

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
```

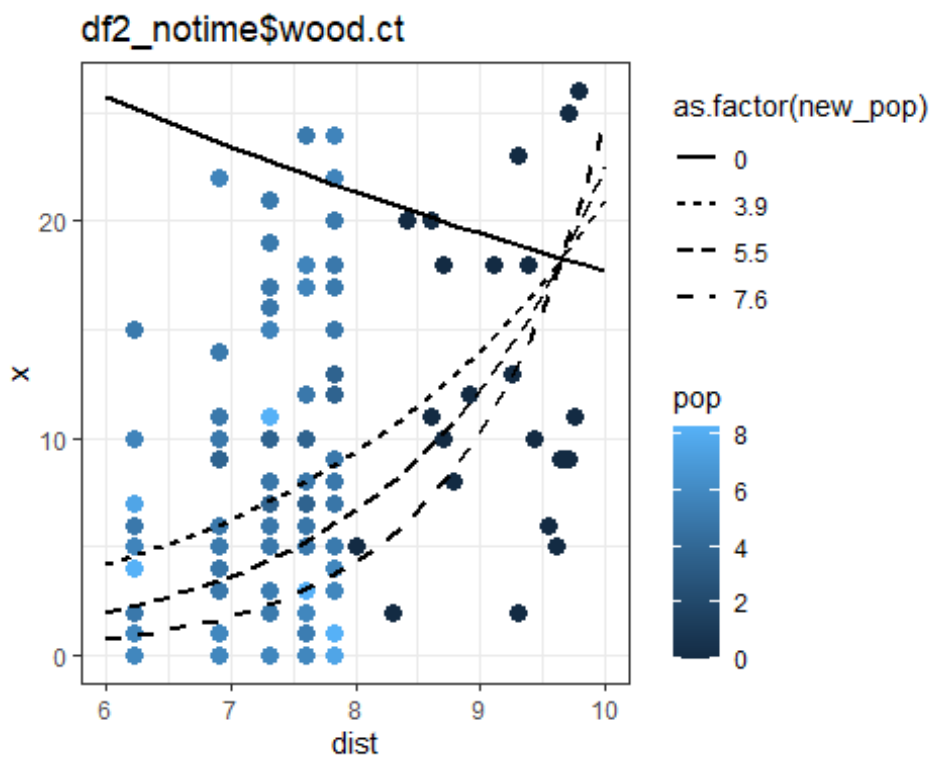
```
## 5.50 | 3.32 | [-1.17, 7.80] | 0.147
## 7.60 | 3.78 | [-2.70, 10.27] | 0.253

##
## 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

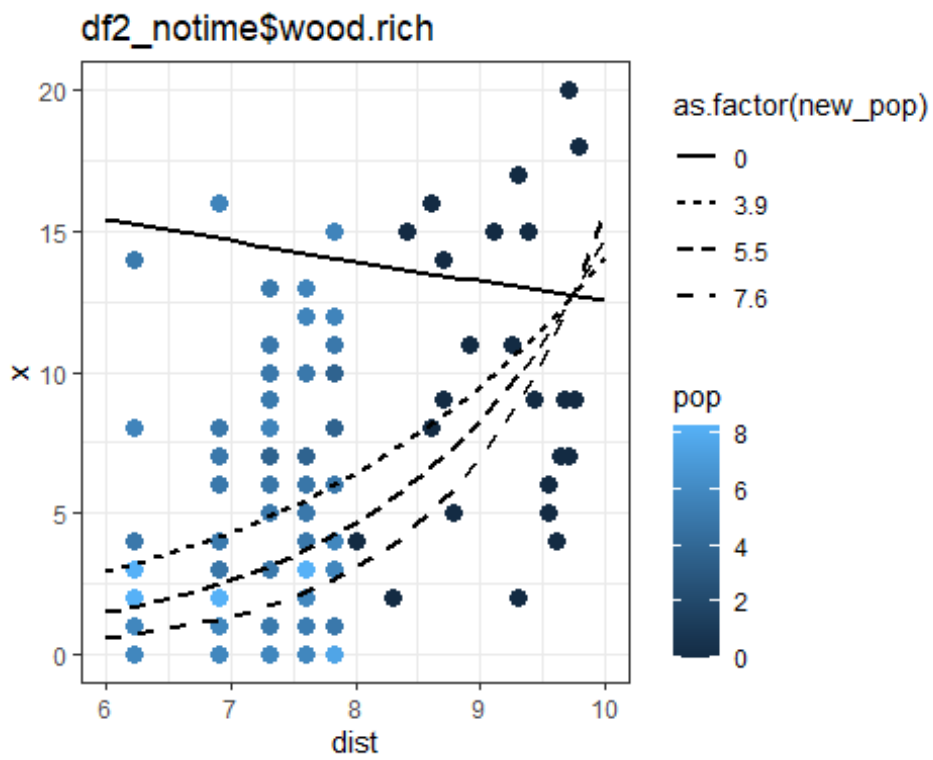
##
##   Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %
## dist    1.616      0.726  2.22  0.0261  0.192  3.040
## pop     -0.955      0.277 -3.45  <0.001 -1.497 -0.413
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
## conf.high
```

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
```

