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Presenter : Yingyi Yang

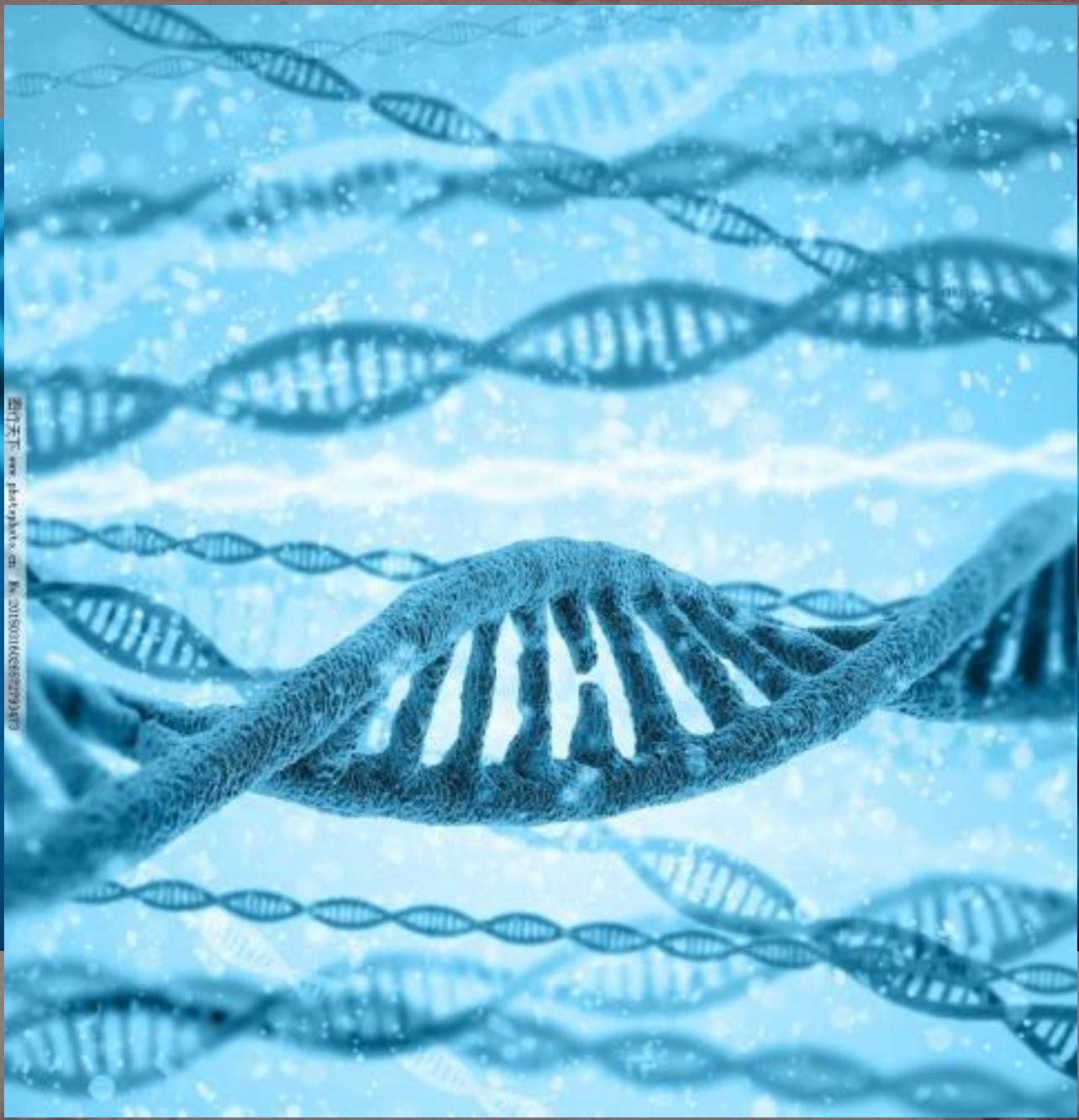
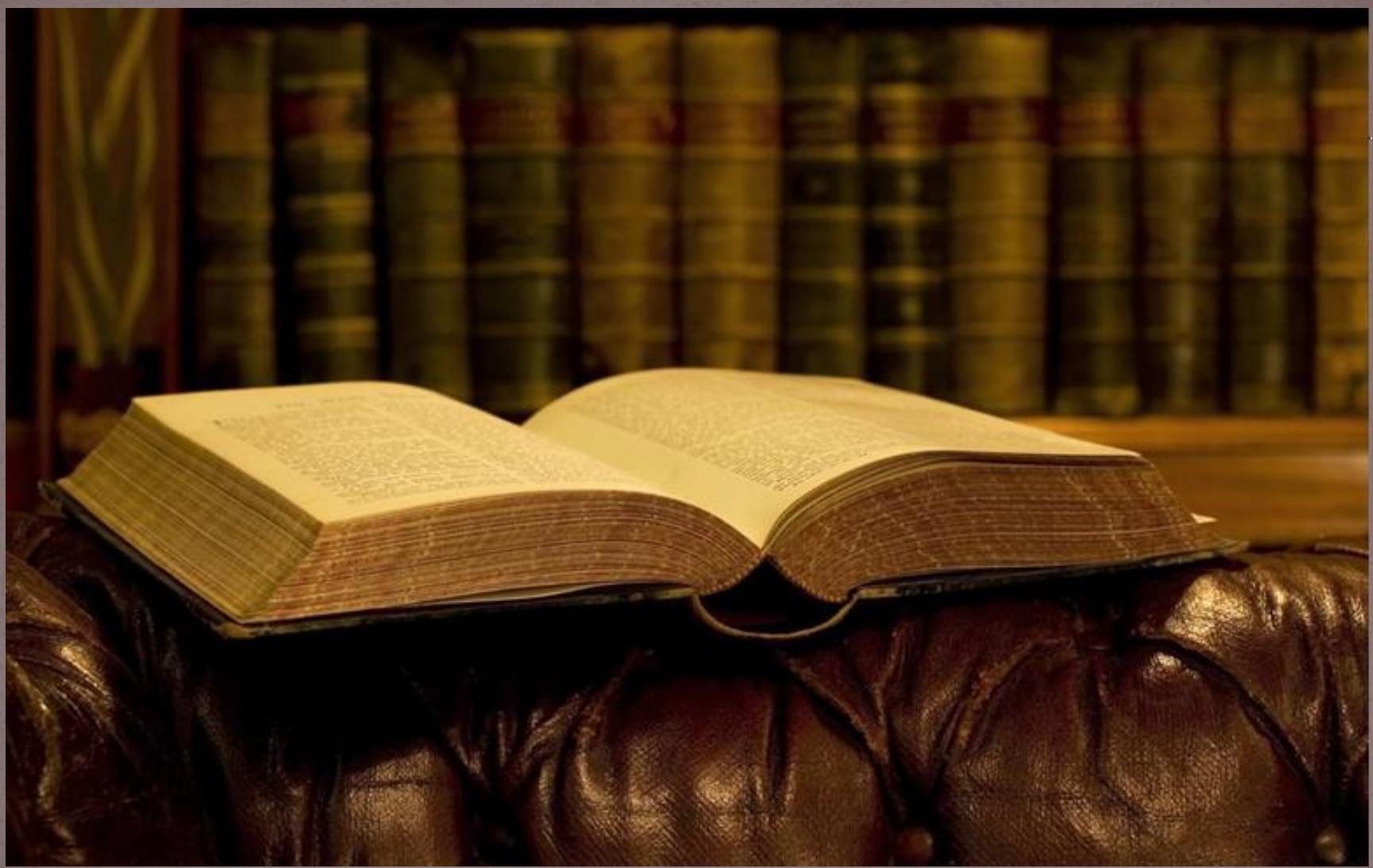
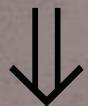


图10-7 www.photopedia.cn No.20150146265279340



- characteristics of individuals



- common ancestors  
( millions of years ago )



