

# KLING et al P&N

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## Modeling Population & Distance

*These analyses include botanical plots inside protected area & near all 13 communities sampled in 2015.*

## Timber & Medicinal Plant Analyses

### TIMBER COUNT

```
fun.mod.notime.aicc(8) # Use function to calculate aicc values of all
possible models
aicc.w # Best model is Full-Int (w = 0.71)

##               fit      delta      w
## Full-Int    905.0079  0.000000  7.112205e-01
## Full-NoInt  907.7983  2.790415  1.762273e-01
## Pop         908.7880  3.780135  1.074381e-01
## Dist        914.8778  9.869989  5.114032e-03
## Null        944.0503  39.042416  2.366199e-09

mod.timc <- glmmTMB(wood.ct ~ pop*dist + (1|site:plot.id), family = poisson,
data = df2_notime)

summary(mod.timc)

## Family: poisson ( log )
## Formula:          wood.ct ~ pop * dist + (1 | site:plot.id)
## Data: df2_notime
##
##      AIC      BIC   logLik deviance df.resid
##    904.6    919.8   -447.3    894.6     150
##
## Random effects:
##
## Conditional model:
##   Groups      Name      Variance Std.Dev.
## site:plot.id (Intercept) 1.467    1.211
## Number of obs: 155, groups: site:plot.id, 155
##
## Conditional model:
```

```
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.34347    2.23395   1.497  0.13448
## pop         -1.22679    0.46630  -2.631  0.00852 **
## dist        -0.09352    0.25251  -0.370  0.71111
## pop:dist      0.12698    0.05716   2.221  0.02633 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How much more likely is this model than the null?

*First number below is dAICc between model & null & second is the actual likelihood (previous number/2 & exponentiated).*

```
##      dAICc likelihood
## 1 39.04242 300575111
```

Main effects: Timber Count

*Are the dist and population slopes significant if averaged over our nested random effects?*

```
main.timc <- avg_slopes(mod.timc)
main.timc

##
##   Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %
##   dist      2.43      1.16   2.10  0.0356  0.163  4.700
##   pop     -1.46      0.44  -3.31  <0.001 -2.320 -0.595
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
## conf.high
```

Marginal effects: Timber Count

*Does distance have a significant effect at certain population values?*

*Note: Population is standardized. Categories examined for marginal effects correspond to population values representative of our sample: (0 ppl, 50, 250, 2000)*

```
me.timc <- ggpredict(mod.timc, terms = c("dist", "pop [0, 3.9, 5.5, 7.6]"),
type = "fixed", allow.new.levels = T)
ggeffects::hypothesis_test(me.timc, test = NULL)

## # Linear trend for dist
##
## pop | Slope |          95% CI |      p
## -----
## 0.00 | -1.33 | [-9.01,  6.34] | 0.734
## 3.90 |  2.75 | [-0.61,  6.11] | 0.109
```

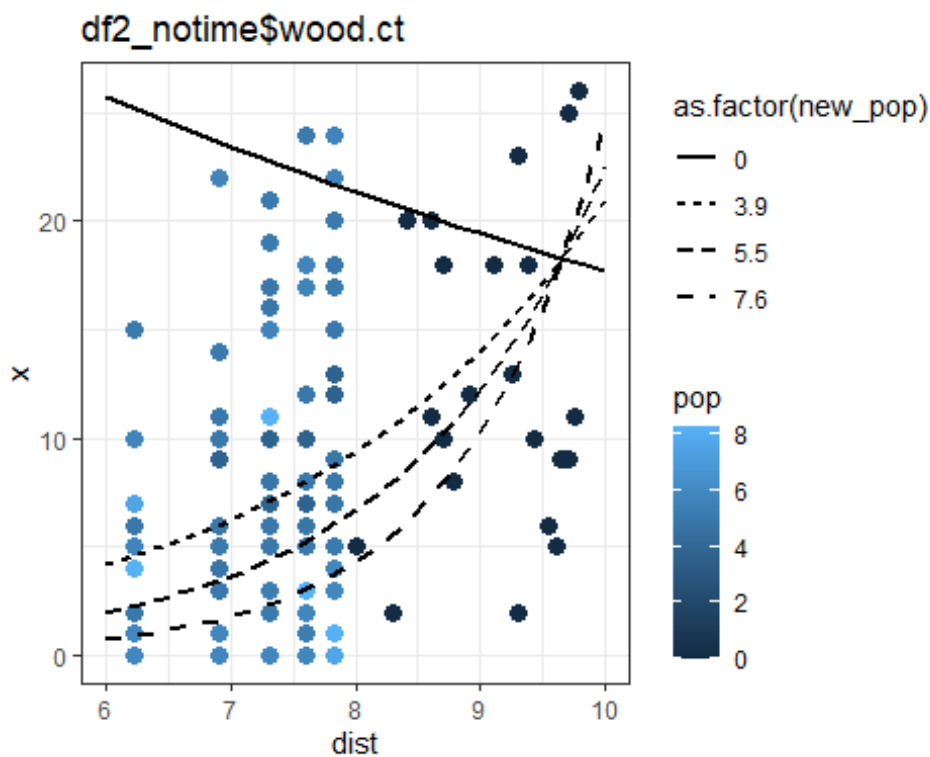
```
## 5.50 | 3.32 | [-1.17, 7.80] | 0.147
## 7.60 | 3.78 | [-2.70, 10.27] | 0.253

##
## Slopes are presented on the response-scale.
```

*Note: All visualizations available either in main text of manuscript or in supplementary materials, as composite figures. These are just quick ones for your reference, as you go through the code!*

### Visualize Data & Model-Predicted Results for Timber Count

*Note: Distance is standardized. Range corresponds to closest botanical plot distance to a community (~ 500 m) to ~ 22 km.*



### TIMBER SPECIES RICHNESS

*## For remaining analyses of pop & dist, using the same process as that for TIMBER COUNT. Refer to Timber Count annotations*

```
fun.mod.notime.aicc(11)
aicc.w # Best model is Full-Int (w = 0.74)

##           fit      delta      w
## Full-Int   805.5110  0.000000  7.437185e-01
## Full-NoInt 808.3593  2.848224  1.790295e-01
## Pop        810.1135  4.602515  7.447066e-02
## Dist       816.6885 11.177471  2.781323e-03
## Null       852.0196 46.508607  5.918245e-11

mod.timr <- glmmTMB(wood.rich ~ pop*dist + (1|site:plot.id), family =
poisson, data = df2_notime)

summary(mod.timr)

## Family: poisson ( log )
## Formula:          wood.rich ~ pop * dist + (1 | site:plot.id)
## Data: df2_notime
##
##      AIC      BIC   logLik deviance df.resid
##    805.1    820.3   -397.6    795.1     150
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev.
## site:plot.id (Intercept) 1.017    1.008
## Number of obs: 155, groups: site:plot.id, 155
##
## Conditional model:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.72529    1.96562   1.387  0.16560
## pop          -1.10856    0.41650  -2.662  0.00778 **
## dist         -0.05127    0.22158  -0.231  0.81702
## pop:dist      0.11370    0.05099   2.230  0.02575 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How much more likely is this model than the null?

```
##      dAICc likelihood
## 1 46.50861 12566537757
```

