# Accompanying R script for Preuss et al 2021 - Herpetozoa

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## R script and results for 'Lurking in the depth: Pond depth predicts microhabitat selection by Rhinella icterica (Anura: Bufonidae) tadpoles at two different sampling scales'

## Load packages

```
library(car)
```

```
## Loading required package: carData
```

```
library(fitdistrplus)
```

```
## Loading required package: MASS

## Loading required package: survival

## Loading required package: npsurv

## Loading required package: lsei
```

```
library(ggplot2)
library(knitr)
library(spdep)
```

```
## Loading required package: sp

## Loading required package: spData

## To access larger datasets in this package, install the spDataLarge
## package with: `install.packages('spDataLarge',
## repos='https://nowosad.github.io/drat/', type='source')`

## Loading required package: sf

## Warning: package 'sf' was built under R version 3.6.2

## Linking to GEOS 3.7.2, GDAL 2.4.2, PROJ 5.2.0
```

```
library(spind)
```

## Checking for multicollinearity

```
glm.plot <- glm(abundance.parcel ~ leaves.coverage.parcel + substrate.parcel + width + depth.parcel +
                    velocity.parcel + turbidity, data=tadpoles.0, family = gaussian(link = "identity"),
                    na.action=na.fail)
glm.subplot <- glm(abundance.quadrat ~ leaves.coverage.quadrat + substrate.quadrat + width.quadrat +
                    depth.quadrat + velocity.quadrat + turbidity, data=tadpoles.0,
                    family = gaussian(link = "identity"), na.action=na.fail)

vif(glm.plot)
```

```
## leaves.coverage.parcel       substrate.parcel                  width
##               1.956014               2.449776               2.517227
##           depth.parcel        velocity.parcel              turbidity
##               2.168100               1.865063               2.184537
```

```
vif(glm.subplot)
```

```
## leaves.coverage.quadrat       substrate.quadrat           width.quadrat
##                1.524434                2.423308                3.413546
##           depth.quadrat        velocity.quadrat              turbidity
##                4.184284                1.385787                2.734184
```

## Investigating spatial autocorrelation

```
pts.tadpoles <- cbind(x=as.integer(1:20), y=as.integer(1:1))
st_multipoint(pts.tadpoles)
```

```
## MULTIPOINT ((1 1), (2 1), (3 1), (4 1), (5 1), (6 1), (7 1), (8 1), (9 1), (10 1), (11 1), (12 1), (
```

```
row.names(pts.tadpoles) = 1:20
knn.tadpoles <- knearneigh(pts.tadpoles, k=2)
nb.tadpoles <- knn2nb(knn.tadpoles)
listtw.tadpoles <- nb2listw(nb.tadpoles)

(m.plot.mc <- moran.mc(tadpoles.0[,1], listtw.tadpoles, nsim=199, alternative = "greater"))
```

```
##
##  Monte-Carlo simulation of Moran I
##
## data:  tadpoles.0[, 1]
## weights: listtw.tadpoles
## number of simulations + 1: 200
##
## statistic = 0.77538, observed rank = 200, p-value = 0.005
## alternative hypothesis: greater
```