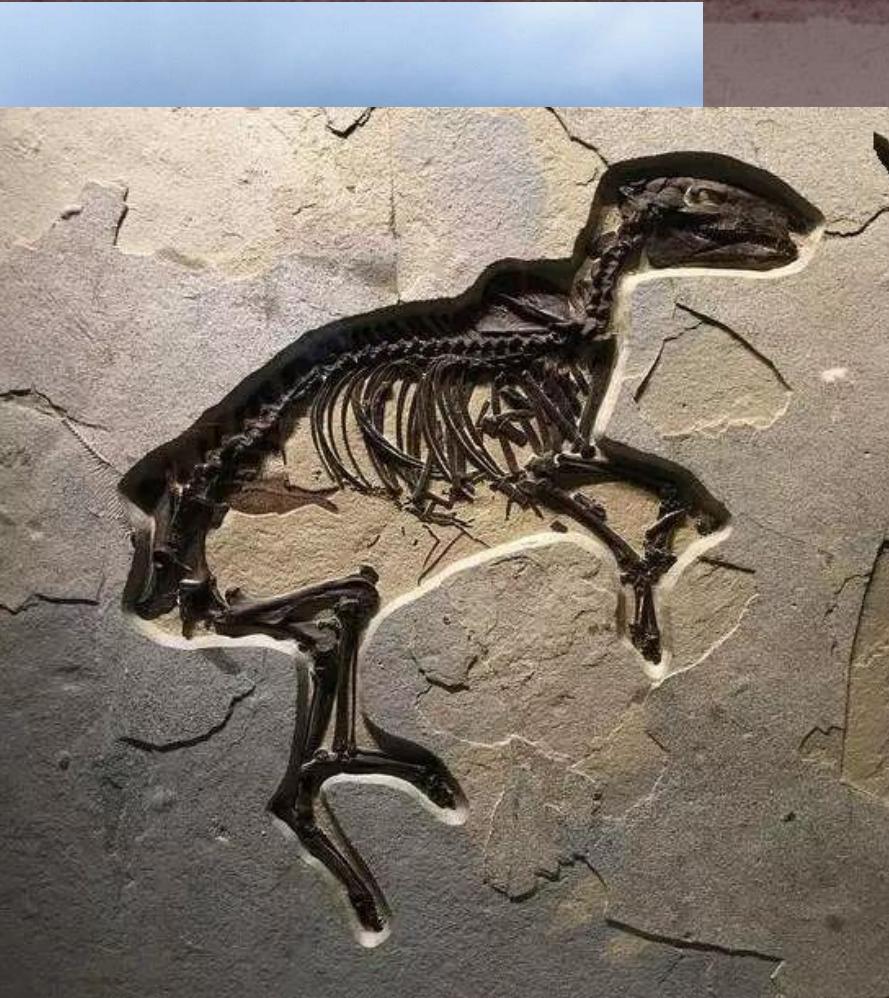
Arctic Ocean

Arctic Ocean

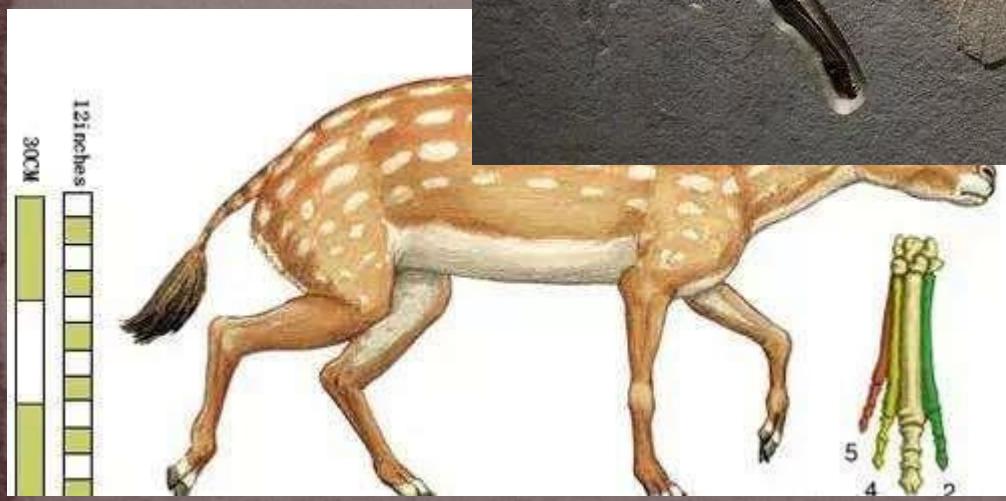
# ⇒ Biogeography



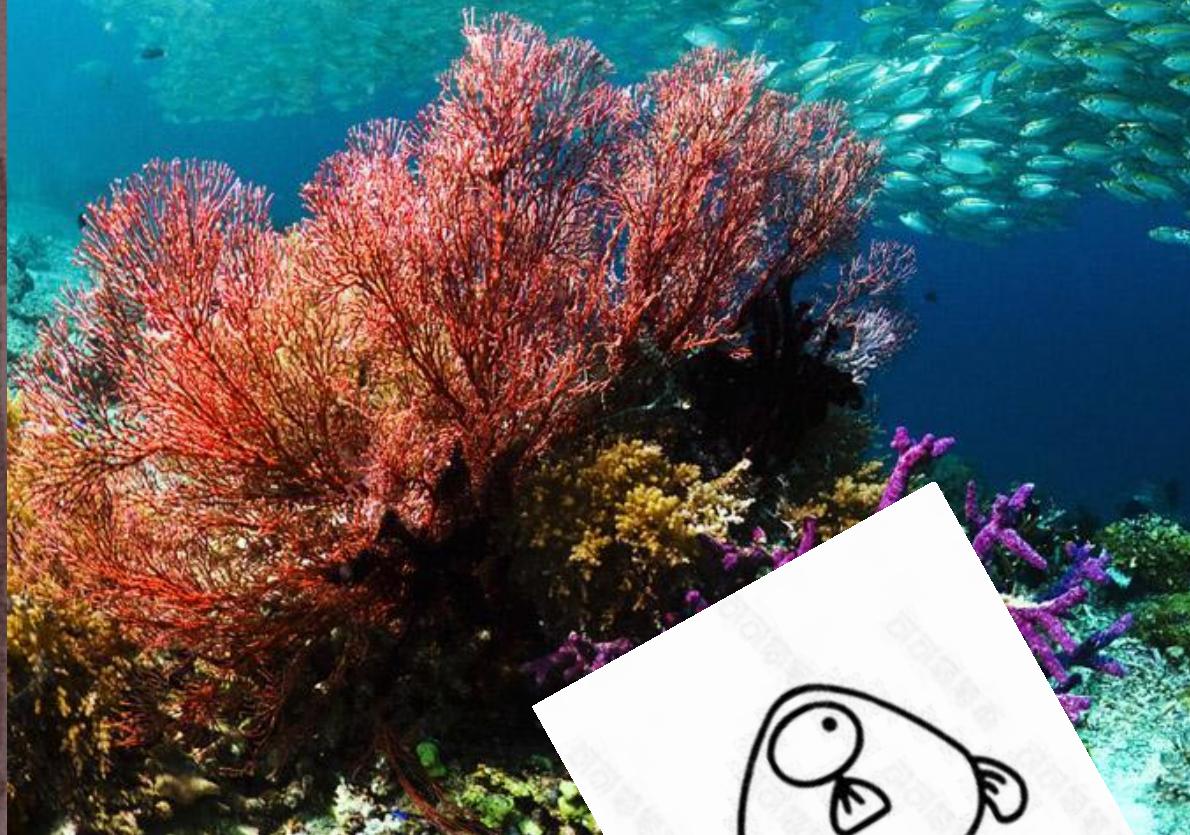
美柏医健



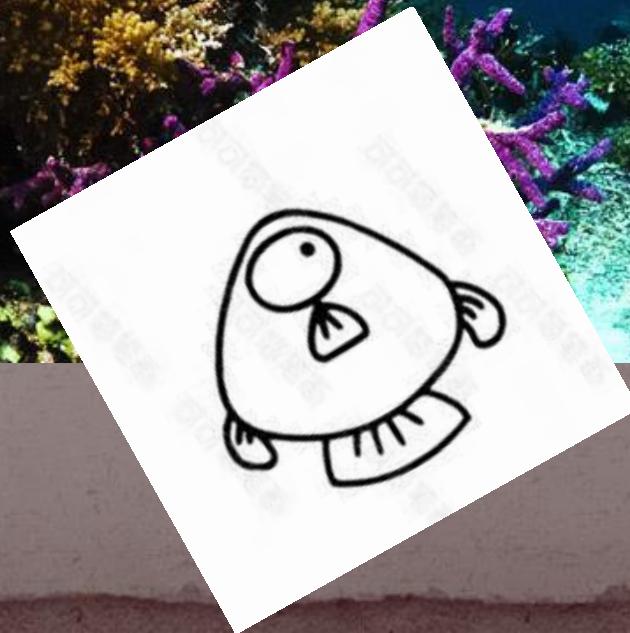
*Macotherium*  
马



⇒Character mapping



... ...



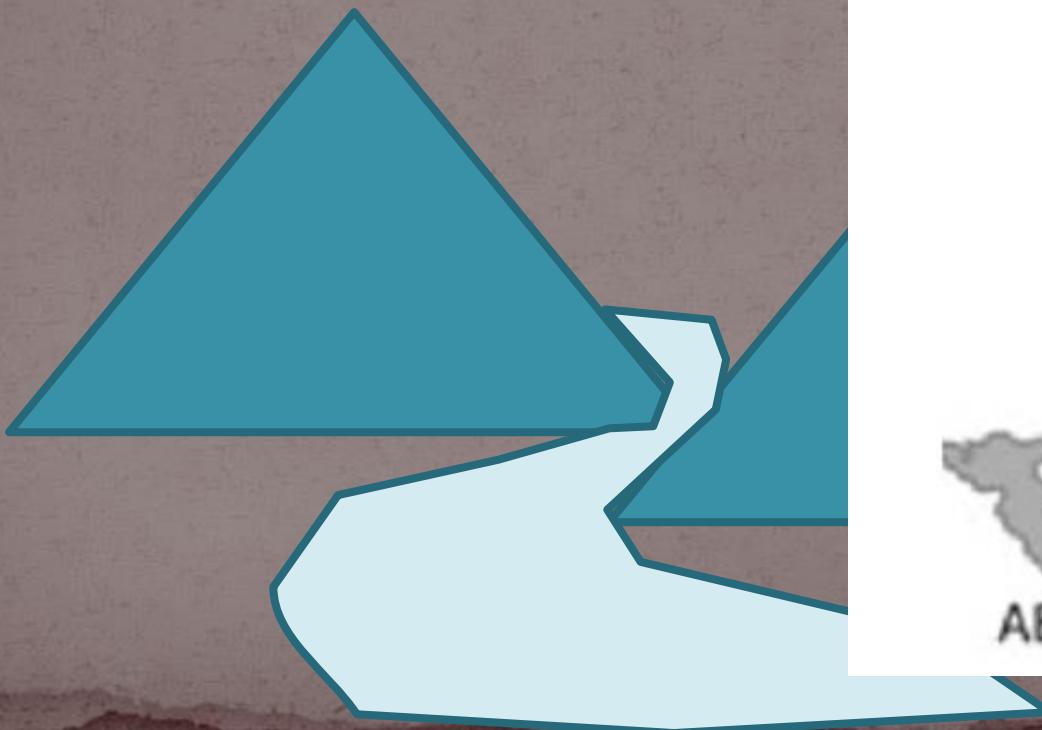


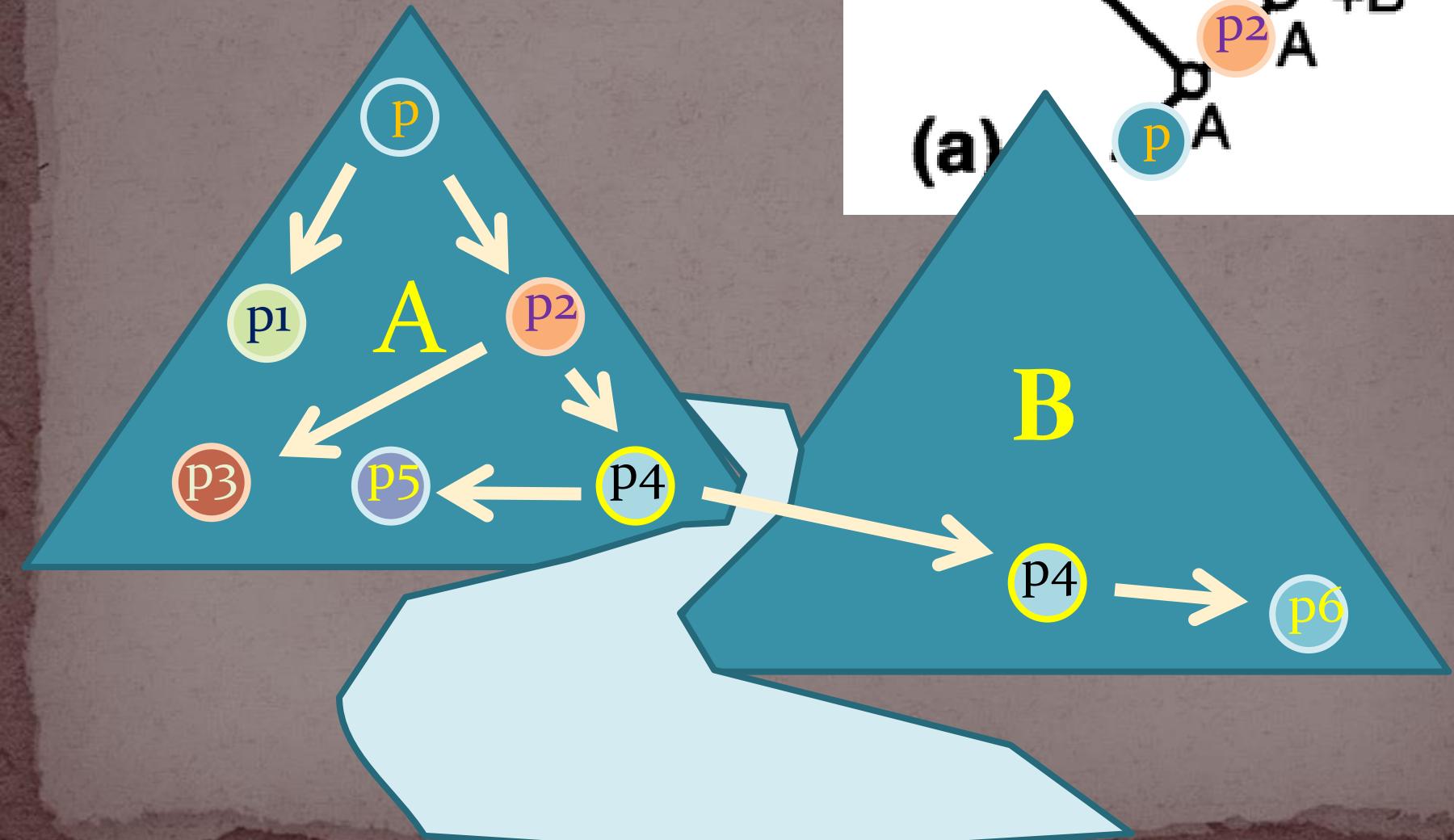


Two model:

- DIVA
- DEC

- —— Dispersal-Vicariance
- 扩散地理隔离分
- Vicariance



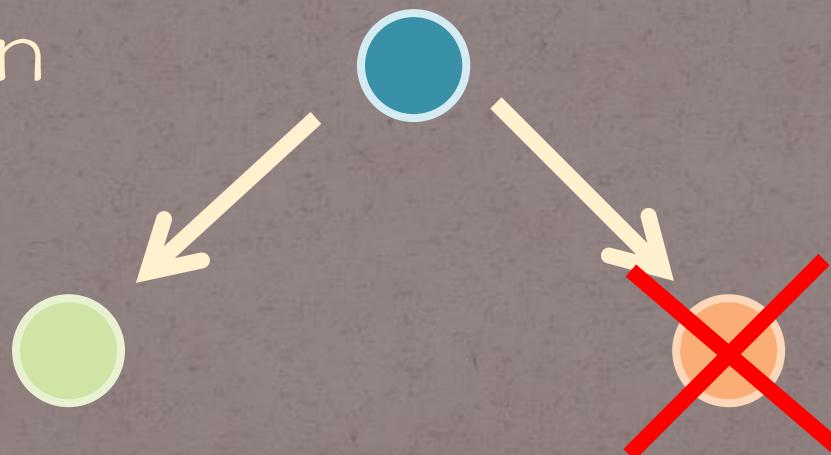


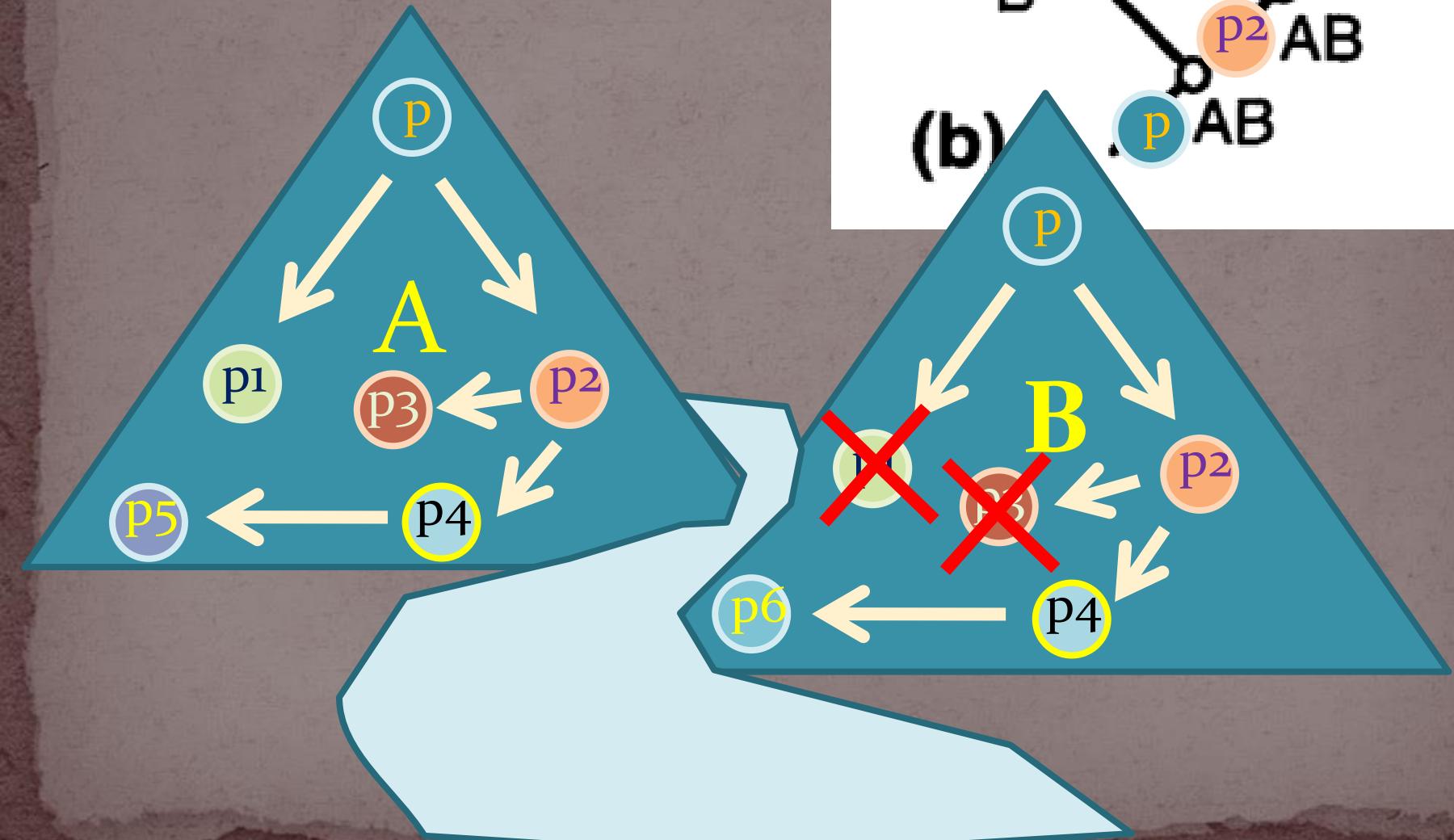
(a)

