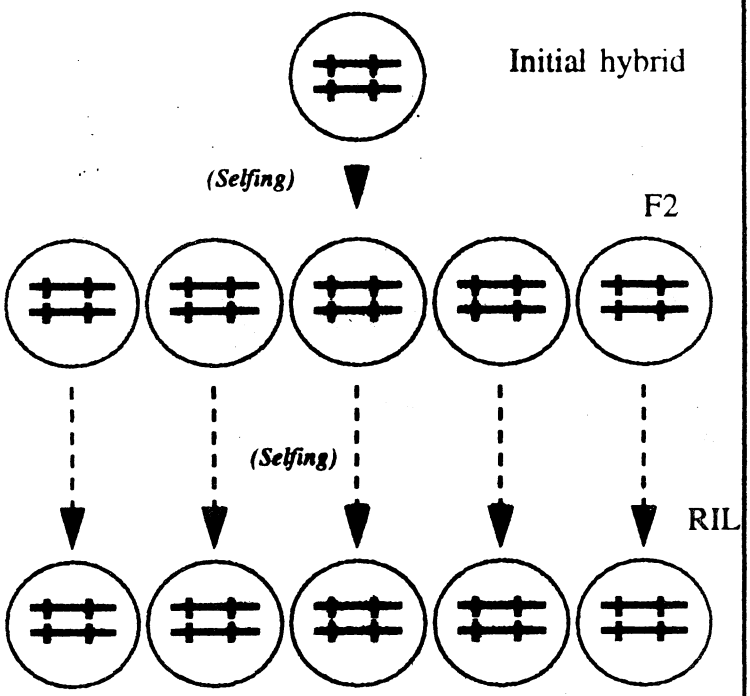
How can two inbred lines be derived each from another ?

Example :

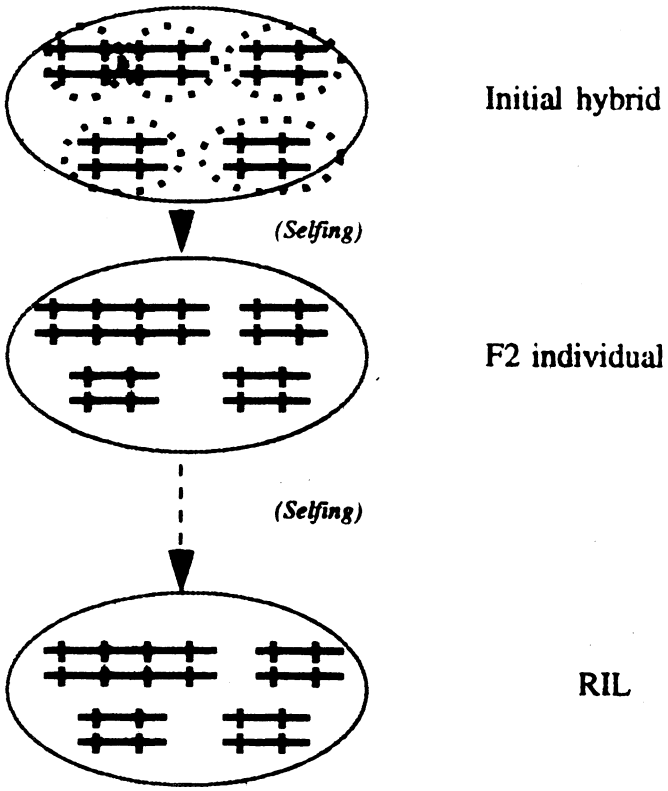
Selfing from an hybrid

The measurement of covariances between distances at marker loci

One couple of loci several individuals



Several couple of loci one individual



Theoretical value

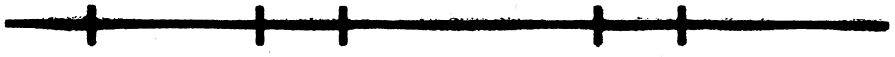
Estimation from the data

The observation of several couples of loci within one individual brings valuable informations about the genetical history of the

