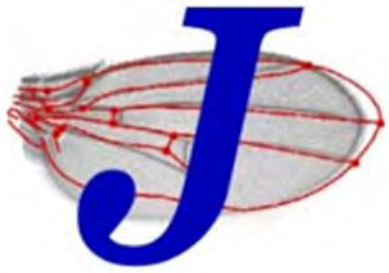
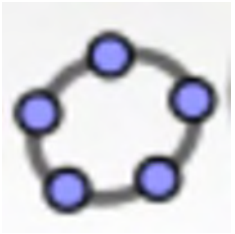
LABORATORIO DE ANATOMÍA ANIMAL

INGENIERIA INVERSA APLICADA A LA ANATOMÍA ANIMAL

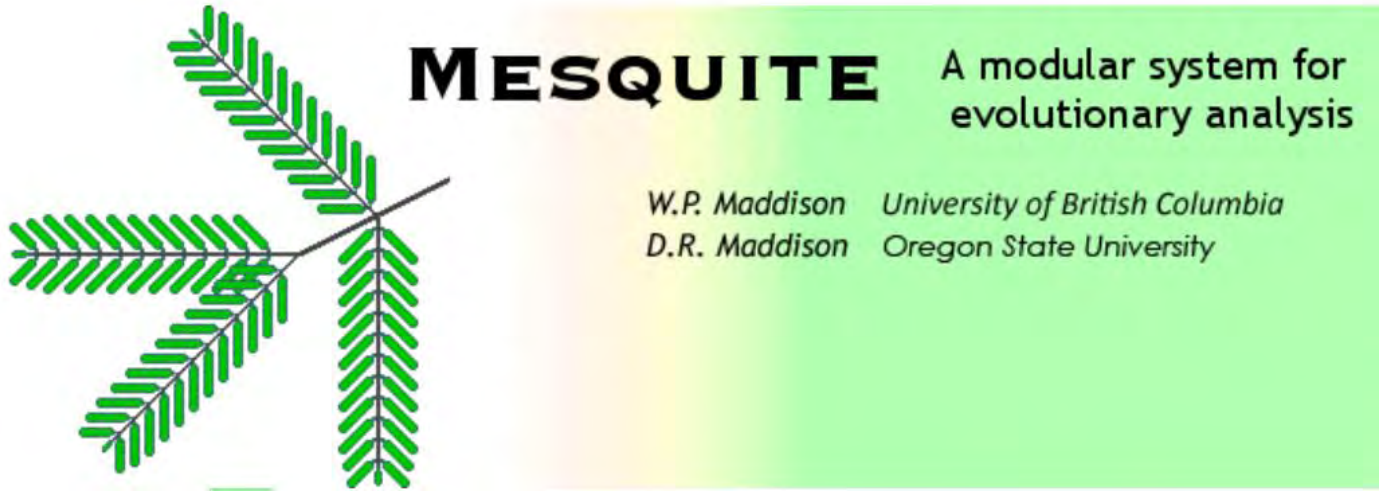
M O O C

9.-Filogenia

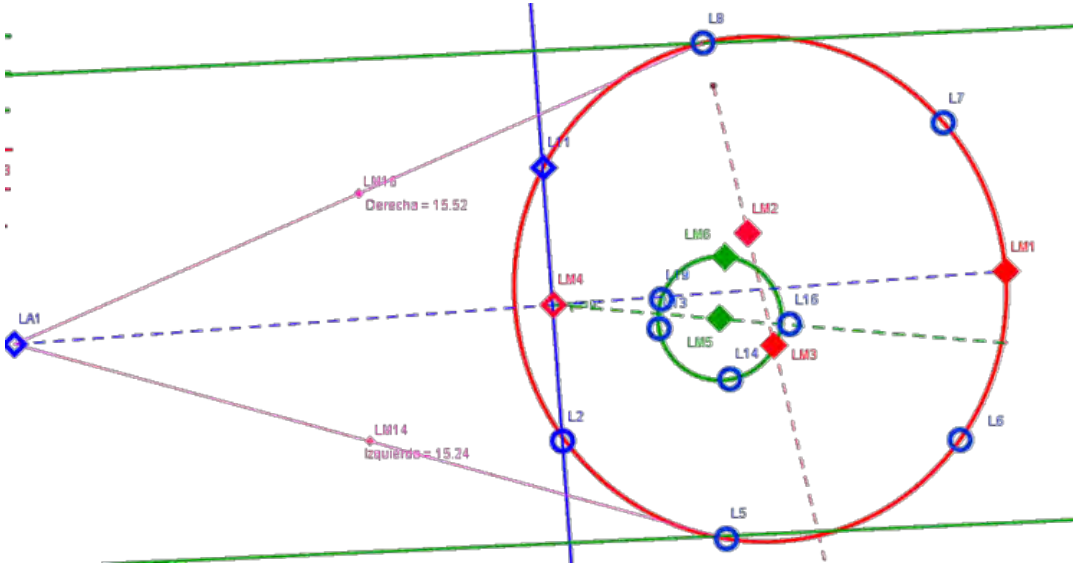


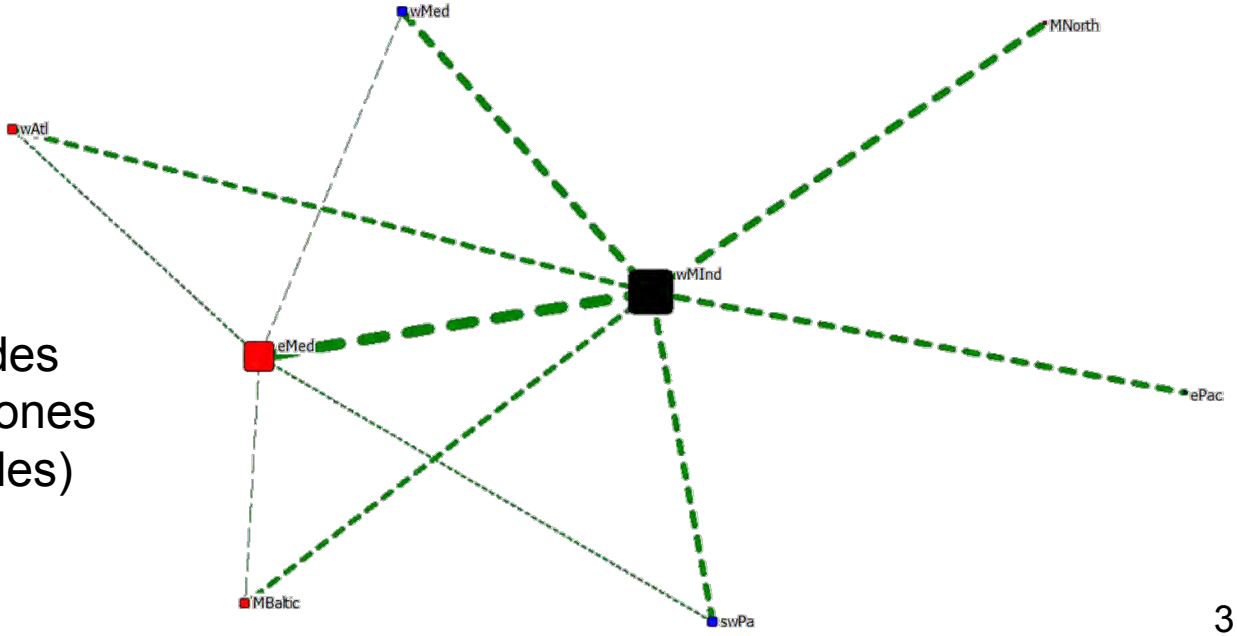


http://mesquiteproject.org/mesquite/mesquite.html



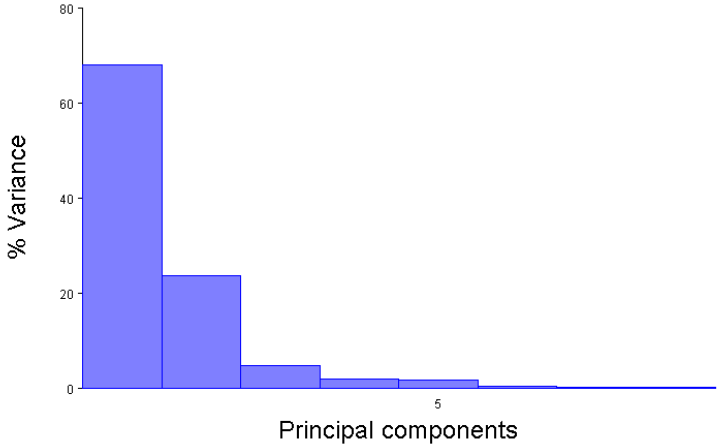
Landmarks matemáticos

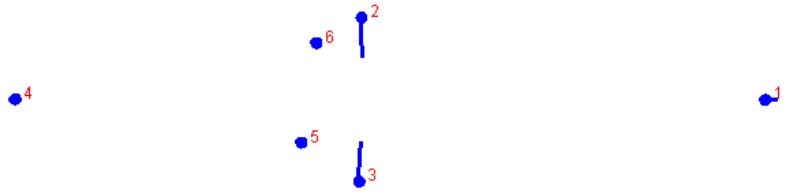




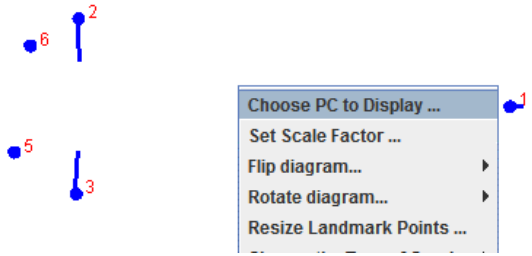
Los nodos mas grandes pertenecen a poblaciones mas aislados (ver redes)

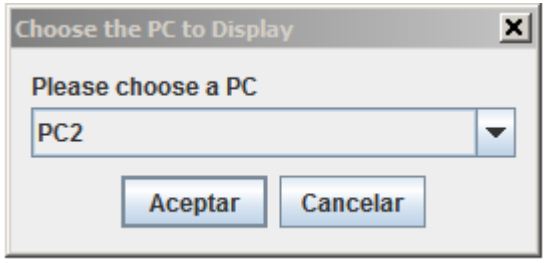

MorphoJ 1.02d
File Preliminaries Variation Covariation Comparison Genetics Help
Project Tree Results Graphics Reports
PCA: CovMatrix, New dorsal, Procrustes coordinates
PC shape changes Eigenvalues PC scores

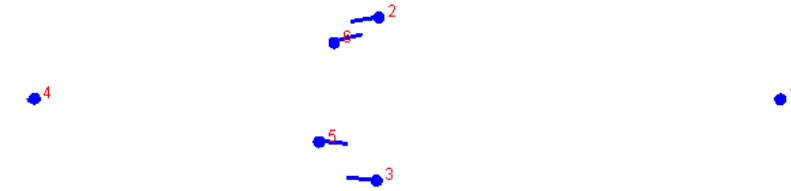

80
60
40
20
0
% Variance
5
Principal components


2
6
4
1
5
3

PC1


2
6
5
3
Choose PC to Display ...
Set Scale Factor ...
Flip diagram...
Rotate diagram...
Resize Landmark Points ...
1