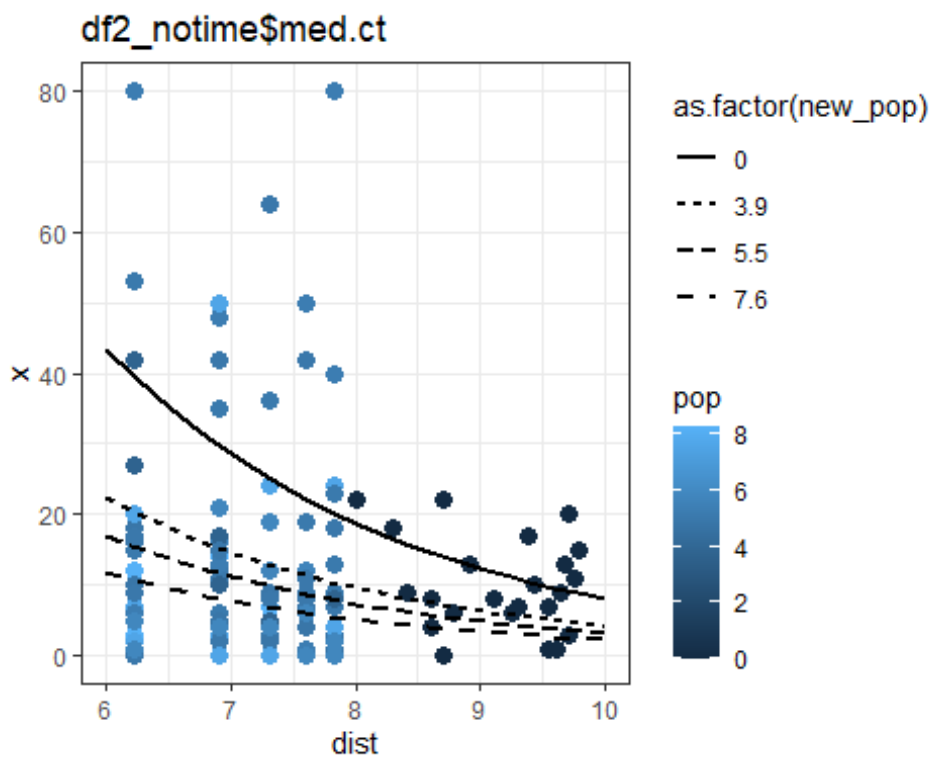
Marginal effects: Medicinal Plants Count

```
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
```