The measurement of covariances between distances at marker loci

estimation from the data

Data set



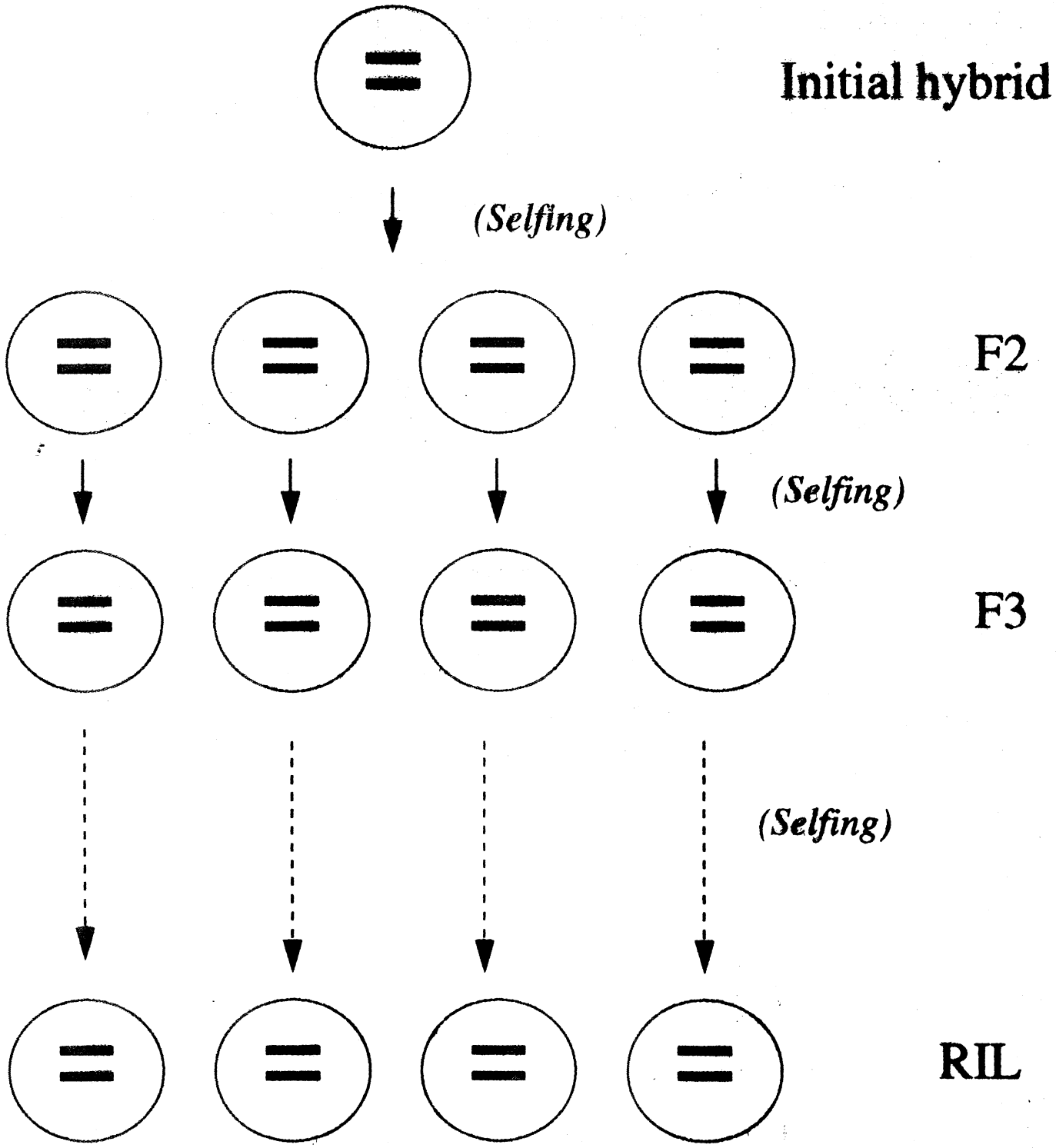
locus	1	2	3	4	5
cM	5	15	20	35	40
d_{AB}^{k}	0	0	1	0	1