Choose the PC to Display
Please choose a PC
PC2
Aceptar
Cancelar


2
6
4
1
5
3

PC2

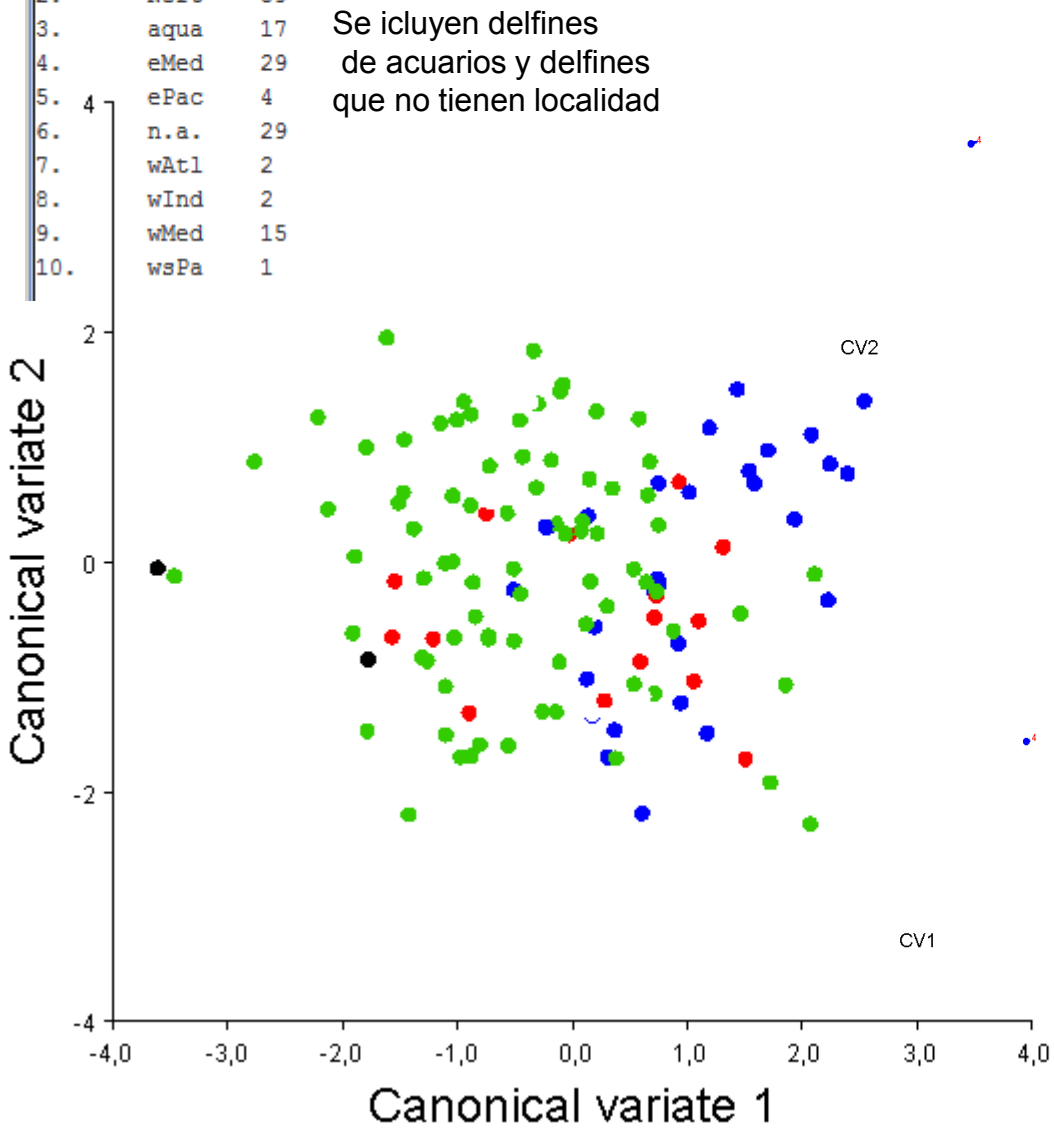
MorphoJ 1.02d

File Preliminaries Variation

Project Tree | Results | Gra

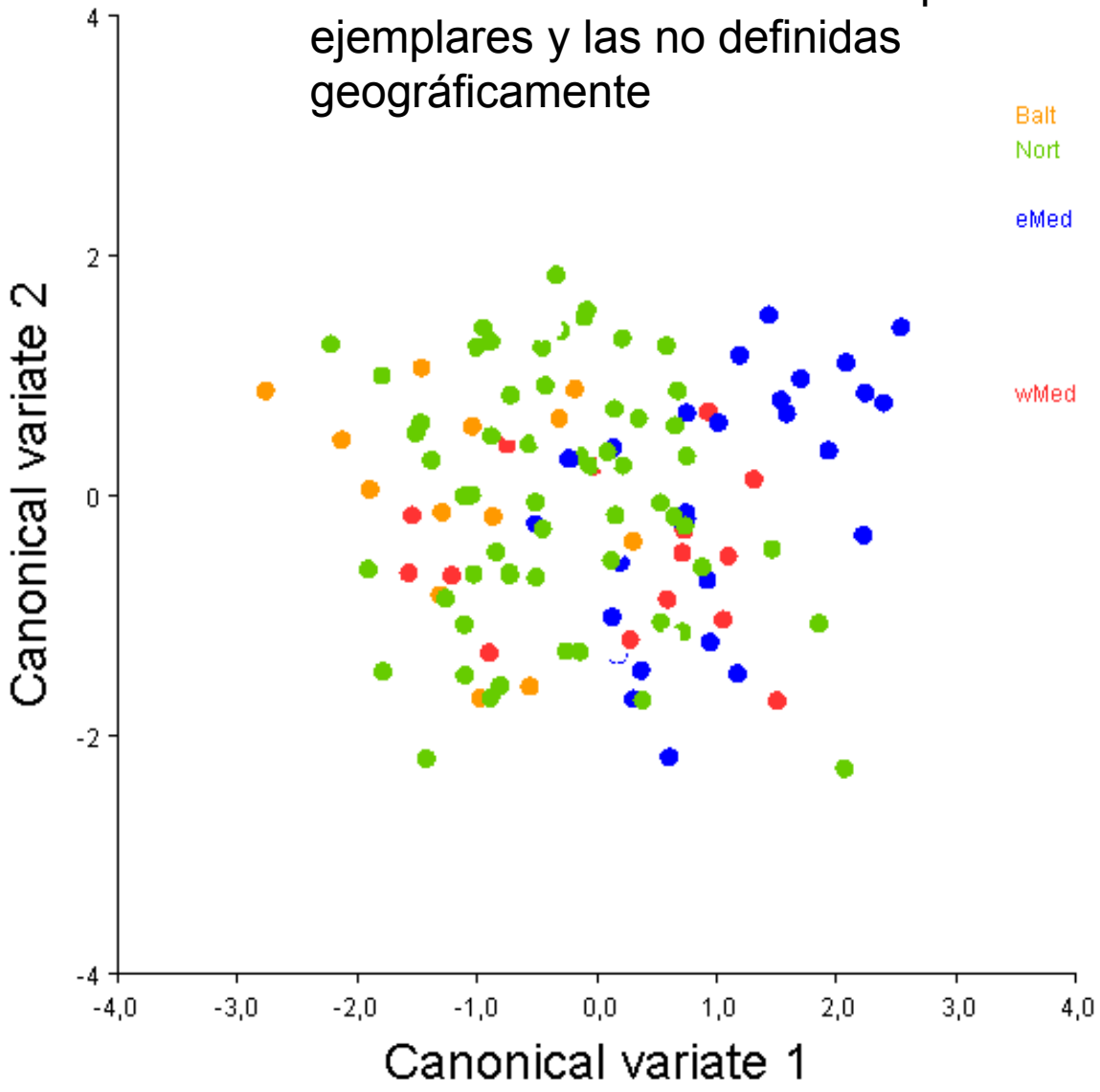
Groups	Observations
1. Balt	13
2. Nort	59
3. aqua	17
4. eMed	29
5. ePac	4
6. n.a.	29
7. wAtl	2
8. wInd	2
9. wMed	15
10. wsPa	1

