

Progressive Change BACIPS

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2/8/2022

1. Data

a. Libraries

```
library(tidyverse) # cleaning
library(here) # directory navigation
library(lubridate) # handling dates
library(janitor) # cleaning up columns

# dependencies for function
library(minpack.lm) # Fitting non-linear models
library(nls2) # Fitting non-linear models
library(AICcmodavg) # calculate second order AIC (AICc)
```

b. Dates for end of the experiment

```
##### a. Naples (NAPL)

# date of last removal
napl_after_date <- as_date("2016-02-09")

napl_after_date_annual <- as_date("2017-02-14")

napl_after_date_continual <- as_date("2016-05-17")

##### b. Mohawk (MOHK)

# date of last removal
mohk_after_date <- as_date("2017-02-13")

mohk_after_date_annual <- as_date("2019-02-12")

mohk_after_date_continual <- as_date("2018-05-15")

##### c. Arroyo Quemado (AQUE)

# date of last removal
```

```

aque_after_date <- as_date("2017-03-02")

aque_after_date_annual <- as_date("2018-02-28")

aque_after_date_continual <- as_date("2017-05-18")

##### d. Carpinteria (CARP)

# date of last removal
carp_after_date <- as_date("2017-02-15")

carp_after_date_annual <- as_date("2018-02-20")

carp_after_date_continual <- as_date("2017-05-19")

##### e. Isla Vista (IVEE)

# date of last removal
ivee_after_date <- as_date("2016-02-18")

ivee_after_date_annual <- as_date("2017-02-09")

```

b. Biomass data

This is data you sent me on the 2nd of February, which is why it has that time appended to the end of the file name to distinguish it from other versions that I pulled down from the online repository.

```

kelp_biomass <- read_csv(here::here("data", "LTE_All_Species_Biomass_at_transect_20220208.csv")) %>%
  clean_names() %>%
  # ANOB is incorrectly coded as having 'SESSILE' mobility
  mutate(mobility = replace(mobility, sp_code == "ANOB", "MOBILE")) %>%
  # replace all -99999 values with NA
  mutate(dry_gm2 = replace(dry_gm2, dry_gm2 < 0, NA), wm_gm2 = replace(wm_gm2,
    wm_gm2 < 0, NA)) %>%
  # create a sample_ID for each sampling date at each treatment at
  # each site
  unite("sample_ID", site, treatment, date, remove = FALSE) %>%
  # change to lower case
  mutate_at(c("group", "mobility", "growth_morph", "treatment", "site"),
    str_to_lower) %>%
  filter(sp_code == "MAPY") %>%
  select(-sp_code)

```

2. Function

Taken from Thiault et al., with modifications so that plots do not print out in quartz viewer.

```

ProgressiveChangeBACIPS <- function(control, impact, time.true, time.model) {
  ### STEP 2 - Calculate the delta at each sampling date
  delta <- impact - control

```

```

# Plot delta against time.true dev.new(width=10, height=5)
# par(mfrow=c(1,2))
plot(delta ~ time.true, type = "n")
time.model.of.impact = max(which(time.model == 0))
rect(time.model.of.impact, min(delta) - 100, max(time.model) + 10,
      max(delta) + 100, col = "grey")
points(delta ~ time.true, pch = 24, bg = "white", cex = 2)

### STEP 3 - Fit and compete models Create a 'period' variable
period <- ifelse(time.model == 0, "Before", "After")

## Fit a step model
step.Model <- aov(delta ~ period)

## Fit a linear model
linear.Model <- lm(delta ~ time.model)

## Fit an asymptotic model Create an asymptotic function
myASYfun <- function(delta, time.model) {
  funAsy <- function(parS, time.model) (parS$M * time.model)/(parS$L +
    time.model) + parS$B
  residFun <- function(p, observed, time.model) observed + funAsy(p,
    time.model)
  parStart <- list(M = mean(delta[time.model.of.impact:length(time.true)]),
    B = mean(delta[1:time.model.of.impact]), L = 1)
  nls_ASY_out <- nls.lm(par = parStart, fn = residFun, observed = delta,
    time.model = time.model, control = nls.lm.control(maxfev = integer(),
    maxiter = 1000))
  foAsy <- delta ~ (M * time.model)/(L + time.model) + B
  startPar <- c(-coef(nls_ASY_out)[1], coef(nls_ASY_out)[2], coef(nls_ASY_out)[3])
  asyFit <- nls2(foAsy, start = startPar, algorithm = "brute-force") # nls2 enables to calculate
  asyFit
}

# Fit the asymptotic model
asymptotic.Model <- myASYfun(delta = delta, time.model = time.model)

## Fit a sigmoid model Create a sigmoid function
mySIGfun <- function(delta, time.model) {
  funSIG <- function(parS, time.model) (parS$M * (time.model/parS$L)^parS$K)/(1 +
    (time.model/parS$L)^parS$K) + parS$B
  residFun <- function(p, observed, time.model) observed + funSIG(p,
    time.model)
  parStart <- list(M = mean(delta[time.model.of.impact:length(time.true)]),
    B = mean(delta[1:time.model.of.impact]), L = mean(time.model),
    K = 5)
  nls_SIG_out <- nls.lm(par = parStart, fn = residFun, observed = delta,
    time.model = time.model, control = nls.lm.control(maxfev = integer(),
    maxiter = 1000))
  foSIG <- delta ~ (M * (time.model/L)^K)/(1 + (time.model/L)^K) +
    B
  startPar <- c(-coef(nls_SIG_out)[1], -coef(nls_SIG_out)[2], coef(nls_SIG_out)[3],
    coef(nls_SIG_out)[4])
  sigFit <- nls2(foSIG, start = startPar, algorithm = "brute-force") # nls2 enables to calculate