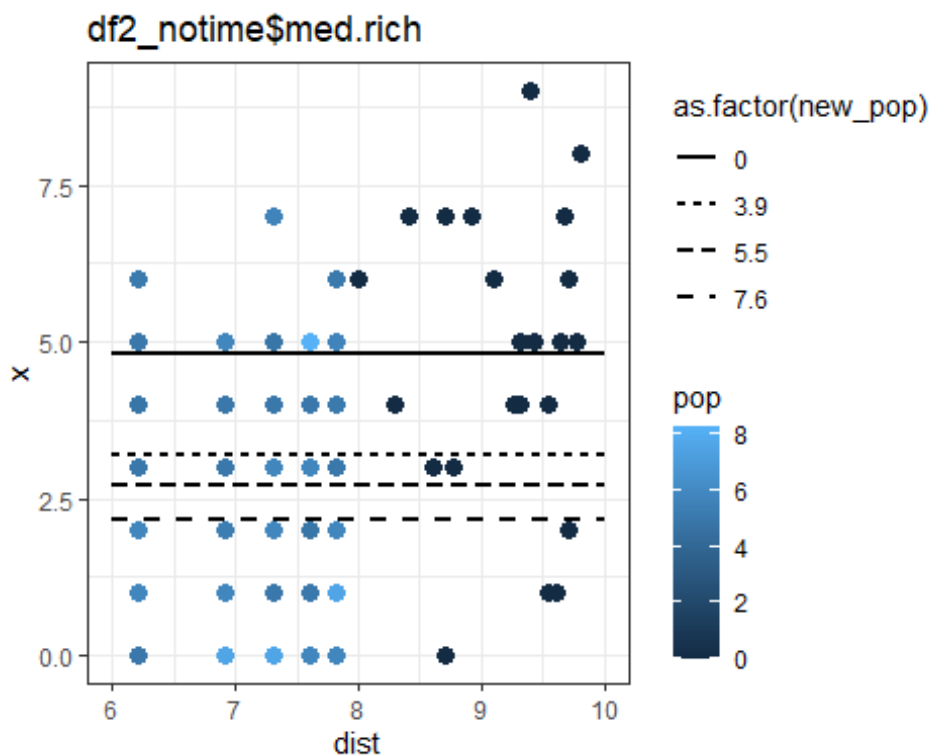
Marginal effects: Medicinal Plants Species Richness

```
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

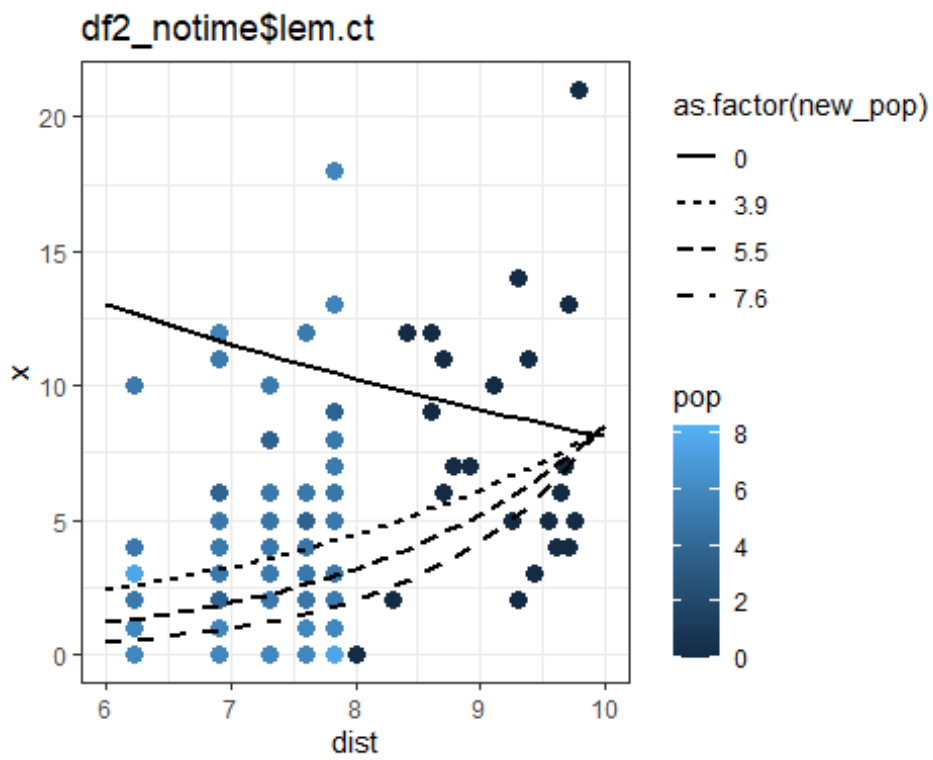
##
##   Term Estimate Std. Error      z Pr(>|z|) 2.5 % 97.5 %
## dist    0.896      0.524   1.71   0.087 -0.13  1.922
## pop    -0.746      0.202  -3.70  <0.001 -1.14 -0.351
##
## Columns: term, estimate, std.error, statistic, p.value, conf.low,
## conf.high
```

