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.
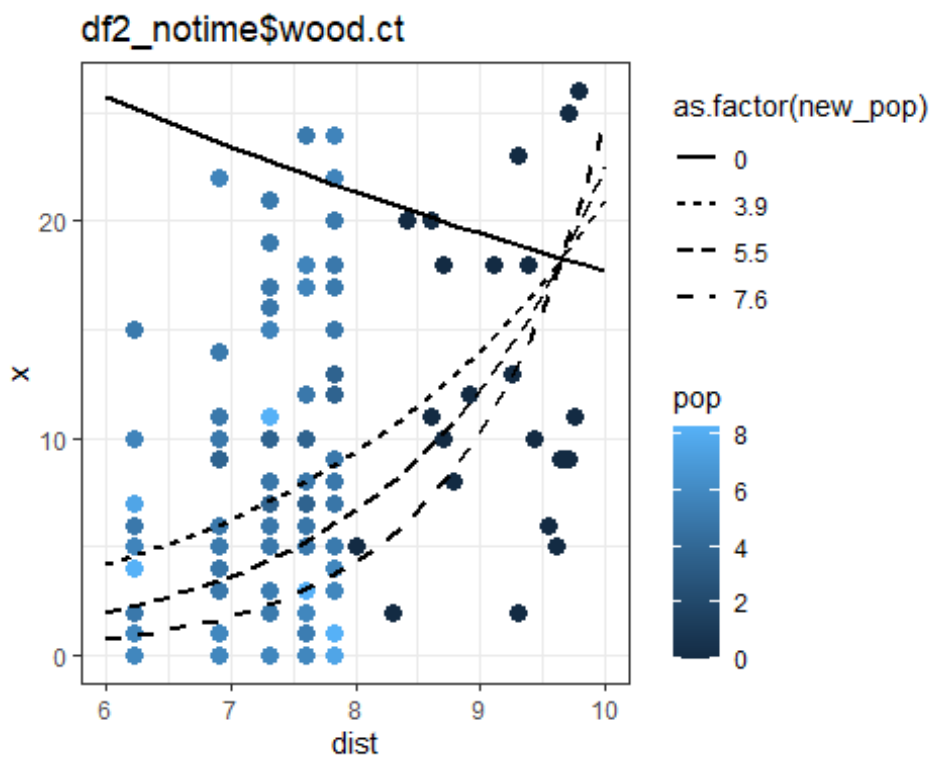
TIMBER SPECIES RICHNESS

```
## 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

df2_notime$wood.rich
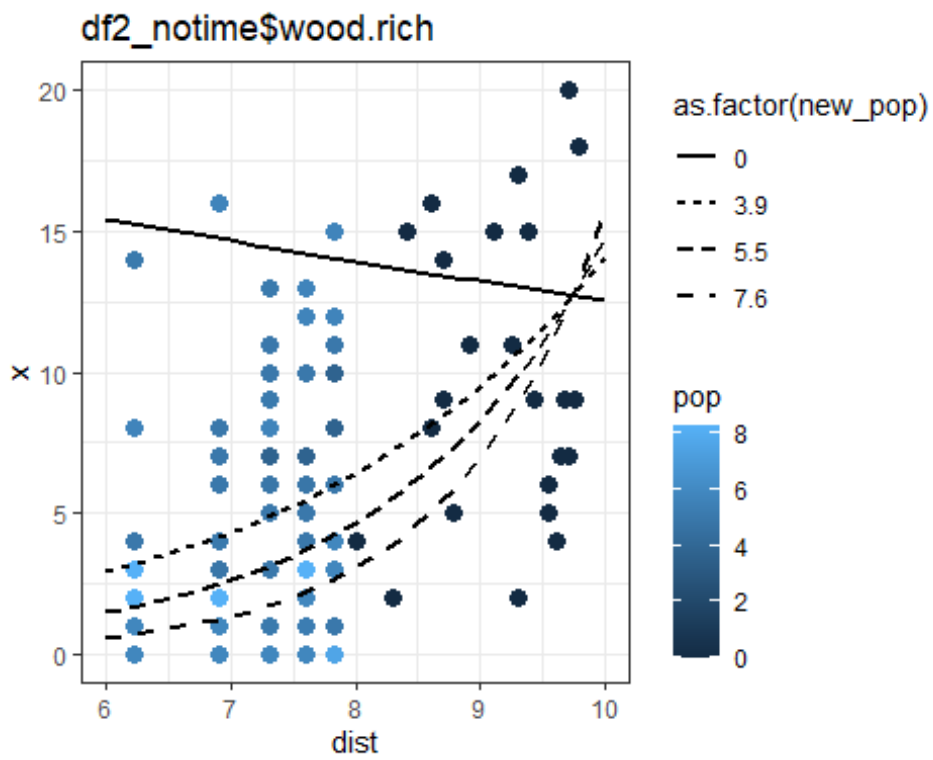
MEDICINAL PLANTS COUNT

```
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
```

```
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.
