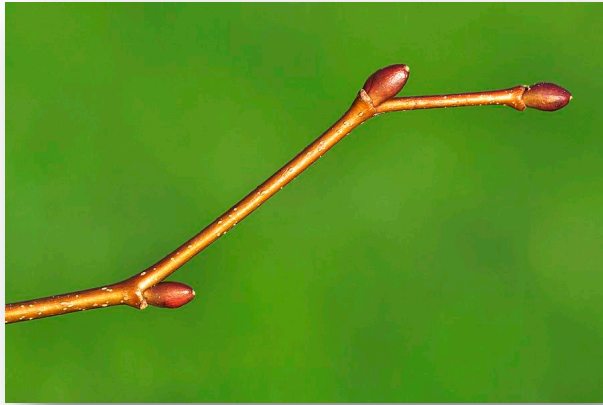


A budding project on buds  
*or* An emerging project on leaf  
emergence

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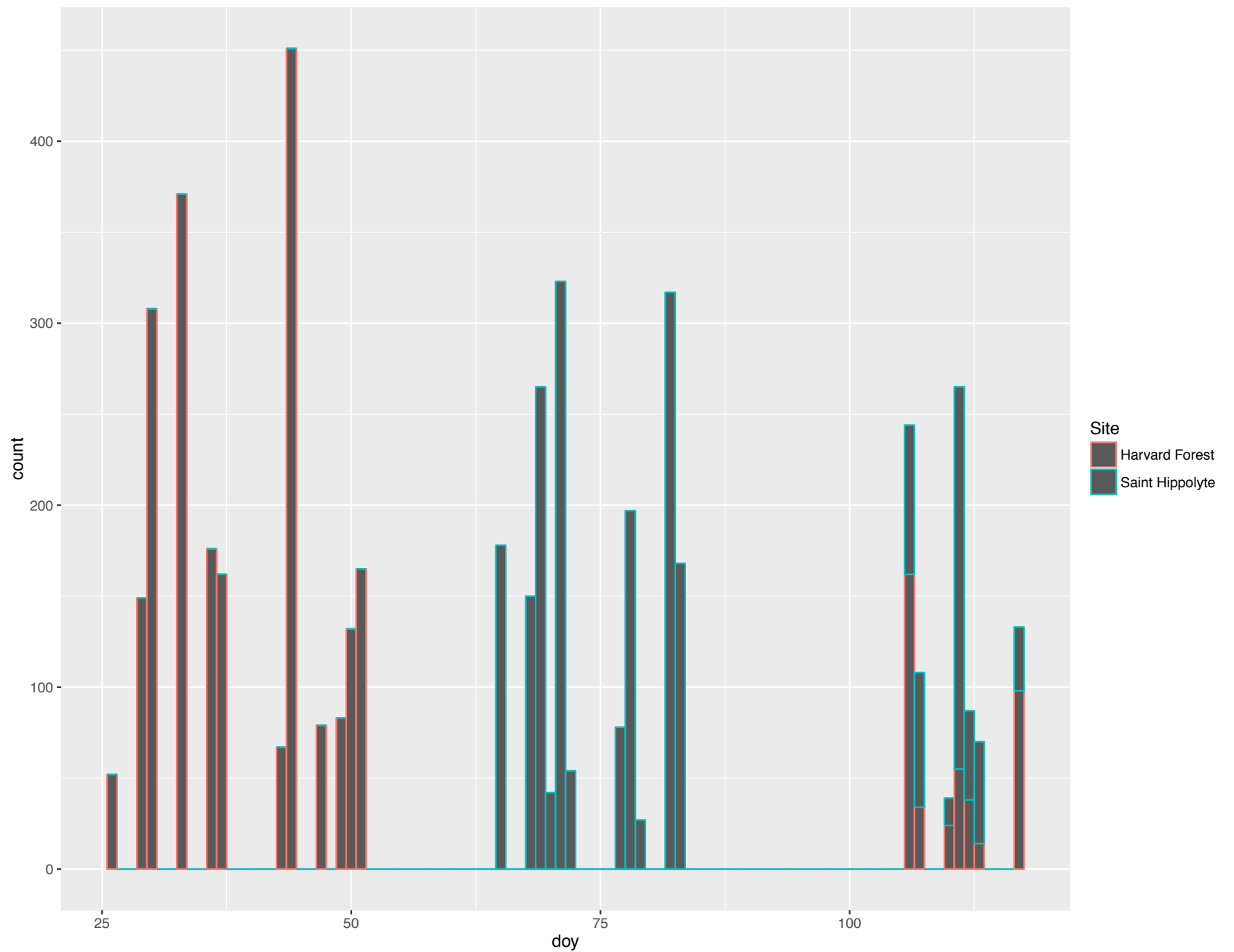
Data set 1:  
6467 rows of bud volume  
27 species (6 reps/species)  
2 sites  
(bud level)



