

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

##	Full-Int	Full-NoInt	Pop	Dist	Null
##	905.0079	907.7983	908.7880	914.8778	944.0503

aicw(aicc) # 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
```

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)
```

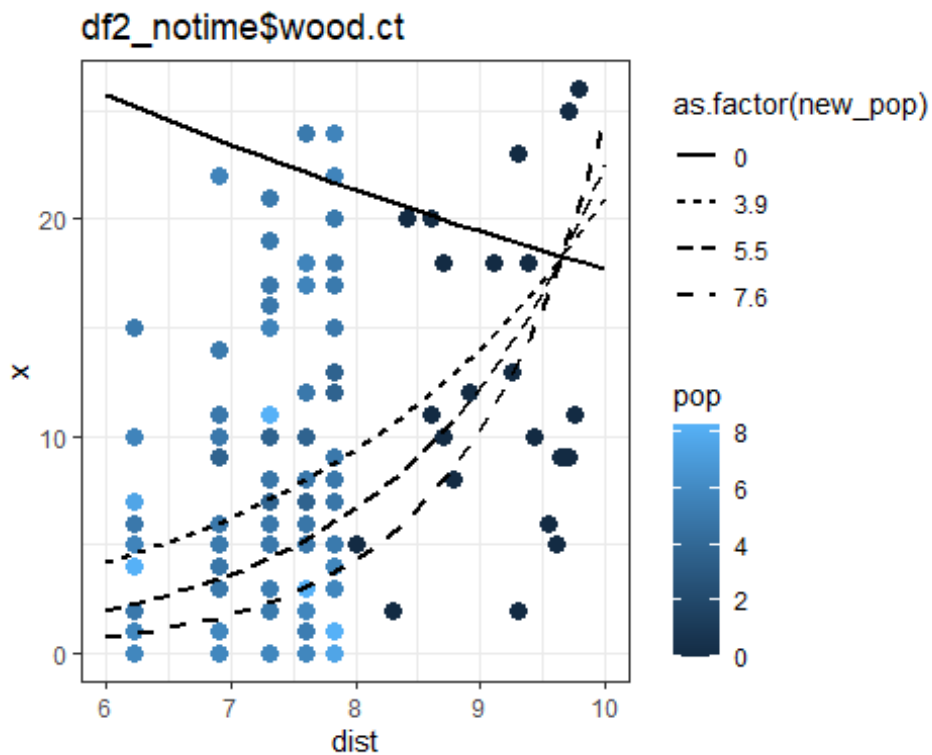
```
## # Linear trend for dist
##
## pop | Slope |          95% CI |      p
## -----
## 0.00 | -1.33 | [-9.01,  6.34] | 0.734
## 3.90 |  2.75 | [-0.61,  6.11] | 0.109
## 5.50 |  3.32 | [-1.17,  7.80] | 0.147
## 7.60 |  3.78 | [-2.70, 10.27] | 0.253
```

```
##  
## 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)

##    Full-Int Full-NoInt      Pop      Dist      Null
##    805.5110   808.3593   810.1135   816.6885   852.0196

aicw(aicc) # 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
```

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
```

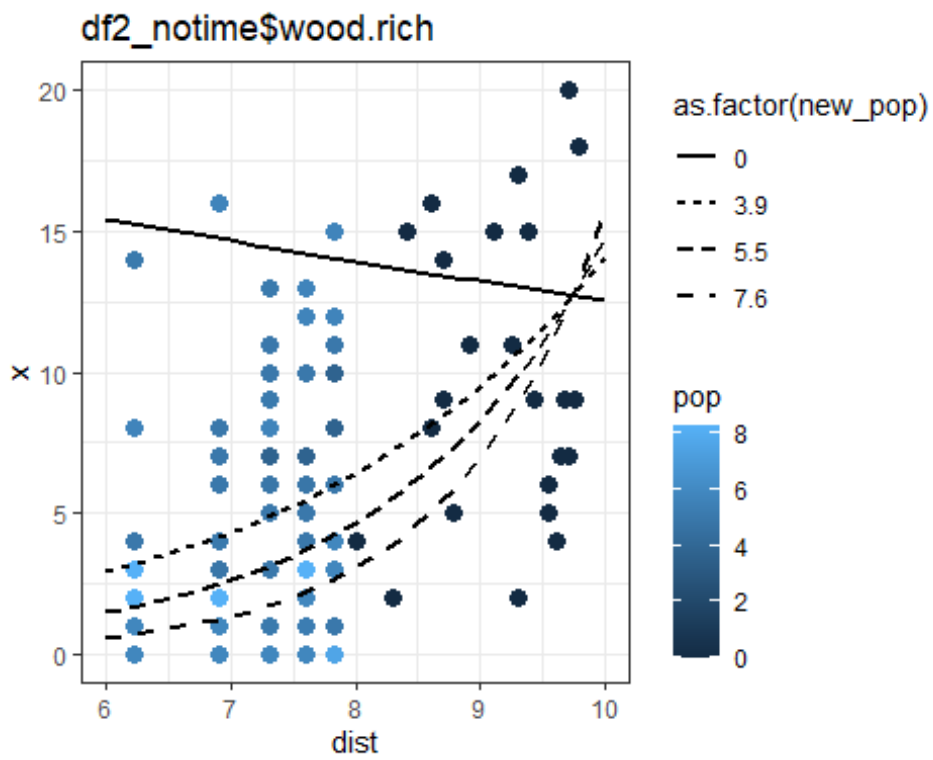
Marginal effects: Timber Species Richness

