Appendix C. Full GLMM diagnostics and results

Supplement to: *Trade-offs in the use of direct and indirect indicators of ecosystem degradation for risk assessment*

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1. Prediction of collapse

Over the time frame of 100 years most of the tropical glacier ecosystem types are predicted to reach collapse by complete loss of ice mass. Since we are using a direct indicator of an ecosystem property (icy substrate) and we are predicting total ice mass for each unit, complete loss of ice is equivalent to a value of $RS_{ice}^{CT=0} = 1$. In the case of an indirect indicator such as bioclimatic suitability, we have more uncertainty in the real value of collapse, and thus use alternative collapse threshold to capture plausible ranges.

We expect that both direct and indirect indicators will have similar performance in describing the magnitude of degradation and predicting collapse. We will use two generalised linear mixed models (GLMM) to test if there are significant differences in inferences based on these estimates of relative severity.

To compare both indicators we used the $RS_{bcs}^{CT=acc}$ and $RS_{bcs}^{CT=ess}$ for the future periods paired with the $RS_{ice}^{CT=0}$ values for the years 2040, 2070 and 2100. We coded these three periods/years as variable time with values $0, 1, 2$ respectively. We use the respective total or mean RS values to calculate the response variable and includes a categorical variable method with three levels indicating either the direct indicator (*ice*) or indirect indicator with two alternative thresholds (*acc* or *ess*).

2. Proportion of models predicting collapse

This table will give us an overview of how many realisations of the predictions reach a point of collapse for each assessment unit:

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```r
valid_methods <- c("ice","ess","acc")
model_data <- model_data %>%
  filter(method %in% valid_methods) %>%
  mutate(
    method=droplevels(method),
    collapsed=case_when(
      method %in% "ice" & RS == 1 ~ 1L,
      !(method %in% "ice") & RS >0.99 ~ 1L,
      TRUE ~ 0L
    )
    )
model_data %>%
  group_by(unit,method) %>%
  summarise(collapse=sum(collapsed,na.rm=T), .groups = "keep") %>%
  pivot_wider(values_from=collapse,names_from=method) %>%
  knitr::kable()
```

unit	ice	acc	ess
Cordillera de Merida	60	16	31
Cordilleras Norte de Peru	0	3	10
Cordilleras Orientales de Peru y Bolivia	0	2	5
Cordilleras de Colombia	0	9	15
Ecuador	0	0	3
Kilimanjaro	22	0	1
Mexico	22	0	1
Mount Kenia	65	10	19
Puncak Jaya	72	0	22
Ruwenzori	47	6	11
Sierra Nevada de Santa Marta	17	0	5
Volcanos de Peru y Chile	0	0	3

3. Binomial GLMM of predicted collapse

We used a binomial GLMM with logit link function, using a response variable with values $y = 1$ when $RS = 1$ and $y = 0$ otherwise. We included fixed effects of scenarios (scenario with three levels) and time, and rabdom effects of assessment unit (unit, 15 levels). [1]

The variable method could be interpreted as a fixed effect and/or as a random effect *grouping* variable. Although it might be interesting to explore its

[1] Each observation corresponds to the prediction of one global circulation model, but since models are not identified in the ice mass balance model, we threat the different models as anonymous replicates, and this implies that the effect of the model is nested within method.

interaction with unit in increasing the variability of the response [1], our primary question is whether there are significant systematic differences between the methods. So we decide to use this variable as a fixed effect and keep the model simple for interpretability:

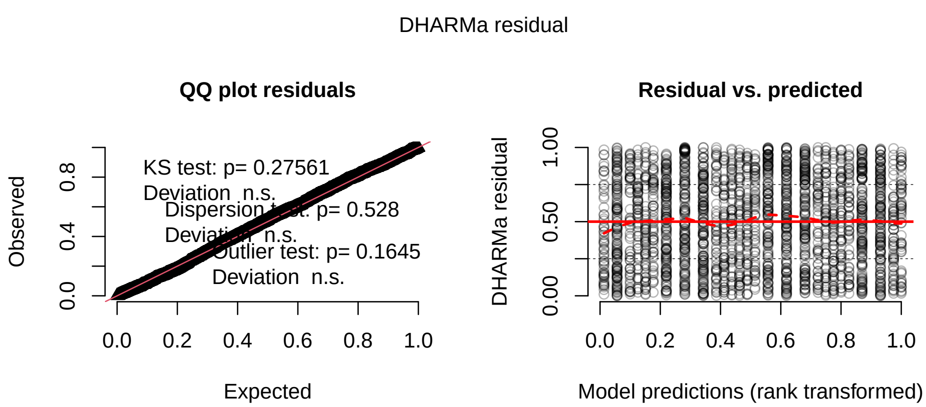
Full model specification in R using the glmmTMB with both fixed and random effects to measure the amount of variability attributed to methods vs. units.

