Appendix C: Model diagnosis

Population aboveground mass and stand density

```
#### Did crop identity and corn weed management affect AMATA aboveground mass in 2018? ####

pop_biom18 <- lm(log(g_m_sq + 0.00025) ~ Block + Crop_ID*Corn_weed_management,
                 data = amata18)
resid_panel(pop_biom18)
```
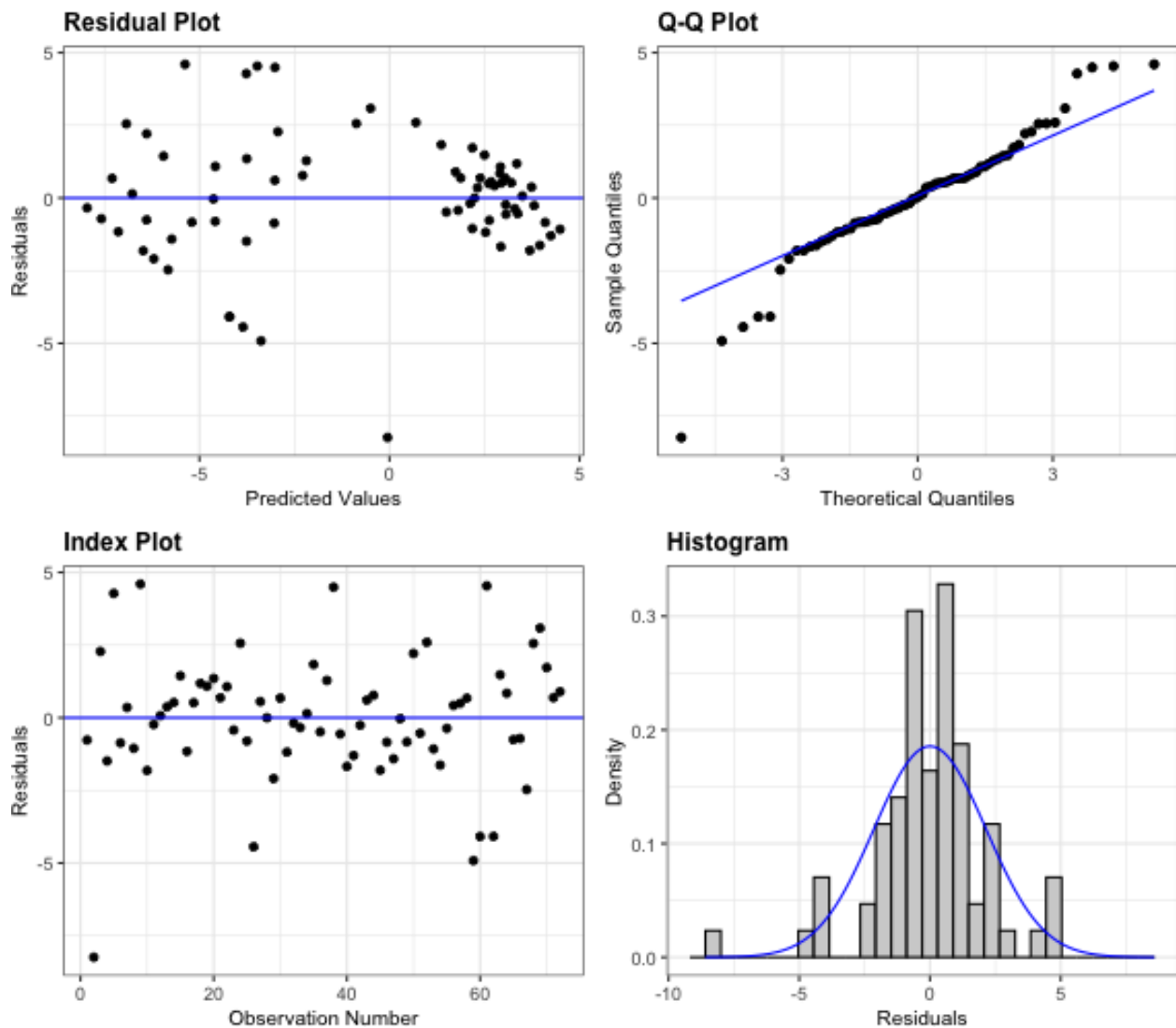
Figure 1: Diagnosis plot for a model of the effects of crop identity and corn weed management on 2018 population aboveground mass.