```
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)

##      Full-Int Full-NoInt      Pop      Dist      Null
##    1092.365   1090.241   1097.626   1098.889   1098.082

aicw(aicc) # 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
```

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
```

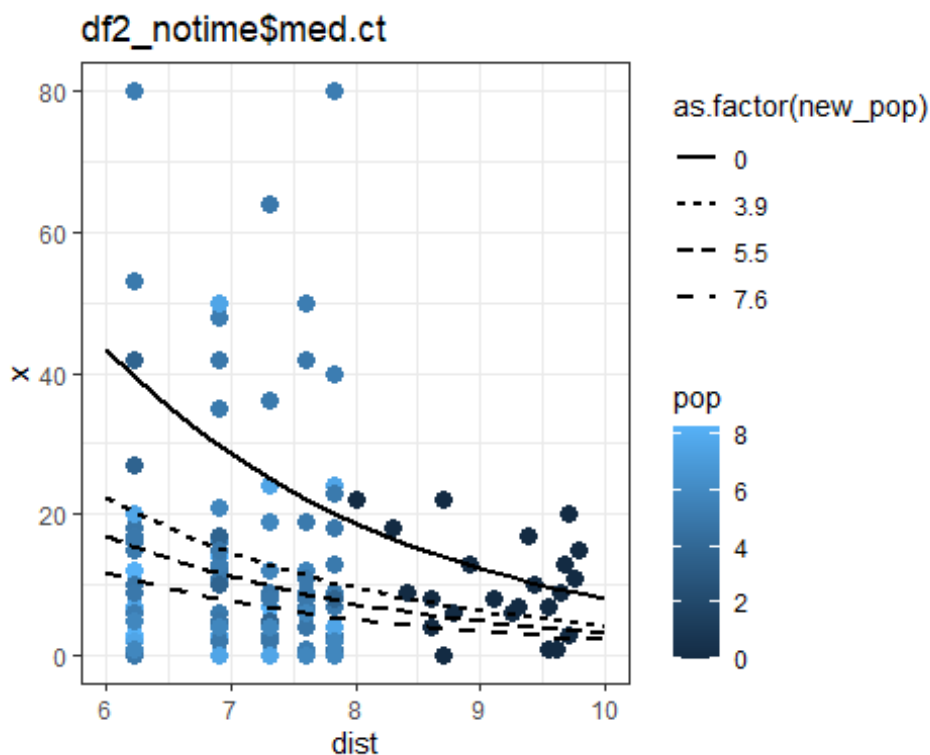
```
##
## pop | Slope |          95% CI |      p
## -----
## 0.00 | -6.14 | [-12.44,  0.15] | 0.056
## 3.90 | -3.15 | [ -5.34, -0.95] | 0.005
## 5.50 | -2.39 | [ -3.80, -0.98] | < .001
## 7.60 | -1.67 | [ -2.50, -0.84] | < .001
```

```
##
```

```
## 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)
```

```
##      Full-Int Full-NoInt      Pop      Dist      Null
##      607.2343   605.2215   604.3955   625.3711   633.3896
```

```
aicw(aicc) # 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
```