### Main effects: Timber Species Richness

```
main.timr <- avg_slopes(mod.timr)
main.timr

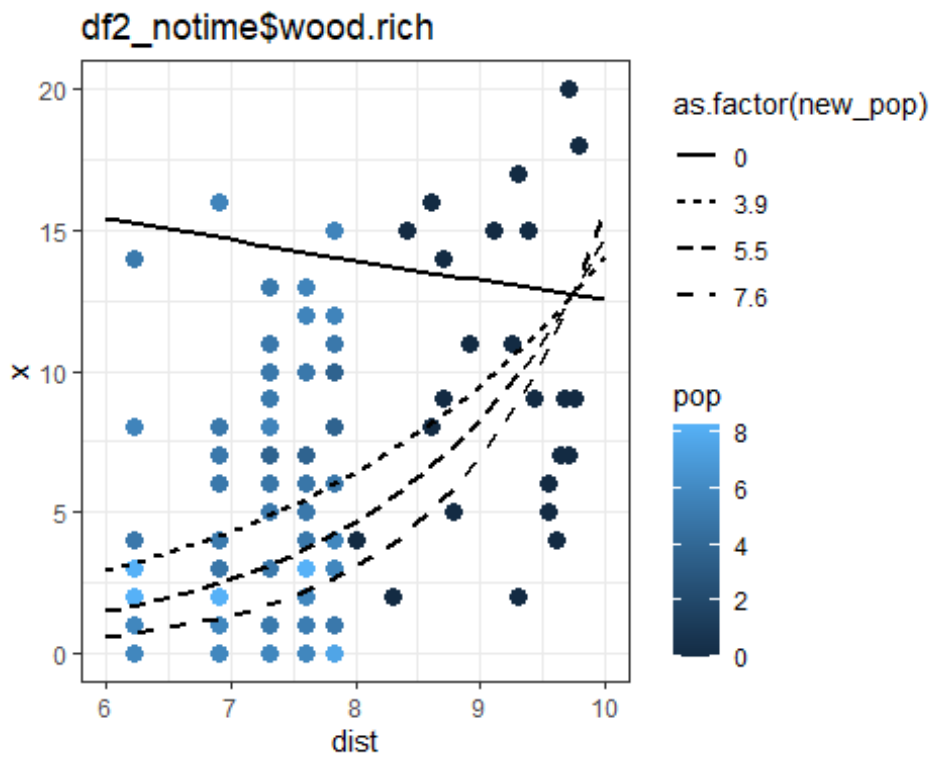
##
##   Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %
##   dist    1.616      0.726   2.22  0.0261  0.192  3.040
##   pop     -0.955      0.277  -3.45  <0.001 -1.497 -0.413
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
## conf.high
```

### Marginal effects: Timber Species Richness

```
me.timr <- ggpredict(mod.timr, terms = c("dist", "pop [0, 3.9, 5.5, 7.6]"),
type = "fixed", allow.new.levels = T)
hypothesis_test(me.timr, test = NULL)

## # Linear trend for dist
##
## pop | Slope |      95% CI |      p
## -----
## 0.00 | -0.54 | [-5.32, 4.24] | 0.825
## 3.90 |  2.07 | [-0.20, 4.35] | 0.073
## 5.50 |  2.44 | [-0.55, 5.43] | 0.109
## 7.60 |  2.72 | [-1.47, 6.91] | 0.204
##
## Slopes are presented on the response-scale.
```

## Visualize Data & Model-Predicted Results for Timber Species Richness



### MEDICINAL PLANTS COUNT

```
fun.mod.notime.aicc(9)
aicc.w # Best model is Full-NoInt (w = 0.71)

##               fit      delta          w
## Full-Int      1092.365 2.123094 0.246395226
## Full-NoInt    1090.241 0.000000 0.712289251
## Pop           1097.626 7.384585 0.017746554
## Dist          1098.889 8.647218 0.009439234
## Null          1098.082 7.840405 0.014129735

mod.medc <- glmmTMB(med.ct ~ pop + dist + (1|site:plot.id), family = poisson,
data = df2_notime)

summary(mod.medc)

## Family: poisson ( log )
## Formula:          med.ct ~ pop + dist + (1 | site:plot.id)
## Data: df2_notime
##
##      AIC      BIC   logLik deviance df.resid
##  1090.0   1102.1   -541.0   1082.0     151
##
## Random effects:
##
## Conditional model:
##   Groups      Name      Variance Std.Dev.
## site:plot.id (Intercept) 1.071    1.035
## Number of obs: 155, groups: site:plot.id, 155
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  5.89354    1.19284   4.941 7.78e-07 ***
## pop          -0.17133    0.05219  -3.283  0.00103 **
## dist         -0.41945    0.13486  -3.110  0.00187 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### How much more likely is this model than the null?

```
##      dAICc likelihood
## 1 7.840405    50.41066
```

### Main effects: Medicinal Plants Count

```
main.medc <- avg_slopes(mod.medc)
main.medc
```

```
##
## Term Estimate Std. Error      z Pr(>|z|) 2.5 % 97.5 %
## dist      -4.93      1.583 -3.11  0.00187 -8.03 -1.822
## pop       -2.01      0.613 -3.28  0.00102 -3.21 -0.811
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
conf.high
```

#### Marginal effects: Medicinal Plants Count

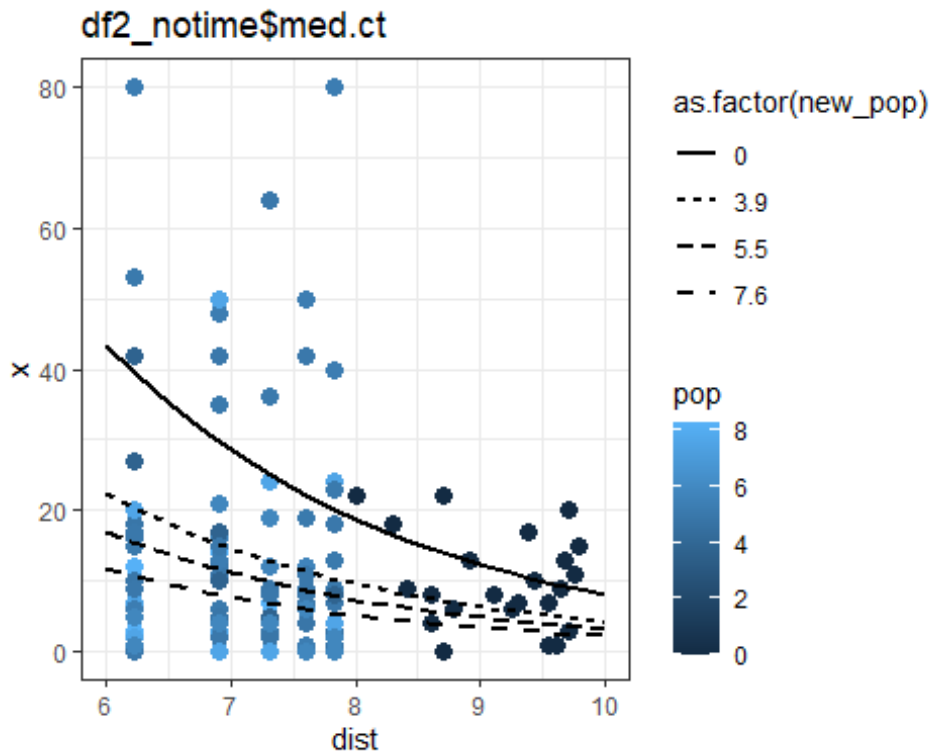
```
me.medc <- ggpredict(mod.medc, terms = c("dist", "pop [0, 3.9, 5.5, 7.6]"),
type = "fixed", allow.new.levels = T)
hypothesis_test(me.medc, test = NULL)
```