```
mod_collapse_both <-
  glmmTMB(collapsed ~ time + scenario + method + (1|unit/method),
     data = model_data,
     family=binomial,
     REML=FALSE)
```

3.1. Model diagnostics

Model diagnostics and residual plots look good for this model specification (small significant effects in the residuals might be spurious due to large sample size).

```
mod_collapse_simres <- simulateResiduals(mod_collapse_both)
plot(mod_collapse_simres)
```



3.2. Explained variance

Approximation of a R^2 statistic for this model suggests more than 90% of the variance explained by the full model (random and fixed effects) and at least 40% explained by the fixed effects alone.

```
MuMIn::r.squaredGLMM(mod_collapse_both)
```

```
                 R2m       R2c
theoretical 0.4446706 0.9063561
delta       0.4076415 0.8308812
```

3.3. Model summary

The summary of the model indicates significant positive effects of time and future scenarios in the proportion of model predicting collapse, as expected. For the method variable, the indirect indicator have negative effects when compared with the direct indicator, but this is only significant for the maximum accuracy threshold. We can interpret this to be the lower, more conservative or optimistic bound of the collapse threshold for this indicator.

Random effect of unit is larger than the random effect of methods within units.

```r
summary(mod_collapse_both)
```

```
 Family: binomial  ( logit )
Formula:          collapsed ~ time + scenario + method + (1 | unit/method)
Data: model_data

     AIC      BIC   logLik deviance df.resid
   828.7    874.9   -406.4    812.7     2368

Random effects:

Conditional model:
 Groups      Name        Variance Std.Dev.
 method:unit (Intercept) 8.692    2.948
 unit        (Intercept) 7.527    2.744
Number of obs: 2376, groups:  method:unit, 36; unit, 12

Conditional model:
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)      -11.6518     1.3951  -8.352   <2e-16 ***
time               3.8584     0.2367  16.298   <2e-16 ***
scenarioSSP3-7.0   3.6845     0.3265  11.284   <2e-16 ***
scenarioSSP5-8.5   4.3241     0.3444  12.556   <2e-16 ***
methodacc         -2.8023     1.4041  -1.996    0.046 *
methodess          1.3094     1.3065   1.002    0.316
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(aov(mod_collapse_both))
```

```
              Df Sum Sq Mean Sq F value Pr(>F)
time           1  54.94   54.94  669.94 <2e-16 ***
```

```
scenario       2  15.46    7.73    94.27 <2e-16 ***
method         2   9.34    4.67    56.92 <2e-16 ***
unit          11  83.89    7.63    93.00 <2e-16 ***
method:unit   22  25.96    1.18    14.39 <2e-16 ***
Residuals   2337 191.65    0.08
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Confidence interval of the coefficients:

```r
confint(mod_collapse_both)
```

```
                                      2.5 %      97.5 %   Estimate
(Intercept)                      -14.386210 -8.91748820 -11.651849
time                               3.394395  4.32240740   3.858401
scenarioSSP3-7.0                   3.044489  4.32446058   3.684475
scenarioSSP5-8.5                   3.649082  4.99901838   4.324050
methodacc                         -5.554398 -0.05026062  -2.802329
methodess                         -1.251400  3.87014437   1.309372
Std.Dev.(Intercept)|method:unit    1.979285  4.39171122   2.948296
Std.Dev.(Intercept)|unit           1.497939  5.02513908   2.743602
```

3.4. Rank order of units

The fitted model suggest a general correlation of values between methods, but this does not mean that the rank order of predicted values is maintained between units. Here we calculate the mean predicted value for each combination of unit, method and scenario:

```r
model_data$pred_collapse <- predict(mod_collapse_both)

pred_collapse_values <- model_data %>%
  group_by(unit, method, scenario) %>%
  summarise(
    pcollapse = mean(pred_collapse),
    .groups="drop") %>%
  pivot_wider(
    names_from = c(scenario, method),
    values_from = pcollapse) %>%
  arrange(desc(`SSP1-2.6_ice`))
```

Now we calculate the rank for each column of this table, and calculate the range of ranks for the direct indicator `ice` and the indirect indicator (suitability) for all three scenarios of socio-economic pathways:

```r
pred_collapse_ranks <- pred_collapse_values %>%
  apply(2,rank)

pred_collapse_values$ice_rank <-
  apply(pred_collapse_ranks[,(2:4)], 1,
    function(x) paste(unique(range(x)), collapse = "-"))
pred_collapse_values$suit_rank <-
  apply(pred_collapse_ranks[,-(1:4)], 1,
    function(x) paste(unique(range(x)), collapse = "-"))
```

