

```

1 ## -----
2 #| eval: false
3 install.packages(c("DHARMa",
4   "data.table",
5   "lme4",
6   "Matrix",
7   "TMB",
8   "glmmTMB",
9   "mgcv",
10  "mgcviz",
11  "gratia",
12  "marginaleffects",
13  "ggplot2",
14  "colorspace",
15  "sf"))
16
17
18 ## -----
19 #| output: false
20 #| cache: false
21 library(DHARMa)
22 library(data.table)
23 library(lme4)
24 library(glmmTMB)
25 library(mgcv)
26 library(marginaleffects)
27 library(ggplot2)
28 library(colorspace)
29 library(sf)
30
31 options(show.signif.stars = FALSE)
32
33
34 ## -----
35 #| include: false
36 #| cache: false
37 base.family <- "BMPlexSansCondensed"
38 base.size <- 11
39 plot_theme <-
40 theme_light(base_size = base.size) +
41 theme(
42   plot.title = element_text(hjust = 0,
43     face = "bold",
44     margin = margin(l = 0, b = base.size/3, t =
45   base.size/3)),
46   plot.tag = element_text(face = "bold"),
47   axis.line.x = element_line(color = "black",
48     linewidth = rel(0.5)),
49   axis.line.y = element_line(color = "black",
50     linewidth = rel(0.5)),
51   axis.title.x = element_text(margin = margin(t = base.size/2)),
52   # axis.title.y = element_text(margin = margin(r = base.size/2)),
53   # axis.text.y = element_text(color = "black", size = rel(1)),
54   # axis.title = element_text(color = "black"),
55   # legend.title = element_text(margin = margin(b = base.size)),
56   legend.position = "right",
57   legend.justification = "top",

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58   panel.grid.major = element_blank(),
59   panel.grid.minor = element_blank(),
60   panel.border = element_blank(),
61   # panel.spacing.x = unit(base.size, "pt"),
62   # panel.spacing.y = unit(base.size/2, "pt"),
63   plot.margin = margin(3, 3, 3, 3),
64   strip.text = element_text(size = rel(0.8),
65     hjust = 0.5,
66     color = "black",
67     margin = margin(base.size/2,
68       base.size/2,
69       base.size/2,
70       base.size/2)),
71   strip.background = element_rect(fill = "gray90", colour = NA))
72 theme_set(plot_theme)
73
74 ## -----
75 #| eval: false
76 base.size <- 11
77 plot_theme <-
78 theme_light(base_size = base.size) +
79 theme(
80   plot.title = element_text(hjust = 0,
81     face = "bold",
82     margin = margin(l = 0, b = base.size/3, t =
83   base.size/3)),
84   plot.tag = element_text(face = "bold"),
85   axis.line.x = element_line(color = "black",
86     linewidth = rel(0.5)),
87   axis.line.y = element_line(color = "black",
88     linewidth = rel(0.5)),
89   axis.title.x = element_text(margin = margin(t = base.size/2)),
90   axis.title.y = element_text(margin = margin(r = base.size/2)),
91   legend.position = "right",
92   legend.justification = "top",
93   legend.key.size = unit(base.size, "pt"),
94   panel.grid.major = element_blank(),
95   panel.grid.minor = element_blank(),
96   panel.border = element_blank(),
97   plot.margin = margin(3, 3, 3, 3),
98   strip.text = element_text(size = rel(0.8),
99     hjust = 0.5,
100    color = "black",
101    margin = margin(base.size/2,
102      base.size/2,
103      base.size/2,
104      base.size/2)),
105   strip.background = element_rect(fill = "gray90", colour = NA))
106 theme_set(plot_theme)
107
108 ## -----
109 #| include: false
110 gutten <- readRDS("../data/gutten.rds")
111
112
113 ## -----
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115 #| eval: false
116 gutten <- readRDS("gutten.rds")