```
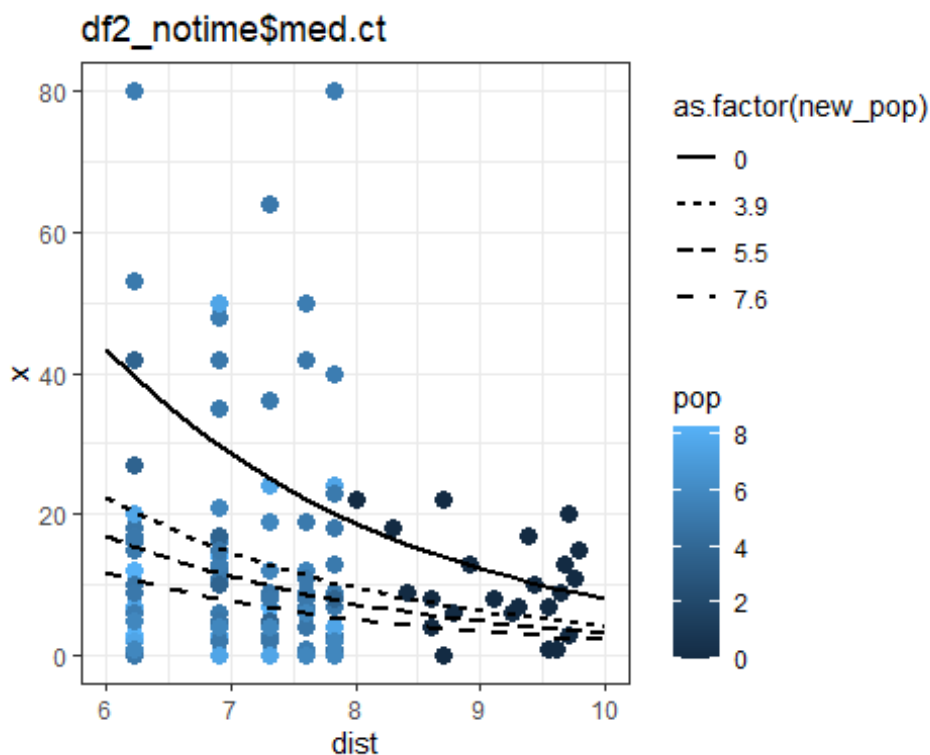
Visualize Data & Model-Predicted Results for Medicinal Plants Count

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.