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
```

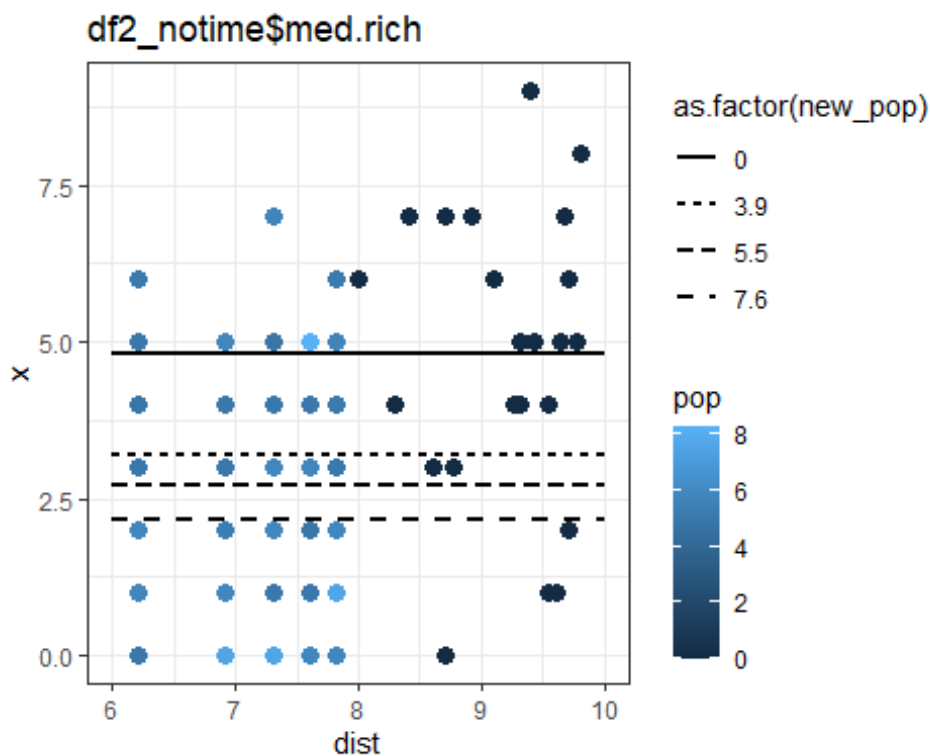
Marginal effects: Medicinal Plants Species Richness

```
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)

##      Full-Int Full-NoInt      Pop      Dist      Null
##      718.2640   720.8157   720.8702   730.9252   763.0890

aicw(aicc) # 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
```

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
```

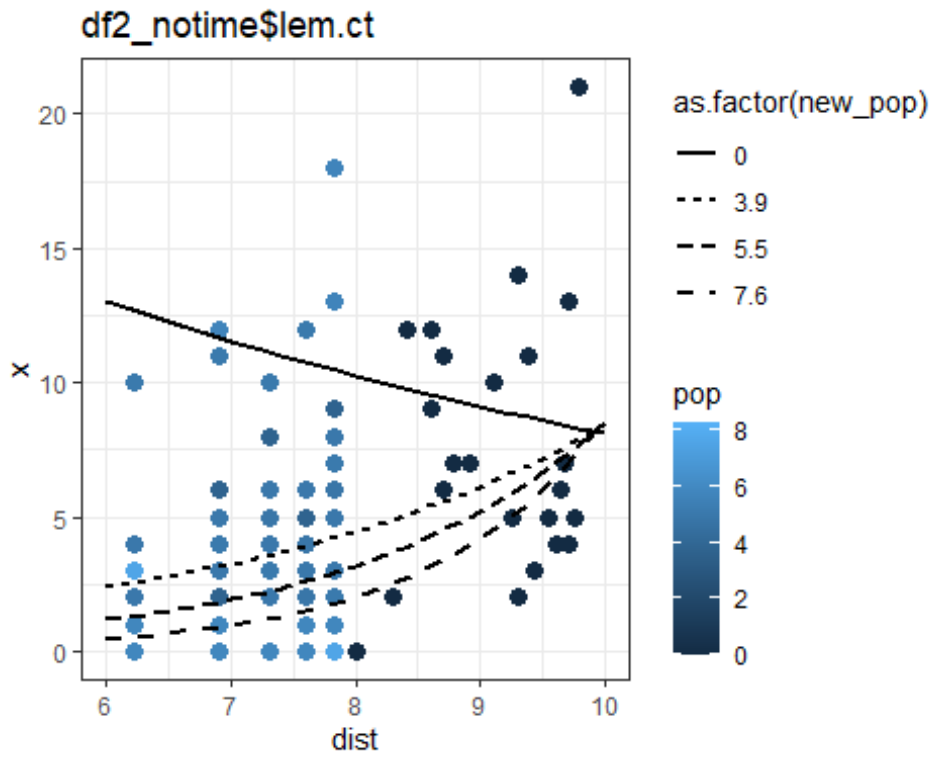
Marginal effects: Lemur Food Trees Count

```
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)
```

##	Full-Int	Full-NoInt	Pop	Dist	Null
##	640.9285	643.7757	644.2823	654.5622	691.5846

aicw(aicc) # 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
```

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
```