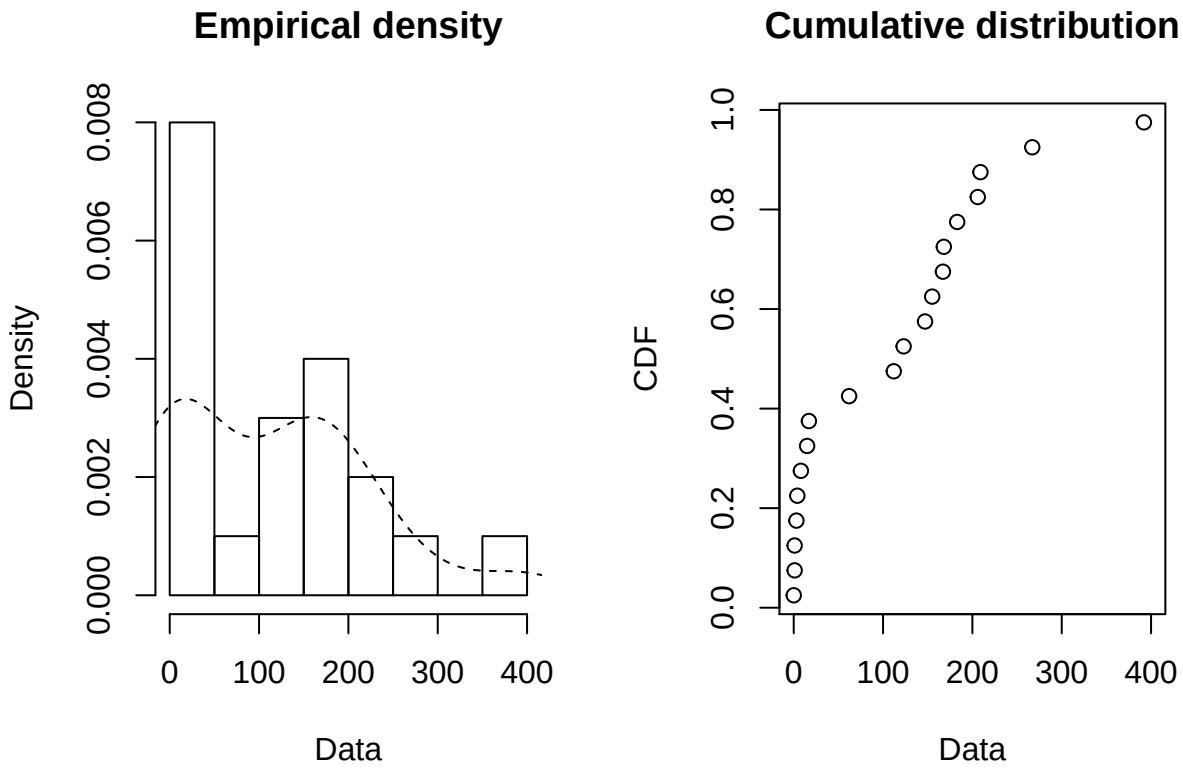
```
(m.subplot.mc <- moran.mc(tadpoles.0[,2], listtw.tadpoles, nsim=199, alternative = "greater"))
```

```
##
##  Monte-Carlo simulation of Moran I
##
## data:  tadpoles.0[, 2]
## weights: listtw.tadpoles
## number of simulations + 1: 200
##
## statistic = 0.87323, observed rank = 200, p-value = 0.005
## alternative hypothesis: greater
```

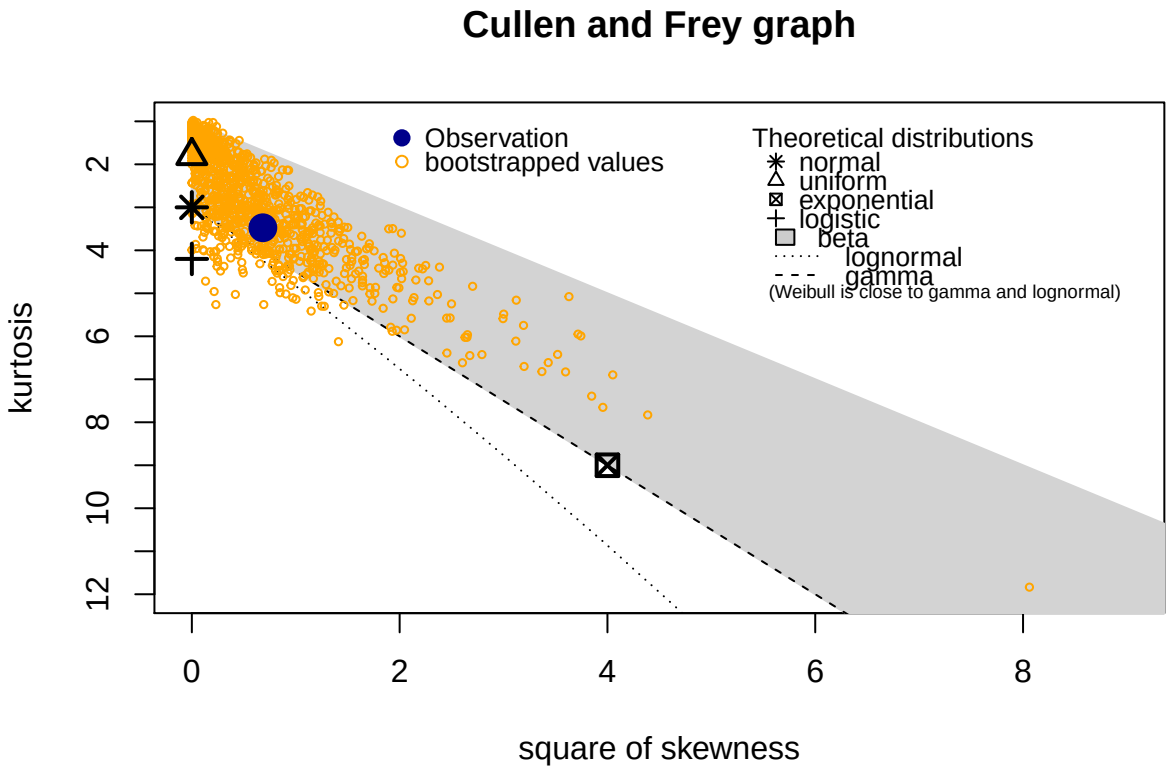
## Data fitting to different distribution families