Data set 2:  
2136 rows phenological  
observations  
12 experimental treatments  
(twig level)

## **Does bud size predict phenological patterns?**

- Inter and intra-species differences



**bday~true.av.bud.vol+(1|treatment)+(1|species)+(1|site)**

- **budvol~doy+(1+doy|sp)**
- **trubudvol=measured.bv+coef(DOY-Constant )**

# Fake data: Varying intercept

```
nsp = 5 # number of species
ntot = 50 # numbers of obs per species.

baseinter <- 5 # baseline intercept (budvol) across all species
spint <- baseinter + c(1:nsp)-mean(1:nsp) # different intercepts by species

# now start building ...
testdat <- vector()

for(i in 1:nsp){ # loop over species. i = 1

  # continuous predictors, generate level (if you will) for each observation
  doy<- rtnorm(ntot,40,10,lower=10,upper=70)

  ## set up effect size
  doycoef<-0.5
  doycoef.sd<-0.05

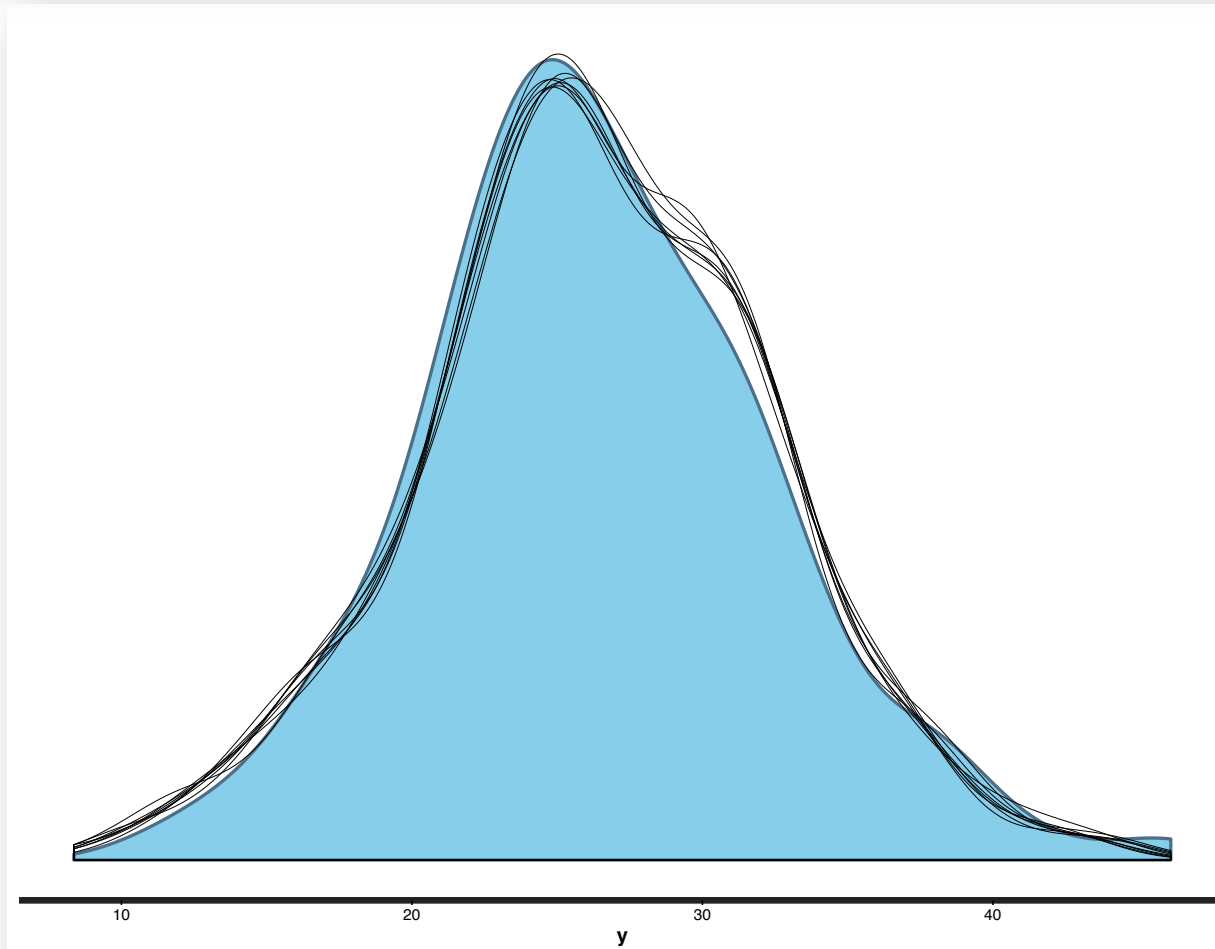
  # build model matrix
  mm <- model.matrix(~doy, data.frame(doy))

  # coefficients need to match the order of the columns in the model matrix (mm)
  coeff <- c(spint[i],
             rnorm(1, doycoef, doycoef.sd))

  bvol <- rnorm(n = ntot, mean = mm %*% coeff, sd = 0.1)

  testdatx <- data.frame(bvol, sp = i,
                        doy)
  testdat <- rbind(testdat, testdatx)
}
```

```
truvol<-stan_lmer(bvol~doy+(1|sp), testdat)
```



