# PhyloDraw Readme

PhyloDraw is a small tool that I created to make drawing phylogenies for zoology lectures easier. Unlike a number of other phylogeny tools I was able to find PhyloDraw does not calculate phylogenies but merely draws phylogenies that you define. This is especially useful when one wishes to draw phylogenies that are incorrect or nonsensical – historical hypotheses that have been disproven or phylogenies that don't display any real data for a test on concepts like monophyly and polyphyly.

PhyloDraw takes input from a spreadsheet saved in CSV format (a format most spreadsheet programs can save to but do not default to). The terminal taxa are written in the first column on the sheet and the final column should contain some clade that all terminal taxa belong to. For instance, a spreadsheet set up like the table below produces the tree shown just below it.

| Unicorns | Equids | Mammals | Mythical beasts |
Pegasi	Equids	Mammals	Mythical beasts
Bugbears	Ursids	Mammals	Mythical beasts
Drop bears	Ursids	Mammals	Mythical beasts
Dragons	Pyrorespirators	Reptiles	Mythical beasts
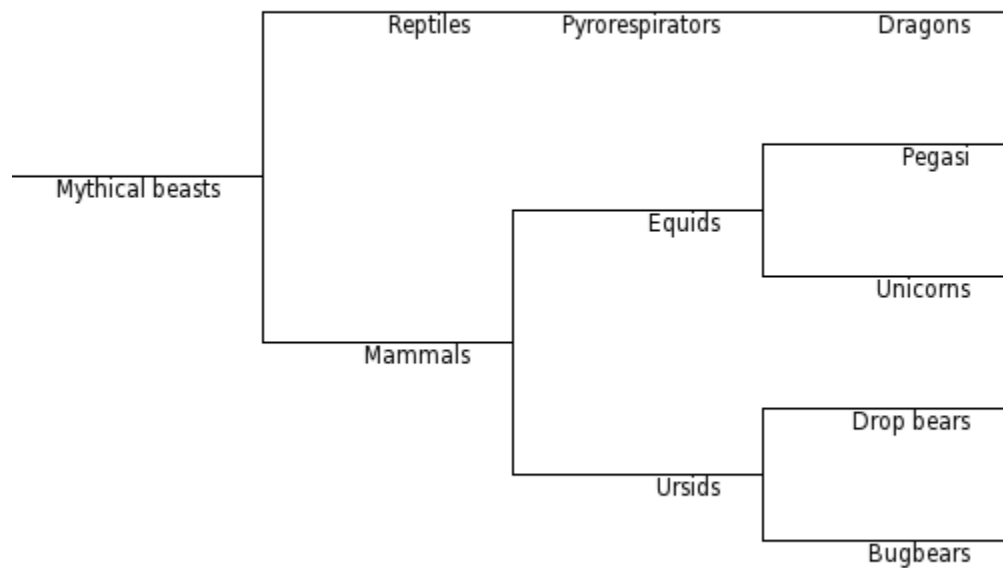
If you wished to suppress all but the first and last set of labels that's also simple – simply start the beginning of each label you want to hide with SKIP (which must be in all caps).

Unicorns	SKIPEquids	SKIPMammals	Mythical beasts
Pegasi	SKIPEquids	SKIPMammals	Mythical beasts
Bugbears	SKIPUrsids	SKIPMammals	Mythical beasts
Drop bears	SKIPUrsids	SKIPMammals	Mythical beasts
Dragons	SKIPPyrorespirators	SKIPReptiles	Mythical beasts
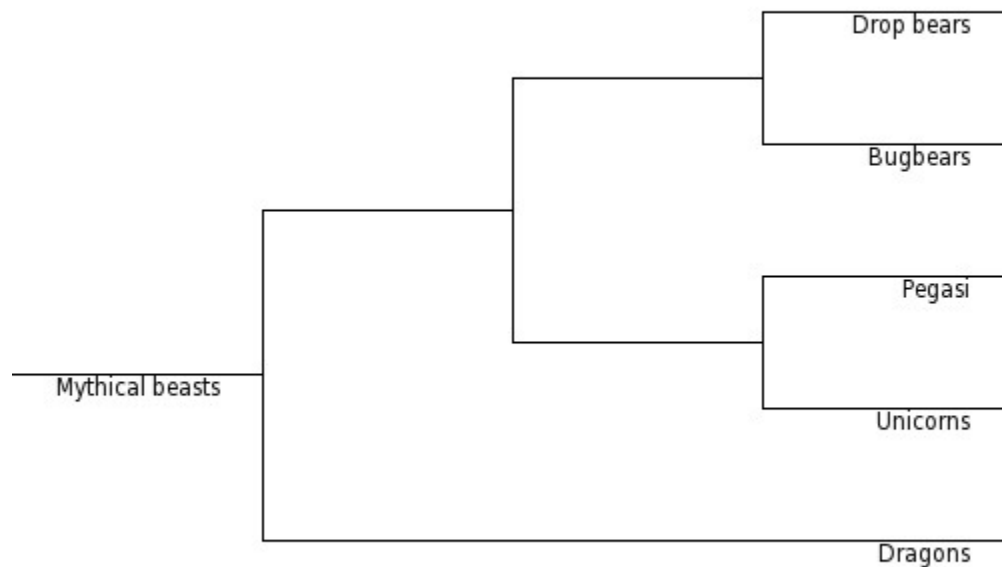
You may notice that the program rearranges trees when you switch options. The default option is not to specify an order to the termini beyond what is required to prevent lines from overlapping. This can be changed however.