### Plot level

```
plotdist(tadpoles.0$abundance.parcel, histo = TRUE, demp = TRUE)
```



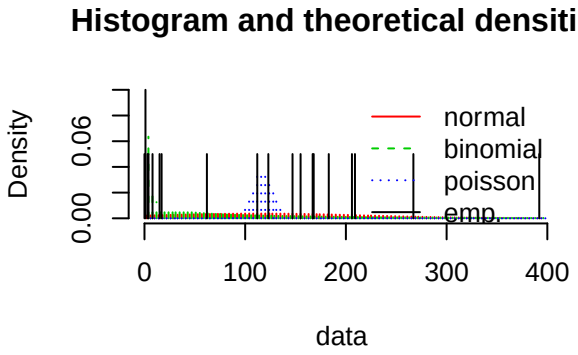

```
descdist(tadpoles.0$abundance.parcel, boot = 1000)
```

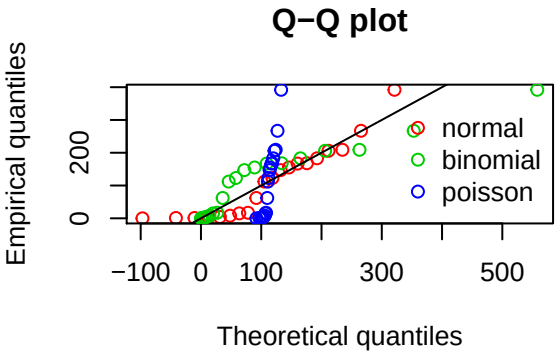


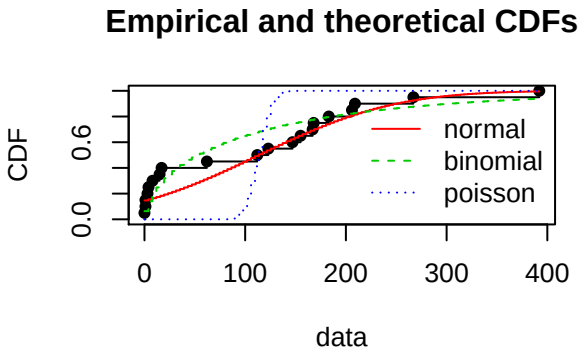

```
## summary statistics
## ------
## min:  0   max:  392
## median:  117.5
## mean:  112
## estimated sd:  109.4359
## estimated skewness:  0.8267059
## estimated kurtosis:  3.475482
```

