

Niche comparisons

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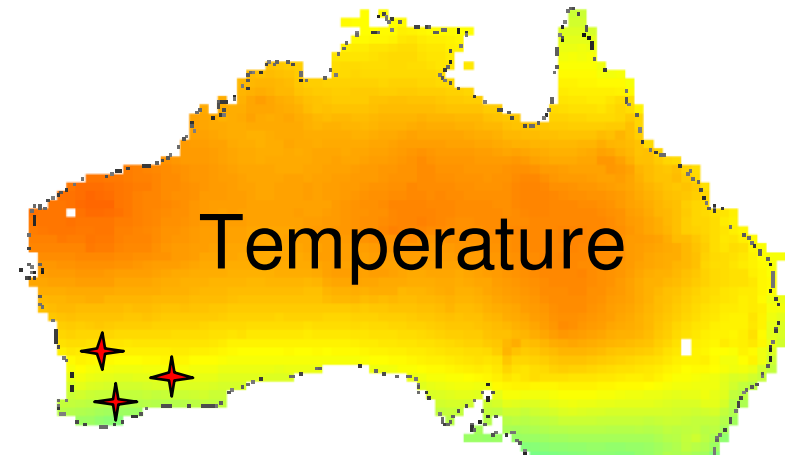
- Often we want to ask how similar are two niches
- There are two approaches we might take
 1. Compare underlying environmental preferences (i.e. single variables)
 2. Compare the areas of the projected niche models



Extracting environmental values

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- openModeller outputs a matrix of environmental values in a table
- Can be done in any good GIS package
- ... or with R



openModeller Desktop - My First Experiment

File Edit Data Preparation Reports Post Processing Help

Experiment

- Experiment
 - Climate Space Model
 - Drosera stolonifera
 - Present day global cli...