After rearranging

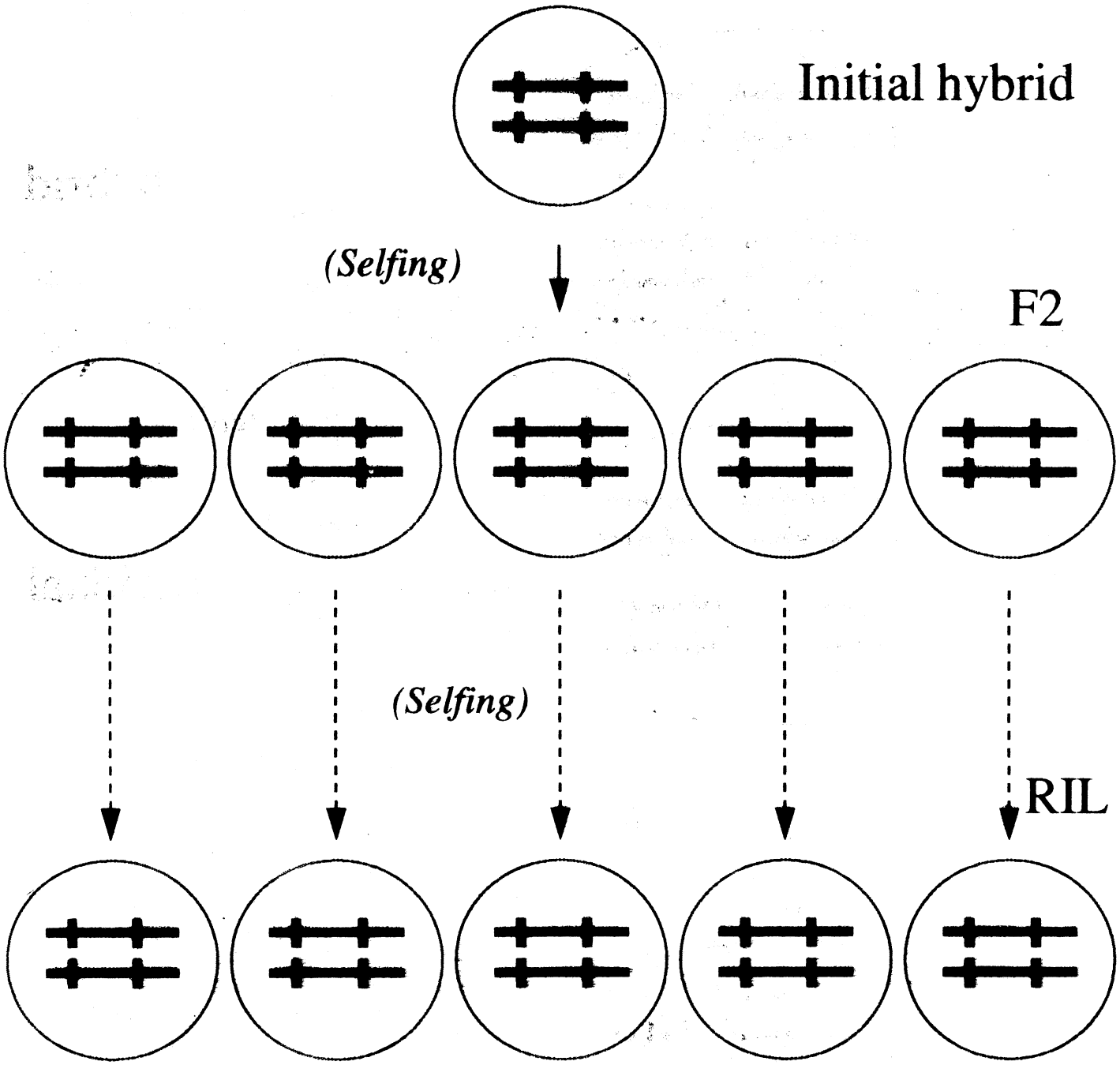
locus	locus	rec. rate	d_{AB}^{k}	d_{AB}^{m}
1	1	0	0	0
1	2	0.10	0	0
1	3	0.15	0	1
1	4	0.30	0	0
1	5	0.35	0	1
2	2	0	0	0
2	3	0.05	0	1

308

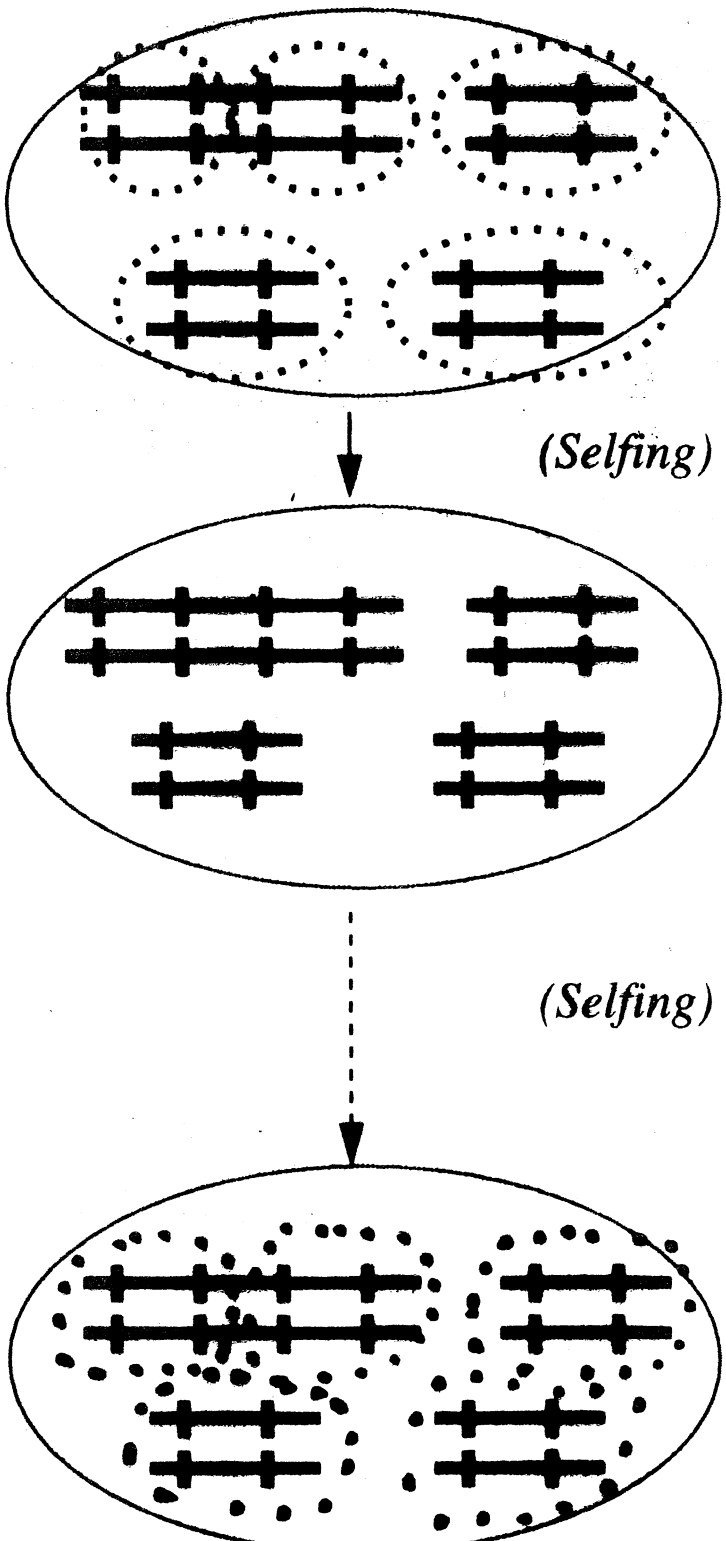
Segregation of one marker locus under selfing