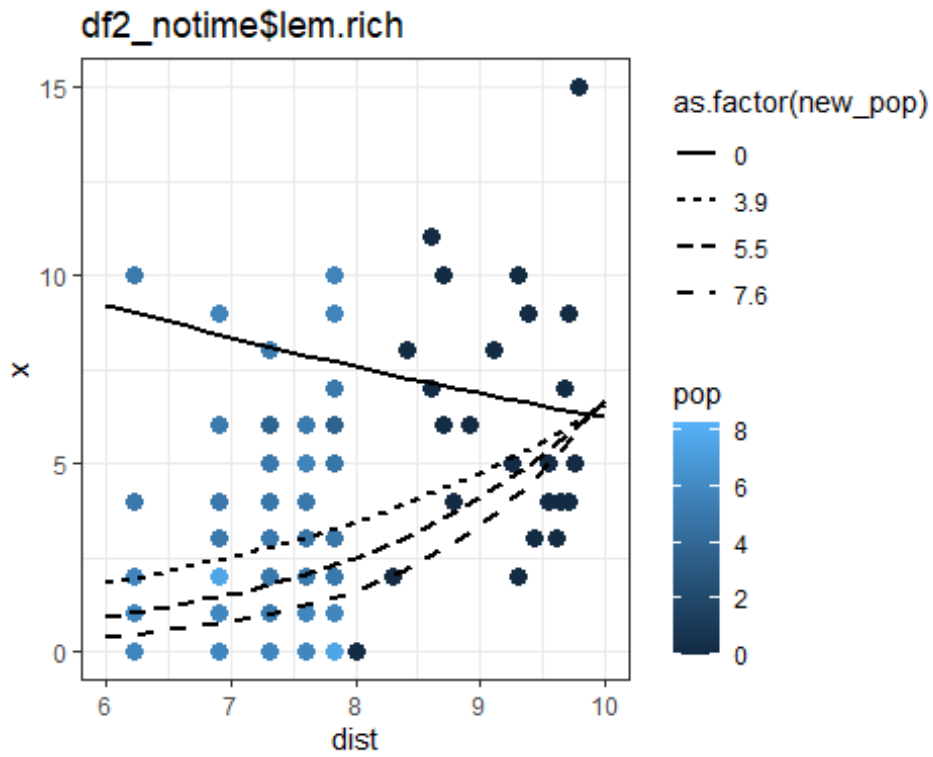
Marginal effects: Lemur Food Trees Species Richness

```
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.

Timber & Medicinal Plant Analyses

TIMBER COUNT

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

summary(mod.time.timc)

## 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
```

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
```

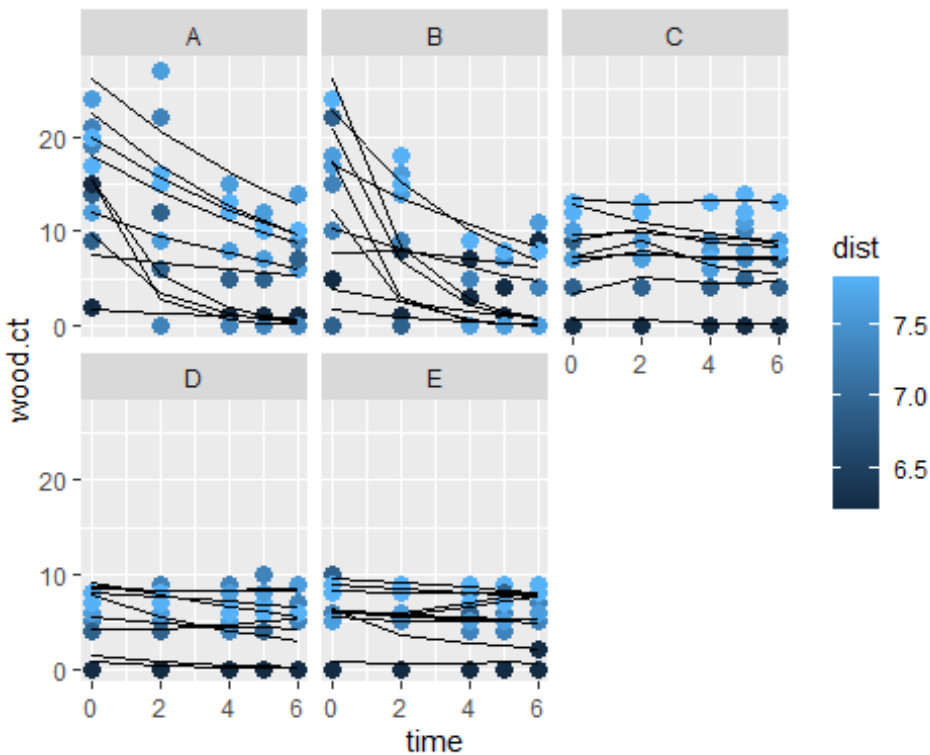
```
## time     -0.835      0.041 -20.342  <0.001 -0.915 -0.754
```

