

Creating a Kinship Matrix using Microsatellite Analyzer (MSA)

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Why create a kinship matrix?

- Visualize family relatedness
- Use in association mapping

The Objective of this Tutorial:

To introduce one approach to generate a kinship matrix for a population

Using Microsatellite Analyzer (MSA)

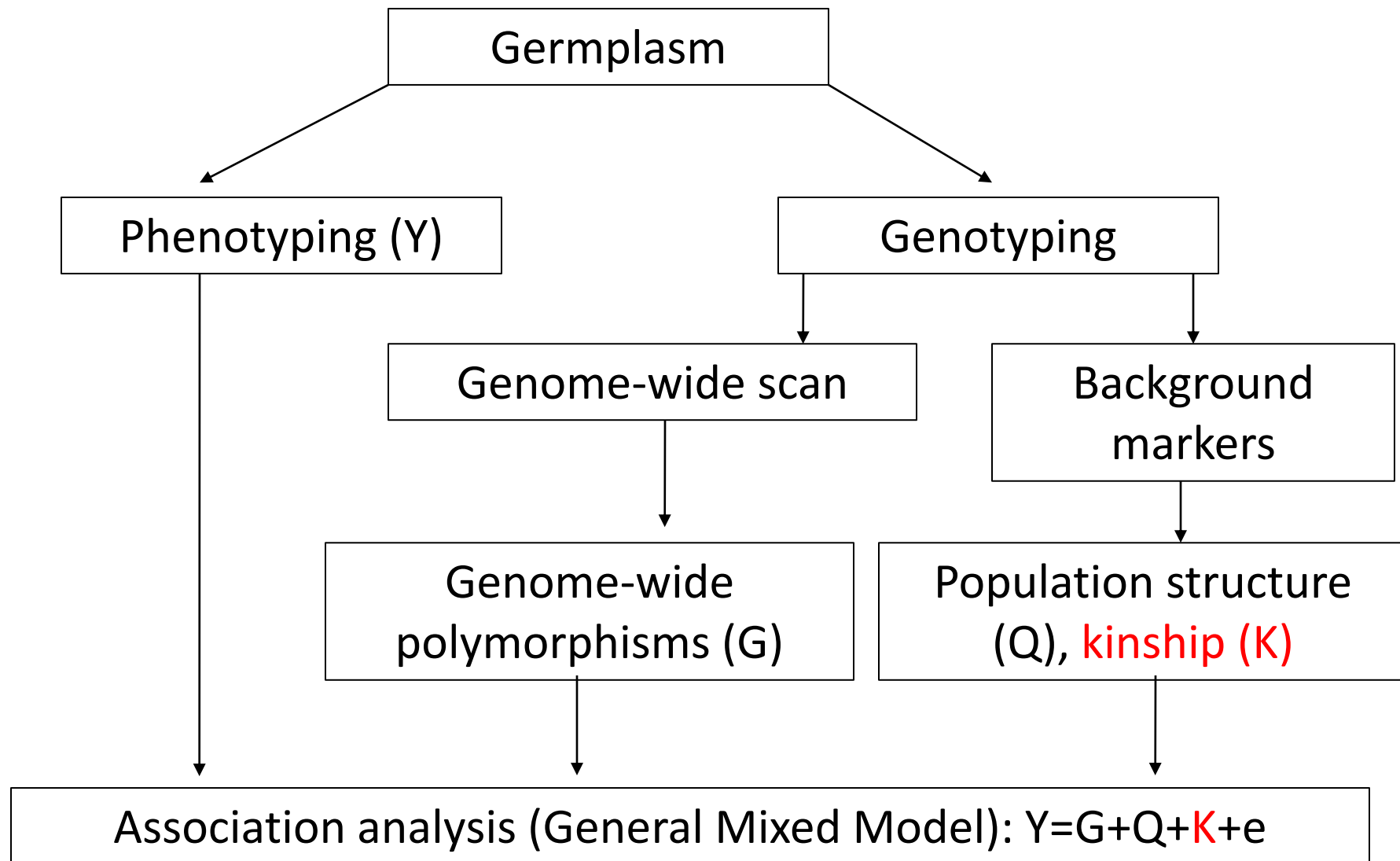
Background

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



Coefficient of Kinship

Coefficient of kinship is used to measure relatedness

DEFINITION: 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

$$K_{ij} = \frac{\sum_k \sum_a (f_{ai} * f_{aj})}{D}$$

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.

An Example

In population 611R2 and 611R3, three loci were studied and summarized.

