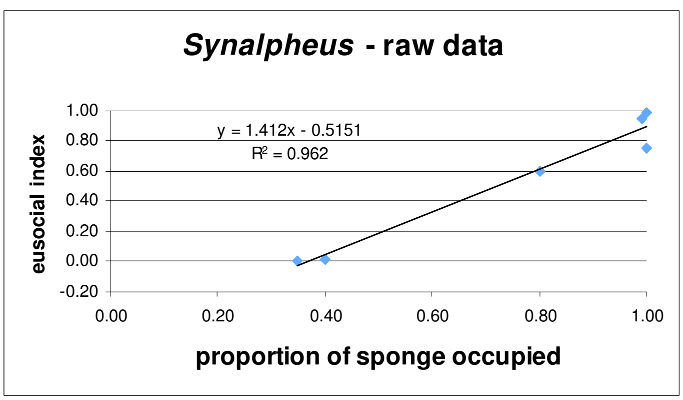
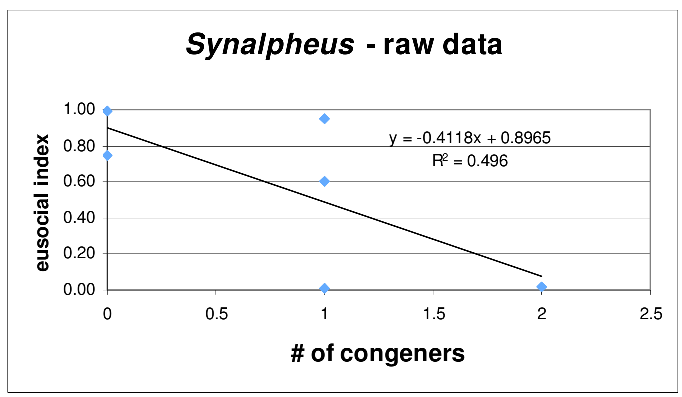
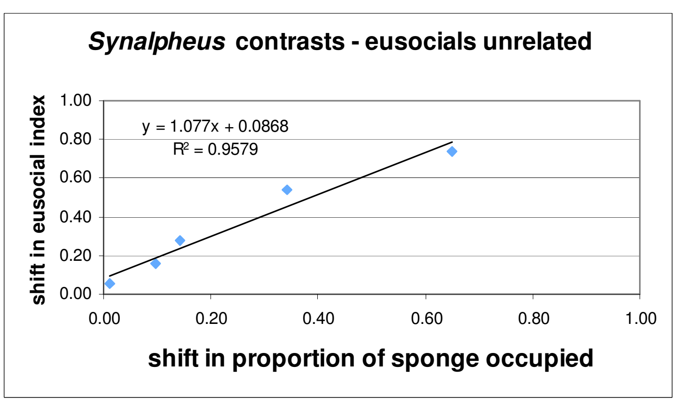
*Synalpheus* is a genus of 100 species distributed world wide among coral reef systems and has obligate associations with sponges and crinoids. About 30 species inhabit the Caribbean region from which the following data were extracted. Certain *Synalpheus* species are to varying degrees eusocial in the sense of "fortress defending" (intense competition for nest resources). The degree to which a species can completely occupy and dominate a particular nest (e.g., individual sponge) appears to be related to the degree of eusociality that subsequently evolves. Given the data below, and the phylogeny given in class, understand how the phylogenetic contrasts (shifts) were calculated.

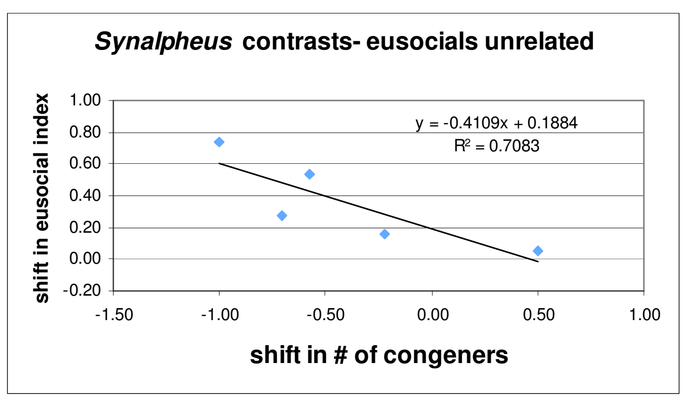
| ***Synalpheus*** | # of congeners | Proportion of sponge occupied | Eusocial index |
|---|---|---|---|
| *bousefieldii* | 2 | 0.40 | 0.02 |
| *chacei* | 1 | 0.99 | 0.95 |
| *paraneptunas* | 1 | 0.35 | 0.01 |
| *paraneptunoides* | 0 | 1.00 | 0.75 |
| *rathbunae* | 1 | 0.80 | 0.60 |
| *regalis* | 0 | 1.00 | 0.99 |
| **Contrasts calculated from phylogeny given in class** | | | |
| *bousefieldii – chacei* | -0.58 | 0.34 | 0.54 |
| *paraneptunas-paraneptunoides* | -1.00 | 0.65 | 0.74 |
| *rathbunae-regalis* | -0.71 | 0.14 | 0.28 |
| Clade A | 0.50 | 0.01 | 0.05 |
| Clade B | -0.22 | 0.10 | 0.16 |

