Summarising Sets of Phylogenies

Consensus Trees and Split/Consensus Networks

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EMBL Heidelberg
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Thanks to...

- Sheila
- Mtakai
- Other course organisers and contributors
- EMBL and Toby Gibson (my supervisor)
- You for your participation!
Consensus Trees and Split/Consensus Networks

A question for the participants...

• Any experience of using/building them?

• Can you describe any applications of them?
Example Applications: Comparing Trees Estimated with Different Methods

Identifying agreement/similarity between tree topologies

Do all East African cichlids share a unique common ancestor?

Maximum Likelihood

Maximum Parsimony

Relatively 'easy' to ask this with just a few trees (2) each with few taxa (35) - more difficult with more trees and more taxa...

Example Applications: Comparing Trees Estimated from Different Loci

Identifying agreement/similarity between tree topologies

Is the simian immunodeficiency virus infecting Western lowland gorillas more closely related to viruses found in chimpanzees or in humans?

Four trees estimated, one from each of four different HIV/SIV genes

Again, as in the previous slide - 'easy' to ask this with just a few trees (4) each with few taxa (25) - again, this is more difficult with more taxa and trees

Origin and biology of simian immunodeficiency virus in wild-living western gorillas.
Figure 4: Copyright © 2010 by the American Society for Microbiology.
Example Applications:
Analysing Trees from Bootstrap/Bayesian Analyses

Identifying clans with unambiguous phylogenetic signal in a set of sampled trees

Characterization of DrCol15a1b, a Novel Component of the Stem-Cell Niche in the Zebrafish Retina.
Gonzalez-Nunez V, Nocco V, Budd A.
Stem Cells. 2010 Jun 14. PMID: 20549708
Example Applications: Analysing Trees from Bootstrap/Bayesian Analyses

SuppFig3A

Fig7

Identifying clans with unambiguous phylogenetic signal in a set of sampled trees

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Example Applications: Analysing Trees from Bootstrap/Bayesian Analyses

Interpreting non-tree-like region of the split network as evidence for reticulate evolution (here recombination in viruses)


“Reticulate” Networks

Describing evolutionary scenarios where some OTUs are believed to share multiple parental lineages

Recombination


Hybridisation

Reconstructing the evolutionary history of polyploids from multilabeled trees. Huber KT, Oxelman B, Lott M, Moulton V. Mol Biol Evol. 2006 Sep;23(9):1784-91. PMID: 16798795
Which of A, B, C, and D is NOT equivalent to E? (i.e., has different topology)
Which of A B C and D is NOT equivalent to E? (i.e. has different topology)
Each branch of a tree describes a **split** of OTUs into two sets. These sets correspond to the two clans associated with the branch.

e.g. black branch of the tree specifies the split $ABCD \mid EFG$

- can also be written $ADCB \mid GFE$ etc.
- i.e. the taxon lists in the two halves of the split are unordered
Splits are either

**trivial**
- example: F | ABCDEG
- associated with **terminal** branches
- provide **no** information about topology structure

**non-trivial**
- example: **ABCD** | **EFG**
- associated with **internal** branches
- provide information about topology structure
Exercise - Identify Splits

For trees 1 and 2 below, write down the list of all non-trivial splits.
For trees 1 and 2 below, write down the list of all non-trivial splits:

**Tree 1**
- CB | EDAF
- EBC | DAF
- BDEC | AF

**Tree 2**
- HE | ABCDFGKMN
- HEN | ABCDFGKMP
- DP | ABCEFGHKMN
- DPM | ABCEFGHKN
- DPMB | ACEFGHKN
- FK | ABCDEGHMNP
- FKG | ABCDEHMNP
- FKGC | ABDEHMNP
- FKGCA | BDEHMNP
Splits

Complete list of splits described by a tree allows reconstruction of that tree’s topology
Splits

Complete list of splits described by a tree allows reconstruction of that tree’s topology

DF | ABCEGH
BCDFGH | AE
ABEGH | CDF
BH | ACDEFG
Splits

Complete list of splits described by a tree allows reconstruction of that tree’s topology

Helps to consider the sets of clans described by the splits

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Complete list of splits described by a tree allows reconstruction of that tree’s topology

Helps to consider the sets of clans described by the splits
Complete list of splits described by a tree allows reconstruction of that tree’s topology

Helps to consider the sets of clans described by the splits

Splits

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Complete list of splits described by a tree allows reconstruction of that tree's topology.

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Complete list of splits described by a tree allows reconstruction of that tree’s topology.

Helps to consider the sets of clans described by the splits.
Splits

Complete list of splits described by a tree allows reconstruction of that tree’s topology

Helps to consider the sets of clans described by the splits

\[
\begin{align*}
DF & \mid ABCEGH \\
BCDFGH & \mid AE \\
ABEGH & \mid CDF \\
BH & \mid ACDEFG
\end{align*}
\]
Draw the unique bifurcating unrooted tree topologies described by each of the two sets of splits, 1 and 2.
Draw the unique bifurcating unrooted tree topologies described by each of the two sets of splits, 1 and 2.