Population	Locus A	Locus B	Locus C
611R2	A	b	c
	A	b	c
611R3	A	B	c
	A	B	c

Coefficient of kinship for populations 611R2 and 611R3:

$$Kf = \sum_k \sum_a (f_{ai} * f_{aj}) / D$$
$$= (1 \times 1 + 1 \times 0 + 0 \times 1 + 1 \times 1) / 3 = 2/3$$

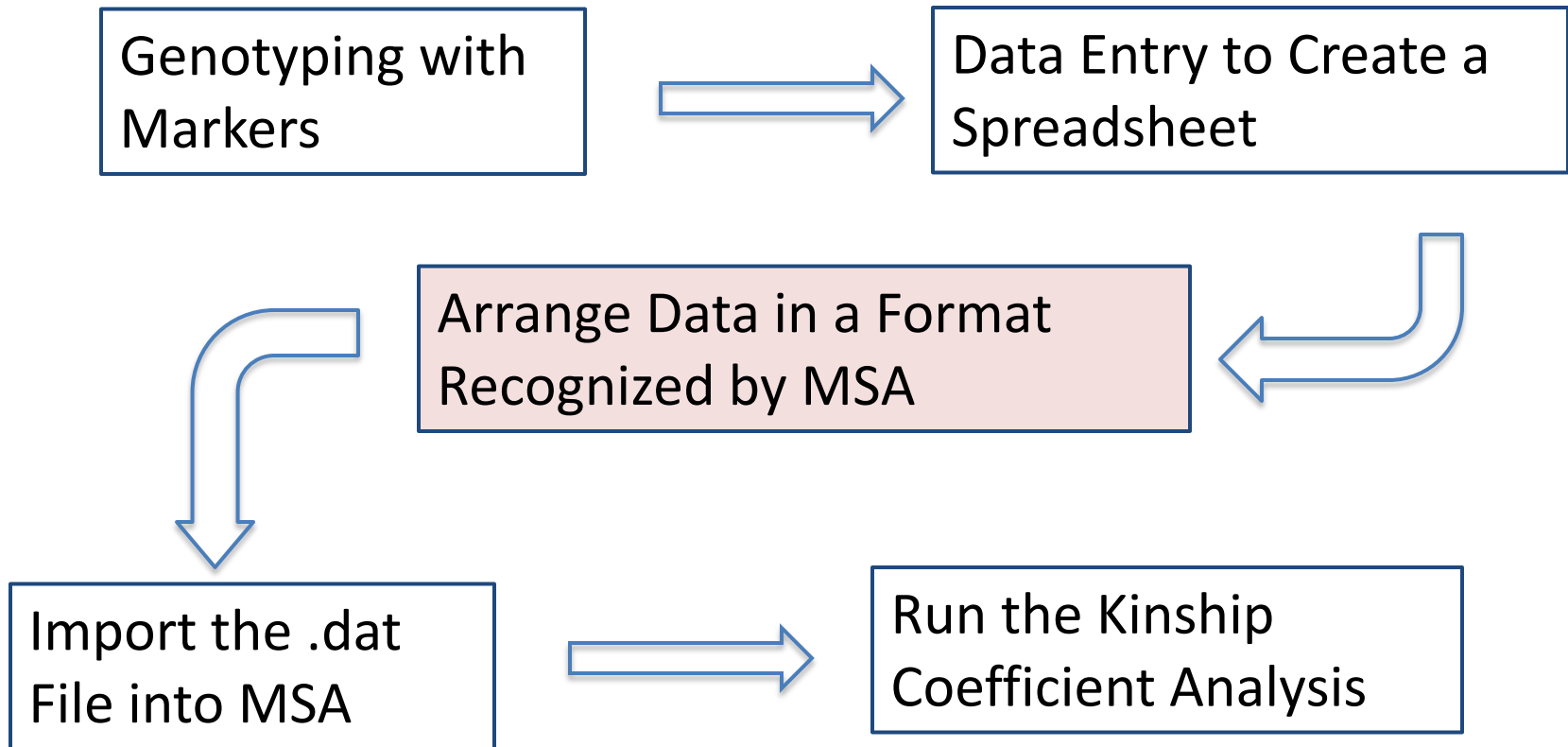
The frequencies of alleles A in populations 611R2 and 611R3 are 1; the frequency of allele b is 1 in population 611R2 but 0 in population 611R3; the frequency of allele B is 0 in population 611R2 but 1 in population 611R3; the frequency of allele c is 1 in each population.

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.

