Creating a Kinship Matrix using Microsatellite Analyzer (MSA)

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Why create a kinship matrix?

- Visualize family relatedness
- Use in association mapping

<u>The Objective of this Tutorial:</u> To introduce one approach to generate a kinship matrix for a population

Using Microsatellite Analyzer (MSA)

Background

Types of Populations for Association Mapping (Yu, et al. 2006):

Population Type	Pros	Cons
"Ideal population"	Minimal population structure and familial relatedness Gives the greatest statistical power	Difficult to collect, small size Narrow genetic basis
Family-based population	Minimal population structure	Limited sample size and allelic diversity
Population with population structure	Larger size and broader allelic diversity	False positives or loss in power due to familial relatedness.
Population with familial relationships within structured population	Larger size and broader allelic diversity	Inadequate control for false positives due to population structure

The highlighted population needs a kinship matrix for analysis.

Scheme of Mapping



Zhu et al. 2006

Coefficient of Kinship

Coefficient of kinship is used to measure relatedness

<u>DEFINITION:</u> Coefficient of kinship is the probability that the alleles of a particular locus chosen randomly from two individuals are identical by descent (Lange, 2002)

* Identical by descent: the identical alleles from two individuals arise from the same allele in an earlier generation

Kinship Matrix Calculation

The kinship coefficient is the probability that an allele (*a*) taken randomly from population *i* (at a given locus) will be identical by descent to an allele taken randomly from population *j* at the same locus

 $Kf = \sum_{k} \sum_{a} (f_{ai} * f_{aj})/D$

Where $\sum_{k}\sum_{a} (f_{ai} * f_{aj})/D$ is the sum of all loci and all alleles; f_{ai} is the frequency of allele a in population *i*, f_{aj} is the frequency of allele *a* in population *j*, *D* is the number of loci.

> Cavalli-Sforza and Bodmer, 1971. MSA manual page 23

An Example

Population	Locus A	Locus B	Locus C
611R2	A	b	С
	A	b	С
611R3	A	В	С
	A	В	С

Coefficient of kinship for populations 611R2 and 611R3: $Kf = \sum_k \sum_a (f_{ai} * f_{aj})/D$ = (1x1+1x0 + 0x1+1x1)/3=2/3

The frequencies of alleles A and c in populations 611R2 and 611R3 are 1; the frequency of allele b in population 611R2 is 1 and 0 while in population 611R3 is 0

Kinship Matrix

In the unified mixed model (Yu et al. 2006), marker-based kinship coefficient matrices are included

A marker-based kinship coefficient matrix can be generated using Microsatellite Analyzer (MSA)

Pipeline for Matrix Generation



A Case Study

Bacterial spot data provided by Dr. David Francis, The Ohio State University

Data Preparation

For genotyping, molecular markers can be: Microsatellite (Simple Sequence Repeat, SSR) SNP (Single Nucleotide Polymorphism) RFLP (Restriction Fragment Length Polymorphism) AFLP (Amplified Fragment Length Polymorphism) Other sequencing markers

MSA was designed for SSR analysis

For other marker types, a value is designated for each allele, e.g. For SNPs, **A** can be 11, **C** can be 12, **G** can be 13, and **T** can be 14.

Data Entry

After genotyping, a spreadsheet of genotypic data can be generated as shown below.

Р	Population Marker Genotype Score											
~			R		D	F						
Ĩ	gen		SL10639	LEOH20	SL10373i	SL10469	SL10	LEOH9				
2	6111R1		0	0	0	0	2	0				
3	6111R2		0	0	0	0	2	0				
4	6111R3		0	0	0	0	2	0				
5	6111S1		0	0	0	5	1	0				
6	6111S2		0	0	0	0	2	0				
7	6115S3		0	0	0	0	1	0				
8	6115S4		0	0	0	0	2	0				
9	6117R1		0	0	0	0	2	0				
10	6117R2		0	0	0	0	0	0				
11	6117S1		0	0	0	0	2	0				
12	6117S2		0	0	0	0	1	0				
13	6117S3		0	0	0	0	0	2				
14	6117S4		0	0	0	0	2	0				

Genotype Score: 0 is homozygous for allele a, 1 is homozygous for allele b, 2 is heterozygous.