```

```

    sigFit
  }
  # Fit the sigmoid model
  sigmoid.Model <- mySIGfun(delta = delta, time.model = time.model)

  ## Compete models Perform AIC tests
  AIC.test <- AIC(step.Model, linear.Model, asymptotic.Model, sigmoid.Model)
  AICc.test <- as.data.frame(cbind(AIC.test[, 1], c(AICc(step.Model),
    AICc(linear.Model), AICc(asymptotic.Model), AICc(sigmoid.Model))))
  rownames(AICc.test) <- rownames(AIC.test)
  names(AICc.test) <- names(AIC.test)

  # Calculate AICc weight and selected the best model
  for (i in 1:dim(AICc.test)[1]) {
    AICc.test$diff[i] <- AICc.test$AIC[i] - min(AICc.test$AIC)
  }
  AICc.test$RL <- exp(-0.5 * AICc.test$diff)
  RL_sum <- sum(AICc.test$RL)
  AICc.test$aicWeights <- (AICc.test$RL/RL_sum) * 100
  w <- AICc.test$aicWeights
  names(w) <- rownames(AICc.test)

  # Display raw AIC values
  print(AICc.test)

  # Display AICc weights print(w)
  barplot(w, col = "white", ylab = "Relative likelihood (%)", cex.names = 0.9,
    names.arg = c("Step", "Linear", "Asymptotic", "Sigmoid"))
  best.Model <- which(w == max(w))

  ### STEP 4 - Derive inference based on the best model (i.e., with
### the higher AICc weight)
  if (best.Model == 1) {
    writeLines(paste("\n\nSTEP MODEL SELECTED - Likelihood = ", round(w[1],
      1), "%\n\n", sep = ""))
    print(summary(step.Model))
  }
  if (best.Model == 2) {
    writeLines(paste("\n\nLINEAR MODEL SELECTED - Likelihood = ", round(w[2],
      1), "%\n\n", sep = ""))
    print(summary(linear.Model))
  }
  if (best.Model == 3) {
    writeLines(paste("\n\nASYMPTOTIC MODEL SELECTED - Likelihood = ",
      round(w[3], 1), "%\n\n", sep = ""))
    print(summary(asymptotic.Model))
  }
  if (best.Model == 4) {
    writeLines(paste("\n\nSIGMOID MODEL SELECTED - Likelihood = ",
      round(w[4], 1), "%\n\n", sep = ""))
    print(summary(sigmoid.Model))
  }
}

```

```

return(c(aicc.test.results = AICc.test, step.model.summary = summary(step.Model),
        linear.model.summary = summary(linear.Model), asy.model.summary = asymptotic.Model,
        sigmoid.model.summary = sigmoid.Model))
}

```

3. Analysis

`time.model.fxn.new`: Function to create a data frame where there are columns for the actual time (i.e. sampling date), the `time.model` (0 for “before” and a sequence of numbers starting at 1 for “after”), kelp biomass in the control, and kelp biomass in the annual or continual treatment depending on the argument supplied.