Population

Marker

Genotype Score

		B	C	D	E	F	G
1	gen	SL10639	LEOH20	SL10373I	SL10469	SL10700	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	0	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

Population #

Mating scheme

Group name: default "1"

Give a new value to each allele for each marker

	A	B	C	D	E	F	G	H	I	J	
1											
2	1			SL10639	LEOH20	SL10373I	SL10469	SL10963	LEOH9	SL10526	Pto
3	6111R1	h	1	33	33	33	33	33	33	33	33
4	6111R1	h	1	33	33	33	33	55	33	33	33
5	6111R2	h	1	33	33	33	33	33	33	33	33
6	6111R2	h	1	33	33	33	33	55	33	33	33
7	6111R3	h	1	33	33	33	33	33	33	33	33
8	6111R3	h	1			33	33	55	33	33	33
9	6111S1	h	1			33	33	55	33	33	33
10	6111S1	h	1				33	55	33	33	33
11	6111S2	h	1			33	33	33	33	33	33
12	6111S2	h	1			33	33	55	33	33	33
13	6115S3	h	1	33	33	33	33	55	33	33	33
14	6115S3	h	1	33	33	33	33	55	33	33	33
15	6115S4	h	1	33	33	33	33	33	33	33	33
16	6115S4	h	1	33	33	33	33	55	33	33	33
17	6117R1	h	1	33	33	33	33	33	33	33	33
18	6117R1	h	1	33	33	33	33	55	33	33	33
19	6117R2	h	1	33	33	33	33	33	33	33	33
20	6117R2	h	1	33	33	33	33	33	33	33	33
21	6117S1	h	1	33	33	33	33	33	33	33	33
22	6117S1	h	1	33	33	33	33	55	33	33	33

These 3 cells should be empty.

Row 1 can be left empty. Columns a, b, and c 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

Homozygotes have the same value in both rows.

Heterozygotes have different values in each row.

A	B	C	D	E	H
1					
			SL10639	LEOH20	SL10963
6111R1	h	1	33	33	33
6111R1	h	1	33	33	55
6111R2	h	1	33	33	33
6111R2	h	1	33	33	55
6111R3	h	1	33	33	33
6111R3	h	1	33	33	55
6111S1	h	1	33	33	55
6111S1	h	1	33	33	55

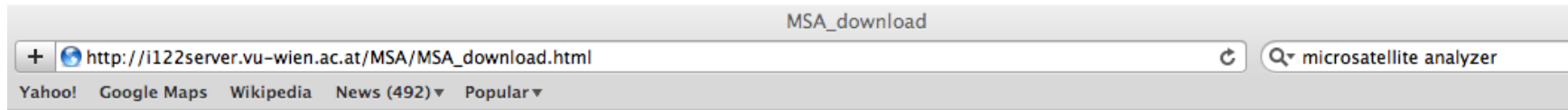
MSA (Microsatellite Analyzer) is available for free, provided by Daniel Dieringer.

The image shows a screenshot of a web browser displaying a Google search for "microsatellite analyzer". The search results page shows several entries, with an orange arrow pointing to the second result, "Microsatellite Analyzer (MSA)".

Search results for "microsatellite analyzer":

- Microsatellite Analyzer - Accurate Leading Edge Applications.** (Ad)
The Most Accurate Workflows.
www.appliedbiosystems.com
- Microsatellite Analyzer (MSA)** ☆ 🔍 - 3 visits - 8:50am
Microsatellite Analyzer (MSA). Information about MSA can be found here. For downloading please click on the required OS icon.
i122server.vu-wien.ac.at/MSA/MSA_download.html - Cached - Similar
- CS lab software** ☆ 🔍
CS lab software. **Microsatellite Analyzer (MSA)**. Provides basic summary ...
i122server.vu-wien.ac.at/CSlab_software.htm - Cached
- [Show more results from vu-wien.ac.at](#)
- Analysis Software** ☆ 🔍
Genealogical **analysis** of linked **microsatellite** and unique event polymorphism haplotypes. Population splitting model and growth models allowed. ...
www2.hawaii.edu/~khayes/Software_links.htm - Cached - Similar
- microsatellites - Evolutionary Genetics Software Links by Sergios ...** ☆ 🔍
Microsatellite Analyzer (MSA), all, Calculates descriptive statistics, distances , ...
microsatellite analysis software list, URL, compiled by David McDonald ...
softlinks.amnh.org/microsatellites.html - Cached - Similar
- [PDF] Microsatellite Analysis on the Applied Biosystems 3130 Series ...** ☆ 🔍 - Feb 14
File Format: PDF/Adobe Acrobat - [Quick View](#)
microsatellite analysis, and the many reasons why the Applied Biosystems ... Fact Sheet
Microsatellite Analysis on the 3130 Series Systems ...
www3.appliedbiosystems.com/cms/groups/mcb.../cms_040581.pdf - Similar
- Microsatellite analysis reveals genetically distinct populations ...** ☆ 🔍
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