117
118
119 ## -----
120 gutten
121
122 ## -----
123
124 ggplot(gutten) +
125   geom_point(aes(x = age.base, y = volume, colour = quality),
126             alpha = 0.5) +
127   facet_wrap(vars(quality)) +
128   labs(y = "Volume (m³/1000)",
129        x = "Age (years)",
130        colour = "Site quality")
131
132 ## -----
133
134 mod <- glm(volume ~ age.base * quality,
135            family = gaussian(link = "identity"),
136            data = gutten)
137
138 summary(mod)
139
140 ## -----
141
142 age.seq <- seq(min(gutten$age.base), max(gutten$age.base), length.out = 100)
143 quality.u <- unique(gutten$quality)
144
145 pred.grid <- datagrid(age.base = age.seq,
146                      quality = quality.u,
147                      model = mod)
148
149 mod.pred <- predictions(mod, newdata = pred.grid)
150
151 mod.pred
152
153 ## -----
154 ggplot(mod.pred) +
155   geom_point(data = gutten,
156             aes(x = age.base, y = volume, colour = quality),
157             alpha = 0.2) +
158   geom_line(aes(x = age.base, y = estimate, colour = quality)) +
159   geom_ribbon(aes(x = age.base, ymin = conf.low, ymax = conf.high,
160                 group = quality),
161             alpha = 0.2) +
162   facet_wrap(vars(quality)) +
163   labs(y = "Volume (m³/1000)",
164        x = "Age (years)",
165        colour = "Site quality")
166
167 ## -----
168
169 #| layout-ncol: 2
170 #| fig-width: 4
171 #| fig-height: 4
172 mod.res <- residuals(mod)

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173 mod.fit <- fitted(mod)
174
175 ggplot() +
176   geom_hline(yintercept = 0, colour = 2) +
177   geom_point(aes(y = mod.res, x = mod.fit), alpha = 0.3) +
178   labs(x = "Fitted", y = "Residual")
179
180 ggplot() +
181   geom_hline(yintercept = 0, colour = 2) +
182   geom_point(aes(y = mod.res, x = rank(mod.fit)), alpha = 0.3) +
183   labs(x = "Fitted (rank)", y = "Residual")
184
185 ## -----
186 #| warning: false
187 #| fig-width: 10
188 #| fig-height: 5.85
189 mod.qres <- simulateResiduals(mod)
190
191 plot(mod.qres)
192
193 ## -----
194 #| eval: false
195 ?simulateResiduals()
196
197 ## -----
198
199 ## -----
200 testUniformity(mod.qres)
201
202 testDispersion(mod.qres)
203
204 testOutliers(mod.qres)
205
206 ## -----
207 testQuantiles(mod.qres)
208
209 ## -----
210
211 mod <- glm(volume ~ age.base * quality,
212           family = Gamma(link = "log"),
213           data = gutten)
214
215 summary(mod)
216
217 ## -----
218
219 age.seq <- seq(min(gutten$age.base), max(gutten$age.base), length.out = 100)
220 quality.u <- unique(gutten$quality)
221
222 pred.grid <- datagrid(age.base = age.seq,
223                      quality = quality.u,
224                      model = mod)
225
226 mod.pred <- predictions(mod, newdata = pred.grid)
227
228 ggplot(mod.pred) +
229   geom_point(data = gutten,
230             aes(x = age.base, y = volume, colour = quality),
231             alpha = 0.2) +

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231 geom_line(aes(x = age.base, y = estimate, colour = quality)) +
232   geom_ribbon(aes(x = age.base, ymin = conf.low, ymax = conf.high,
233                 group = quality),
234             alpha = 0.2) +
235   facet_wrap(vars(quality)) +
236   labs(y = "Volume (m3/1000)",
237        x = "Age (years)",
238        colour = "Site quality")
239
240
241 ## -----
242 #| fig-width: 10
243 #| fig-height: 5.85