Data Formatting



Row 1 can be left empty except for columns a, b, and c, which have to be filled. In cell A1, enter '1'. Row 2 is marker name. Genotype data start in row 3.

Data Formatting

Two-row entry for each individual (we are treating individuals as populations) to specify heterozygotes and homozygotes



After Formatting

Save the file in a "Tab Delimited" text format, change the extension name ".txt" into ".dat".

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12	6111S2	h										55	33	33
13	6115S3	h	Le	arn more about	file formats							33	33	55
14	611553	h										33	33	55
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20	611754	h	1	33	33	33	33	33	33	33	33	33	33	33
28	611754	h	1	33	33	33	33	55	33	33	55	33	33	55
20	6124P1	h	1	33	33	33	33	55	33	33	33	33	33	55
30	6124R1	h	1	33	33	33	33	55	33	33	55	55	33	55
31	6124R2	h	1	33	33	33	33	33	33	33	33	33	33	55
32	6124R2	h	1	33	33	33	33	55	33	33	55	33	33	55
33	6124R3	h	1	33	33	33	33	33	33	33	33	33	33	55
34	6124R3	h	1	33	33	33	33	55	33	33	55	33	33	55
35	6124R4	h	1	33	33	33	33	33	33	33	55	33	33	33
36	6124R4	h	1	33	33	33	33	55	33	33	55	33	33	55
37	6124S1	h	1	33	33	33	33	55	33	33	55	33	33	55

MSA (Microsatellite Analyzer) is available for free, provided by Daniel Dieringer.

000	0	microsatellite analyzer – Google Search					
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		Microsatellite analysis reveals genetically distinct populations ☆ Q by J Boys - 2005 - Cited by 30 - Related articles In an analysis of over 500 individuals representing 17 red pine populations from Manitoba					

MSA is compatible with different operation systems

MSA_download

+ Shttp://i122server.vu-wien.ac.at/MSA/MSA_download.html

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Microsatellite Analyzer (MSA)

information about MSA can be found here

For downloading please click on the required OS icon. You will receive a folder containing the following items:

> executables documentation sample input file

Choose the operating system you use and install it as other software

Q. microsatellite analyzer

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Install MSA

For Mac, a folder for MSA will be formed after you extract the downloaded file

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exit:
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If you are interested in this function
please read the documentation!
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Import your data file to MSA by dragging it to the MSA window

After the data file is imported,

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Each line will be treated as a population in this study

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(c) ... Pairwise populations distances calc: OFF

    Pairwise individual distances calc : OFF

 (1)
        Dps, Proportion of shared allels : ON
 (2)
        Dfs, Fuzzy set similarity
                                        : 0FF
        Dad, Absolute difference algorithm:OFF
 (3)
 (4) Dkf, Kinship coefficient
                                        : ON
 (5) Dmu, Delta mu squared
                                        : ON
 (6) D1 , Average squared difference : OFF
 (7) Dc , Chord distance
                                        : ON
 (8) Da , Nei's-distance (1983)
                                    : ON
  (9) D , Nei standard genetic distance:OFF
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    (r) ... Number of loci used by boots.: Use all loci
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    (m) ... back to main menu
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    (!) ... Run
    (q) ... Quit
                          populations distances calc"
Please enter command:c
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After the analysis, a folder of results will be created automatically in the same folder as your data file

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	Errorreport.txt		Today, 2:36 PM	4 KB	Plain Text	
•	🚞 Formats&Data		Today, 2:36 PM		Folder	
►	🚞 Group_data		Today, 2:36 PM		Folder	
	MSA.log		Today, 2:36 PM	4 KB	Log File	
►	🚞 Single_data		Today, 2:36 PM		Folder	
	📄 Summary.xls		Today, 2:36 PM	557 KB	Microrkbook	

The kinship matrix is in the folder of "Distance _data"

The Kinship matrix is saved as a file named "KSC_Pop.txt"