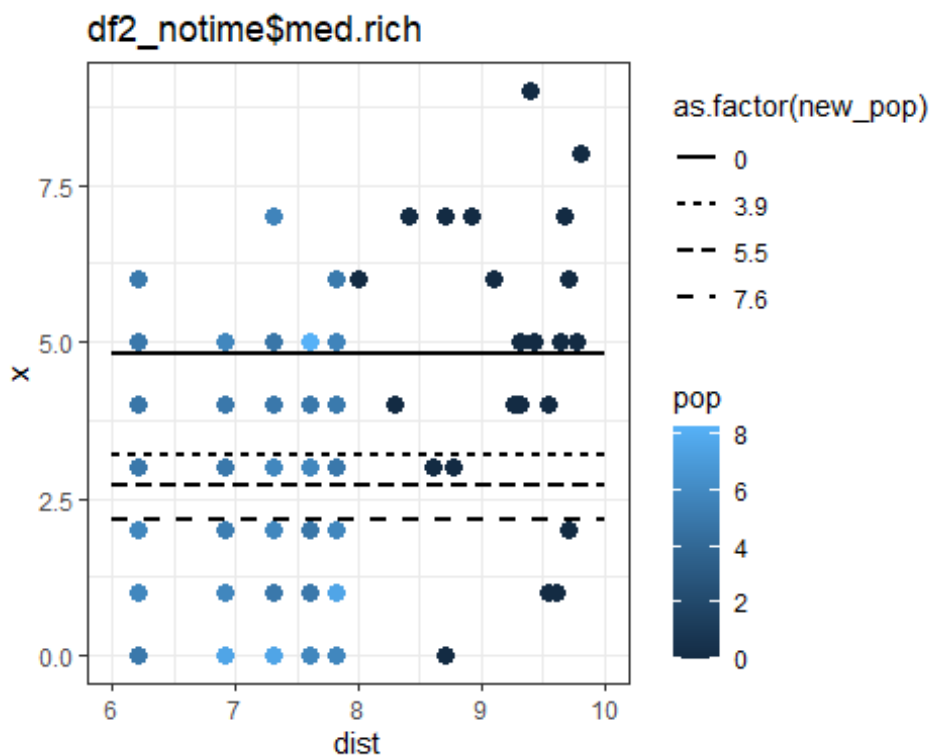
Lemur Food Trees Analyses

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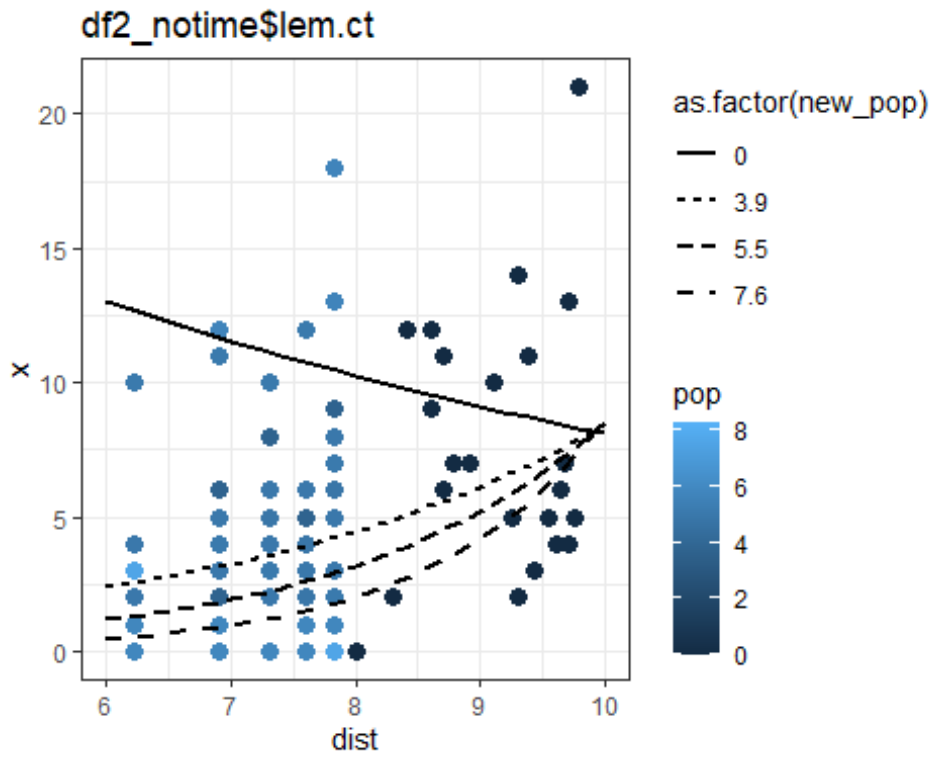
Marginal effects: Lemur Food Trees Count
```
me.lemc <- ggpredict(mod.lemc, terms = c("dist", "pop [0, 3.9, 5.5, 7.6]"),
type = "fixed", allow.new.levels = T)
hypothesis_test(me.lemc, test = NULL)