```
#### Did crop identity and corn weed management affect AMATA aboveground mass in 2018? ####

pop_biom19<- lm(log(g_m_sq + 0.002) ~ Block + Crop_ID*Corn_weed_management,
                data = amata19)
```
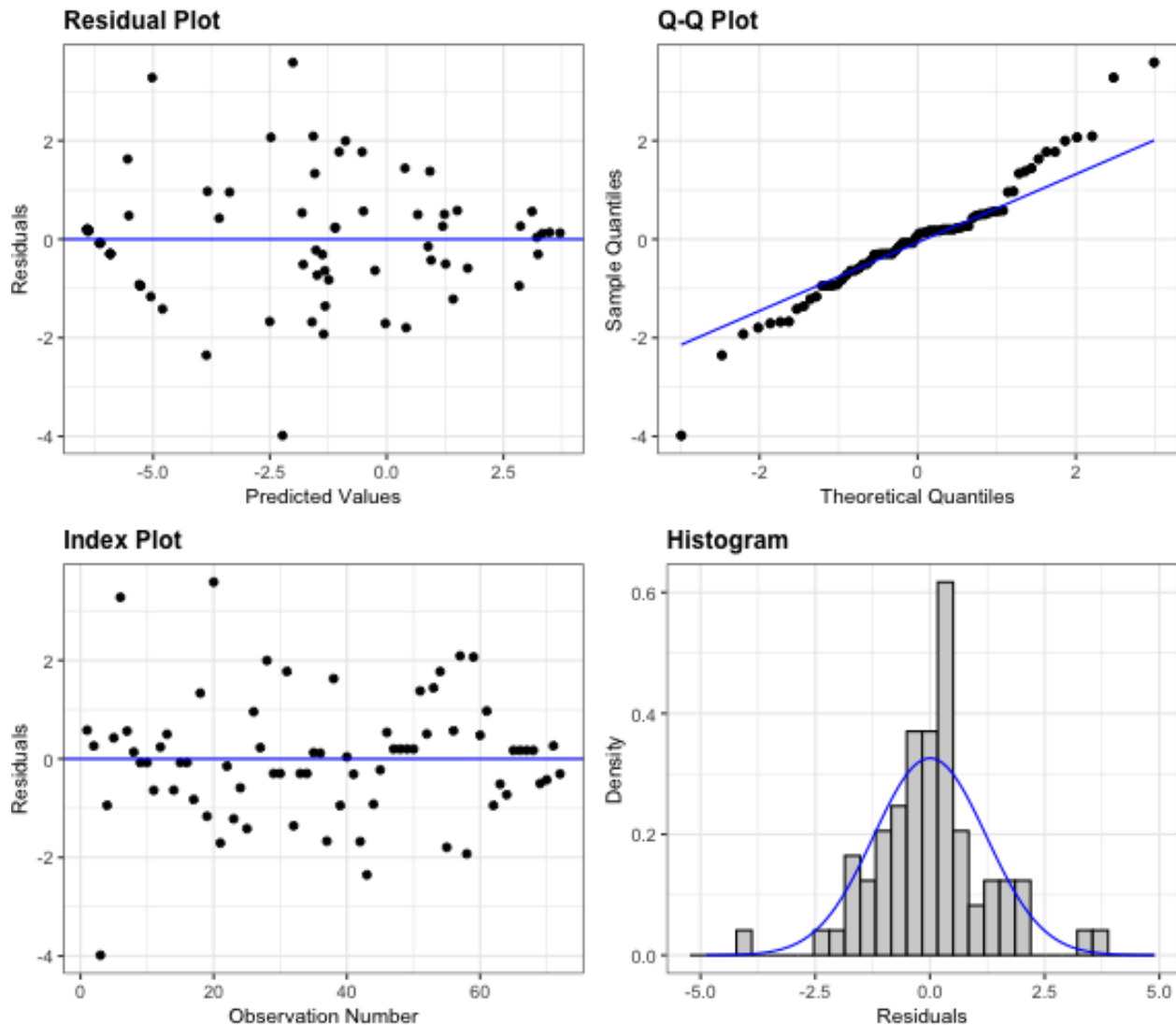
1

```
resid_panel(pop_biom19)
```


Figure 2: Diagnosis plot for a model of the effects of crop identity and corn weed management on 2019 population aboveground mass.

```
#### Did crop identity and corn weed management affect AMATA density in 2018? ####

pop_dens18 <- lm(log(plant_m_sq + 0.025) ~ Block + Crop_ID*Corn_weed_management,
