Supplemental file to "Testing for heterogeneous rates of discrete character evolution on phylogenies" – hidden-rates analysis of *Anolis* dewlap evolution

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```
## load packages
library(phytools)
```

```
## Loading required package: ape
```

```
## Loading required package: maps
```

```
## load data & results from non-HRM analysis
load("../dewlap-analysis/dewlap-analysis.Rdata")
```

```
## fit hidden-rate models
## equal-rates
er_hrm.dewlap<-fitHRM(as.phylo(treedC),DomCol,
  model="ER",parallel=TRUE,niter=10)
er_hrm.dewlap
```

```
## Object of class "fitHRM".
##
## Observed states: [ black, orange, pink, red, white, yellow ]
## Number of rate categories per state: [ 2, 2, 2, 2, 2, 2 ]
##
## Fitted (or set) value of Q:
##              black       black*      orange      orange*        pink        pink*
## black     -0.037130     0.026764    0.002073     0.000000    0.002073     0.000000
## black*     0.026764 -25000.026768   0.000000  5000.000001    0.000000  5000.000001
## orange     0.002073     0.000000   -0.037130     0.026764    0.002073     0.000000
## orange*    0.000000  5000.000001    0.026764 -25000.026768   0.000000  5000.000001
## pink       0.002073     0.000000    0.002073     0.000000   -0.037130     0.026764
## pink*      0.000000  5000.000001    0.000000  5000.000001    0.026764 -25000.026768
## red        0.002073     0.000000    0.002073     0.000000    0.002073     0.000000
## red*       0.000000  5000.000001    0.000000  5000.000001    0.000000  5000.000001
## white      0.002073     0.000000    0.002073     0.000000    0.002073     0.000000
## white*     0.000000  5000.000001    0.000000  5000.000001    0.000000  5000.000001
## yellow     0.002073     0.000000    0.002073     0.000000    0.002073     0.000000
## yellow*    0.000000  5000.000001    0.000000  5000.000001    0.000000  5000.000001
##               red         red*       white       white*      yellow      yellow*
## black       0.002073     0.000000    0.002073     0.000000    0.002073     0.000000
## black*      0.000000  5000.000001    0.000000  5000.000001    0.000000  5000.000001
## orange      0.002073     0.000000    0.002073     0.000000    0.002073     0.000000
## orange*     0.000000  5000.000001    0.000000  5000.000001    0.000000  5000.000001
## pink        0.002073     0.000000    0.002073     0.000000    0.002073     0.000000
```

```
## pink*      0.000000    5000.000001   0.000000    5000.000001   0.000000    5000.000001
## red       -0.037130       0.026764    0.002073       0.000000   0.002073       0.000000
## red*       0.026764  -25000.026768    0.000000    5000.000001   0.000000    5000.000001
## white      0.002073       0.000000   -0.037130       0.026764   0.002073       0.000000
## white*     0.000000    5000.000001    0.026764  -25000.026768   0.000000    5000.000001
## yellow     0.002073       0.000000    0.002073       0.000000  -0.037130       0.026764
## yellow*    0.000000    5000.000001    0.000000    5000.000001   0.026764  -25000.026768
##
## Fitted (or set) value of pi:
##     black    black*   orange   orange*      pink     pink*       red      red*
## 0.083333  0.083333  0.083333  0.083333  0.083333  0.083333  0.083333  0.083333
##     white    white*   yellow   yellow*
## 0.083333  0.083333  0.083333  0.083333
## due to treating the root prior as (a) flat.
##
## Log-likelihood: -306.42736
##
## Optimization method used was "nlminb"
##
## R thinks it has found the ML solution.
```

```r
## symmetric
sym_hrm.dewlap<-fitHRM(treedC,DomCol,model="SYM",parallel=TRUE,
  corHMM_model=TRUE,niter=10)
sym_hrm.dewlap
```

```
## Object of class "fitHRM".
##
## Observed states: [ black, orange, pink, red, white, yellow ]
## Number of rate categories per state: [ 2, 2, 2, 2, 2, 2 ]
##
## Fitted (or set) value of Q:
##              black     black*    orange   orange*      pink     pink*       red
## black     -0.017388   0.005619  0.006061  0.000000  0.000000  0.000000  0.000000
## black*     0.005619  -0.019540  0.000000  0.000000  0.000000  0.000000  0.000000
## orange     0.006061   0.000000 -0.084164  0.005619  0.000000  0.000000  0.035418
## orange*    0.000000   0.000000  0.005619 -0.121890  0.000000  0.006675  0.000000
## pink       0.000000   0.000000  0.000000  0.000000 -0.161314  0.005619  0.000000
## pink*      0.000000   0.000000  0.000000  0.006675  0.005619 -0.022270  0.000000
## red        0.000000   0.000000  0.035418  0.000000  0.000000  0.000000 -0.116815
## red*       0.000000   0.000000  0.000000  0.000000  0.000000  0.000000  0.005619
## white      0.005708   0.000000  0.000000  0.000000  0.056938  0.000000  0.000000
## white*     0.000000   0.004290  0.000000  0.033465  0.000000  0.000000  0.000000
## yellow     0.000000   0.000000  0.037066  0.000000  0.098757  0.000000  0.075777
## yellow*    0.000000   0.009631  0.000000  0.076130  0.000000  0.009976  0.000000
##               red*    white     white*    yellow    yellow*
## black      0.000000  0.005708  0.000000  0.000000  0.000000
## black*     0.000000  0.000000  0.004290  0.000000  0.009631
## orange     0.000000  0.000000  0.000000  0.037066  0.000000
## orange*    0.000000  0.000000  0.033465  0.000000  0.076130
## pink       0.000000  0.056938  0.000000  0.098757  0.000000
## pink*      0.000000  0.000000  0.000000  0.000000  0.009976
## red        0.005619  0.000000  0.000000  0.075777  0.000000
## red*      -0.005619  0.000000  0.000000  0.000000  0.000000
## white      0.000000 -0.068265  0.005619  0.000000  0.000000
```