This table show the results:

```r
pred_collapse_values %>%
  select(unit, ice_rank, suit_rank) %>%
  knitr::kable()
```

unit	ice_rank	suit_rank
Puncak Jaya	1—4	2—7
Mount Kenia	2—3	1—3
Cordillera de Merida	2—3	1—3
Ruwenzori	1—4	4—5
Kilimanjaro	5.5	9.5—11.5
Mexico	5.5	9.5—11.5
Sierra Nevada de Santa Marta	7	7—8
Cordilleras de Colombia	8	3—4
Cordilleras Norte de Peru	9	5—6
Cordilleras Orientales de Peru y Bolivia	10	6—8
Ecuador	11.5	9.5—11.5
Volcanos de Peru y Chile	11.5	9.5—11.5

The first four units have overlapping ranks, but Kilimanjaro and Mexico have lower ranks and the cordilleras of Colombia and North Peru are ranked higher by the indicator based on suitability. This discrepancies are in line with the different number of realisations reaching collapse in each unit.

4. Magnitude of degradation

We expect that both direct and indirect indicators will have similar performance in describing the magnitude of degradation and predicting collapse. We will use two generalised linear mixed models (GLMM) to test if there are significant differences in inferences based on these estimates of relative severity.

For the combinations of units and models that did not reach a point of collapse, we wanted to compare the magnitude of degradation as indicated by the value of $\overline{\mathrm{RS}}$, $cED(0.30)$, $cED(0.50)$, $cED(0.80)$ and AUC_{cED}.

To compare both indicators we used the $RS_{bcs}^{CT=acc}$ and $RS_{bcs}^{CT=ess}$ for the future periods paired with the $RS_{ice}^{CT=0}$ values for the years 2040, 2070 and 2100. We coded these three periods/years as variable time with values $0, 1, 2$ respectively. We use the respective total or mean RS values to calculate the response variable and includes a categorical variable method with three levels indicating either the direct indicator (ice) or indirect indicator with two alternative thresholds (acc or ess).

```
valid_methods <- c("ice","ess","acc")
model_data <- model_data %>%
  filter(method %in% valid_methods) %>%
  mutate(
    method=droplevels(method),
    collapsed=case_when(
      method %in% "ice" & RS == 1 ~ 1L,
      !(method %in% "ice") & RS >0.99 ~ 1L,
      TRUE ~ 0L
    )
    )
```

We have to consider two issues with the data:

1. The bioclimatic suitability model perform better in the Andes than outside, probably as an effect of uneven sample sizes, so we use an additional variable for region, and
2. Kilimanjaro has a very poor fit, and we remove it as an outlier.

4.1. β distribution GLMM of $\overline{\mathrm{RS}}$

Given that $\overline{\mathrm{RS}}$ represent a relative measure (proportion between 0 and 1), we use a beta distribution GLMM with logit link function with $y = \overline{\mathrm{RS}}$ for all observations where $\overline{\mathrm{RS}} < 1$. Just as the binomial GLMM, we included fixed effects of scenarios (scenario with three levels) and time, and nested effect of method within each assessment unit (unit, 15 levels) and implied nested effects of model within method.

We prepare the data by applying the necessary filters and including a categorial variable representing Andean vs non-Andean units:

```
model_data_ss <- model_data %>%
  filter(RS < 1 & RS > 0, !unit %in% "Kilimanjaro") %>%
  mutate(
    andes = grepl("Peru|Colombia|Ecuador|Merida",unit),
```

```
  )
```

We fit the full model, and alternative versions with modelled dispersion parameters and additional fixed effects as:

```
mod_degradation_both <-
  glmmTMB(RS ~ time + scenario + method + (1|unit/method),
        data = model_data_ss,
        family = beta_family,
        REML = FALSE)

mod_degradation_andes <-
  glmmTMB(RS ~ time + scenario + method + (1|unit/method) + (1|method:andes),
        dispformula = ~ method,
        data = model_data_ss,
        family = beta_family,
        REML = FALSE)

mod_degradation_disp <-
  glmmTMB(RS ~ time + scenario + method + (1|unit/method),
        dispformula = ~ method,
        data = model_data_ss,
        family = beta_family,
        REML = FALSE)

mod_degradation_dispandes <-
  glmmTMB(RS ~ time + scenario + method + (1|unit/method),
        dispformula = ~ method + andes,
        data = model_data_ss,
        family = beta_family,
        REML = FALSE)
```

The AIC criterion favours a model with the original fixed and random effect but an additional dispersion formula including method and region (Andean vs. non-Andean) :

```
bbmle::AICtab(
  mod_degradation_disp,
  mod_degradation_dispandes,
  mod_degradation_andes,
  mod_degradation_both
  )
```