Se icluyen delfines
de acuarios y delfines
que no tienen localidad

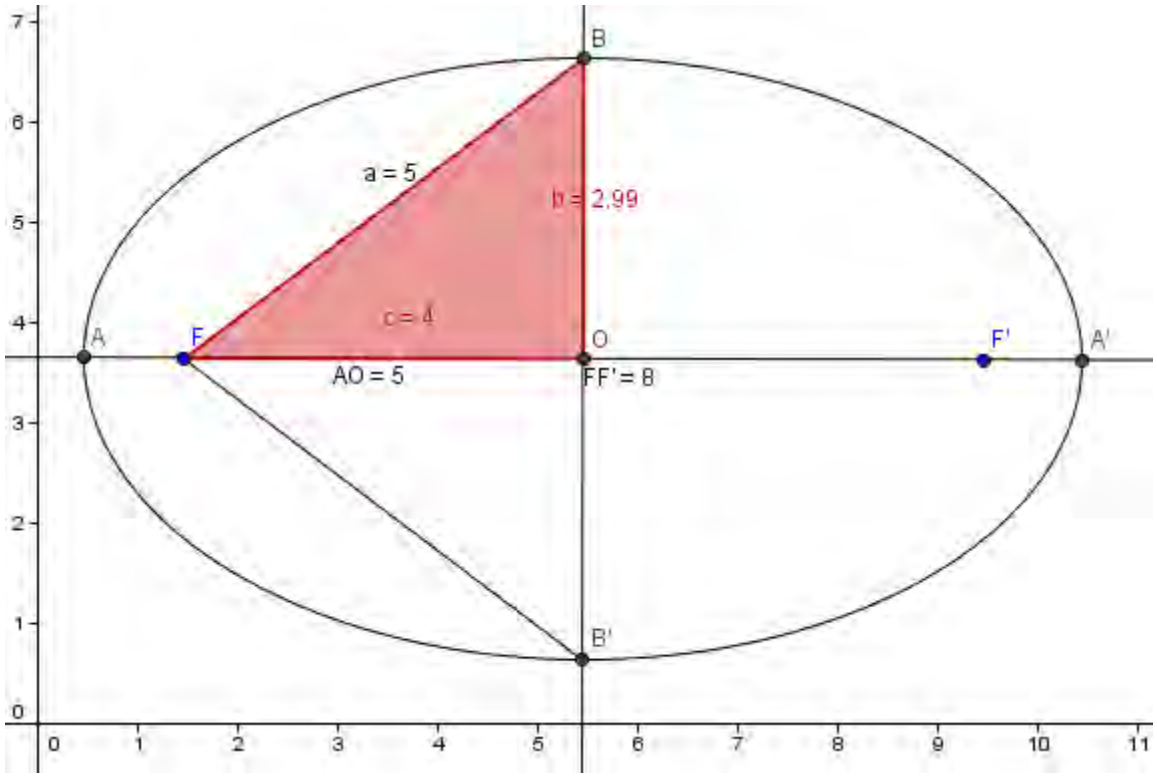



2
6
4
1
5
3
Adult -- Juveniles
2
6
4
1
5
3
F -- M

Quitamos las localidades con pocos ejemplares y las no definidas geográficamente

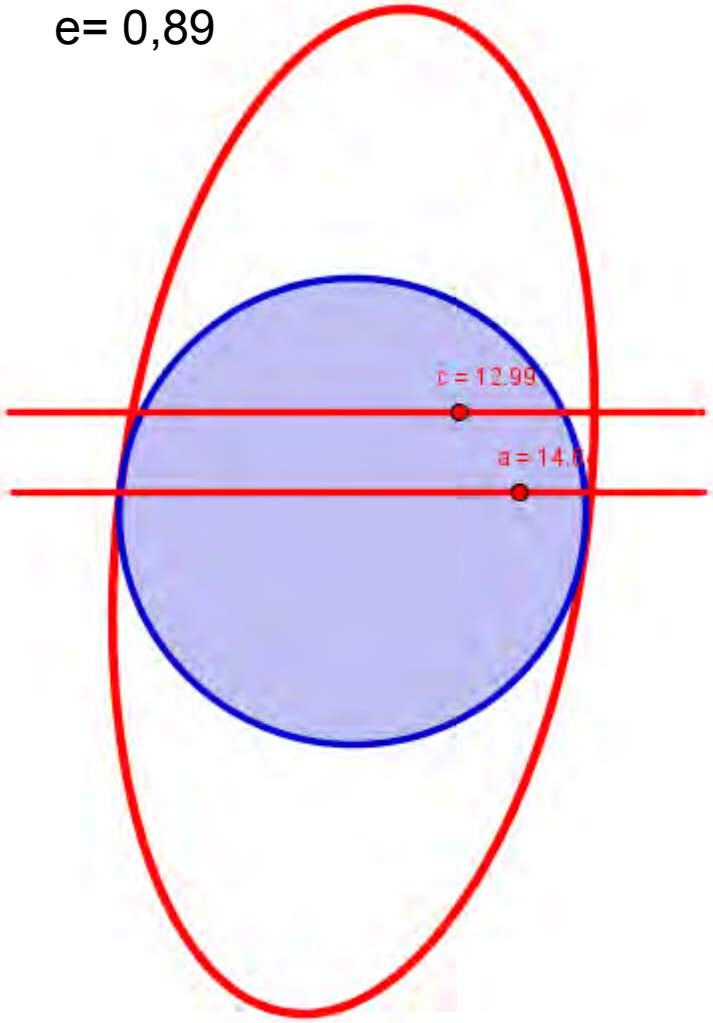


Al ser BB' < BF+B'F =2a=AA' a las magnitudes BB' y AA' se les conoce como **eje menor** y **eje mayor** respectivamente de la curva. En el triángulo OBF se verifica que $a^2 = b^2 + c^2$, relación entre los semiejes y distancia focal. c/a = e se denomina **excentricidad de la curva** y al ser c<a e es siempre <1. Cuanto mayor es la excentricidad más achatada es la elipse, acercándose los focos a los vértices. Si e es igual a 0 la elipse se convierte en un círculo en el que los focos se confunden con el centro.

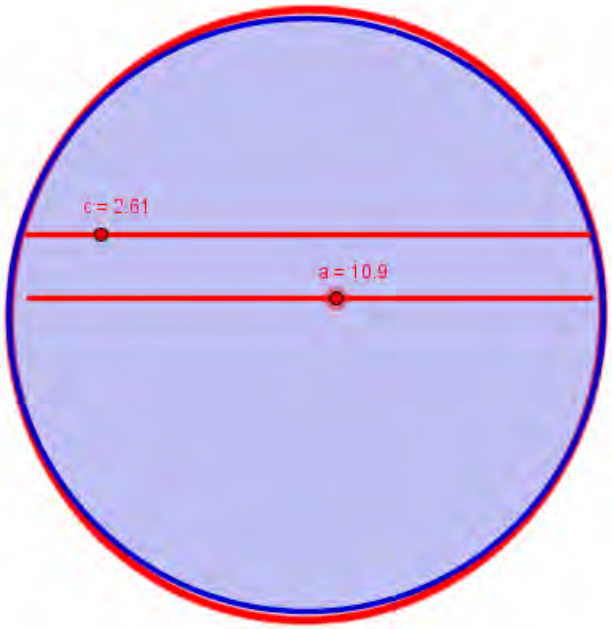


Representación de excentricidades

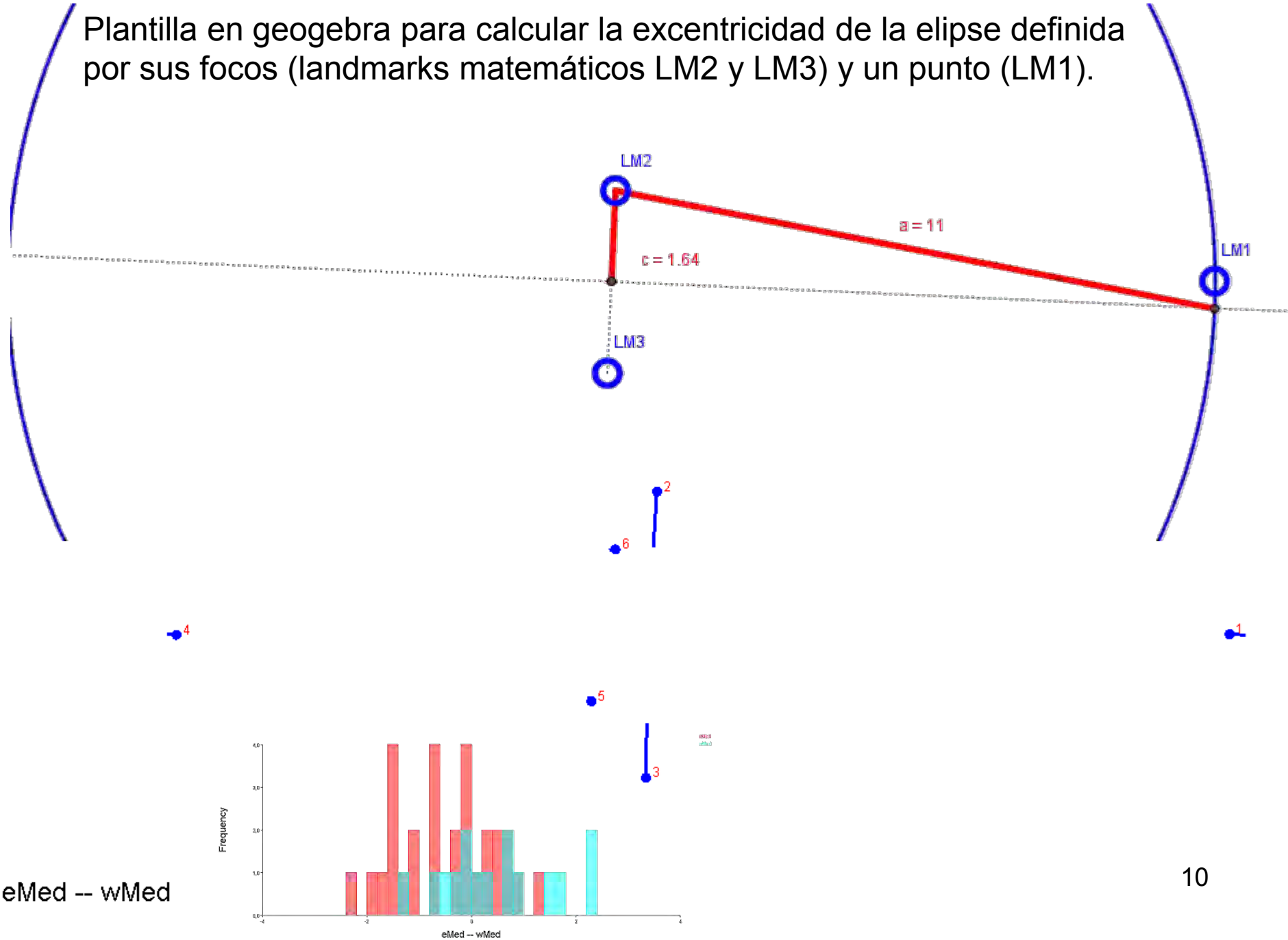
e= 0,89



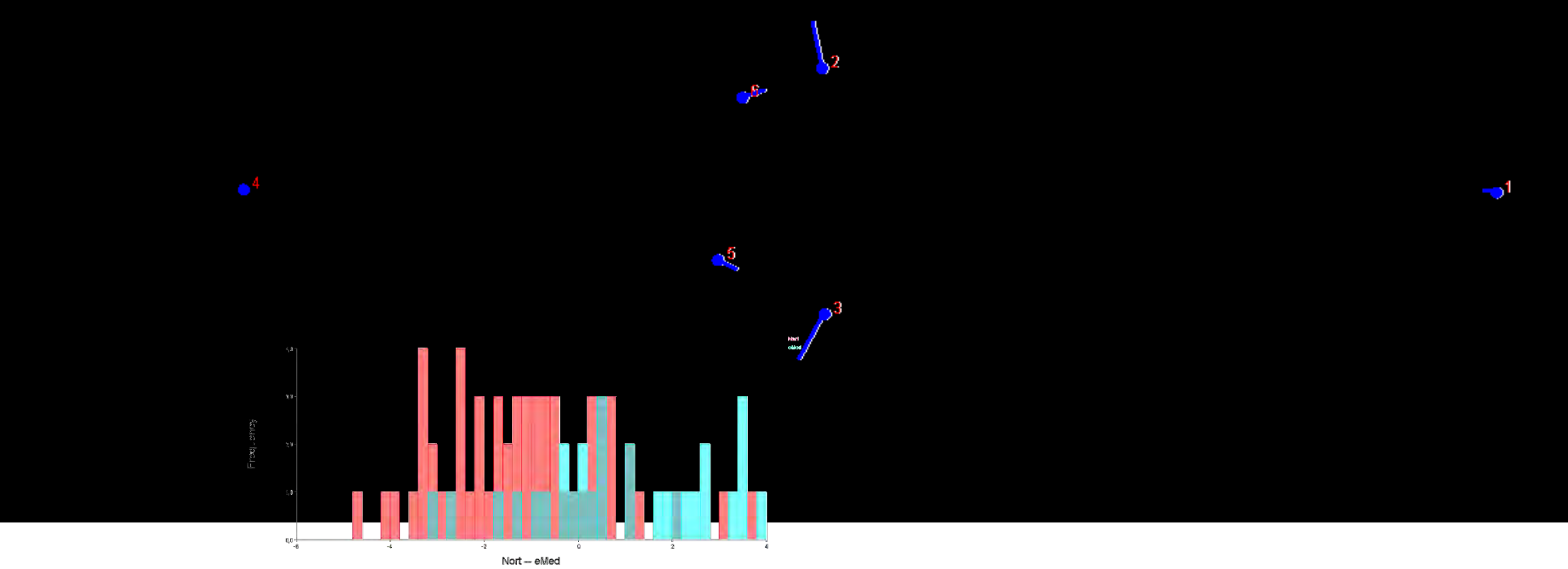
e= 0,24

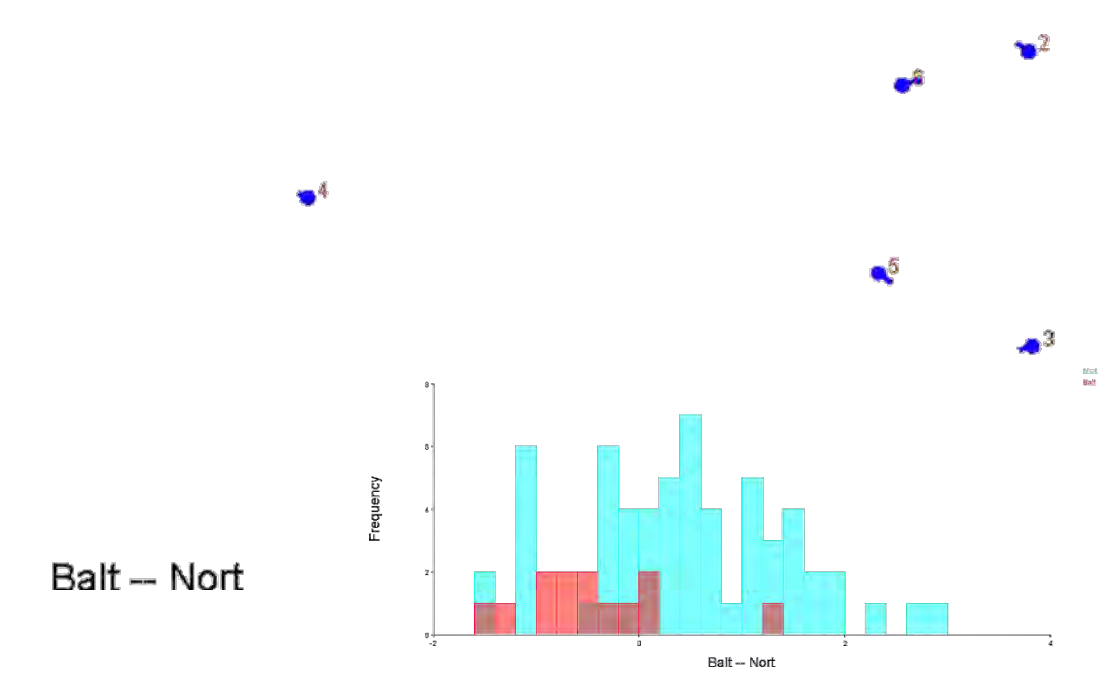


Plantilla en geogebra para calcular la excentricidad de la elipse definida por sus focos (landmarks matemáticos LM2 y LM3) y un punto (LM1).