This is more or less the original function from the paper, but with some edits to 1) print the results in the console instead of the quartz viewer, and 2) print the results for all 4 models instead of the one selected by AIC.

`biomass.pcbacips`: Function to pull columns out of the intermediate data frame created by `time.model.fxn.new` to do Progressive Change BACIPS.

```

time.model.fxn.new <- function(site, treatment) {
  # select an after date based on site and treatment
  treatment_after_date <- if(site == "aque" & treatment == "annual") {
    aque_after_date_annual
  } else if(site == "aque" & treatment == "continual") {
    aque_after_date_continual
  } else if(site == "napl" & treatment == "annual") {
    napl_after_date_annual
  } else if(site == "napl" & treatment == "continual") {
    napl_after_date_continual
  } else if(site == "ivee" & treatment == "annual") {
    ivee_after_date_annual
  } else if(site == "mohk" & treatment == "annual") {
    mohk_after_date_annual
  } else if(site == "mohk" & treatment == "continual") {
    mohk_after_date_continual
  } else if(site == "carp" & treatment == "annual") {
    carp_after_date_annual
  } else if(site == "carp" & treatment == "continual") {
    carp_after_date_continual
  }
}

kelp_biomass %>%
  select(site, year, month, treatment, date, wm_gm2) %>%
  filter(site == {{ site }} & treatment %in% c({{ treatment }}, "control")) %>%
  pivot_wider(names_from = "treatment", values_from = "wm_gm2") %>%
  drop_na() %>%
  mutate(exp_dates = case_when(
    date > treatment_after_date ~ "after",
    TRUE ~ "during"
  )) %>%
  mutate(exp_dates = fct_relevel(exp_dates, c("after", "during"))) %>%
  arrange(exp_dates) %>%
  # assign everything a "time step number" using the row numbers...
  rownames_to_column("time.model") %>%

```

```

# only keep the time step numbers for the "after dates"
# make everything else 0 (i.e. everything else is before the "after")
mutate(time.model = case_when(
  exp_dates == "during" ~ 0,
  TRUE ~ as.numeric(as.numeric(time.model))
)) %>%
# rearrange the sampling dates to be in logical order
mutate(exp_dates = fct_relevel(exp_dates, c("during", "after"))) %>%
arrange(exp_dates)
}

biomass.pcbacips <- function(df) {
  ProgressiveChangeBACIPS(
    control = pull(df, 6), # control column
    impact = pull(df, 7), # treatment column
    time.true = pull(df, 5), # date column
    time.model = pull(df, 1) # time.model column
  )
}

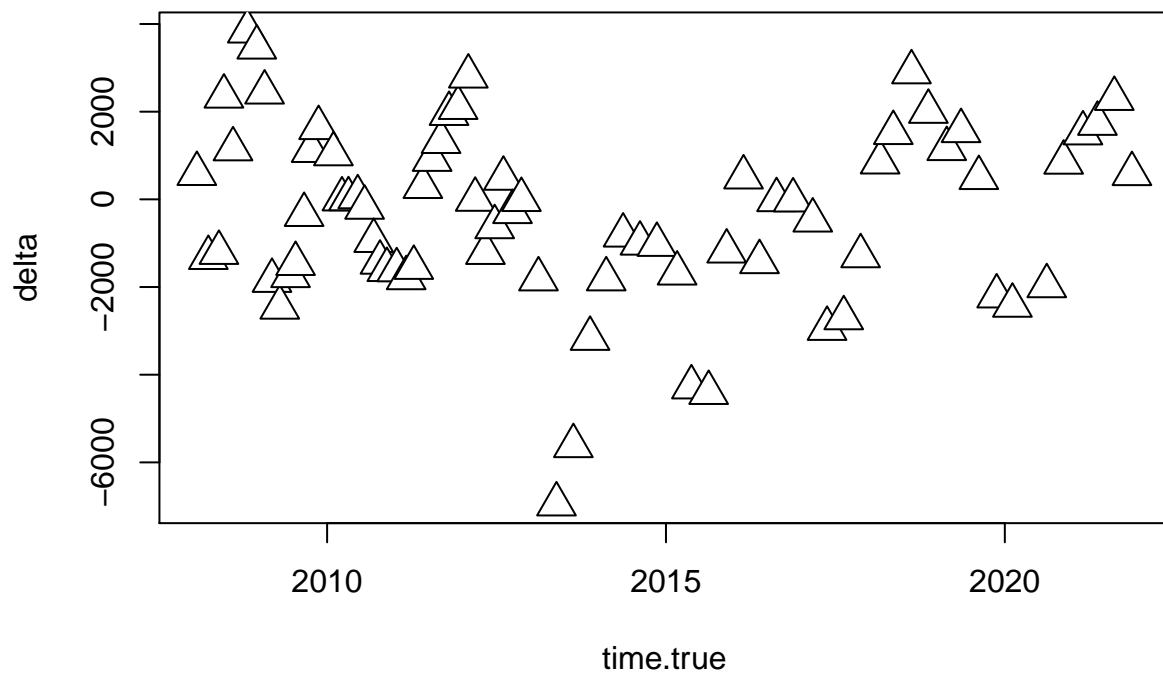
```