What if you wanted to create a tree like the one below, perhaps for a test question about monophyly?
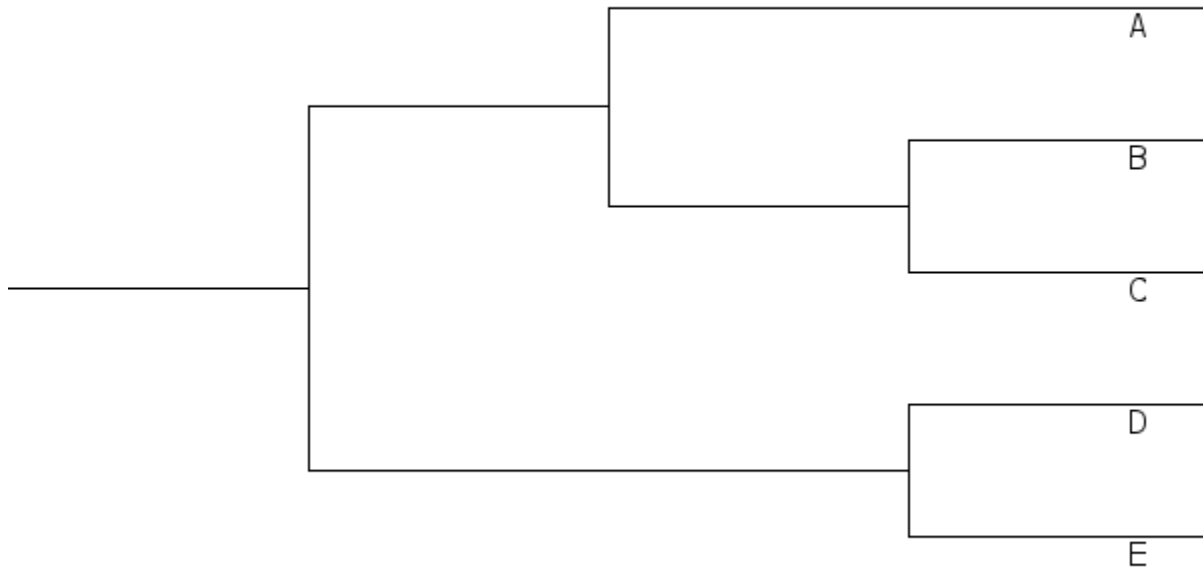
There isn't any particular name for any of the larger clades and it would be a pain to make up unique names for each group even if you just used letters. However, PhyloDraw knows that every column on a spreadsheet is a different block of names and so if you reuse the same few letters on every column it treats them as if they were different. The tree above came from the output below which only uses A, B, and C (with the SKIP prefix) to create groups.

A	SKIPA	SKIPA	SKIPA
B	SKIPB	SKIPA	SKIPA
C	SKIPB	SKIPA	SKIPA
D	SKIPC	SKIPB	SKIPA
E	SKIPC	SKIPB	SKIPA

Behind the scenes PhyloDraw assigns numbers to the names in each column so that the SKIPA in column 2 is actually SKIPA002 whereas the SKIPA in column 3 is SKIPA003. This means that you can be as uninventive as you want with names and not worry that the tree will be drawn in some odd manner.