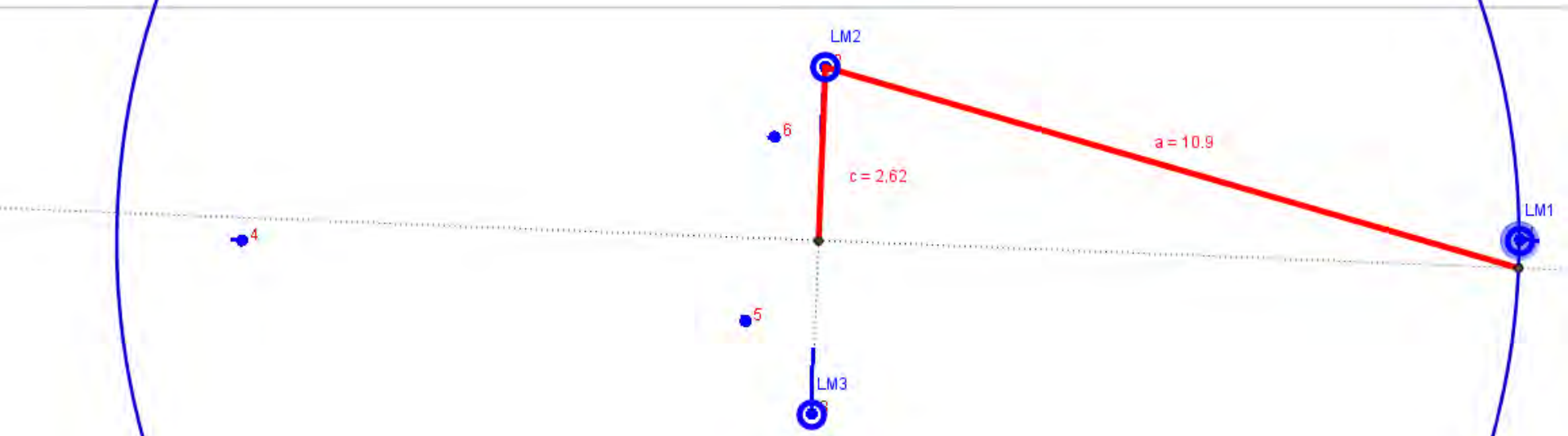


eMed -- wMed



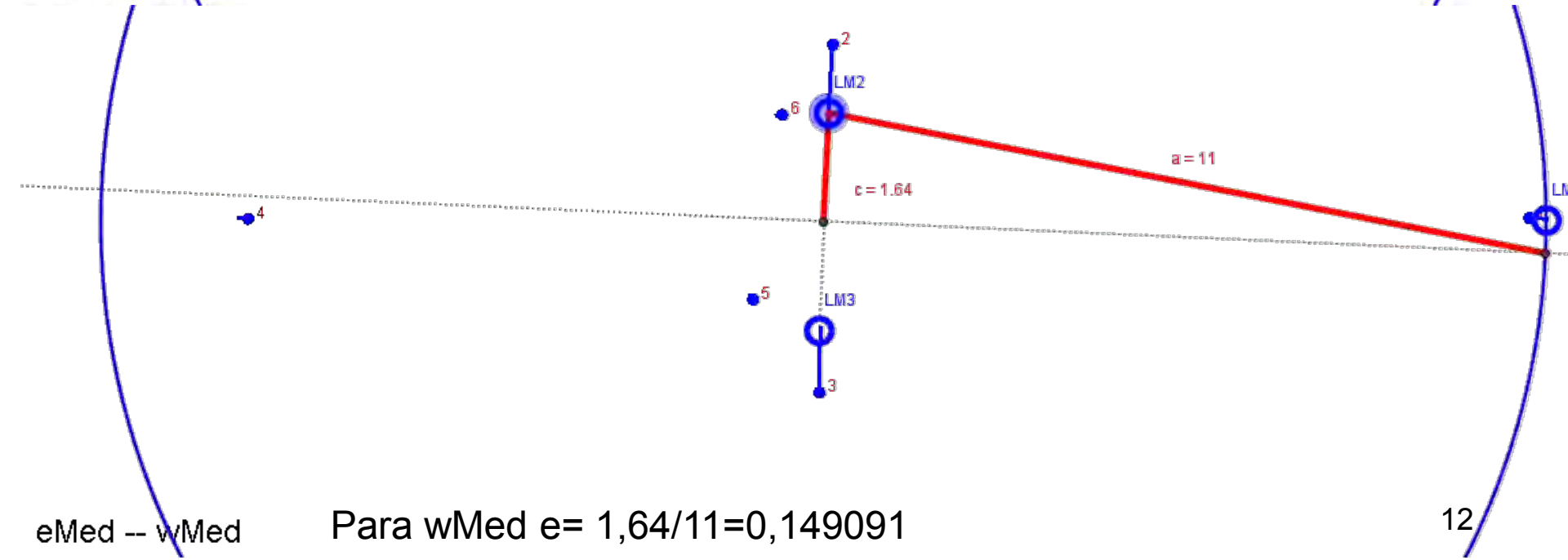


Balt -- Nort



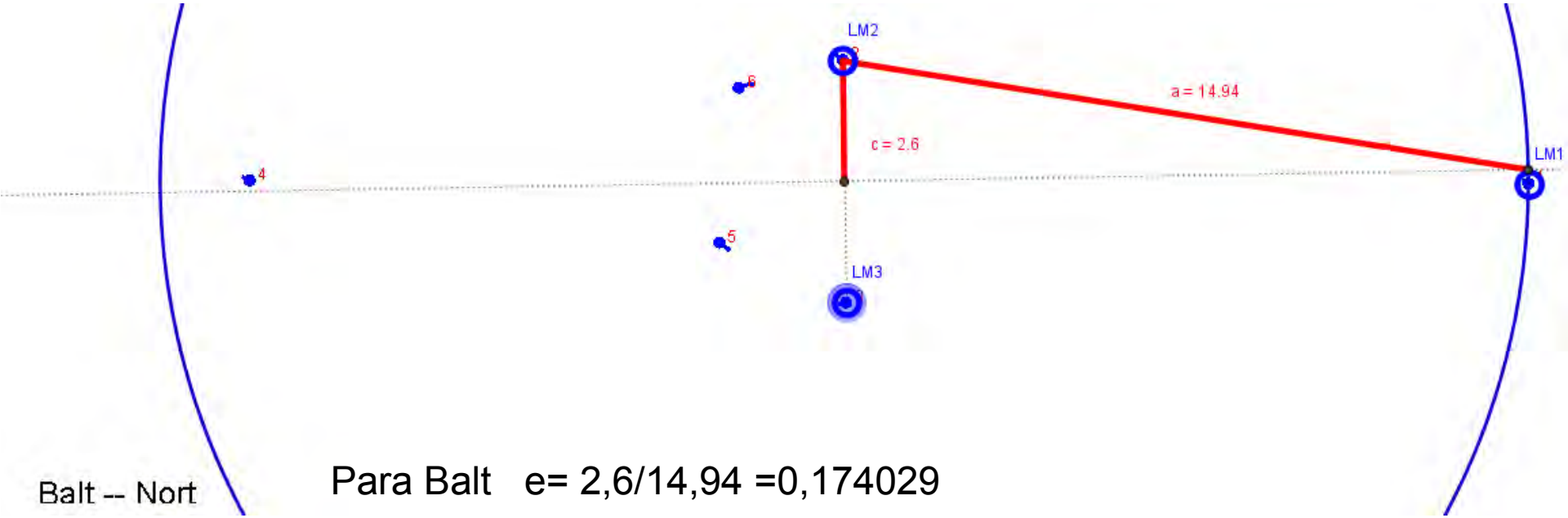
Para eMed e= 2,62/10,9 = 0,240367

eMed -- wMed

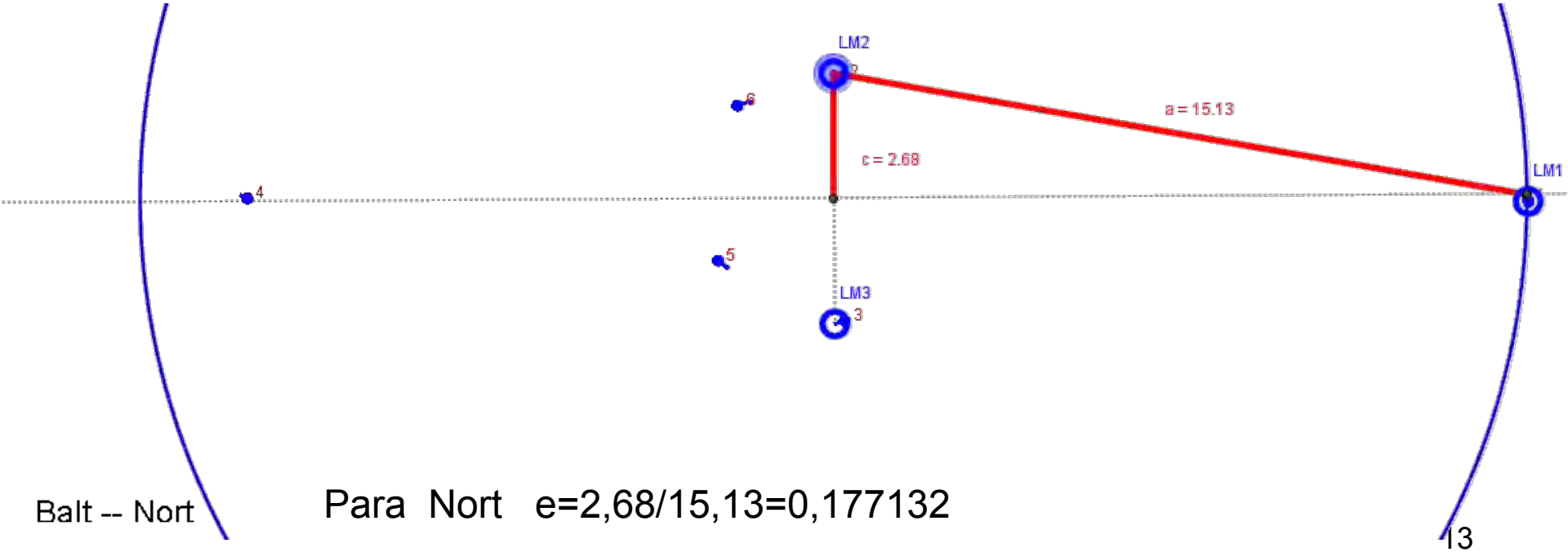


eMed -- wMed

Para wMed e= 1,64/11=0,149091



Para Balt e= 2,6/14,94 =0,174029



Para Nort e=2,68/15,13=0,177132

eMed e= 0,240367

wMed e= 0149091

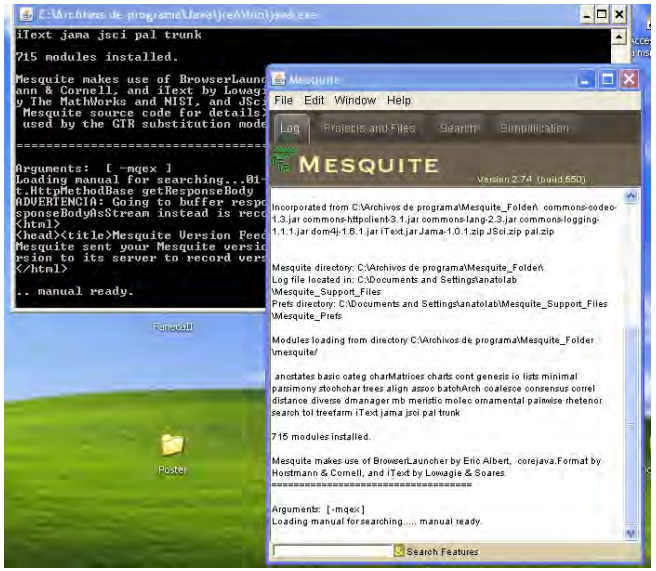