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
```

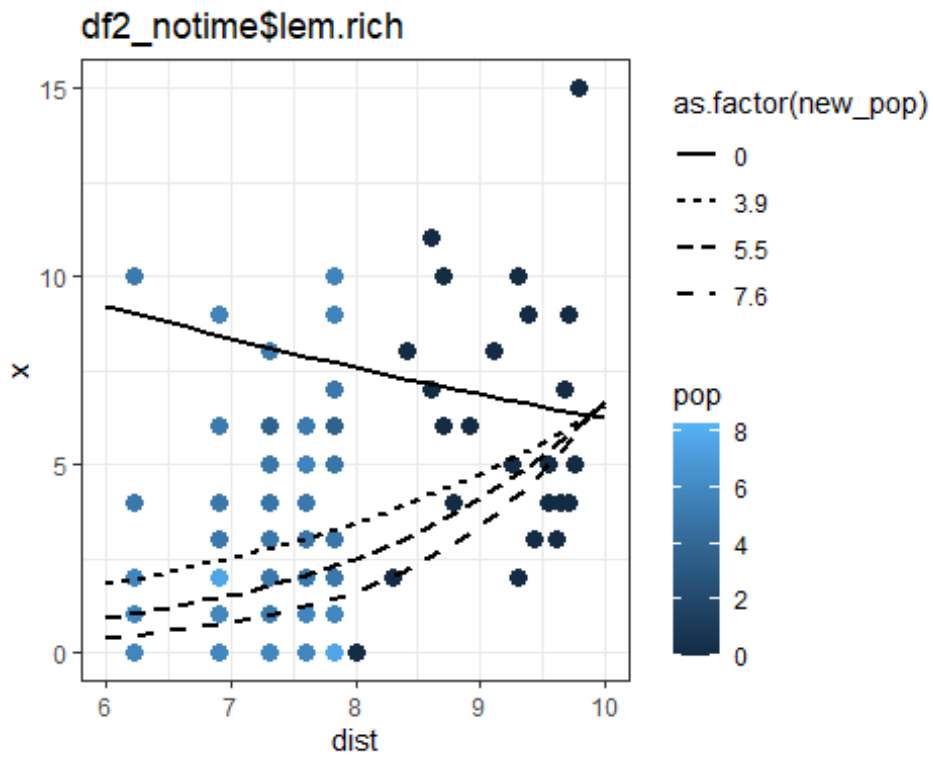
Marginal effects: Lemur Food Trees Species Richness

```
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.

Timber & Medicinal Plant Analyses

TIMBER COUNT & TIME

```
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
```

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 & Time

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
```

Marginal effects: Timber Count & Time

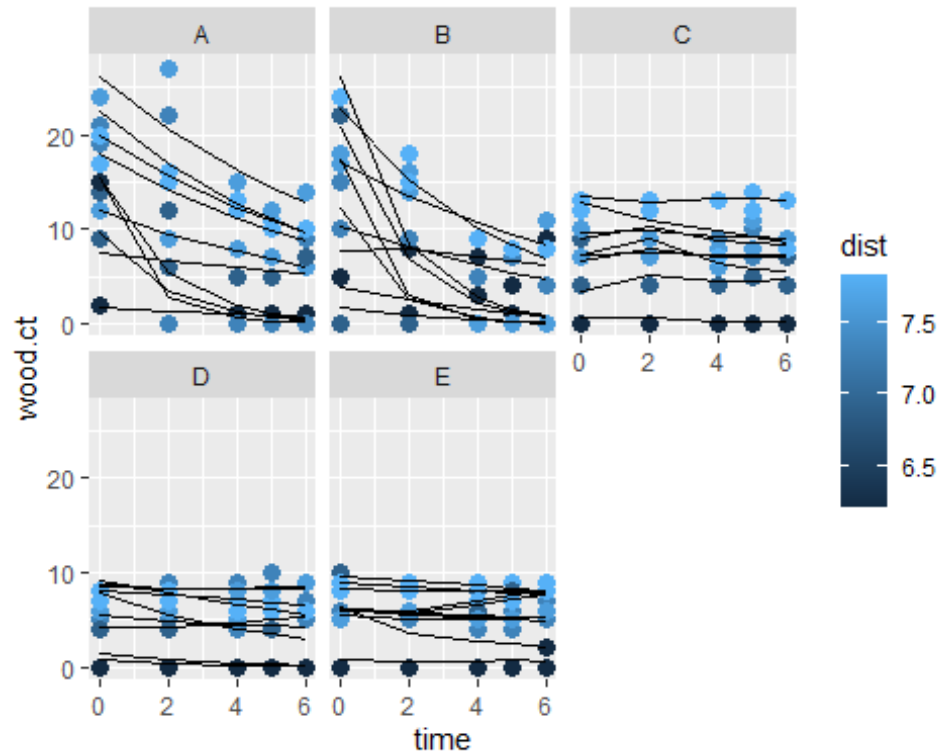
Does time have a significant effect at each site surveyed (i.e., villages A-E)?

