## 13.xi.

1. a posteriori weighting
2. optimization
3. summary

## CHARACTER WEIGHT



## CHARACTER WEIGHT



## CHARACTER WEIGHT

information from ch. Y is more reliable than from ch. X
in analysis more weight for $Y$ than $X$
weighting made using rescaled consistency index ( $r \times c$ )

## CHARACTER WEIGHT

A POSTERIOR/ (after analysis)

1) cladistic analysis
2) $\mathrm{rx} \times \mathrm{c}$ calculated for all characters on shortest tree
3) characters weighted with the value of $r \times c$
4) re-analysis Farris, J.S. 1969. A successive approximations
5) back to 2) approach to character weighting. Systematic Zoology 18:374-385.
2-5 repeated until result stabilizes (tree length \& ch. weights), i.e. in two analyses following each other same result obtained

## CHARACTER WEIGHT

central assumption in a posteriori weighting is that characters with lots of homoplasy (those WITHOUT reliable signal about evolutionary history) are not as reliable hypotheses of homology as characters with very little homoplasy (part of historical signal), i.e. congruent with other characters

## IMPLIED CHARACTER WEIGHTING

Goloboff, P.A. 1993. Estimating character weights during tree search. Cladistics 9:83-91.
differential weighting is performed from the very start of the analysis
weighting performed during analysis using consistency
related index $c=m / s$, CONCAVE weighting function

## CHARACTER WEIGHT



## IMPLIED CHARACTER WEIGHTING

differential weighting is performed from the very start of the analysis
weighting performed during analysis using consistency related index $(k+1) / s+k+1-m$
this means that increase/decrease of ch. state changes in characters with less homoplasy (high index value) affect result more than same kind of changes in characters with much homoplasy (low index value) ---->

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this means that increase/decrease of ch. state changes in characters with less homoplasy affect result more than same kind of changes in characters with much homoplasy (low index value) ----> preference of trees were CHARACTERS WITH LESS HOMOPLASY ARE MORE DECISIVE
instead of trying to find a tree with smallest number of ch. state changes this approach tries to find a TREE MAXIMIZING FIT

Stomatophyta


Källersjö, M., V.A. Albert, \& J.S. Farris 1999. Homoplasy increases phylogenetic structure. Cladistics 15:91-95
nucleotide triplets coding for aminoacids


## INDICES DESCRIBING TREES

## individual character

$$
c=\frac{m}{\mathrm{~m}}
$$



ALL characters (ensemble indices

$$
C=\frac{\sum m}{\sum s}
$$

$$
R=\frac{\sum g-\sum s}{\sum g-\Sigma m}
$$

ATTENTION! it might be HIGHLY informative to calculate indices also LOCALLY, i.e. for certain clades


58 evolutionary changes

## OPTIMIZATION






## OPTIMIZATION

Farris, J.S. 1970. Methods for computing Wagner trees.
Systematic Zoology19: 83-92.

Fitch, W.M. 1971. Toward defining the course of evolution : minimal change for a specific tree topology.

Systematic Zoology 20: 406-416.




ATTENTION! LENGTH of diagram, number of ch. state changes, calculated already at this stage. Unions ( $\cup$ ) add always one ch. state change.

" upward pass" rules (Fitch 1971, Wheeler 2012)

- root final state set $=$ root preliminary state set $(F=P)$

RULE 1. If the overlap of the preliminary state, $P$, of the node and its ancestor, $A$, is equal to $A$, (if $A \cap P=A$ ) then the final state set, $F$, is equal to that of the ancestor $(F=A)$.

RULE 2. If Rule 1 does not apply and the union of final/preliminary states of the 2 descendants of the current node (Left and Right) are equal to preliminary states of the current node $(P=L \cup R)$, then $F=P \cup A$.

RULE 3. If Rule 1 and 2 do not apply the final state set is the preliminary state set, supplemented by state set that is common to the ancestor and descendants $(F=P \cup(L \cap A) \cup(R \cap A))$.


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o
1
$\{0,1\}$

24 E F
$\{2,4\}$
$\{0,1,2,4\}$

RULE 2. If Rule 1 does not apply and union of final/preliminary states of 2 descendants of current node (Left and Right) are equal to preliminary states of current node $(P=L \cup R)$, then $F=P \cup A$.
$\{0,1\}$
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## Wagner optimization

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Systematic Zoology 20: 406-416.

## FITCH PARSIMONY <br> 

WAGNER PARSIMONY
o <--> 1 <--> 2


RULE 1: if terminals share character state this will be marked also for their ancestor (intersection, $\cap$ )

RULE 2: if terminals do not share ch. states (intersection, $\cap=\varnothing$ ) assign smallest closed interval between states of terminals for their ancestor, i.e.
$[a, b]=\{x \mid a \leq x \leq b\}$

FITCH PARSIMONY

$$
\begin{array}{ll}
A=\{0,1,2,3\} & \\
B=\{\cap B=\varnothing \\
B=\{5,6\} & \\
A \cup B=\{0,1,2,3,4,5,6\}
\end{array}
$$

WAGNER PARSIMONY $0<-->1<-->2$

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\begin{aligned}
& A=\{0,1,2,3\} \\
& B=\{5,6\}
\end{aligned}
$$

$$
A \cap B=\varnothing
$$

$$
A \cup B=[3,5]=\{x \mid 3 \leq x \leq 5\}
$$

## WAGNER PARSIMONY <br> o <--> 1 <--> 2

$$
\begin{array}{rl}
A & =\{0,1,2,3\} \\
B & A \cap\{5,6\} \\
& A \cup B=\{3,4,5\}=\{x \mid 3 \leq x \leq 5\}
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"upward pass" rules (Goloboff 1993)

- PRELIMINARY $(P)$ state set for root and terminals is their final set ( $P=F$ )

RULE 1. If $A \cap P=A, F=A$.
$A$, character state of immediate ancestor

RULE 2. If rule 1 does not apply, and $(L \cup R) \cap A \neq \varnothing$, define $X$ as $X=(L \cup R \cup P) \cap A$. If $X \cap P \neq \varnothing, F=X$. If $X \cap P=\varnothing, F$ equals the LARGEST closed interval between $X$ and state in $P$ closest to $X$.

RULE 3. If rules $1 \& 2$ do not apply, $F$ equals the LARGEST closed interval between the state in $P$ closest to $A$ and the state in ( $L \cup R$ ) closest to A.




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WAGNER PARSIMONY $0<-->1<-->2$

RULE 2.

$X=\{0,1,2,3\}$
$P=\{5,6\}$
$X \cap P=\varnothing$
$F=[0,5]=\{x \mid 0 \leq x \leq 5\}$

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## UPWARD <br> PASS




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## [0,1]

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## UPWARD PASS

$[0,1]$







## SUMMARY

a posteriori character weighting is objective but justification
still debated implied weighting made during the search
optimization has to be used in order to find shortest tree \&
to find character states for internal nodes
MULTIPLE equally parsimonious reconstructions are possible