                 data = amata18)

resid_panel(pop_dens18)
```

```
#### Did crop identity and corn weed management affect AMATA density in 2019? ####
pop_dens19 <- lm(log(plant_m_sq + 0.025) ~ Block + Crop_ID*Corn_weed_management,
                 data = amata19)

resid_panel(pop_dens19)
```
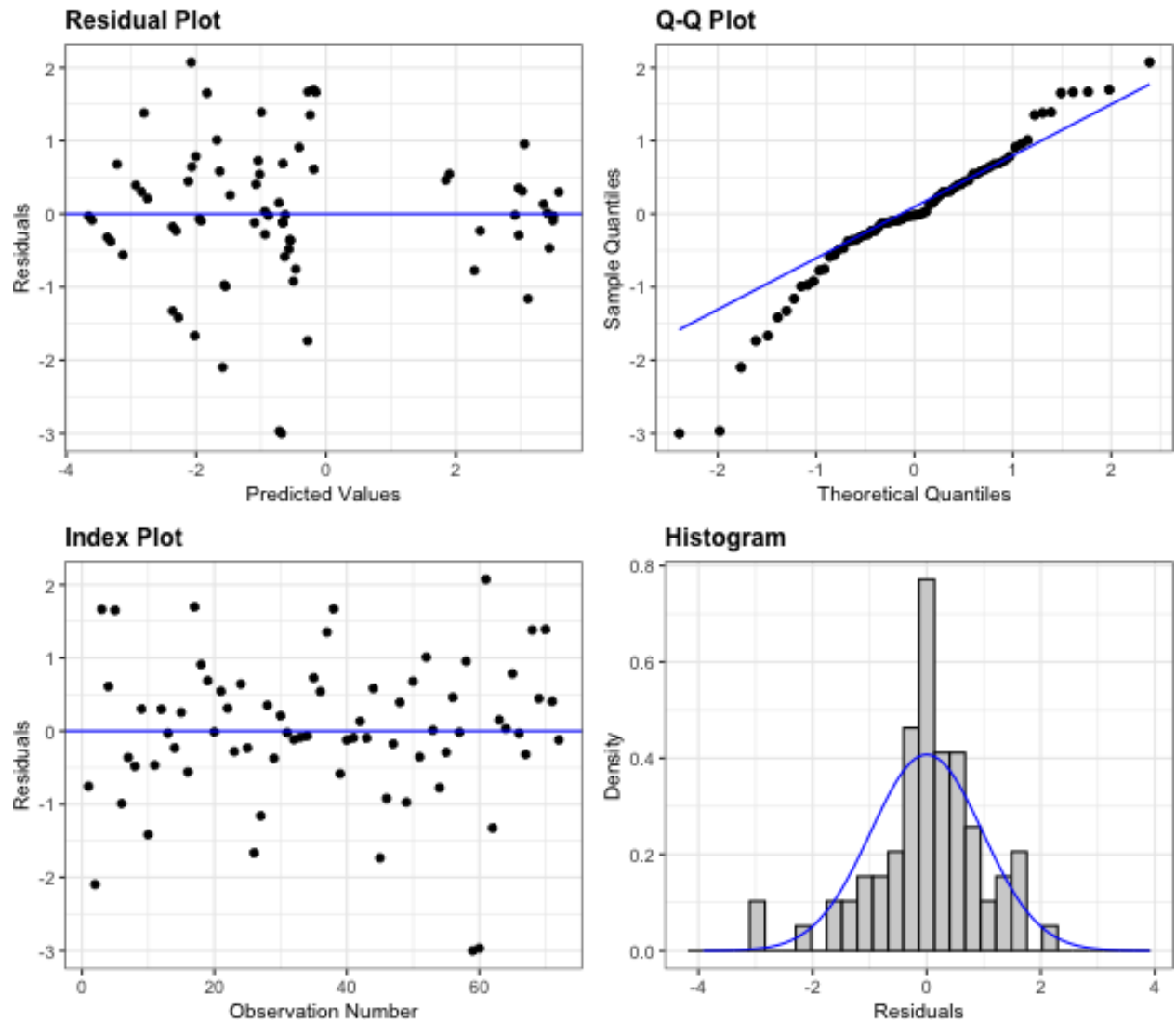
Figure 3: Diagnosis plot for a model of the effects of crop identity and corn weed management on 2018 population density.
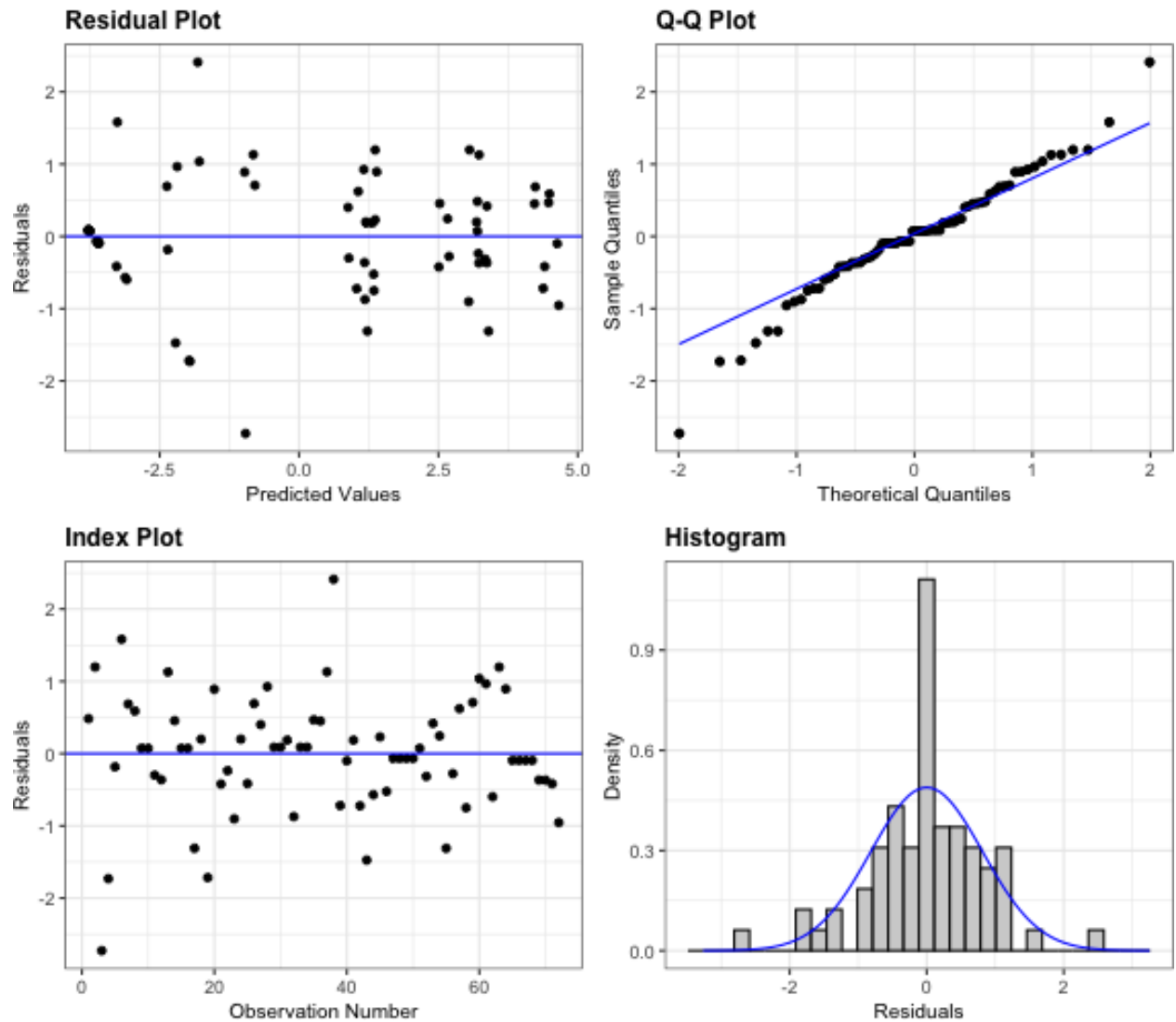
Figure 4: Diagnosis plot for a model of the effects of crop identity and corn weed management on 2019 population density.