```
## # Linear trend for dist
##
## pop | Slope |          95% CI |      p
## -----
## 0.00 | -6.14 | [-12.44,  0.15] | 0.056
## 3.90 | -3.15 | [ -5.34, -0.95] | 0.005
## 5.50 | -2.39 | [ -3.80, -0.98] | < .001
## 7.60 | -1.67 | [ -2.50, -0.84] | < .001
##
## Slopes are presented on the response-scale.
```



## Visualize Data & Model-Predicted Results for Medicinal Plants Count

*Note: There is no interaction between pop & dist for medicinal plants count.*



### MEDICINAL PLANTS SPECIES RICHNESS

```
fun.mod.notime.aicc(12)
aicc.w # Best model is Pop only (w = 0.53)

##               fit      delta      w
## Full-Int    607.2343  2.8387274 1.270606e-01
## Full-NoInt  605.2215  0.8259879 3.475937e-01
## Pop         604.3955  0.0000000 5.253308e-01
## Dist        625.3711 20.9755705 1.464352e-05
## Null        633.3896 28.9940488 2.657389e-07

mod.medr <- glmmTMB(med.rich ~ pop + (1|site:plot.id), family = poisson, data
= df2_notime)

summary(mod.medr)

## Family: poisson ( log )
## Formula:          med.rich ~ pop + (1 | site:plot.id)
## Data: df2_notime
##
##      AIC      BIC   logLik deviance df.resid
##    604.2    613.4   -299.1    598.2     152
##
## Random effects:
##
## Conditional model:
##   Groups      Name      Variance Std.Dev.
## site:plot.id (Intercept) 2.582e-09 5.081e-05
## Number of obs: 155, groups: site:plot.id, 155
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.56745    0.08594  18.239  < 2e-16 ***
## pop          -0.10404    0.01756  -5.924 3.14e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### How much more likely is this model than the null?

```
##      dAICc likelihood
## 1 28.99405    1976868
```

### Main effects: Medicinal Plants Species Richness

```
main.medr <- avg_slopes(mod.medr)
main.medr

##
##   Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %
```

```
##   pop    -0.313      0.0549 -5.71   <0.001 -0.421 -0.206
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
## conf.high
```

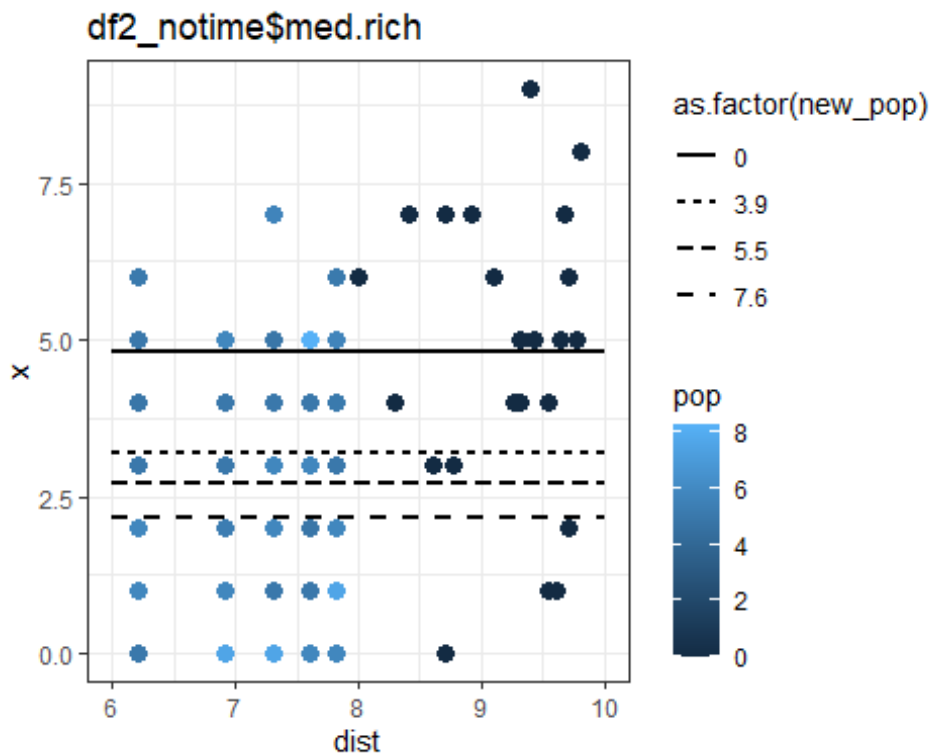
### Marginal effects: Medicinal Plants Species Richness

```
me.medr <- ggpredict(mod.medr, terms = c("pop [0, 3.9, 5.5, 7.6]"), type =
"fixed", allow.new.levels = T)
hypothesis_test(me.medr, test = NULL)
```

```
## # Linear trend for pop
##
## Slope |          95% CI |      p
## -----
## -0.31 | [-0.42, -0.21] | < .001
##
## Slopes are presented on the response-scale.
```

### Visualize Data & Model-Predicted Results for Medicinal Plants Species Richness

*Note: There is no distance term in the model for medicinal plants species richness.*



## Lemur Food Trees Analyses

### LEMUR FOOD TREES COUNT

```
fun.mod.notime.aicc(10)
aicc.w # Best model is Full-Int (w = 0.64)

##               fit      delta      w
## Full-Int    718.2640  0.000000 6.440495e-01
## Full-NoInt  720.8157  2.551669 1.798172e-01
## Pop         720.8702  2.606136 1.749863e-01
## Dist        730.9252 12.661181 1.147041e-03
## Null        763.0890 44.824983 1.189318e-10

mod.lemc <- glmmTMB(lem.ct ~ pop*dist + (1|site:plot.id), family = poisson,
data = df2_notime)

summary(mod.lemc)

## Family: poisson ( log )
## Formula:      lem.ct ~ pop * dist + (1 | site:plot.id)
## Data: df2_notime
##
##      AIC      BIC   logLik deviance df.resid
##   717.9    733.1   -353.9    707.9     150
##
## Random effects:
##
## Conditional model:
##   Groups      Name      Variance Std.Dev.
## site:plot.id (Intercept) 0.857    0.9257
## Number of obs: 155, groups: site:plot.id, 155
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.02425    1.93726   1.561   0.11850
## pop          -1.09937    0.42067  -2.613   0.00897 **
## dist         -0.11790    0.21767  -0.542   0.58806
## pop:dist      0.11080    0.05143   2.154   0.03122 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### How much more likely is this model than the null?