Options

The top line of PhyloDraw's window displays the CSV file that you have selected to read from. Choose a file with the "Select Spreadsheet" button. If you select a file that does not end in ".csv" you will see the word "INVALID". If the file does end in ".csv" you will see a directory path to the file you have selected.
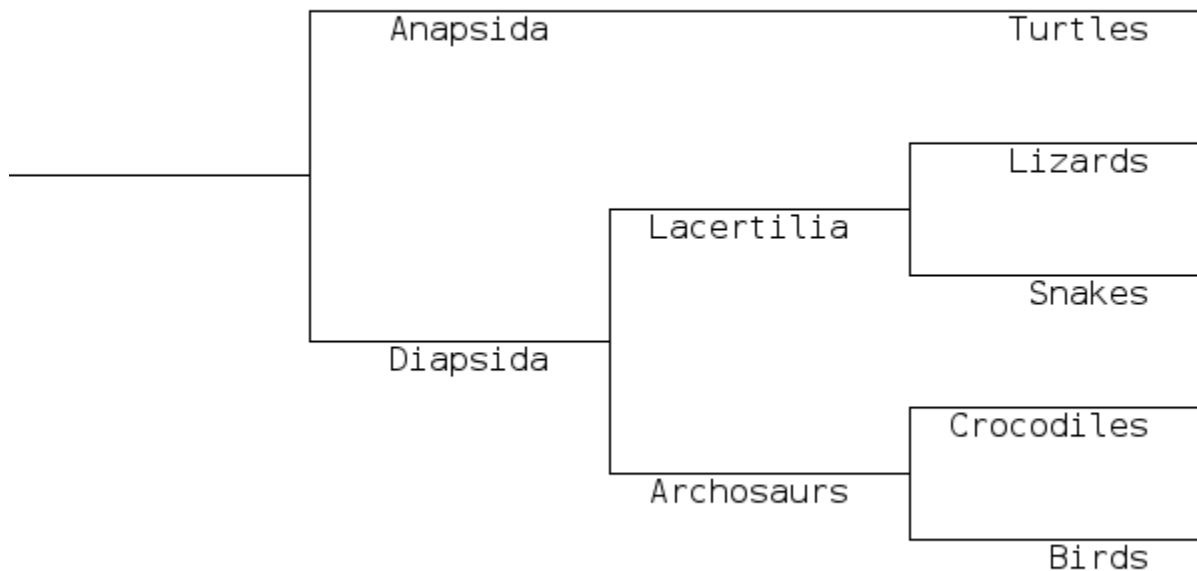
Keep order of names

As I said above there is no naturally preferred way to arrange the termini in the program – if you specified that A, B, and C are related so that A and B are most closely related you might get a tree with the termini in order A, B, C, or C, A, B, or C, B, A, or B, A, C. The only order you wouldn't get is one with C in the middle since this would cause the tree to be drawn with lines crossing. If you wish to specify a specific order for the termini you can do so in the spreadsheet and select "keep order of names". I frequently do this when I am drawing trees for a class and I want the order of the termini to reflect the order in which the taxa have been or will be reviewed in class.
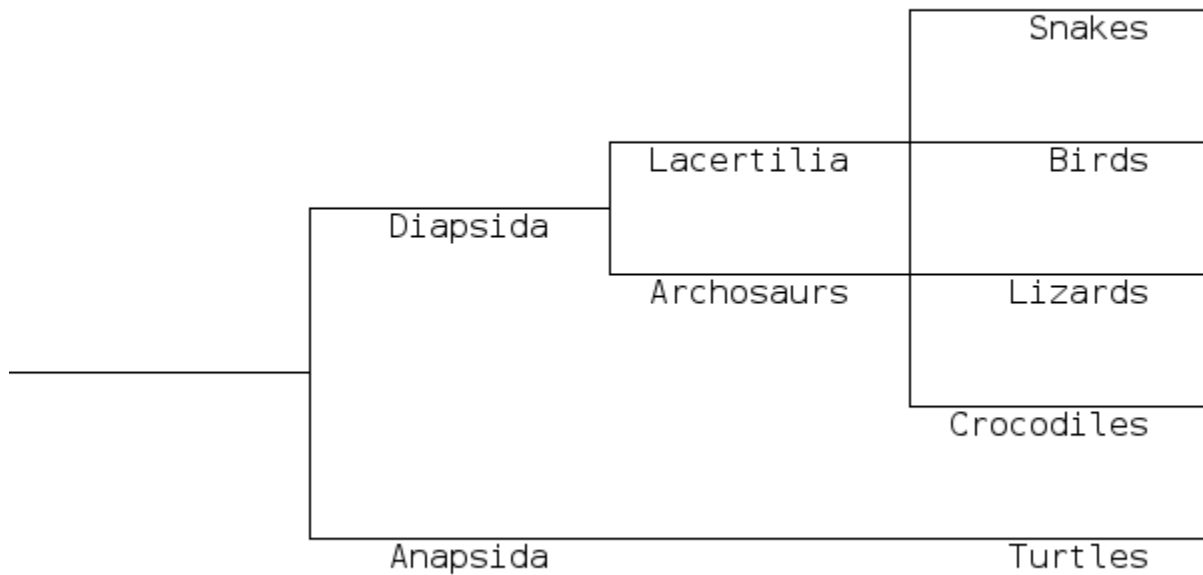
Do be aware that keeping the order of names overrides the program's own procedures for arranging the tree and so if the order you have in the spreadsheet is problematic those problems will not be fixed. The following spreadsheet data are out of order – the Lacertilia and Archosaurs are intermixed.