244 mod.qres <- simulateResiduals(mod)
245
246 plot(mod.qres)
247
248 ## -----
249 #| layout-nrow: 2
250 plotResiduals(mod.qres, gutten$quality)
251 plotResiduals(mod.qres, gutten$age.base)
252
253
254 ## -----
255 mod <- glm(volume ~ poly(age.base, 2) * quality,
256            family = Gamma(link = "log"),
257            data = gutten)
258
259 summary(mod)
260
261 ## -----
262 #| fig-width: 10
263 #| fig-height: 5.85
264 mod.qres <- simulateResiduals(mod)
265
266 plot(mod.qres)
267
268 ## -----
269 plotResiduals(mod.qres, gutten$age.base)
270
271 ## -----
272 #| fig-width: 10
273 #| fig-height: 5.85
274 mod <- glm(volume ~ poly(age.base, 5) * quality,
275            family = Gamma(link = "log"),
276            data = gutten)
277
278 summary(mod)
279
280 ## -----
281 #| fig-width: 10
282 #| fig-height: 5.85
283 mod.qres <- simulateResiduals(mod)
284
285 plot(mod.qres)
286
287
288
289
290 ## -----
291 #| layout-nrow: 2
292 plotResiduals(mod.qres, gutten$quality)
293 plotResiduals(mod.qres, gutten$age.base)
294
295
296 ## -----
297 age.seq <- seq(min(gutten$age.base), max(gutten$age.base), length.out = 100)
298 quality.u <- unique(gutten$quality)
299
300 pred.grid <- datagrid(age.base = age.seq,
301                      quality = quality.u,
302                      model = mod)
303
304 mod.pred <- predictions(mod, newdata = pred.grid)
305
306 ggplot(mod.pred) +
307   geom_point(data = gutten,
308             aes(x = age.base, y = volume, colour = quality),
309             alpha = 0.3) +
310   geom_line(aes(x = age.base, y = estimate, colour = quality)) +
311   geom_ribbon(aes(x = age.base, ymin = conf.low, ymax = conf.high,
312                 group = quality),
313             alpha = 0.2) +
314   facet_wrap(vars(quality)) +
315   labs(y = "Volume (m3/1000)",
316        x = "Age (years)",
317        colour = "Site quality")
318
319 ## -----
320 mod <- glmmTMB(volume ~ poly(age.base, 5) * quality + (1 | site + tree.id),
321               family = Gamma(link = "log"),
322               data = gutten)
323
324 summary(mod)
325
326 ## -----
327 #| fig-width: 10
328 #| fig-height: 5.85
329 mod.qres <- simulateResiduals(mod)
330
331 plot(mod.qres)
332
333 ## -----
334 age.seq <- seq(min(gutten$age.base), max(gutten$age.base), length.out = 100)
335 quality.u <- unique(gutten$quality)
336
337 pred.grid <- datagrid(age.base = age.seq,
338                      quality = quality.u,
339                      model = mod)
340
341 mod.pred <- predictions(mod, newdata = pred.grid, re.form = NA)
342
343 ggplot(mod.pred) +

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347 geom_point(data = gutten,
348             aes(x = age.base, y = volume, colour = quality),
349             alpha = 0.3) +
350 geom_line(aes(x = age.base, y = estimate, colour = quality)) +
351 geom_ribbon(aes(x = age.base, ymin = conf.low, ymax = conf.high,
352               group = quality),
353            alpha = 0.2) +
354 facet_wrap(vars(quality)) +
355 labs(y = "Volume (m³/1000)",
356      x = "Age (years)",
357      colour = "Site quality")
358
359
360
361 ## -----
362 mod <- glmTMB(volume ~ poly(age.base, 5) * quality + (1 | site + tree.id),
363              family = tweedie(link = "log"),
364              data = gutten)
365
366 summary(mod)
367 AIC(mod)
368
369 ## -----
370 #| fig-width: 10
371 #| fig-height: 5.85
372 mod.qres <- simulateResiduals(mod)