```
##      dAICc likelihood
## 1 44.82498 5415284488
```

### Main effects: Lemur Food Trees Count

```
main.lemc <- avg_slopes(mod.lemc)
main.lemc

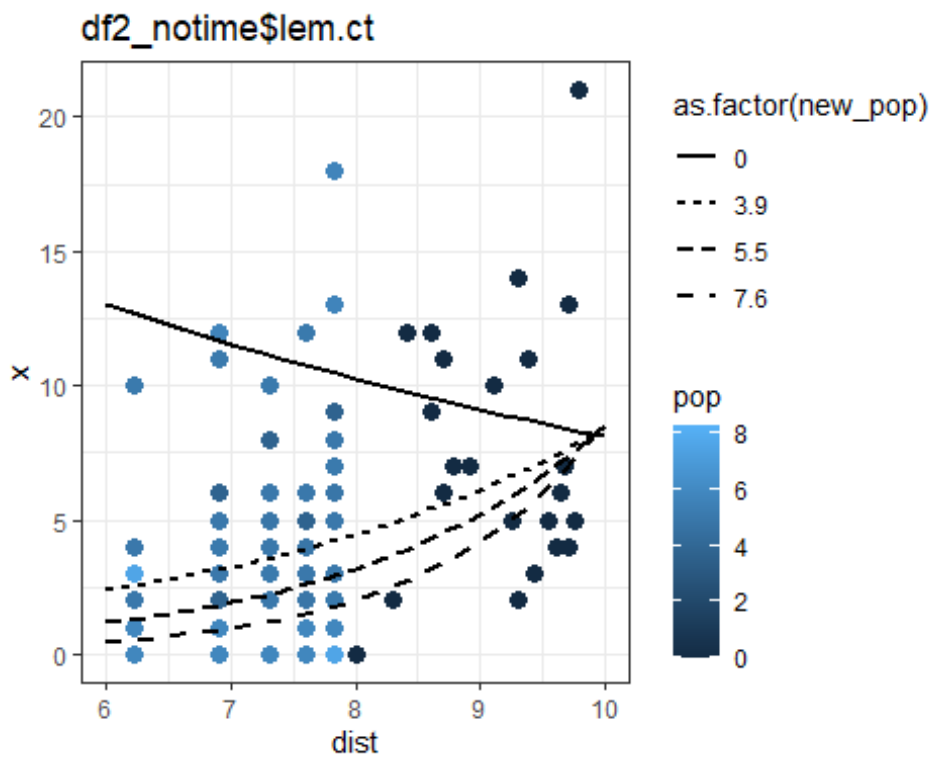
##
##   Term Estimate Std. Error      z Pr(>|z|) 2.5 % 97.5 %
## dist    0.896      0.524   1.71   0.087 -0.13  1.922
## pop    -0.746      0.202  -3.70  <0.001 -1.14 -0.351
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
## conf.high
```

### Marginal effects: Lemur Food Trees Count

```
me.lemc <- ggpredict(mod.lemc, terms = c("dist", "pop [0, 3.9, 5.5, 7.6]"),
type = "fixed", allow.new.levels = T)
hypothesis_test(me.lemc, test = NULL)

## # Linear trend for dist
##
## pop | Slope |      95% CI |      p
## -----
## 0.00 | -0.98 | [-4.96, 3.00] | 0.629
## 3.90 |  1.20 | [-0.30, 2.69] | 0.117
## 5.50 |  1.45 | [-0.44, 3.33] | 0.133
## 7.60 |  1.59 | [-0.94, 4.12] | 0.217
##
## Slopes are presented on the response-scale.
```

## Visualize Data & Model-Predicted Results for Lemur Food Trees Count



## LEMUR FOOD TREES SPECIES RICHNESS

# Lemur Food Tree SPECIES RICHNESS

```
fun.mod.notime.aicc(13)
```

aicc.w # Best model is Full-Int (w = 0.70)

```
##               fit      delta      w
## Full-Int    640.9285  0.000000 6.998338e-01
## Full-NoInt  643.7757  2.847120 1.685585e-01
## Pop         644.2823  3.353715 1.308413e-01
## Dist        654.5622 13.633673 7.664438e-04
## Null        691.5846 50.656040 7.001251e-12
```

```
mod.lemr <- glmmTMB(lem.rich ~ pop*dist + (1|site:plot.id), family = poisson,
data = df2_notime)
```

```
summary(mod.lemr)
```

```
## Family: poisson ( log )
## Formula:      lem.rich ~ pop * dist + (1 | site:plot.id)
## Data: df2_notime
##
##      AIC      BIC   logLik deviance df.resid
##   640.5    655.7   -315.3    630.5     150
##
## Random effects:
##
## Conditional model:
##   Groups      Name      Variance Std.Dev.
## site:plot.id (Intercept) 0.6036   0.7769
## Number of obs: 155, groups: site:plot.id, 155
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.65397    1.78518   1.487   0.13710
## pop           -1.06075    0.39929  -2.657   0.00789 **
## dist          -0.09857    0.19993  -0.493   0.62199
## pop:dist       0.10736    0.04874   2.203   0.02762 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How much more likely is this model than the null?

```
##      dAICc likelihood
## 1 50.65604 99958393047
```

## Main effects: Lemur Food Trees Species Richness

```
main.lemr <- avg_slopes(mod.lemr)
main.lemr
```

```
##
##   Term Estimate Std. Error      z Pr(>|z|)    2.5 % 97.5 %
## dist    0.676      0.367  1.84  0.0657 -0.0439  1.396
## pop     -0.533      0.141 -3.77  <0.001 -0.8099 -0.256
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
## conf.high
```

