Theory on Genetic Diversity Analysis

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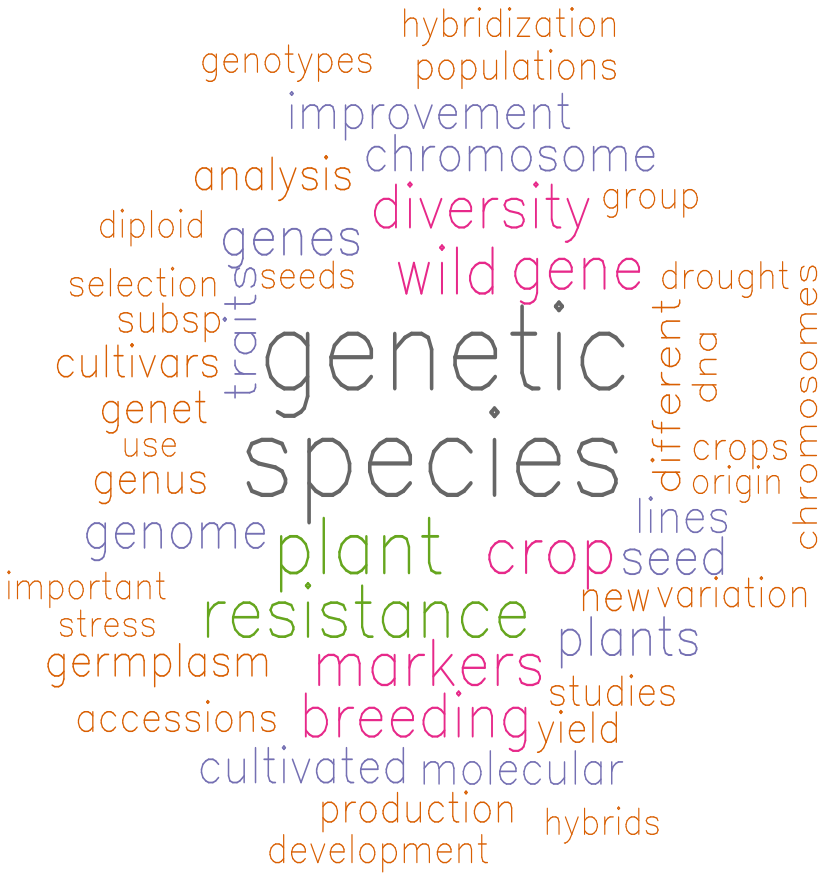


Outline:

Some definitions
- Population Genetics
- Genetic Markers

Genetic Distances

Intraspecific Diversity
- Anova & Complete Randomized Design
- Wright Statistics

Find Clusters and Groups

The software BIO-R
- Getting BIO-R
  - Check Output and Estimates

Some Definitions ...

- **Genotype:**

  Genotype is ... _____

  _____

  _____

  _____.

- **Markers:**

  Genetic Markers are ... _____

  _____

  _____

  _____.

- **Population:** ... [CONT]

Population Genetics ...

- **Population Genetics:** Studies the heredity's mechanisms at the population level.
- **Population:** Set of conspecifics individuals in the *same place and time*, which have the ability to mate (exchange alleles).

In a population, the individual has a transitory importance, what matters are the alleles it has, which will be transmitted to subsequent generations

Reproductive systems

- **Allogamous:** frequency of cross polination is ≥ 95% *e.g.*, maize
- **Autogamous:** frequency of cross pollination is ≤ 5% *e.g.*, wheat.

Allele and Genotypic Frequencies ...

Genotype		Phenotype	Observed	Frequency
BB	$\longrightarrow$	White	100	0.05
Bb	$\longrightarrow$	Yellow	1000	0.50
bb	$\longrightarrow$	Red	900	0.45
		Total:	2000	1.00

$$f(B) = p = 0.05 + \frac{0.50}{2} = 0.30$$

$$\begin{aligned} f(b) &= q = 0.45 + \frac{0.50}{2} = 0.70 \\ &= (1 - p) \end{aligned}$$

Onion is a autogamous specie ...

Any plant can mate with any other one i.e., panmixia & HWE

		B	b
		p	q
B	p	p^2	$p \cdot q$
b	q	$p \cdot q$	q^2

BB	p^2	$0,30^3 = 0,09$
Bb	$2 \cdot p \cdot q$	$2 \cdot 0,30 \cdot 0,70 = 0,42$
bb	q^2	$0,70^2 = 0,49$

If not, considering selfcross ...

The plants mate by themselves

Genotype	G_0	G_1	
BB	$p^2 = f_{BB_0}$	$f_{BB_0} + 1/4 \cdot f_{Bb_0}$	$p^2 + 1/2 \cdot p \cdot q$
Bb	$2 \cdot p \cdot q = f_{Bb_0}$	$f_{Bb_0} - 1/2 \cdot f_{Bb_0}$	$p \cdot q$
bb	$q^2 = f_{bb_0}$	$f_{bb_0} + 1/4 \cdot f_{Bb_0}$	$q^2 + 1/2 \cdot p \cdot q$

$$
\begin{aligned}
p' &= p^2 + 1/2 \cdot p \cdot q + 1/2 \cdot p \cdot q \\
&= p^2 + 1/2 \cdot p \cdot (1 - p) + 1/2 \cdot p \cdot (1 - p) \\
&= p^2 + 1/2 \cdot (p^2 - p) + 1/2 \cdot (p^2 - p) \\
&= p^2 + 1/2 \cdot p^2 - 1/2 \cdot p + 1/2 \cdot p^2 - 1/2 \cdot p \\
&= p^2 - p^2 + p \\
p' &= p
\end{aligned}
$$

1. **Alogamous**

$$\begin{aligned} f_{BB} &:= p^2 \\ f_{Bb} &:= 2 \cdot p \cdot q \\ f_{bb} &:= q^2 \end{aligned}$$

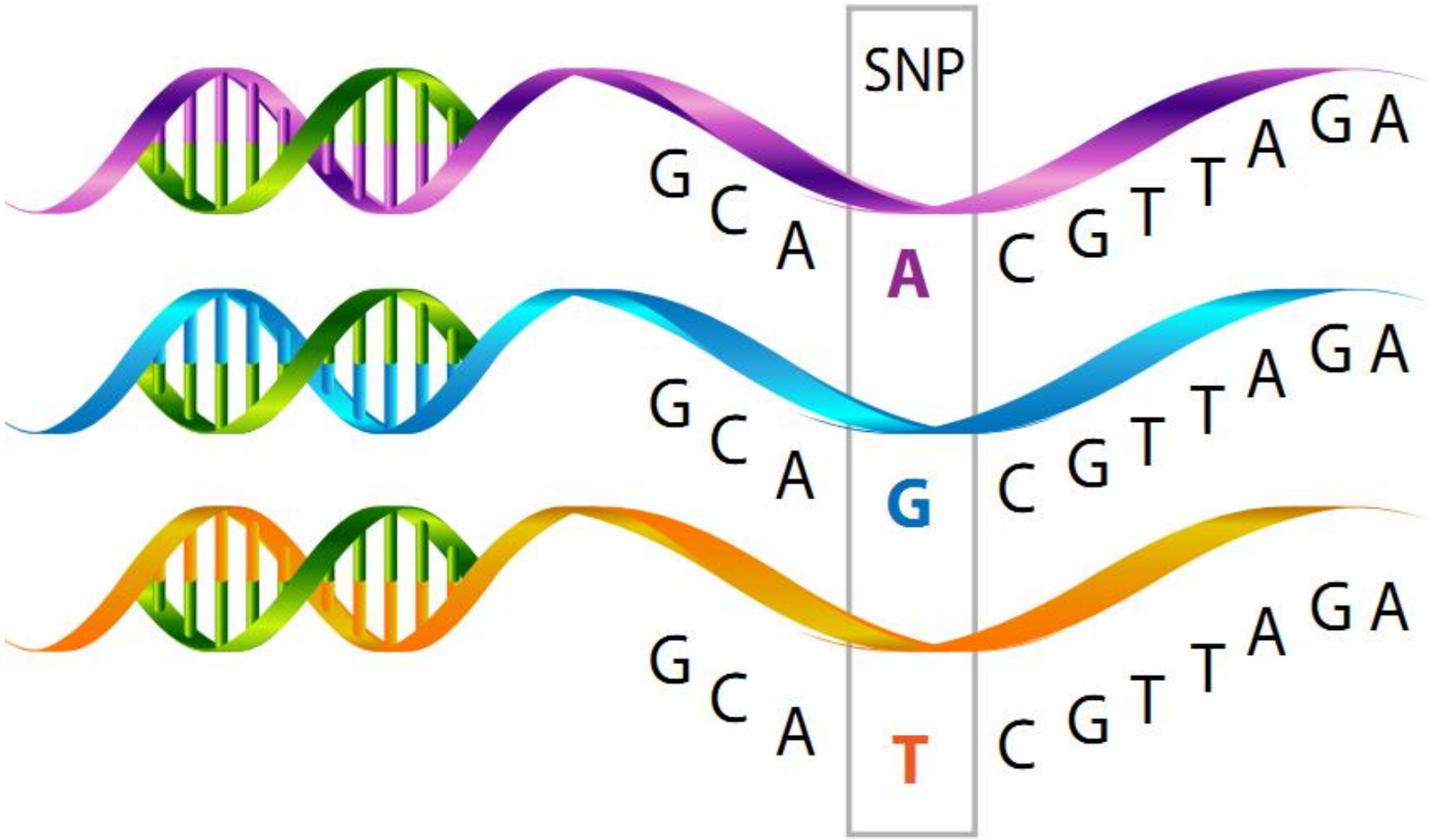
2. **Autogamous**

$$\begin{aligned} f_{BB} &:= p^2 + 1/2 \cdot p \cdot q \\ f_{Bb} &:= 2 \cdot p \cdot q - 1/2^* \cdot 2 \cdot p \cdot q \\ f_{bb} &:= q^2 + 1/2 \cdot p \cdot q \end{aligned}$$

3. **Mixed type**...taking $^*1/2 = I$ or Wright's Equilibrium

$$\begin{aligned} f_{BB} &:= p^2 + I \cdot p \cdot q \\ f_{Bb} &:= 2 \cdot p \cdot q - I \cdot 2 \cdot p \cdot q \\ f_{bb} &:= q^2 + I \cdot p \cdot q \end{aligned}$$

Genetic Markers ...