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Name		Date Modified	Size	Kind			
CAS_Pop.txt		Today, 2:36 PM	111 KB	Plain Text			
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DMS_Pop.txt		Today, 2:36 PM	115 KB	Plain Text			
KSC_Pop.txt		Today, 2:36 PM	111 KB	Plain Text			
POSA_Pop.txt		Today, 2:36 PM	111 KB	Plain Text			

Open the file with Excel to read the the matrix

Number of individuals

Kinship Matrix

The population (line) code

\diamond	A B	C	D	E	F	G	Н	1	J	K	L	M	N
1	109												
2	6111R1	0	0.17568	0.16216	0.13514	0.16216	0.17568	0.29167	0.375	0.14865	0.25676	0.27027	0.36
3	6111R2	0.17568	0	0.24324	0.25676	0.28378	0.24324	0.34722	0.36111	0.28378	0.33784	0.31081	0.36
4	6111R3	0.16216	0.24324	0	0.13158	0.14865	0.21053	0.32432	0.37838	0.21053	0.26316	0.32895	0.31
5	6111S1	0.13514	0.25676	0.13158	0	0.12162	0.18421	0.25676	0.33784	0.18421	0.21053	0.30263	0.28
6	6111S2	0.16216	0.28378	0.14865	0.12162	0	0.17568	0.30556	0.40278	0.18919	0.27027	0.33784	0.2
7	6115S3	0.17568	0.24324	0.21053	0.18421	0.17568	0	0.32432	0.32432	0.25	0.30263	0.31579	0.32
8	6115S4	0.29167	0.34722	0.32432	0.25676	0.30556	0.32432	0	0.22222	0.31081	0.27027	0.24324	0.27
9	6117R1	0.375	0.36111	0.37838	0.33784	0.40278	0.32432	0.22222	0	0.37838	0.27027	0.24324	0.32
10	6117R2	0.14865	0.28378	0.21053	0.18421	0.18919	0.25	0.31081	0.37838	0	0.23684	0.25	0.28
11	6117S1	0.25676	0.33784	0.26316	0.21053	0.27027	0.30263	0.27027	0.27027	0.23684	0	0.23684	0.31
12	6117S2	0.27027	0.31081	0.32895	0.30263	0.33784	0.31579	0.24324	0.24324	0.25	0.23684	0	0.30
13	6117S3	0.36486	0.36486	0.31579	0.28947	0.2973	0.32895	0.27027	0.32432	0.28947	0.31579	0.30263	
14	6117S4	0.37838	0.36486	0.38158	0.32895	0.41892	0.35526	0.21622	0.18919	0.36842	0.25	0.23684	0.28
15	6124R1	0.27027	0.33784	0.32895	0.31579	0.2973	0.28947	0.27027	0.27027	0.25	0.26316	0.22368	0.28
16	6124R2	0.41892	0.36486	0.38158	0.34211	0.40541	0.35526	0.22973	0.21622	0.38158	0.31579	0.27632	0.27
17	6124R3	0.35135	0.31081	0.34211	0.32895	0.36486	0.30263	0.27027	0.27027	0.34211	0.34211	0.26316	0.30
18	6124R4	0.40541	0.39189	0.36842	0.31579	0.36486	0.34211	0.17568	0.17568	0.36842	0.28947	0.26316	0.28
19	6124S1	0.39189	0.32432	0.36842	0.32895	0.36486	0.30263	0.25676	0.22973	0.38158	0.27632	0.26316	0.28