## # 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.
```

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
```
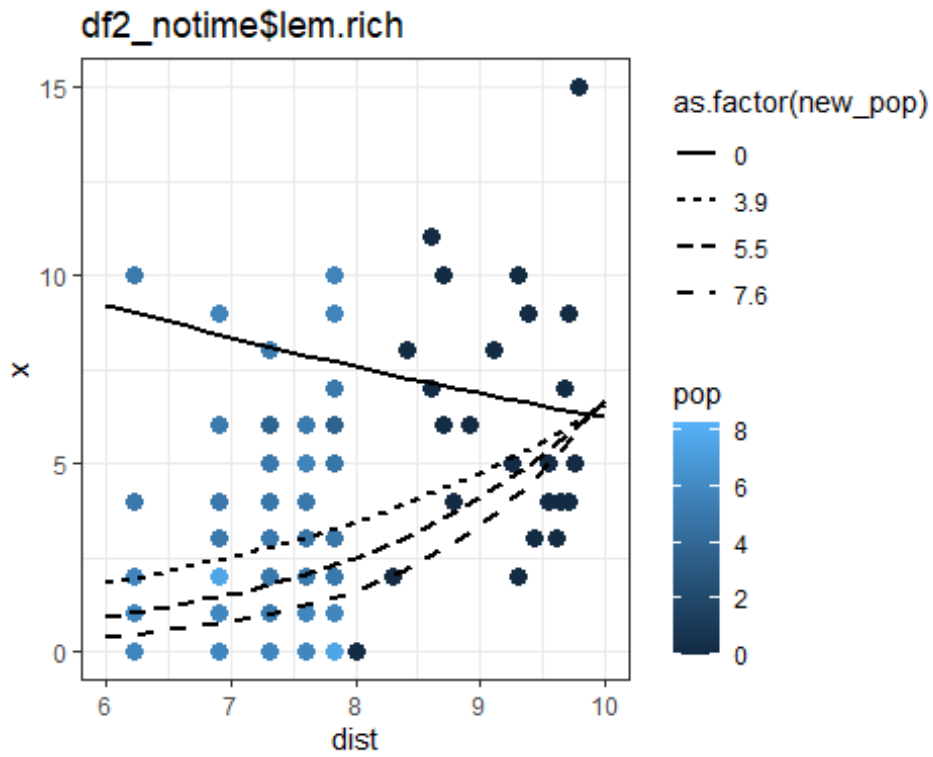
Marginal effects: Lemur Food Trees Species Richness

```
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.
```

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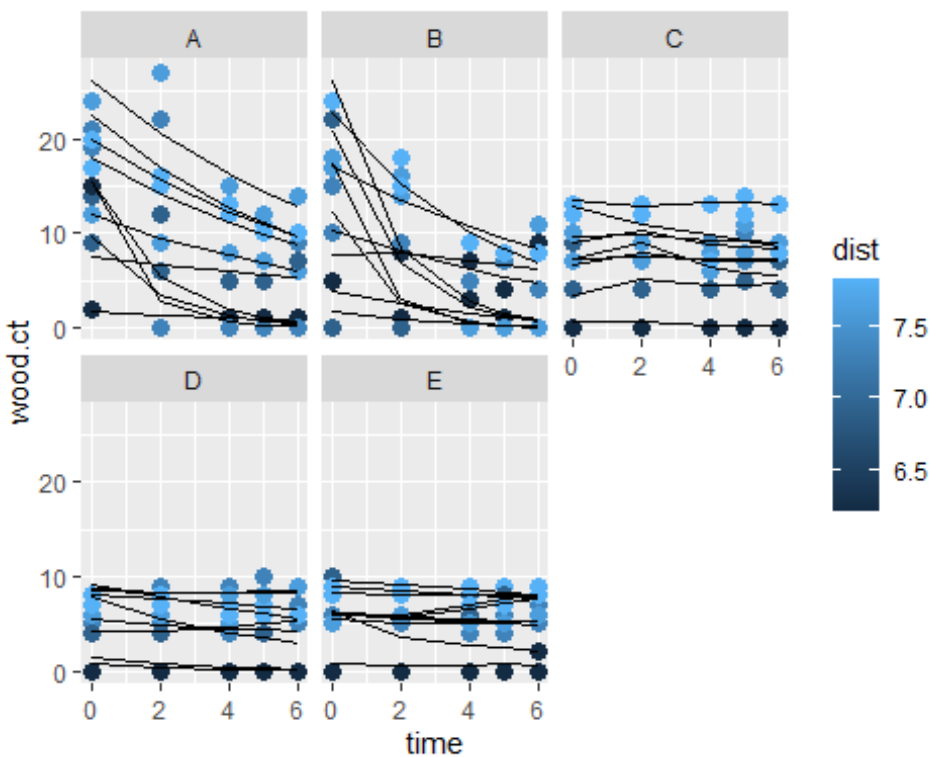
Visualize Data & Model-Predicted Results for Timber Count Change over Time BY SITE