- The dispersal-extinction-cladogenesis model

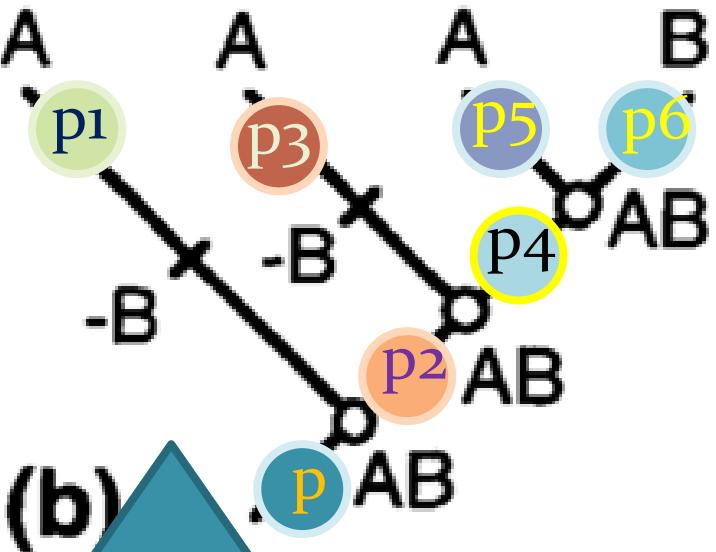
传播灭绝分枝进化模型

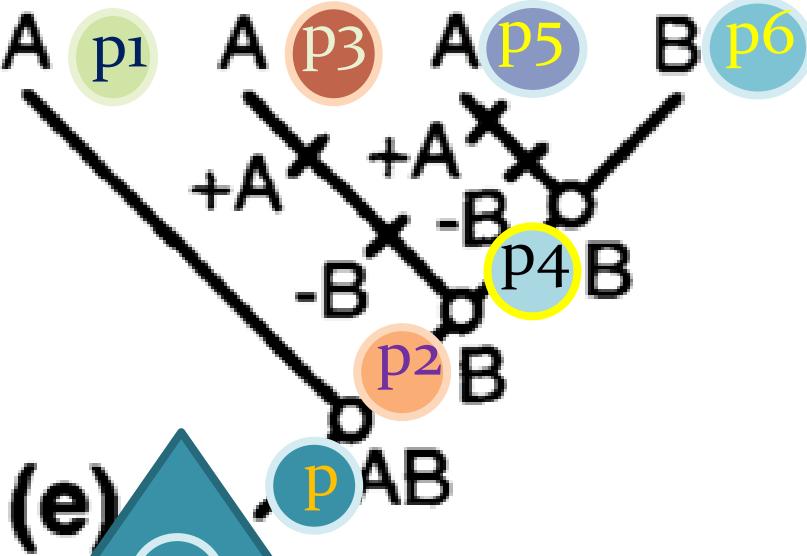
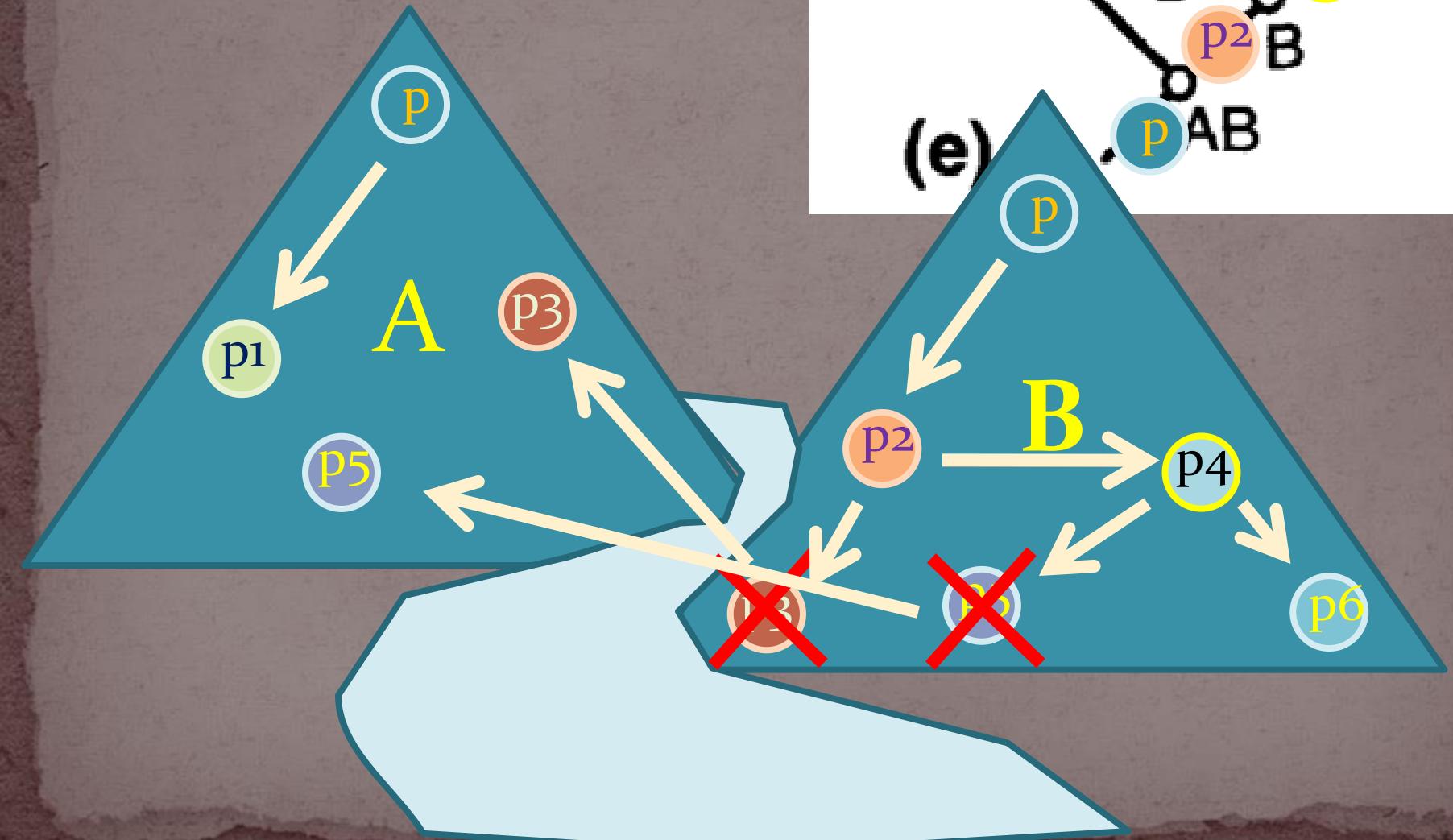
- extinction

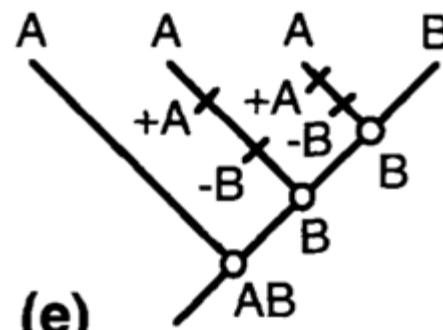
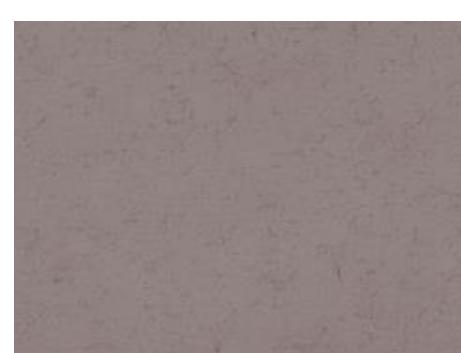
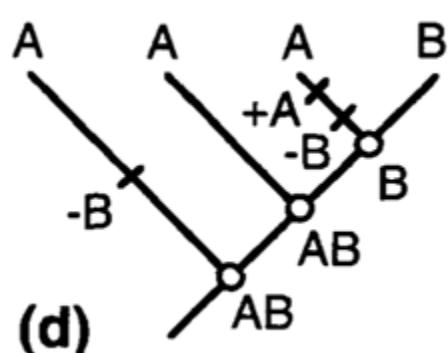
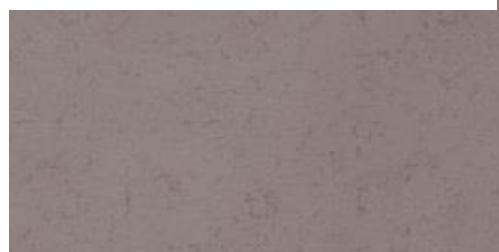
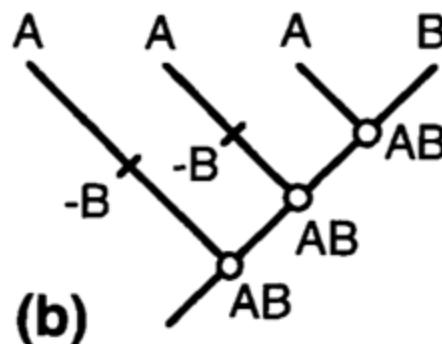
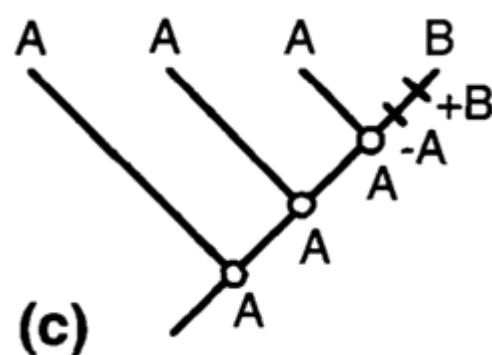
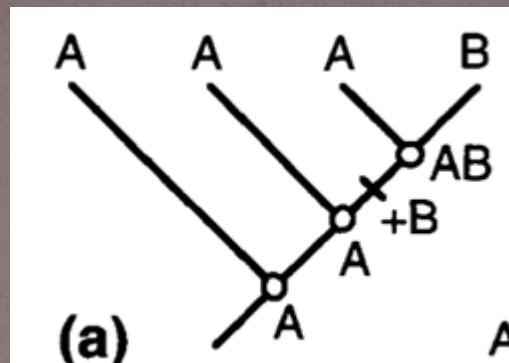




(b)







：

# 重建系统发育的祖先状态

：

- Detailed operating procedures:
- <http://www.docin.com/p-2090319329.html>

## S-DIVA 1.5c

File   Graphic   Analysis   Help

ID      Taxon      Distribution

## Option

Amount of trees:

0

Burn-in:

0

 Random trees

100

 Use Tree File Use DIVA output file Estimate P for a single node With an undefined sister (x) With omitted taxa distributed in  Hide status output

## Optimize

 Allow Reconstruction Max areas at each node  Age Weight Hold Bound Set command for final tree

Optimize Printrecs Maxareas=4 Weight=

- File->load tree

RASP (Reconstruct Ancestral State in Phylogenies) 3.2 Build 20150410 WIN32

File Graphic Analysis Tools Help

ID	Taxon	Distribution	Selected
6	P_mauiensis_		<input type="checkbox"/>
7	P_axillaris_H_		<input type="checkbox"/>
8	P_greenerella_		<input type="checkbox"/>
9	P_greenerella_		<input type="checkbox"/>
10	P_mammana_		<input type="checkbox"/>
11	P_hawaiiensis_		<input type="checkbox"/>
12	P_mammana_		<input type="checkbox"/>
13	P_mammana_		<input type="checkbox"/>
14	P_axillarisDL7_		<input type="checkbox"/>
15	P_grindelia_		<input type="checkbox"/>
16	P_hexandra_Rosa		<input type="checkbox"/>
17	P_hexandra_K1		<input type="checkbox"/>
18	P_hexandra_M		<input type="checkbox"/>
19	P_hexandra_O		<input type="checkbox"/>

Tree Options

Binary trees:

Amount of trees:

Oscillate trees:

Random trees:

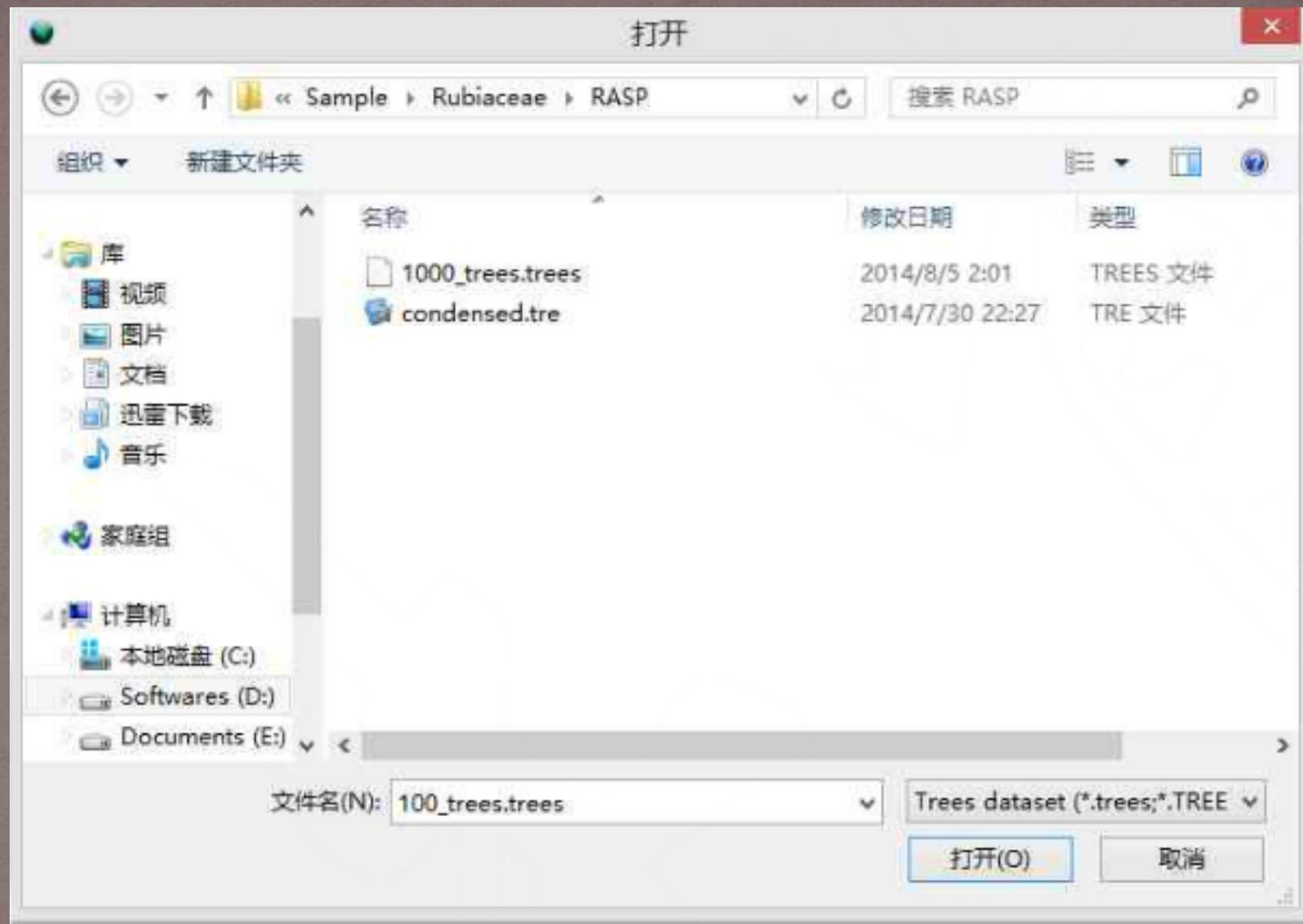
Current Condensed Tree:

PLEASE CHECK THE STATUS BEFORE ANALYSES

CHECK STATUS

Loading Trees Database...  
Load Trees Database Successfully!

- File->save distribution



- File->load tree->load trees

RASP (Reconstruct Ancestral State in Phylogenies) 3.2 Build 20150410 WIN32

File Graphic Analysis Tools Help

ID	Taxon	Distribution	Selected
1	Cecropia		
2	Cheirodora_alea		
3	Cissampela_p.		
4	Cinchona_cali		
5	Cinchona_ma.		
6	Cinchona_mit.		
7	Cinchona_ofic.		
8	Cinchona_oRa		
9	Cinchona_julis		
10	Circlospora_		
11	Condaminia_		
12	Coimbraea_		
13	Cubanota_du_		
14	Erosrema_sire		

Tree Options  
Binary tree: 1000  
Amount of trees: 1000  
Decent trees: 0  
 Random trees: 100

Current Condensed Tree:  
((109 53 407 105 445 287 95, (59 23 495))

**PLEASE CHECK THE STATUS BEFORE ANALYSIS**

10000 3.202480620289226 21 10.376047505253978 (1 0000 10.15928502505642)  
1 0000 18.575193868514524 (1 0900 5.352428259946325 40.53 56445547757235)  
1 0000 17.614035376281768 (44.53 860428203.64421  
0) (47.25 81671566384894.45 26.51671689884894)  
1 0000 11.56237085749 88298.43 38.4804252434872761  
1 0000 11.542577945567201 39.50 42388918902446  
0.6986 1.5643348206944817 46.52 107338005015971 1 0000 1.753099257252402  
1 0000 12.338362590209008 (1 0900 11.788957939965216 1 0000 5.963336809115167.  
Load Condensed Tree Successfully!

CHECK STATUS

- File->load Condense Tree

RASP (Reconstruct Ancestral State in Phylogenies) 3.2 Build 20150410 WIN32

**File** **Graphic** **Analysis** **Tools** **Help**

ID	Taxon	Distribution	Selected
1	Cephalanthus...		Γ
2	Chionoxa_alexa	ABCDEFISH	Γ
3	Citrusmusa_p	CF	Γ
4	Cinchona_cali	D	Γ
5	Cinchona_mia	CD	Γ
6	Cinchona_miaE	C	Γ
7	Cinchona_pfcc	C	Γ
8	Cinchona_pfca	C	Γ
9	Cinchona_pfcb	ACD	Γ
10	Cinchonostyle	F	Γ
11	Combretumka...	ACDEGH	Γ
12	Coimbraura...	ACDEFG	Γ
13	Cuscuta_dsi	B	Γ
14	Erythrina_bra...	B	Γ

**Tree Options:**

- Binarytree: 1000
- Amount of taxa: 1000
- Discard trees: 0
- Random trees: 100

**Current Condensed Tree:**  
((63 53 40 18 85 44 50 87 795, 59 33 4 854

**PLEASE CHECK THE STATUS BEFORE ANALYSIS!**

0.0000 19.6771938825 14524(1.0000 5.7524283 909420125 40.53 53.56445547757235)  
 1.0000 -12.5343353782817699 (44.53 3.6034242013.64421  
 0)147.26 8.16718666884934.45 26 0)197.16653344324  
 1.0000 11.663708574832235 43 29 483425241487276)  
 1.0000 11.942577845667201.39 50 423000 383024480  
 0.8938 1.5043548206944617.46 52.10733800 39188971.0000 1.7630982537252402)  
 1.0000 -12.321362500330009(1.0000 11.73895702036516)1.0000 5.083338600115197;  
 Load Condensed Tree Successfully!  
 Load Distributions Successfully!

**CHECK STATUS**

- File->load Distribution

Range

**Operation**

Range constraints		Fossils								
A	B	C	D	E	F	G	H	I	J	K
<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
B	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
C	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
D	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
E	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
F	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
G	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
H	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
I	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
J	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
K	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

**include**

- AB
- ABC
- ABCU
- ABCE
- ABCF
- ABCG
- ABCH
- ABCI
- ABCIJ
- ABCK
- ABD
- ABDE
- ABDF
- ABDO
- ABDH
- ABDI
- ABDU
- ABDK
- ABE
- ABEF
- ABEC
- ABFH
- ABEL
- ABEJ
- ABFK

**Exclude**

RASP (Reconstruct Ancestral State in Phylogenies) 3.2 Build 20150410 WIN32

**File** **Graph** **Analysis** **Tools** **Help**

ID	Taxon	Distribution	Selected
1	Cephalanthus_	All	<input type="checkbox"/>
2	Chionodora_ata	BCDEFGH	<input type="checkbox"/>
3	Chiosmaea_p	CF	<input type="checkbox"/>
4	Clethra_cst	D	<input type="checkbox"/>
5	Clethra_ma	CD	<input type="checkbox"/>
6	Clethra_mlf	C	<input type="checkbox"/>
7	Clethra_ofc	C	<input type="checkbox"/>
8	Clethra_spa	C	<input type="checkbox"/>
9	Clethra_pus	ACD	<input type="checkbox"/>
10	Clethraopis	F	<input type="checkbox"/>
11	Condaliarea_	ACDEGH	<input type="checkbox"/>
12	Comptonia_	ACDEFG	<input type="checkbox"/>
13	Cotinolia_st	B	<input type="checkbox"/>
14	Eriothema_lne	B	<input type="checkbox"/>

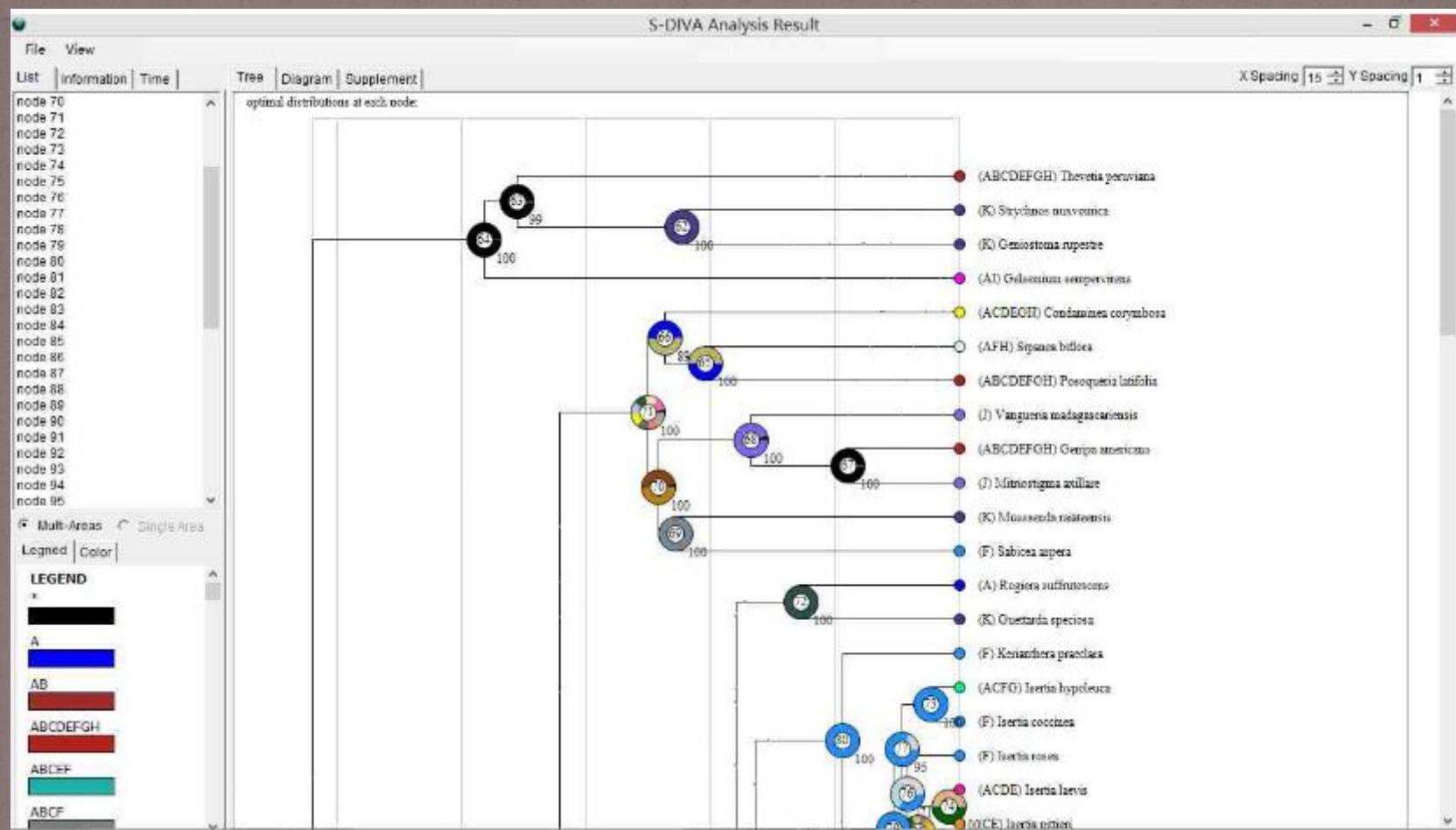
Load Condensed Tree Successfully!  
Load Distributions Successfully!