Balt e= 0,174029

Nort e= 0177132

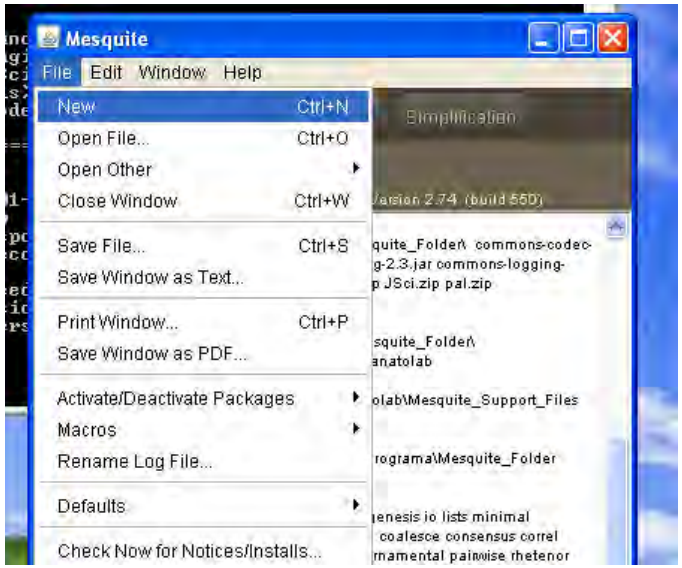
X 100 y quitando decimales queda

24
15
17
18

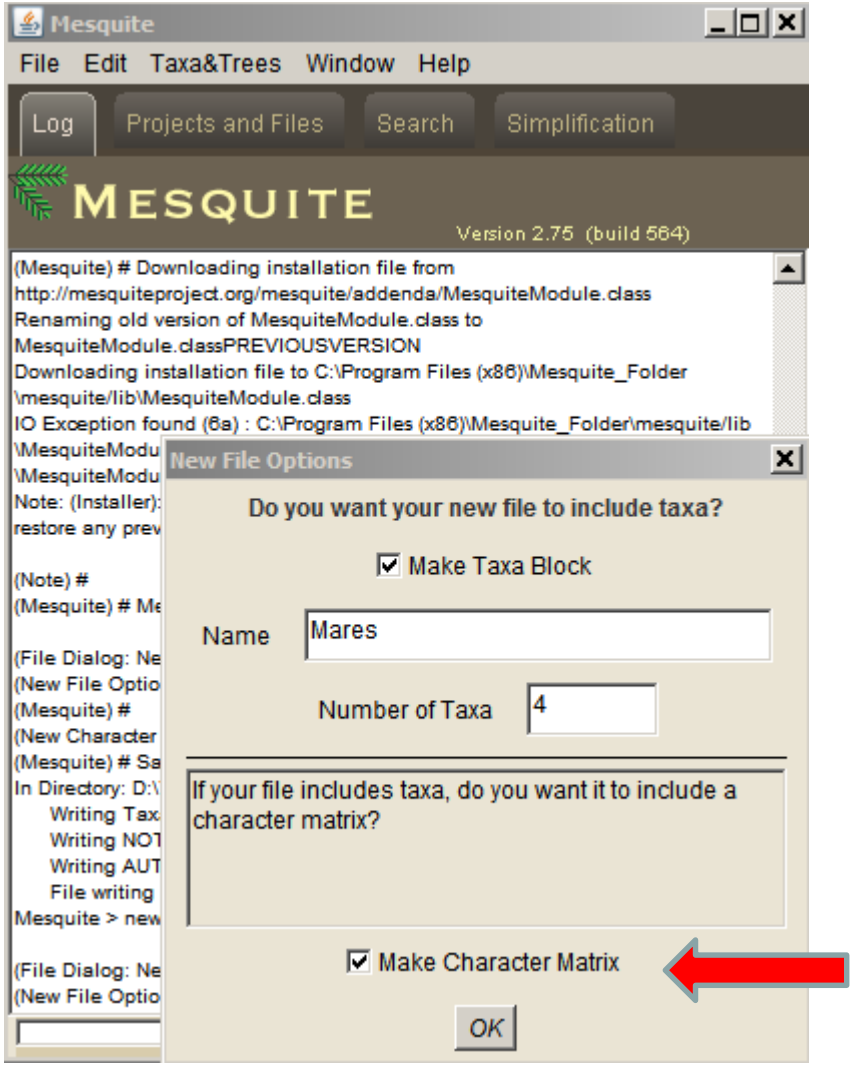
Abrimos el soft mesquite:



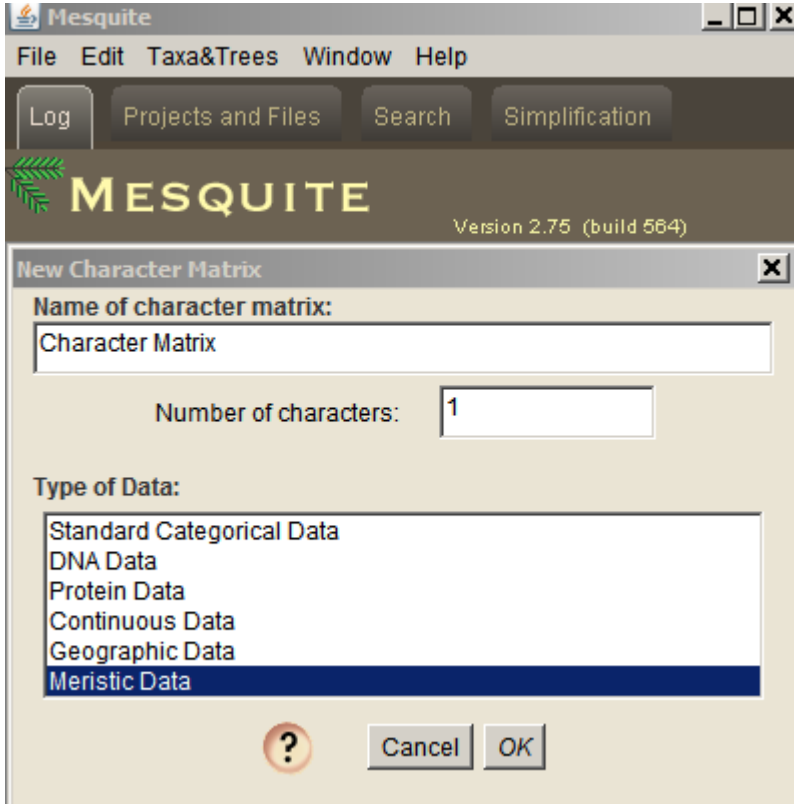
Y creamos un nuevo fichero:

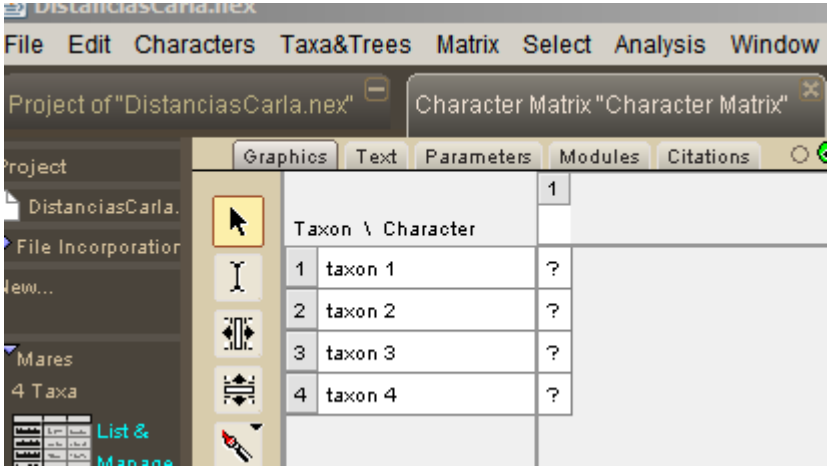


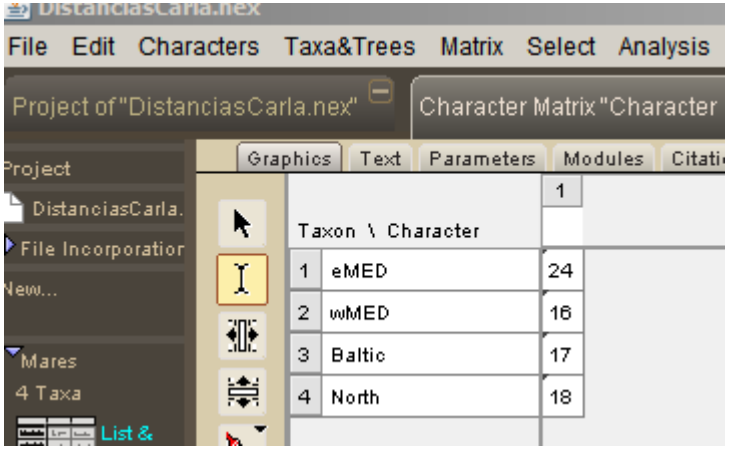
Nos pregunta el número de grupos que tenemos, en nuestro caso es 4