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

```
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
```
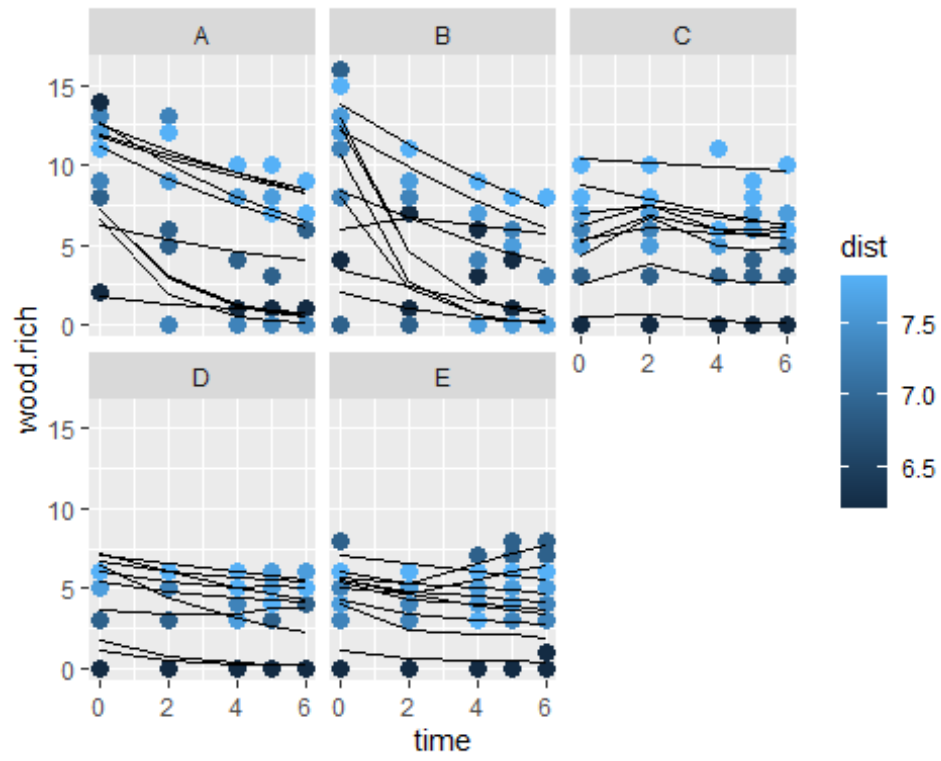
Main effects: Timber Species Richness

```
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
```

```
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
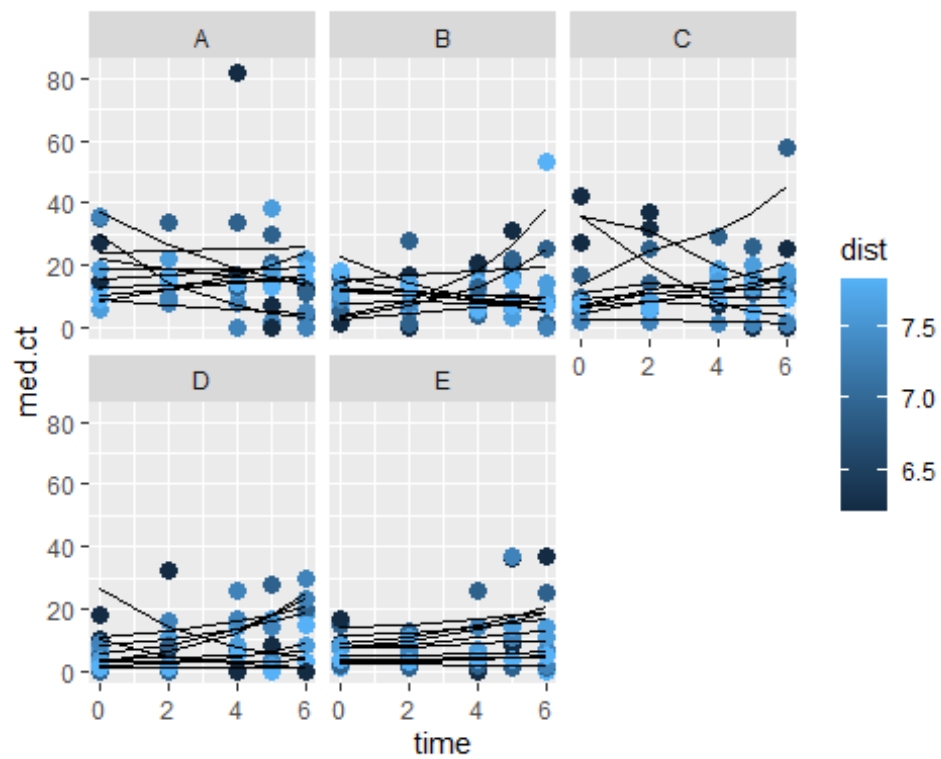
MEDICINAL PLANTS SPECIES RICHNESS

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.