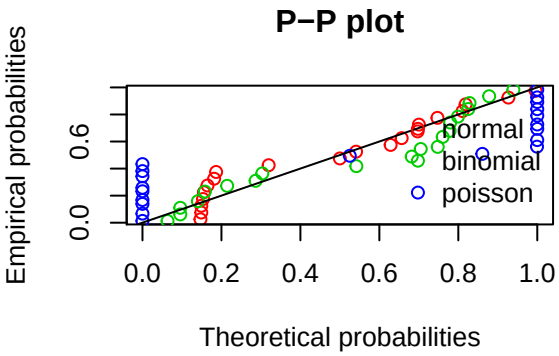
```
tad.normal <- fitdist(tadpoles.0$abundance.parcel, "norm")
tad.binomial <- fitdist(tadpoles.0$abundance.parcel, "nbinom")
tad.poisson <- fitdist(tadpoles.0$abundance.parcel, "pois")

par(mfrow = c(2, 2))
plot.legend <- c("normal", "binomial", "poisson")
denscomp(list(tad.normal, tad.binomial, tad.poisson), legendtext = plot.legend)
qqcomp(list(tad.normal, tad.binomial, tad.poisson), legendtext = plot.legend)
cdfcomp(list(tad.normal, tad.binomial, tad.poisson), legendtext = plot.legend)
ppcomp(list(tad.normal, tad.binomial, tad.poisson), legendtext = plot.legend)
```




```
fit.plot <- gofstat(list(tad.normal, tad.binomial, tad.poisson),
                    fitnames = c("normal", "binomial", "poisson"))
fit.plot$cvm # Cramer-Von Mises
```

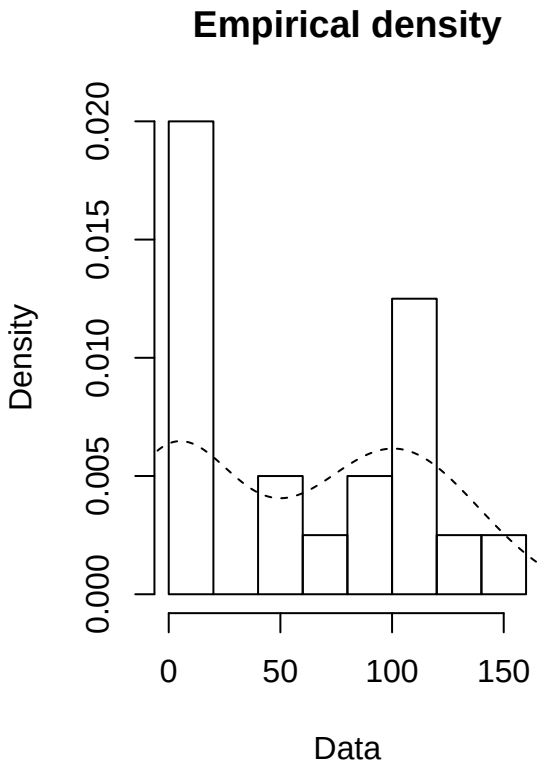
```
##    normal  binomial   poisson
## 0.1201342 0.1796843 1.3301498
```

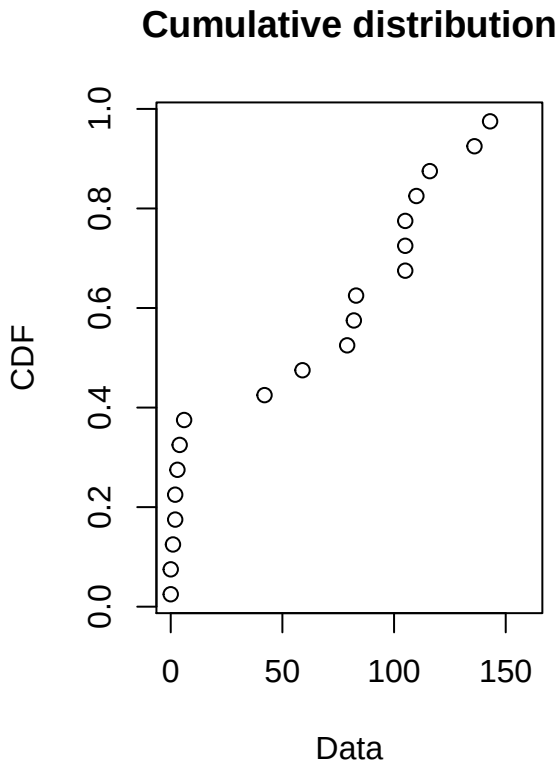
```
fit.plot$ks # Kolmogorov-Smirnov
```

```
##    normal  binomial   poisson
## 0.2134388 0.2320121 0.4499998
```

