All possible trees

Forming all 4-species trees by adding the next species in all possible places
The number of rooted bifurcating trees:

$$1 \times 3 \times 5 \times 7 \times \ldots \times (2n - 3)$$

$$= \frac{(2n - 3)!}{(n - 2)! \ 2^{n-2}}$$
which is:

<table>
<thead>
<tr>
<th>species</th>
<th>number of trees</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>4</td>
<td>15</td>
</tr>
<tr>
<td>5</td>
<td>105</td>
</tr>
<tr>
<td>6</td>
<td>945</td>
</tr>
<tr>
<td>7</td>
<td>10,395</td>
</tr>
<tr>
<td>8</td>
<td>135,135</td>
</tr>
<tr>
<td>9</td>
<td>2,027,025</td>
</tr>
<tr>
<td>10</td>
<td>34,459,425</td>
</tr>
<tr>
<td>11</td>
<td>654,729,075</td>
</tr>
<tr>
<td>12</td>
<td>13,749,310,575</td>
</tr>
<tr>
<td>13</td>
<td>316,234,143,225</td>
</tr>
<tr>
<td>14</td>
<td>7,905,853,580,625</td>
</tr>
<tr>
<td>15</td>
<td>213,458,046,676,875</td>
</tr>
<tr>
<td>16</td>
<td>6,190,283,353,629,375</td>
</tr>
<tr>
<td>17</td>
<td>191,898,783,962,510,625</td>
</tr>
<tr>
<td>18</td>
<td>6,332,659,870,762,850,625</td>
</tr>
<tr>
<td>19</td>
<td>221,643,095,476,699,771,875</td>
</tr>
<tr>
<td>20</td>
<td>8,200,794,532,637,891,559,375</td>
</tr>
<tr>
<td>30</td>
<td>$4.9518 \times 10^{38}$</td>
</tr>
<tr>
<td>40</td>
<td>$1.00985 \times 10^{57}$</td>
</tr>
<tr>
<td>50</td>
<td>$2.75292 \times 10^{76}$</td>
</tr>
</tbody>
</table>
Rooting an unrooted tree
A global maximum is not easy to find

end up here

but global maximum is here

if start here
Nearest-neighbor interchanges (NNIs)

a subtree

is rearranged by dissolving the connections to an interior branch:

and reforming them in one of the two possible alternative ways:

(The triangles are subtrees)
all 15 trees, connected by NNIs
with parsimony scores
Subtree pruning and regrafting (SPR) rearrangement

Break a branch, remove a subtree

Add it in, attaching it to one (*) of the other branches

Here is the result:
Tree bisection and reconnection (TBR) rearrangement

- Break a branch, separate the subtrees
- Connect a branch of one to a branch of the other

Here is the result:

Lecture 25. Phylogeny methods, part 2 (Searching tree space) – p.11/22
Greedy search by sequential addition

Greedy search by addition of species in a fixed order (A, B, C, D, E) in the best place each time.
Goloboff’s time-saving trick

Goloboff’s economy in computing scores of rearranged trees
"Star decomposition" search for best tree can happen in multiple ways
Disk-covering

“Disk covering” – assembly of a tree from overlapping estimated subtrees
Shortest Hamiltonian path problem

(a) 

(b) 

(c) 

(d)
same, with parsimony scores in place of trees
Some references


Graham, R. L. and L. R. Foulds. 1982. Unlikelihood that minimal phylogenies for a realistic biological study can be constructed in reasonable computational time. *Mathematical Biosciences* **60**: 133-142. [ ... and more]

continued


How it was done

This projection produced

- using the prosper style in LaTeX,
- using Latex to make a .dvi file,
- using dvips to turn this into a Postscript file,
- using ps2pdf to mill it into a PDF file, and
- displaying the slides in Adobe Acrobat Reader.

Result: nice slides using freeware.