```
##
```

```
## 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)
```

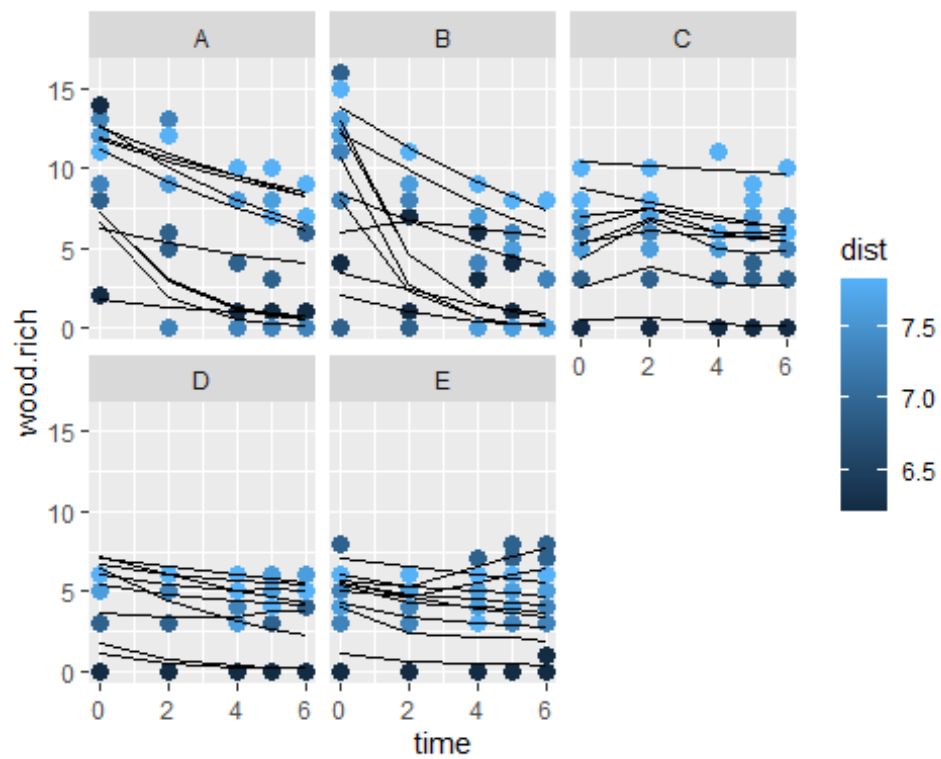
```
## Family: poisson ( log )  
## Formula: wood.rich ~ pop * dist + time + (1 + time |  
site:plot.id)  
## Data: df3_time  
##  
##      AIC      BIC   logLik deviance df.resid  
##  1100.0   1128.2   -542.0   1084.0     242  
##  
## Random effects:  
##  
## Conditional model:  
## Groups      Name      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
```

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)
```

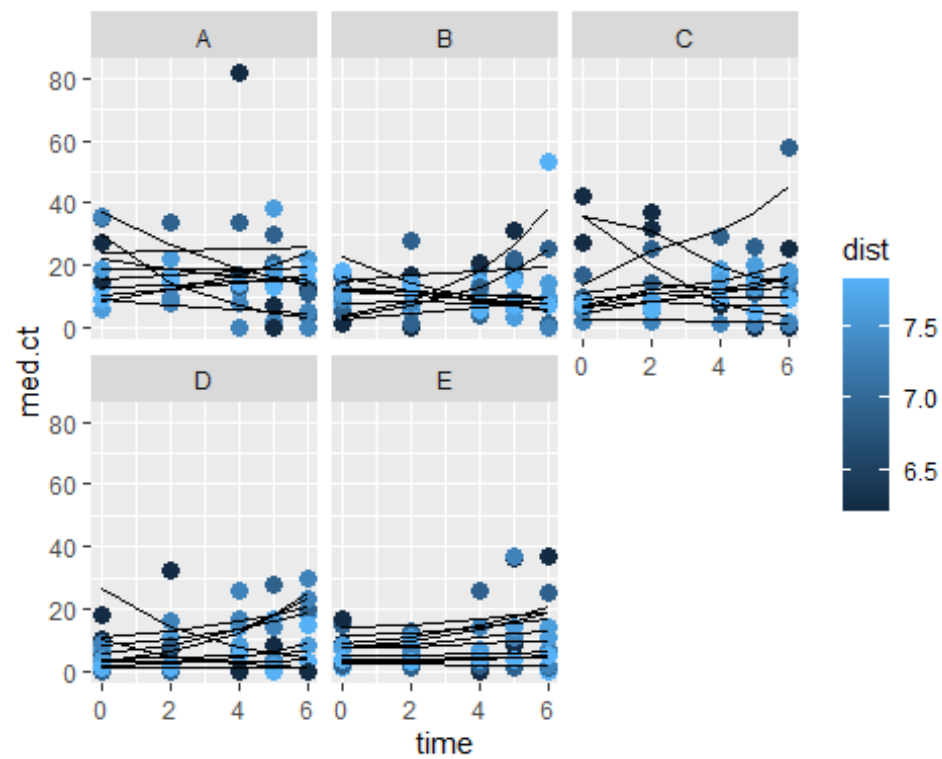
```
## Family: poisson ( log )  
## Formula: med.ct ~ pop + dist + time + (1 + time | site:plot.id)  
## Data: df3_time  
##  
##      AIC      BIC   logLik deviance df.resid  
##  2146.7   2171.4  -1066.4   2132.7      243  
##  
## Random effects:  
##  
## Conditional model:  
## Groups      Name      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
```