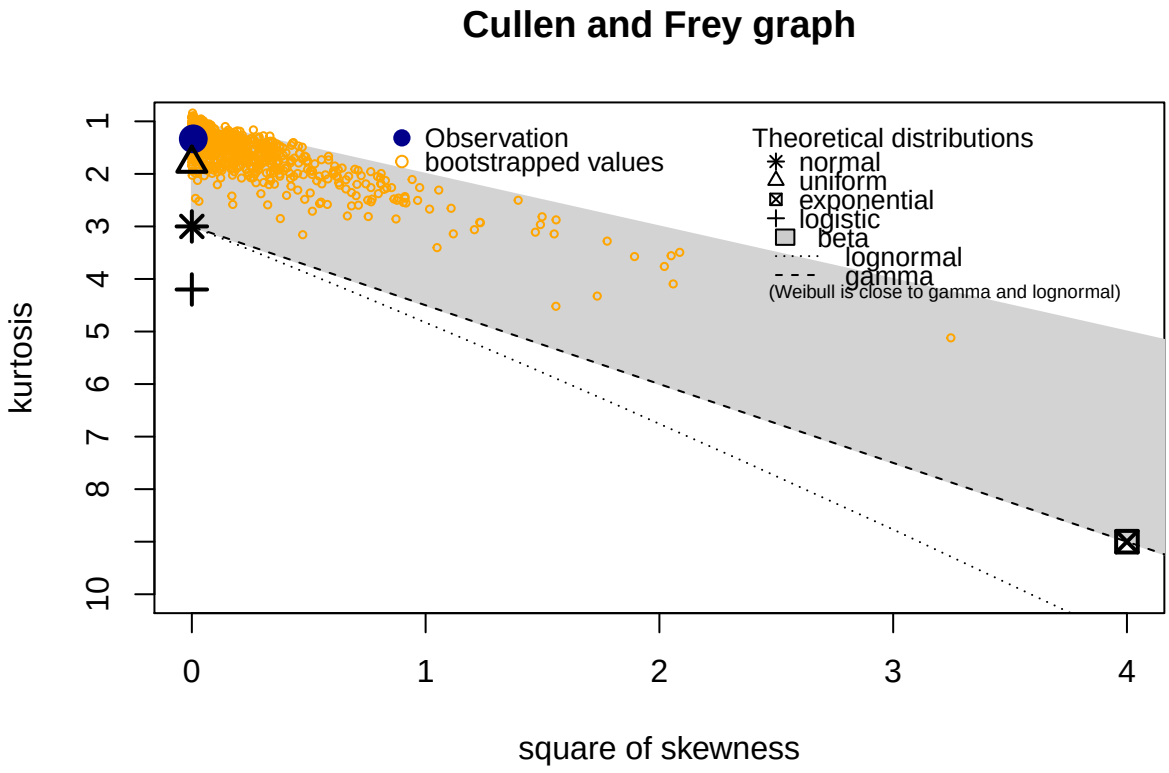
### Subplot level

```
plotdist(tadpoles.0$abundance.quadrat, histo = TRUE, demp = TRUE)
```