Population sex ratio

```
#### Did crop identity and corn weed management had any effect on 2018 population sex ratio? ####
sexed18.glm <- glm(cbind(Female, Male) ~ Block + Crop_ID*Corn_weed_management,
  data=amata18, family=quasibinomial(link = "logit"))

glm.diag.plots(sexed18.glm) #in boot package
```
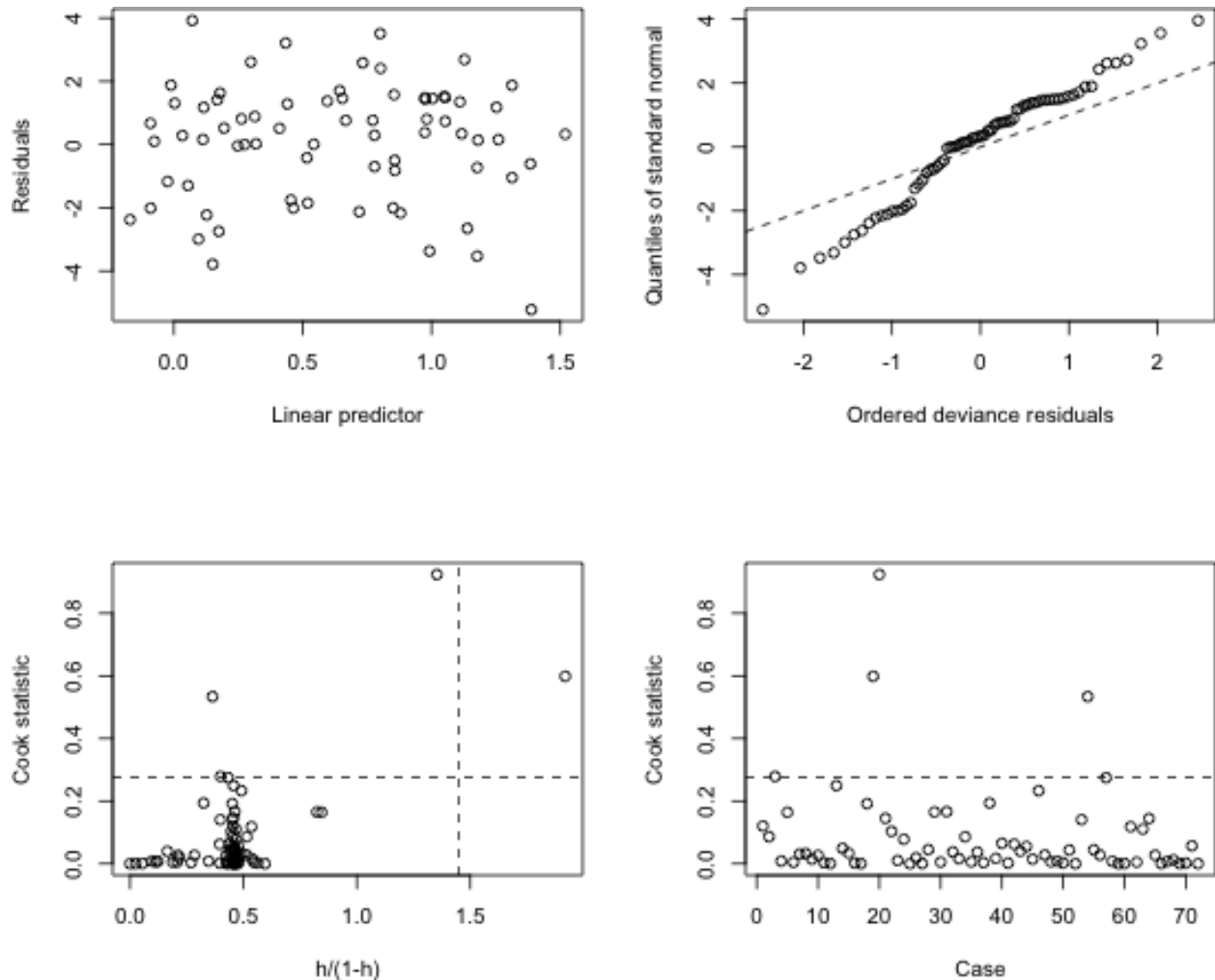

Figure 5: Diagnosis plot for a model of the effects of crop identity, corn weed management, and population aboveground mass on 2018 population sex ratio. Deviance = 165.91.