Statistical Dispersal-Vicariance Analysis™

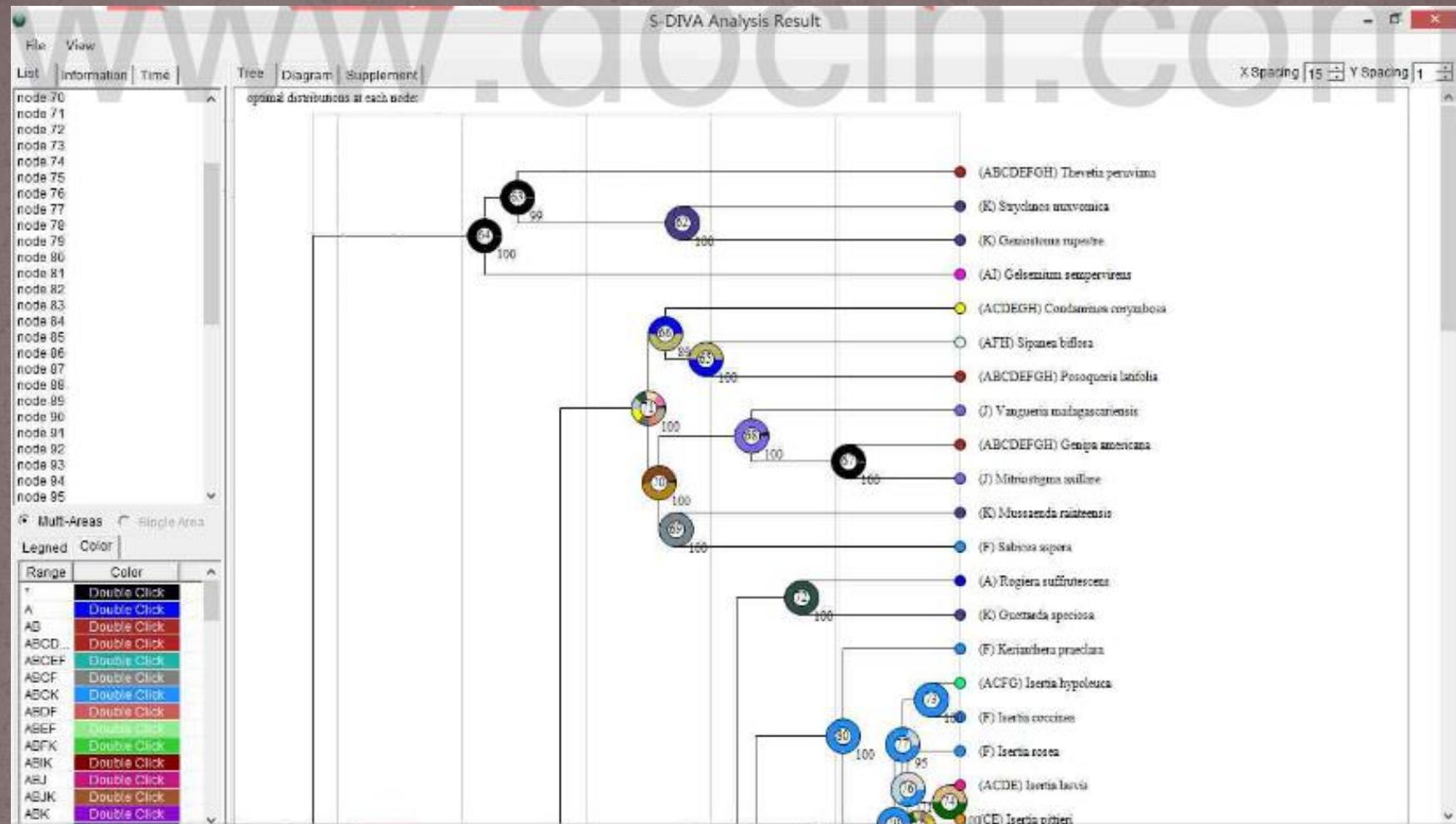
Process began at 5/1/2015 6:58:11 PM  
Using command: optimize Maxareas=4 min\_bsf1 rnf2 keep=5536  
Condensed tree used command: optimize Maxareas=4 min\_bsf1 rnf2 keep=5536

**Optimize...**

- Analysis-> Statistical Dispersal Vicariance Analysis



## • Graphic->Tree view

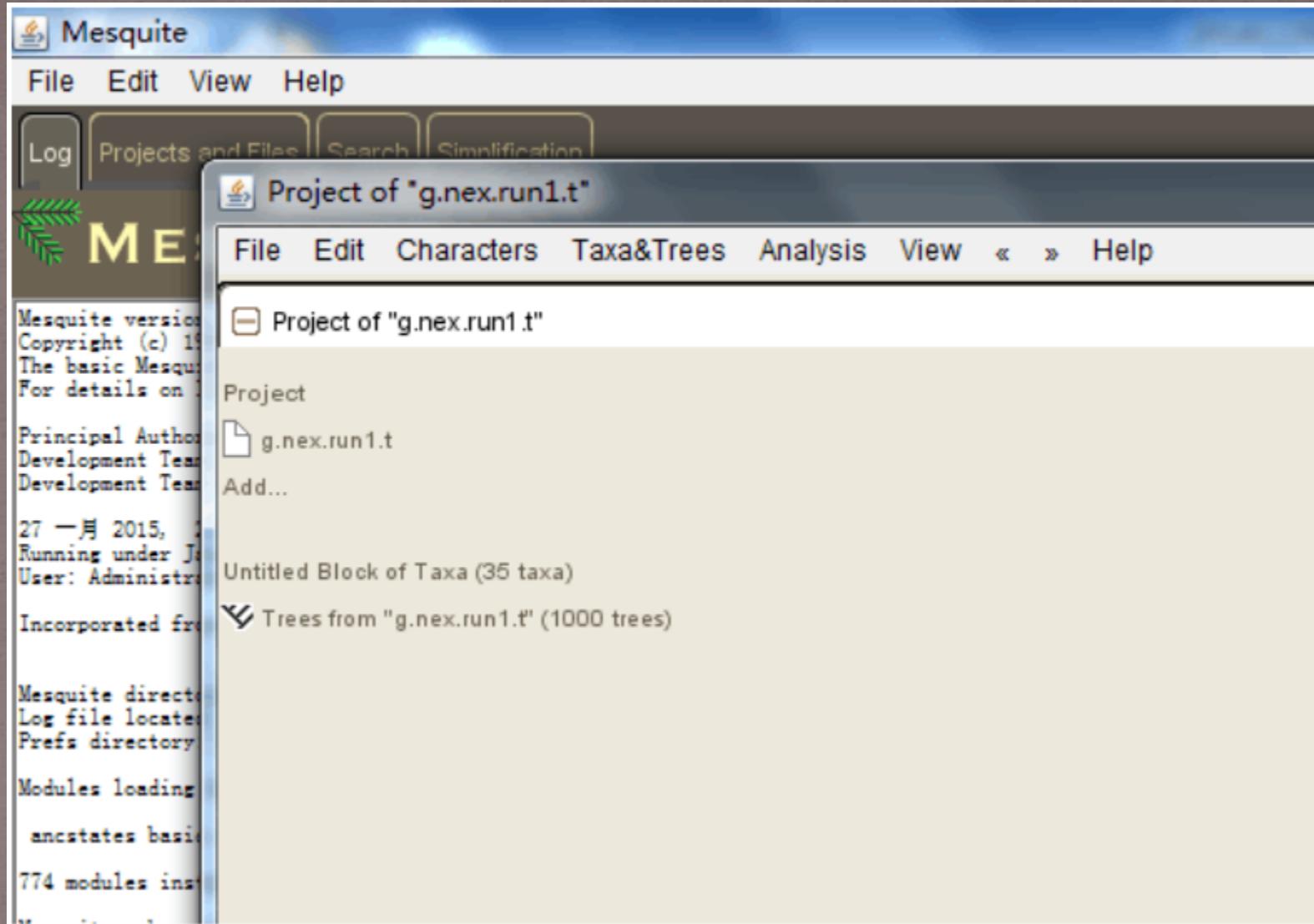


- Color
- File-> Export Graphic

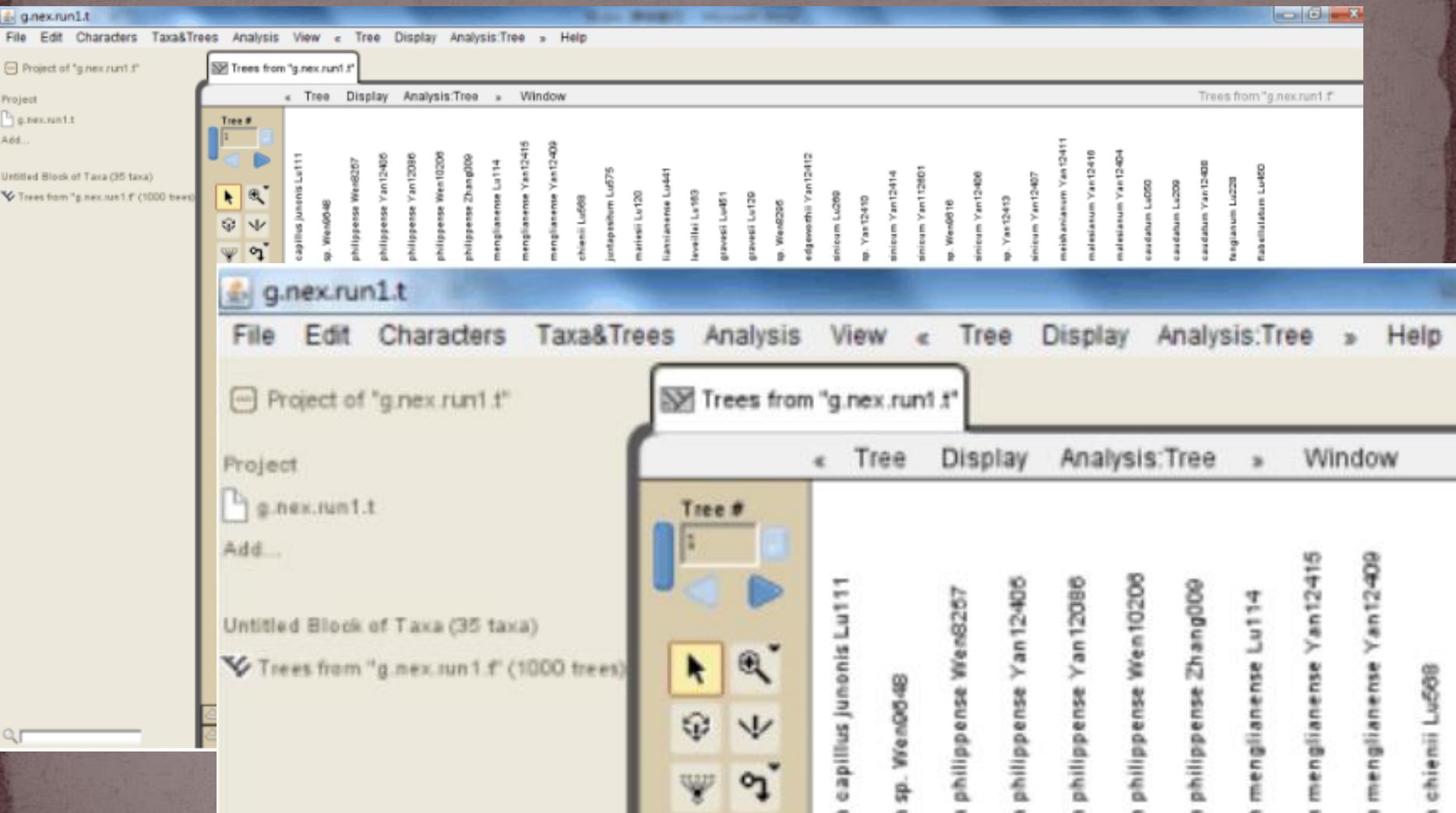




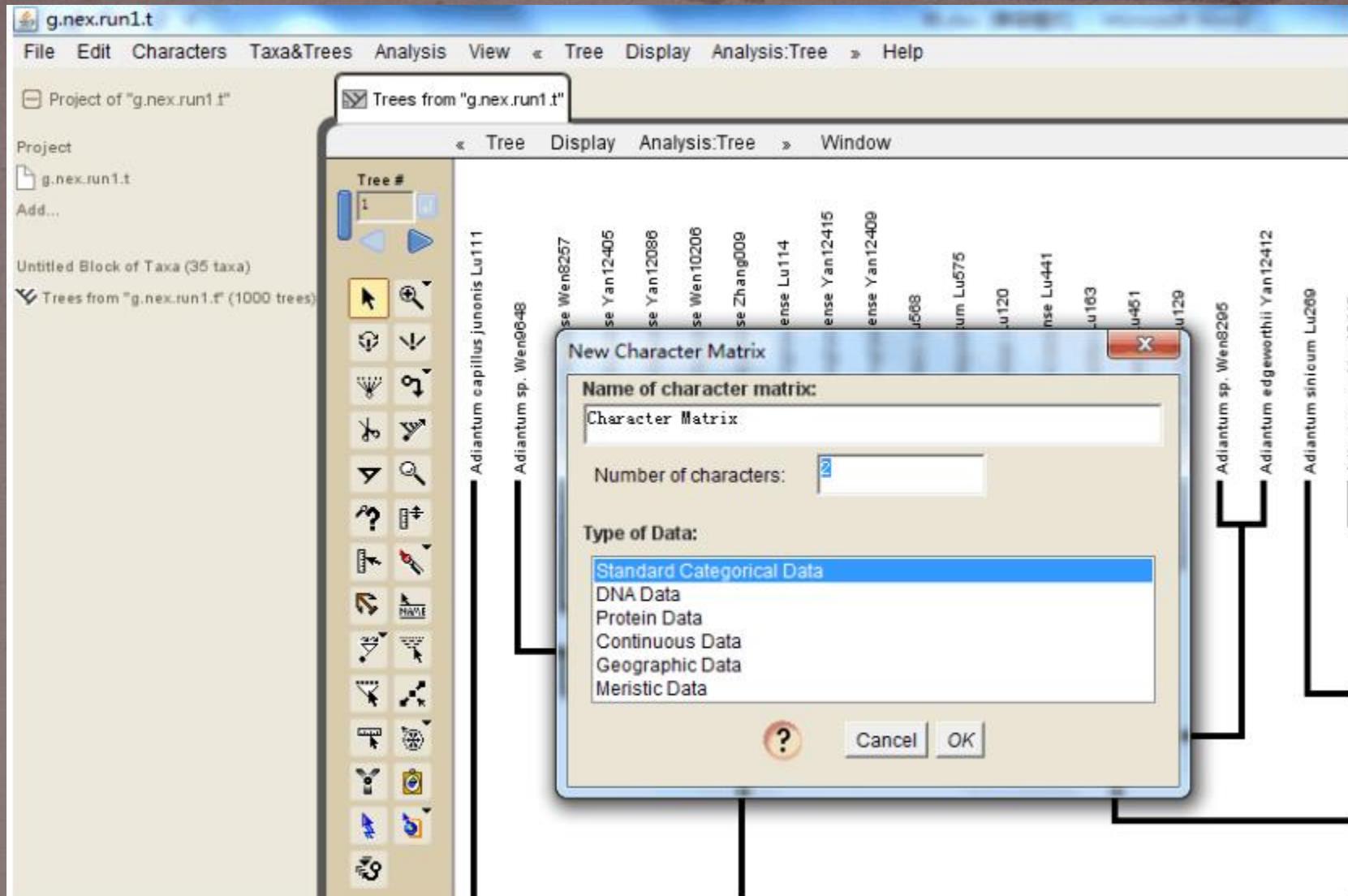
- Detailed operating procedures:
- <https://wenku.baidu.com/view/f17a326cf18583do496459ce.html>



- File->load tree



• Trees from " " ->view tree



- Characters->New empty matrix (Number of characters)->ok

g.nex.run1.t

File Edit Characters Taxa&Trees Analysis View « Matrix Select Display Analysis:Matrix

Project of "g.nex.run1.t"

Trees from "g.nex.run1.t" Character Matrix

Matrix Select Display Analysis:Matrix Window

g.nex.run1.t

Add...

