

```

> m1=glmm(N_niphargus~Pre.Post_COVID_LOCKDOWN+s(Date_n,k=5)+Area+Dist_ingresso,random=list(Site.sampled.name=~1),family=quasipoisson,data=Dati_totali)

Maximum number of PQL iterations: 20
iteration 1
iteration 2
iteration 3
iteration 4
iteration 5
> summary(m1$gam)

Family: quasipoisson
Link function: log

Formula:
N_niphargus ~ Pre.Post_COVID_LOCKDOWN + s(Date_n, k = 5) + Area +
  Dist_ingresso

Parametric coefficients:

              Estimate Std. Error t value Pr(>|t|)
(Intercept)   -0.181616    0.408061  -0.445    0.6571
Pre.Post_COVID_LOCKDOWNpost  0.405293    0.366670   1.105    0.2714
Area           0.052962    0.046510   1.139    0.2573
Dist_ingresso  -0.004287    0.002091  -2.050    0.0427 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:
              edf Ref.df    F p-value
s(Date_n)    1      1 3.09 0.0815 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.0369
Scale est. = 1.5817    n = 115
> (((exp(0.405293-0.181616)-exp(-0.181616))/exp(-0.181616))*100
[1] 49.97419

```

The dependent variable is the number of Niphargus crustaceans; other than the period pre/post lockdown we considered also the area of the site and the distance of the site from the cave entrance. As random factors we considered the cave, the year and the survey.

```
> m2=gamm(N_dendrocoelum~Pre.Post_COVID_LOCKDOWN+s(Date_n,k=5)+Area+Dist_ingresso,random=list(Site.sampled.name=~1),family=quasipoisson,data=Dati_totali)
```

```
Maximum number of PQL iterations: 20
```

```
iteration 1
iteration 2
iteration 3
iteration 4
iteration 5
iteration 6
iteration 7
iteration 8
```

```
> summary(m2$gam)
```

```
Family: quasipoisson
```

```
Link function: log
```

```
Formula:
```

```
N_dendrocoelum ~ Pre.Post_COVID_LOCKDOWN + s(Date_n, k = 5) +
  Area + Dist_ingresso
```

```
Parametric coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-0.7622808	0.6582769	-1.158	0.2497
Pre.Post_COVID_LOCKDOWNpost	-0.6987586	0.3753774	-1.861	0.0656
Area	0.0299599	0.0710952	0.421	0.6744
Dist_ingresso	0.0002528	0.0028326	0.089	0.9291

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Approximate significance of smooth terms:
```

	edf	Ref.df	F	p-value
s(Date_n)	1	1	0.004	0.949

```
R-sq.(adj) = -0.0275
```

```
Scale est. = 1.2292    n = 104
```

```
> (((exp(-0.6987586-0.7622808 )-exp(-0.7622808 ))/exp(-0.7622808 )))*100
```

```
[1] -50.27979
```

The dependent variable is the number of Dendrocoelum flatworms; other than the period pre/post lockdown we considered also the area of the site and the distance of the site from the cave entrance. As random factors we considered the site.

```

> m3=gamm(N_monolistra~Pre.Post_COVID_LOCKDOWN+s(Date_n,k=4)+Area+Dist_ingresso,random=list(Site.sampled.name=~1),family=quasipoisson,data=Dati_totali)

Maximum number of PQL iterations: 20
iteration 1
iteration 2
iteration 3
iteration 4
iteration 5
> summary(m3$gam)

Family: quasipoisson
Link function: log

Formula:
N_monolistra ~ Pre.Post_COVID_LOCKDOWN + s(Date_n, k = 4) + Area +
  Dist_ingresso

Parametric coefficients:

              Estimate Std. Error t value Pr(>|t|)
(Intercept)   -11.260579    4.610038  -2.443  0.02060 *
Pre.Post_COVID_LOCKDOWNpost  0.868132    0.403994   2.149  0.03972 *
Area           0.743780    0.251060   2.963  0.00588 **
Dist_ingresso  0.025835    0.009573   2.699  0.01126 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

              edf Ref.df    F p-value
s(Date_n) 2.589  2.589 5.354  0.0366 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.463
Scale est. = 5.2575    n = 37
> (((exp(0.868132-11.260579)-exp(-11.260579))/exp(-11.260579)))*100
[1] 138.2456

```

The dependent variable is the number of *Monolistra pavani*; other than the period pre/post lockdown we considered also the area of the site and the distance of the site

```

> m4<-glmmPQL(Bufo.bufo~Pre.Post_COVID_LOCKDOWN,family=quasipoisson,random=~1|Locality,data=R2_Mortality_amphibiansreptiles)
iteration 1
iteration 2
iteration 3
iteration 4
> summary(m4)
Linear mixed-effects model fit by maximum likelihood
Data: R2_Mortality_amphibiansreptiles
   AIC BIC logLik
   NA  NA    NA

Random effects:
Formula: ~1 | Locality
      (Intercept) Residual
StdDev:   0.3621409 4.110145

Variance function:
Structure: fixed weights
Formula: ~invwt
Fixed effects: Bufo.bufo ~ Pre.Post_COVID_LOCKDOWN
              Value Std.Error DF   t-value p-value
(Intercept)   3.922648  0.2776719   6 14.126921   0.000
Pre.Post_COVID_LOCKDOWNduring -2.670002  0.9181186   6 -2.908123   0.027
Correlation:
              (Intr)
Pre.Post_COVID_LOCKDOWNduring -0.214

Standardized Within-Group Residuals:
      Min       Q1       Med       Q3      Max
-1.2733031 -0.5353301 -0.2722460  0.1955929  2.1989425

Number of Observations: 14
Number of Groups: 7

```

Mortality Bufo bufo

```
> m5<-glm(N~COVID_LOCKDOWN+Habitat,family=quasipoisson,data=R3_Porcupine_Italy)
> summary(m5)
```

Call:

```
glm(formula = N ~ COVID_LOCKDOWN + Habitat, family = quasipoisson,
     data = R3_Porcupine_Italy)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.52792	-0.45927	-0.00225	0.36086	0.51458

We analysed the number of Porcupine observed in urban and not urban environments.

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.30581	0.08798	3.476	0.00109
COVID_LOCKDOWNDuring	0.17947	0.11790	1.522	0.13450
COVID_LOCKDOWNPost	0.12083	0.11915	1.014	0.31559
HabitatUrban	-0.03043	0.13496	-0.225	0.82257

We tested also the interaction between lockdown period and habitat.

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasipoisson family taken to be 0.1725193)

Null deviance: 8.8347 on 51 degrees of freedom

Residual deviance: 8.4180 on 48 degrees of freedom

AIC: NA

Number of Fisher Scoring iterations: 4