### Marginal effects: Lemur Food Trees Species Richness

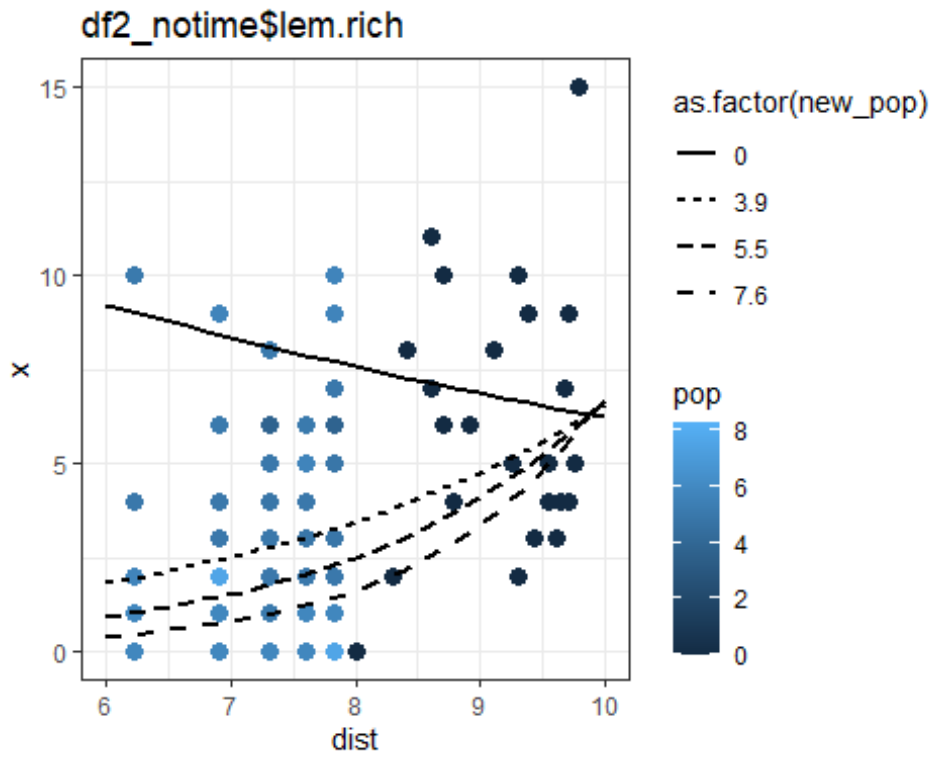
```
me.lemr <- ggpredict(mod.lemr, terms = c("dist", "pop [0, 3.9, 5.5, 7.6]"),
type = "fixed", allow.new.levels = T)
hypothesis_test(me.lemr, test = NULL)
```

```
## # Linear trend for dist
##
## pop | Slope |          95% CI |      p
## -----
## 0.00 | -0.65 | [-3.51, 2.20] | 0.655
## 3.90 |  1.02 | [-0.15, 2.19] | 0.088
## 5.50 |  1.23 | [-0.27, 2.73] | 0.109
## 7.60 |  1.36 | [-0.67, 3.40] | 0.190
```

```
##
## Slopes are presented on the response-scale.
```



## Visualize Data & Model-Predicted Results for Lemur Food Trees Species Richness



## Modeling Changes in Plot Metrics Over Time

*These analyses include all plots that were repeat-sampled near 5 communities between 2015-2021. Each plot was sampled 5x.*

*Note: All changes over time analyses use the same fixed effect model structure for population & distance as that used in the first set of analyses for that plant trait (e.g., TIMBER COUNT's model of population & distance included the following as its fixed effects: pop x dist, so its fixed effects for the model of change over time would be pop x dist + time).*

### Timber & Medicinal Plant Analyses

#### TIMBER COUNT

```
mod.time.tmc <- glmmTMB(wood.ct ~ pop*dist + time + (1+time|site:plot.id),  
family = poisson, data = df3_time)
```

```
summary(mod.time.tmc)
```

```
## Family: poisson ( log )  
## Formula: wood.ct ~ pop * dist + time + (1 + time | site:plot.id)  
## Data: df3_time  
##  
##      AIC      BIC   logLik deviance df.resid  
## 1239.2 1267.4 -611.6 1223.2      242  
##  
## Random effects:  
##  
## Conditional model:  
## Groups      Name      Variance Std.Dev. Corr  
## site:plot.id (Intercept) 0.50693  0.7120  
##              time      0.07053  0.2656  -0.37  
## Number of obs: 250, groups: site:plot.id, 50  
##  
## Conditional model:  
##              Estimate Std. Error z value Pr(>|z|)  
## (Intercept) -22.49004    9.29200 -2.420  0.01550 *  
## pop          3.00793    1.82068  1.652  0.09852 .  
## dist         3.25121    1.25623  2.588  0.00965 **  
## time        -0.18827    0.04518 -4.167 3.08e-05 ***  
## pop:dist     -0.38940    0.24576 -1.584  0.11308  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How much more likely is this model than the null? What is its model weight?

```
##      dAICc    likelihood weight
## 1 265.6346 4.806403e+57      1
```

Main effects: Timber Count

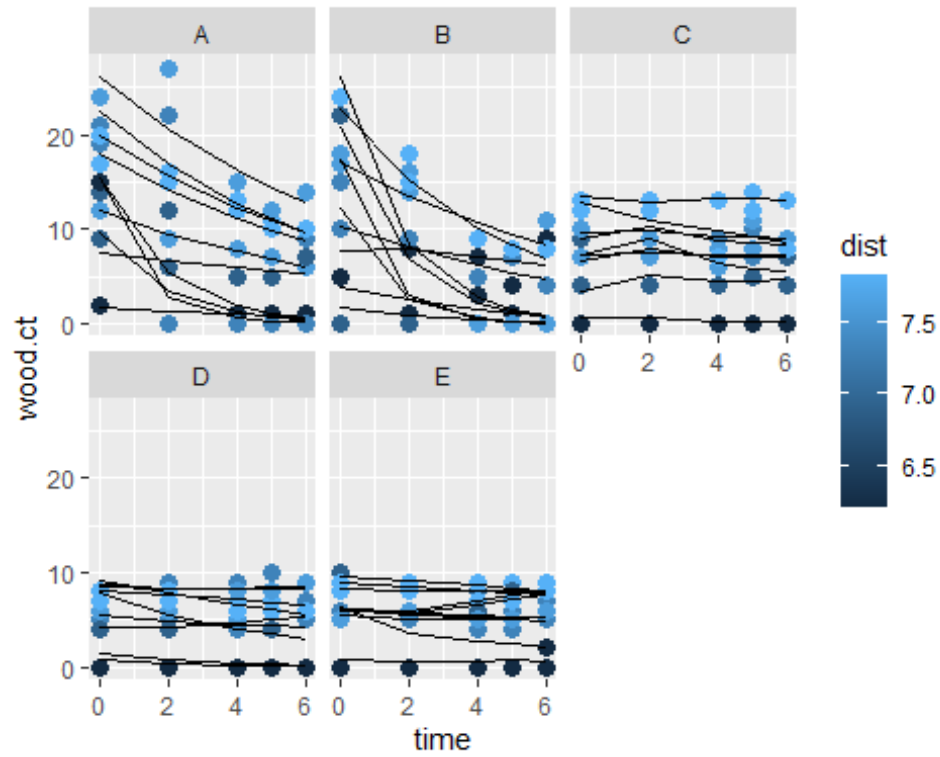
*Is the effect of time (& dist and population for this subset of repeat-sampled plots) significant if averaged over our nested random effects?*

```
main.time.timc <- avg_slopes(mod.time.timc)
main.time.timc
```

```
##
##   Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %
## dist      8.426      1.396   6.035  <0.001   5.689 11.163
## pop       0.735      0.777   0.946   0.344  -0.788  2.259
## time     -0.835      0.041 -20.342  <0.001  -0.915 -0.754
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
##          conf.high
```

## Visualize Data & Model-Predicted Results for Timber Count Change over Time BY SITE

*Note: Lines represent change over time for each individual plot per site.*



### TIMBER SPECIES RICHNESS