The following graphs shows the relationship of the ability to dominate a nest (proportion of a sponge occupied) and exclude congeneric competitors (number of congeners) to evolving a high degree of eusocial behavior. Notice how the phylogenetic contrasts are more evenly distributed and explain as much or more of the data than do the raw data. The independent evolution of eusocial behavior sets up a natural experiment by which certain causes of eusocial behavior can be detected (notably, if eusocial species formed a monophyletic group, traits involved in the evolution of eusociality would be poorly if at all detected). These results strongly suggest that the evolution of eusocial behavior has been in part a cause of population divergence (speciation) in *Synalpheus*.



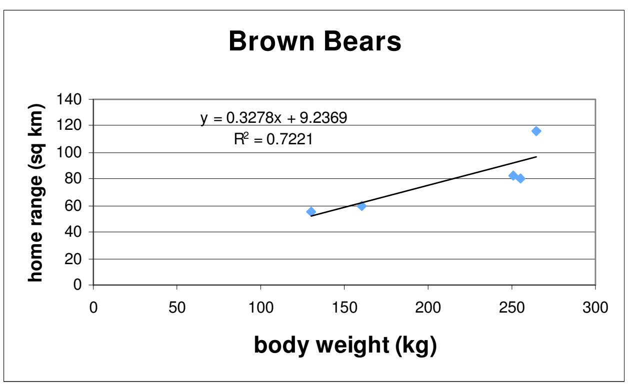



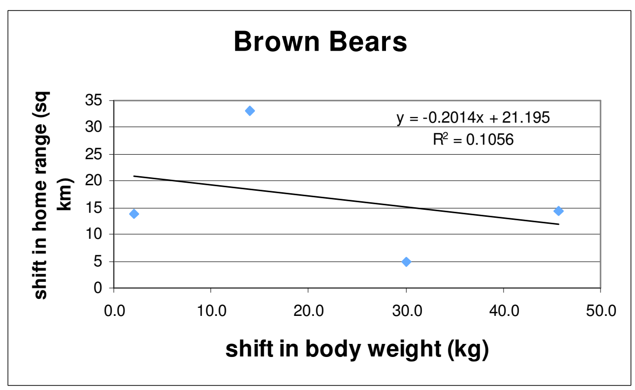
The following example on Brown and Polar Bears contrasts to the on *Synalpheus* example. These data are derived in part from pages 376-381 of the text, including Box 10.2. Use the following phylogeny to calculate the phylogenetic contrasts:

- Polar and ABC Brown Bears are sister lineage that trace back in time to 0.5 Ma (1 Ma total)
- The Kodiak Bear is sister to the Polar-ABC-Bear lineages, tracing back to 1.0 Ma (2 Ma total)
- The Balkan-Iberian Brown Bear sister relationship traces back in time to 0.5 Ma (1 Ma total)
- The Polar-ABC-Kodiak-Bear lineage is sister to the Balkan-Iberian-Bear lineage tracing back in time 3 Ma (6 Ma total)

| **Lineage**: | Body size (kg) | Minimum home range size (sq km) |
|---|---|---|
| Polar Bear | 265 | 116 |
| ABC Brown | 251 | 83 |
| Kodiak Bear | 255 | 80 |
| Balkan Brown | 160 | 60 |
| Iberian Brown | 130 | 55 |
| | | |
| **Phylogenetic contrasts**: | | |
| Polar-ABC | 14.0 | 33 |
| Polar-ABC-Kodiak | 2.1 | 13.8 |
| Balkan-Iberian | 30.0 | 5.0 |
| Polar-ABC-Kodiak and Balkan-Iberian | 45.7 | 14.5 |

Plot the raw data (body weight on x axis, home range on y), then plot the phylogenetic contrasts (shift in body weight on x, shift in home range on y). Notice how the relationship differs between the two plots. What does this suggest about the evolution of body size and home range during the diversification (speciation) of Brown Bears and relatives?




**<u>Aside</u>** – How to calculate least squares line for each graph (y=eusociality index, x=prop. sponge occupied):

*Synalpheus* raw data: n=6, sum(x)=4.54, sum(y)=3.32, sum($x^2$)=3.9026, sum(xy)=3.172

Slope = b1 = SSxy/SSxx = [sum(xy)-(sum(x)*sum(y))/n]/[sum($x^2$)-$(\text{sum}(x))^2$/n]

Slope = b1 = [3.172-(4.54*3.32)/6]/[3.9026-$4.54^2$/6] = 0.6598667/0.4673333 = 1.411983

y-intercept = b0 = mean(y)-b1*mean(x) = 0.5533333 – 1.411983*0.7566667 = -0.515067