

Predicting budburst of woody species using functional traits

Research Question:

What functional traits best predict budburst by woody species under variable climate conditions?

Goal for FRST 507:

Model the relationship between phenology and 5 functional traits, with partial pooling across both sites and species

The Data:

- 2 populations
- 28 species

Budburst data:

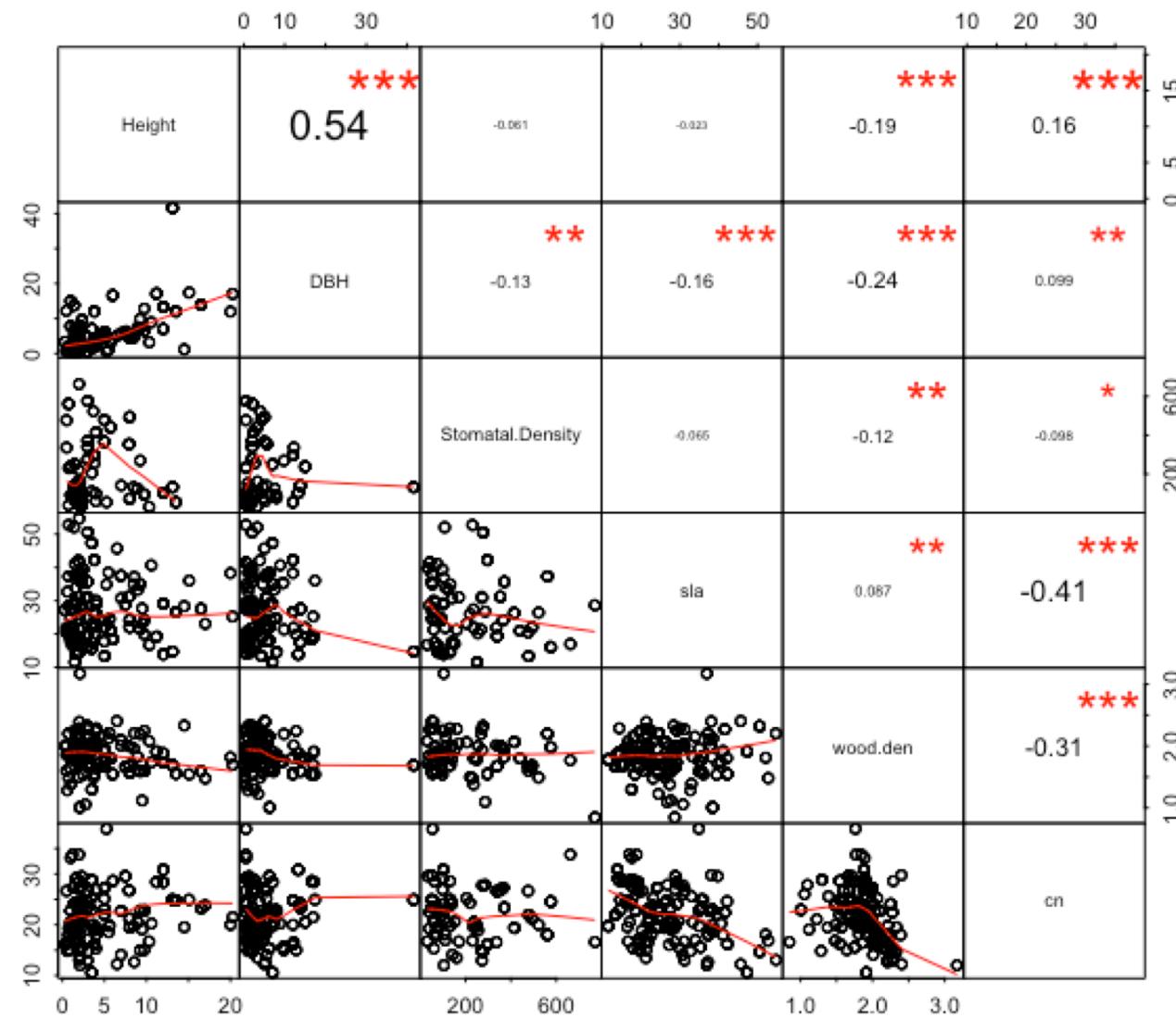
- 2 warming trt
- 2 photoperiods trt
- 3 winter chilling trt