373
374 plot(mod.qres)
375
376 ## -----
377 age.seq <- seq(min(gutten$age.base), max(gutten$age.base), length.out = 100)
378 quality.u <- unique(gutten$quality)
379
380 pred.grid <- datagrid(age.base = age.seq,
381                       quality = quality.u,
382                       model = mod)
383
384 mod.pred <- predictions(mod, newdata = pred.grid, re.form = NA)
385
386 ggplot(mod.pred) +
387   geom_point(data = gutten,
388             aes(x = age.base, y = volume, colour = quality),
389             alpha = 0.3) +
390   geom_line(aes(x = age.base, y = estimate, colour = quality)) +
391   geom_ribbon(aes(x = age.base, ymin = conf.low, ymax = conf.high,
392                 group = quality),
393             alpha = 0.2) +
394   facet_wrap(vars(quality)) +
395   labs(y = "Volume (m³/1000)",
396        x = "Age (years)",
397        colour = "Site quality")
398
399
400 ## -----
401 mod <- glmTMB(volume ~ poly(age.base, 5) * quality + (1 | site + tree.id),
402              formula = ~ age.base * quality,
403              family = Gamma(link = "log"),
404              data = gutten)

```

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405 summary(mod)
406
407 ## -----
408 #| fig-width: 10
409 #| fig-height: 5.85
410 mod.qres <- simulateResiduals(mod)
411
412 plot(mod.qres)
413
414 ## -----
415 age.seq <- seq(min(gutten$age.base), max(gutten$age.base), length.out = 100)
416 quality.u <- unique(gutten$quality)
417
418 pred.grid <- datagrid(age.base = age.seq,
419                       quality = quality.u,
420                       model = mod)
421
422 mod.pred <- predictions(mod, newdata = pred.grid, re.form = NA)
423
424 ggplot(mod.pred) +
425   geom_point(data = gutten,
426             aes(x = age.base, y = volume, colour = quality),
427             alpha = 0.3) +
428   geom_line(aes(x = age.base, y = estimate, colour = quality)) +
429   geom_ribbon(aes(x = age.base, ymin = conf.low, ymax = conf.high,
430                 group = quality),
431             alpha = 0.2) +
432   facet_wrap(vars(quality)) +
433   labs(y = "Volume (m³/1000)",
434        x = "Age (years)",
435        colour = "Site quality")
436
437 ## -----
438 #| include: false
439 sitka <- readRDS("../data/sitka.rds")
440
441 ## -----
442 #| eval: false
443 sitka <- readRDS("sitka.rds")
444
445 ## -----
446 #| eval: false
447 sitka <- readRDS("sitka.rds")
448
449 ## -----
450 sitka
451
452 ## -----
453 ggplot(sitka) +
454   geom_line(data = sitka,
455             aes(x = day, y = size,
456                 group = tree.id, colour = treatment),
457             alpha = 0.5) +
458   scale_colour_brewer(type = "qual", palette = "Set1") +
459   labs(x = "Time (days)",
460        y = "Size (cm²m)",
461

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463 colour = "Treatment")
464
465
466 ## -----
467 mod <- glmTMB(size ~ day * treatment + (1 | tree.id),
468 data = sitka,
469 family = Gamma(link = "log"))
470
471 summary(mod)
472
473
474 ## -----
475 day.seq <- seq(min(sitka$day), max(sitka$day), length.out = 100)
476 treatment.u <- unique(sitka$treatment)
477
478 pred.grid <- datagrid(day = day.seq,
479 treatment = treatment.u,
480 model = mod)
481
482
483 ggplot(mod.pred) +
484 geom_line(data = sitka, aes(x = day, y = size, group = tree.id),
485 alpha = 0.2) +
486 geom_ribbon(aes(x = day, ymin = conf.low, ymax = conf.high,
487 fill = treatment),
488 alpha = 0.2) +