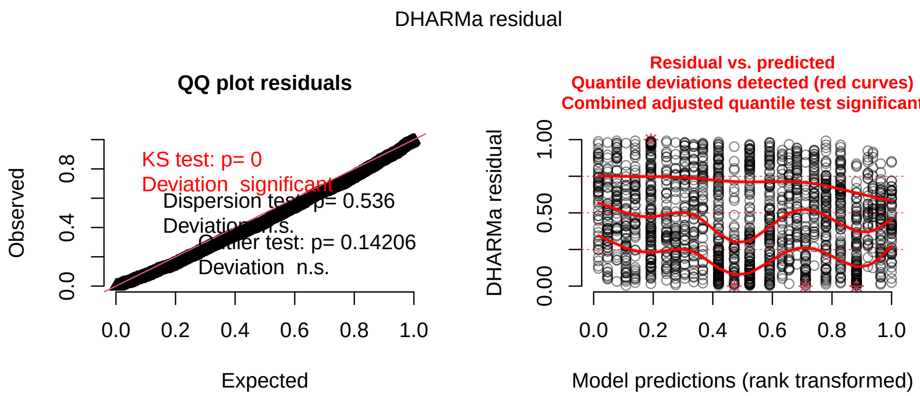
```
                          dAIC  df
mod_degradation_dispandes   0.0 12
```

```
mod_degradation_andes       38.2 12
mod_degradation_disp        52.4 11
mod_degradation_both       134.9 9
```

4.1.1. Model diagnostics

Model diagnostics and residual plots show important deviations, there is probably some effect of the unequal sample sizes between units, as we are excluding observations with $RS = 1$ and these are not evenly distributed among the assessment units. Particularly, the residuals are lower for the observation with high predicted values.

```
mod_degradation_simres <- simulateResiduals(mod_degradation_dispandes)
plot(mod_degradation_simres)
```



4.1.2. Outliers

When we examine the outliers, these are all related to the most optimistic scenario.

```
mod_degradation_simres$fittedModel$frame %>%
 slice(outliers(mod_degradation_simres))
```

```
          RS time scenario method                          unit andes
1  0.1166621    2 SSP1-2.6    acc                    Ruwenzori FALSE
2  0.1908056    2 SSP1-2.6    acc Sierra Nevada de Santa Marta FALSE
3  0.2202120    2 SSP1-2.6    acc Sierra Nevada de Santa Marta FALSE
4  0.3647246    2 SSP1-2.6    ess Sierra Nevada de Santa Marta FALSE
5  0.4837541    2 SSP1-2.6    ice     Cordilleras Norte de Peru  TRUE
6  0.4999853    2 SSP1-2.6    ice     Cordilleras Norte de Peru  TRUE
7  0.5723302    2 SSP1-2.6    ice     Cordilleras Norte de Peru  TRUE
8  0.6793231    2 SSP1-2.6    ice       Cordilleras de Colombia  TRUE
9  0.6668170    2 SSP1-2.6    ice       Cordilleras de Colombia  TRUE
```

```
10 0.4923106    2 SSP1-2.6    ice                             Ecuador  TRUE
11 0.6043740    2 SSP1-2.6    ice                             Ecuador  TRUE
12 0.5666947    2 SSP1-2.6    ice                             Ecuador  TRUE
13 0.4980398    2 SSP1-2.6    ice                             Ecuador  TRUE
14 0.3657955    2 SSP1-2.6    ice                             Ecuador  TRUE
15 0.3622036    2 SSP1-2.6    ice                             Ecuador  TRUE
16 0.4327956    2 SSP1-2.6    ice                             Ecuador  TRUE
17 0.5654804    2 SSP1-2.6    ice                             Ecuador  TRUE
18 0.9991269    0 SSP1-2.6    ice                         Puncak Jaya FALSE
19 0.9989429    0 SSP1-2.6    ice                         Puncak Jaya FALSE
20 0.9867472    0 SSP1-2.6    ice                           Ruwenzori FALSE
```

4.1.3. Model summary

The summary of the model indicates significant positive effects of time and future scenarios in the magnitude of RS, as expected. For the method variable, the indirect indicator have significant negative effects when compared with the direct indicator, but the effect is larger for the maximum accuracy threshold. We can interpret this to be the lower, more conservative or optimistic bound of RS for this indicator. In general, variability between units is considerably larger than variability between methods, thus we can expect all three methods to reflect general patterns, but will require closer inspection to rule out interaction with the random effects of assessment units.

```r
options(width=120)
summary(mod_degradation_dispandes)
```

```
 Family: beta  ( logit )
Formula:          RS ~ time + scenario + method + (1 | unit/method)
Dispersion:          ~method + andes
Data: model_data_ss

     AIC      BIC   logLik deviance df.resid
 -4137.0  -4071.1   2080.5  -4161.0     1787

Random effects:

Conditional model:
 Groups      Name        Variance Std.Dev.
 method:unit (Intercept) 0.3238   0.5690
 unit        (Intercept) 0.2840   0.5329
Number of obs: 1799, groups:  method:unit, 33; unit, 11

Conditional model:
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)       0.77427    0.23810    3.25  0.00115 **
```

```
time                1.05534    0.02399   43.99  < 2e-16 ***
scenarioSSP3-7.0  0.71553    0.04045   17.69  < 2e-16 ***
scenarioSSP5-8.5  0.93131    0.04124   22.58  < 2e-16 ***
methodacc        -1.35694    0.24749   -5.48 4.19e-08 ***
methodess        -0.62014    0.24894   -2.49  0.01274 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.33828    0.06848   34.15  < 2e-16 ***
methodacc   -0.53841    0.07823   -6.88 5.89e-12 ***
methodess   -0.50491    0.08449   -5.98 2.29e-09 ***
andesTRUE    0.49988    0.06867    7.28 3.34e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4.1.4. Rank order of units

The fitted model suggest a general correlation of values between methods, but this does not mean that the rank order of predicted values is maintained between units. Here we calculate the mean predicted value for each combination of unit, method and scenario:

```
model_data_ss$pred_beta <- predict(mod_degradation_dispandes)

pred_degradation_values <- model_data_ss %>%
  group_by(unit, method,scenario) %>%
  summarise(
    pdeg = mean(pred_beta),
    .groups="drop") %>%
  pivot_wider(
    names_from = c(scenario, method),
    values_from = pdeg) %>%
  arrange(`SSP1-2.6_ice`)
```

Now we calculate the rank for each column of this table, and calculate the range of ranks for the direct indicator `ice` and the indirect indicator (suitability) for all three scenarios of socio-economic pathways:

```
pred_degradation_ranks <- pred_degradation_values %>%
  apply(2,rank) %>% data.frame()

pred_degradation_values$ice_rank <-
  apply(pred_degradation_ranks[,(2:4)], 1,
```

```
    function(x) paste(unique(range(x)),collapse="-"))
pred_degradation_values$suit_rank <-
  apply(pred_degradation_ranks[,-(1:4)], 1,
    function(x) paste(unique(range(x)),collapse="-"))
```

This table show the results:

```
pred_degradation_values %>%
  select(unit, ice_rank, suit_rank) %>%
  knitr::kable()
```

unit	ice_rank	suit_rank
Ecuador	1	2—5
Cordilleras Norte de Peru	2	6—10
Volcanos de Peru y Chile	3	1—9
Cordilleras Orientales de Peru y Bolivia	4—5	3—6
Cordilleras de Colombia	5—6	7—9
Mexico	4—6	1—10
Sierra Nevada de Santa Marta	7	1—11
Mount Kenia	8	8—10
Puncak Jaya	9—11	2—7
Cordillera de Merida	9—10	9—11
Ruwenzori	10—11	4—6

Predictions are very variable for the indirect indicators, generating very wide ranges and strong discrepancies in rank order.

4.2. β distribution GLMM of $\mathrm{cED}(x)$

Given that $\mathrm{cED}(x)$ represent a relative measure (proportion between 0 and 1), we can also use a beta distribution GLMM with logit link function with $y = \mathrm{cED}(x)$ for all observations where $\mathrm{cED}(x) < 1$.

First let's prepare the dataframe considering the filters and modification applied before:

```
cED_model_data <-
  cED_model_data %>%
    filter(
      method %in% valid_methods,
      !unit %in% "Kilimanjaro"
      ) %>%
    mutate(
      method=factor(method, levels = valid_methods),
```

```
    andes = grepl("Peru|Colombia|Ecuador|Merida", unit)
  )
```

4.2.1. cED(0.3)

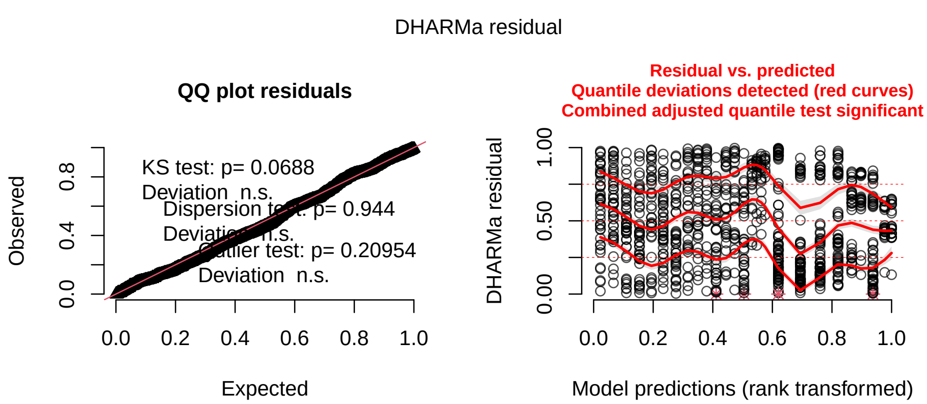
Just as the model above, we included fixed effects of scenarios (scenario with three levels) and time, and nested effect of method within each assessment unit (unit, 15 levels) and implied nested effects of model within method.