```
mod.time.timr <- glmmTMB(wood.rich ~ pop*dist + time + (1+time|site:plot.id),  
family = poisson, data = df3_time)
```

```
summary(mod.time.timr)
```

```
## Family: poisson ( log )  
## Formula: wood.rich ~ pop * dist + time + (1 + time |  
site:plot.id)  
## Data: df3_time  
##  
##      AIC      BIC   logLik deviance df.resid  
##  1100.0   1128.2   -542.0   1084.0     242  
##  
## Random effects:  
##  
## Conditional model:  
## Groups      Name      Variance Std.Dev. Corr  
## site:plot.id (Intercept) 0.2847  0.5335  
##              time        0.0537  0.2317  -0.18  
## Number of obs: 250, groups: site:plot.id, 50  
##  
## Conditional model:  
##              Estimate Std. Error z value Pr(>|z|)  
## (Intercept) -24.05962    9.32671  -2.580  0.00989 **  
## pop          3.66609     1.81456   2.020  0.04334 *  
## dist         3.37542     1.26638   2.665  0.00769 **  
## time        -0.18065     0.04235  -4.266 1.99e-05 ***  
## pop:dist    -0.46921     0.24597  -1.908  0.05645 .  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How much more likely is this model than the null? What is its model weight?

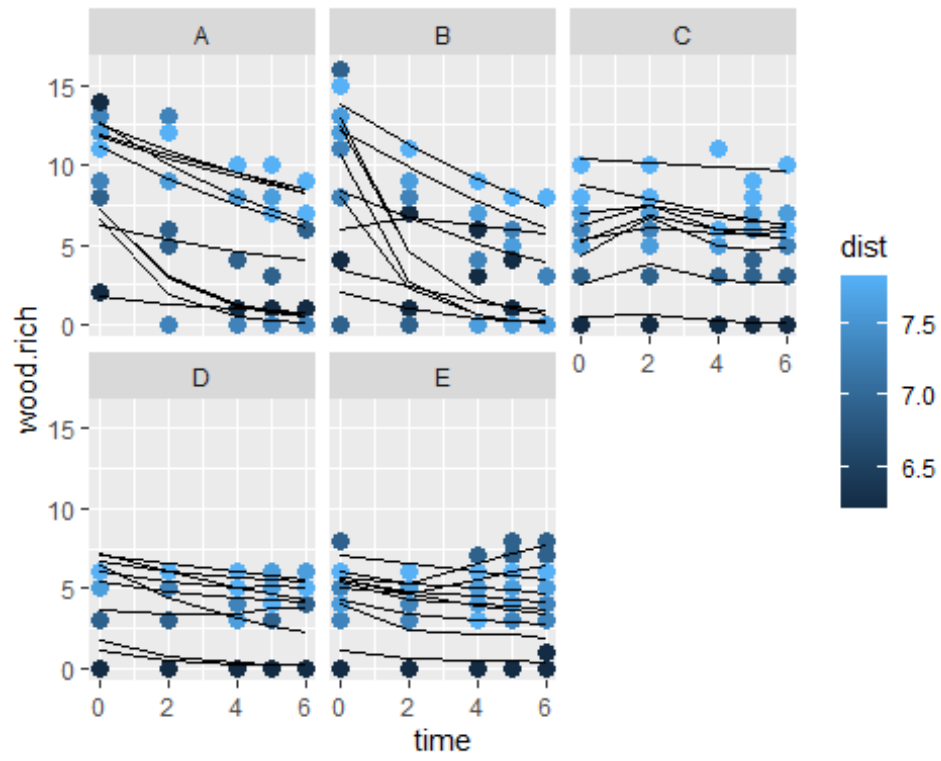
```
##      dAICc  likelihood weight  
## 1 134.6359 1.721093e+29      1
```

### Main effects: Timber Species Richness

```
main.time.timr <- avg_slopes(mod.time.timr)  
main.time.timr
```

```
##  
## Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %  
## dist    4.863    0.9410    5.17  <0.001  3.019  6.708  
## pop     0.885    0.6188    1.43   0.153 -0.328  2.098  
## time   -0.498    0.0452  -11.02  <0.001 -0.586 -0.409  
##  
## Columns: term, estimate, std.error, statistic, p.value, conf.low,  
conf.high
```

## Visualize Data & Model-Predicted Results for Timber Species Richness Change over Time BY SITE



### MEDICINAL PLANTS COUNT

```
mod.time.medc <- glmmTMB(med.ct ~ pop + dist + time + (1+time|site:plot.id),  
family = poisson, data = df3_time)
```

```
summary(mod.time.medc)
```

```
## Family: poisson ( log )  
## Formula: med.ct ~ pop + dist + time + (1 + time | site:plot.id)  
## Data: df3_time  
##  
##      AIC      BIC   logLik deviance df.resid  
##  2146.7   2171.4  -1066.4   2132.7      243  
##  
## Random effects:  
##  
## Conditional model:  
## Groups      Name      Variance Std.Dev. Corr  
## site:plot.id (Intercept) 0.71321  0.8445  
##              time        0.03584  0.1893  -0.56  
## Number of obs: 250, groups: site:plot.id, 50  
##  
## Conditional model:  
##              Estimate Std. Error z value Pr(>|z|)  
## (Intercept)  3.26135    1.44892   2.251   0.0244 *  
## pop          0.19504    0.08860   2.201   0.0277 *  
## dist        -0.29380    0.19147  -1.534   0.1249  
## time         0.02102    0.02937   0.716   0.4743  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How much more likely is this model than the null? What is its model weight?

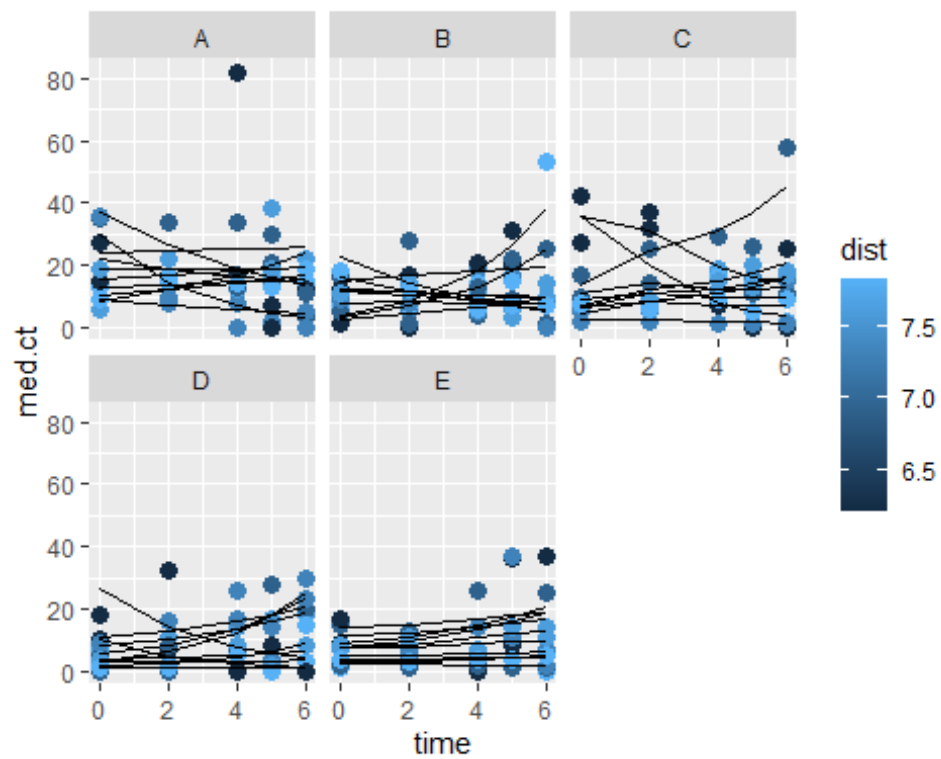
```
##      dAICc  likelihood weight  
## 1 315.6227 3.440369e+68      1
```

### Main effects: Medicinal Plants Count