489 geom_line(aes(x = day, y = estimate, colour = treatment)) +
490 scale_colour_brewer(type = "qual", palette = "Set1") +
491 scale_fill_brewer(type = "qual", palette = "Set1",
492 guide = "none") +
493 labs(x = "Time (days)",
494 y = "Size (cm2m)",
495 colour = "Treatment")
496
497
498 ## -----
499
500 #| fig-width: 10
501 #| fig-height: 5.85
502 mod.qres <- simulateResiduals(mod)
503
504 plot(mod.qres)
505
506 ## -----
507 #| warning: false
508 #| fig-width: 10
509 #| fig-height: 5.85
510 mod.qres.time <- recalculateResiduals(mod.qres, group = sitka$day)
511
512 testTemporalAutocorrelation(residuals(mod.qres.time), unique(sitka$day))
513
514
515 ## -----
516 mod <- gam(size ~ s(day) + treatment + s(tree.id, bs = "re"),
517 data = sitka,
518 family = Gamma(link = "log"),
519 method = "REML")
520
521
522 summary(mod)
523
524 ## -----
525 #| fig-width: 10
526 #| fig-height: 5.85
527 mod.qres <- simulateResiduals(mod)
528
529
530 plot(mod.qres)
531
532 ## -----
533 day.seq <- seq(min(sitka$day), max(sitka$day), length.out = 100)
534 treatment.u <- unique(sitka$treatment)
535
536 pred.grid <- datagrid(day = day.seq,
537 treatment = treatment.u,
538 model = mod)
539
540 mod.pred <- predictions(mod, newdata = pred.grid, re.form = NA)
541
542
543 ggplot(mod.pred) +
544 geom_line(data = sitka, aes(x = day, y = size, group = tree.id),
545 alpha = 0.2) +
546 geom_ribbon(aes(x = day, ymin = conf.low, ymax = conf.high,
547 fill = treatment),
548 alpha = 0.2) +
549 geom_line(aes(x = day, y = estimate, colour = treatment)) +
550 scale_colour_brewer(type = "qual", palette = "Set1") +
551 scale_fill_brewer(type = "qual", palette = "Set1",
552 guide = "none") +
553 labs(x = "Time (days)",
554 y = "Size (cm2m)",
555 colour = "Treatment")
556
557
558 ## -----
559 #| warning: false
560 #| fig-width: 10
561 #| fig-height: 5.85
562 mod.qres.time <- recalculateResiduals(mod.qres, group = sitka$day)
563
564 testTemporalAutocorrelation(residuals(mod.qres.time), unique(sitka$day))
565
566 ## -----
567 mod <- gam(size ~
568 s(day) + treatment +
569 s(day, treatment, bs = "sz") +
570 s(tree.id, bs = "re"),
571 data = sitka,
572 family = Gamma(link = "log"),
573 method = "REML")
574
575
576 summary(mod)
577
578

```

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579 ## -----
580 #| fig-width: 10
581 #| fig-height: 5.85
582 mod.qres <- simulateResiduals(mod)
583
584 plot(mod.qres)
585
586
587
588 ## -----
589 day.seq <- seq(min(sitka$day), max(sitka$day), length.out = 100)
590 treatment.u <- unique(sitka$treatment)
591
592 pred.grid <- datagrid(day = day.seq,
593                       treatment = treatment.u,
594                       model = mod)
595 mod.pred <- predictions(mod,
596                        newdata = pred.grid,
597                        exclude = "s(tree.id)")
598
599 ggplot(mod.pred) +
600   geom_line(data = sitka, aes(x = day, y = size, group = tree.id),
601            alpha = 0.2) +
602   geom_ribbon(aes(x = day, ymin = conf.low, ymax = conf.high,
603                  fill = treatment),
604              alpha = 0.2) +
605   geom_line(aes(x = day, y = estimate, colour = treatment)) +
606   scale_colour_brewer(type = "qual", palette = "Set1") +
607   scale_fill_brewer(type = "qual", palette = "Set1",
608                     guide = "none") +
609   labs(x = "Time (days)",
610        y = "Size (cm²m)",
611        colour = "Treatment")