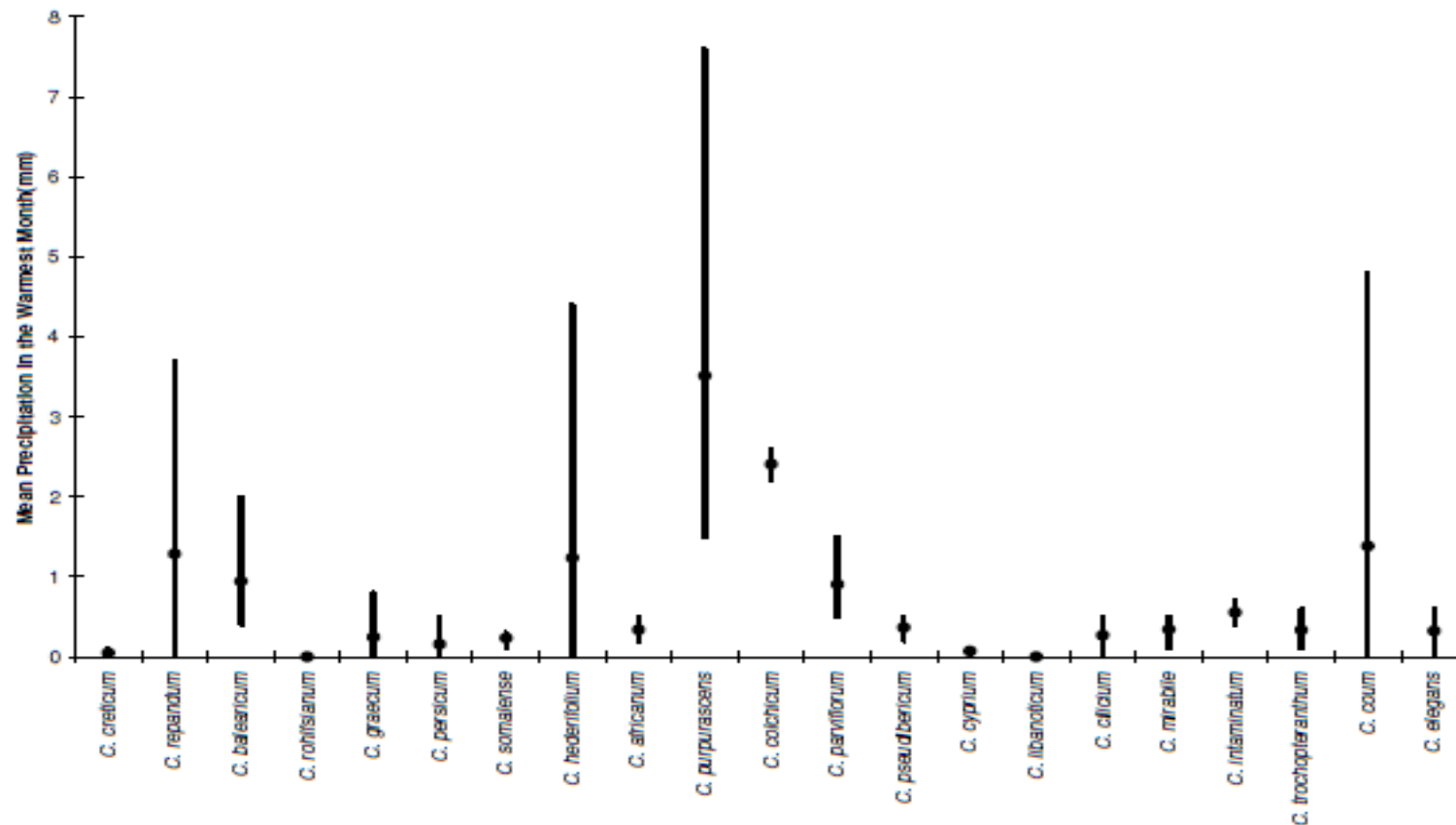
Report Table Output Map Logs

	ID	Lon	Lat	Count	mperature_in_warm	mperature_in_cool	an_daily_prec
0	4067	113.71	-26.695	1	33.9	9.9	0.825
1	4068	113.86	-25.3	1	35.1	10.4	0.716667
2	4069	113.864	-26.6986	1	33.9	9.9	0.825
3	4070	114.03	-26.74	1	35	9.6	0.783333
4	4071	114.03	-27.2614	1	34.4	9.5	0.891667
5	4072	114.13	-26.27	1	35.5	9.8	0.691667
6	4073	114.133	-27.7333	1	33.7	9.5	1.00833

Comparing individual variables

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- Extract observed values for the locations
- Compare the values



Whole niche comparison

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- Many modelling algorithms attempt to account for correlated components by discarding, downweighting or transforming the original layers
- This means the resulting models are not comparable directly
- What we can compare is the predicted area of the projected niche



Projected niche comparison



- Correlations between projected niches have been used widely
- Several measures have been used, for example evaluating one species' model with another species' localities data
- Other measures only use the projected niche, such as the D and I statistics
- The phylodlim R-package calculates D and I

Schoener's D



- Ranges from 0 (no overlap) to 1 (niches identical)
- Developed to compare microhabitats and/or diet
- Assumes values of p_X , p_Y are direct measures of local species density (which is not the case for our niche models)

$$D(p_X, p_Y) = 1 - \frac{1}{2} \sum_i |p_{X,i} - p_{Y,i}|$$

See Warren et al. (2008) *Evolution* 62(11):2868-2883

I statistic based on Hellinger distance

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- Range from 0 to 1
- Previously used for comparing community composition

$$H(p_X, p_Y) = \sqrt{\sum_i (\sqrt{p_{X,i}} - \sqrt{p_{Y,i}})^2}$$

$$I(p_X, p_Y) = 1 - \frac{1}{2}H(p_X, p_Y)$$

D and I

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- The phyloclim R-package by Christoph Heibl measures D and I for given pairs of projected niches



## I \ D	D.pelt	D.gig	D.bin
## D.pelt	NA	0.02008929	0.37276786
## D.gig	0.3242765	NA	0.02547771
## D.bin	0.5487119	0.31632008	NA

- The phyloclim R-package by Christoph Heibl measures D and I for given pairs of projected niches

```
## Load projected niches
```

```
D.p<-import.asc("Data/Drosera_peltata.asc")
```

```
D.g<-import.asc("Data/Drosera_gigantea.asc")
```

```
D.b<-import.asc("Data/Drosera_binata.asc")
```