```
# deviance(sexed18.glm) # 165.9

#### Did population aboveground mass, crop identity and corn weed management had any effect on 2018 popu

sexr18_biom_glm <- glm(cbind(Female, Male) ~ Block +  Crop_ID + Corn_weed_management +
                        log(g_m_sq + 0.00025) +
                      Crop_ID:Corn_weed_management +
                      log(g_m_sq + 0.00025):Crop_ID +
                      log(g_m_sq + 0.00025):Corn_weed_management +
                      log(g_m_sq + 0.00025):Crop_ID:Corn_weed_management ,
```

```
    data=amata18, family=quasibinomial(link = "logit"))
```
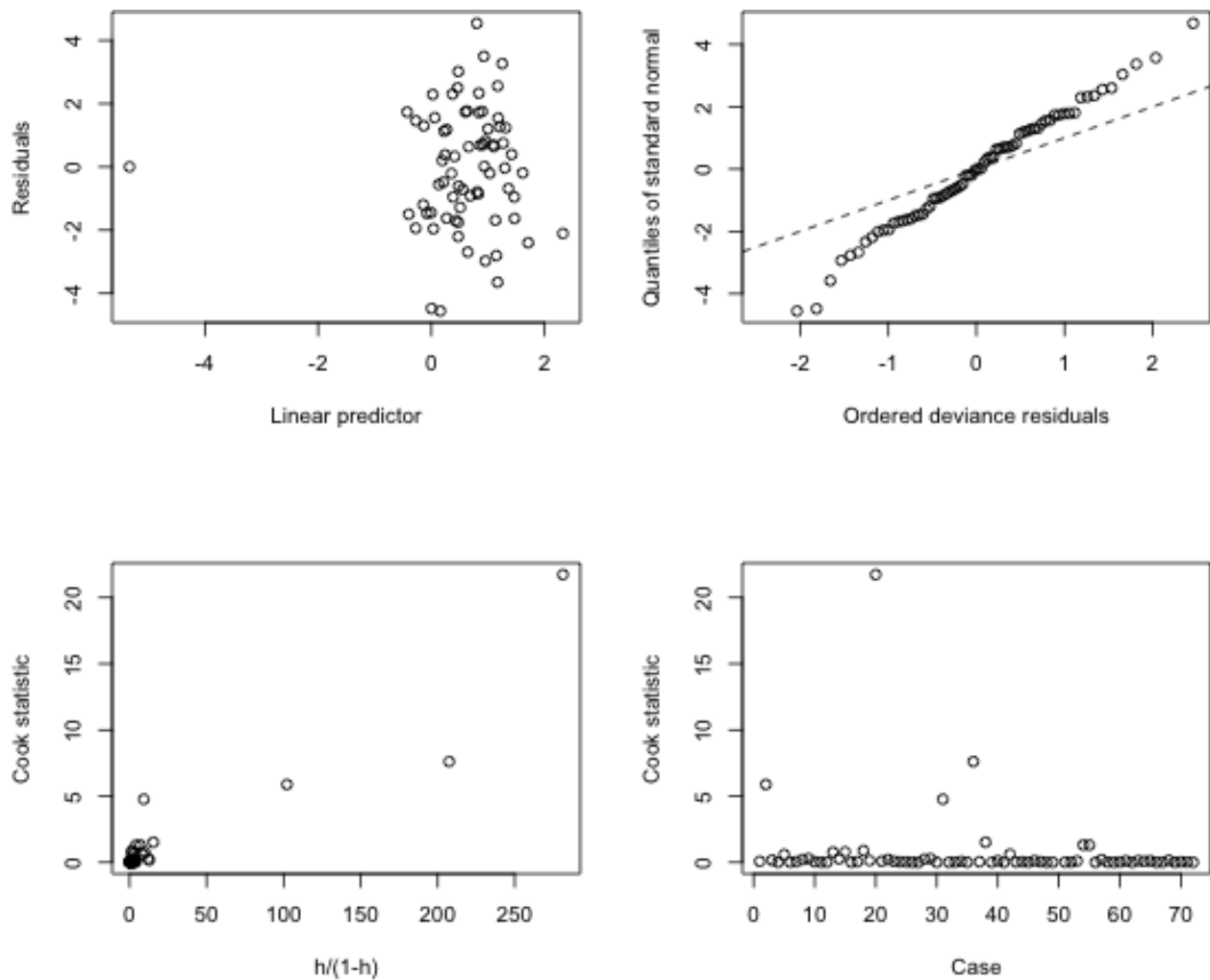
```
glm.diag.plots(sexr18_biom_glm)
```


Figure 6: Diagnosis plot for a model of the effects of crop identity, corn weed management, and population aboveground mass on 2018 population sex ratio. Deviance = 104.26.

```
#deviance(sexr18_biom_glm3) # 104.256
```

```
#### Did crop identity, corn weed management and plant density affect AMATA aboveground mass in 2018? #
```

```
sexr18_dens_glm3 <- glm(cbind(Female, Male) ~ Block  + Crop_ID + Corn_weed_management +