# Bias correction

```
76  
77 ###make adjusted bvol  
78 testdat<-dplyr::mutate(testdat, offset=40-doy)  
79 testdat<-dplyr::mutate(testdat, deltabv= offset*0.5)  
80 testdat<-dplyr::mutate(testdat, trubudvol= bvol-deltabv)  
81
```

```
> head(testdat)
```

	bvol	sp	doy	offset	deltabv	trubudvol
1	27.81795	1	38.54953	1.450469	0.7252345	27.09271
2	30.57948	1	42.91358	-2.913580	-1.4567900	32.03627
3	29.42414	1	40.93797	-0.937974	-0.4689870	29.89312
4	27.82368	1	38.72632	1.273679	0.6368394	27.18684
5	23.12146	1	31.53169	8.468310	4.2341552	18.88731
6	29.56401	1	41.41166	-1.411659	-0.7058293	30.26984

```
> |
```

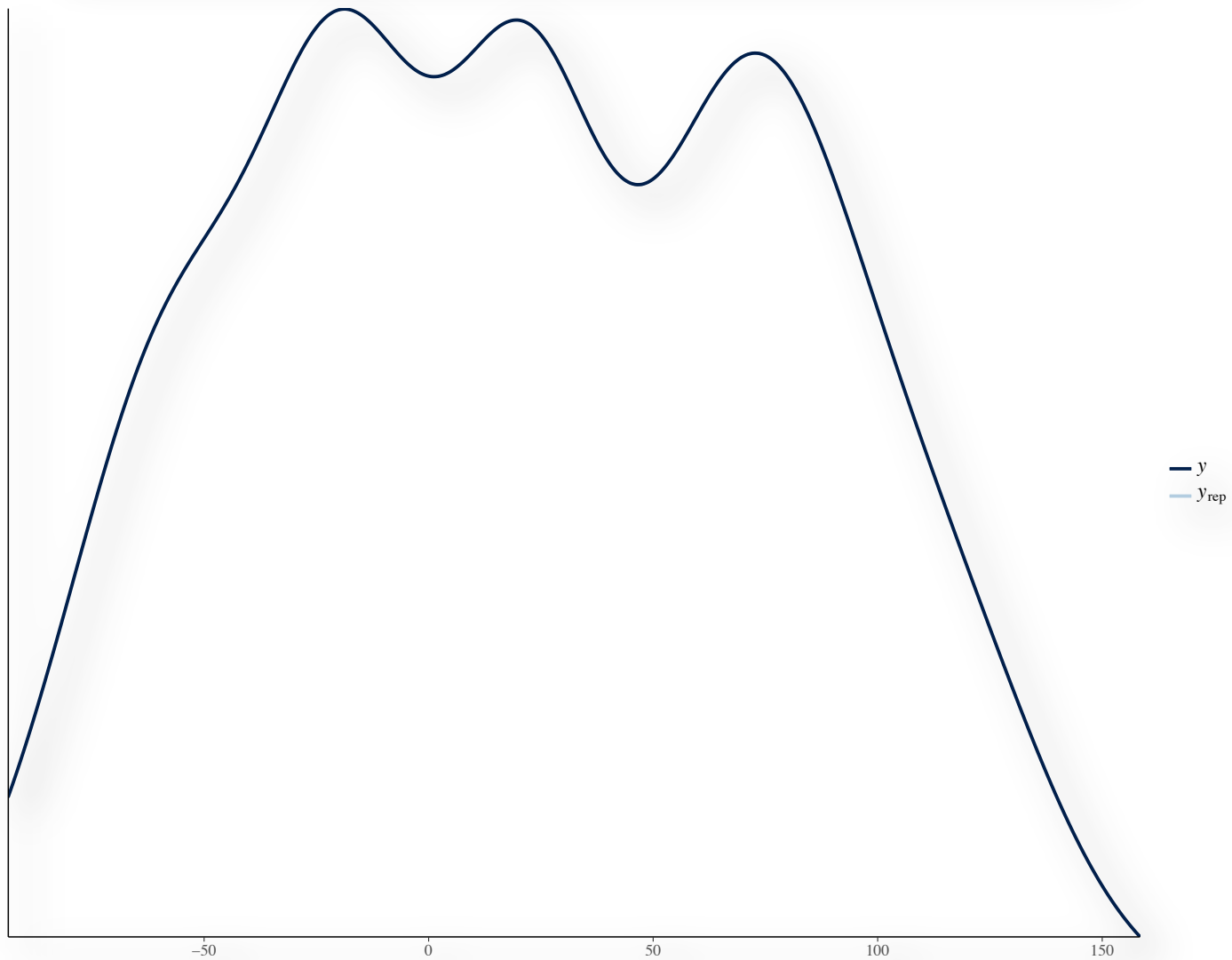
How to account for error on coefficient?  
Is there a less hacky way to do this?