```
me.time.timc <- ggpredict(mod.time.timc, terms = c("time", "site"), type =
"random", allow.new.levels = T)
ggeffects::hypothesis_test(me.time.timc, test = NULL)
```

```
## # Linear trend for time
##
## site | Slope |          95% CI |      p
## -----
## A    | -0.93 | [-1.19, -0.67] | < .001
## B    | -0.89 | [-1.14, -0.63] | < .001
## C    | -0.62 | [-0.88, -0.36] | < .001
## D    | -0.62 | [-0.88, -0.37] | < .001
## E    | -0.62 | [-0.88, -0.36] | < .001
##
## Slopes are presented on the response-scale.
```

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 & TIME

```
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 & Time

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

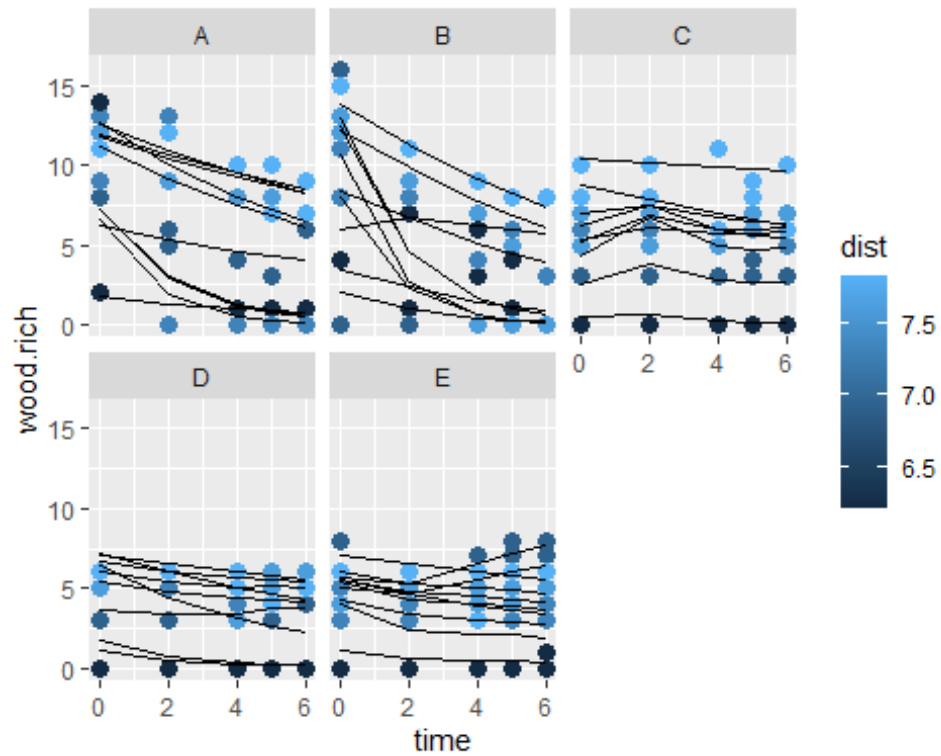
```
##
## Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %
## dist    4.863    0.9410    5.17  <0.001   3.019  6.708
## pop      0.885    0.6188    1.43   0.153  -0.328  2.098
## time    -0.498    0.0452  -11.02  <0.001  -0.586 -0.409
##
## Columns: term, estimate, std.error, statistic, p.value,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

Marginal effects: Timber Species Richness & Time

```
me.time.timr <- ggpredict(mod.time.timr, terms = c("time", "site"), type =
"random", allow.new.levels = T)
ggeffects::hypothesis_test(me.time.timr, test = NULL)
```

```
## # Linear trend for time
##
## site | Slope |           95% CI |           p
## -----
## A    | -0.62 | [-0.80, -0.43] | < .001
## B    | -0.62 | [-0.80, -0.43] | < .001
## C    | -0.48 | [-0.66, -0.29] | < .001
## D    | -0.49 | [-0.68, -0.31] | < .001
## E    | -0.47 | [-0.66, -0.29] | < .001
##
## Slopes are presented on the response-scale.
```

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



MEDICINAL PLANTS COUNT & TIME

```
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 & Time

```
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
```