Arroyo Quemado

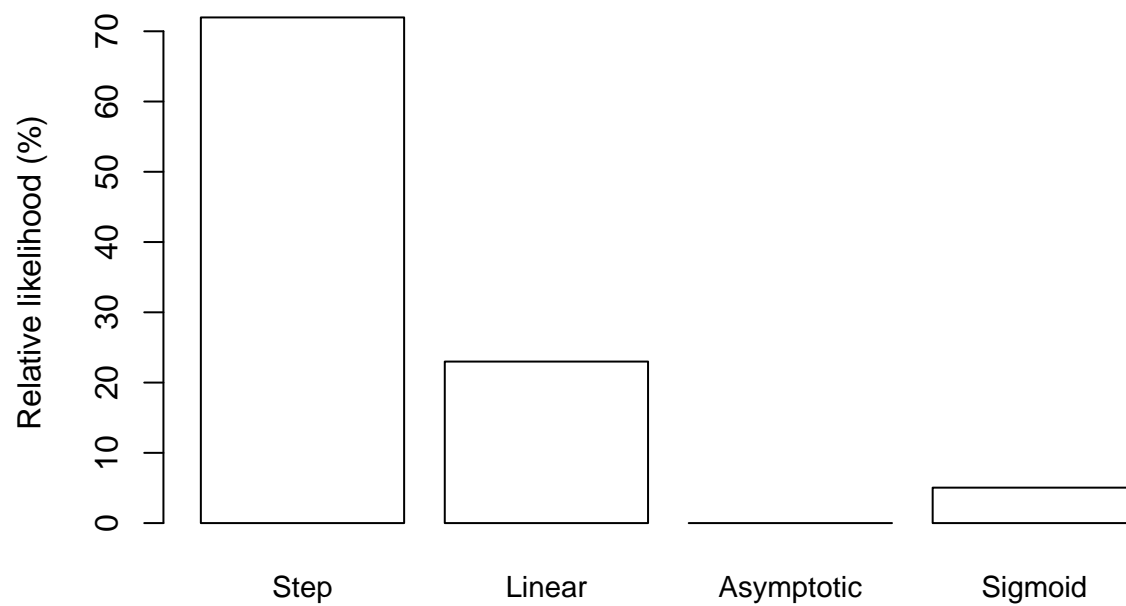
```

aque_biomass_annual <- time.model.fxn.new("aque", "annual")
aque_biomass_continual <- time.model.fxn.new("aque", "continual")
aque_annual_bacips_results <- biomass.pcbacips(aque_biomass_annual)