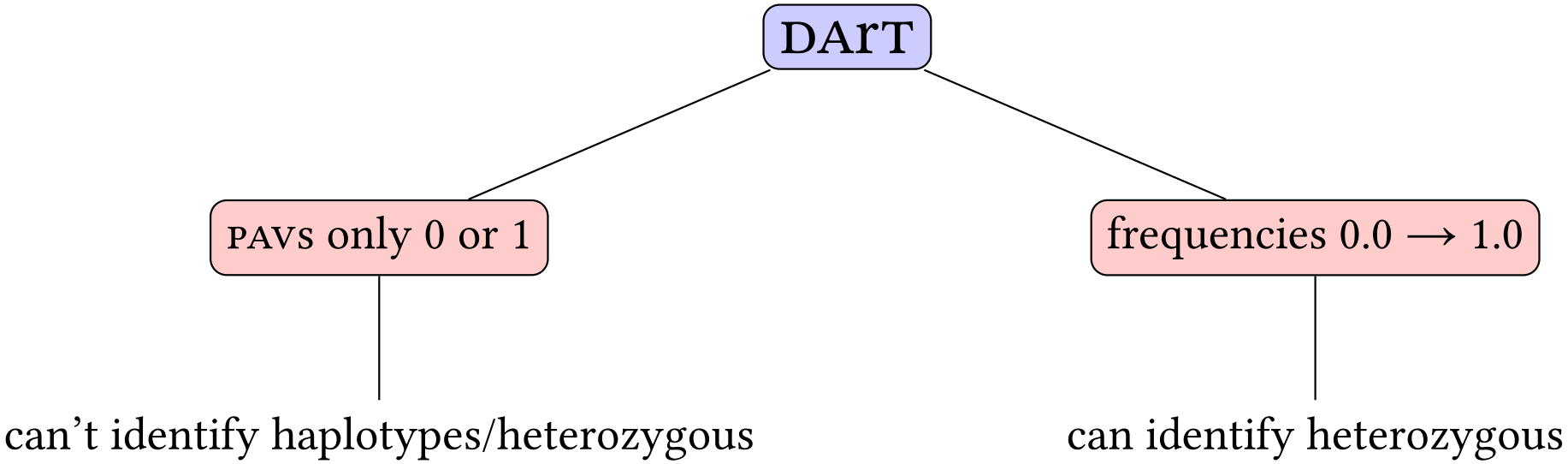
Examples

Marker	Amount	Expression	Polymorphic degree	Specific by locus
Isoenzyme	< 100	codominant	low	✓
RFLP	∞	codominant	medium	✓
RAPD	∞	dominant	medium	–
SSR	∞	codominant	very high	✓
SCAR	∞*	both	low	✓
AFLP	∞	dominant	high	–
SNP	∞	codominant	very high	✓
DArT	∞	both	very high	✓**

* After the deployment of other kind of markers.

** Clone aren't but markers are.

DArT flexibility...



Maize Bulks w/ frequencies

Marker	Allele	Bulks					
		1	2	3	4	⋯	g
1	1	0.67	*NA**	0.57	*NA*	⋯	0.36
1	2	0.33	*NA*	0.43	*NA*	⋯	0.64
2	1	*NA*	1.00	1.00	1.00	⋯	1.00
2	2	*NA*	0.00	0.00	0.00	⋯	0.00
⋮	⋮	⋮	⋮	⋮	⋮	⋱	⋮
m	1	0.00	*NA*	1.00	0.00	⋯	1.00
m	2	1.00	*NA*	0.00	1.00	⋯	0.00

* *NA* means *Not Available* or missing.

Frequencies, so:

$$p + q = 0.67 + 0.33 = 1.00$$

Maize Genotypes w/ *PAV* – (presence/absence)

Marker	Allele	Bulks					
		1	2	3	4	⋯	g
1	1	1	*NA*	1	*NA*	⋯	1
2	1	*NA*	1	1	1	⋯	1
⋮	⋮	⋮	⋮	⋮	⋮	⋱	⋮
m	1	1	*NA*	1	1	⋯	1

* *NA* means *Not Available* or missing.

Allele is always 1…the reference allele.

When Genotypes belong to the same bulk, the summary of their *PAV* generates frequencies

Genetic Distances ...

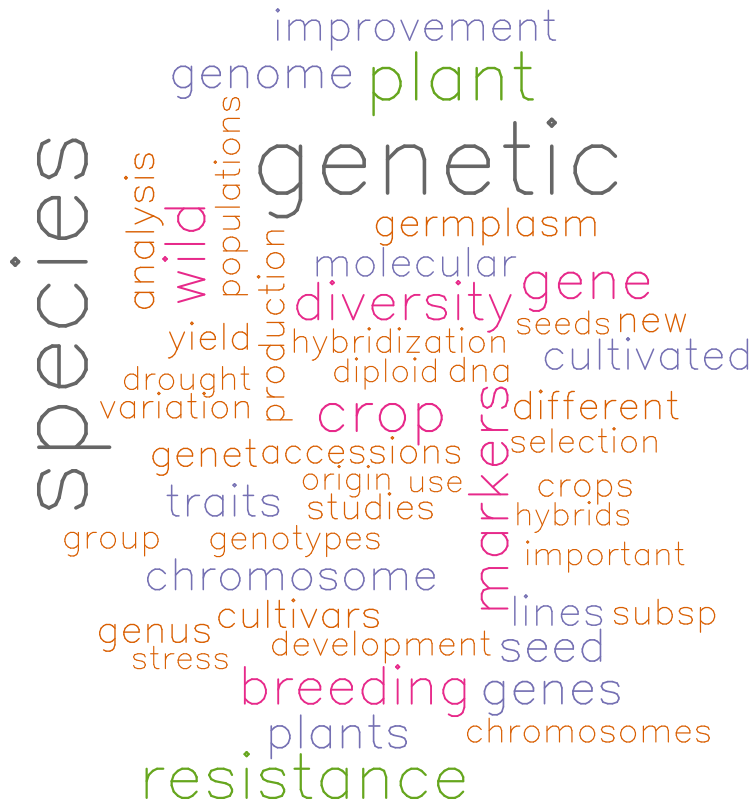
Genetic Distances

Markers w/ allelic information

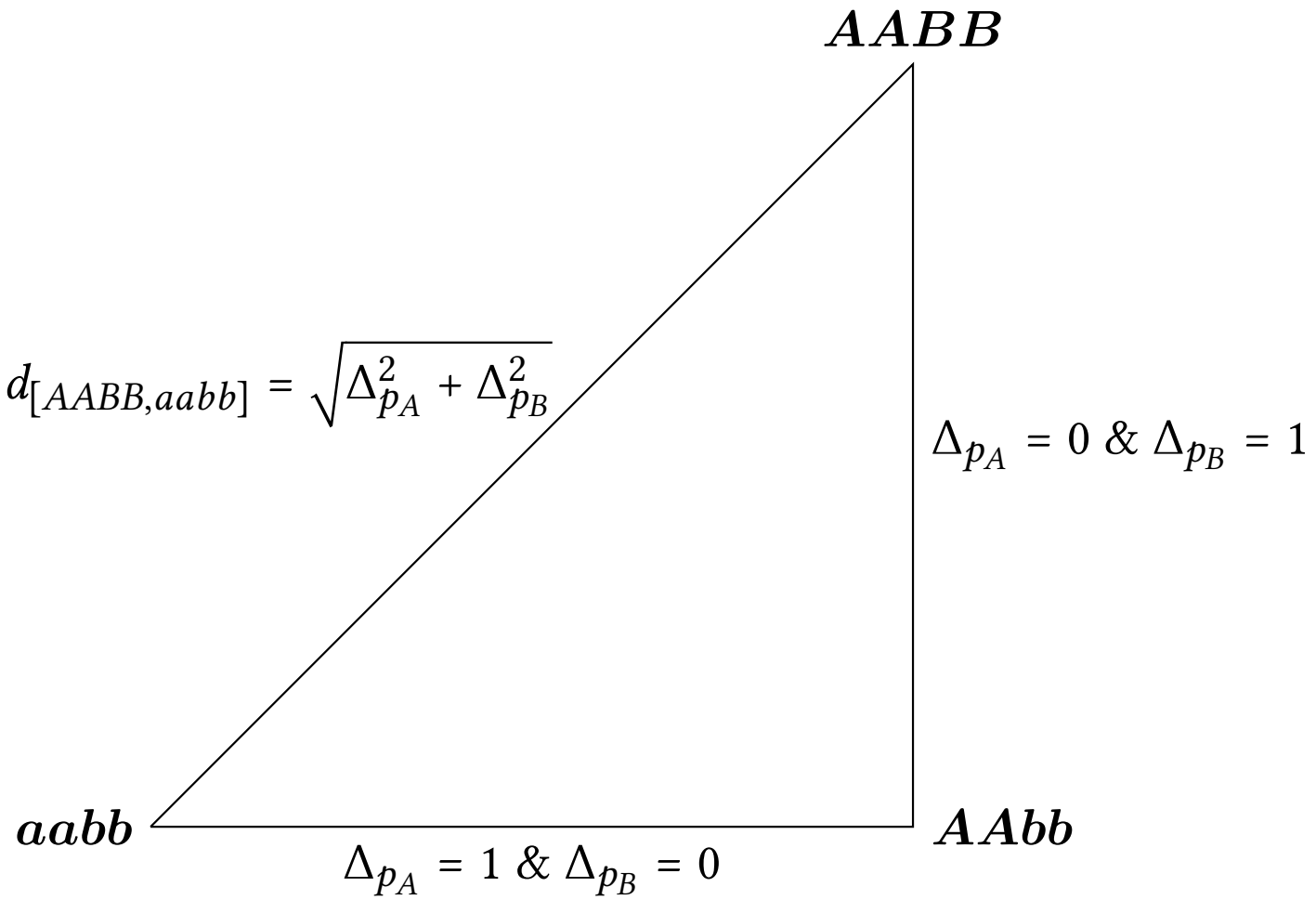
For example: SSR, SNP and DArT.