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



contact: [Daniel Dieringer](#)

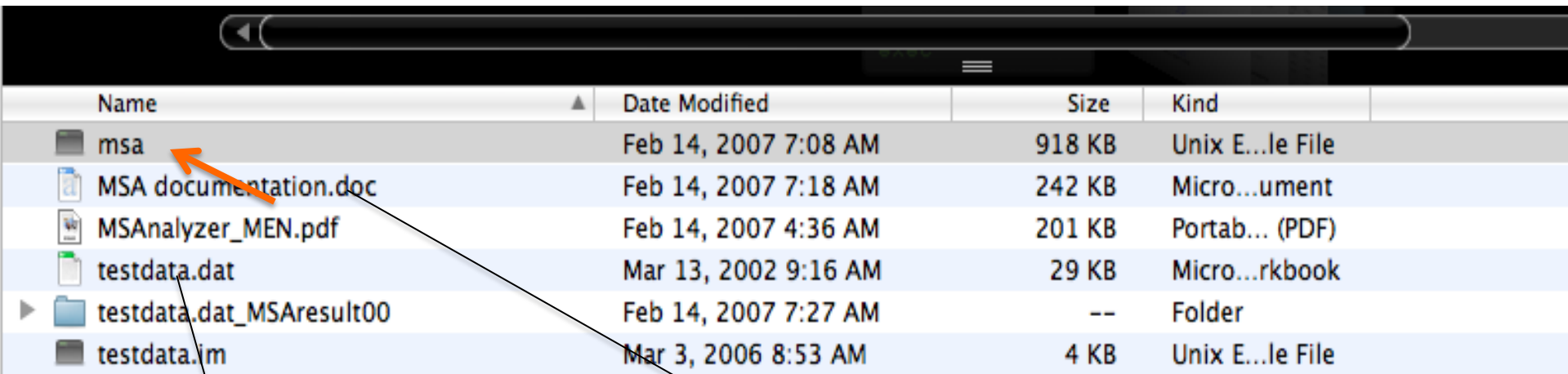
Choose the
operating system
you use and install it
as other software

Install MSA

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

Name	Date Modified
▶ MSA_OSX.1	Feb 14, 2007 7:41 AM
MSA_OSX.sit	Feb 14, 2007 8:14 AM
▶ GB_ESTs_Feb_2007.sp.Heli_annu.clean.cap3.80.90.Align	Feb 21, 2007 5:59 PM
2yrlyc.xls	Apr 1, 2008 10:50 AM
f2f3lyc.xls	Apr 1, 2008 10:50 AM
Grad Progress Rpt ADV 10.doc	May 29, 2010 11:53 PM
Description of financial need.doc	Jun 2, 2010 11:37 AM
Grad Course Forms Au 2009.pdf	Jun 2, 2010 11:35 PM
FINAL Attendee List.pdf	Jul 1, 2010 2:32 PM
Certificate of Attendance.pdf	Jul 1, 2010 2:33 PM
Zhang.pdf	Jul 1, 2010 2:34 PM
July 8 2010.pdf	Jul 9, 2010 9:26 AM
GS start and projected grad dates.pdf	Jul 12, 2010 3:43 PM
nrg2808.pdf	Jul 20, 2010 5:35 PM
nrg2838.pdf	Jul 20, 2010 5:37 PM
science.1190532v1.pdf	Jul 20, 2010 5:39 PM
nrq2834.pdf	Jul 20, 2010 5:39 PM

Use MSA



Name	Date Modified	Size	Kind
msa	Feb 14, 2007 7:08 AM	918 KB	Unix E...le File
MSA documentation.doc	Feb 14, 2007 7:18 AM	242 KB	Micro...ument
MSAnalyzer_MEN.pdf	Feb 14, 2007 4:36 AM	201 KB	Portab... (PDF)
testdata.dat	Mar 13, 2002 9:16 AM	29 KB	Micro...rkbook
testdata.dat_MSAresult00	Feb 14, 2007 7:27 AM	--	Folder
testdata.im	Mar 3, 2006 8:53 AM	4 KB	Unix E...le File