Segregation of one couple of marker loci under selfing



Segregation of five couples of marker loci within one individual under selfing



311

The estimation of genetic distances in Maize for DUS and ED protocols

The measurement of covariances between distances at marker loci

Experimental results

Data set 1 :

50 Maize Recombinant Inbred lines derived by selfing from an hybrid without selection.

Molecular datas on 170 public RFLP probes. (A. Charcosset)

Data set 2 :

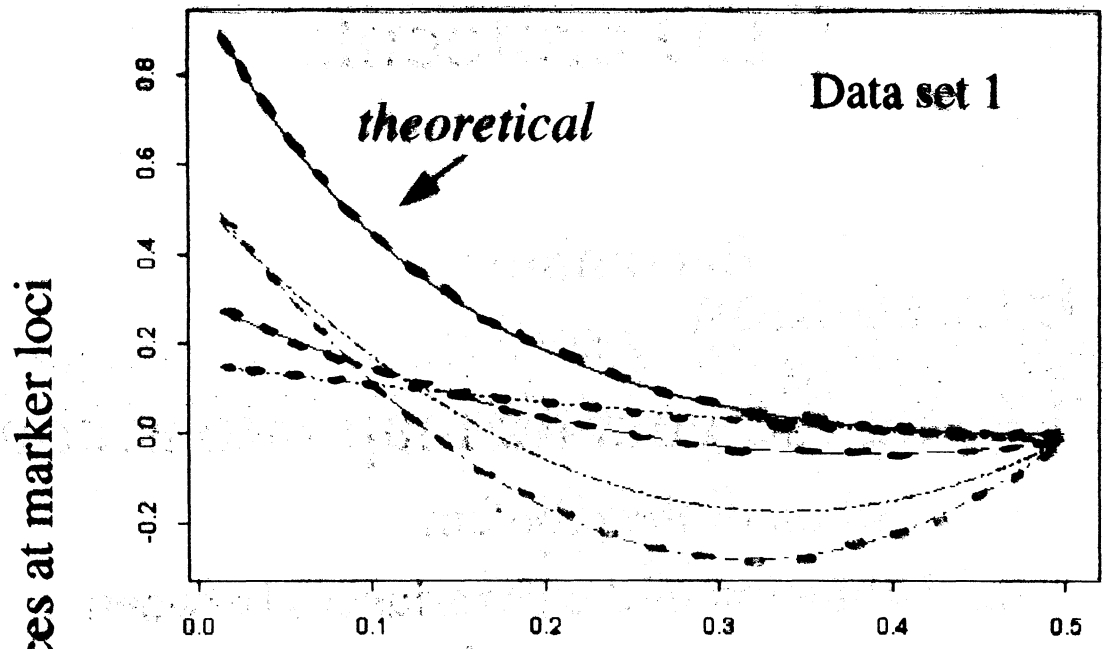
37 highly selected, elite inbred lines of Maize from the central US Corn Belt.