Marginal effects: Medicinal Plants Count & Time

```
me.time.medc <- ggpredict(mod.time.medc, terms = c("time", "site"), type =  
"random", allow.new.levels = T)  
ggeffects::hypothesis_test(me.time.medc, test = NULL)
```

```
## # Linear trend for time
```

```
##
```

```
## site | Slope |          95% CI |      p
```

```
## -----
```

```
## A      |  0.07 | [-0.37, 0.50] | 0.770
```

```
## B      |  0.26 | [-0.18, 0.70] | 0.246
```

```
## C      |  0.27 | [-0.17, 0.71] | 0.231
```

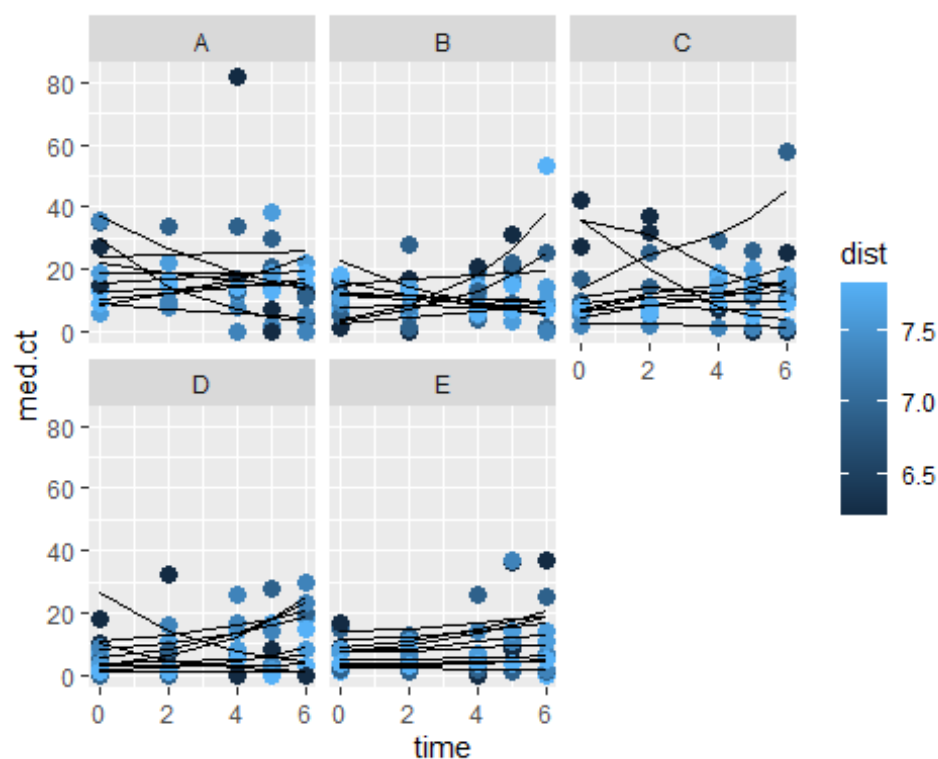
```
## D      |  0.35 | [-0.09, 0.79] | 0.120
```

```
## E      |  0.29 | [-0.14, 0.73] | 0.189
```

```
##
```

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

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



MEDICINAL PLANTS SPECIES RICHNESS & TIME

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 & Time

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

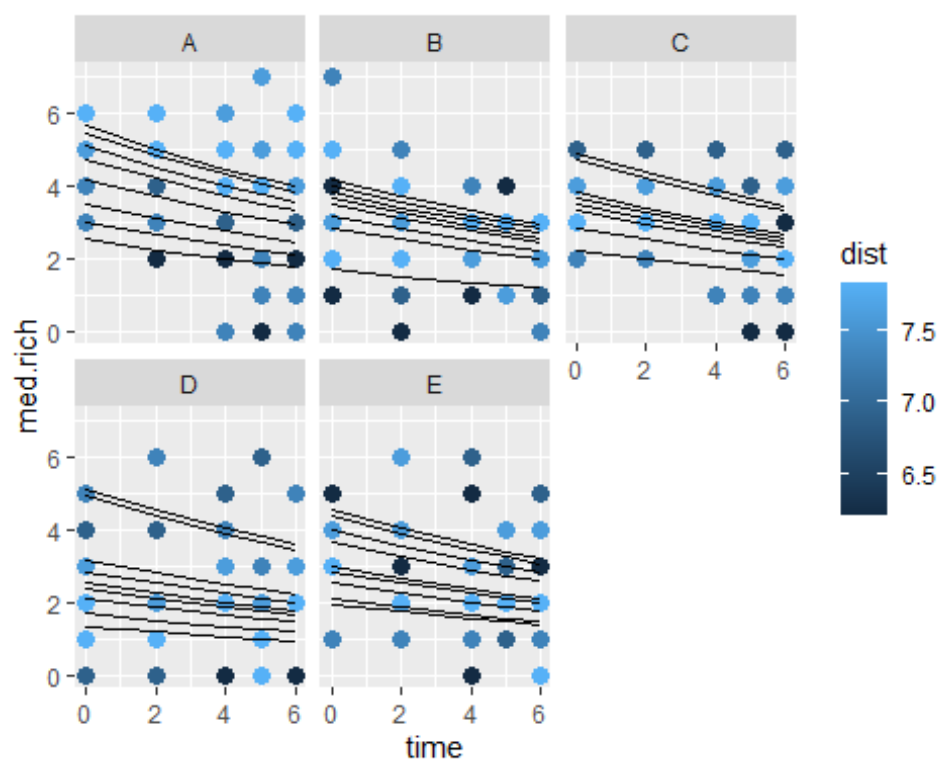
```
##  
## Term Estimate Std. Error      z Pr(>|z|)  2.5 % 97.5 %  
## pop    0.0185    0.2763  0.0668  0.947 -0.523  0.5599  
## time  -0.1637    0.0485 -3.3756 <0.001 -0.259 -0.0687  
##  
## Columns: term, estimate, std.error, statistic, p.value, conf.low,  
conf.high
```