                        + log(plant_m_sq + 0.025)  +
                    Crop_ID:Corn_weed_management +
                    log(plant_m_sq + 0.025):Crop_ID +
                    log(plant_m_sq + 0.025):Corn_weed_management +
                    log(plant_m_sq + 0.025):Crop_ID:Corn_weed_management ,
  data=amata18, family=quasibinomial(link = "logit"))
```
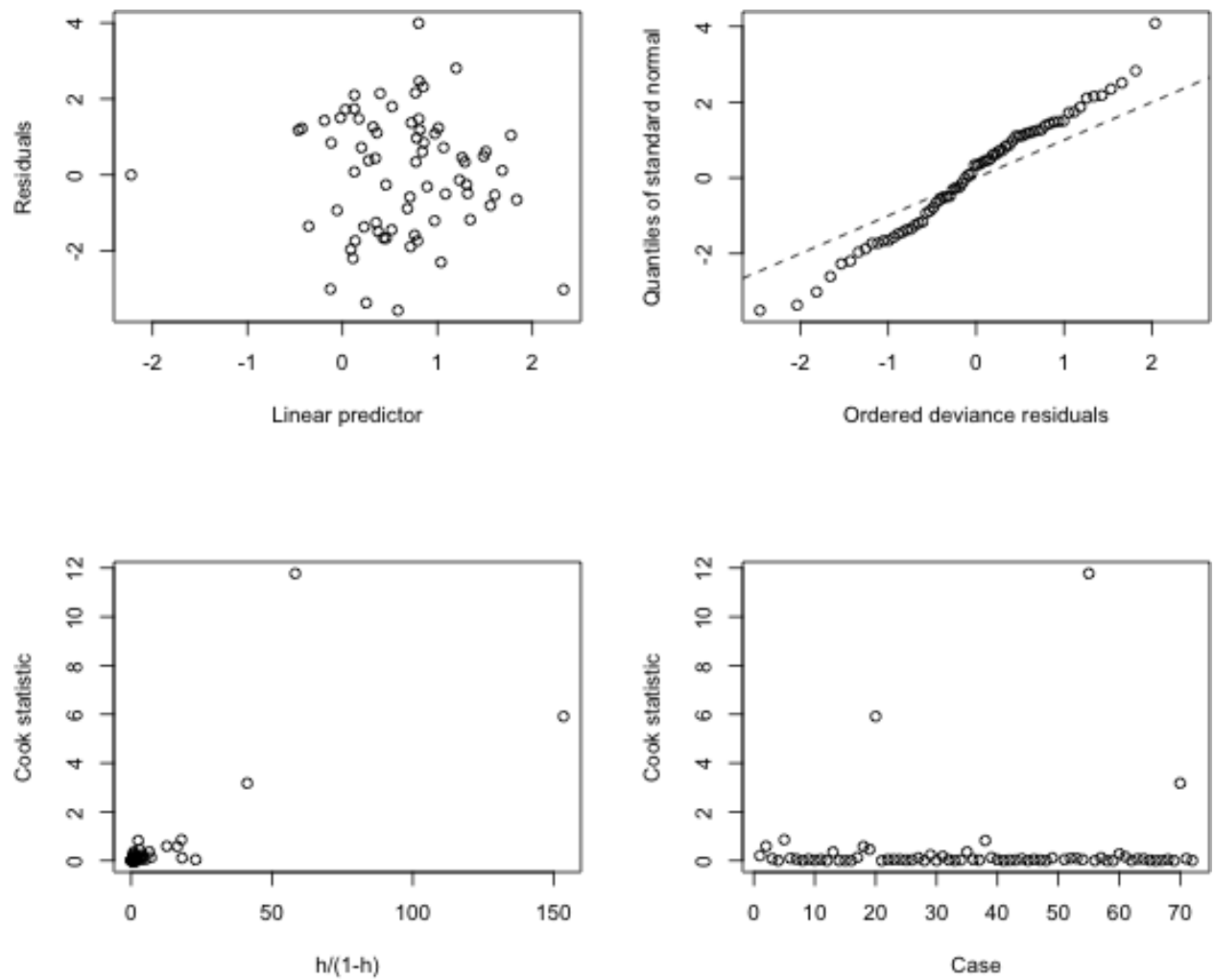
```
glm.diag.plots(sexr18_dens_glm3)
```

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Figure 7: Diagnosis plot for a model of the effects of crop identity, corn weed management, and population density on 2018 population sex ratio. Deviance = 82.12.

```
# GLM link function explained <http://web.pdx.edu/~newsomj/cdaclass/ho_glm.pdf>

# deviance(sexr18_dens_glm3 )   # = 82.12
```

Individual female aboveground mass and fecundity

```
#### Did crop identity and corn weed management affect individual aboveground mass? ####
# Keep rows with no NAs only, fecundity18_b for Biomass

fecundity18_b <- fecundity18[complete.cases(fecundity18$Biomass), ]