Molecular data on 110 public RFLP probes. (S. Smith)

theoretical value = expected For R11

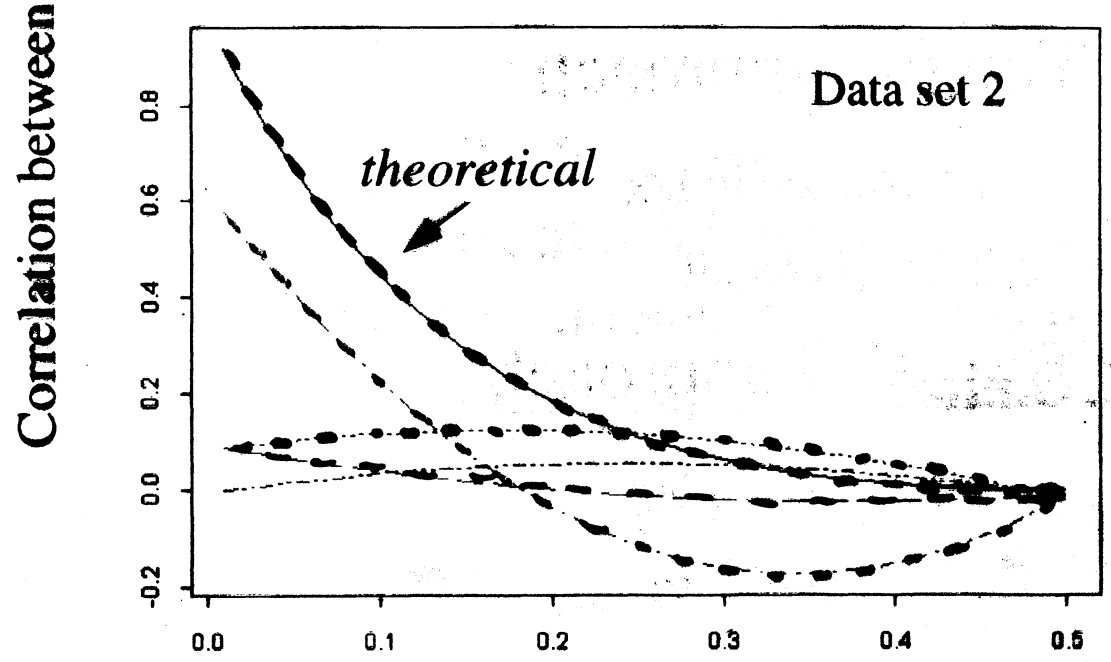
The measurement of covariances between distances at marker loci

Experimental results



Rogers

0.233
0.398
0.331
0.173



Rogers

0.318
0.518
0.482
0.145

Correlation between distances at marker loci

Recombination rate between the two loci

314

The estimation of genetic distances in Maize for DUS and ED protocols

The ED approach

determination of the distance

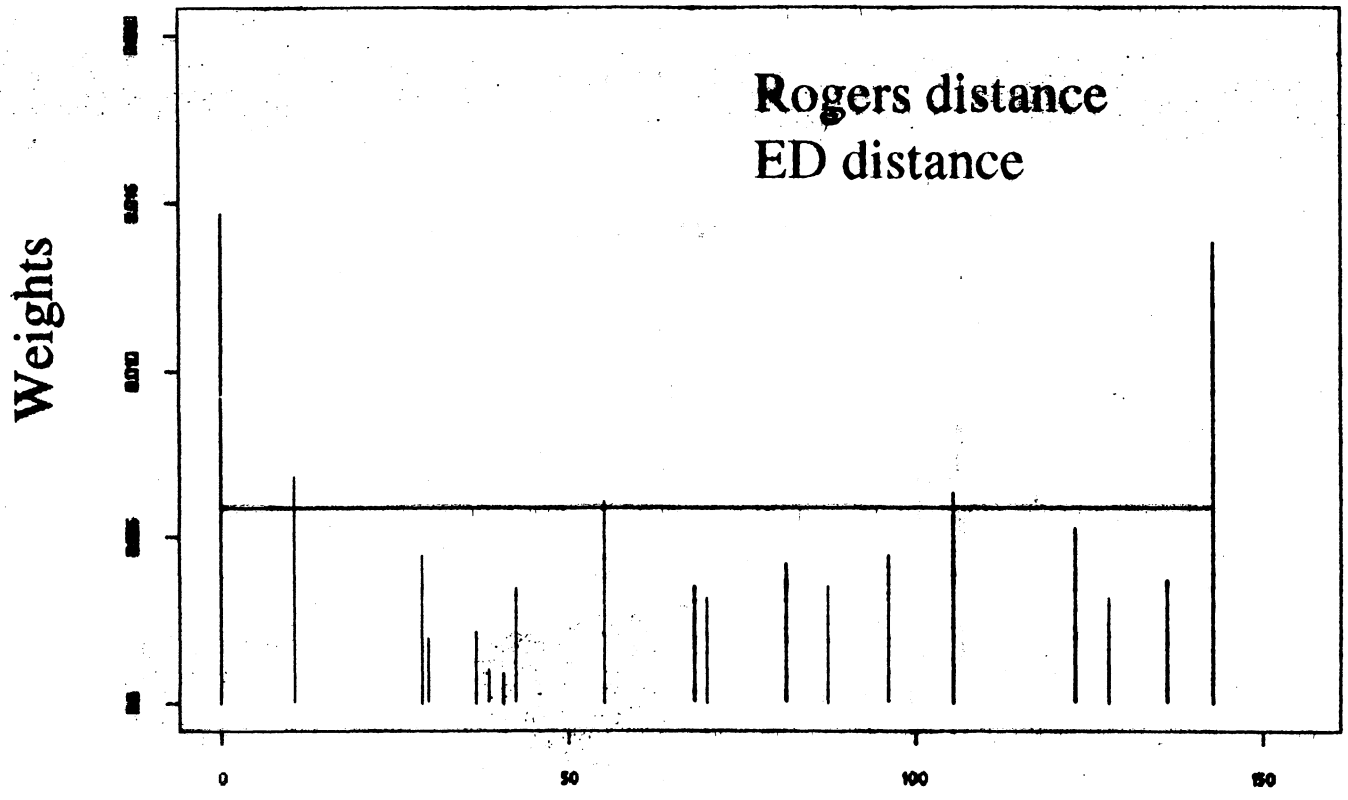
The ED distance
weights each marker locus in order to minimize the sampling variance, conditionally to the genetic map.