Untitled Block of Taxa (35 taxa)

Character Matrix (2 characters)

Trees from "g.nex.run1.t" (1000 trees)

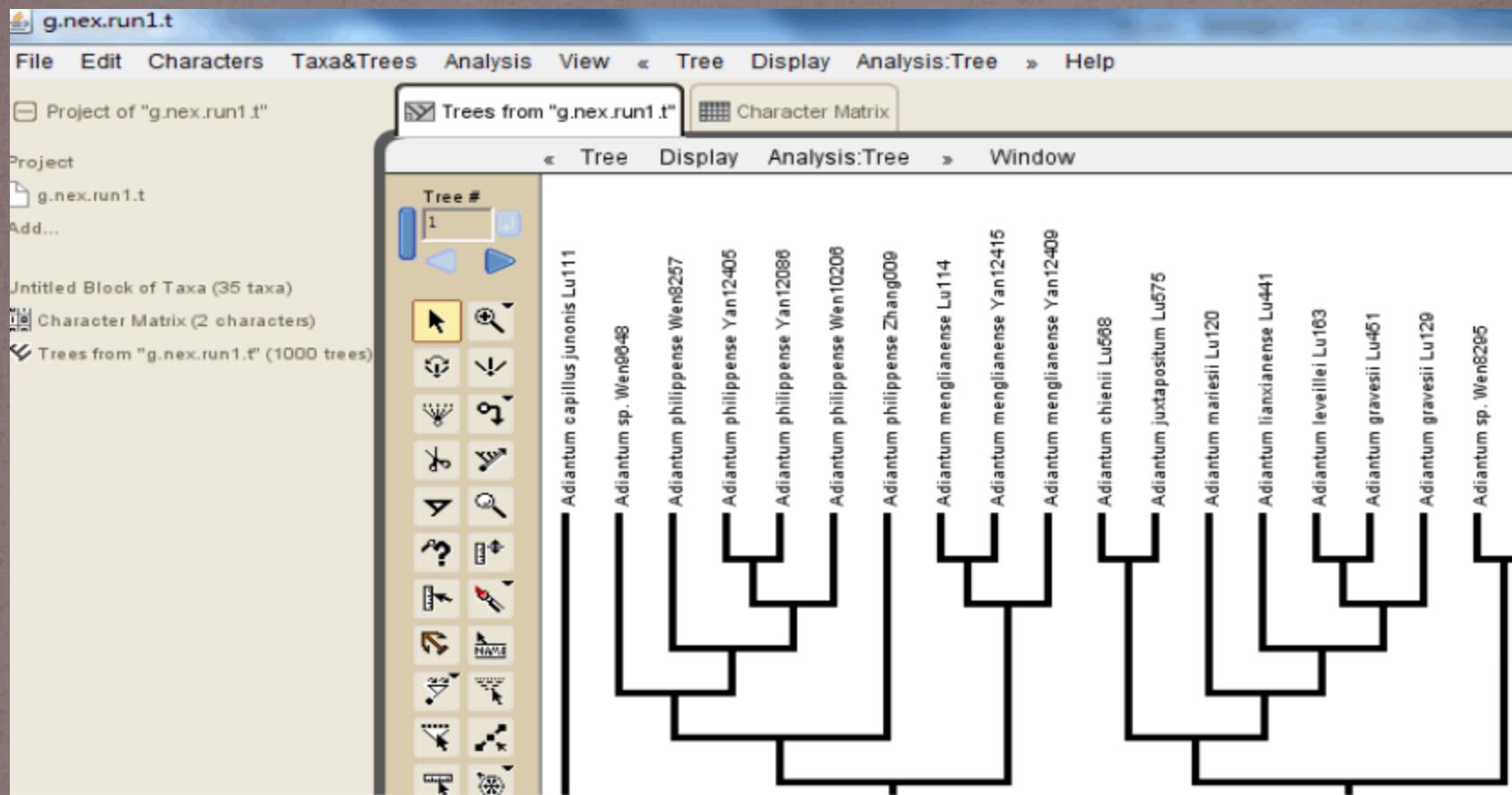
« Matrix Select Display Analysis:Matrix » Window

Taxon \ Character

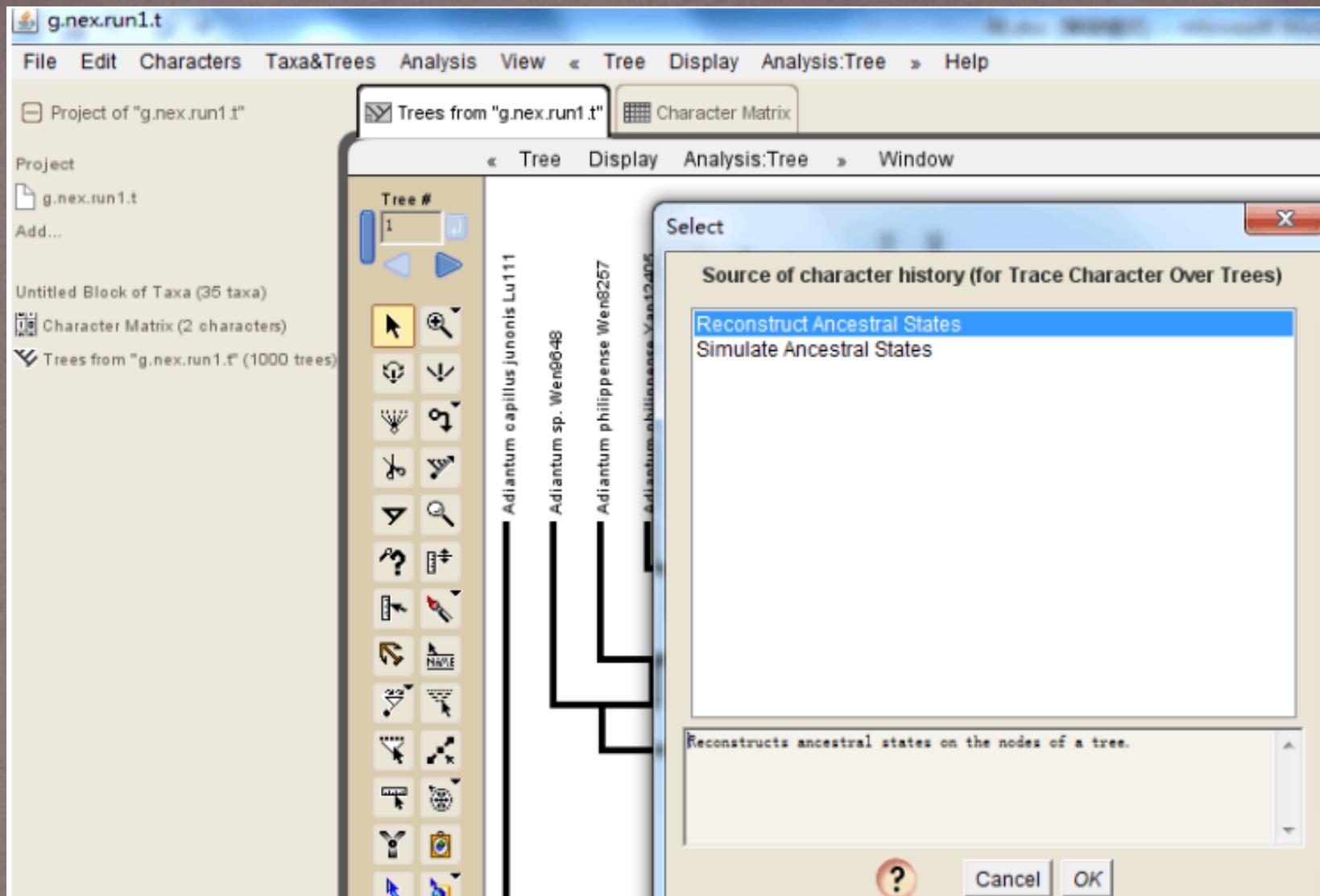
	1	2	?
1	Adiantum caudatum	2	2
2	Adiantum edgeworthii	1	1
3	Adiantum malesianum	2	2
4	Adiantum malesianum	2	2
5	Adiantum meishanianum	1	0
6	Adiantum menglianense	0	0
7	Adiantum menglianense	0	?

The screenshot shows the Mesquite software interface. The title bar reads "g.nex.run1.t". The menu bar includes File, Edit, Characters, Taxa&Trees, Analysis, View, « Matrix, Select, Display, Analysis:Matrix, » Window. A toolbar on the left lists Project, g.nex.run1.t, Add..., Untitled Block of Taxa (35 taxa), Character Matrix (2 characters), and Trees from "g.nex.run1.t" (1000 trees). The main window displays a character matrix titled "Trees from 'g.nex.run1.t'" with "Character Matrix" as the active tab. The matrix table has columns for Taxon (1-7) and Character (1-2). Some cells contain values like RF, RA, or question marks. A vertical toolbar on the left contains icons for selection, zoom, and other functions. A red arrow points to the "Select" tab in the top menu bar.