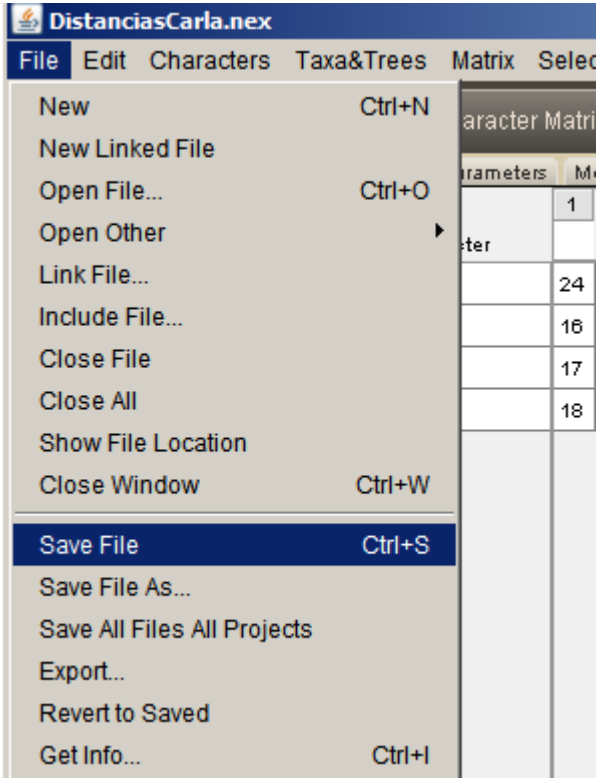


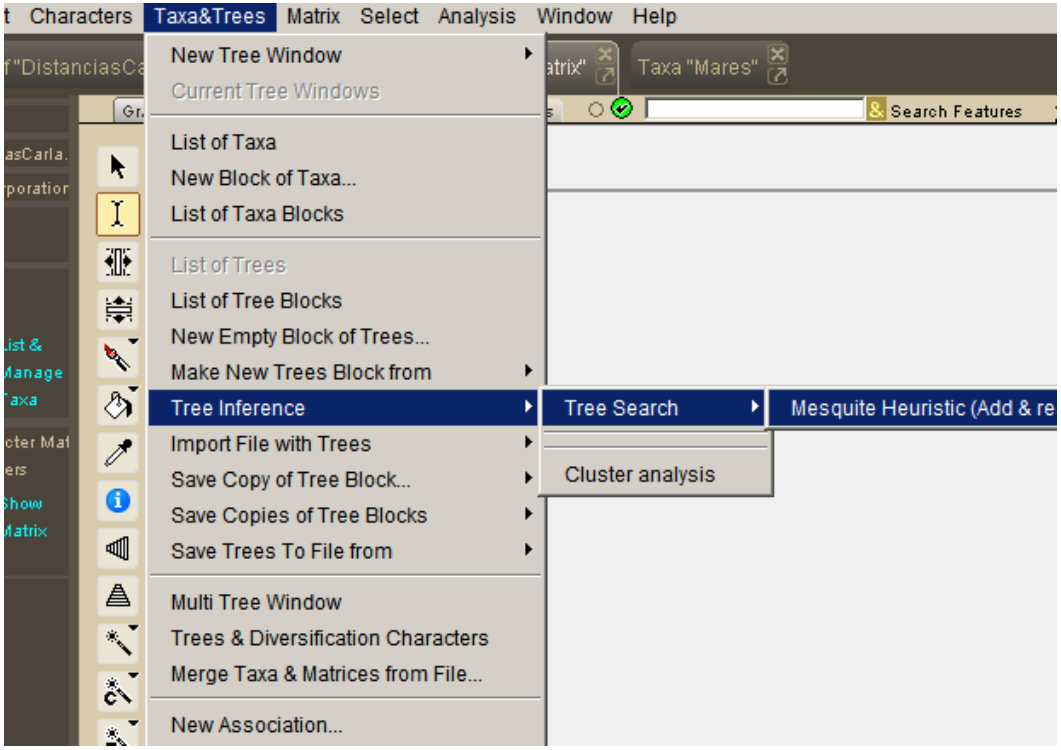
Y el número de columnas de la matriz asi como el tipo de matriz

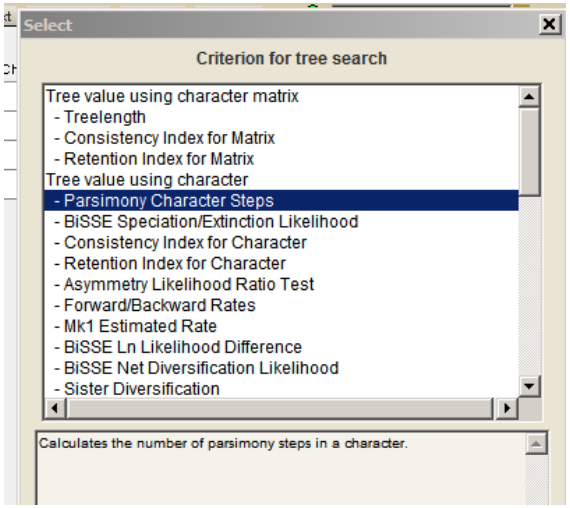


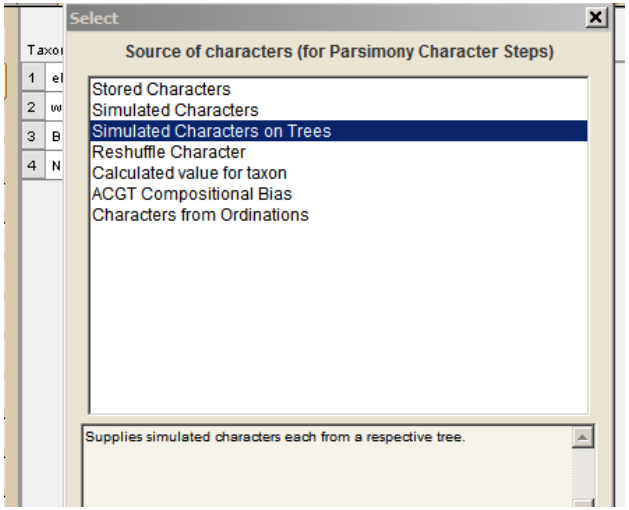

File Edit Characters Taxa&Trees Matrix Select Analysis Window
Project of "DistanciasCarla.nex"
Character Matrix "Character Matrix"
Graphics Text Parameters Modules Citations
Taxon \ Character
1 taxon 1 ?
2 taxon 2 ?
3 taxon 3 ?
4 taxon 4 ?

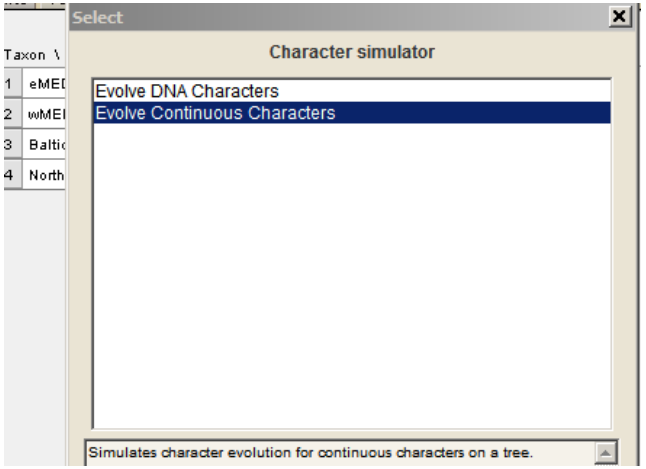

File Edit Characters Taxa&Trees Matrix Select Analysis
Project of "DistanciasCarla.nex"
Character Matrix "Character
Graphics Text Parameters Modules
Taxon \ Character
1 eMED 24
2 wMED 16
3 Baltic 17
4 North 18

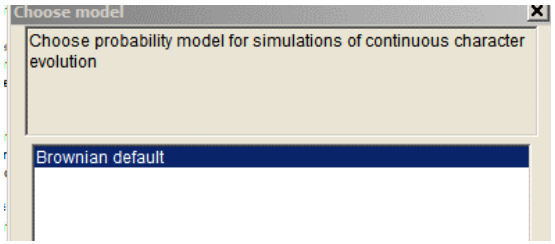

DistanciasCarla.nex
File Edit Characters Taxa&Trees Matrix
New Ctrl+N
New Linked File
Open File... Ctrl+O
Open Other
Link File...
Include File...
Close File
Close All
Show File Location
Close Window Ctrl+W
Save File Ctrl+S
Save File As...
Save All Files All Projects
Export...
Revert to Saved
Get Info... Ctrl+I

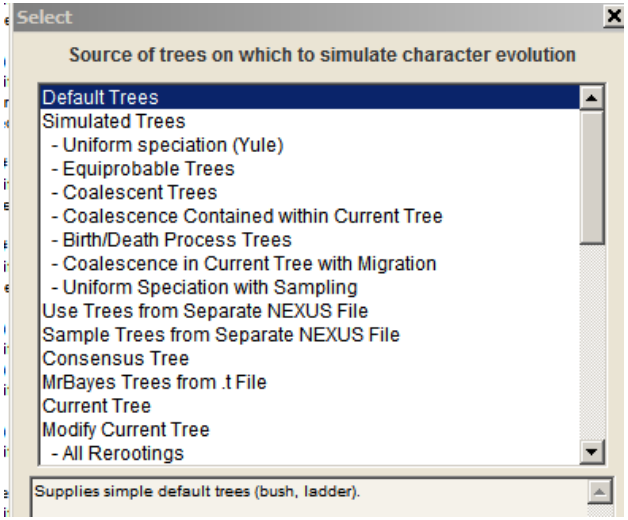

Characters Taxa&Trees Matrix Select Analysis Window Help
New Tree Window
Current Tree Windows
List of Taxa
New Block of Taxa...
List of Taxa Blocks
List of Trees
List of Tree Blocks
New Empty Block of Trees...
Make New Trees Block from
Tree Inference
Import File with Trees
Save Copy of Tree Block...
Save Copies of Tree Blocks
Save Trees To File from
Multi Tree Window
Trees & Diversification Characters
Merge Taxa & Matrices from File...
New Association...
Tree Search
Mesquite Heuristic (Add & re
Cluster analysis
Taxa "Mares"
Search Features

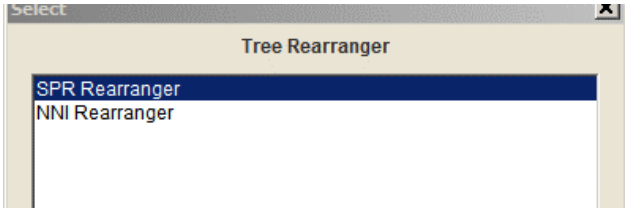

Select
Criterion for tree search
Tree value using character matrix
- Treelength
- Consistency Index for Matrix
- Retention Index for Matrix
Tree value using character
- Parsimony Character Steps
- BiSSE Speciation/Extinction Likelihood
- Consistency Index for Character
- Retention Index for Character
- Asymmetry Likelihood Ratio Test
- Forward/Backward Rates
- Mk1 Estimated Rate
- BiSSE Ln Likelihood Difference
- BiSSE Net Diversification Likelihood
- Sister Diversification
Calculates the number of parsimony steps in a character.

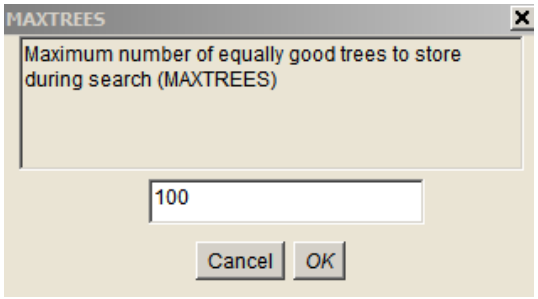

Select
Source of characters (for Parsimony Character Steps)
Stored Characters
Simulated Characters
Simulated Characters on Trees
Reshuffle Character
Calculated value for taxon
ACGT Compositional Bias
Characters from Ordinations
Supplies simulated characters each from a respective tree.