20	6124S2	0.375	0.375	0.37838	0.31081	0.31944	0.31081	0.20833	0.26389	0.33784	0.28378	0.25676	0.25
21	6125R1	0.33784	0.33784	0.30263	0.28947	0.31081	0.31579	0.24324	0.27027	0.35526	0.27632	0.30263	0.28
22	6125R2	0.45833	0.375	0.39189	0.36486	0.38889	0.32432	0.25	0.21622	0.44595	0.33784	0.31081	0.28
23	6125R3	0.34722	0.31944	0.33784	0.27027	0.31944	0.27027	0.26389	0.25	0.37838	0.31081	0.31081	0.32
24	6125R4	0.36111	0.34722	0.2973	0.28378	0.27778	0.31081	0.34722	0.375	0.33784	0.35135	0.37838	0.36
25	6125S1	0.37838	0.28378	0.31579	0.27632	0.32432	0.27632	0.27027	0.25676	0.35526	0.34211	0.28947	0.23
26	6125S2	0.25714	0.28571	0.27778	0.20833	0.24286	0.23611	0.22857	0.29167	0.30556	0.33333	0.31944	0.26
27	6125S3	0.27027	0.28378	0.27632	0.19737	0.22973	0.23684	0.27027	0.31081	0.27632	0.31579	0.30263	0.27
28	6125S4	0.37838	0.32432	0.38158	0.32895	0.35135	0.28947	0.28378	0.25676	0.36842	0.31579	0.28947	0.35
29	6126R4	0.33333	0.29167	0.36486	0.36486	0.34722	0.28378	0.36111	0.33333	0.36486	0.40541	0.33784	0.32
30	6126R5	0.31081	0.37838	0.34211	0.30263	0.31081	0.36842	0.37838	0.41892	0.39474	0.31579	0.40789	0.46
31	6132R4	0.30556	0.34722	0.40541	0.35135	0.38889	0.37838	0.44444	0.45833	0.43243	0.39189	0.43243	0.47
32	6132S3	0.2027	0.28378	0.23684	0.17105	0.17568	0.25	0.32432	0.39189	0.18421	0.23684	0.31579	0.31
33	6132S4	0.30556	0.31944	0.32432	0.32432	0.29167	0.28378	0.38889	0.38889	0.2973	0.36486	0.36486	0.33
34	6133R1	0.29167	0.31944	0.32432	0.28378	0.27778	0.28378	0.36111	0.38889	0.2973	0.35135	0.36486	0.40
35	6133R2	0.375	0.36111	0.31081	0.31081	0.29167	0.32432	0.44444	0.45946	0.37838	0.44595	0.47297	0.41
36	6133R3	0.43056	0.375	0.43243	0.43243	0.41667	0.36486	0.375	0.36486	0.45946	0.44595	0.41892	0.44
37	6133S1	0.37838	0.35135	0.36842	0.35526	0.37838	0.38158	0.45946	0.48649	0.43421	0.42105	0.47368	0.44
38	6133S2	0.40278	0.43056	0.40541	0.39189	0.38889	0.39189	0.44444	0.44444	0.45946	0.44595	0.45946	0.48
39	6133S3	0.47222	0.47222	0.52703	0.5	0.5	0.45946	0.47222	0.45833	0.52703	0.47297	0.48649	0.54
40	6133S4	0.51351	0.45946	0.52632	0.51316	0.51351	0.47368	0.45946	0.44595	0.59211	0.48684	0.48684	0.52
41	6135R3	0.47297	0.40541	0.46053	0.46053	0.47297	0.42105	0.48649	0.44595	0.52632	0.48684	0.48684	0.44
42	612601	0 20270	0.26496	0.20047	0.26216	0.25676	0.20047	0.25676	0.22022	0.27622	0 22269	0.26216	0.20