```
main.time.medc <- avg_slopes(mod.time.medc)  
main.time.medc
```

```
##  
## Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %  
## dist  -3.499    2.2806  -1.53  0.1249  -7.969  0.971  
## pop    2.323    1.0553   2.20  0.0277   0.255  4.391  
## time   0.375    0.0445   8.43  <0.001   0.288  0.462  
##  
## Columns: term, estimate, std.error, statistic, p.value, conf.low,  
## conf.high
```

## Visualize Data & Model-Predicted Results for Medicinal Plants Count Change over Time BY SITE





## MEDICINAL PLANTS SPECIES RICHNESS

*Note: There is a singular convergence issue is time is included as a random slope. This is the only time analysis that does NOT include time as a random slope. Time is still included as a fixed effect.*

```
mod.time.medr <- glmmTMB(med.rich ~ pop + time + (1|site:plot.id), family =  
poisson, data = df3_time) # Singular convergence issue when time was included  
as a random slope
```

```
summary(mod.time.medr) # Medicinal plant species richness significantly  
decreases over time
```

```
## Family: poisson ( log )  
## Formula: med.rich ~ pop + time + (1 | site:plot.id)  
## Data: df3_time  
##  
##      AIC      BIC   logLik deviance df.resid  
##  901.1    915.1   -446.5    893.1      246  
##  
## Random effects:  
##  
## Conditional model:  
## Groups      Name      Variance Std.Dev.  
## site:plot.id (Intercept) 0.1574  0.3967  
## Number of obs: 250, groups: site:plot.id, 50  
##  
## Conditional model:  
##      Estimate Std. Error z value Pr(>|z|)  
## (Intercept)  1.114065   0.496837  2.242 0.024941 *  
## pop          0.006645   0.099431  0.067 0.946720  
## time        -0.058923   0.017411 -3.384 0.000714 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How much more likely is this model than the null? What is its model weight?

```
##      dAICc likelihood    weight  
## 1 7.420269    40.85929 0.9761104
```

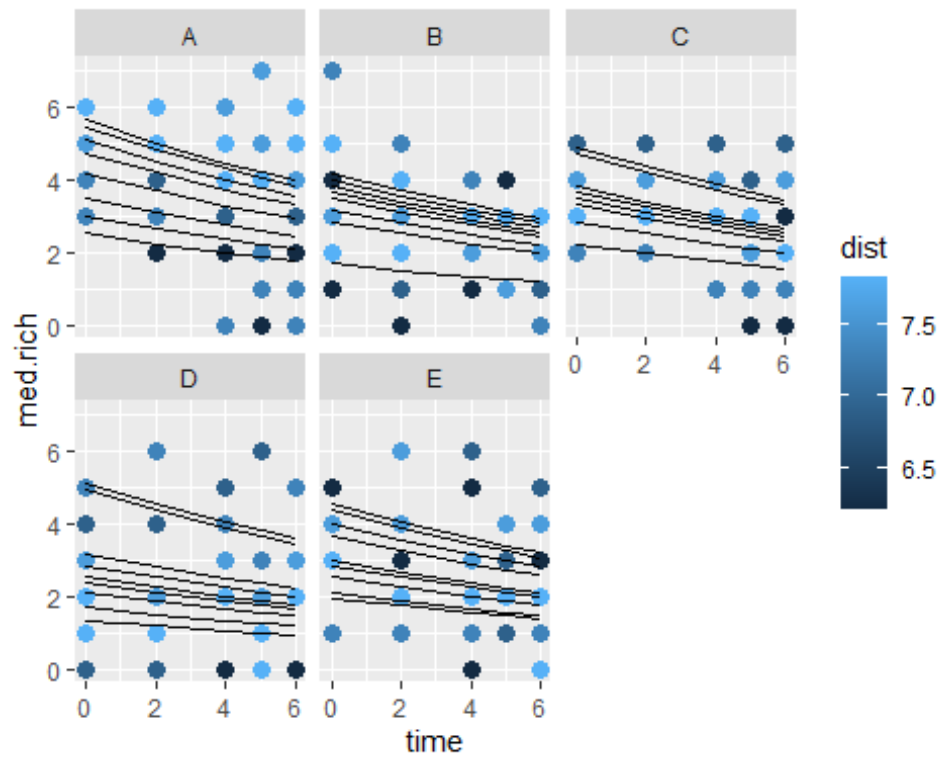
### Main effects: Medicinal Plants Species Richness

```
main.time.medr <- avg_slopes(mod.time.medr)  
main.time.medr
```

```
##  
## Term Estimate Std. Error      z Pr(>|z|)  2.5 %  97.5 %  
## pop      0.0185     0.2763  0.0668    0.947 -0.523  0.5599  
## time    -0.1637     0.0485 -3.3756   <0.001 -0.259 -0.0687  
##
```

```
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
conf.high
```

Visualize Data & Model-Predicted Results for Medicinal Plants Species Richness Change over Time BY SITE