# min(fecundity18_b$Biomass[fecundity18_b$Biomass > 0])

biomass.gls <- gls(log(Biomass + 0.005) ~ Block + Crop_ID +
                    Corn_weed_management + Crop_ID:Corn_weed_management,
                  correlation=corCompSymm(form= ~1 | bt), #identifies each treatment within block
  data=fecundity18_b)

# Ho testing reference <http://web.pdx.edu/~newsomj/cdaclass/ho_glm.pdf>

diag_biom(biomass.gls, tag= "")

#### Did crop identity and corn weed management affect individual fecundity? {-}

# Keep rows with no NAs only, fecundity18_s for Number of seeds
fecundity18_s <- fecundity18[complete.cases(fecundity18$Seed), ]

# min(fecundity18_s$Seed[fecundity18_s$Seed > 0])

seeds.gls <- gls(log(Seed + 1) ~ Block +
                  Crop_ID*Corn_weed_management,
                correlation=corCompSymm(form= ~1 | bt), #identifies each treatment within block
  data=fecundity18_s)

diag_seed(seeds.gls , tag= "")

### 18-mean full compound symmetry model
#### Did crop identity, corn weed management, and individual aboveground mass affect AMATA aboveground
fecundity18_sb <- fecundity18[complete.cases(fecundity18$Seed, fecundity18$Biomass), ]