- **Euclidean**;
- **Modified Rogers**; and
- **Cavalli-Sforza & Edwards**.

References: [1, 2, 3]



Euclidean Distance ...



So, . . . :

$$Ed_{[x,y]} = \sqrt{\sum_{l}^{L}\sum_{a}^{A}(\hat{p}_{x\,la} - \hat{p}_{y\,la})^2} \;, \left(0.0 \leq Ed_{[x,y]} \leq \sqrt{2L}^{*}\right)$$

where:
$\hat{p}_{x\,la}$ is the allele frequency for allele a at *locus* l in the genotypes x;
$\hat{p}_{y\,la}$ is the same as above for genotype y;
L is the number of *locus*; and
A is the number of alleles at *locus* l.

*This is the estimator and its respective domain as shown by [3].

Roger's Distance ...

$$Rd_{[x,y]} = \frac{1}{L}\sum_{l}^{L}\sqrt{\frac{1}{2}\sum_{a}^{A}(\hat{p}_{x\,la} - \hat{p}_{y\,la})^2}\ , \left(0.0 \leq Rd_{[x,y]} \leq 1.0\right)$$

where:
$\hat{p}_{x\,la}$ is the allele frequency for allele a at *locus* l in the genotypes x;
$\hat{p}_{y\,la}$ is the same as above for genotype y;
L is the number of *locus*; and
A is the number of alleles at *locus* l.

It hasn't relationship with Euclidean Geometry. So, ...

Modified Roger's Distance ...

$$MRd_{[x,y]} = \frac{1}{\sqrt{2L}}\sqrt{\sum_{l}^{L}\sum_{a}^{A}(\hat{p}_{x\,la} - \hat{p}_{y\,la})^2}\ , \left(0.0 \leq MRd_{[x,y]} \leq 1.0\right)$$

where:
$\hat{p}_{x\,la}$ is the allele frequency for allele a at *locus* l in the genotypes x;
$\hat{p}_{y\,la}$ is the same as above for genotype y;
L is the number of *locus*; and
A is the number of alleles at *locus* l.

For non-diploid species, replace $2L$ by the number of copies.

Cavalli-Sforza & Edwards ...

$$Cd_{[x,y]} = \sqrt{\frac{1}{L}\sum_{l}^{L}\left(1 - \sum_{a}^{A}\sqrt{\hat{p}_{x\,la} \times \hat{p}_{y\,la}}\right)}\ , \left(0.0 \leq Cd_{[x,y]} \leq 1.0\right)$$

where:
$\hat{p}_{x\,la}$ is the allele frequency for allele a at *locus* l in the genotypes x;
$\hat{p}_{y\,la}$ is the same as above for genotype y;
L is the number of *locus*; and
A is the number of alleles at *locus* l.

Means, Variances and Standard Errors ...

$d_{[x,y]}$ is the distance between genotypes x and y, thus:

- **Mean:** $\mu_{d_{[x,y]}} = \frac{1}{\frac{A(A-1)}{2}} \sum_{x<y} d_{[x,y]}$;
- **Variance:** $\sigma^2_{d_{x,y}} = \frac{1}{\frac{A(A-1)}{2}-1} \sum_{x<y} \left(d_{[x,y]} - \mu_{d_{[x,y]}} \right)^2$; and
- **Standard Error:** $S_{\bar{d}_{[x,y]}} = \sqrt{\frac{\sigma^2_{d_{[x,y]}}}{\frac{A(A-1)}{2}}}$.

$\frac{A(A-1)}{2}$ is the 2×2 combination of the alleles i.e., pairs in the distances estimators

Markers w/o Allelic Information ...

		Genotype x	
		1	0
Genotype y	1	a	b
	0	c	d

- **Simple Matching:** $d_{[x,y]} = \frac{b+c}{a+b+c+d}$;
- **Jaccard:** $d_{[x,y]} = \frac{b+c}{a+b+c}$; and
- **Nei and Li (or Dice):** $d_{[x,y]} = \frac{2(b+c)}{2a+b+c}$.

The same references for the previous cases i.e., [1, 2, 3].

Diversity Indices ...

A locus is polymorphic if, and only if, its allele frequency is ≤ 0.95 or 0.99

Raw ...

- **Polymorphic proportion:**

$$P = \frac{n_{poly}}{n_{total}}$$

- **Mean allele number by locus:**

$$n_a = \frac{1}{L} \sum_{l}^{L} n_l$$

Applied ...

- **Observed Heterozygosity** (Ho);
- **Expected Heterozygosity** (He);
- **Effective Number of Alleles** (Ae); and
- **Shannon Index** (SH).

Observed Heterozygosity:

It is defined as the percentage of heterozygous loci per individual or the number of heterozygous individuals per locus.

Expected Heterozygosity:

$$He = \frac{1}{L}\sum_{l}^{L}\left(1 - \sum_{a}^{A}\hat{p}_{la}^{2}\right) \quad ,(0.0 \leq He \leq 1.0)$$

where:
$\hat{p}_{la}$ is the estimated frequency of the allele a at locus l; and
the other quantities (L and A) were already defined.

NOTE:

$$\sum_{a}^{A}\hat{p}_{la} = 1.0$$

Effective Number of Alleles:

$$Ae_l = \frac{1}{\sum_a^A \hat{p}_a^2}$$

$$Ae = \frac{1}{L} \sum_l^L Ae_l$$

NOTE:

$$Ae_l = \frac{1}{1-He_l}$$

Shannon Index:

- Total Frequencies:

$$SH_{\text{Total}} = -\sum_{a}^{A} \hat{p}_a \log_{10}\left(\hat{p}_a\right) \ , \sum_{a}^{A} \hat{p}_a = 1.0$$

- By Locus Frequencies:

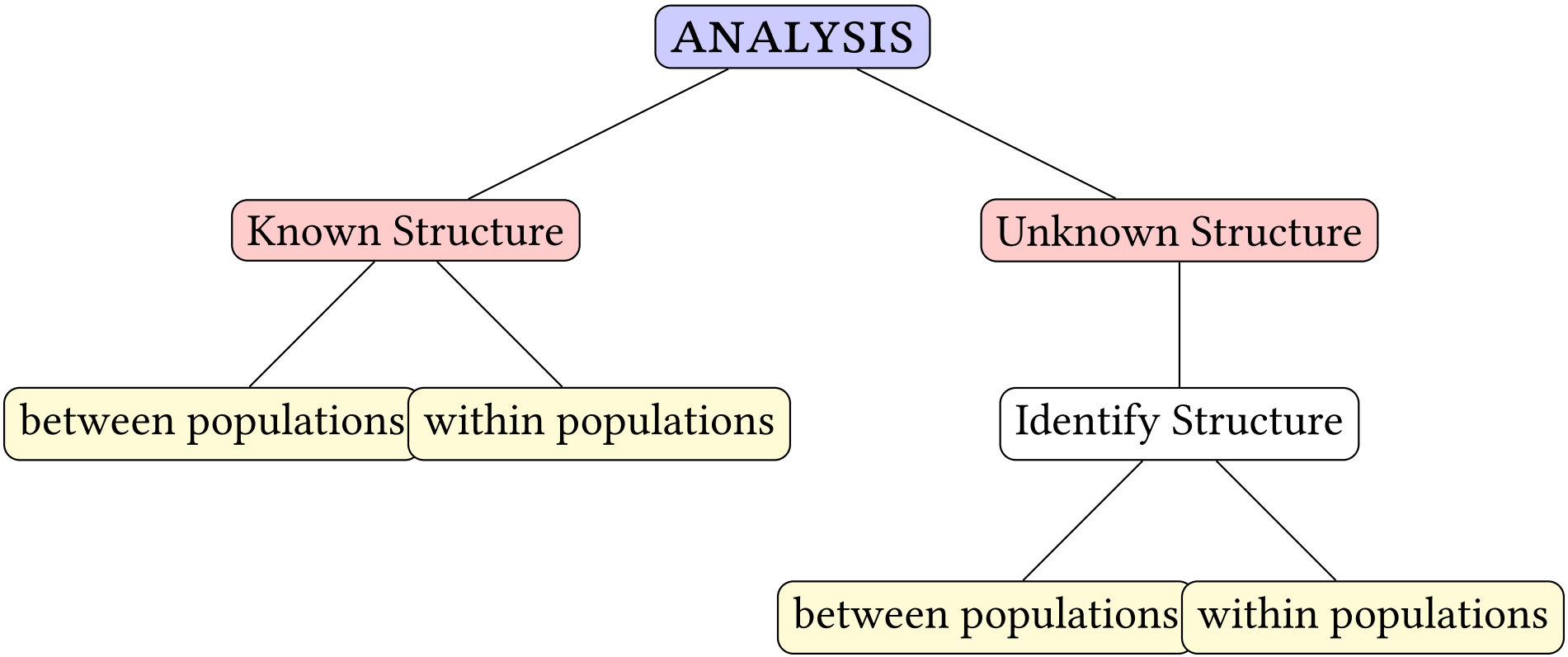
$$SH_{\text{Locus}} = -\sum_{a}^{A} \hat{p}_a \log_{2}\left(\hat{p}_a\right) \ , \sum_{a}^{A} \hat{p}_a = L \therefore \left(0.0 \leq SH_{\text{Locus}} \leq L\right)$$