## Lemur Food Trees Analyses

### LEMUR FOOD TREES COUNT

```
mod.time.lemc <- glmmTMB(lem.ct ~ pop*dist + time + (1+time|site:plot.id),
family = poisson, data = df3_time)

summary(mod.time.lemc)

## Family: poisson ( log )
## Formula:      lem.ct ~ pop * dist + time + (1 + time | site:plot.id)
## Data: df3_time
##
##      AIC      BIC   logLik deviance df.resid
##   987.0   1015.1   -485.5    971.0     242
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev. Corr
## site:plot.id (Intercept) 0.47870  0.6919
##              time        0.03966  0.1991  -0.20
## Number of obs: 250, groups:  site:plot.id, 50
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -23.69840   10.80574  -2.193   0.0283 *
## pop          3.36018    2.09666   1.603   0.1090
## dist         3.39960    1.46985   2.313   0.0207 *
## time        -0.17469    0.04097  -4.264 2.01e-05 ***
## pop:dist     -0.45131    0.28497  -1.584   0.1133
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How much more likely is this model than the null? What is its model weight?

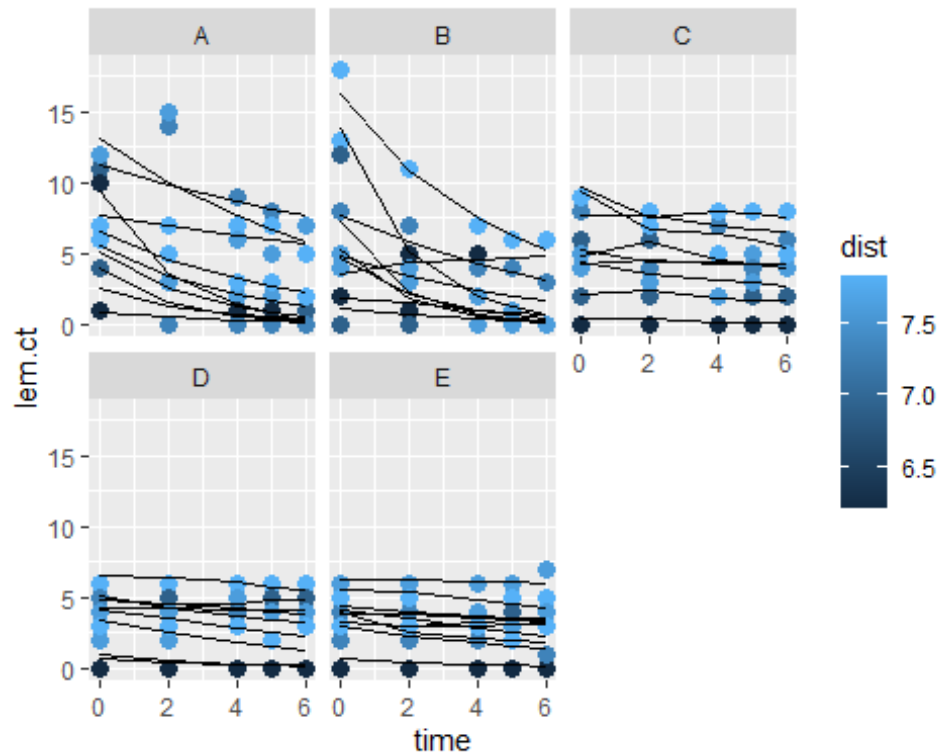
```
##      dAICc  likelihood weight
## 1 109.4422 5.821925e+23      1
```

### Main effects: Lemur Food Trees Count

```
main.time.lemc <- avg_slopes(mod.time.lemc)
main.time.lemc

##
## Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %
## dist  4.0841    0.8403   4.861  <0.001  2.437  5.73
## pop   0.0557    0.5168   0.108   0.914 -0.957  1.07
## time -0.3991    0.0404  -9.887  <0.001 -0.478 -0.32
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
conf.high
```

## Visualize Data & Model-Predicted Results for Lemur Food Trees Count Change over Time BY SITE



### LEMUR FOOD TREES SPECIES RICHNESS

```
mod.time.lemr <- glmmTMB(lem.rich ~ pop*dist + time + (1+time|site:plot.id),
family = poisson, data = df3_time)

summary(mod.time.lemr)

## Family: poisson ( log )
## Formula:      lem.rich ~ pop * dist + time + (1 + time | site:plot.id)
## Data: df3_time
##
##      AIC      BIC   logLik deviance df.resid
##    899.7    927.9   -441.9    883.7      242
##
## Random effects:
##
## Conditional model:
## Groups          Name          Variance Std.Dev. Corr
## site:plot.id (Intercept) 0.26267  0.5125
##              time         0.03203  0.1790  0.07
## Number of obs: 250, groups:  site:plot.id, 50
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -22.0968    10.6871  -2.068   0.0387 *
## pop          3.4083     2.0604   1.654   0.0981 .
## dist         3.0850     1.4606   2.112   0.0347 *
## time        -0.1740     0.0411  -4.234 2.29e-05 ***
## pop:dist     -0.4444     0.2814  -1.579   0.1143
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

How much more likely is this model than the null? What is its model weight?

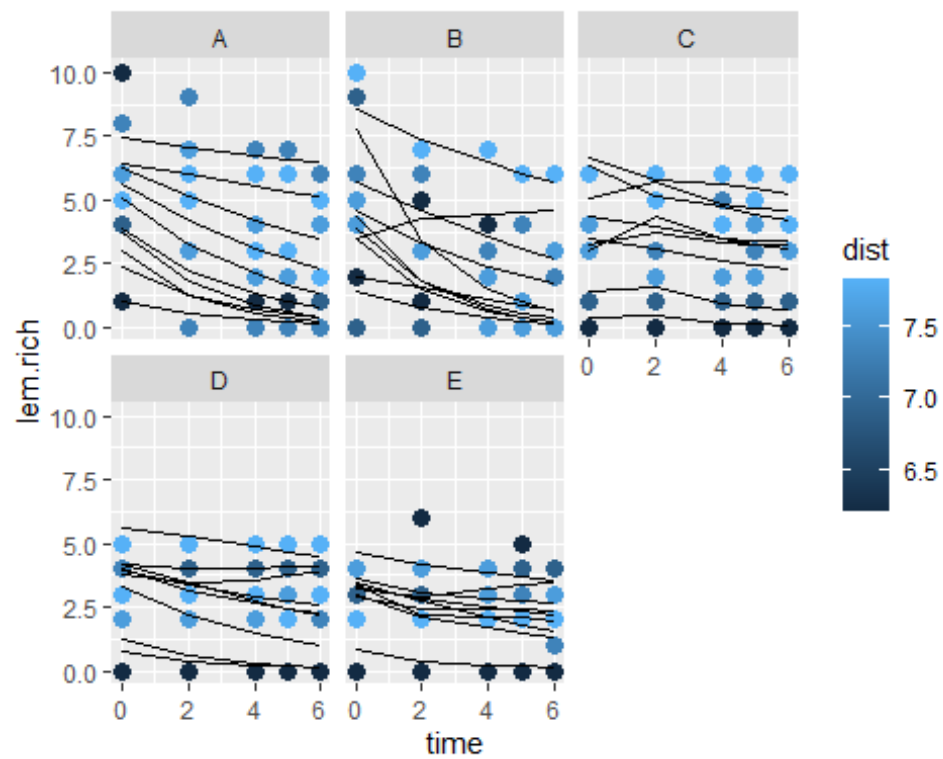
```
##      dAICc  likelihood weight
## 1 65.59039 1.748933e+14      1
```

### Main effects: Lemur Food Trees Species Richness

```
main.time.lemr <- avg_slopes(mod.time.lemr)
main.time.lemr

##
## Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %
## dist    2.381    0.6049   3.936  <0.001   1.196  3.567
## pop     0.346    0.4211   0.822   0.411  -0.479  1.171
## time   -0.276    0.0458  -6.026  <0.001  -0.366 -0.186
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
conf.high
```

## Visualize Data & Model-Predicted Results for Lemur Food Trees Species Richness Change over Time BY SITE



## Bonus Plot!

*Plot showing Incidence Rate Ratios for all models. Note that plant metrics were not standardized and thus are not directly comparable.*