Trait data:

- Specific Leaf Area
- Height
- Wood density
- C:N
- Stomatal density

```
> str(comb)
'data.frame': 880 obs. of 15 variables:
 $ ind       : chr  "ACEPEN02_HF" "ACEPEN02_HF" "ACEPEN02_HF" "ACEPEN02_HF" ...
 $ sp        : chr  "ACEPEN" "ACEPEN" "ACEPEN" "ACEPEN" ...
 $ site      : chr  "HF" "HF" "HF" "HF" ...
 $ treatcode : Factor w/ 12 levels "CL0","CL1","CL2",...: 1 2 3 4 5 6 7 8 9 10 ...
 $ warm      : Factor w/ 2 levels "15","20": 1 1 1 1 1 1 2 2 2 2 ...
 $ photo     : Factor w/ 2 levels "08","12": 2 2 2 1 1 1 2 2 2 1 ...
 $ chill     : Factor w/ 3 levels "chill0","chill1",...: 1 2 3 1 2 3 1 2 3 1 ...
 $ tleaffm   : num  0 0 0 0 0 0 0 0 0 ...
 $ lleaffm   : num  0 0 0 0 0 0 0 0 0 ...
 $ Height    : num  3 3 3 3 3 3 3 3 3 ...
 $ DBH       : num  2 2 2 2 2 2 2 2 2 ...
 $ Stomatal.Density: num  277 277 277 277 277 ...
 $ sla        : num  50.5 50.5 50.5 50.5 50.5 ...
 $ wood.den  : num  2.32 2.32 2.32 2.32 2.32 ...
 $ cn         : num  14.7 14.7 14.7 14.7 14.7 ...
```

Correlations:



Test Data:

```
int<-11 # days into the experiment of bb
sigma<-2

nsite = 2 #number of sites
nsp = 28 #number of species
rep = 50 # A large number to increase the size of the dataset
ntot<-nsite*nsp*rep #2800

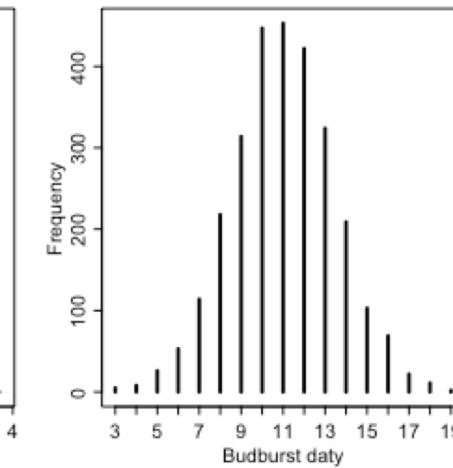
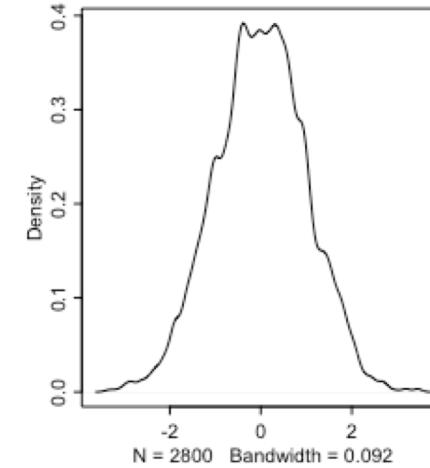
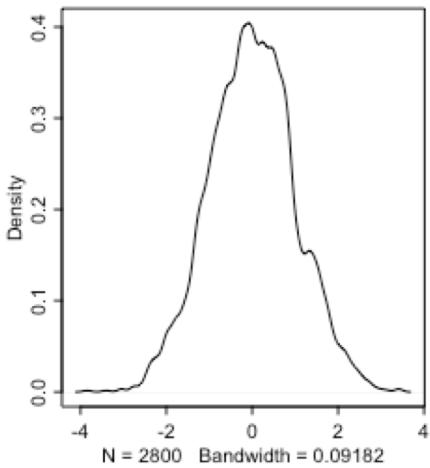
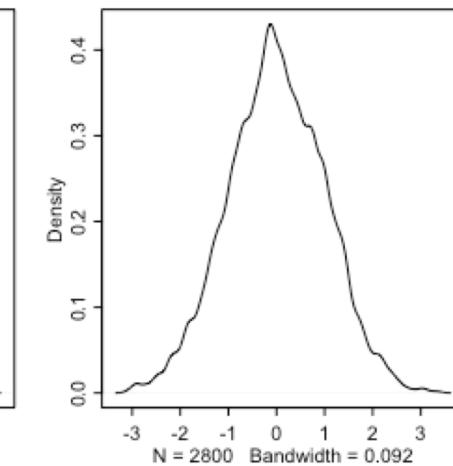
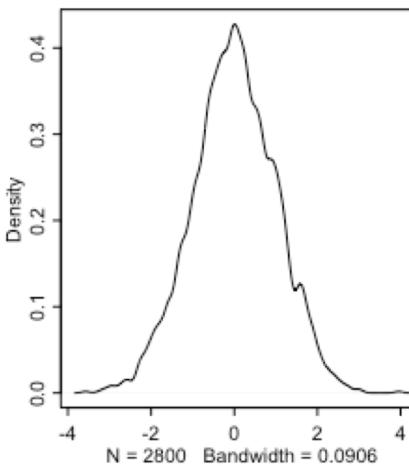
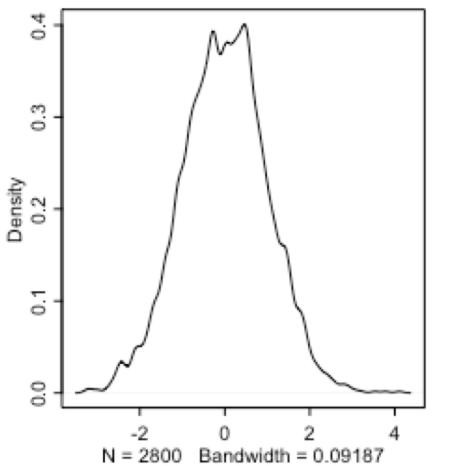
# Trait values (trait name + v for value)
slav= rnorm(ntot, 5, 1);
htv=rnorm(ntot, 11, 3)
cnv=rnorm(ntot, 10, 2)
woodv=rnorm(ntot, 0.5, 0.05)
stomv=rnorm(ntot, 20, 5)

#effect sizes
site.diff=2
sladiff= -0.5
htdiff=0.5
cndiff=-0.5
wooddiff=0.3
stomdiff=1

phenfull<-vector()
for (i in 1:ntot){
  phenfull[i]<-int+sladiff*slav[i]+htdiff*htv[i]+cndiff*cnv[i]+wooddiff*woodv[i]+stomdiff
  *stomv[i]+rnorm(1, 0, sigma)
}
```

Getting started:

```
> head(fakecent)
  phencent X.Intercept. site2      slav       htv       cnv      woodv      stomv
1 4.260948          1 1.3037428 -2.0683050 2.9245375 -1.0760992 0.5109427
2 8.742628          1 0.4823260 0.1082784 0.4747702 0.7906126 -1.1304780
3 17.524791         1 0 -0.5820891 0.6268206 -0.6011590 0.6346397 1.3002006
4 16.317983         1 0 0.3022609 1.0908223 -2.3853452 -0.3659183 -0.3678685
5 10.368237         1 0 1.6564534 -0.3000259 0.2948016 -1.5791134 -0.7375435
6 10.363664         1 0 -0.2490465 1.1795484 0.5337240 2.7227835 0.8214160
```



Getting started:

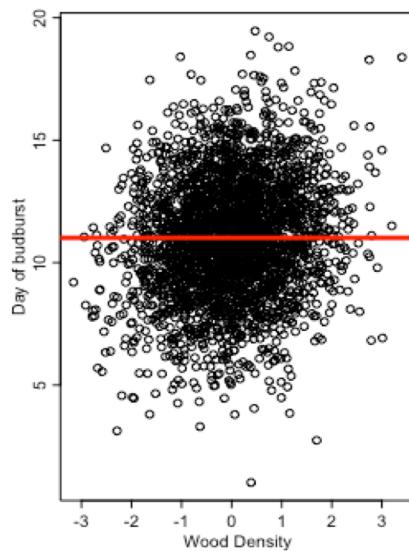
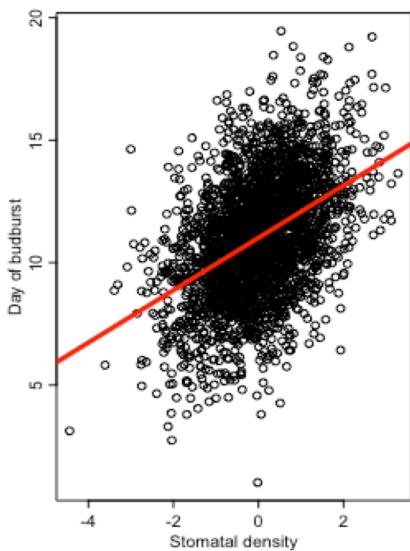
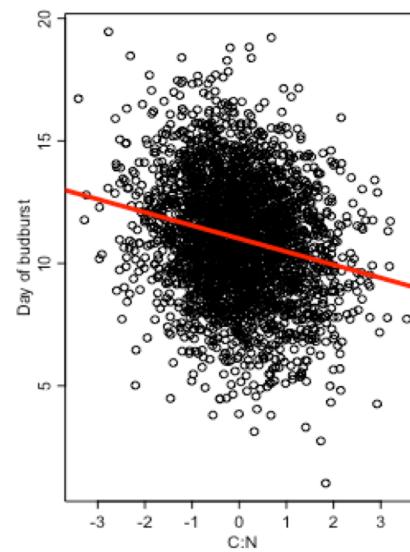
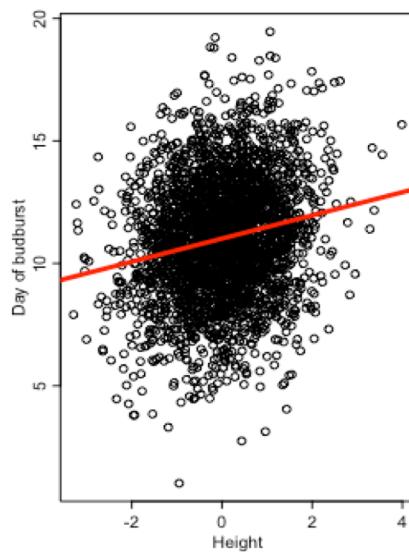
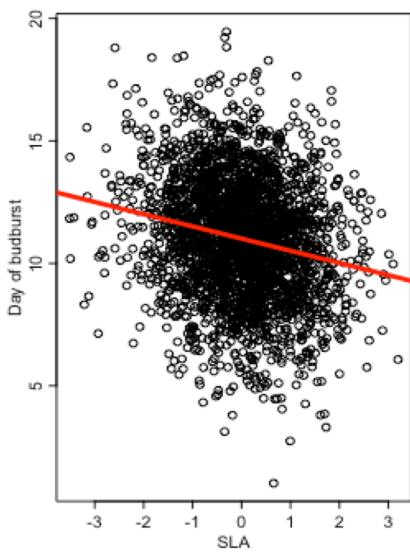
```
> full.m<- mapC  
+   alist(  
+     phencent~dnorm(mu, sigmahere),  
+     mu<-a+bsla*slav+bht*htv+bcn*cnv+bstom*stomv+bwood*woodv,  
+     a~dnorm(0, 10),  
+     bsla~dnorm(0, 10),  
+     bht~dnorm(0, 10),  
+     bcn~dnorm(0, 10),  
+     bstom~dnorm(0, 10),  
+     bwood~dnorm(0, 10),  
+     sigmahere~dunif(0,10)  
+   ),  
+   data=fakecent)
```

```
> precis(full.m)  
      Mean StdDev 5.5% 94.5% #effect sizes  
a    11.01  0.04 10.95 11.07 site.diff=2  
bsla -0.50  0.04 -0.56 -0.44 sladiff= -0.5  
bht   0.47  0.04  0.41  0.53 htdiff=0.5  
bcn   -0.54  0.04 -0.60 -0.47 cndiff=-0.5  
bstom  1.07  0.04  1.01  1.13 wooddiff=0.3  
bwood  0.32  0.04  0.26  0.38 stomdiff=1  
sigmahere 2.00  0.03  1.95  2.04
```