Diversity Indices for PAVs

Statistics . . . :

- **Polymorphic proportion** ⊘
- **Mean number of alleles by locus** ⊘
- **Observed Heterozygosity** (Ho) ⊘
- **Expected Heterozygosity** (He) ⊘
- **Effective Number of Alleles** (Ae) ⊘
- **Shannon Index** (SH) ⊘

Intraspecific Diversity ...



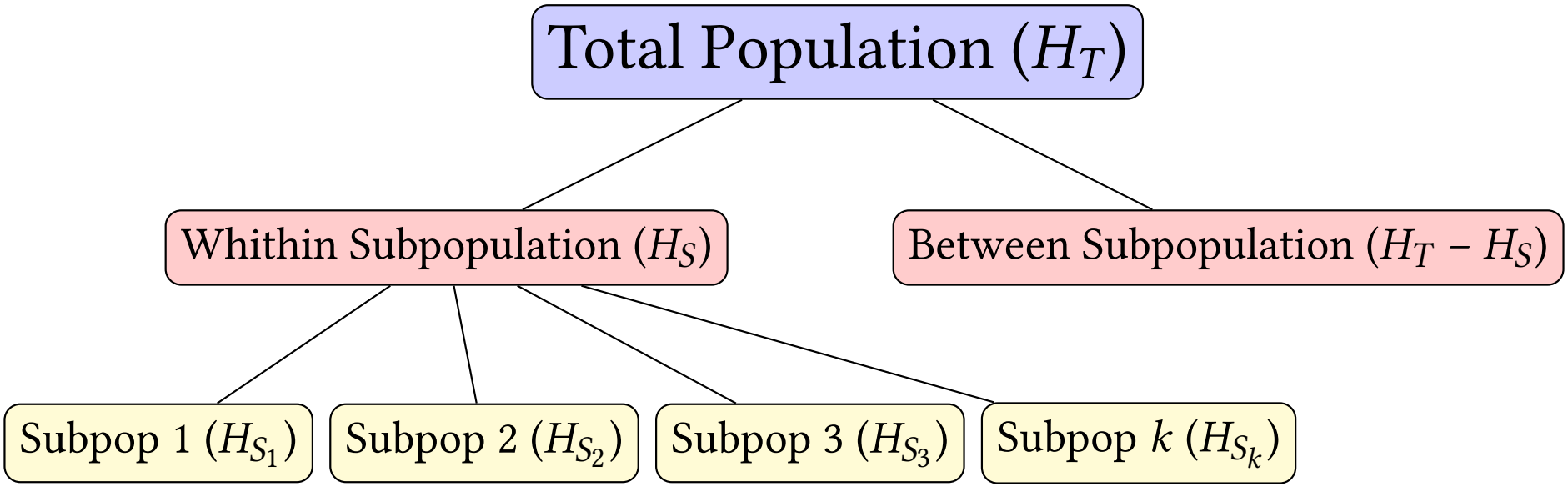
ANOVA & CR Designs ...

	D.F.	M.S.
Between	$T - 1$	"variance between means"
Within	$T \times (R - 1)$	"mean of within variances"
Total	$T \times R - 1$	

Recapping ...

Parameter	Estimator
Population (by locus)	$He_l(H_{T_l}) = 1 - \sum_a^2 \hat{p}_{a_l}^2$
Population (average)	$He(H_T) = \frac{1}{L} \sum_l^L He_l$
Subpopulation$_i$ (by locus)	$He_{i_l} = 1 - \sum_a^2 \hat{p}_{i_{a_l}}^2$
Subpopulation$_i$ (average)	$He_i = \frac{1}{L} \sum_l^L He_{i_l}$
Within Subpopulation	$H_S = \frac{1}{I} \sum_i^I He_i$
Between Subpopulation	$D_{ST} = H_T - H_S$

Total = Between + Within



Wright Statistics (F) ...

F_{IS} Heterozygosis proportional deviations within subpopulations:

$$F_{IS} = \frac{H_S - Ho}{H_S} \; [-1; 1]$$

F_{IT} Overall heterozygosis proportional deviation (inbreeding coefficient):

$$F_{IT} = \frac{H_T - Ho}{H_T} \; [-1, 1]$$

F_{ST} Heterozygosis proportional deviation between subpopulations:

$$F_{ST} = \frac{H_T - H_S}{H_T} \; [0; 1]$$

Nei, 1987 [4] ...:

1. Obtain H_T:

$$H_T = \frac{1}{L} \sum_{l}^{L} He_l$$

2. Obtain H_s (by locus):

$$H_S = \frac{1}{L} \sum_{l}^{L} He_{S_l}$$

3. Thus, obtain G_{ST}:

$$G_{ST} = \frac{D_{ST}}{HT} = \frac{H_T - H_S}{H_T} = 1 - \frac{H_S}{H_T}$$

Berg, 1997 [1] . . . :

1. Obtain G_{ST} by locus:

$$G_{ST} = \frac{D_{ST}}{HT} = \frac{H_T - H_S}{H_T} = 1 - \frac{H_S}{H_T}$$

2. Summarize as average:

$$\bar{G}_{ST} = \frac{1}{n_a} \sum_{n}^{n_a} G_{ST_n}$$

3. That is the same as:

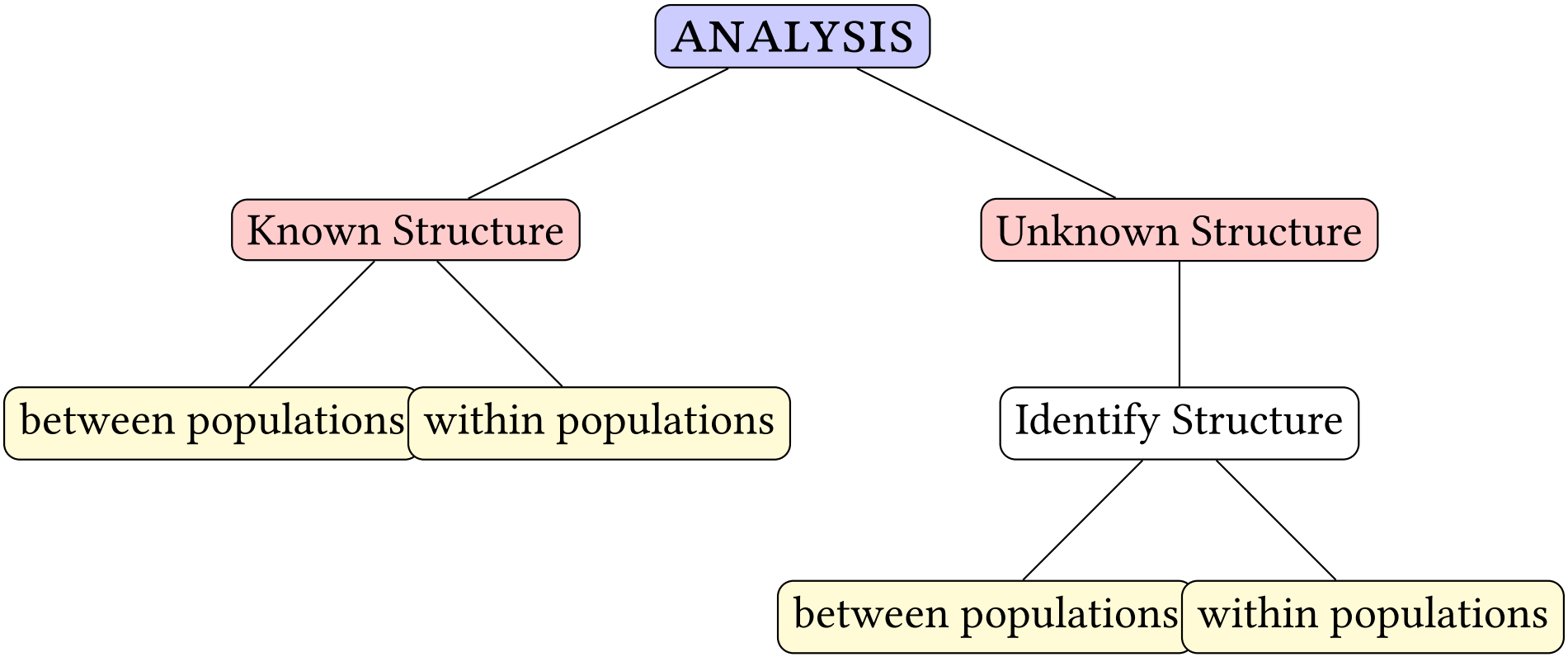
$$\bar{G}_{ST} = 1 - \frac{\sum_{n}^{n_a} \left(\frac{H_{S_n}}{H_{T_n}} \right)}{n_a}$$

Be aware ...