Manual for MSA is available in the folder

Sample data is available

Use MSA

Terminal — msa — 80x24

```
Last login: Fri Mar  4 14:29:56 on ttys000
/Users/zhifenzhang/Downloads/MSA_OSX.1/msa ; exit;
dhcp-140-254-186-156:~ zhifenzhang$ /Users/zhifenzhang/Downloads/MSA_OSX.1/msa ;
exit;
MSA can now also handle command line arguments!
If you are interested in this function
please read the documentation!

Welcome to MSAnalyzer 4.05 !
```

```
(i) ... Inputfile:none (MSA will use testdata.dat)
(d) ... Distance settings
(c) ... Data conversion settings
(a) ... Number of ind's for allelic richness:
           : Minimal sample number per locus
(r) ... Heterozygosity range settings

(!) ... Run
(q) ... Quit
```

Please enter command:i

Enter command “i” to import file

Menu of
Commands

Use MSA

View Quick Look Schoeffl 1998 revi...ent regulation.pdf other Action Search

```
Terminal — msa — 80x24
/Users/zhifenzhang/Downloads/MSA_OSX.1/msa ; exit;
dhcp-140-254-186-156:~ zhifenzhang$ /Users/zhifenzhang/Downloads/MSA_OSX.1/msa ;
exit;
MSA can now also handle command line arguments!
If you are interested in this function
please read the documentation!

Welcome to MSAAnalyzer 4.05 !

-----
(i) ... Inputfile:none (MSA will use testdata.dat)
(d) ... Distance settings
(c) ... Data conversion settings
(a) ... Number of ind's for allelic richness:
      : Minimal sample number per locus
(r) ... Heterozygosity range settings

(!) ... Run
(q) ... Quit
Please enter command:i

Please enter the filename:/Users/zhifenzhang/Downloads/MSA_OSX.1/T1_MarkerData_1
10301.dat
```

Name

- msa
- MSA documentation.doc
- MSAnalyzer_MEN.pdf
- T1_MarkerData_110301.dat
- testdata.dat
- testdata.dat_MSAresult00
- testdata.im

Import your data file to MSA easily by dragging it to the MSA window

Use MSA

After the data file is imported,

```
Terminal — msa — 80x24
(d) ... Distance settings
(c) ... Data conversion settings
(a) ... Number of ind's for allelic richness:
      : Minimal sample number per locus
(r) ... Heterozygosity range settings

(!) ... Run
(q) ... Quit
Please enter command:
Unknown command!

-----
(i) ... Inputfile:/Users/zhifenzhang/Downloads/MSA_OSX.1/T1_MarkerData_1103
01.dat (1)
(X) ... Remove Data from Memory

(d) ... Distance settings
(c) ... Data conversion settings
(a) ... Number of ind's for allelic richness:
      : Minimal sample number per locus
(r) ... Heterozygosity range settings

(!) ... Run
(q) ... Quit
Please enter command:d
```

Enter command “d” to access submenu of “Distance setting”

Use MSA

Terminal — msa — 80x24

```
(c) ... Pairwise populations distances calc: OFF
(i) ... Pairwise individual distances calc : OFF
(1)  Dps, Proportion of shared alleles : ON
(2)  Dfs, Fuzzy set similarity          : OFF
(3)  Dad, Absolute difference algorithm:OFF
(4)  Dkf, Kinship coefficient           : OFF
(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
(l)  ... Use -ln(similarity factor)
      instead of 1-(similarity factor)  : OFF
      This option will only used for Dps, Dfs, Dkf, D
(o)  ... Distance per population pair and locus: OFF
(n)  ... Number of bootstraps          : No bootstrapping!

(r)  ... Number of loci used by boots.: Use all loci
(b)  ... back to distance menu
(m)  ... back to main menu

(!)  ... Run
(q)  ... Quit
```

Please enter command:4

Enter "4" to turn on kinship coefficient module.

Use MSA

Each line will be treated as a population in this study

```
(c) ... Pairwise populations distances calc: OFF
(i) ... Pairwise individual distances calc : OFF
(1)  Dps, Proportion of shared alleles : ON
(2)  Dfs, Fuzzy set similarity          : OFF
(3)  Dad, Absolute difference algorithm:OFF
(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
(l)  ... Use -ln(similarity factor)
      instead of 1-(similarity factor)  : OFF
      This option will only used for Dps, Dfs, Dkf, D
(o)  ... Distance per population pair and locus: OFF
(n)  ... Number of bootstraps           : No bootstrapping!

(r)  ... Number of loci used by boots.: Use all loci
(b)  ... back to distance menu
(m)  ... back to main menu
```

```
(!) ... Run
(q) ... Quit
```