```
## white*   0.000000  0.005619 -0.043375  0.000000  0.000000
## yellow   0.000000  0.000000  0.000000 -0.217219  0.005619
## yellow*  0.000000  0.000000  0.000000  0.005619 -0.101355
##
## Fitted (or set) value of pi:
##    black    black*   orange   orange*     pink     pink*      red      red*
## 0.083333 0.083333 0.083333 0.083333 0.083333 0.083333 0.083333 0.083333
##    white    white*   yellow   yellow*
## 0.083333 0.083333 0.083333 0.083333
## due to treating the root prior as (a) flat.
##
## Log-likelihood: -281.838774
##
## Optimization method used was "optim"
##
## R thinks optimization may not have converged.
```

```r
ard_hrm.dewlap<-fitHRM(treedC,DomCol,model="ARD",parallel=TRUE,
  corHMM_model=TRUE,niter=50)
ard_hrm.dewlap
```

```
## Object of class "fitHRM".
##
## Observed states: [ black, orange, pink, red, white, yellow ]
## Number of rate categories per state: [ 2, 2, 2, 2, 2, 2 ]
##
## Fitted (or set) value of Q:
##              black    black*   orange   orange*     pink     pink*      red
## black    -0.051796  0.000003  0.044346  0.000000  0.000204  0.000000  0.006800
## black*    0.005860 -0.046761  0.000000  0.000000  0.000000  0.000007  0.000000
## orange    0.000005  0.000000 -0.129986  0.000003  0.000666  0.000000  0.054075
## orange*   0.000000  0.006404  0.005860 -0.147920  0.000000  0.000005  0.000000
## pink      0.000000  0.000000  0.004787  0.000000 -0.021557  0.000003  0.000000
## pink*     0.000000  0.000527  0.000000  0.000018  0.005860 -0.109873  0.000000
## red       0.008315  0.000000  0.054535  0.000000  0.025642  0.000000 -0.088531
## red*      0.000000  0.000005  0.000000  0.075771  0.000000  0.000052  0.005860
## white     0.000001  0.000000  0.000070  0.000000  0.045549  0.000000  0.000014
## white*    0.000000  0.005826  0.000000  0.034665  0.000000  0.012755  0.000000
## yellow    0.000045  0.000000  0.102106  0.000000  0.000001  0.000000  0.000024
## yellow*   0.000000  0.006308  0.000000  0.000000  0.000000  0.000001  0.000000
##              red*    white    white*   yellow   yellow*
## black    0.000000  0.000437  0.000000  0.000006  0.000000
## black*   0.000003  0.000000  0.000001  0.000000  0.040889
## orange   0.000000  0.013316  0.000000  0.061921  0.000000
## orange*  0.019105  0.000000  0.116547  0.000000  0.000000
## pink     0.000000  0.000000  0.000000  0.016767  0.000000
## pink*    0.000017  0.000000  0.000004  0.000000  0.103447
## red      0.000003  0.000033  0.000000  0.000003  0.000000
## red*    -0.089701  0.000000  0.008007  0.000000  0.000006
## white    0.000000 -0.069043  0.000003  0.023406  0.000000
## white*   0.000006  0.005860 -0.059110  0.000000  0.000000
## yellow   0.000000  0.000032  0.000000 -0.102211  0.000003
## yellow*  0.000000  0.000000  0.010810  0.005860 -0.022979
##
## Fitted (or set) value of pi:
```

```
##    black   black*   orange  orange*     pink    pink*      red     red*
## 0.083333 0.083333 0.083333 0.083333 0.083333 0.083333 0.083333 0.083333
##    white   white*   yellow  yellow*
## 0.083333 0.083333 0.083333 0.083333
## due to treating the root prior as (a) flat.
##
## Log-likelihood: -272.3408
##
## Optimization method used was "optim"
##
## R thinks optimization may not have converged.
```

```
## check likelihood
ard_hrm.dewlap$lik(as.Qmatrix(er_hrm.dewlap))
```

```
## [1] -306.4274
```

```
## compare models
options(scipen=0)
anova(fitER1,fitERmulti1,er_hrm.dewlap,
  fitSYM1,fitSYMmulti1,sym_hrm.dewlap,
  fitARD1,fitARDmulti1,ard_hrm.dewlap)
```

```
##                   log(L) d.f.      AIC       weight
## fitER1         -308.6466    1 619.2931 7.740347e-03
## fitERmulti1    -308.6463    2 621.2926 2.848295e-03
## er_hrm.dewlap  -306.4274    3 618.8547 9.637337e-03
## fitSYM1        -289.8064   15 609.6128 9.790675e-01
## fitSYMmulti1   -285.6250   30 631.2501 1.960363e-05
## sym_hrm.dewlap -281.8388   31 625.6775 3.179792e-04
## fitARD1        -282.6902   30 625.3804 3.689051e-04
## fitARDmulti1   -272.6277   60 665.2554 8.094335e-13
## ard_hrm.dewlap -272.3408   62 668.6816 1.459445e-13
```

```
## save results
save(er_hrm.dewlap,sym_hrm.dewlap,ard_hrm.dewlap,
  file="dewlap-hrm-analysis.rda")
```