```
model_data_ss <- cED_model_data %>%
  filter(cED_30>0 & cED_30<1)

mod_cED_30_andes <-
  glmmTMB(cED_30 ~ time + scenario + method + (1|unit/method),
        dispformula = ~ method + andes,
    data = model_data_ss,
    family = beta_family,
    REML = FALSE)
```

Model diagnostics and residual plots deviate strongly, thus this model is not considered further.

```
mod_cED_simres <- simulateResiduals(mod_cED_30_andes)
plot(mod_cED_simres)
```



4.2.2. cED(0.5)

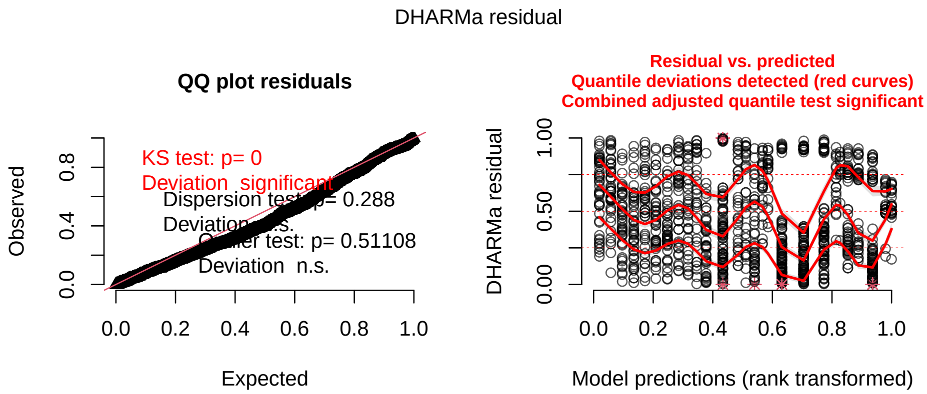
We fit similar models for cED(0.5):

```
model_data_ss <- cED_model_data %>%
  filter(cED_50>0 & cED_50<1)
```

```r
mod_cED_50_andes <-
  glmmTMB(cED_50 ~ time + scenario + method + (1|unit/method),
        dispformula = ~ method + andes,
    data = model_data_ss,
    family = beta_family,
    REML = FALSE)
```

But model diagnostics and residual plots deviate strongly again.

```r
mod_cED_simres <- simulateResiduals(mod_cED_50_andes)
plot(mod_cED_simres)
```



4.3. cED(0.8)

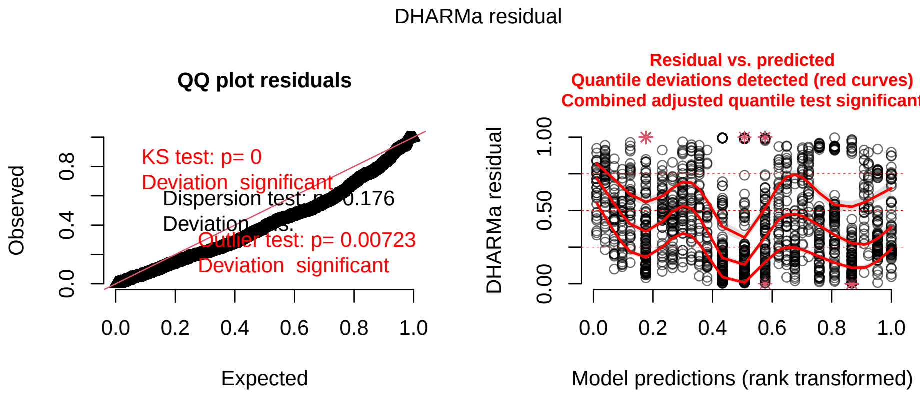
We fit similar models for cED(0.8):

```r
model_data_ss <- cED_model_data %>%
  filter(cED_80>0 & cED_80<1)

mod_cED_80_andes <-
  glmmTMB(cED_80 ~ time + scenario + method + (1|unit/method),
        dispformula = ~ method + andes,
        data = model_data_ss,
    family = beta_family,
    REML = FALSE)
```

But model diagnostics and residual plots deviate strongly again.

```r
mod_cED_simres <- simulateResiduals(mod_cED_80_andes)
plot(mod_cED_simres)
```



4.4. β distribution GLMM of $\mathrm{AUC}_{\mathrm{cED}}$

We also use a beta distribution GLMM with logit link function with $y = \mathrm{AUC}_{\mathrm{cED}}$ for all observations where $\mathrm{AUC}_{\mathrm{cED}} < 1$. Just as the model above, we included fixed effects of scenarios (scenario with three levels) and time, and nested effect of method within each assessment unit (unit, 15 levels) and implied nested effects of model within method.