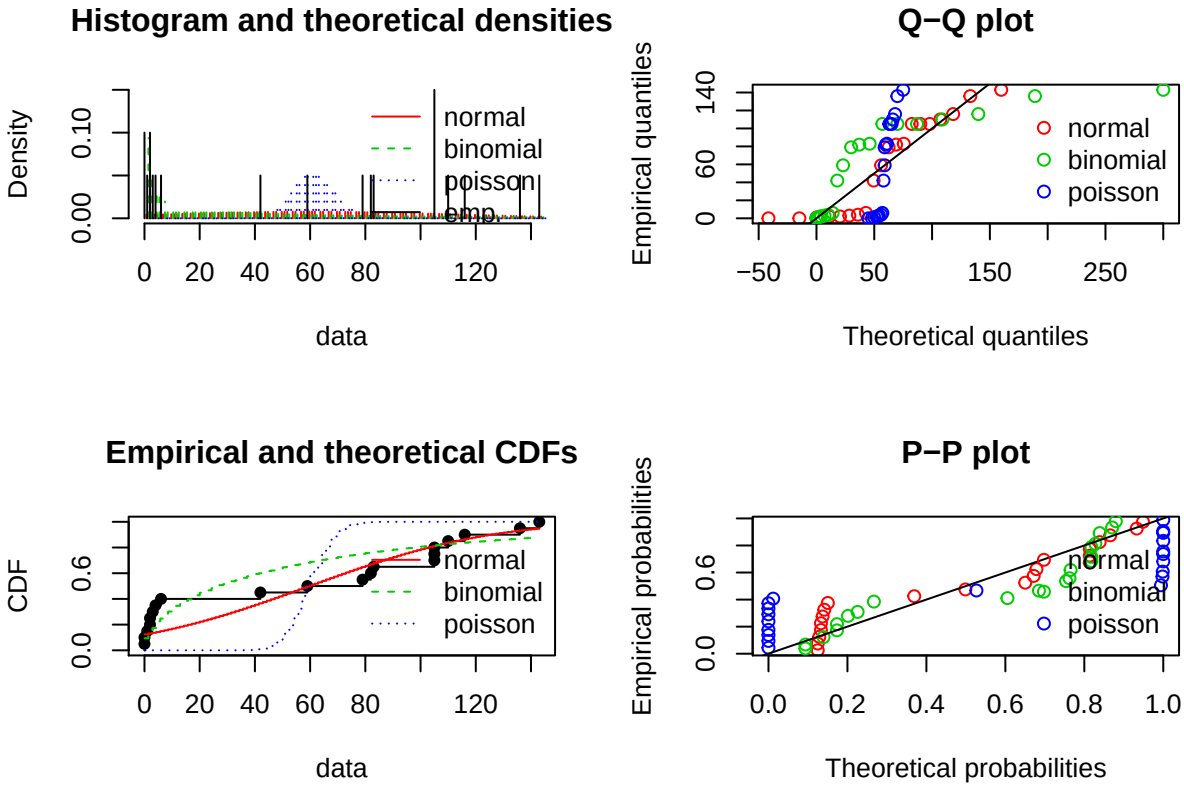

```
descdist(tadpoles.0$abundance.quadrat, boot = 1000)
```




```
## summary statistics
## ------
## min:  0   max:  143
## median:  69
## mean:  59.15
## estimated sd:  52.70102
## estimated skewness:  0.07882528
## estimated kurtosis:  1.333389
```

```
tad.sub.normal <- fitdist(tadpoles.0$abundance.quadrat, "norm")
tad.sub.binomial <- fitdist(tadpoles.0$abundance.quadrat, "nbinom")
tad.sub.poisson <- fitdist(tadpoles.0$abundance.quadrat, "pois")

par(mfrow = c(2, 2))
plot.legend <- c("normal", "binomial", "poisson")
denscomp(list(tad.sub.normal, tad.sub.binomial, tad.sub.poisson), legendtext = plot.legend)
qqcomp(list(tad.sub.normal, tad.sub.binomial, tad.sub.poisson), legendtext = plot.legend)
cdfcomp(list(tad.sub.normal, tad.sub.binomial, tad.sub.poisson), legendtext = plot.legend)
ppcomp(list(tad.sub.normal, tad.sub.binomial, tad.sub.poisson), legendtext = plot.legend)
```




```
fit.sub <- gofstat(list(tad.sub.normal, tad.sub.binomial, tad.sub.poisson),
                   fitnames = c("normal", "binomial", "poisson"))
fit.sub$cvm # Cramer-Von Mises
```

```
##    normal  binomial   poisson
## 0.1914100 0.2670143 1.4256683
```

```
fit.sub$ks # Kolmogorov-Smirnov
```

```
##    normal  binomial   poisson
## 0.2495999 0.2538380 0.4943490
```