```



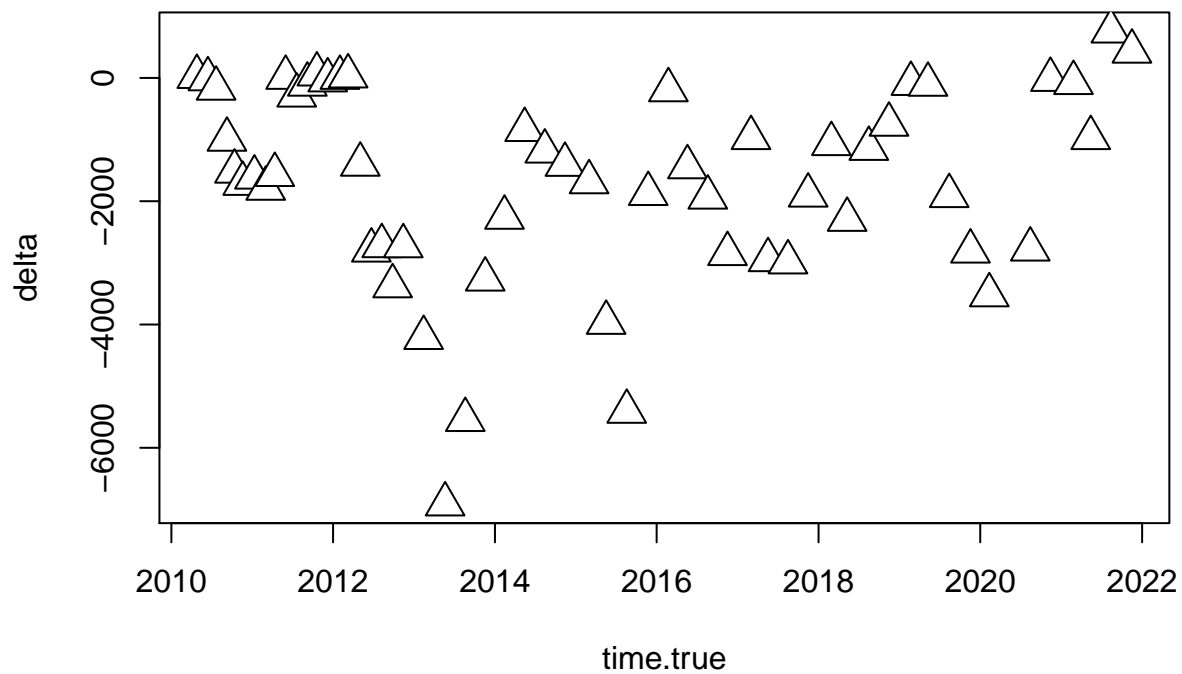
##		df	AIC	diff	RL	aicWeights
##	step.Model	3	1319.258	0.000000	1.000000e+00	7.196853e+01
##	linear.Model	3	1321.541	2.282512	3.194176e-01	2.298801e+01
##	asymptotic.Model	4	1345.180	25.921349	2.350989e-06	1.691972e-04
##	sigmoid.Model	5	1324.575	5.316342	7.007629e-02	5.043288e+00



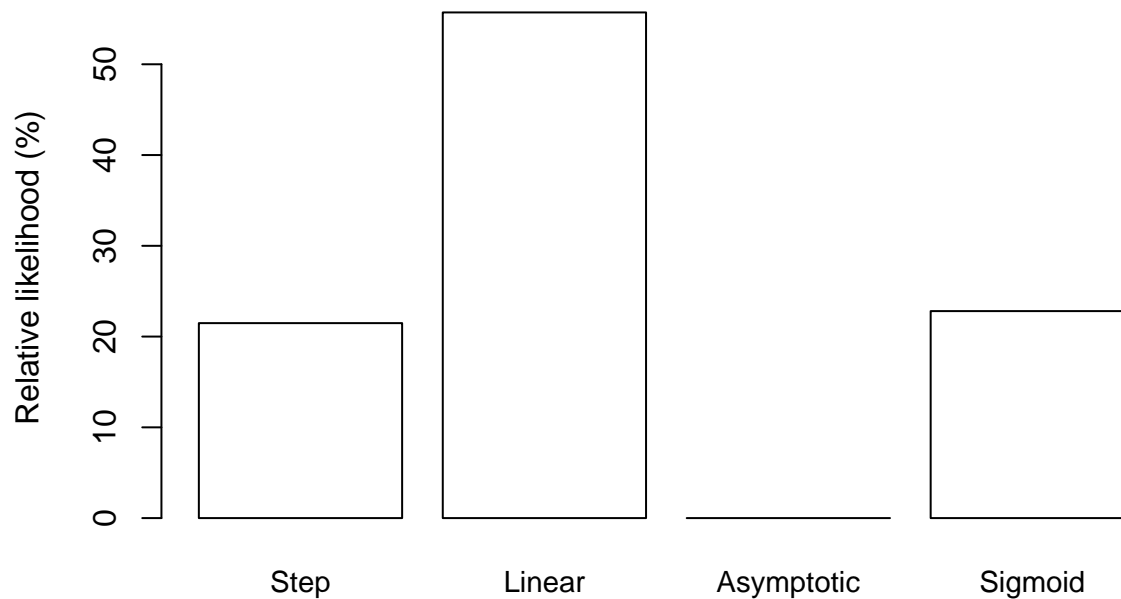
```
##
##
## STEP MODEL SELECTED - Likelihood = 72%
##
##
##           Df      Sum Sq  Mean Sq F value Pr(>F)
## period      1 19596560 19596560   5.032  0.028 *
## Residuals   71 276482324  3894117
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# STEP MODEL SELECTED - Likelihood = 72%
```

```
aque_continual_bacips_results <- biomass.pcbacips(aque_biomass_continual)
```