```
model_data_ss <- cED_model_data %>%
  filter(AUC_cED>0 & AUC_cED<1)


mod_degradation_both <-
  glmmTMB(AUC_cED ~ time + scenario + method + (1|unit/method),
        data = model_data_ss,
        family = beta_family,
        REML = FALSE)

mod_degradation_andes <-
  glmmTMB(AUC_cED ~ time + scenario + method + (1|unit/method) + (1|method:andes),
        dispformula = ~ method,
        data = model_data_ss,
        family = beta_family,
        REML = FALSE)

mod_degradation_disp <-
  glmmTMB(AUC_cED ~ time + scenario + method + (1|unit/method),
        dispformula = ~ method,
        data = model_data_ss,
        family = beta_family,
        REML = FALSE)
```

```r
mod_degradation_dispandes <-
  glmmTMB(AUC_cED ~ time + scenario + method + (1|unit/method),
        dispformula = ~ method + andes,
        data = model_data_ss,
        family = beta_family,
        REML = FALSE)
```

The AIC criterion favours the initial specification with all variables and without dispersion model:

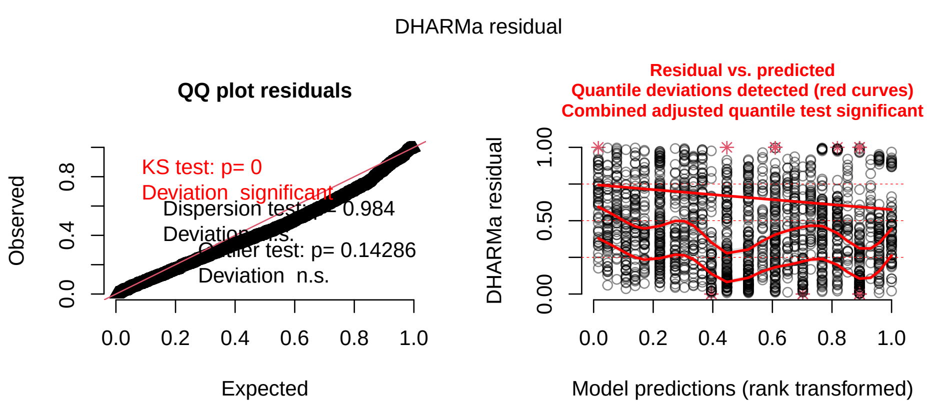
```r
bbmle::AICtab(
  mod_degradation_disp,
  mod_degradation_dispandes,
  mod_degradation_andes,
  mod_degradation_both
  )
```

```
                          dAIC  df
mod_degradation_dispandes   0.0 12
mod_degradation_andes     143.9 12
mod_degradation_disp      160.1 11
mod_degradation_both      186.4 9
```

4.4.1. Model diagnostics

Model diagnostics and residual plots look more or less ok, but there is probably some effect of the unequal sample sizes between units, as we are excluding observations with $RS = 1$ and these are not evenly distributed among the assessment units.

```r
mod_cED_simres <- simulateResiduals(mod_degradation_dispandes)
plot(mod_cED_simres)
```



4.4.2. Outliers

When we examine the outliers, these are mostly related to the more optimistic scenario, or to regions with extreme risk of collapse.

```
mod_cED_simres$fittedModel$frame %>%
  slice(outliers(mod_cED_simres))
```

```
     AUC_cED time scenario method                      unit andes
1  0.0110632    2 SSP1-2.6    ess               Mount Kenia FALSE
2  0.2410671    2 SSP1-2.6    ess                 Ruwenzori FALSE
3  0.0110632    2 SSP1-2.6    acc               Mount Kenia FALSE
4  0.1266893    2 SSP1-2.6    acc                 Ruwenzori FALSE
5  0.9289891    0 SSP1-2.6    acc       Cordillera de Merida  TRUE
6  1.0000000    1 SSP1-2.6    ice               Puncak Jaya FALSE
7  1.0000000    1 SSP1-2.6    ice                 Ruwenzori FALSE
8  0.4902343    2 SSP1-2.6    ice Cordilleras Norte de Peru  TRUE
9  1.0000000    1 SSP1-2.6    ice       Cordillera de Merida  TRUE
10 1.0000000    1 SSP1-2.6    ice       Cordillera de Merida  TRUE
11 1.0000000    2 SSP1-2.6    ice       Cordillera de Merida  TRUE
12 1.0000000    2 SSP1-2.6    ice       Cordillera de Merida  TRUE
13 1.0000000    2 SSP1-2.6    ice       Cordillera de Merida  TRUE
14 0.4924969    2 SSP1-2.6    ice                   Ecuador  TRUE
15 0.5024112    2 SSP1-2.6    ice                   Ecuador  TRUE
16 0.3733117    2 SSP1-2.6    ice                   Ecuador  TRUE
17 0.3634823    2 SSP1-2.6    ice                   Ecuador  TRUE
18 0.4376313    2 SSP1-2.6    ice                   Ecuador  TRUE
19 1.0000000    0 SSP3-7.0    ice               Puncak Jaya FALSE
20 1.0000000    1 SSP5-8.5    ice       Cordillera de Merida  TRUE
```

4.4.3. Model summary

The summary of the model for AUC_{cED} indicates significant positive effects of time and future scenarios in the magnitude of degradation, with similar patterns as those described for $\overline{\mathrm{RS}}$ above.