Number of individuals

Kinship Matrix

The population (line) code

Please remember that the value in the matrix is "1-kinship coefficient".

\diamond	AB	C	D	E	F	G	Н	1	J	K	L	M	N
1	109												
2	6111R1	0	0.17568	0.16216	0.13514	0.16216	0.17568	0.29167	0.375	0.14865	0.25676	0.27027	0.36
3	6111R2	0.17563	0	0.24324	0.25676	0.28378	0.24324	0.34722	0.36111	0.28378	0.33784	0.31081	0.36
4	6111R3	0.16216	0.24524	0	0.13158	0.14865	0.21053	0.32432	0.37838	0.21053	0.26316	0.32895	0.31
5	6111S1	0.13514	0.25676	0.15158	0	0.12162	0.18421	0.25676	0.33784	0.18421	0.21053	0.30263	0.28
6	6111S2	0.16216	0.28378	0.14865	0.12162	0	0.17568	0.30556	0.40278	0.18919	0.27027	0.33784	0.2
7	6115S3	0.17568	0.24324	0.21053	0.18421	0.17568	0	0.32432	0.32432	0.25	0.30263	0.31579	0.32
8	6115S4	0.29167	0.34722	0.32432	0.25676	0.30556	0.32432	0	0.22222	0.31081	0.27027	0.24324	0.27
9	6117R1	0.375	0.36111	0.37838	0.33784	0.40278	0.32432	0.22222	0	0.37838	0.27027	0.24324	0.32
10	6117R2	0.14865	0.28378	0.21053	0.18421	0.18919	0.25	0.31081	0.37838	0	0.23684	0.25	0.28
11	6117S1	0.25676	0.33784	0.26316	0.21053	0.27027	0.30263	0.27027	0.27027	0.23684	0	0.23684	0.31
12	6117S2	0.27027	0.31081	0.32895	0.30263	0.33784	0.31579	0.24324	0.24324	0.25	0.23684	0	0.30
13	6117S3	0.36486	0.36486	0.31579	0.28947	0.2973	0.32895	0.27027	0.32432	0.28947	0.31579	0.30263	
14	6117S4	0.37838	0.36486	0.38158	0.32895	0.41892	0.35526	0.21622	0.18919	0.36842	0.25	0.23684	0.28
15	6124R1	0.27027	0.33784	0.32895	0.31579	0.2973	0.28947	0.27027	0.27027	0.25	0.26316	0.22368	0.28
16	6124R2	0.41892	0.36486	0.38158	0.34211	0.40541	0.35526	0.22973	0.21622	0.38158	0.31579	0.27632	0.27
17	6124R3	0.35135	0.31081	0.34211	0.32895	0.36486	0.30263	0.27027	0.27027	0.34211	0.34211	0.26316	0.30
18	6124R4	0.40541	0.39189	0.36842	0.31579	0.36486	0.34211	0.17568	0.17568	0.36842	0.28947	0.26316	0.28
19	6124S1	0.39189	0.32432	0.36842	0.32895	0.36486	0.30263	0.25676	0.22973	0.38158	0.27632	0.26316	0.28
20	6124S2	0.375	0.375	0.37838	0.31081	0.31944	0.31081	0.20833	0.26389	0.33784	0.28378	0.25676	0.25
21	6125R1	0.33784	0.33784	0.30263	0.28947	0.31081	0.31579	0.24324	0.27027	0.35526	0.27632	0.30263	0.28