Ask your neighbour to check your answers, and discuss any disagreements you have between yourselves.

### Set 1

- **EC** | **HNGA**
- **ECH** | **GAN**
- **GA** | **NHEC**

### Set 2

- **CB** | **ADEFGHKMNP**
- **EH** | **ABCDGHKMN**
- **BCEH** | **ADFGKMN**
- **FN** | **ABCDEGHKMP**
- **FNM** | **ABCDEGHKP**
- **FNMK** | **ABCDEGHP**
- **FNMKA** | **BCDEGHP**
- **GP** | **ABCDEFHKMN**
- **GPD** | **ABCEFHKMN**

2
Exercise - Split Compatibility

Sets (e.g. pairs) of splits are either:

- **compatible**
  - a tree can be drawn that contains all splits in the set

- **incompatible**
  - a tree cannot be drawn that contains all splits in the set

Which of these sets of splits is incompatible?

i.e. for which set can you NOT build a tree which contains all the splits?

(i) AB | CDE
    DE | ABC

(ii) BCDFGH | AE
     ABEGH | CDF
     BG | ACDEFH

(iii) AB | CDE
     AC | BDE
Exercise - Split Compatibility: ANSWERS

(i)

AB | CDE
DE | ABC

(ii)

BCDFGH | AE
ABEGH | CDF
BG | ACDEFH

(iii)

AB | CDE
AC | BDE
Strict Consensus Trees

(i) A - C - D - E - F
(ii) C - D - E - F
(iii) E - D - C - F
(iv) A - F - C - D
(v) A - D - E - F
(vi) D - E - C - F
(vii) A - C - F - E
(viii) D - E - C - F
Strict Consensus Trees

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      E | F

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       D | F

(iv) A | F
      E | D
      C | B

(v) A | D
     B | C
     E | F

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      A | B
      E | F

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Exercise - Strict Consensus Trees

Draw the strict consensus tree for this set of 6 trees

Begin by listing the set of splits found in the trees and counting their frequency
Exercise - Strict Consensus Trees

Trees

Draw the strict consensus tree for this set of 6 trees

Split Frequencies

Begin by listing the set of splits found in the trees and counting their frequency
Exercise - Strict Consensus Trees

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Trees

Split
Frequencies
Exercise - Strict Consensus Trees

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Split Frequencies
50%/Majority Rule Consensus Trees

(i) A C E D B F
(ii) B D C E A F
(iii) B D C E A F
(iv) B D C E A F
(v) A C E D B F
(vi) B D C E A F
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50%/Majority Rule Consensus Trees

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50%/Majority Rule Consensus Trees

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Diagram:

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(viii) A
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50%/Majority Rule Consensus Trees

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(iv) A
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(vi) A
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Exercise - 50%/Majority Rule Consensus Trees

Draw the 50%/Majority Rule consensus trees for these 6 trees

Work again with the same table of split frequencies as for previous exercise
Exercise - 50%/Majority Rule Consensus Trees

Draw the 50%/Majority Rule consensus trees for these 6 trees

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Split Frequencies
Exercise - 50%/Majority Rule Consensus Trees

Draw the 50%/Majority Rule consensus trees for these 6 trees

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Exercise - 50%/Majority Rule Consensus Trees

Draw the 50%/Majority Rule consensus trees for these 6 trees

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Majority Rule (Extended) Consensus Tree

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Majority Rule (Extended) Consensus Tree

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## Majority Rule (Extended) Consensus Tree

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### Table Explanation:
- Each row represents a combination of taxa.
- The columns represent different trees labeled (i) to (viii).
- A star (*) indicates the presence of a taxon in the consensus tree.
- The number at the end of each row indicates the number of trees in which the combination is present.
- A red X in tree (iv) denotes a node that is inconsistent with other trees.

### Diagrams:
- Trees (i) to (viii) are shown, with nodes labeled A to F.
- Tree (iv) has a red X at the node B, indicating an inconsistency.

### Analysis:
- The consensus tree is derived by combining the majority rule (extended) across multiple phylogenetic trees.
- The table summarizes the presence of taxa across different tree combinations, helping to identify the consensus among the trees.
Majority Rule (Extended) Consensus Tree

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Majority Rule (Extended) Consensus Tree

(i) A | CDEF
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     B  D  E  F

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      B  D  E  F

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(v) A | CDEF
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Split Networks - Visualising Split Incompatibility

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Split Networks - Visualising Split Incompatibility

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Split Networks - Visualising Split Incompatibility

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  F

(iv) A F
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  C D

(v) A D
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  E F

(vi) A D
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  E F

(vii) A C E
    B D
  F

(viii) A F
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Split Networks - Visualising Split Incompatibility

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Split Networks - Visualising Split Incompatibility

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#### Diagrams

(i) A C E (ii) A C D (iii) A C F (iv) A F E
(v) A D E (vi) B D C (vii) B D F (viii) B C F
Causes of Split Incompatibility