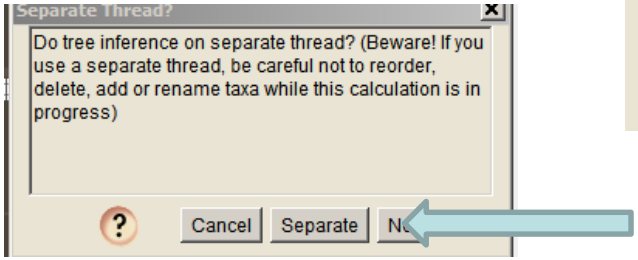

Select
Character simulator
Evolve DNA Characters
Evolve Continuous Characters
Simulates character evolution for continuous characters on a tree.

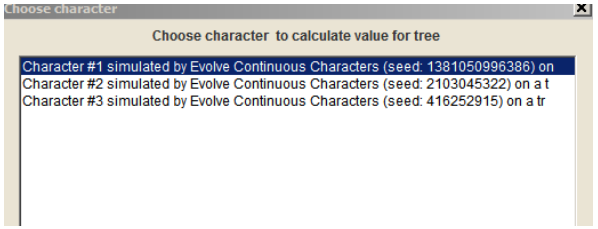

Choose model
Choose probability model for simulations of continuous character evolution
Brownian default

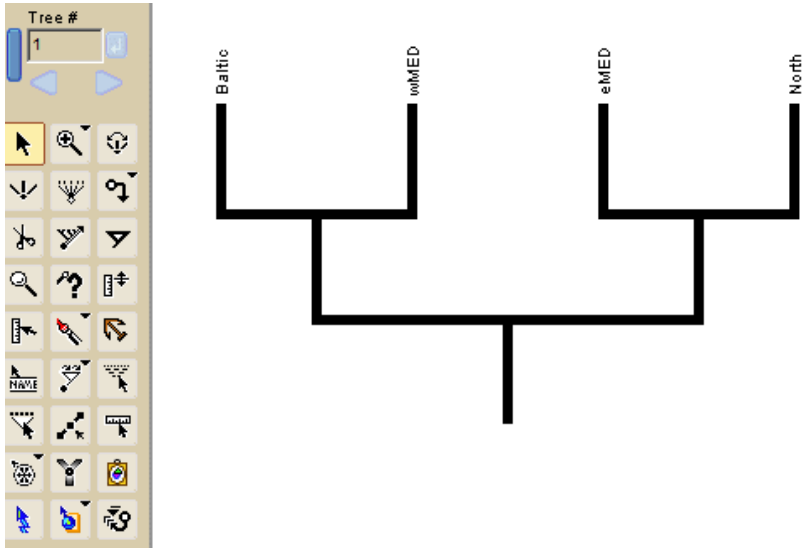

Select
Source of trees on which to simulate character evolution
Default Trees
Simulated Trees
- Uniform speciation (Yule)
- Equiprobable Trees
- Coalescent Trees
- Coalescence Contained within Current Tree
- Birth/Death Process Trees
- Coalescence in Current Tree with Migration
- Uniform Speciation with Sampling
Use Trees from Separate NEXUS File
Sample Trees from Separate NEXUS File
Consensus Tree
MrBayes Trees from .t File
Current Tree
Modify Current Tree
- All Rerootings
Supplies simple default trees (bush, ladder).

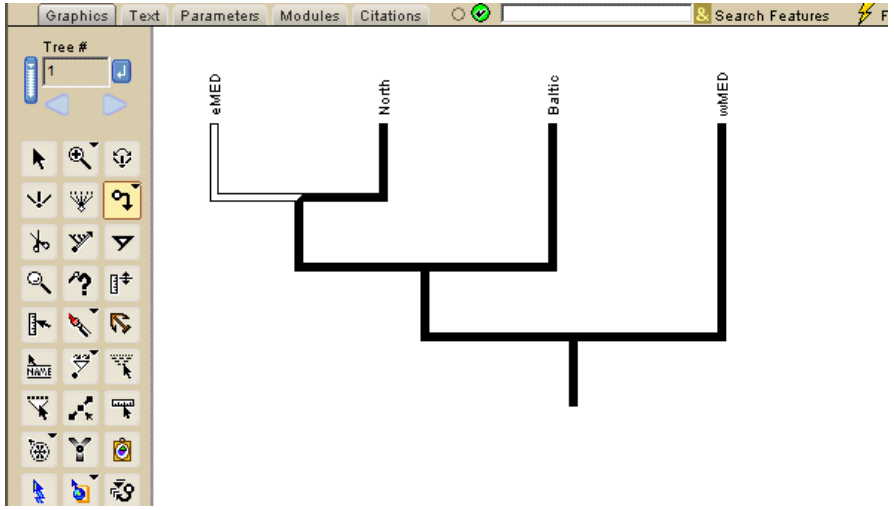

Select
Tree Rearranger
SPR Rearranger
NNI Rearranger

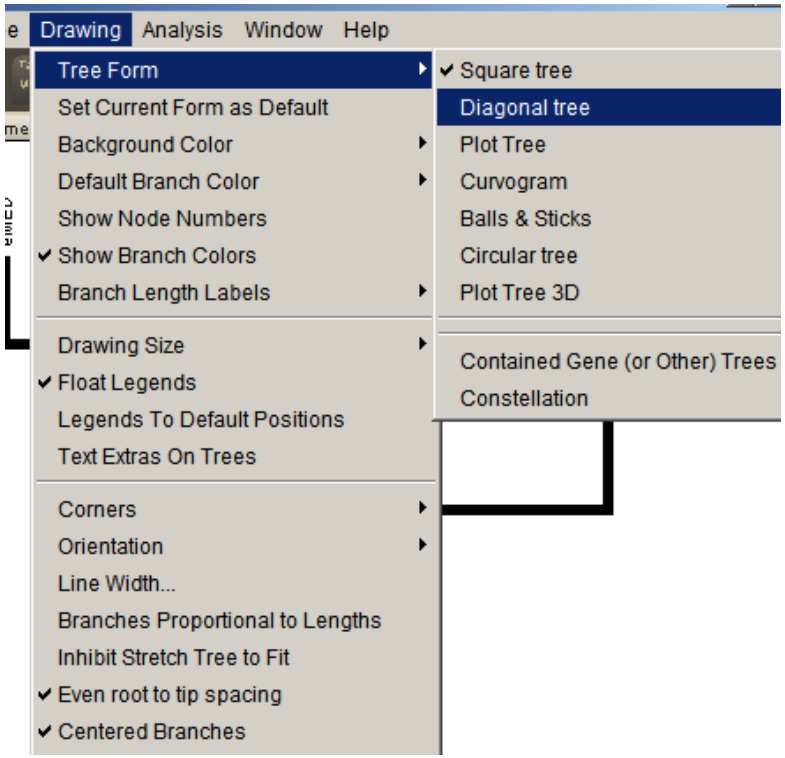

MAXTREES
Maximum number of equally good trees to store during search (MAXTREES)
100
Cancel
OK

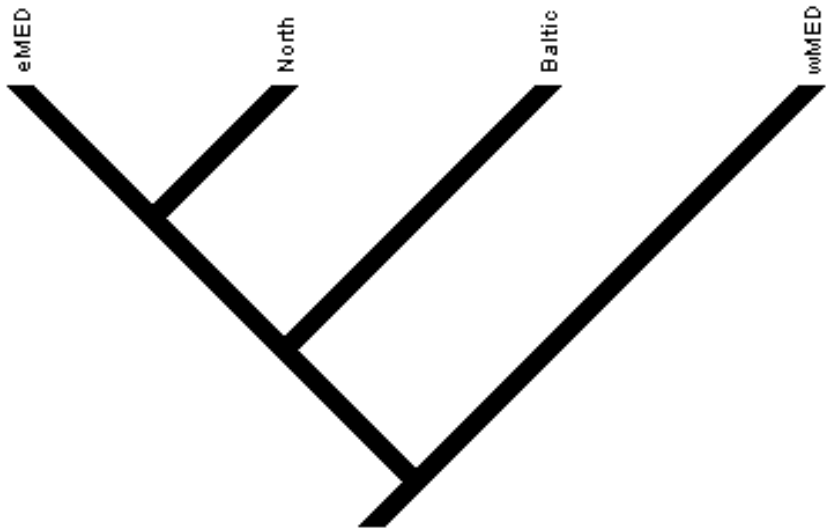

Separate Thread?
Do tree inference on separate thread? (Beware! If you use a separate thread, be careful not to reorder, delete, add or rename taxa while this calculation is in progress)
Cancel
Separate


Choose character
Choose character to calculate value for tree
Character #1 simulated by Evolve Continuous Characters (seed: 1381050996386) on
Character #2 simulated by Evolve Continuous Characters (seed: 2103045322) on a t
Character #3 simulated by Evolve Continuous Characters (seed: 416252915) on a tr

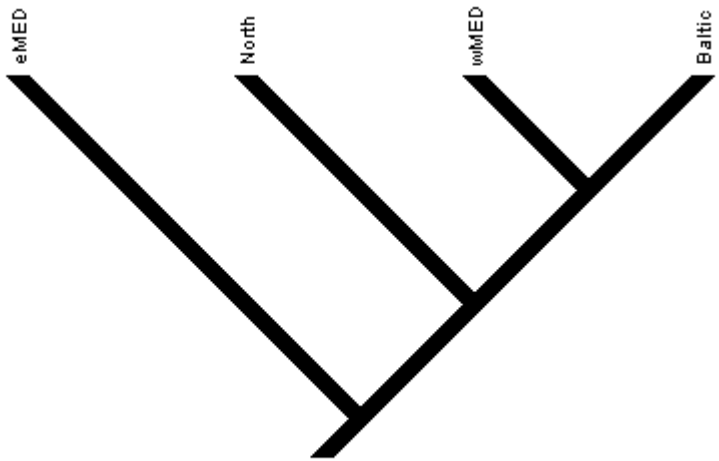

Tree #
1
Baltic
wMED
eMED
North

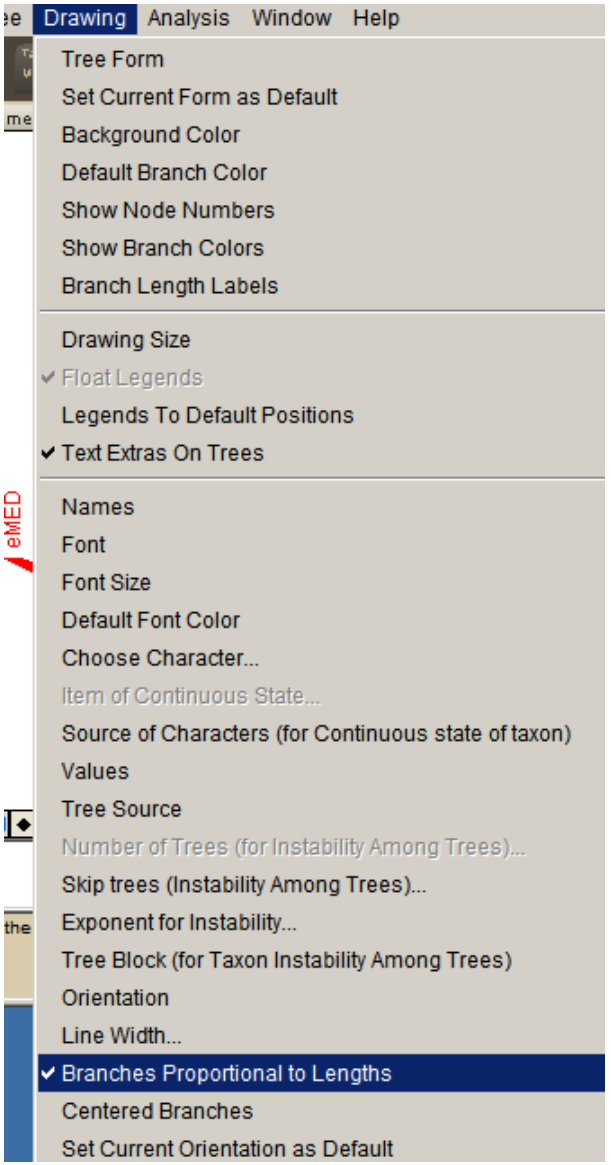

Graphics
Text
Parameters
Modules
Citations
Search Features
Tree #
1
eMED
North
Baltic
wMED