# Fake Data: Varying slope & intercept

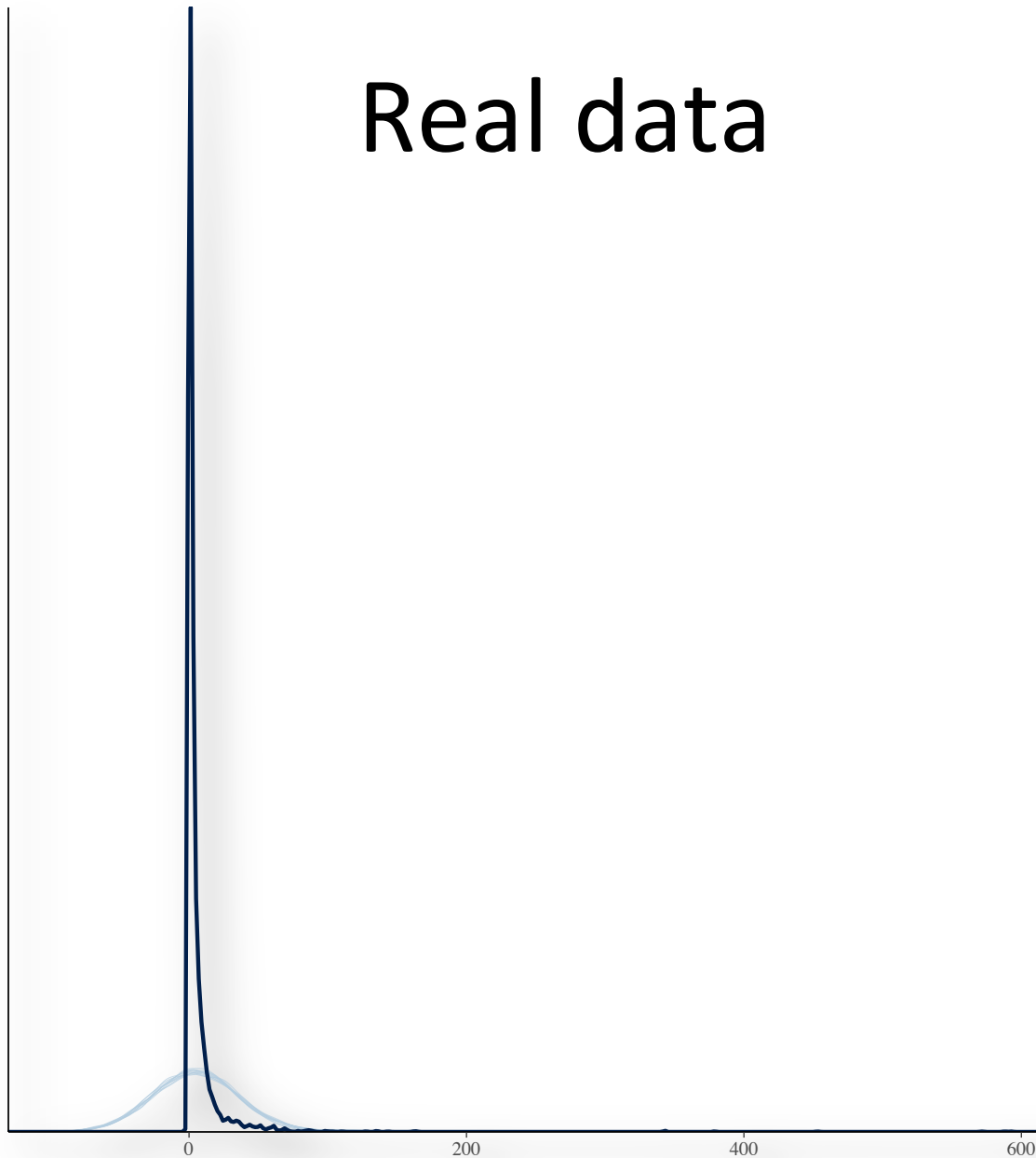
```
9 ##### fake data for doyc effect varying slope
0 nsp = 5 # number of species
1 ntot = 50 # numbers of obs per species.
2 baseinter <- 5 # baseline intercept (budvol) across all species
3 spint <- baseinter + c(1:nsp)-mean(1:nsp) # different intercepts by species
4 baseeff<-.5 ##baseline effect size
5 speff<- baseeff + c(1:nsp)-mean(1:nsp) ##different effect by sdpecies
6 # now start building ...
7 testdat2 <- vector()
8 for(i in 1:nsp){ # loop over species. i = 1
9   # continuous predictors, generate level for each observation
0   doyc<- rtnorm(ntot,40,10,lower=10,upper=70)
1   ## set up effect size
2   doyccoef<-speff
3   doyccoef.sd<-0.05
4   # build model matrix
5   mm <- model.matrix(~doyc, data.frame(doyc))
6   # coefficients need to match the order of the columns in the model matrix (mm)
7   coeff <- c(spint[i],
8             rtnorm(1, doyccoef[i], doyccoef.sd))
9
0   bvol <- rtnorm(n = ntot, mean = mm %*% coeff, sd = 0.1)
1   |
2   testdatx <- data.frame(bvol, sp = i,
3                         doyc)
4   testdat2 <- rbind(testdat2, testdatx)
5 }
```



```
truvol.slope<-brm(bvol~doy+(doy|sp), testdat2)
```



# Real data



# Next steps

- Improve fake data
- Better method/script for bias correct?
- What's the deal with real data???
- rough model to predict phenology from tru.bud.vol