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
```

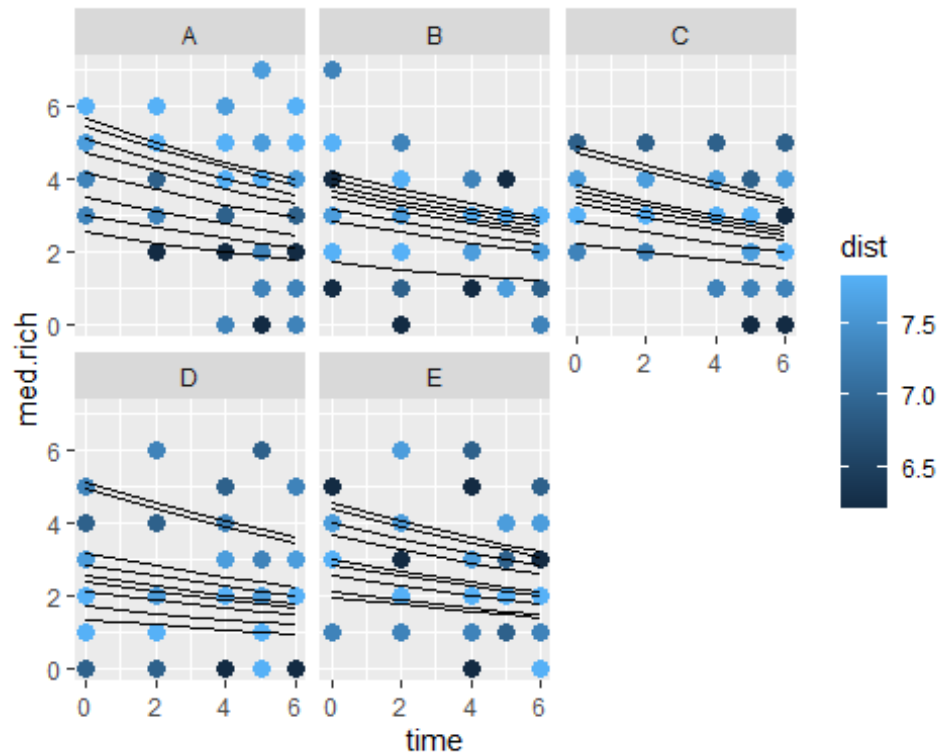
```
## Family: poisson ( log )  
## Formula: med.rich ~ pop + time + (1 | site:plot.id)  
## Data: df3_time  
##  
##      AIC      BIC   logLik deviance df.resid  
##  901.1    915.1   -446.5    893.1     246  
##  
## Random effects:  
##  
## Conditional model:  
## Groups      Name      Variance 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
```

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)

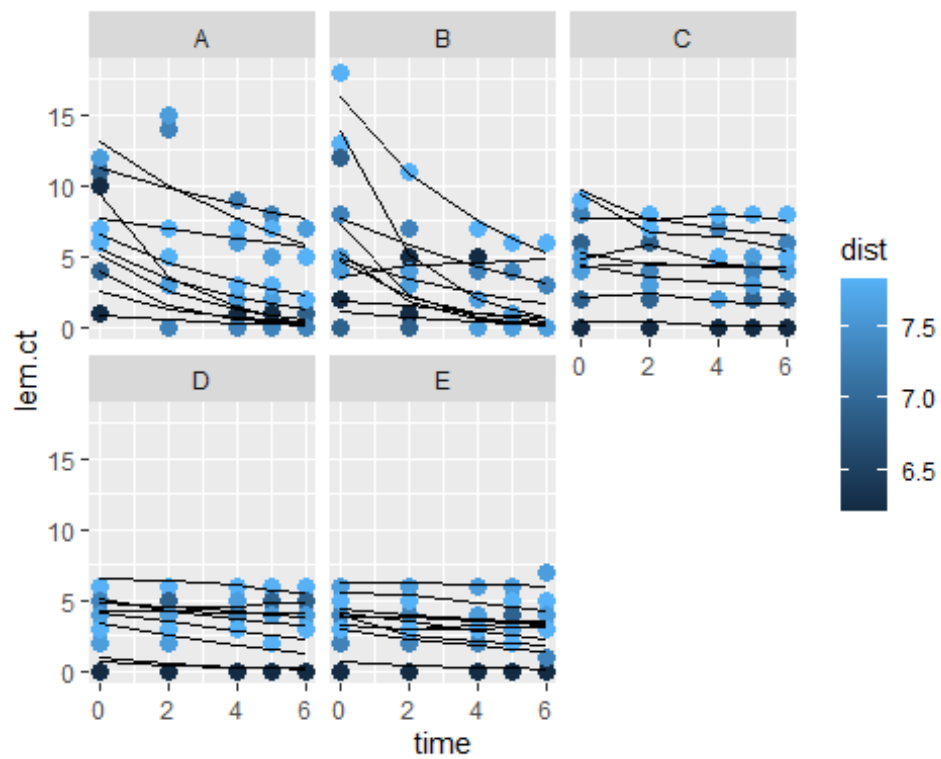
## Family: poisson ( log )
## Formula:      lem.ct ~ pop * dist + time + (1 + time | site:plot.id)
## Data: df3_time
##
##      AIC      BIC   logLik deviance df.resid
##   987.0   1015.1   -485.5    971.0     242
##
## Random effects:
##
## Conditional model:
## Groups      Name      Variance Std.Dev. 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
```