Please enter command:c

Input command “c” to turn on “Pair-wise populations distances calc”

Use MSA

```
Terminal — msa — 80x24
(c) ... Pairwise populations distances calc: ON
(i) ... Pairwise individual distances calc : OFF
(1)  Dps, Proportion of shared alleles : ON
(2)  Dfs, Fuzzy set similarity          : OFF
(3)  Dad, Absolute difference algorithm:OFF
(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
(l)  ... Use -ln(similarity factor)
      instead of 1-(similarity factor)  : OFF
      This option will only used for Dps, Dfs, Dkf, D
(o)  ... Distance per population pair and locus: OFF
(n)  ... Number of bootstraps          : No bootstrapping!

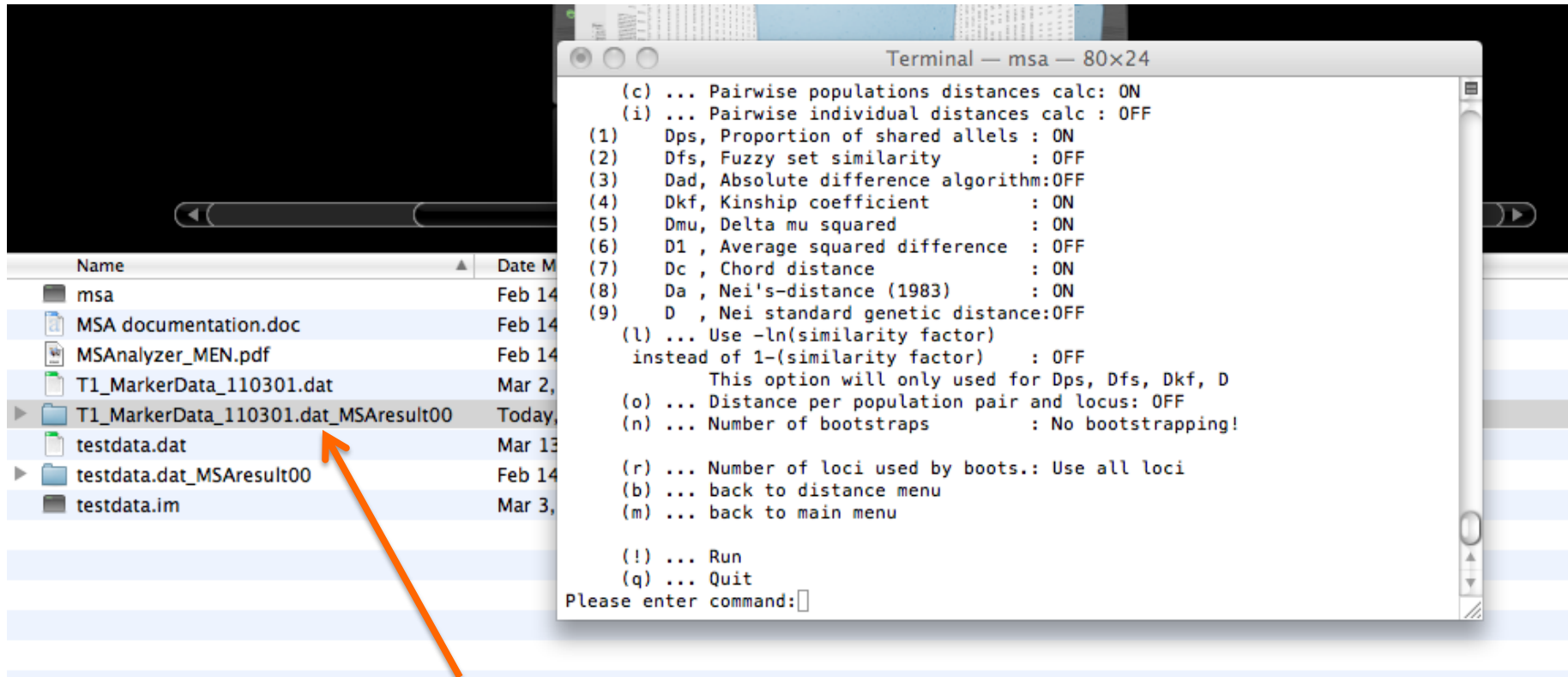
(r)  ... Number of loci used by boots.: Use all loci
(b)  ... back to distance menu
(m)  ... back to main menu

(!)  ... Run
(q)  ... Quit
Please enter command:!
```

NOTE: Dkf in the matrix will be 1-kf in default.