Snakes	Lacertilia	Diapsida	SKIPA
Birds	Archosaurs	Diapsida	SKIPA
Lizards	Lacertilia	Diapsida	SKIPA
Crocodiles	Archosaurs	Diapsida	SKIPA
Turtles	SKIPA	Anapsida	SKIPA

In the following tree these data are drawn without keeping the order of names. The program figures out a new order to draw these groups in so that none of the lines cross.
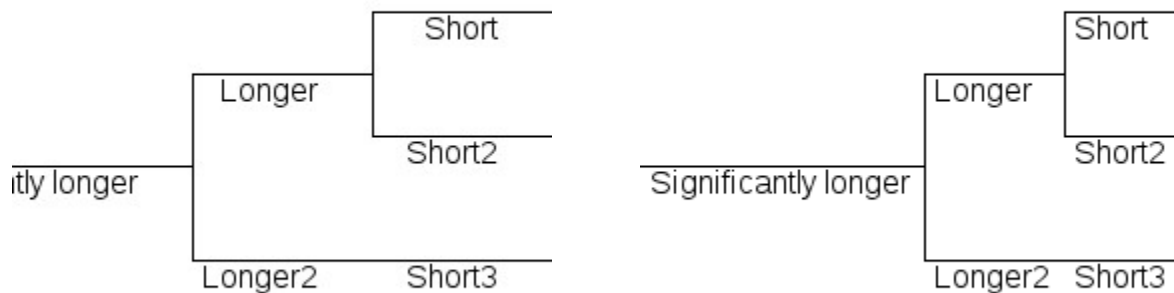

However, if you kept the order of names without fixing them on the spreadsheet you would override this behavior and get this:

```
                                              ┌───────  Snakes
                                   ┌──────────┤
                                   │ Lacertilia          Birds
                        ┌──────────┤
                        │ Diapsida │
                        │          │          ┌───────  Lizards
             ┌──────────┤          └──────────┤
─────────────┤          │            Archosaurs         Crocodiles
             │          │
             │          └──────────────────────────────  Turtles
               Anapsida
```

Dynamic spacing
If this is not checked the program divides the root-to-termini space into equal sections (as on the left).
In this case there is actually enough room to fit all the words in the space allowed if each column were
only allowed the needed space ("Short", for instance, does not need nearly as much room as
"Significantly longer" but both have been given the same amount of space). The Dynamic Spacing
option allows you to tell the program to use only the needed space for each label as in the picture on the
right (where all the text fits). This allows for more compact trees in cases where one or two columns
require significantly more space than the others.

```
                            ┌────── Short              ┌──── Short
              ┌─── Longer ──┤              ┌── Longer ─┤
              │             └─ Short2      │           └─── Short2
──itly longer ┤              ──Significantly longer ──┤
              └─ Longer2   Short3          └ Longer2  Short3
```

Image width and Image height

These do exactly what you think they should – they alter the size of the image that gets drawn. Note that if you have checked **Allow automatic width resizing** and also **Dynamic spacing** the program will expand the tree in the root-to-branches direction if the size you have specified is not large enough to fit all of your text.

Tree root orientation

These options rotate the tree so that the root of the tree faces in the specified direction. This works by actually rotating the tree after it has been drawn with the root aimed to the left. This means that the text is also rotated. In the case of facing the root to the right this means that the text actually ends up upside down. At some point I may fix this so that the text is drawn post-rotation.

Font Options

The program will look for fonts on your system and give you options to use the ones it finds. You can also specify a font size. Note that the imaging library used by the program (Python Imaging Library) cannot always draw every font and so I have provided an option for you to have the program draw the word "Font" in a small window next to the font options using whatever options you have selected. DO also note that the program currently does not resize any part of the tree to fit labels and so if you select particular combinations of image size and font size the labels will overlap the tree.

Text padding

Text padding is just blank space that is either appended ("after label" option) or prepended ("before label") to the text. I added this option because without it text can run into lines that join branches (on either side). However there are probably other formatting uses for this option.

Line width

This specifies the line width for the tree itself.

Allow automatic width resizing

This is meant for use with the Dynamic Spacing option. It allows the program to override your width selection (root-to-termini) if there is not enough room to fit all the labels.

Minimum root length

Dynamic spacing can resize the root of the tree to the point where it appears oddly short. This option allows you to specify a minimum length for the root so that it does not look so odd.

Draw tree

This draws the tree in the PhyloDraw window. If you don't like the way it looks alter some options and redraw it.

Save image

If you like the way the tree looks and want to use it hit this button and you can select a place and name to save the image under. Images are saved in PNG format.