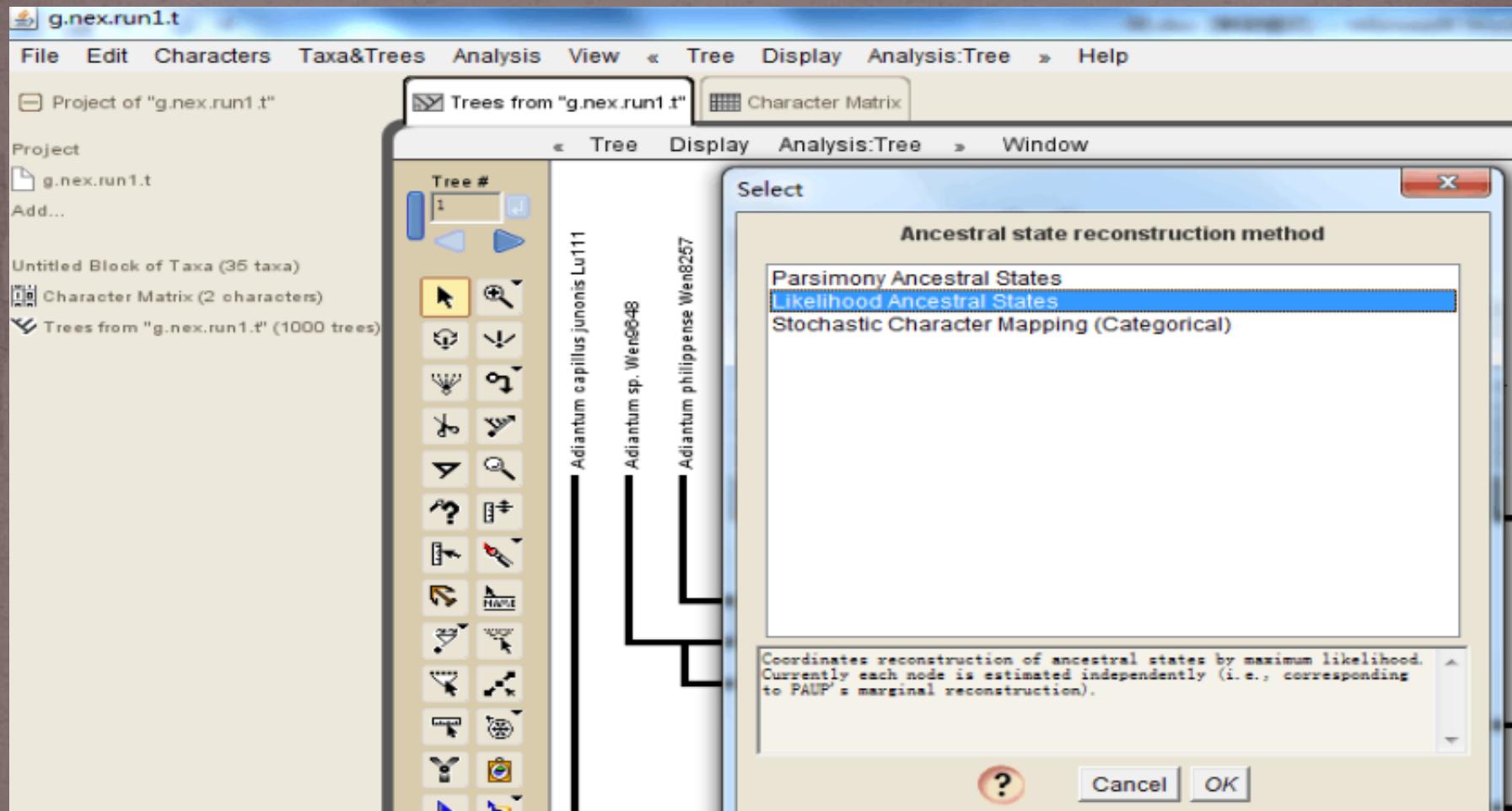
- Edit character name



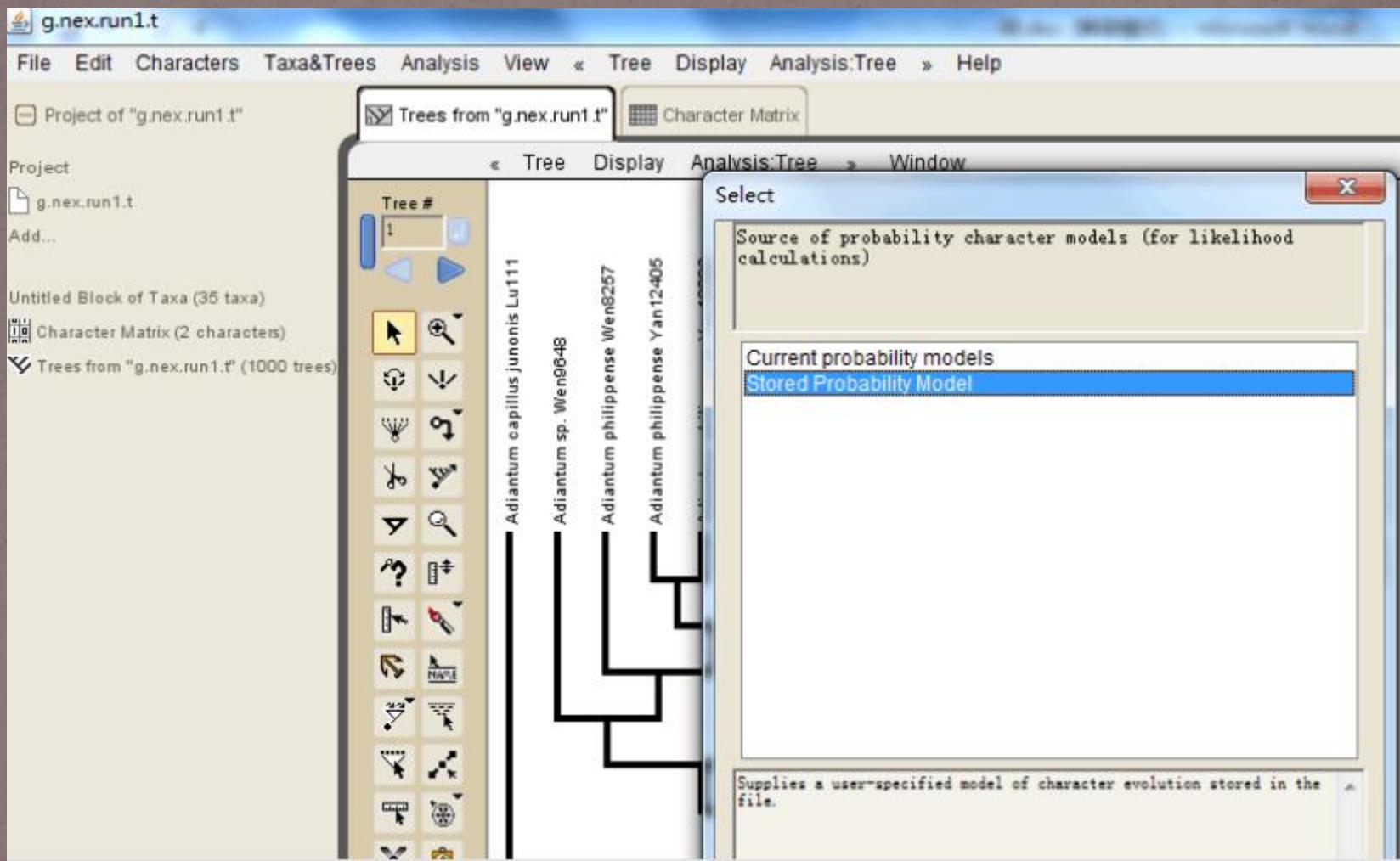
- Click: Trees from " " "



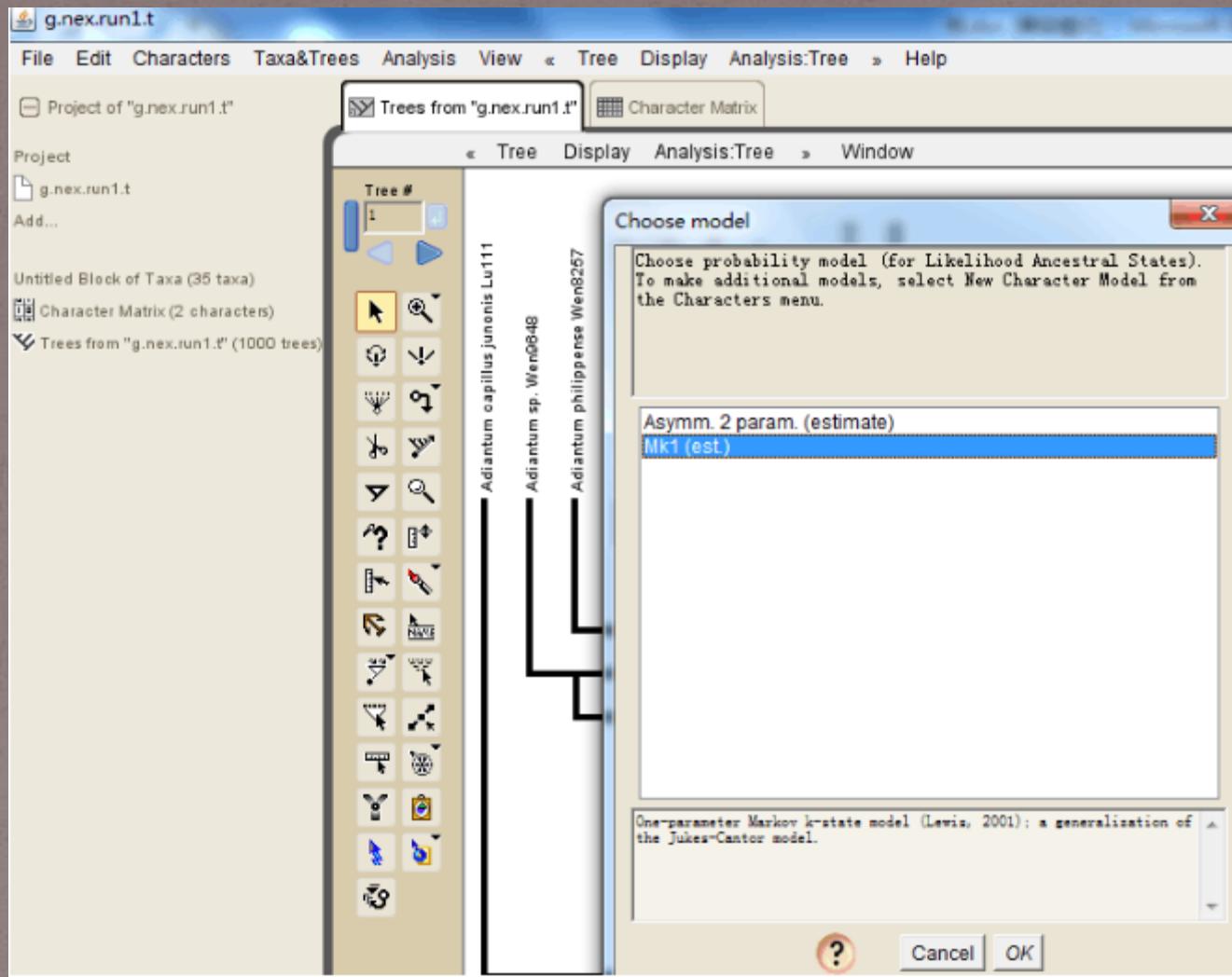
- Analysis: trace characters over trees->ok