After everything is set, input “!” command to run the analysis.

Use MSA



The image shows a file manager window on the left and a terminal window on the right. The file manager displays a directory listing with columns for Name and Date Modified. An orange arrow points from the terminal window to a folder named 'T1_MarkerData_110301.dat_MSAresult00' in the file manager. The terminal window shows a menu of MSA analysis options.

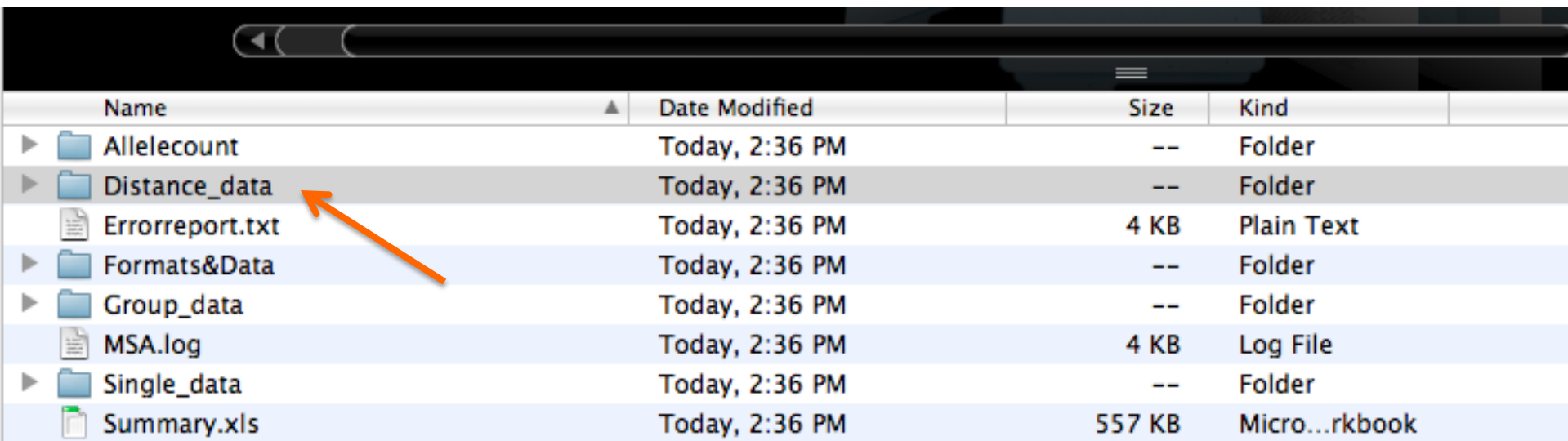
Name	Date Modified
msa	Feb 14
MSA documentation.doc	Feb 14
MSAnalyzer_MEN.pdf	Feb 14
T1_MarkerData_110301.dat	Mar 2,
T1_MarkerData_110301.dat_MSAresult00	Today,
testdata.dat	Mar 13
testdata.dat_MSAresult00	Feb 14
testdata.im	Mar 3,

```
Terminal — msa — 80x24
(c) ... Pairwise populations distances calc: ON
(i) ... Pairwise individual distances calc : OFF
(1) Dps, Proportion of shared alleles : ON
(2) Dfs, Fuzzy set similarity : OFF
(3) Dad, Absolute difference algorithm:OFF
(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
(l) ... Use -ln(similarity factor)
    instead of 1-(similarity factor) : OFF
    This option will only used for Dps, Dfs, Dkf, D
(o) ... Distance per population pair and locus: OFF
(n) ... Number of bootstraps : No bootstrapping!
(r) ... Number of loci used by boots.: Use all loci
(b) ... back to distance menu
(m) ... back to main menu

(!) ... Run
(q) ... Quit
Please enter command:
```

After the analysis, a folder of results will be created automatically in the same folder as your data file

Use MSA



A screenshot of a file explorer window showing a directory listing. The window has a dark header with navigation arrows and a hamburger menu icon. The main area displays a table of files and folders. An orange arrow points to the 'Distance_data' folder.