Split incompatibility is identified by applying phylogeny estimation method(s) to a multiple sequence alignment (MSA)

Most phylogeny estimation methods analyse MSAs column-by-column

All phylogeny estimation methods incorporate (implicitly or explicitly) a model of evolution (almost always a model of residue substitution)

Split incompatibility is due to the presence of columns in the MSA which are more likely to be observed (given the model used to estimate the tree) under trees with split-incompatible topologies

Thus, it depends on the substitution model and method of estimation used in the analysis
Causes of Split Incompatibility

1. Sampling/random error associated with stochastic nature of mutation events

2. Alignment error

3. Substitution model misspecification

4. 'Reticulate' evolutionary processes
   • Recombination
   • Hybridisation
   • Horizontal/Lateral Gene Transfer

Split incompatibility could be due to any/several/all of these...

...thus, additional analysis is required to identify more/less likely explanations
Label the Branches!

Branches of consensus tree labeled to indicate proportion of trees containing that branch/split

Resolving an ancient, rapid radiation in Saxifragales.
Jian S, Soltis PS, Gitzendanner MA, Moore MJ, Li R, Hendry TA, Qiu YL, Dhingra A, Bell CD, Soltis DE.
PMID: 18275001
**Nodes** with greater than 90% posterior probability support from analysis of seven individual loci (TBOXX) in MrBayes are marked with a box (□).
Label the Branches!

Nodes with greater than 90% posterior probability support from analysis of seven individual loci (TBOXX) in MrBayes are marked with a box (□).
• Consensus trees and split/consensus networks are useful tools for exploring the signal in a phylogenetic dataset

• Split incompatibility can have many (multiple) causes - once it is observed, further analysis is required to determine causes

• Absence of split incompatibility indicates that your data strongly supports just one of the many different possible tree topologies
Polytomies
Polytomies

Internal nodes with two daughter branches are bifurcations.
Polytomies

Internal nodes with more than two daughter branches are bifurcations.

How many bifurcations on the tree?  
(a) 4  (b) 5  (c) 6
Interpreting Polytomies

**Soft Polytomy**

Lineages only bifurcate - internal lineages so short that no identifiable change/evolution occurred along them.

Thus true pattern of lineage divergence cannot be resolved.

**Hard Polytomy**

Ancestral lineage diverged into 3+ lineages simultaneously.

**NB:** Some software only accepts bifurcating trees.
Tree Topologies and Representations
Tree Topology

The branch intersections (i.e. internal nodes) of a tree specify its **topology**

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<th>Node</th>
<th>Branches</th>
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<td>xy yw yz</td>
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<td>yw wc wd</td>
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Trees with **identical** topologies

Trees “rotated” around internal branches have the **same topology**

For rooted trees, different topologies describe different patterns of relatedness of OTUs
Tree Representations

Most rooted tree figures use a “rectangular” rather than a “diagonal” representation.

Diagonal

Rectangular
Most rooted tree figures use a “rectangular” rather than a “diagonal” representation.

Rectangular trees represent internal nodes with lines perpendicular to lines representing the branches.
Unrooted Phylogenies
Unrooted Trees

There’s no root on the tree

Thus, there is no statement about the DIRECTION of time 
(i.e. of direction of divergence of lineages in the tree)

thus - we can’t distinguish daughter from parent branches

Many applications of phylogenies require a rooted tree

But many tree estimation tools yield only unrooted trees!
There are multiple rooted trees possible from a given unrooted tree.

The number of possible rooted tree topologies is the number of branches on the unrooted tree (assuming a bifurcating root).
There are multiple rooted trees possible from a given unrooted tree.

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There are multiple rooted trees possible from a given unrooted tree

If you allow a polytomy at the root...

there is one additional rooted tree possible for each internal node in the unrooted tree
Which sequence is d most closely related to?

a
b
c

Quiz
Which sequence is d most closely related to?

None of them - It depends where the root is!
Which sequence is \textbf{d} most closely related to?

\begin{itemize}
  \item \textbf{a}
  \item \textbf{b}
  \item \textbf{c}
\end{itemize}

None of them - It depends where the root is!

However, if \textbf{d} is most closely related to a single OTU and not to a group, then that OTU must be \textbf{c} (see previous slide)

i.e. \textbf{d} is certainly NOT most closely related to \textbf{a} or to \textbf{b}
Clans
Clans

Group of OTUs are a **clan** if there is at least one rooted phylogeny where they form a clade.

Of clades and clans: terms for phylogenetic relationships in unrooted trees.

Wilkinson M, McInerney JO, Hirt RP, Foster PG, Embley TM.


PMID: 17239486
Clans

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PMID: 17239486
Group of OTUs are a **clan** if there is at least one rooted phylogeny where they form a clade.
Group of OTUs are a **clan** if there is at least one rooted phylogeny where they form a monophyletic group/clade.

NO rooted trees place EG in a monophyletic group

Therefore **EG is not** a clan