Marginal effects: Medicinal Plants Species Richness & Time

```
me.time.medr <- ggpredict(mod.time.medr, terms = c("time", "site"), type =  
"random", allow.new.levels = T)  
ggeffects::hypothesis_test(me.time.medr, test = NULL)
```

```
## # Linear trend for time  
##  
## site | Slope |          95% CI |      p  
## -----  
## A    | -0.16 | [-0.26, -0.07] | < .001  
## B    | -0.15 | [-0.25, -0.06] | < .001  
## C    | -0.16 | [-0.25, -0.06] | < .001  
## D    | -0.15 | [-0.24, -0.06] | < .001  
## E    | -0.15 | [-0.24, -0.06] | < .001  
  
##  
## Slopes are presented on the response-scale.
```

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



Lemur Food Trees Analyses

LEMUR FOOD TREES COUNT & TIME

```
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 & Time

```
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
```

Marginal effects: Lemur Food Trees Count & Time

```
me.time.lemc <- ggpredict(mod.time.lemc, terms = c("time", "site"), type =  
"random", allow.new.levels = T)  
ggeffects::hypothesis_test(me.time.lemc, test = NULL)
```

```
## # Linear trend for time
```

```
##
```

```
## site | Slope |          95% CI |      p
```

```
## -----
```

```
## A      | -0.46 | [-0.60, -0.31] | < .001
```

```
## B      | -0.43 | [-0.58, -0.28] | < .001
```

```
## C      | -0.34 | [-0.49, -0.19] | < .001
```

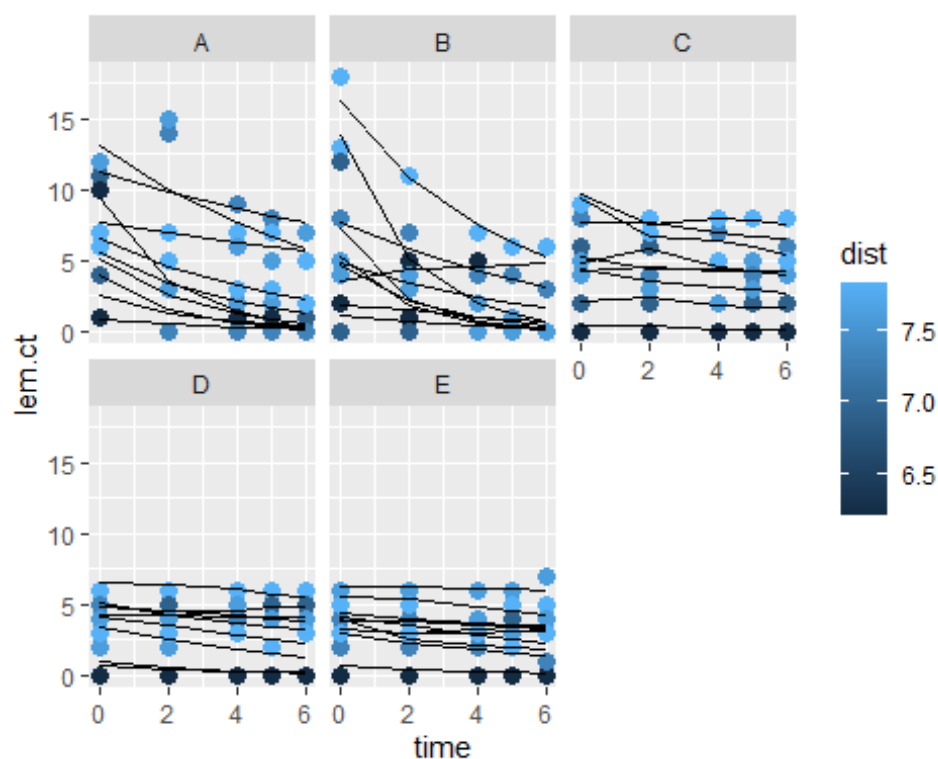
```
## D      | -0.34 | [-0.48, -0.19] | < .001
```