Name	Date Modified	Size	Kind
▶ Allelecount	Today, 2:36 PM	--	Folder
▶ Distance_data	Today, 2:36 PM	--	Folder
▶ 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	Micro...rkbook

The kinship matrix is in the folder of “Distance_data”

Use MSA

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

KSC_Pop.txt

Name	Date Modified	Size	Kind
CAS_Pop.txt	Today, 2:36 PM	111 KB	Plain Text
DAN_Pop.txt	Today, 2:36 PM	111 KB	Plain Text
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

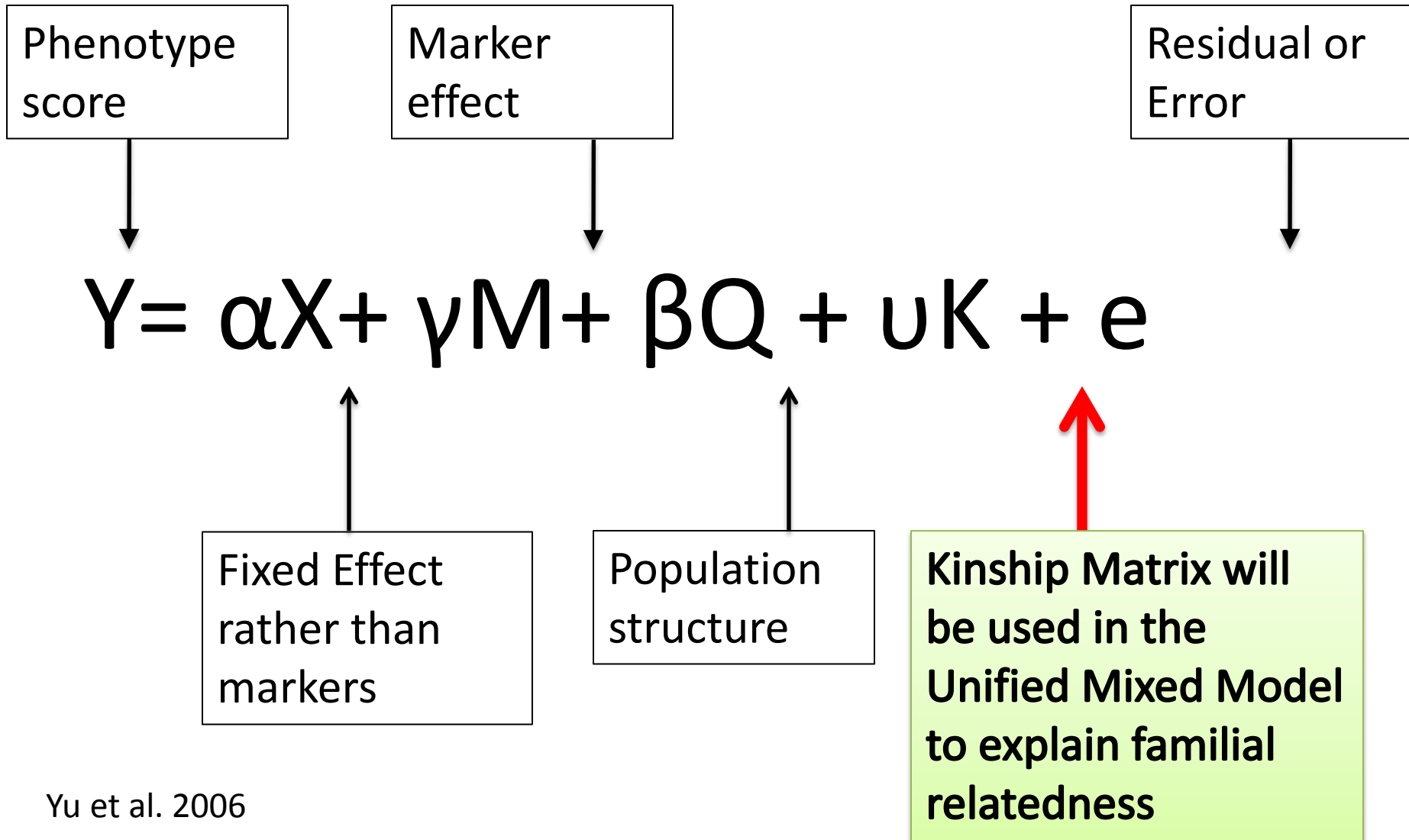
◇	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	109													
2		6111R1	0	0.17568	0.16216	0.13514	0.16216	0.17568	0.29167	0.375	0.14865	0.25676	0.27027	0.36
3		6111R2	0.17568	0	0.24324	0.25676	0.28378	0.24324	0.34722	0.36111	0.28378	0.33784	0.31081	0.36
4		6111R3	0.16216	0.24324	0	0.13158	0.14865	0.21053	0.32432	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		6135R1	0.28378	0.36486	0.38158	0.32895	0.35135	0.28947	0.25676	0.27027	0.36842	0.31579	0.28947	0.35

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				
◇	A	B	C	D	E	F	G	H	I	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

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Thank you and good luck!