22	6125R2	0.45833	0.375	0.39189	0.36486	0.38889	0.32432	0.25	0.21622	0.44595	0.33784	0.31081	0.28
23	6125R3	0.34722	0.31944	0.33784	0.27027	0.31944	0.27027	0.26389	0.25	0.37838	0.31081	0.31081	0.32
24	6125R4	0.36111	0.34722	0.2973	0.28378	0.27778	0.31081	0.34722	0.375	0.33784	0.35135	0.37838	0.36
25	6125S1	0.37838	0.28378	0.31579	0.27632	0.32432	0.27632	0.27027	0.25676	0.35526	0.34211	0.28947	0.23
26	6125S2	0.25714	0.28571	0.27778	0.20833	0.24286	0.23611	0.22857	0.29167	0.30556	0.33333	0.31944	0.26
27	6125S3	0.27027	0.28378	0.27632	0.19737	0.22973	0.23684	0.27027	0.31081	0.27632	0.31579	0.30263	0.27
28	6125S4	0.37838	0.32432	0.38158	0.32895	0.35135	0.28947	0.28378	0.25676	0.36842	0.31579	0.28947	0.35
29	6126R4	0.33333	0.29167	0.36486	0.36486	0.34722	0.28378	0.36111	0.33333	0.36486	0.40541	0.33784	0.32
30	6126R5	0.31081	0.37838	0.34211	0.30263	0.31081	0.36842	0.37838	0.41892	0.39474	0.31579	0.40789	0.46
31	6132R4	0.30556	0.34722	0.40541	0.35135	0.38889	0.37838	0.44444	0.45833	0.43243	0.39189	0.43243	0.47
32	6132S3	0.2027	0.28378	0.23684	0.17105	0.17568	0.25	0.32432	0.39189	0.18421	0.23684	0.31579	0.31
33	6132S4	0.30556	0.31944	0.32432	0.32432	0.29167	0.28378	0.38889	0.38889	0.2973	0.36486	0.36486	0.33
34	6133R1	0.29167	0.31944	0.32432	0.28378	0.27778	0.28378	0.36111	0.38889	0.2973	0.35135	0.36486	0.40
35	6133R2	0.375	0.36111	0.31081	0.31081	0.29167	0.32432	0.44444	0.45946	0.37838	0.44595	0.47297	0.41
36	6133R3	0.43056	0.375	0.43243	0.43243	0.41667	0.36486	0.375	0.36486	0.45946	0.44595	0.41892	0.44
37	6133S1	0.37838	0.35135	0.36842	0.35526	0.37838	0.38158	0.45946	0.48649	0.43421	0.42105	0.47368	0.44
38	613352	0.40278	0.43056	0.40541	0.39189	0.38889	0.39189	0.44444	0.44444	0.45946	0.44595	0.45946	0.48
39	6133S3	0.47222	0.47222	0.52703	0.5	0.5	0.45946	0.47222	0.45833	0.52703	0.47297	0.48649	0.54
40	613354	0.51351	0.45946	0.52632	0.51316	0.51351	0.47368	0.45946	0.44595	0.59211	0.48684	0.48684	0.52
41	6135R3	0.47297	0.40541	0.46053	0.46053	0.47297	0.42105	0.48649	0.44595	0.52632	0.48684	0.48684	0.44
42	612601	0 20270	0.26496	0.20047	0.26216	0.25676	0.20047	0.25676	0.27027	0.27622	0 22269	0.26216	0.20