Main effects: Medicinal Plants Species Richness

```
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
```

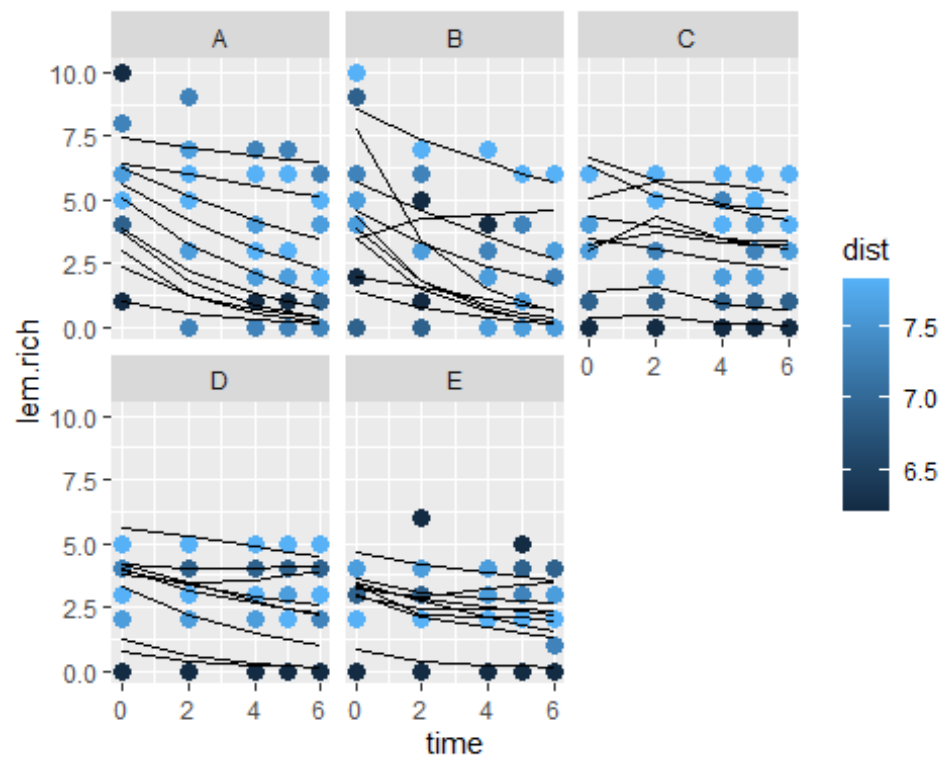
Main effects: Lemur Food Trees Species Richness

```
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



Examining Models Goodness of Fit

Likelihood ratio tests between best model for each plant metric & null.

Population & Distance Models

TIMBER COUNT

```
anova(fun.m0(8), mod.timc, test = "LRT")

## Data: df2_notime
## Models:
## fun.m0(8): df2_notime[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.timc: wood.ct ~ pop * dist + (1 | site:plot.id), zi=~0, disp=~1
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## fun.m0(8)  2 943.97 950.06 -469.99   939.97
## mod.timc   5 904.61 919.82 -447.30   894.61 45.366      3 7.735e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

TIMBER SPECIES RICHNESS

```
# TIMR
anova(fun.m0(11), mod.timr, test = "LRT")

## Data: df2_notime
## Models:
## fun.m0(11): df2_notime[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.timr: wood.rich ~ pop * dist + (1 | site:plot.id), zi=~0, disp=~1
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## fun.m0(11)  2 851.94 858.03 -423.97   847.94
## mod.timr    5 805.11 820.33 -397.55   795.11 52.832      3 1.991e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

MEDICINAL PLANTS COUNT

```
anova(fun.m0(9), mod.medc, test = "LRT")

## Data: df2_notime
## Models:
## fun.m0(9): df2_notime[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.medc: med.ct ~ pop + dist + (1 | site:plot.id), zi=~0, disp=~1
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## fun.m0(9)  2 1098 1104.1 -547.00   1094
## mod.medc   4 1090 1102.2 -540.99   1082 12.028      2 0.002444 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