# Wavelet-Revised Models

## Plot level

```
pts.tadpoles <- cbind(x=as.integer(1:20), y=as.integer(1:1))
plot.wrm <- WRM(abundance.parcel ~ leaves.coverage.parcel + substrate.parcel + width + depth.parcel +
                  velocity.parcel + turbidity, data=tadpoles.0, family = "gaussian",
                  coord = pts.tadpoles, level = 1, wavelet = "la8", wtrafo = "dwt",
                  moran.params = list(0,1))
sswrm <- step.spind(object = plot.wrm, data = tadpoles.0, AICc=TRUE, trace = FALSE)
sswrm
```

```
## $model
## abundance.parcel ~ substrate.parcel + depth.parcel
##
## $table
##       Deleted.Vars    LogLik      AIC     AICc
## 1           <none> -82.82232 173.6446 176.3113
## 2 substrate.parcel -88.53329 183.0666 184.5666
## 3     depth.parcel -85.15285 176.3057 177.8057
```

```
best.wrm <- WRM(formula = sswrm$model, family="gaussian", data=tadpoles.0, coord=pts.tadpoles,
                level = 1)
summary(best.wrm)
```

```
##
##  Call:
## WRM(formula = sswrm$model, family = "gaussian", data = tadpoles.0,
##     coord = pts.tadpoles, level = 1)
##
##  Pearson Residuals:
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
## -90.0893 -12.7858   0.3403   0.0000  18.2195 111.5593
## ---
##  Coefficients:
##                   Estimate   Std.Err t value  Pr(>|t|)
## (Intercept)      -67.48524  33.76771 -1.9985 0.0619133 .
## substrate.parcel   2.57949   0.61025  4.2269 0.0005677 ***
## depth.parcel       5.93507   2.09736  2.8298 0.0115571 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ---
##  Number of observations n:  20 ,  n.eff:  15 ,  AIC:  174.0188
##
##  Number of iterations:  2
## ---
## Autocorrelation of glm.residuals
##  [1] -0.07446892 -0.20296692 -0.07517668  0.19645107 -0.24201901 -0.34408044
##  [7]  0.07891455  0.21805077 -0.10221289  0.23296475
## Autocorrelation of wavelet.residuals
##  [1] -0.26511129 -0.02233657 -0.09567405  0.19799399 -0.27308701 -0.12828268
##  [7]  0.09313922  0.25300658 -0.17558315  0.18326199
```

## Subplot level

```
subplot.wrm <- WRM(abundance.quadrat ~ leaves.coverage.quadrat + substrate.quadrat + width.quadrat +
                     depth.quadrat + velocity.quadrat + turbidity, data=tadpoles.0,
                     family = "gaussian", coord = pts.tadpoles, level = 1, wavelet = "haar",
                     wtrafo = "dwt", moran.params = list(0,1))
sswrm.sub <- step.spind(object = subplot.wrm, data = tadpoles.0, AICc=TRUE, trace = FALSE)
sswrm.sub
```

```
## $model
```

```
## abundance.quadrat ~ depth.quadrat + turbidity
##
## $table
##    Deleted.Vars    LogLik      AIC     AICc
## 1        <none> -68.17345 144.3469 147.0136
## 2 depth.quadrat -78.36623 162.7325 164.2325
## 3     turbidity -70.11151 146.2230 147.7230
```

```
best.wrm.sub <- WRM(formula = sswrm.sub$model, family="gaussian", data=tadpoles.0,
                    coord=pts.tadpoles, level = 1)
summary(best.wrm.sub)
```

```
##
##  Call:
## WRM(formula = sswrm.sub$model, family = "gaussian", data = tadpoles.0,
##     coord = pts.tadpoles, level = 1)
##
##  Pearson Residuals:
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -23.578 -10.489  -1.795   0.000   8.474  45.889
## ---
##  Coefficients:
##                Estimate   Std.Err t value Pr(>|t|)
## (Intercept)   -10.09758  11.53387 -0.8755  0.39352
## depth.quadrat  10.12428   1.35003  7.4993  8.7e-07 ***
## turbidity      -2.18700   0.79129 -2.7639  0.01328 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ---
##  Number of observations n:  20 ,  n.eff:  15 ,  AIC:  144.3469
##
##  Number of iterations:  2
## ---
## Autocorrelation of glm.residuals
##  [1]  0.04956623 -0.12076712  0.23204814  0.15934318 -0.13034117 -0.49560640
##  [7]  0.37603866  0.02660686 -0.20931275  0.12914488
## Autocorrelation of wavelet.residuals
##  [1] -0.21537014 -0.10561333  0.25936921  0.08323627 -0.01839557 -0.44707457
##  [7]  0.56490988 -0.12467440 -0.23297588  0.20660082
```