- When we have just one (1) allele: $G_{ST} = F_{ST}$;
- G_{ST} generalizes F_{ST};
- G_{ST} is the proportion of total diversity that is between subpopulations; and
- Thus, $(1 - G_{ST})$ is the proportion of total diversity within subpopulations.
- The meaning of diversity according to F_{ST}:

F_{ST}	means
$[0; 0.05)$	small
$[0.05; 0.15)$	medium
$[0.15; 0.25)$	high
≥ 0.25	very high

...Intraspecific Diversity (*2nd branch*)



Clusters & Groups ...

OBJECTIVE:

Minimize within variability $\longrightarrow$ Maximize between variability

References can be consulted for deep understanding:

- Fundation book ... [5];
- Fundation paper in genetics (Nei) ... [4]; and
- More modern reference ... [6].

$$\boldsymbol{Y}_{n\times p} = \begin{bmatrix} y_{1,1} & y_{1,2} & y_{1,3} & \cdots & y_{1,p} \\ y_{2,1} & y_{2,2} & y_{2,3} & \cdots & y_{2,p} \\ y_{3,1} & y_{3,2} & y_{3,3} & \cdots & y_{3,p} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ y_{n,1} & y_{n,2} & y_{n,3} & \cdots & y_{n,p} \end{bmatrix}$$

Note:

Everything starts from obtaining the distance matrix between all 2×2 pairs ...

$$\frac{n(n-1)}{2}$$

$$\boldsymbol{D} = \begin{bmatrix} 0 & d_{1,2} & d_{1,3} & \cdots & d_{1,j} & \cdots & d_{1,n} \\ & 0 & d_{2,3} & \cdots & d_{2,j} & \cdots & d_{2,n} \\ & & 0 & \cdots & d_{3,j} & \cdots & d_{3,n} \\ & & & \ddots & \vdots & & \vdots \\ & & & & 0 & \cdots & d_{j,n} \\ & & & & & \ddots & \vdots \\ & & & & & & 0 \end{bmatrix}$$

$d_{i,i} = 0.0$ and D is symmetric $\therefore d_{i,j} = d_{j,i}$

Clustering Methods

- **Geometrical:**
  - Hierarchical;
  - Neighbor Joining;
  - *k-means* (density search); and others
- **MANOVA:**

$$\text{Total} = \text{Between} + \text{Within}$$

- **Statistical:**

  Mixture and Bayesian (STRUCTURE)

Hierarchical:

1. All distances;
2. Find the most close individuals (smaller distance); and
3. Iterate over that.
    - UPGMA: merge groups with smaller distance;
    - WARD: merge groups that generate a new one with smaller $S.S._W$; and
    - NJ: merge groups if: (*i*) smaller distance & (*ii*) higher distances in comparison to the others.

Bayesian:

The model account for the presence of HW or LD, introduces population structure...find population structure (groups) with the smaller possible disequilibrium [6].

Multidimensional Scaling ...

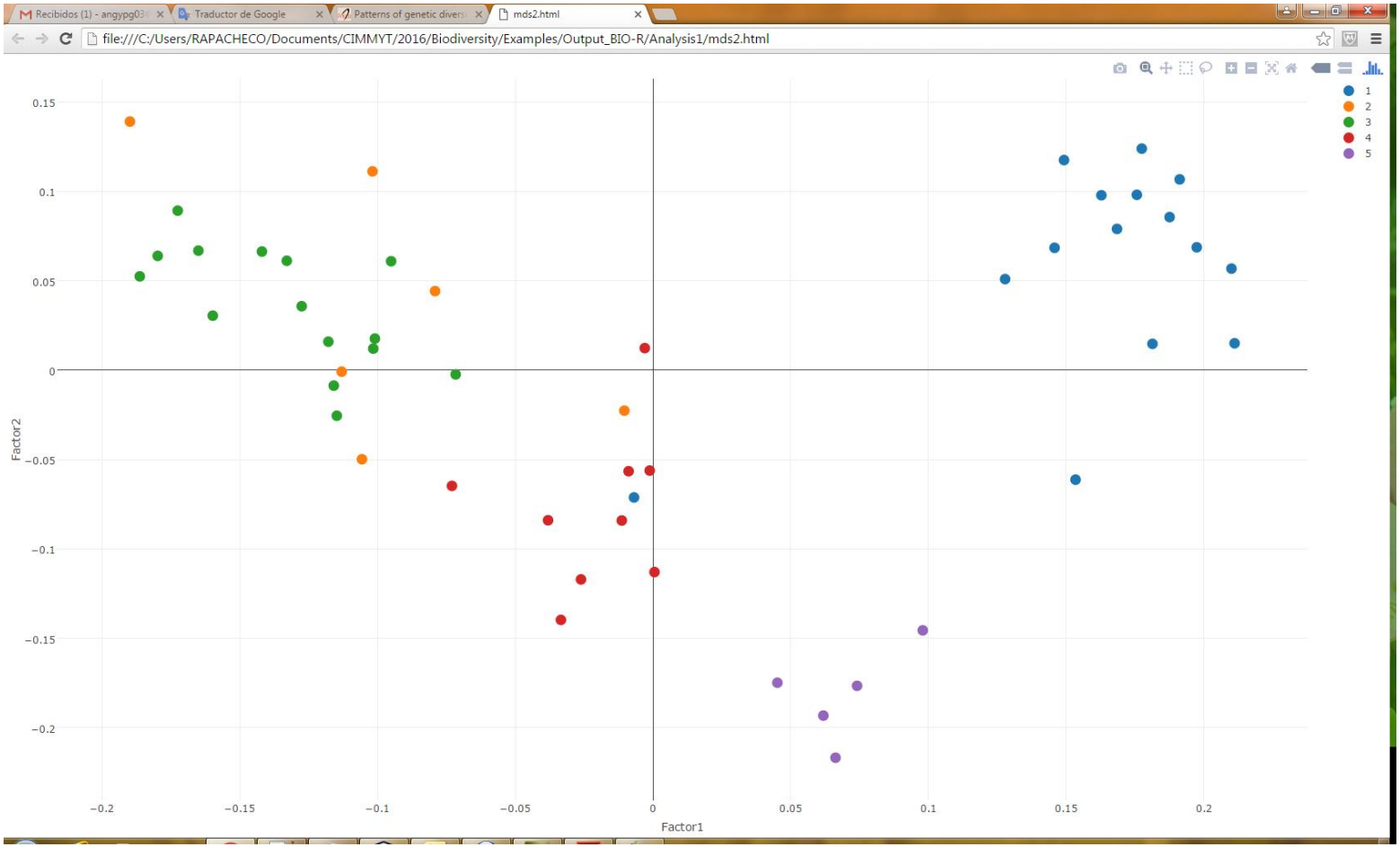
Two concepts:

1. **Similarity** ($s_{[x,y]}$): $d_{[x,y]} = \sqrt{2 \times \left(1 - s_{[x,y]}\right)}$;

2. ***stress*** (S): $S = \sqrt{\frac{\sum_x \sum_y \left(d_{[x,y]} - \mu_{d_{[x,y]}}\right)^2}{\frac{n(n-1)}{2}}}$

NOTE:

Search for the reduced representation (2 or 3 dimensions) that minimizes the $S.S._B$ in the p dimensional space and with minimum the estimated distance.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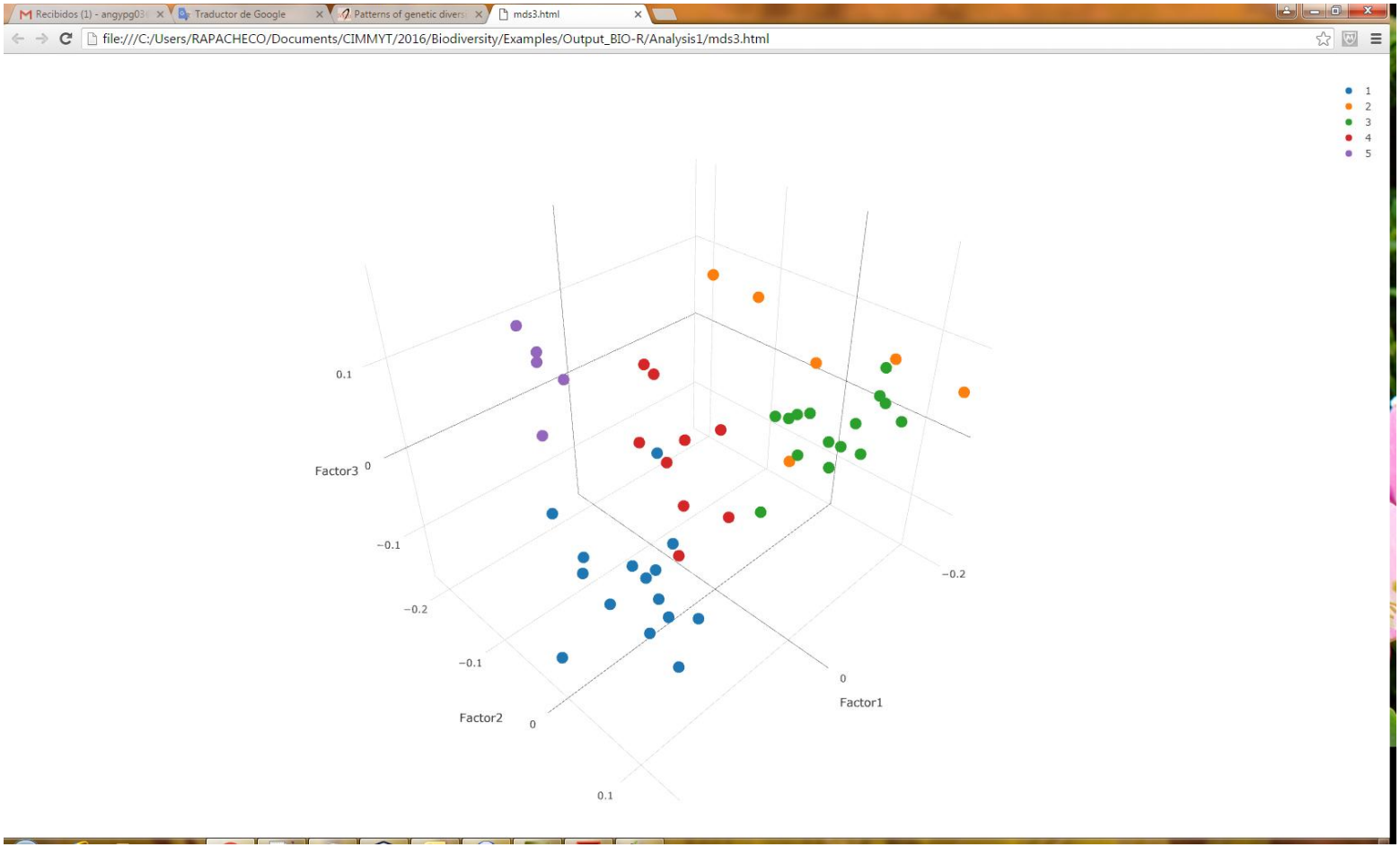
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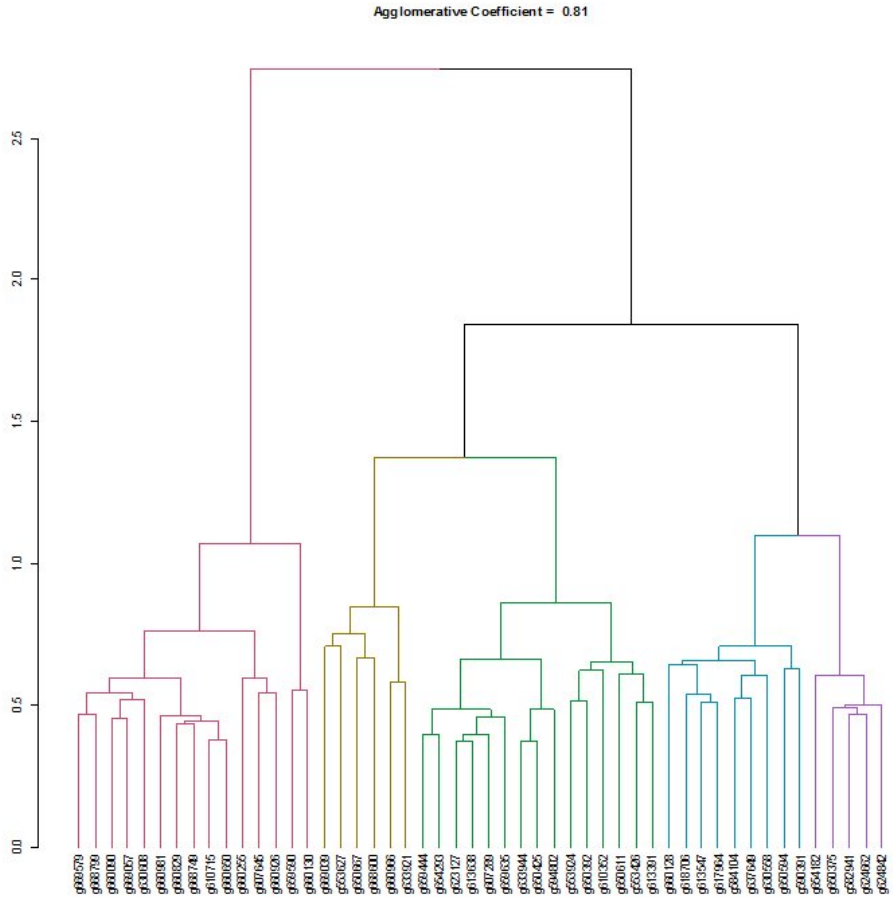
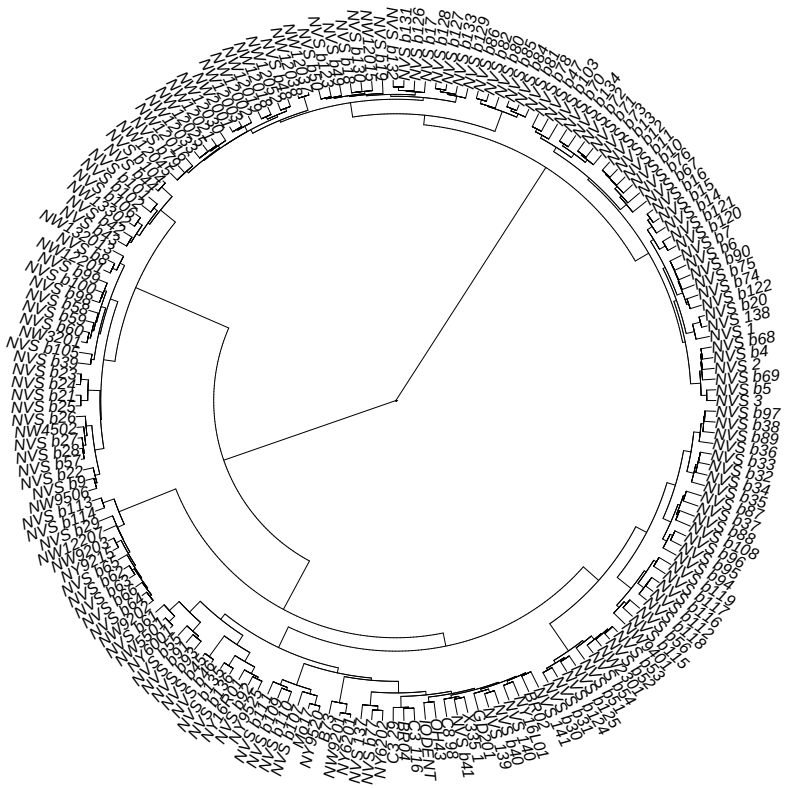
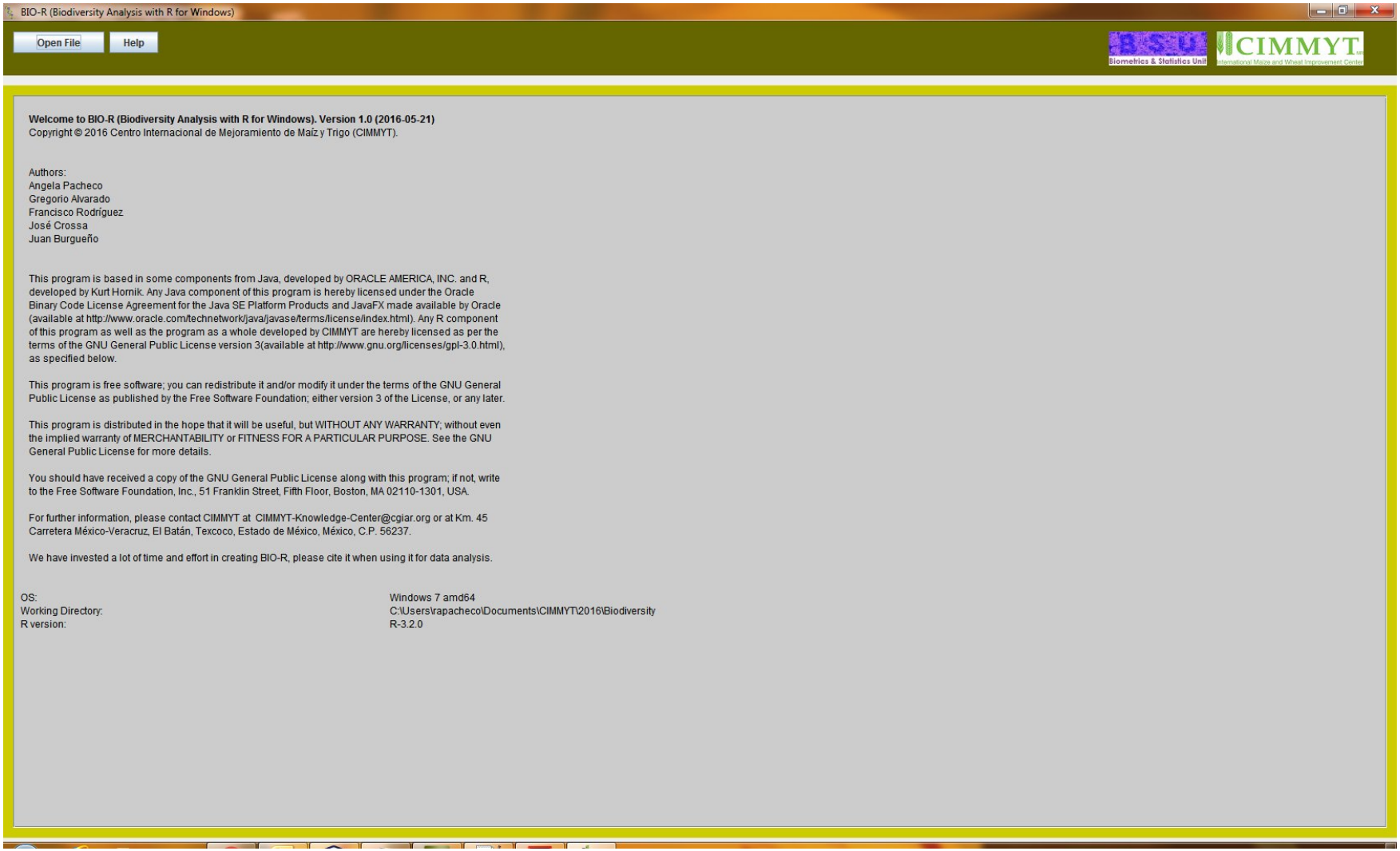
Dendograms ...