The weight of each marker locus is proportional to the covariances between this locus and all the other marker loci

316

The ED distance example

Weights of 17 Maize RFLP markers on chromosome 8



position of the markers in the chromosome

ED protocol

(1) Choose an appropriate set of markers whith known position on the genetic map

(2) Compute the $d_{AB}{}^{k}$'s

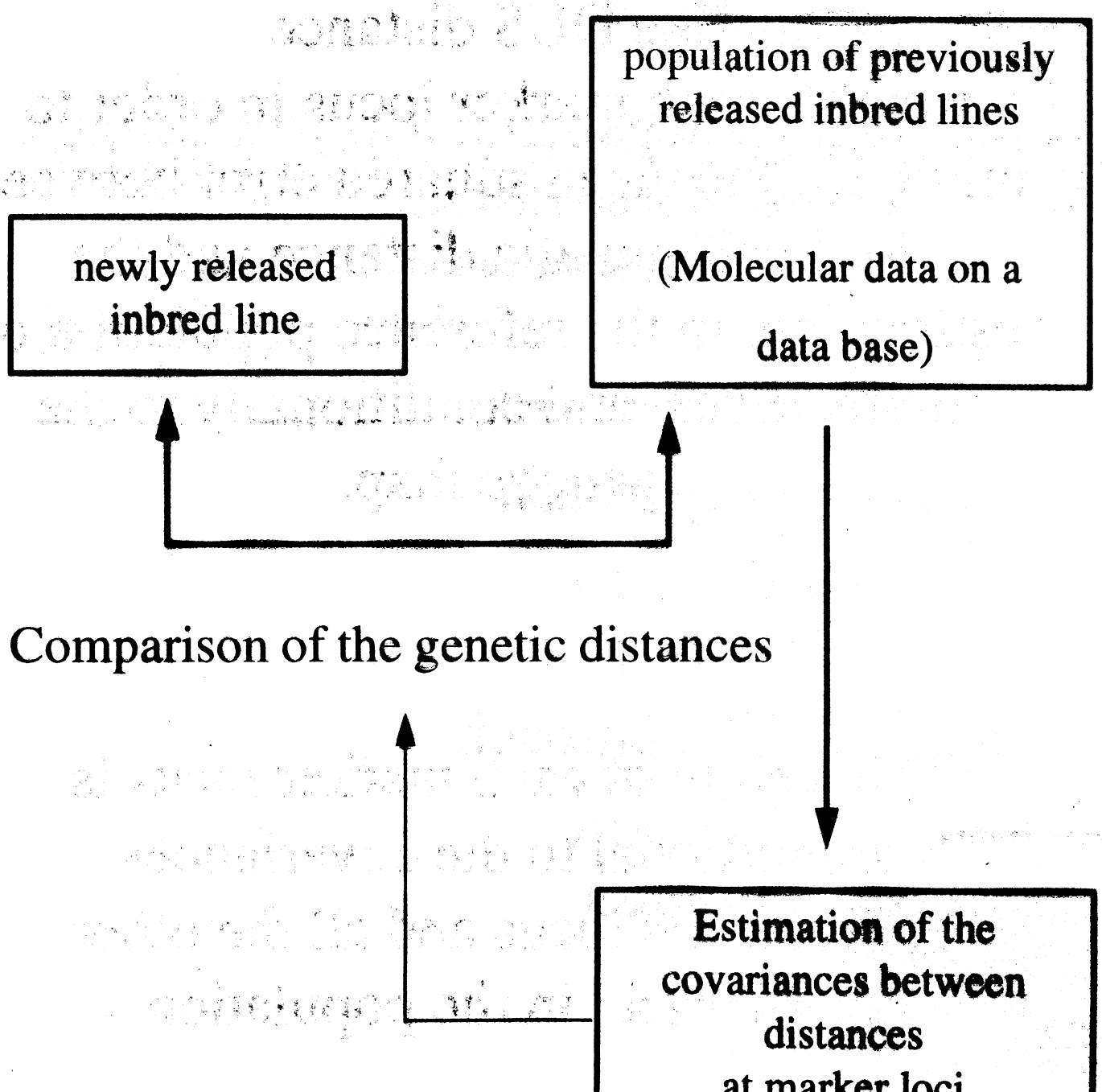
(3) Use the data to find the best suited value for the covariances between distances

