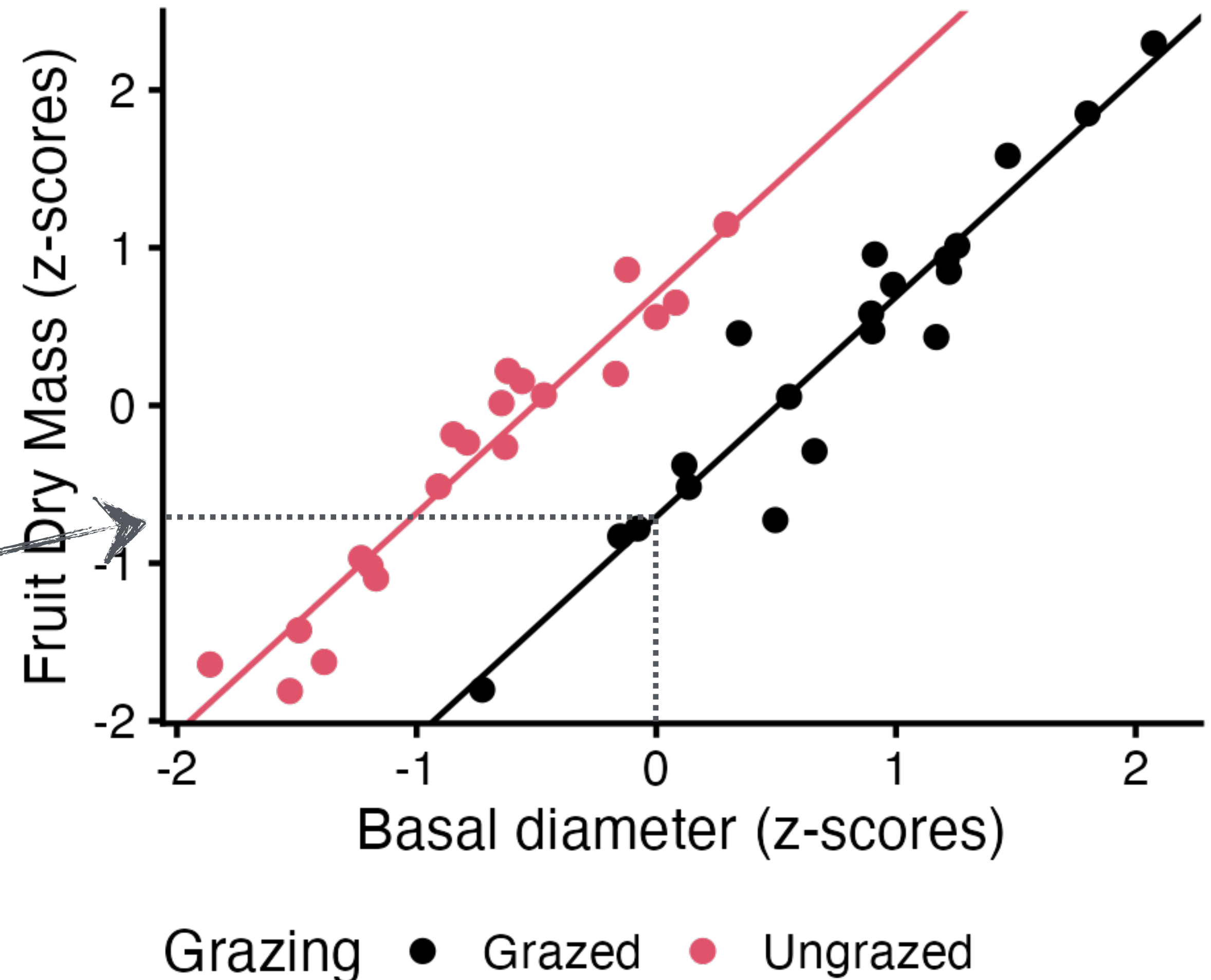


# Model with treatment and size

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m2 = ulam(alist(  
  Fruit ~ normal(mu, sigma),  
  mu <- a + b*Grazing0 + c*Root,  
  a ~ normal(0, 1),  
  b ~ normal(0, 1),  
  c ~ normal(0, 1),  
  sigma ~ exponential(1)),  
  data = df, chains = 4, cores = 4)
```

```
> precis(m2, prob = 0.95)
```

	mean	sd	2.5%	97.5%
a	-0.71	0.08	-0.86	-0.54
b	1.42	0.14	1.13	1.67
c	1.39	0.07	1.26	1.53
sigma	0.28	0.03	0.23	0.36



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