Correlation matrix:

	a	bsla	bht	bcn	bstom	bwood	sigmahere
a	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000	-0.000111
bsla	0.000000	1.000000	0.009333	0.025189	-0.001650	0.016672	0.000005
bht	0.000000	0.009333	1.000000	-0.020311	0.017033	-0.021356	-0.000005
bcn	0.000000	0.025189	-0.020311	1.000000	-0.025244	0.025828	0.000006
bstom	0.000000	-0.001650	0.017033	-0.025244	1.000000	-0.024013	-0.000011
bwood	0.000000	0.016672	-0.021356	0.025828	-0.024013	1.000000	-0.000002
sigmahere	-0.000111	0.000005	-0.000005	0.000006	-0.000011	-0.000002	1.000000
.

Visualizing the data:



Next steps:

Evaluating priors

- Posterior predictive checks

Adding hierarchy

- pooling across species
- pooling across sites

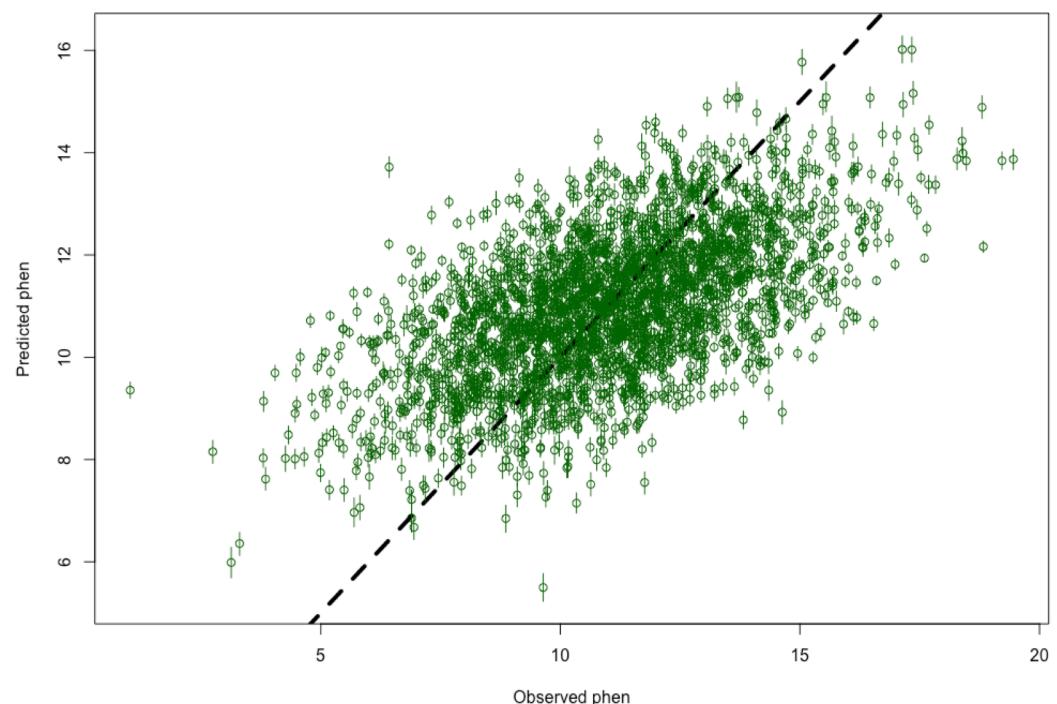


Fig 1. Example of a ppc showing the observed and predicted budburst dates