Final Matrix

Use "1-X" (X is the value of each cell in the matrix) to generate a new matrix that will be the kinship matrix in Excel.

					Sheets	Charts	SmartArt Graphics		WordArt	-		
\diamond	Α	В	С	D	E	F	G	H	1	J	K	L
1	109											
2		6111R1	1	0.80681	0.82307	0.85482	0.82307	0.80681	0.65516	0.53	0.83907	0.70327
3		6111R2	0.80681	1	0.72129	0.70327	0.66623	0.72129	0.57348	0.55198	0.66623	0.58776
4		6111R3	0.82307	0.72129	1	0.85892	0.83907	0.76361	0.60796	0.52458	0.76361	0.69462
5		6111S1	0.85482	0.70327	0.85892	1	0.87032	0.7964	0.70327	0.58776	0.7964	0.76361
6		6111S2	0.82307	0.66623	0.83907	0.87032	1	0.80681	0.63536	0.48453	0.79028	0.68492
7		6115S3	0.80681	0.72129	0.76361	0.7964	0.80681	1	0.60796	0.60796	0.71232	0.63956
8		6115S4	0.65516	0.57348	0.60796	0.70327	0.63536	0.60796	1	0.74869	0.62776	0.68492
9		6117R1	0.53	0.55198	0.52458	0.58776	0.48453	0.60796	0.74869	1	0.52458	0.68492
10		6117R2	0.83907	0.66623	0.76361	0.7964	0.79028	0.71232	0.62776	0.52458	1	0.72971
11		6117S1	0.70327	0.58776	0.69462	0.76361	0.68492	0.63956	0.68492	0.68492	0.72971	1
12		6117S2	0.68492	0.62776	0.60109	0.63956	0.58776	0.62051	0.72129	0.72129	0.71232	0.72971
13		6117S3	0.54608	0.54608	0.62051	0.65825	0.64718	0.60109	0.68492	0.60796	0.65825	0.62051
14		6117S4	0.52458	0.54608	0.51941	0.60109	0.45714	0.56109	0.75638	0.79028	0.54047	0.71232
15		6124R1	0.68492	0.58776	0.60109	0.62051	0.64718	0.65825	0.68492	0.68492	0.71232	0.69462
16		6124R2	0.45714	0.54608	0.51941	0.58129	0.48012	0.56109	0.73899	0.75638	0.51941	0.62051
17		6124R3	0.56714	0.62776	0.58129	0.60109	0.54608	0.63956	0.68492	0.68492	0.58129	0.58129
18		6124R4	0.48012	0.5026	0.54047	0.62051	0.54608	0.58129	0.80681	0.80681	0.54047	0.65825
19		6124S1	0.5026	0.60796	0.54047	0.60109	0.54608	0.63956	0.70327	0.73899	0.51941	0.6766
20		6124S2	0.53	0.53	0.52458	0.62776	0.61515	0.62776	0.76639	0.69363	0.58776	0.66623
21		6125R1	0.58776	0.58776	0.63956	0.65825	0.62776	0.62051	0.72129	0.68492	0.56109	0.6766
22		6125R2	0.3869	0.53	0.5026	0.54608	0.50752	0.60796	0.71232	0.75638	0.40951	0.58776
23		6125R3	0.57348	0.61515	0.58776	0.68492	0.61515	0.68492	0.69363	0.71232	0.52458	0.62776
24		6125R4	0.55198	0.57348	0.64718	0.66623	0.67458	0.62776	0.57348	0.53	0.58776	0.56714
25		6125S1	0.52458	0.66623	0.62051	0.6766	0.60796	0.6766	0.68492	0.70327	0.56109	0.58129
26		6125S2	0.70275	0.66353	0.67458	0.76639	0.7218	0.73067	0.74049	0.65516	0.63536	0.59453
27		6125S3	0.68492	0.66623	0.6766	0.78014	0.73899	0.72971	0.68492	0.62776	0.6766	0.62051
28		6125S4	0.52458	0.60796	0.51941	0.60109	0.56714	0.65825	0.66623	0.70327	0.54047	0.62051
29		6126R4	0.59453	0.65516	0.54608	0.54608	0.57348	0.66623	0.55198	0.59453	0.54608	0.48012
30		6126R5	0.62776	0.52458	0.58129	0.63956	0.62776	0.54047	0.52458	0.45714	0.49791	0.62051
31		6132R4	0.63536	0.57348	0.48012	0.56714	0.50752	0.52458	0.41221	0.3869	0.4336	0.5026
32		6132S3	0.77347	0.66623	0.72971	0.8124	0.80681	0.71232	0.60796	0.5026	0.7964	0.72971
33		6132S4	0.63536	0.61515	0.60796	0.60796	0.65516	0.66623	0.50752	0.50752	0.64718	0.54608
34		6133R1	0.65516	0.61515	0.60796	0.66623	0.67458	0.66623	0.55198	0.50752	0.64718	0.56714
35		6133R2	0.53	0.55198	0.62776	0.62776	0.65516	0.60796	0.41221	0.38481	0.52458	0.40951
36		6133R3	0.43691	0.53	0.4336	0.4336	0.461	0.54608	0.53	0.54608	0.38481	0.40951
37		6133S1	0.52458	0.56714	0.54047	0.56109	0.52458	0.51941	0.38481	0.33352	0.43047	0.45346

The Mixed Model



References Cited & External Link

References Cited

- Cavalli-Sforza, L. L., and W. F. Bodmer. 1971. The genetics of human populations, W.H. Freeman and Company, NY.
- Lange, K. 2002. Mathematical and statistical methods for genetic analysis, 2nd edition. Springer-Verlag, NY.
- Yu, J. G. Pressoir, W. H. Briggs, I. V. Bi, M. Yamasaki, J. F. Doebley, M. D. McMullen, B. S. Gaut, D. M. Nielsen, J. B. Holland, S. Kresovich, and E. S. Buckler. 2006. A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. Nature Genetics 38: 203-208. (Available online at: http://dx.doi.org/10.1038/ng1702) (verified 8 July 2011).
- Zhu, C. M. Gore, E. S. Buckler, and J. Yu. 2008. Status and prospects of association mapping in plants. The Plant Genome 1: 5-20. (Available online at: http://dx.doi.org/10.3835/plantgenome2008.02.0089) (verified 8 July 2011).

External Link

 Dieringer, D. Microsatellite analyzer (MSA) [Online]. Available at: http://i122server.vu-wien.ac.at/MSA/MSA_download.html (verified 8 July 2011).

Thank you and good luck!