#log(fecundity18_sb$Biomass )
allcrops.biom.seed.gls <- gls(log(Seed+1) ~ Block + log(Biomass + 0.005) +
                              Crop_ID + Corn_weed_management +
                    Crop_ID:Corn_weed_management +
                    Crop_ID:log(Biomass + 0.005) +
                      Corn_weed_management:log(Biomass + 0.005) +
                    Crop_ID:Corn_weed_management:log(Biomass + 0.005),
  correlation=corCompSymm(form= ~1 | bt), #identifies each treatment within block
  data=fecundity18_sb)

diag_seed(allcrops.biom.seed.gls, tag = "")
```
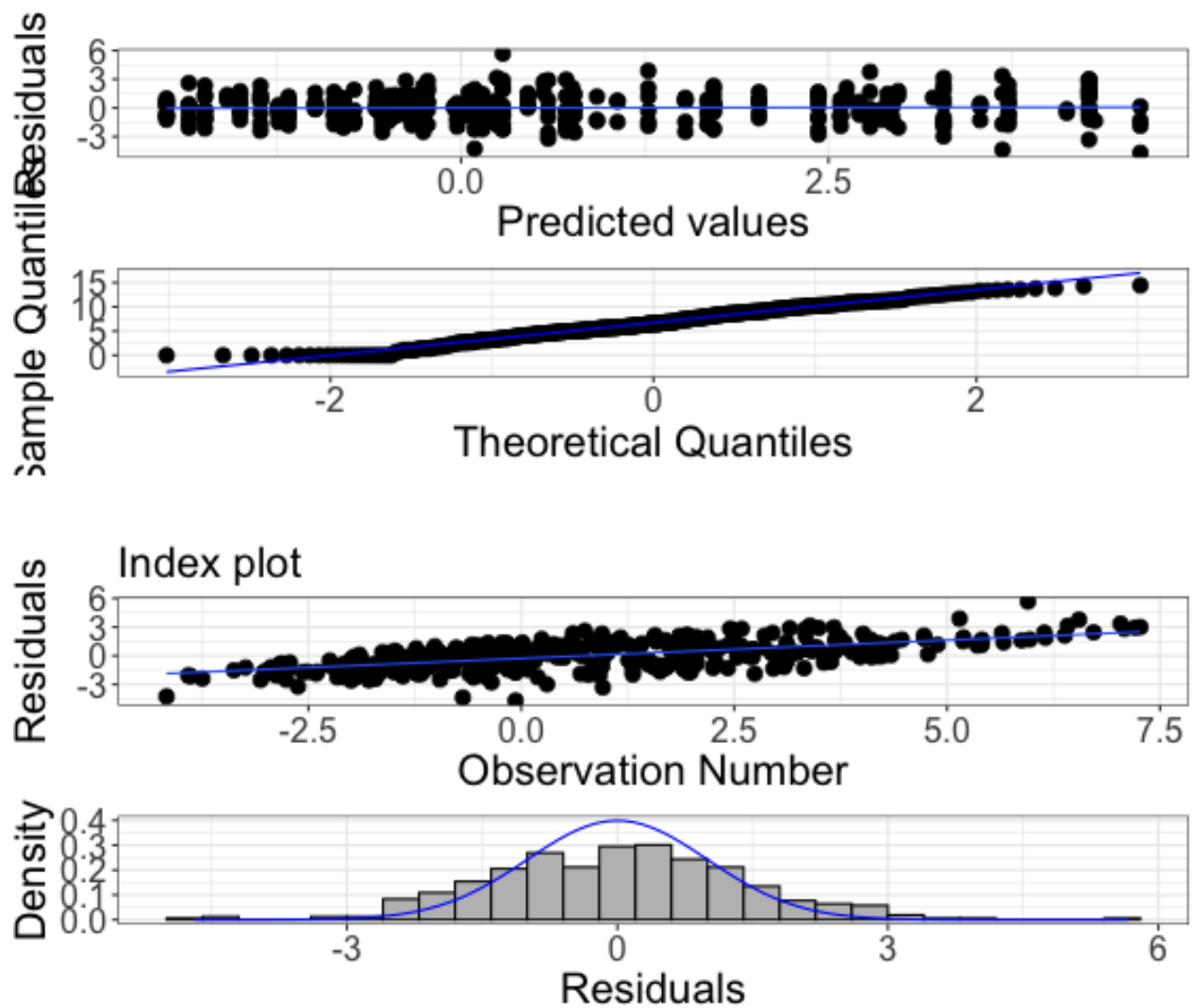
Figure 8: Diagnosis plot for a model of crop identity and corn weed management effects on individual biomass.
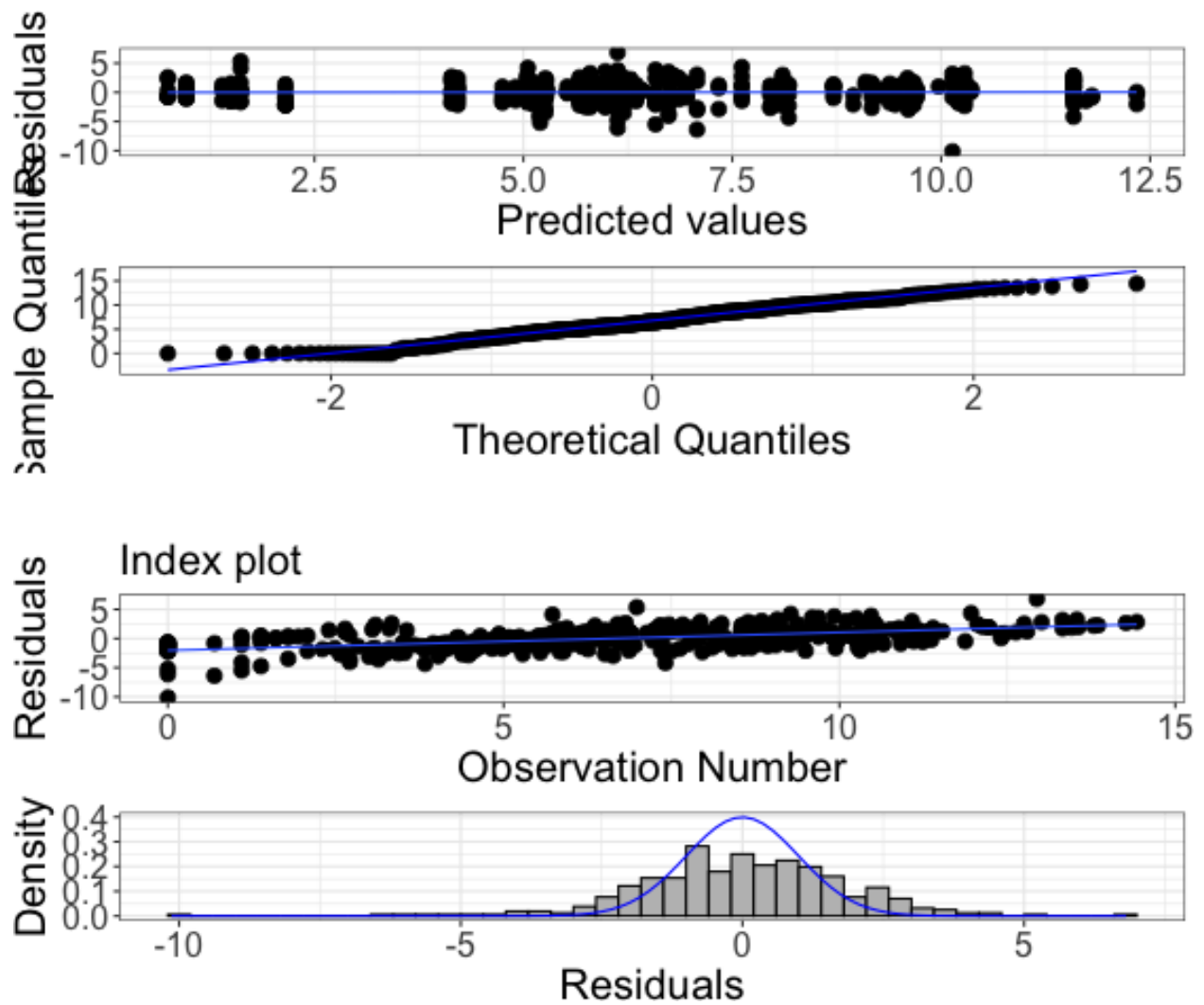
Figure 9: Diagnosis plot for a model of crop identity and corn weed management effect on individual fecundity.
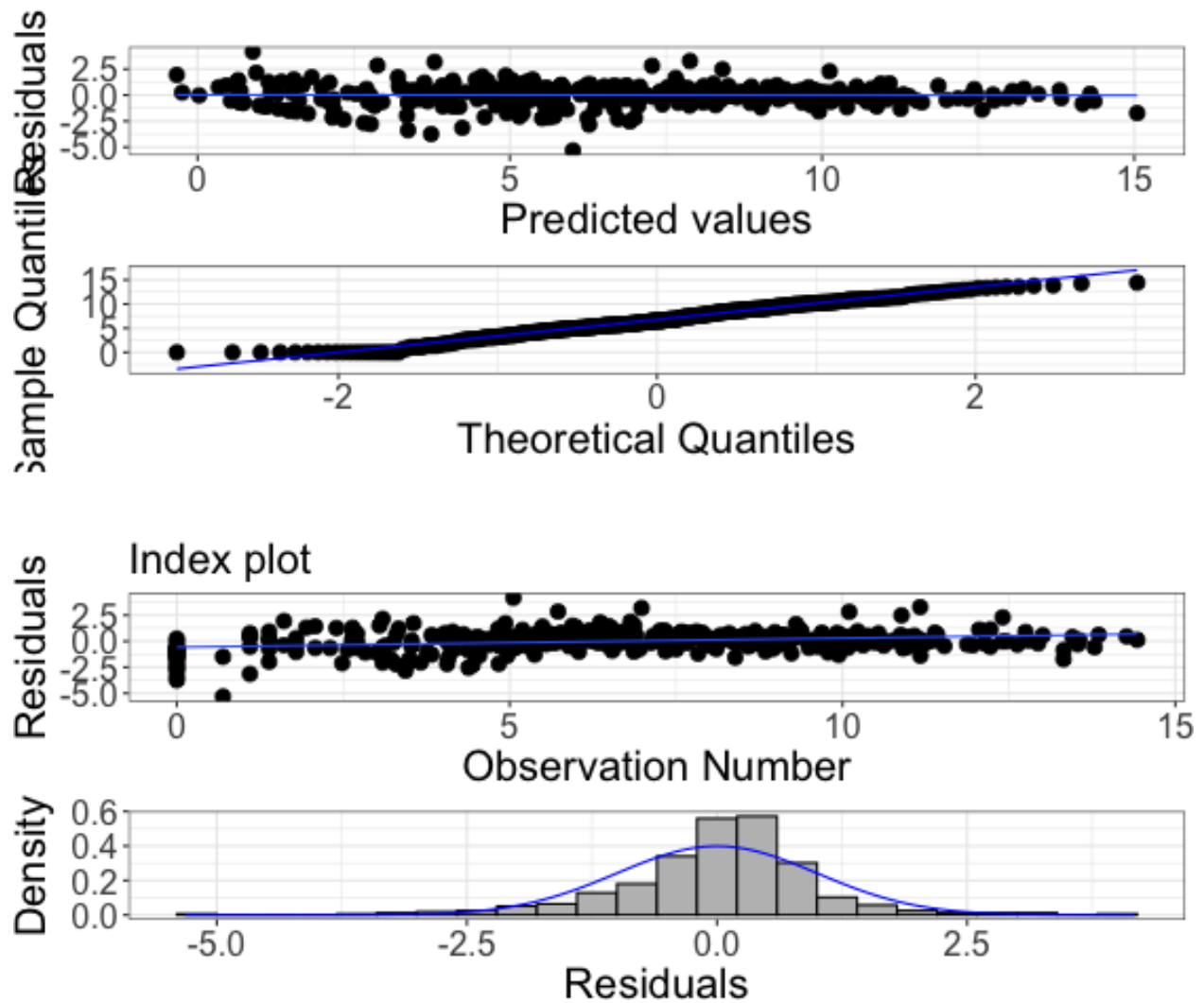
Figure 10: Diagnosis plot for a model of crop identity and corn weed management effect on individual fecundity.