(4) Compute the ED genetic distance and it's sampling variance by using (2) and (3).

The estimation of genetic distances in Maize for DUS and ED protocols

The DUS approach

determination of the distance



320

The DUS approach

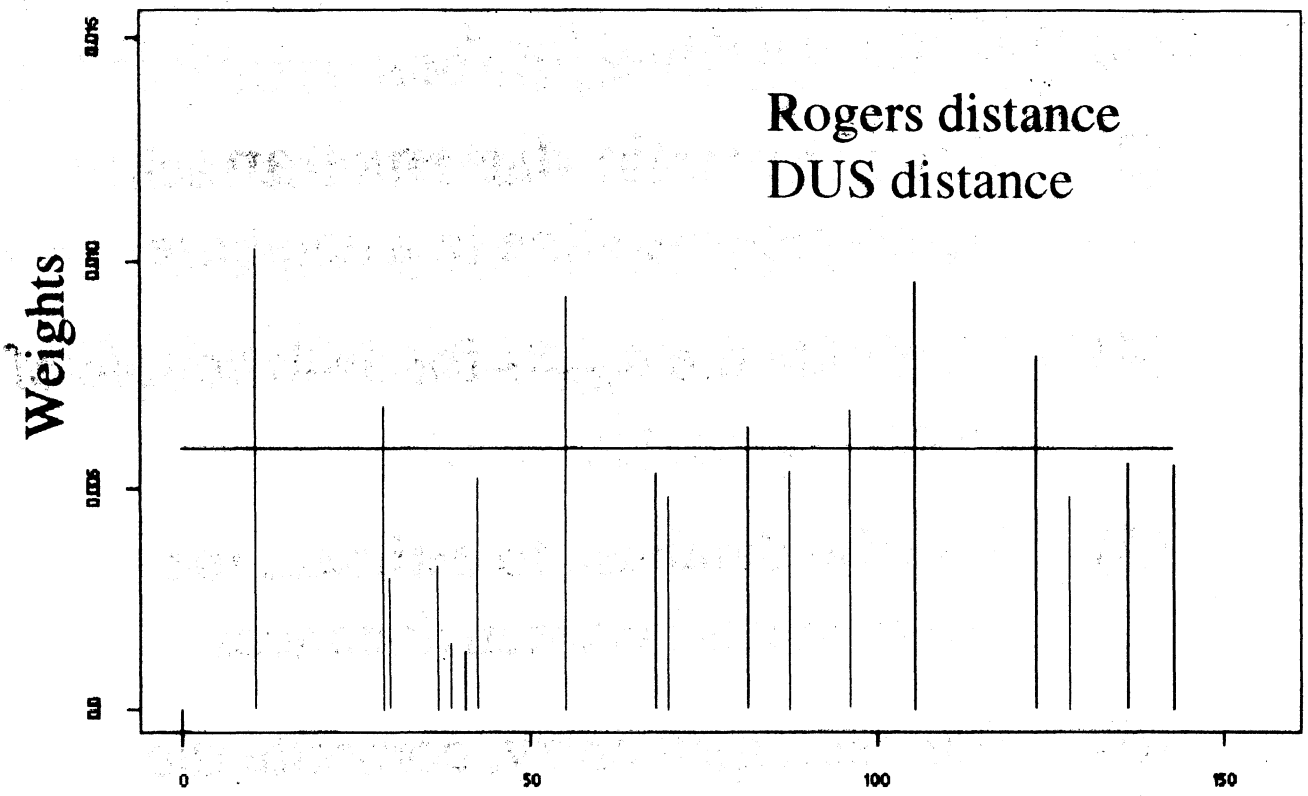
determination of the distance

The DUS distance
weights each marker locus in order to minimize the mean squared error between the "real" genetic distance and the estimation, in the reference population of inbred lines and conditionally to the genetic map.