612
613
614 ## -----
615 #| warning: false
616 #| fig-width: 10
617 #| fig-height: 5.85
618 mod.qres.time <- recalculateResiduals(mod.qres, group = sitka$day)
619
620 testTemporalAutocorrelation(residuals(mod.qres.time), unique(sitka$day))
621
622
623 ## -----
624 gratia: draw(mod)
625
626
627 ## -----
628 #| include: false
629 lichen <- readRDS("../data/lichen.rds")
630 swe <- st_read("../data/adm_swe.gpkg")
631
632
633 ## -----
634 #| eval: false
635 lichen <- readRDS("lichen.rds")
636 swe <- st_read("adm_swe.gpkg")

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637 ## -----
638
639 lichen
640
641
642 ## -----
643 lichen.usneal <- lichen[species == "Usnea" & ip == 1]
644
645
646
647 ## -----
648 plot_theme <-
649   plot_theme +
650   theme(panel.grid.major = element_line(linewidth = rel(1)))
651
652 theme_set(plot_theme)
653
654
655 ## -----
656 #| fig-width: 8
657 #| fig-height: 10
658 lichen.prop.agg <-
659   lichen[,
660     .(occurrence = mean(occurrence)),
661     by = .(ip, species, east.agg, north.agg)]
662
663 ggplot(lichen.prop.agg) +
664   geom_raster(aes(x = east.agg, y = north.agg, fill = occurrence)) +
665   geom_sf(data = swe, fill = NA, colour = "black") +
666   scale_fill_viridis_c() +
667   facet_grid(rows = vars(ip), cols = vars(species)) +
668   labs(x = NULL, y = NULL, fill = "Occurrence probability")
669
670
671 ## -----
672
673 mod <-
674   glm(occurrence ~ temp * rain,
675       data = lichen.usneal,
676       family = binomial(link = "logit"))
677 summary(mod)
678
679
680 ## -----
681 mod.pred <- avg_predictions(mod, by = c("east.agg", "north.agg"))
682
683
684 ggplot(mod.pred) +
685   geom_raster(aes(x = east.agg, y = north.agg, fill = estimate)) +
686   geom_sf(data = swe, fill = NA, colour = "black") +
687   scale_fill_viridis_c() +
688   labs(x = NULL, y = NULL, fill = "Estimated occurrence\probability")
689
690
691 ## -----
692 #| fig-width: 10
693 #| fig-height: 5.85
694 mod.qres <- simulateResiduals(mod)

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695
696
697
698
699
700 #| warning: false
701 #| fig-width: 10
702 #| fig-height: 5.85
703 mod.res.agg <- recalculateResiduals(mod.qres, lichen.usneal$rast.agg.id)
704
705 plot(mod.res.agg, quantreg = TRUE)
706
707
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plot(mod.qres, quantreg = TRUE)

## -----
700 #| warning: false
701 #| fig-width: 10
702 #| fig-height: 5.85
703 mod.res.agg <- recalculateResiduals(mod.qres, lichen.usneal$rast.agg.id)
704
705 plot(mod.res.agg, quantreg = TRUE)
706
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plot(mod.qres, quantreg = TRUE)
plotResiduals(mod.qres, lichen.usneal$bas, quantreg = TRUE)
plotResiduals(mod.qres, lichen.usneal$age, quantreg = TRUE)

## -----
mod <-
  glm(occurrence ~
    temp + rain +
    mat + ndep +
    dbh + cri +
    bas + age,
    data = lichen.usneal,
    family = binomial(link = "logit"))
summary(mod)

## -----
mod.pred <- avg_predictions(mod, by = c("east.agg", "north.agg"))

ggplot(mod.pred) +
  geom_raster(aes(x = east.agg, y = north.agg, fill = estimate)) +
  geom_sf(data = swe, fill = NA, colour = "black") +
  scale_fill_viridis_c() +
  labs(x = NULL, y = NULL, fill = "Estimated occurrence\nprobability")

## -----
800 #| fig-width: 10
801 #| fig-height: 5.85
802 mod.qres <- simulateResiduals(mod)
803
804 plot(mod.qres, quantreg = TRUE)
805