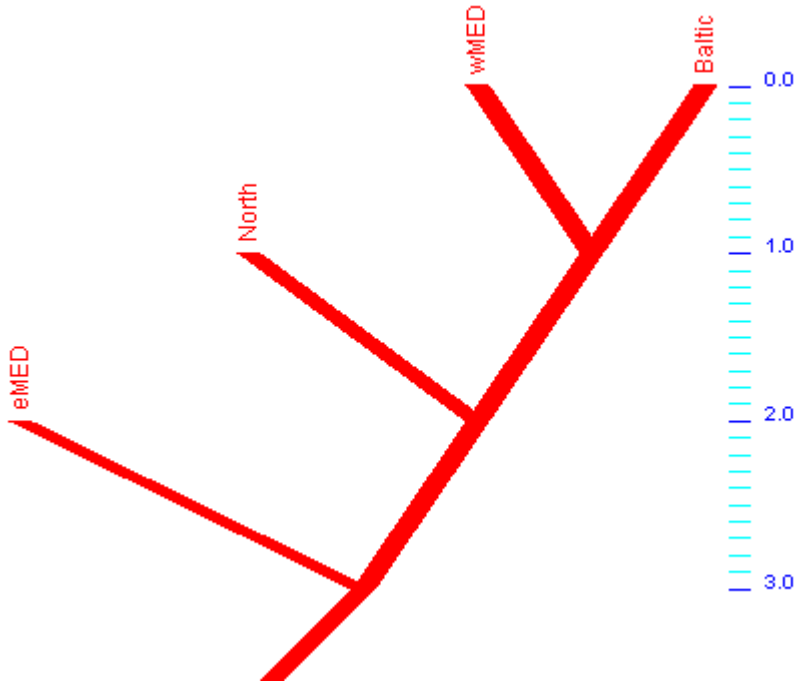

Drawing
Analysis
Window
Help
Tree Form
Set Current Form as Default
Background Color
Default Branch Color
Show Node Numbers
Show Branch Colors
Branch Length Labels
Drawing Size
Float Legends
Legends To Default Positions
Text Extras On Trees
Corners
Orientation
Line Width...
Branches Proportional to Lengths
Inhibit Stretch Tree to Fit
Even root to tip spacing
Centered Branches
Square tree
Diagonal tree
Plot Tree
Curvogram
Balls & Sticks
Circular tree
Plot Tree 3D
Contained Gene (or Other) Trees
Constellation


eMED
North
Baltic
wMED


Tree #
1


eMED
North
wMED
Baltic


Drawing
Analysis
Window
Help
Tree Form
Set Current Form as Default
Background Color
Default Branch Color
Show Node Numbers
Show Branch Colors
Branch Length Labels
Drawing Size
Float Legends
Legends To Default Positions
Text Extras On Trees
Names
Font
Font Size
Default Font Color
Choose Character...
Item of Continuous State...
Source of Characters (for Continuous state of taxon)
Values
Tree Source
Number of Trees (for Instability Among Trees)...
Skip trees (Instability Among Trees)...
Exponent for Instability...
Tree Block (for Taxon Instability Among Trees)
Orientation
Line Width...
Branches Proportional to Lengths
Centered Branches
Set Current Orientation as Default

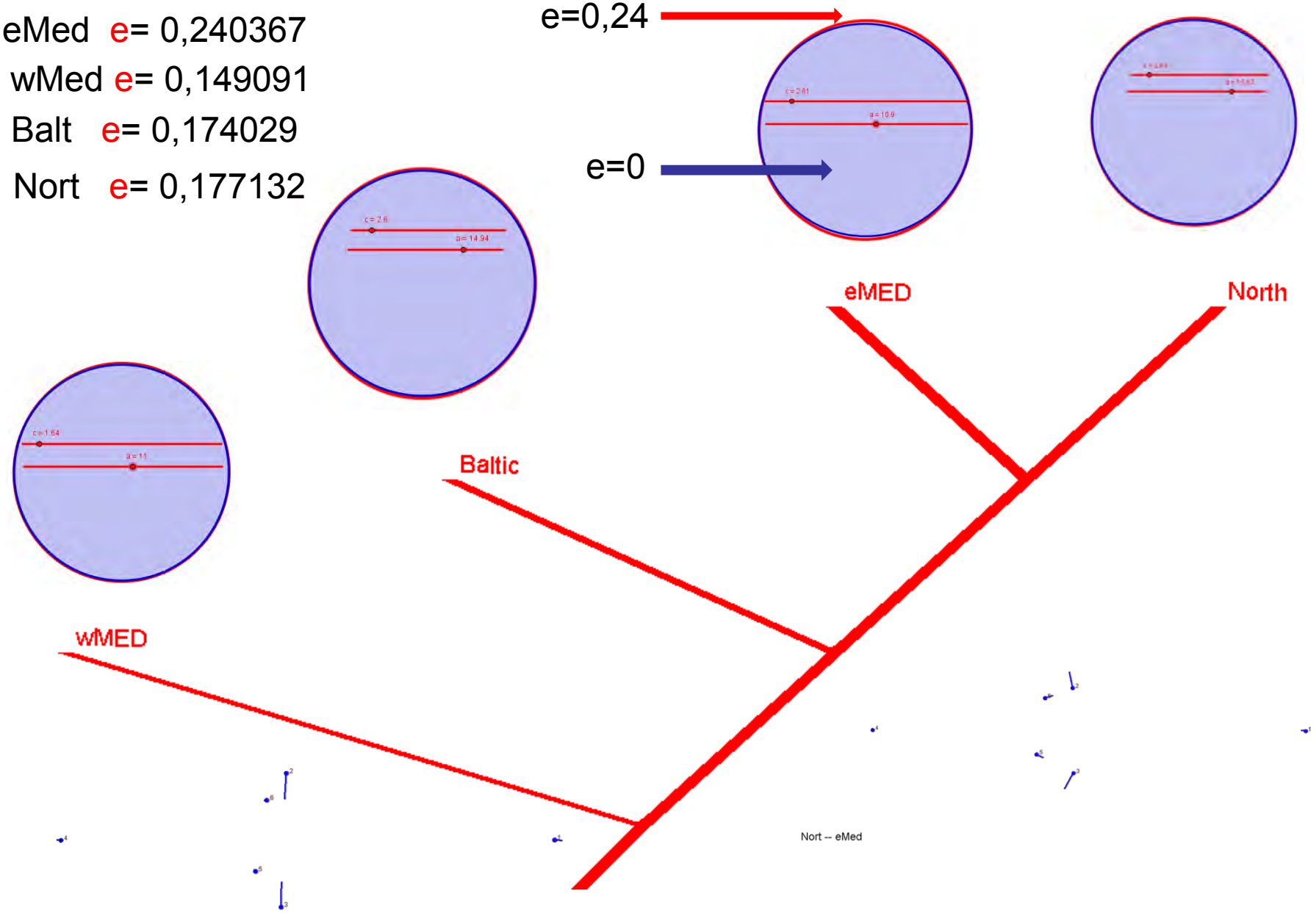

wMED
Baltic
North
eMED
0.0
1.0
2.0
3.0

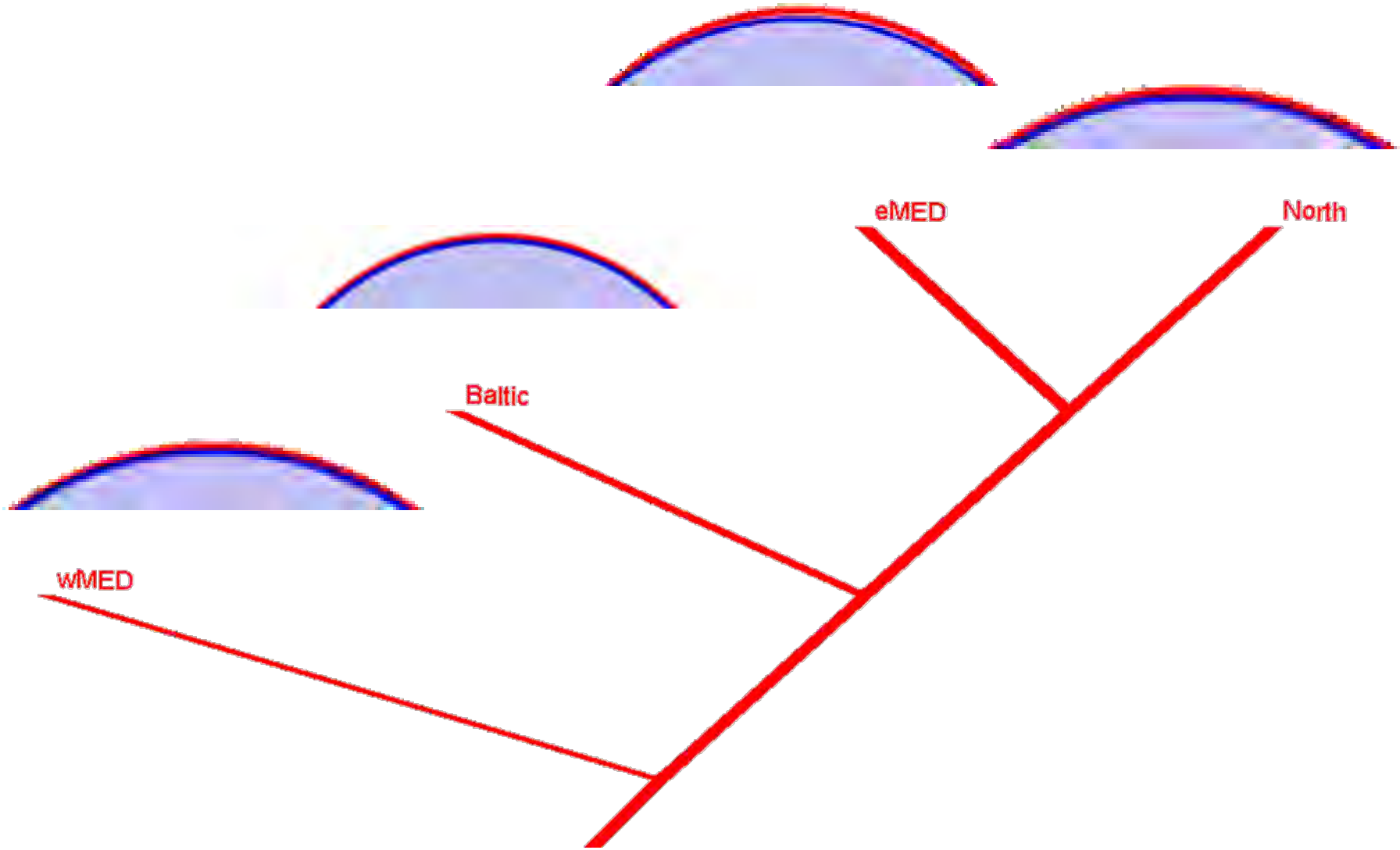
eMed e= 0,240367

wMed e= 0,149091

Balt e= 0,174029

Nort e= 0,177132




eMED
North
Baltic
wMED