```
options(width=120)
summary(mod_degradation_dispandes)
```

```
 Family: beta  ( logit )
Formula:          AUC_cED ~ time + scenario + method + (1 | unit/method)
Dispersion:               ~method + andes
Data: model_data_ss

     AIC      BIC   logLik deviance df.resid
 -7389.6  -7323.6   3706.8  -7413.6     1792
```

```
Random effects:

Conditional model:
 Groups      Name        Variance Std.Dev.
 method:unit (Intercept) 0.4280   0.6542
 unit        (Intercept) 0.3511   0.5926
Number of obs: 1804, groups:  method:unit, 33; unit, 11

Conditional model:
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)       0.93848    0.26985    3.48 0.000506 ***
time              1.10740    0.02499   44.31  < 2e-16 ***
scenarioSSP3-7.0  0.73008    0.04317   16.91  < 2e-16 ***
scenarioSSP5-8.5  0.93173    0.04388   21.24  < 2e-16 ***
methodess        -0.83180    0.28541   -2.91 0.003564 **
methodacc        -1.56336    0.28405   -5.50 3.71e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion model:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.81310    0.06954  26.073  < 2e-16 ***
methodess   -0.22808    0.08535  -2.672 0.007536 **
methodacc   -0.29254    0.07903  -3.702 0.000214 ***
andesTRUE    0.86508    0.06922  12.497  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

5. R session info

Analysis was conducted in R using following packages and versions:

```r
options(width=120)
sessionInfo()
```

```
R version 4.3.1 (2023-06-16)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Sonoma 14.2.1

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.3-arm64/Resources/lib/libRlapack.dylib;

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
time zone: Australia/Sydney
tzcode source: internal

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
 [1] DHARMa_0.4.6  lme4_1.1-35.1 Matrix_1.6-4  glmmTMB_1.1.8 tidyr_1.3.0   readr_2.1.4   pu
 [9] stringr_1.5.1 units_0.8-5   ggplot2_3.4.4 dplyr_1.1.4

loaded via a namespace (and not attached):
 [1] tidyselect_1.2.0    fastmap_1.1.1       TH.data_1.1-2       promises_1.2.1      digest_
 [6] mime_0.12           estimability_1.4.1  lifecycle_1.0.4     ellipsis_0.3.2      surviva
[11] magrittr_2.0.3      compiler_4.3.1      rlang_1.1.2         tools_4.3.1         utf8_1.
[16] yaml_2.3.8          knitr_1.45          bit_4.0.5           here_1.0.1          plyr_1.
[21] gap.datasets_0.0.6  multcomp_1.4-25     withr_2.5.2         numDeriv_2016.8-1.1 grid_4.
[26] stats4_4.3.1        fansi_1.0.6         xtable_1.8-4        colorspace_2.1-0    emmeans
[31] scales_1.3.0        iterators_1.0.14    MASS_7.3-60         bbmle_1.0.25.1      cli_3.6
[36] mvtnorm_1.2-4       rmarkdown_2.25      crayon_1.5.2        generics_0.1.3      rstudio
[41] tzdb_0.4.0          bdsmatrix_1.3-6     minqa_1.2.6         splines_4.3.1       paralle
[46] vctrs_0.6.5         boot_1.3-28.1       sandwich_3.1-0      jsonlite_1.8.8      hms_1.1
[51] bit64_4.0.5         qgam_1.3.4          foreach_1.5.2       gap_1.5-3           glue_1.
[56] nloptr_2.0.3        codetools_0.2-19    stringi_1.8.3       gtable_0.3.4        later_1
[61] munsell_0.5.0       tibble_3.2.1        pillar_1.9.0        htmltools_0.5.7     R6_2.5.
[66] TMB_1.9.10          Rdpack_2.6          doParallel_1.0.17   rprojroot_2.0.4     vroom_1
[71] evaluate_0.23       shiny_1.8.0         lattice_0.22-5      rbibutils_2.2.16    httpuv_
[76] Rcpp_1.0.11         nlme_3.1-164        mgcv_1.9-0          MuMIn_1.47.5        xfun_0.
[81] zoo_1.8-12          pkgconfig_2.0.3
```

References

[1] D. J. Barr, R. Levy, C. Scheepers, H. J. Tily, Random effects structure for confirmatory hypothesis testing: Keep it maximal, Journal of Memory and Language 68 (2013). doi:10.1016/j.jml.2012.11.001.