The weight of each marker locus is proportional to the covariances between this locus and all the other marker loci in the population

The DUS distance example

Weights of 17 Maize RFLP markers on chromosome 8



position of the markers in the chromosome

population = RIL

DUS protocol

(1) Choose an appropriate set of markers whith known position on the genetic map

(2) Choose a value for d_{MIN}

(3) Enter the molecular data for each newly released line in a database

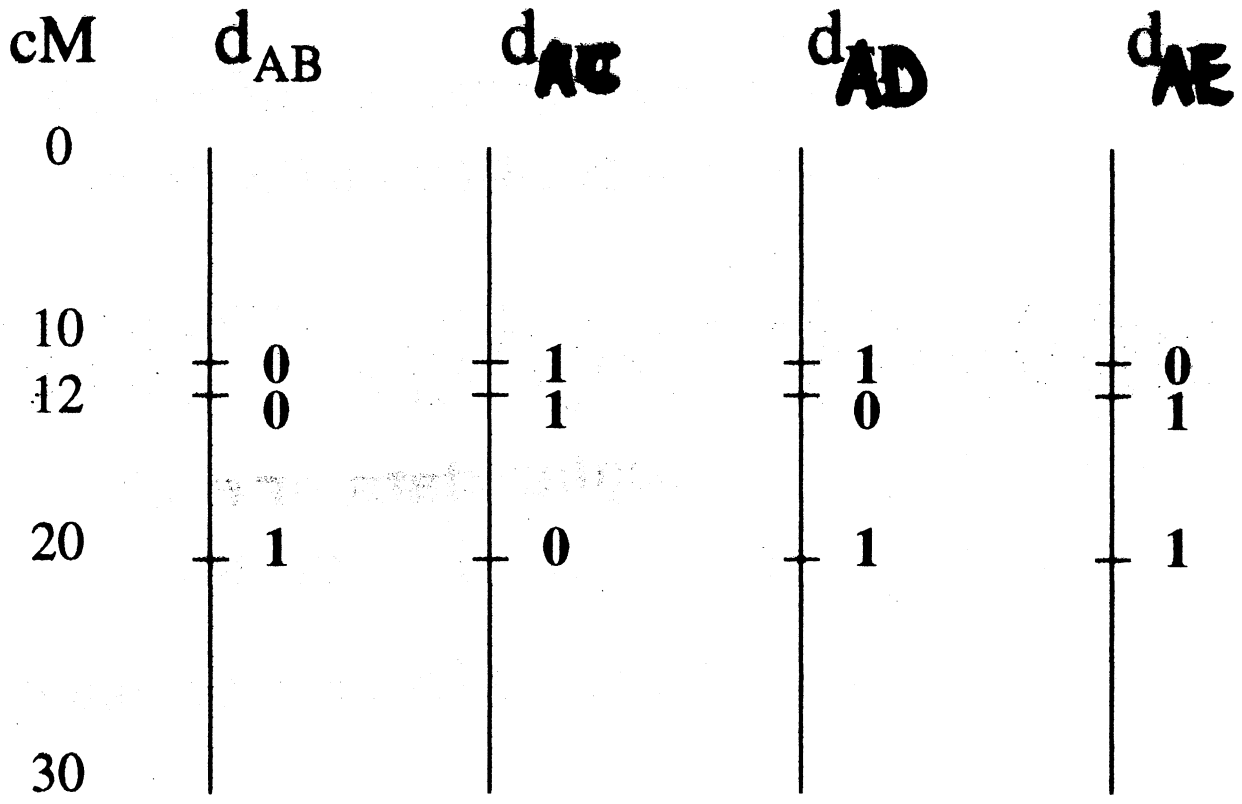
(4) Compute the $d_{AB}{}^{k}$'s for each couple of lines

(5) Use the database to estimate the covariances between distances

(6) For each new entry, compute the DUS genetic distance and it's sampling variance by using (4) and (5)

(7) Test $H_0 : d_{AB} < d_{MIN}$

Discussion
Comparison of the three distances



	d_{AB}	d_{AC}	d_{AD}	d_{AE}
Rogers	0.33	0.66	0.66	0.66
Wished	0.5	0.5	>0.66	<0.66
ED	0.48	0.52	0.92	0.56
DUS	0.48	0.52	0.89	0.59

[End of document]