806
807
808
809
810

## -----
800 #| warning: false
801 #| fig-width: 10
802 #| fig-height: 5.85
803 mod.res.agg <- recalculateResiduals(mod.qres, lichen.usneal$rast.agg.id)
804
805 plot(mod.res.agg, quantreg = TRUE)
806
807
808
809
810

## -----
testSpatialAutocorrelation(mod.qres, lichen.usneal$east, lichen.usneal$north)

## -----
lichen.usneal[, qres := residuals(mod.qres)]

lichen.usneal[,
  .(qres = sum(qres)/N),
  by = c("east.agg", "north.agg")] |>
ggplot() +
  geom_raster(aes(x = east.agg, y = north.agg, fill = qres)) +
  geom_sf(data = swe, fill = NA, colour = "black") +
  scale_fill_continuous_diverging("Blue-Red", mid = 0.5) +
  labs(x = NULL, y = NULL, fill = "Quantile residual")

## -----
726 #| layout-ncol: 2
727 #| fig-width: 4
728 #| fig-height: 4
729 #| fig-height: 4
730 plotResiduals(mod.qres, lichen.usneal$temp, quantreg = TRUE)
731 plotResiduals(mod.qres, lichen.usneal$rain, quantreg = TRUE)
732
733
734
735 #| layout-ncol: 2
736 #| fig-width: 4
737 #| fig-height: 4
738 plotResiduals(mod.qres, lichen.usneal$ndep, quantreg = TRUE)
739 plotResiduals(mod.qres, lichen.usneal$mat, quantreg = TRUE)
740
741
742
743 #| layout-ncol: 2
744 #| fig-width: 4
745 #| fig-height: 4
746 plotResiduals(mod.qres, lichen.usneal$dbh, quantreg = TRUE)
747 plotResiduals(mod.qres, lichen.usneal$cri, quantreg = TRUE)
748
749
750
751 #| layout-ncol: 2
752 #| fig-width: 4

ggplot() +
  geom_raster(aes(x = east.agg, y = north.agg, fill = qres)) +

```

```

811 geom_sf(data = swe, fill = NA, colour = "black") +
812 scale_fill_continuous_diverging("Blue-Red", mid = 0.5) +
813 labs(x = NULL, y = NULL, fill = "Quantile residual")
814
815 ## -----
816
817
818 mod <-
819 gam(occurrence ~
820     s(east, north, k = 60) +
821     mat * ndep +
822     dbh + age,
823     data = lichen.usnea1,
824     family = binomial(link = "logit"),
825     method = "REML")
826
827 summary(mod)
828
829
830 ## -----
831
832 mod.pred <- avg_predictions(mod, by = c("east.agg", "north.agg"))
833
834
835 ggplot(mod.pred) +
836   geom_raster(aes(x = east.agg, y = north.agg, fill = estimate)) +
837   geom_sf(data = swe, fill = NA, colour = "black") +
838   scale_fill_viridis.c() +
839   labs(x = NULL, y = NULL, fill = "Estimated occurrence\nprobability")
840
841 ## -----
842
843 #| fig-width: 10
844 #| fig-height: 5.85
845 mod.qres <- simulateResiduals(mod)
846
847 plot(mod.qres, quantreg = TRUE)
848
849 ## -----
850
851 #| warning: false
852 #| fig-width: 10
853 #| fig-height: 5.85
854 mod.res.agg <- recalculateResiduals(mod.qres, lichen.usnea1$rast.agg.id)
855
856 plot(mod.res.agg, quantreg = TRUE)
857
858
859 ## -----
860
861 testSpatialAutocorrelation(mod.qres, lichen.usnea1$east, lichen.usnea1$north)
862
863 ## -----
864
865 lichen.usnea1[, qres := residuals(mod.qres)]
866
867 lichen.usnea1[,
868   .(qres = mean(qres)),
869   by = c("east.agg", "north.agg")] |>

```

```

869 ggplot() +
870   geom_raster(aes(x = east.agg, y = north.agg, fill = qres)) +
871   geom_sf(data = swe, fill = NA, colour = "black") +
872   scale_fill_continuous_diverging("Blue-Red", mid = 0.5) +
873   labs(x = NULL, y = NULL, fill = "Quantile residual")
874
875 ## -----
876
877 lichen.usnea <- lichen[species == "Usnea"]
878
879 mod <-
880   gam(occurrence ~
881     s(east, north, by = ip, k = 60) +
882     temp * rain +
883     mat * ndep +
884     dbh + c1l +
885     bas + age,