BIO-R Tutorial

- **Phenotypic data**
  - *Experimental Design:* ADEL, AUDE & STAD;
  - *Individual & Multi-Env:* META (> 1500), AGD (> 1300);
  - *Interaction/Stability:* GEA (> 1800); and
  - *Spatial Analysis:* SPAT.
- **Genotypic data**
  - *kinship:* BROWSE & COP; and
  - *Diversity:* BIO.
- **Fusion data**
  - *Relationship/Interaction:* GEA;
  - *Genome prediction:* BGLR (*R package & application tool); and
  - *Selection Index:* SI (> 300), RINDSEL.
- **Decision:** *Eval L × T*.


BIO-R (Biodiversity Analysis with R for Windows)
Open File
Help
Biometrics & Statistics Unit
CIMMYT
International Maize and Wheat Improvement Center
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For further information, please contact CIMMYT at CIMMYT-Knowledge-Center@cgiar.org or at Km. 45 Carretera México-Veracruz, El Batán, Texcoco, Estado de México, México, C.P. 56237.
We have invested a lot of time and effort in creating BIO-R, please cite it when using it for data analysis.
OS: Windows 7 amd64
Working Directory: C:\Users\rapacheco\Documents\CIMMYT\2016\Biodiversity
R version: R-3.2.0

Downloading and Installation

- BIO-R is already available **go to:** `http://data.cimmyt.org`;
- Java interface/application for embedding *R* [7] scripts to perform Diversity analysis; and
- heterozygosity, diversity B & W groups, shannon index, number of effective allele, % of polymorphic loci, Rogers & Nei distance, clusters and multidimensional scaling (2 & 3d plots).

CREDITS: BSU/CIMMYT

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CIMMYT
International Maize and Wheat Improvement Center

Research Software Repository

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BIO-R (BIODIVERSITY ANALYSIS WITH R FOR WINDOWS) VERSION 1.0

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hdl:11529/10820

Version: 2– Released: Tue Dec 06 09:03:26 CST 2016

CATALOGING INFORMATION | Data & Analysis | Comments | Versions

If you use these data, please add the following citation to your scholarly references. Why cite?

Data Citation

Pacheco, Ángela; Alvarado, Gregorio; Rodríguez, Francisco; Burgueño, Juan, 2016-12-06, "BIO-R (Biodiversity analysis with R for Windows) Version 1.0", http://hdl.handle.net/11529/10820 nternational Maize and Wheat Improvement Center [Distributor] V2 [Version]

Citation Format Print

Data Citation Details

Study Global ID	hdl:11529/10820
Other ID	CIMMYT: cimmytswdvn-0
Authors	Pacheco, Ángela (BSU - CIMMYT); Alvarado, Gregorio (BSU - CIMMYT); Rodríguez, Francisco (BSU - CIMMYT); Burgueño, Juan (BSU - CIMMYT)
Producer	International Maize and Wheat Improvement Center (CIMMYT) CIMMYT
Production Date	diciembre 06, 2016
Distributor	nternational Maize and Wheat Improvement Center (CIMMYT) CIMMYT
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Deposit Date	diciembre 06, 2016
Provenance	CIMMYT Research Software Dataverse

Getting Help & Manual

The Help button will provide you two options:

- **Manual:** `*.pdf` document descripting all options, methods and outputs.

- **About:** How to cite BIO-R and any associated license (GNU & Oracle)

Data Format – *MyData.csv*

mark	g1	g2	g3	g4	...	gX
1	0.67	NA	0.57	NA	...	1
2	NA	1	1	1	...	NA
3	1	1	0.52	0.50	...	0.80
4	1	NA	0.50	1	...	NA
5	1	NA	1	NA	...	1
6	0.67	0	0.71	1	...	0.33
7	1	NA	0	1	...	1
8	1	NA	1	1	...	1
9	NA	1	0.60	0.22	...	0.71
⋮	⋮	⋮	⋮	⋮	⋱	⋮
N	1	1	1	1	...	1

Setup ...

1. `Markers` – selects the column that identify the **markers**;
2. `# Clusters` – type the number of groups to split the population;
3. `Output folder` – type the path of the output folder where results will be saved;
    - It will be created inside the BIO-R's Output folder;
    - You can change the name for different sets; and
    - It is necessary to change the name for each analysis.
4. `Genotypes` – selects the columns that identify the **genotypes**;
5. `Distance` – selects the method to calculate **distances**; and
6. `ColorMDSPlot` ...*[CONT.]*

ColorMDSPlot

Specify a `*.csv` file containing additional information for colors in MDS plot

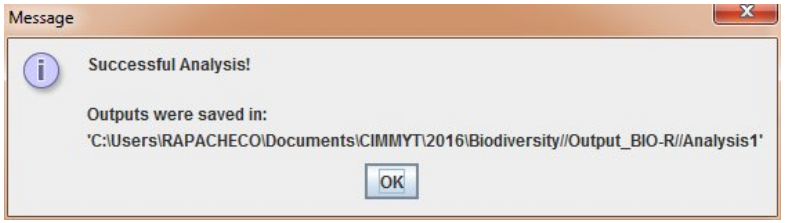
Collumn 1: the name of the genotypes – should be equal to the input data;

Collumn 2: the variable to identify the groups of different colours; and

Collumn 3: any additonal information.

Genotype	NumColor	Something
g669579	11	I
g669039	3	A
g659444	8	F
g660128	11	I
⋮	⋮	⋮
g660829	11	I

Outputs ...



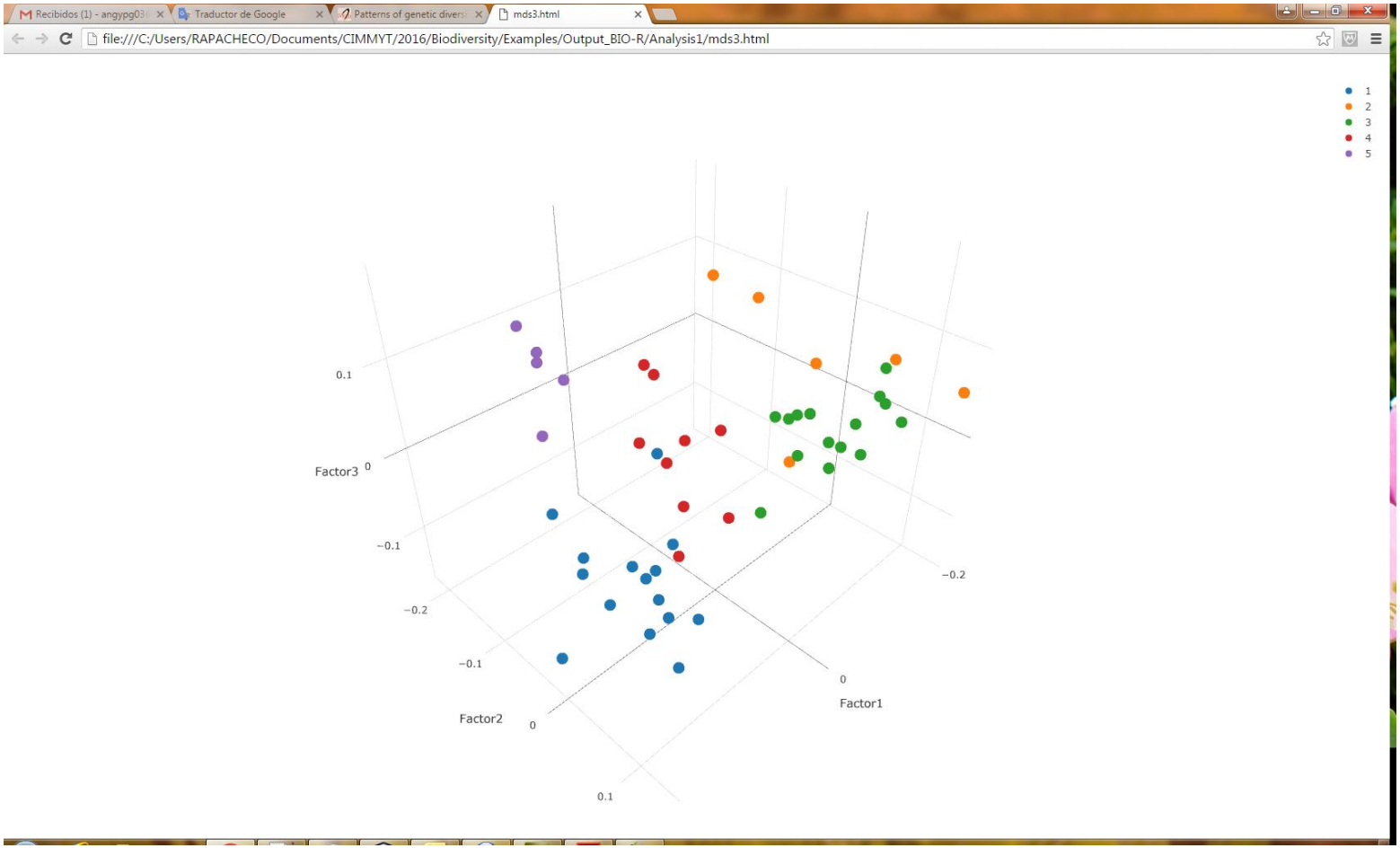
- Output
  - Analysis 1
    - CalculusPerGenotype.csv
    - CalculusPerLocus.csv
    - Dendogram.wmf
    - mds2.html
    - mds3.html
    - MDStable.csv
    - RogersDistances.csv
    - SummaryDiversityAnalysis.csv
    - mds2_files
    - mds3_files