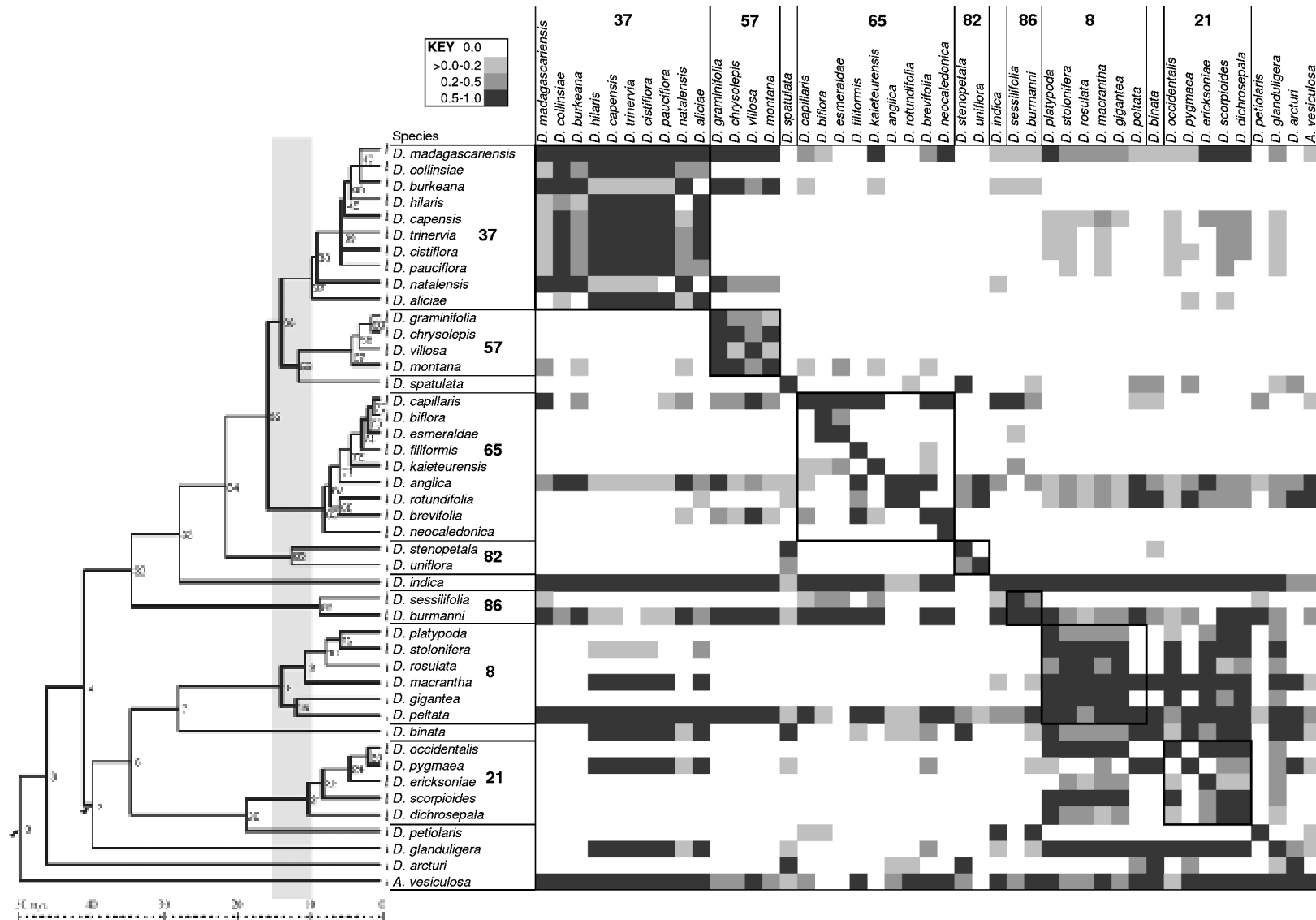
```
## run analysis
```

```
niche.overlap(list(D.pelt=D.p,D.gig=D.g,D.bin=D.b))
```

```
## I \ D      D.pelt      D.gig      D.bin
## D.pelt      NA 0.02008929 0.37276786
## D.gig 0.3242765      NA 0.02547771
## D.bin 0.5487119 0.31632008      NA
```