886     data = lichen.usnea,
887     family = binomial(link = "logit"),
888     method = "REML")
889
890 summary(mod)
891
892 ## -----
893
894 mod.pred <- avg_predictions(mod, by = c("east.agg", "north.agg", "ip"))
895
896
897 ggplot(mod.pred) +
898   geom_raster(aes(x = east.agg, y = north.agg, fill = estimate)) +
899   geom_sf(data = swe, fill = NA, colour = "black") +
900   scale_fill_viridis.c() +
901   facet_wrap(vars(ip)) +
902   labs(x = NULL, y = NULL, fill = "Estimated occurrence\nprobability")
903
904 ## -----
905
906 #| fig-width: 10
907 #| fig-height: 5.85
908 mod.qres <- simulateResiduals(mod)
909
910 plot(mod.qres, quantreg = TRUE)
911
912 ## -----
913
914 #| warning: false
915 #| fig-width: 10
916 #| fig-height: 5.85
917 mod.res.agg <- recalculateResiduals(mod.qres, lichen.usnea$rast.agg.id)
918
919 plot(mod.res.agg, quantreg = TRUE)
920
921 ## -----
922
923 lichen.usnea[, qres := residuals(mod.qres)]
924
925 lichen.usnea[,
926   .(qres = mean(qres)),

```



```

927 ggplot() +
928   geom_raster(aes(x = east_agg, y = north_agg, fill = qres)) |>
929   geom_sf(data = swe, fill = NA, colour = "black") +
930   scale_fill_continuous_diverging("Blue-Red", mid = 0.5) +
931   facet_wrap(vars(ip)) +
932   labs(x = NULL, y = NULL, fill = "Quantile residual")
933
934
935
936
937
938
939 mod <-
940   gam(occurrence ~
941     s(east, north, by = ip, k = 60) +
942     ti(temp, k = 5) +
943     ti(rain, k = 5) +
944     ti(temp, rain, k = c(5, 5)) +
945     s(mat) +
946     s(ndep) +
947     s(dbh) +
948     s(crl) +
949     s(bas) +
950     s(age),
951     data = lichen.usnea,
952     family = binomial(link = "logit"),
953     method = "REML",
954     select = TRUE,
955     optimizer = "ef5")
956
957 summary(mod)
958
959
960 mod_pred <- avg_predictions(mod, by = c("east_agg", "north_agg", "ip"))
961
962 ggplot(mod_pred) +
963   geom_raster(aes(x = east_agg, y = north_agg, fill = estimate)) +
964   geom_sf(data = swe, fill = NA, colour = "black") +
965   scale_fill_viridis_c() +
966   facet_wrap(vars(ip)) +
967   labs(x = NULL, y = NULL, fill = "Estimated occurrence\probability")
968
969
970
971 #| fig-width: 10
972 #| fig-height: 5.85
973 mod_qres <- simulateResiduals(mod)
974
975 plot(mod_qres, quantreg = TRUE)
976
977
978
979 #| warning: false
980 #| fig-width: 10
981 #| fig-height: 5.85
982 mod_res_agg <- recalculateResiduals(mod_qres, lichen.usnea$rast_agg_id)
983
984 plot(mod_res_agg, quantreg = TRUE)

```

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```

```

## -----
## lichen.usnea[, qres := residuals(mod.qres)]
##
lichen.usnea[,
  .(qres = mean(qres)),
  by = c("ip", "east_agg", "north_agg")] |>
ggplot() +
  geom_raster(aes(x = east_agg, y = north_agg, fill = qres)) +
  geom_sf(data = swe, fill = NA, colour = "black") +
  scale_fill_continuous_diverging("Blue-Red", mid = 0.5) +
  facet_wrap(vars(ip)) +
  labs(x = NULL, y = NULL, fill = "Quantile residual")
## -----
##
gratia::draw(mod, rug = FALSE, select = 1:2)
## -----
##
gratia::draw(mod, rug = FALSE, select = 3:5)
## -----
##
#| fig-height: 3
gratia::draw(mod, rug = FALSE, select = 6:7)
## -----
##
#| fig-height: 3
gratia::draw(mod, rug = FALSE, select = 8:9)
## -----
##
#| fig-height: 3
gratia::draw(mod, rug = FALSE, select = 10:11)
## -----
##
sessionInfo()
## -----
##
#| include: false
knitr::purl(input = "cef_dharma.qmd", output = "cef_dharma.R")

```