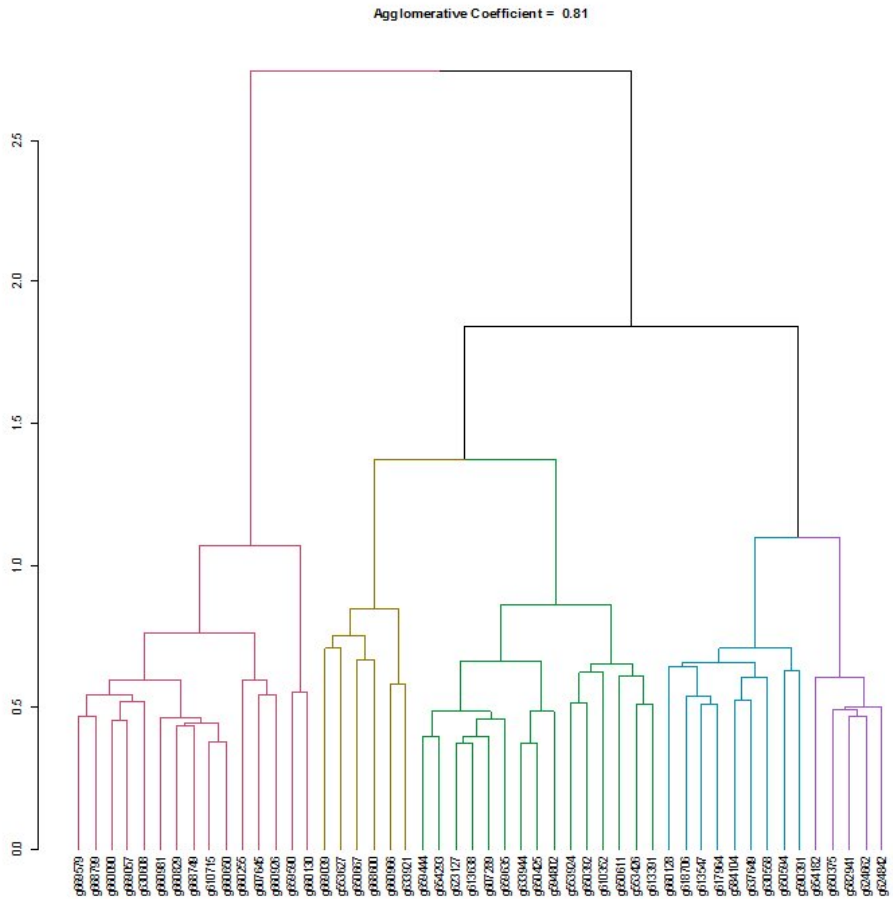
Output : `CalculusPerLocus.csv`

Marker	He	Ho	Ae	Shannon	%NA
1	0.50	0.29	1.99	0.95	0.22
2	0.01	-0.05	1.01	0.02	0.08
3	0.45	0.38	1.82	0.93	0.16
4	0.41	0.42	1.69	0.87	0.24
5	0.03	-0.08	1.03	0.11	0.10
6	0.40	0.43	1.68	0.86	0.20
7	0.50	0.31	2.00	0.99	0.24
8	0.49	0.47	1.94	0.98	0.18
9	0.45	0.47	1.82	0.93	0.14
⋮	⋮	⋮	⋮	⋮	⋮
N	0.08	-0.03	1.09	0.26	0.12

Output : `CalculusPerGenotype.csv`

Genotype	He	Ho	Ae	Shannon	%NA	clusterGroup
1	0.39	0.06	1.63	0.83	0.11	1
2	0.38	-1.46	1.62	0.82	0.37	2
3	0.40	0.51	1.67	0.85	0.03	3
4	0.39	0.03	1.64	0.83	0.19	4
5	0.37	0.39	1.60	0.81	0.03	3
6	0.41	-3.56	1.69	0.86	0.42	1
7	0.39	0.34	1.65	0.84	0.04	3
8	0.37	-0.28	1.54	0.81	0.24	5
9	0.40	-0.70	1.61	0.82	0.32	1
⋮	⋮	⋮	⋮	⋮	⋮	⋮
X	0.38	0.33	1.66	0.84	0.04	3


Recibidos (1) - angypg03
Traductor de Google
Patterns of genetic divers
mds3.html
file:///C:/Users/RAPACHECO/Documents/CIMMYT/2016/Biodiversity/Examples/Output_BIO-R/Analysis1/mds3.html
1
2
3
4
5
0.1
Factor3
0
−0.1
−0.2
−0.1
Factor2
0
0.1
0
Factor1
−0.2


Agglomerative Coefficient = 0.81
0.0
0.5
1.0
1.5
2.0
2.5

Summary : ***SummaryDiversitysAnalysis.csv***

- **% of polymorphic loci:** 0.94;
- **Exp. Heterozygosity:** 0.30;
- **Std. Dev. of** He**:** 0.01;
- **Obs. Heterozygosity:** 0.22;
- **Std. Dev. of** Ho**:** 0.01;
- **Number of effective alleles:** 1.55;
- **Std. Dev. of** Ae**:** 0.02;
- **Shannon Index:** 0.63;
- **Std. Dev. Shannon:** 0.02 ...

Remarks

- Frequency of Alleles & Genotypes;

  (Population Genetics) The fundamental concept!

- Distances & Diversity Indices;

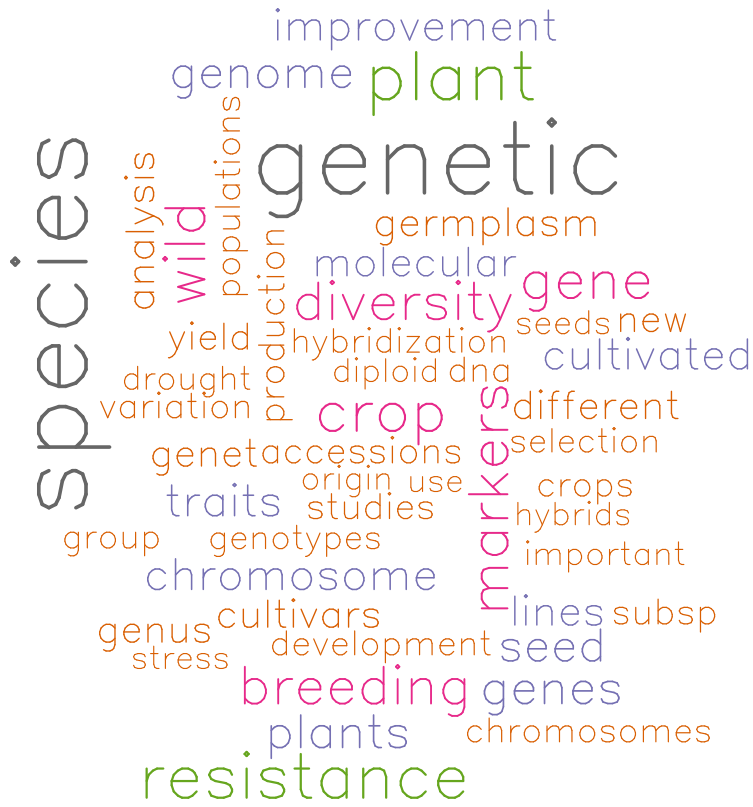
  (Genetic Diversity) Several ways and flavors.

- Wright Statistics;

  (Intraspecific Diversity) Between/Within variability

- BIO-R; and

  (Software) it has been built considering everything you may want



Questions/Suggestions??

For Further Studies:

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[5] KAUFMAN, L.; ROUSSEEUW, P. J. *Finding groups in data: an introduction to cluster analysis.* New York: John Wiley, 1990. 368 p.

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[7] R Core Team. *R: A Language and Environment for Statistical Computing*. Vienna, Austria, 2016. Disponível em: <https://www.R-project.org/>.