MEDICINAL PLANTS SPECIES RICHNESS

```
anova(fun.m0(12), mod.medr, test = "LRT")

## Data: df2_notime
## Models:
## fun.m0(12): df2_notime[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.medr: med.rich ~ pop + (1 | site:plot.id), zi=~0, disp=~1
##           Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fun.m0(12)  2 633.31 639.40 -314.65   629.31
## mod.medr    3 604.24 613.37 -299.12   598.24 31.074      1 2.484e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

LEMUR FOOD TREES COUNT

```
anova(fun.m0(10), mod.lemc, test = "LRT")

## Data: df2_notime
## Models:
## fun.m0(10): df2_notime[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.lemc: lem.ct ~ pop * dist + (1 | site:plot.id), zi=~0, disp=~1
##           Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fun.m0(10)  2 763.01 769.10 -379.51   759.01
## mod.lemc    5 717.86 733.08 -353.93   707.86 51.149      3 4.548e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

LEMUR FOOD TREES SPECIES RICHNESS

```
anova(fun.m0(13), mod.lemr, test = "LRT")

## Data: df2_notime
## Models:
## fun.m0(13): df2_notime[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.lemr: lem.rich ~ pop * dist + (1 | site:plot.id), zi=~0, disp=~1
##           Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fun.m0(13)  2 691.51 697.59 -343.75   687.51
## mod.lemr    5 640.53 655.74 -315.26   630.53 56.98      3 2.596e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Change over Time Models

TIMBER COUNT

```
anova(fun.m0t(8), mod.time.timc, test = "LRT")

## Data: df3_time
## Models:
## fun.m0t(8): df3_time[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.time.timc: wood.ct ~ pop * dist + time + (1 + time | site:plot.id),
zi=~0, disp=~1
##           Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fun.m0t(8)   2 1505.4 1512.4 -750.70   1501.4
## mod.time.timc 8 1239.2 1267.4 -611.61   1223.2 278.18      6 < 2.2e-16
***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

TIMBER SPECIES RICHNESS

```
anova(fun.m0t(11), mod.time.timr, test = "LRT")

## Data: df3_time
## Models:
## fun.m0t(11): df3_time[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.time.timr: wood.rich ~ pop * dist + time + (1 + time | site:plot.id),
zi=~0, disp=~1
##           Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fun.m0t(11)   2 1235.2 1242.2 -615.60   1231.2
## mod.time.timr 8 1100.0 1128.2 -542.01   1084.0 147.18      6 < 2.2e-16
***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

MEDICINAL PLANTS COUNT

```
anova(fun.m0t(9), mod.time.medc, test = "LRT")

## Data: df3_time
## Models:
## fun.m0t(9): df3_time[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.time.medc: med.ct ~ pop + dist + time + (1 + time | site:plot.id),
zi=~0, disp=~1
##           Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fun.m0t(9)   2 2462.8 2469.8 -1229.4   2458.8
## mod.time.medc 7 2146.7 2171.4 -1066.4   2132.7 326.04      5 < 2.2e-16
***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

MEDICINAL PLANTS SPECIES RICHNESS

```
anova(fun.m0t(12), mod.time.medr, test = "LRT")

## Data: df3_time
## Models:
## fun.m0t(12): df3_time[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.time.medr: med.rich ~ pop + time + (1 | site:plot.id), zi=~0, disp=~1
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## fun.m0t(12)  2 908.59 915.64 -452.30   904.59
## mod.time.medr  4 901.06 915.14 -446.53   893.06 11.535      2  0.003128
## ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

LEMUR FOOD TREES COUNT

```
anova(fun.m0t(10), mod.time.lemc, test = "LRT")

## Data: df3_time
## Models:
## fun.m0t(10): df3_time[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.time.lemc: lem.ct ~ pop * dist + time + (1 + time | site:plot.id),
##               zi=~0, disp=~1
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## fun.m0t(10)  2 1096.96 1104.0 -546.48  1092.96
## mod.time.lemc  8  986.97 1015.1 -485.48   970.97 121.99      6 < 2.2e-16
## ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

LEMUR FOOD TREES SPECIES RICHNESS

```
anova(fun.m0t(13), mod.time.lemr, test = "LRT")

## Data: df3_time
## Models:
## fun.m0t(13): df3_time[, x] ~ 1 + (1 | site:plot.id), zi=~0, disp=~1
## mod.time.lemr: lem.rich ~ pop * dist + time + (1 + time | site:plot.id),
##               zi=~0, disp=~1
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## fun.m0t(13)  2 965.87 972.91 -480.93   961.87
## mod.time.lemr  8 899.73 927.90 -441.86   883.73 78.139      6 8.652e-15
## ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Bonus Plot!

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