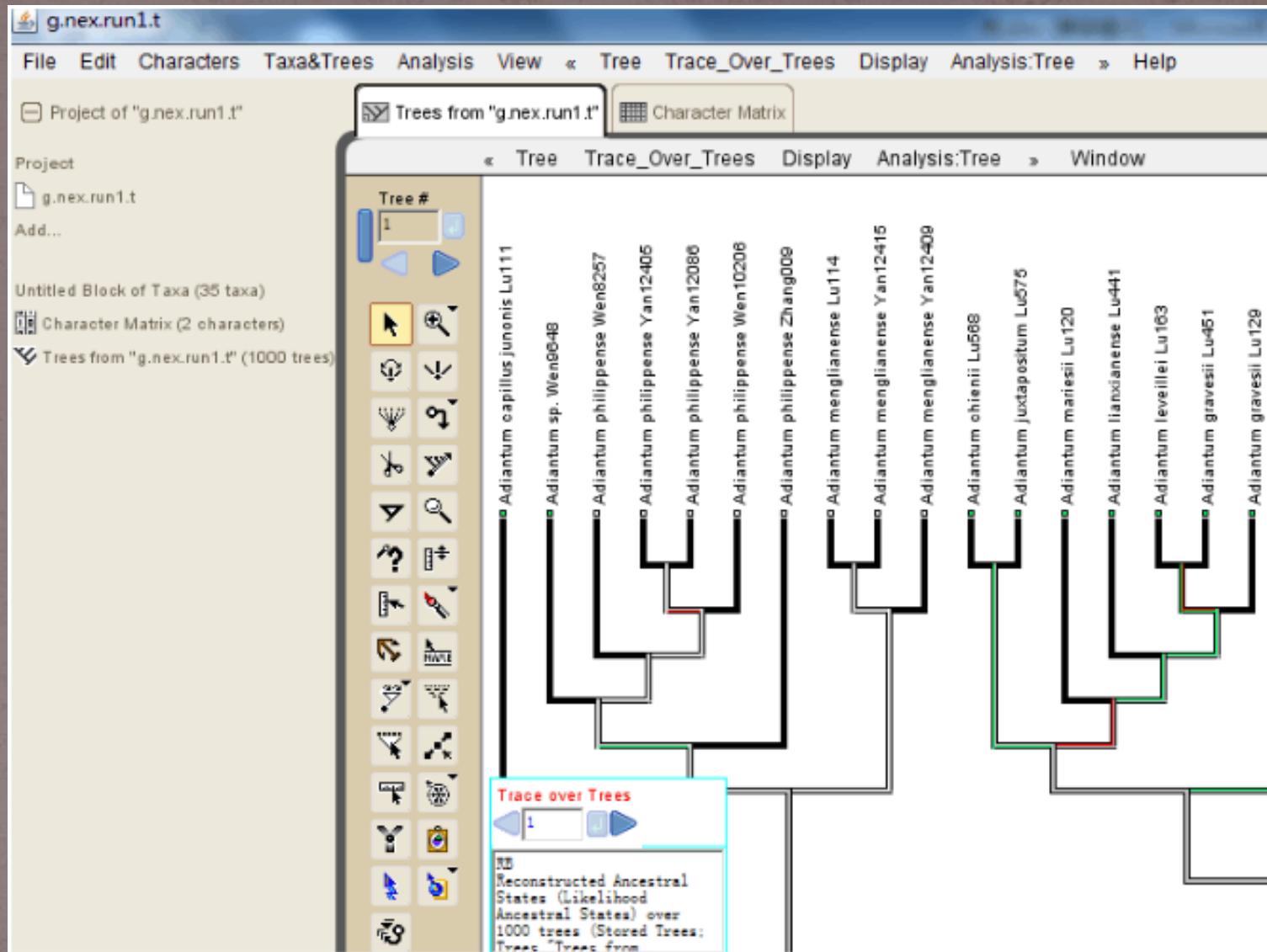
- Likelihood ancestral states



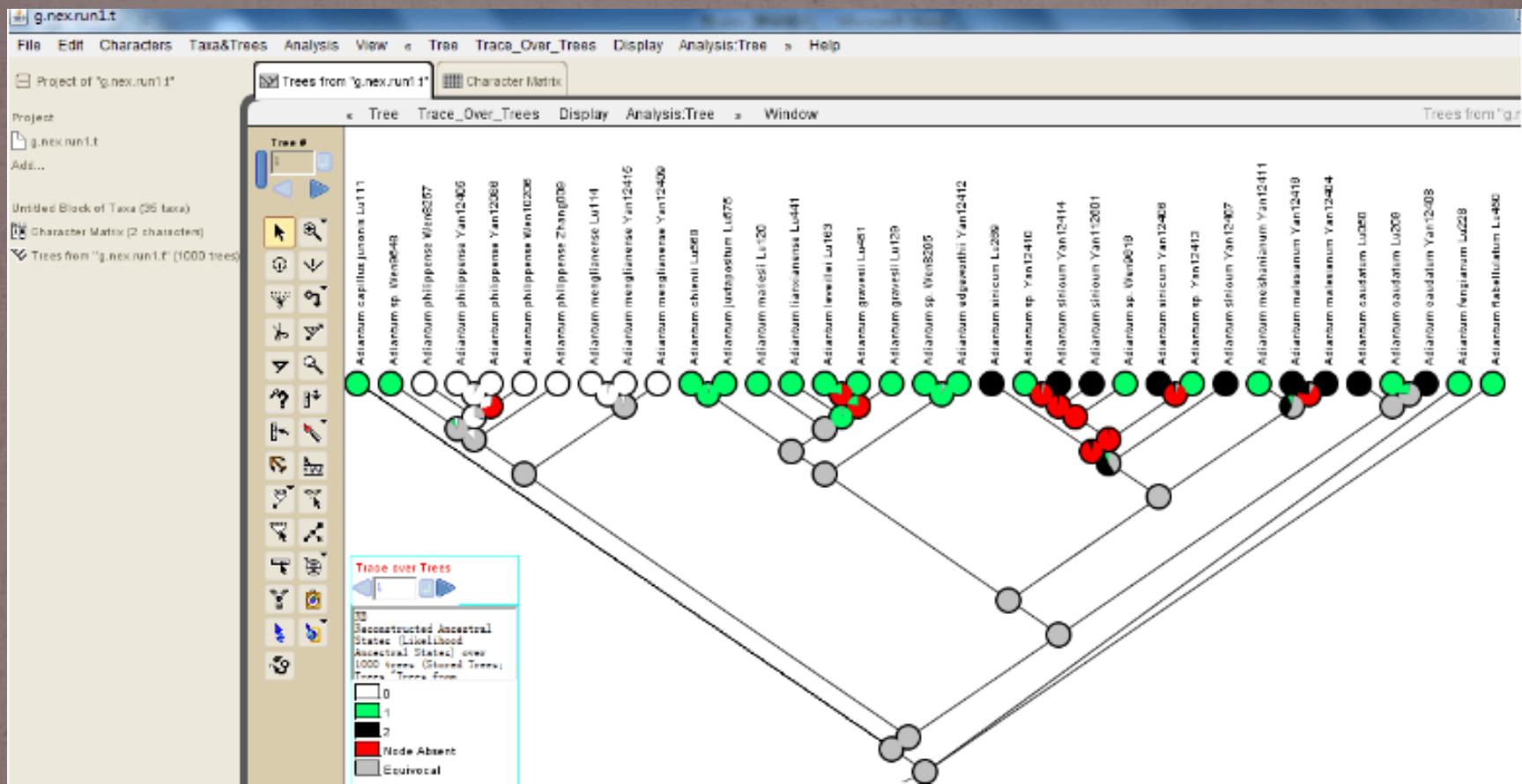
- Stored probability model



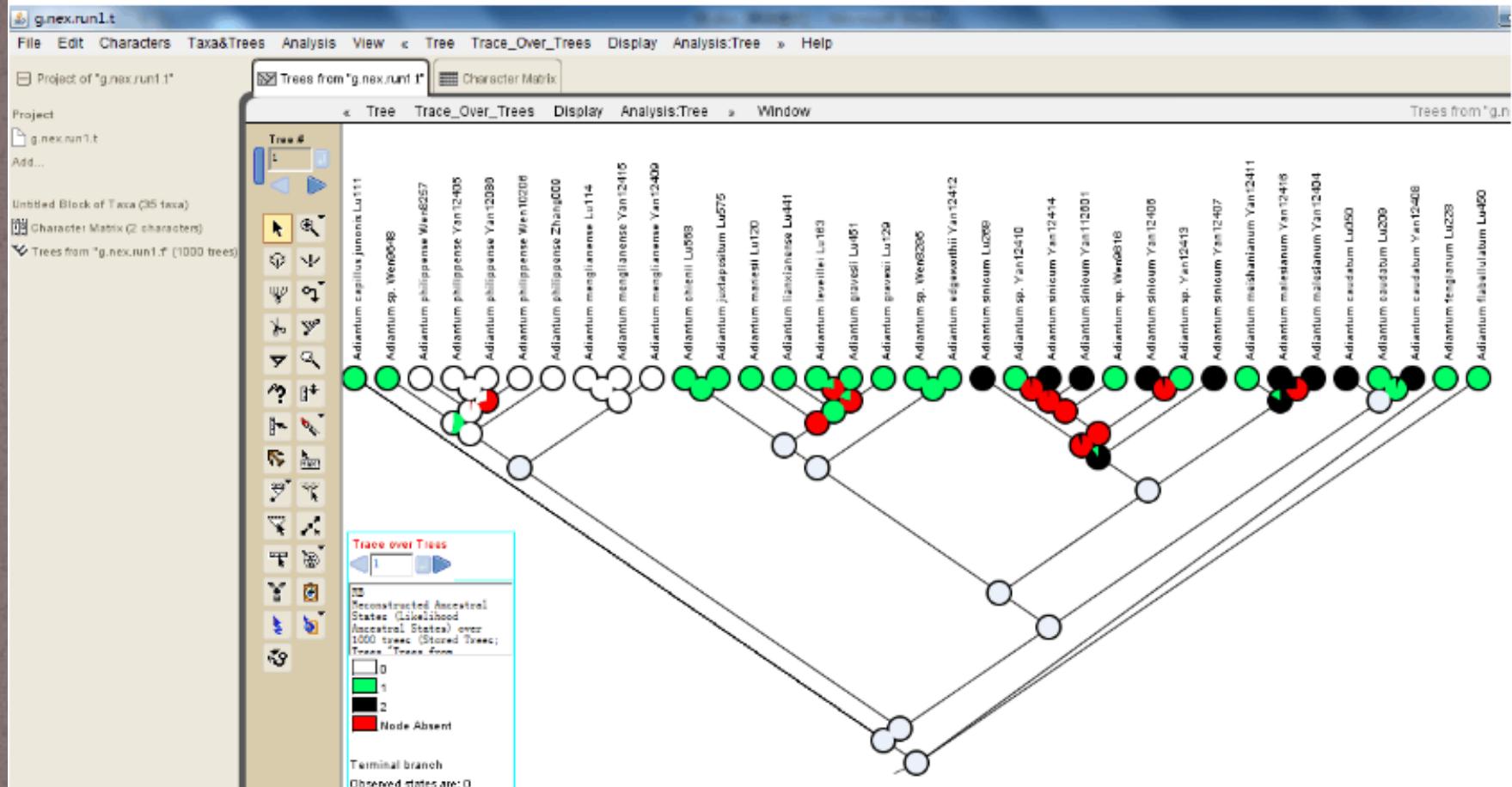
- Shade states-> stored trees->MK1(est)



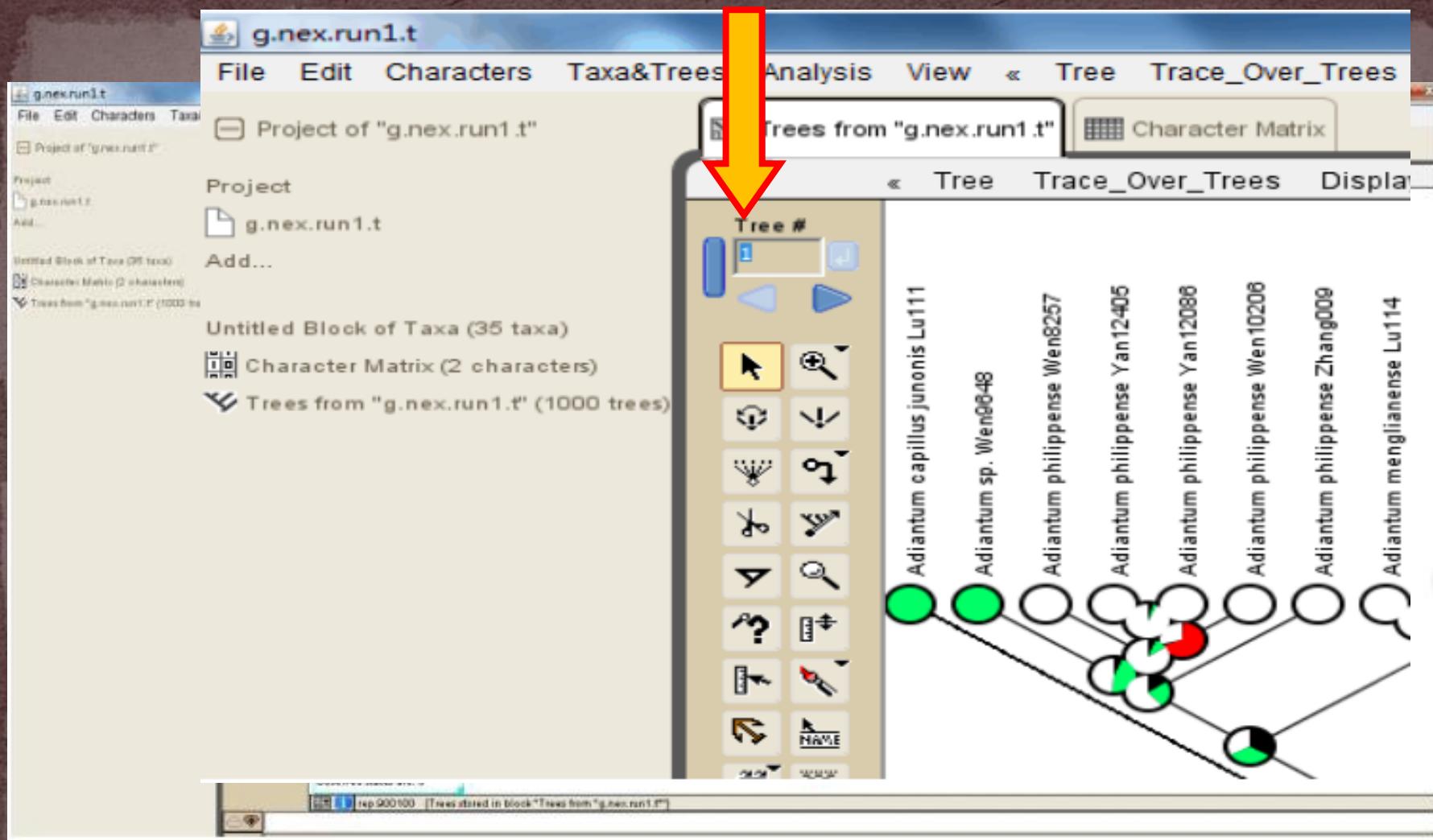
- Display->tree from->Ball & sticks



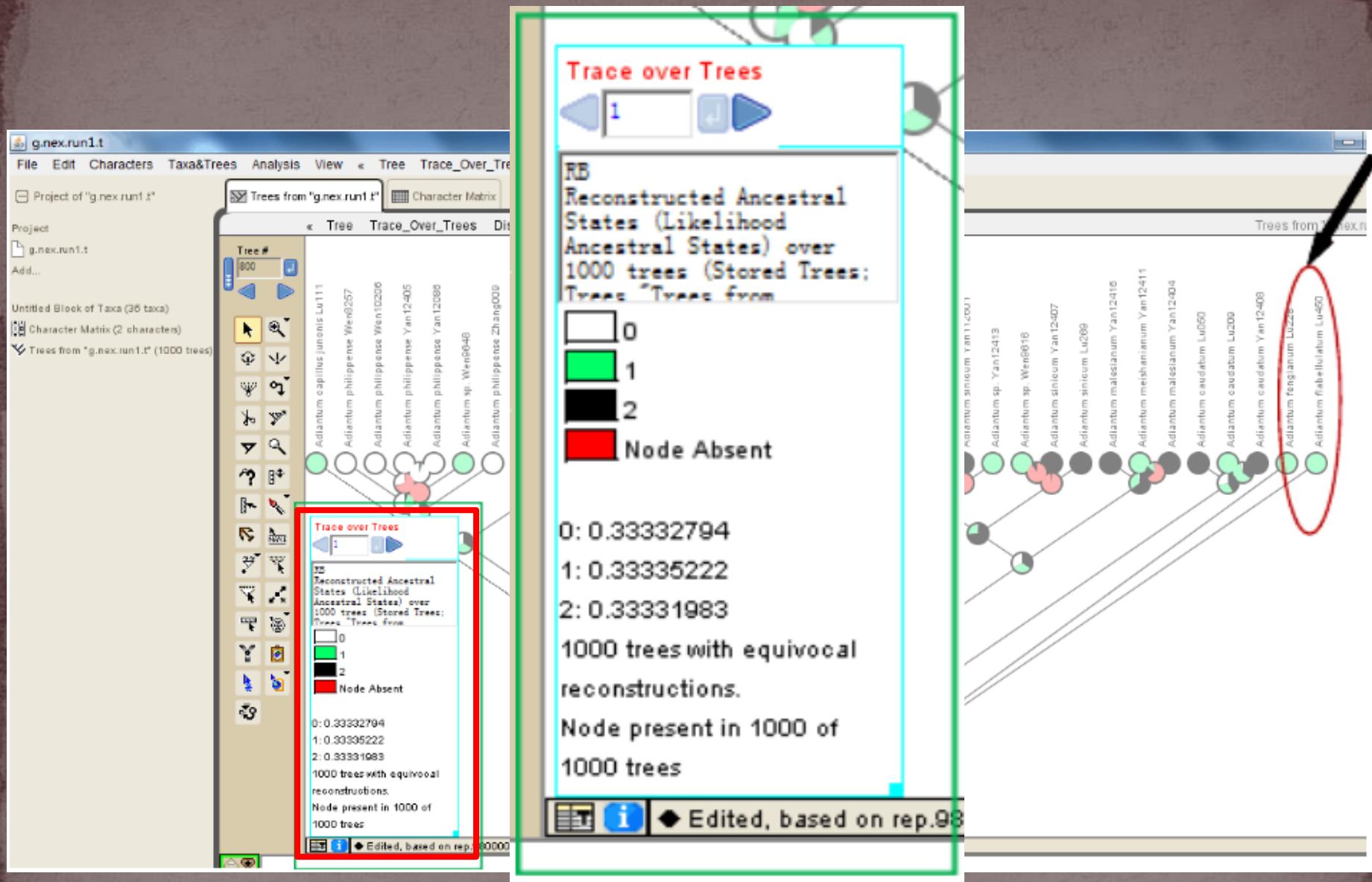
- trace over trees-> Show fractions of trees with Equivocal (Remove the “✓” )



- trace over trees-> Calculate-> Average frequencies across trees



- Likelihood ancestral states->



## • Character of ancestor