```r
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

```r
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
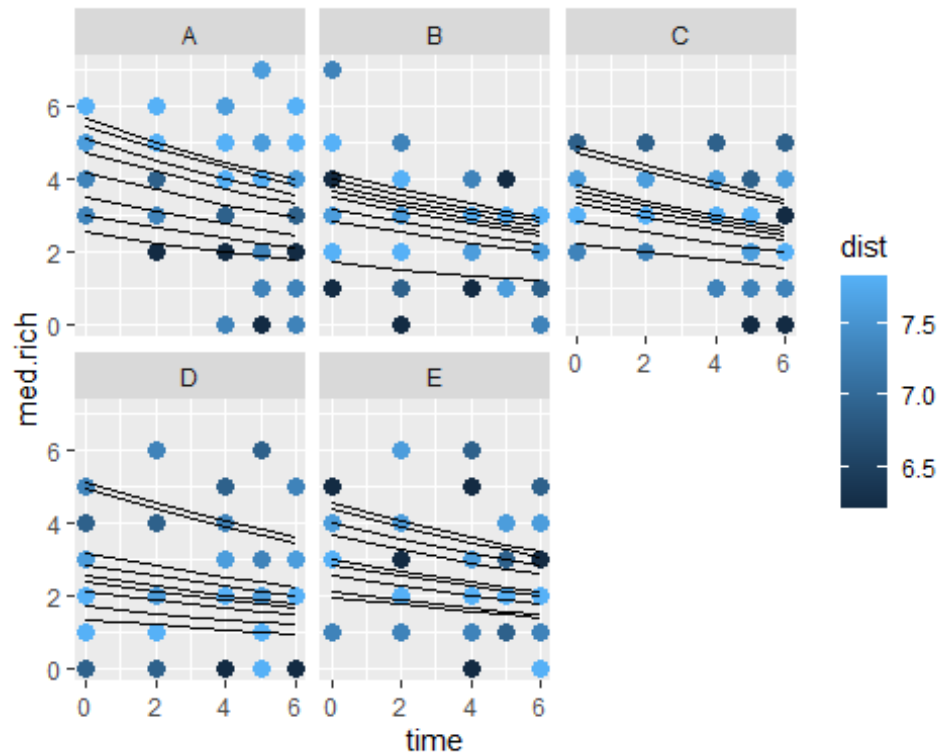
Lemur Food Trees Analyses

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
```
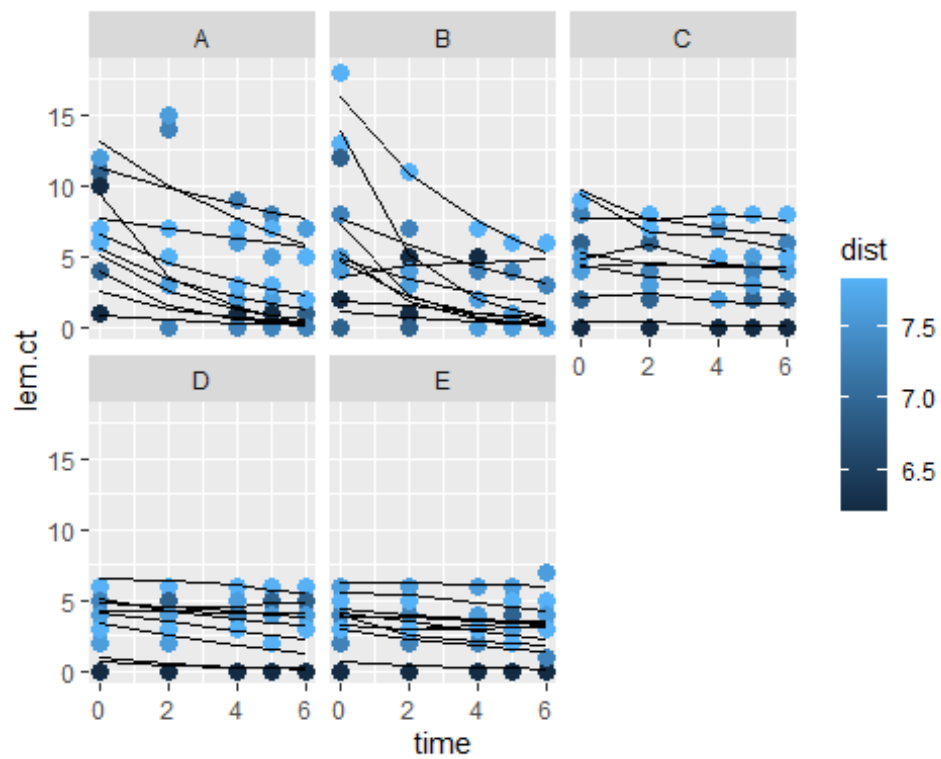
Main effects: Medicinal Plants Species Richness

```