```
## E      | -0.34 | [-0.49, -0.20] | < .001
```

```
##
```

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

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



LEMUR FOOD TREES SPECIES RICHNESS & TIME

```
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 & Time

```
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
```

Marginal effects: Lemur Food Trees Species Richness & Time

```
me.time.lemr <- ggpredict(mod.time.lemr, terms = c("time", "site"), type =  
"random", allow.new.levels = T)
```

```
ggeffects::hypothesis_test(me.time.lemr, test = NULL)
```

```
## # Linear trend for time
```

```
##
```

```
## site | Slope |          95% CI |      p
```

```
## -----
```

```
## A      | -0.34 | [-0.47, -0.22] | < .001
```

```
## B      | -0.33 | [-0.46, -0.21] | < .001
```

```
## C      | -0.29 | [-0.41, -0.17] | < .001
```

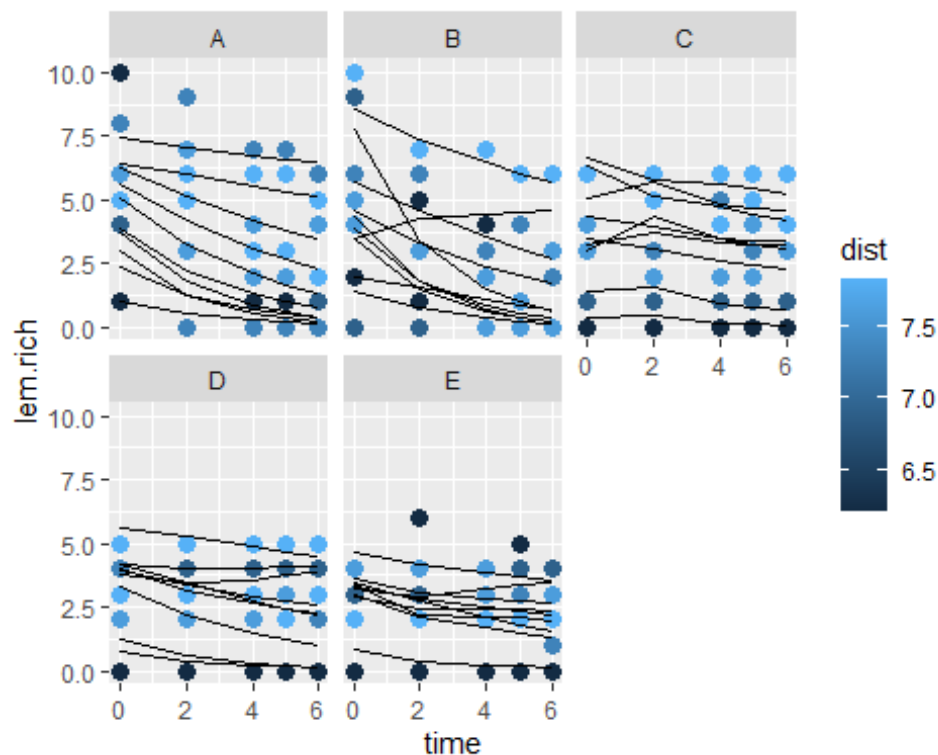
```
## D      | -0.29 | [-0.42, -0.17] | < .001
```

```
## E      | -0.29 | [-0.42, -0.17] | < .001
```

```
##
```

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

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.

```
## Warning: The `size` argument of `element_rect()` is deprecated as of
## i Please use the `linewidth` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.

## Warning: Removed 3 rows containing missing values (`geom_effect()`).
## Warning: Removed 3 rows containing missing values (`geom_effect()`).
```