Niche correlations can reveal phylogenetic pattern

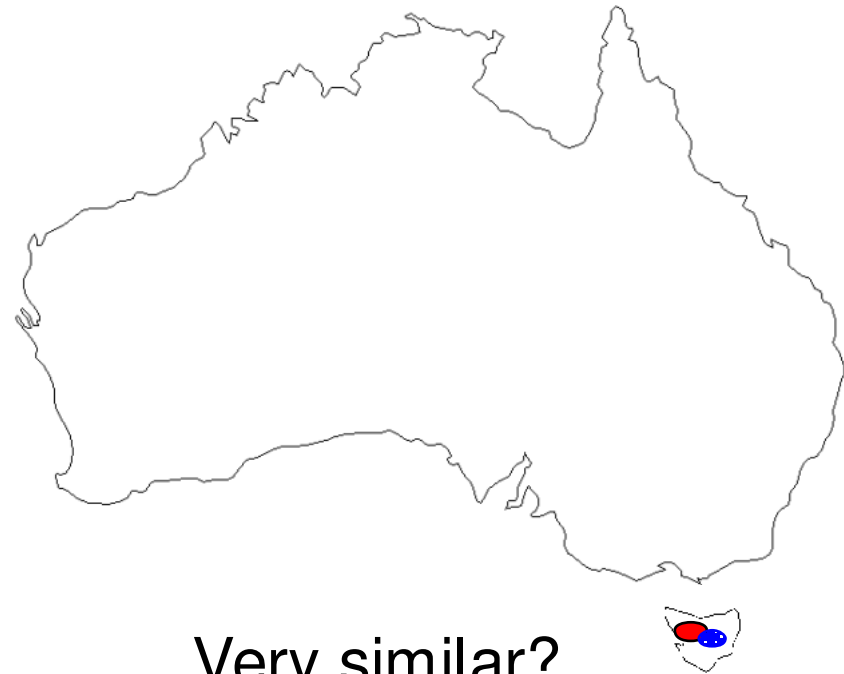
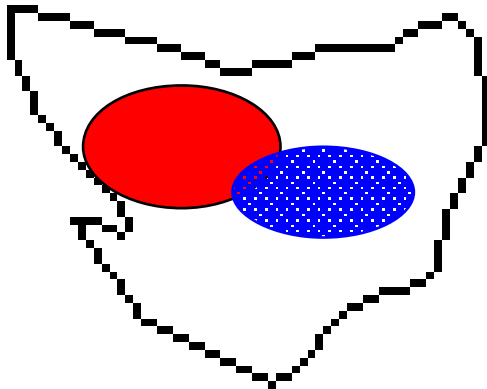
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A warning on niche comparisons

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Very different?



Very similar?

Niche and Age correlation

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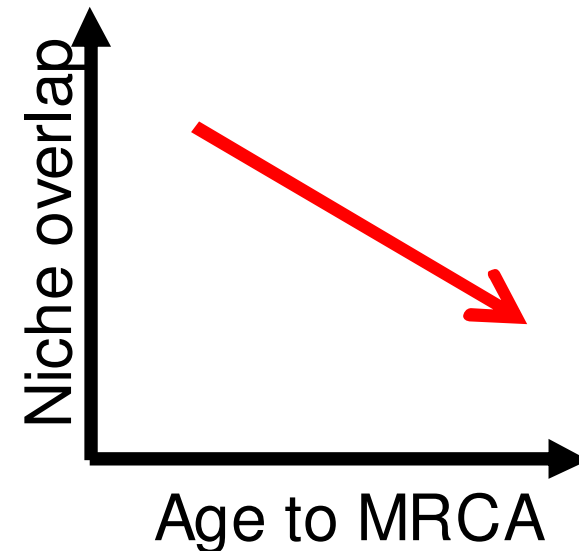
- Compare niche overlap with age to most recent common ancestor to test phylogenetic conservancy
- Can be performed in R using “age.range.correlation” in phyloclim

```
# load test data  
data(palmatifoliae_pno)
```

```
# calculate niche overlap between species  
no <- niche.overlap(palmatifoliae_pno$AnnualMeanTemperature)
```

```
# load phylogeny and PNOs of Oxalis sect. Palmatifoliae  
data(palmatifoliae_tree)
```

```
# age-range correlation  
x <- age.range.correlation(phy=palmatifoliae_tree, overlap=no)
```



Try to recreate this example

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