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
```

```
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
```
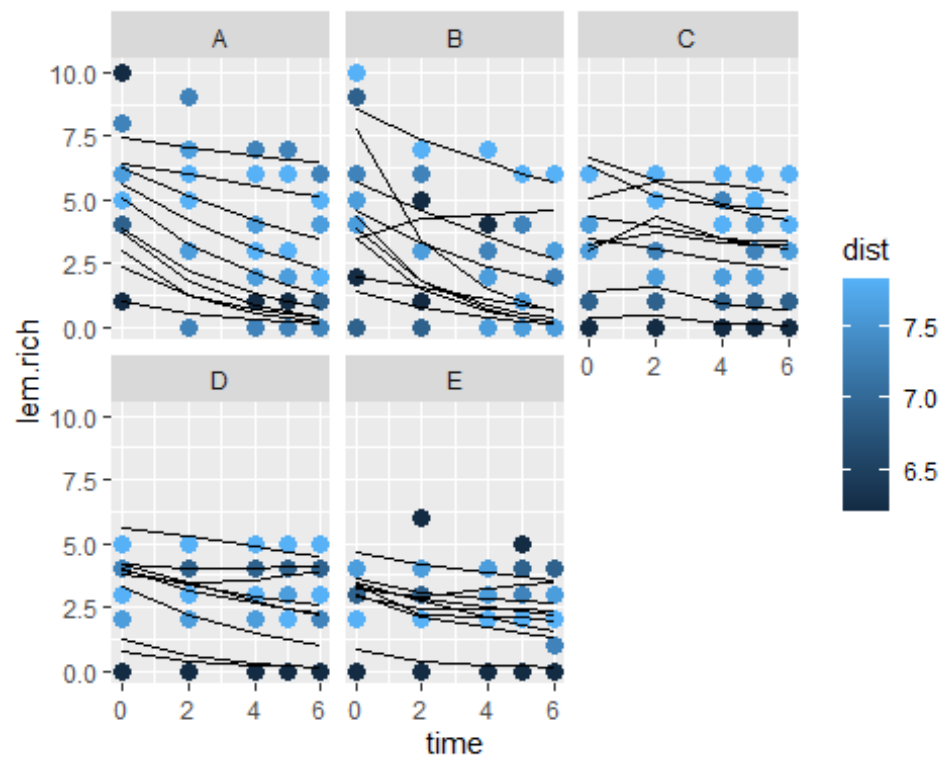
Main effects: Lemur Food Trees Species Richness

```
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
```

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.

Incidence Rate Ratios
for Plot Count & Species Richness (95% CI