##		df	AIC	diff	RL	aicWeights
##	step.Model	3	989.5379	1.906045	3.855739e-01	2.148127e+01
##	linear.Model	3	987.6319	0.000000	1.000000e+00	5.571247e+01
##	asymptotic.Model	4	1098.3659	110.734014	9.003564e-25	5.016108e-23
##	sigmoid.Model	5	989.4182	1.786338	4.093564e-01	2.280626e+01

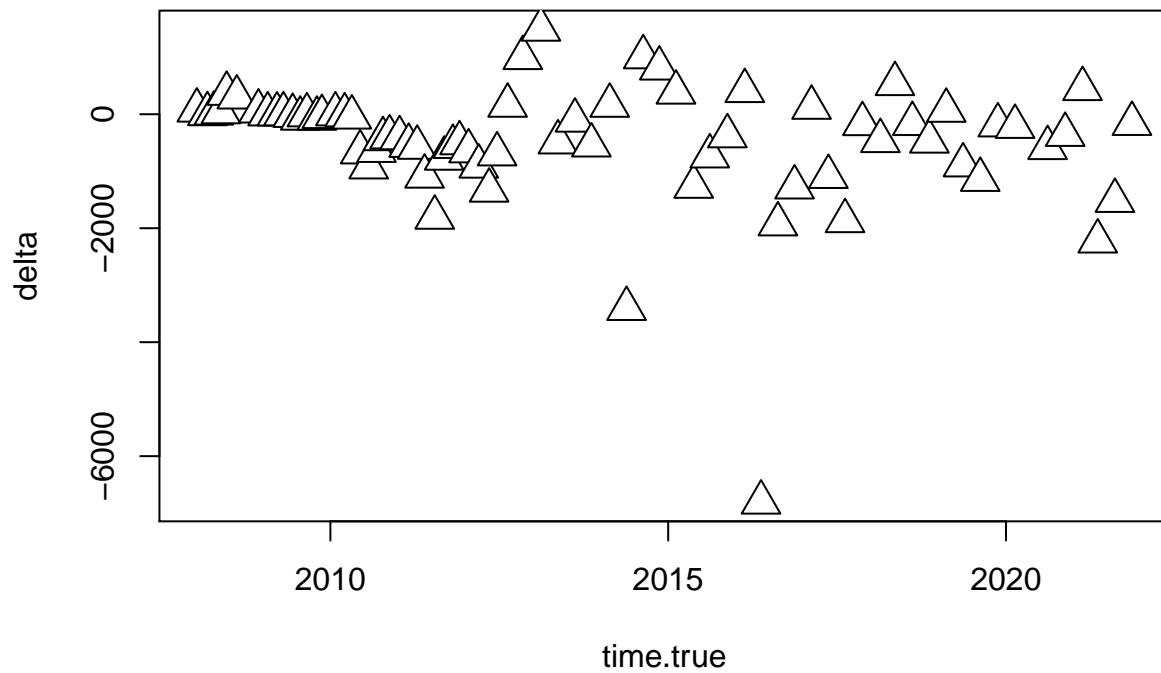


```
##
##
## LINEAR MODEL SELECTED - Likelihood = 55.7%
##
##
## Call:
## lm(formula = delta ~ time.model)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5036.6  -866.5   319.8  1061.0  1937.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1878.84     239.95  -7.830 1.86e-10 ***
## time.model    79.69       42.50   1.875  0.0662 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1571 on 54 degrees of freedom
## Multiple R-squared:  0.06113,    Adjusted R-squared:  0.04374
## F-statistic: 3.516 on 1 and 54 DF,  p-value: 0.0662
```

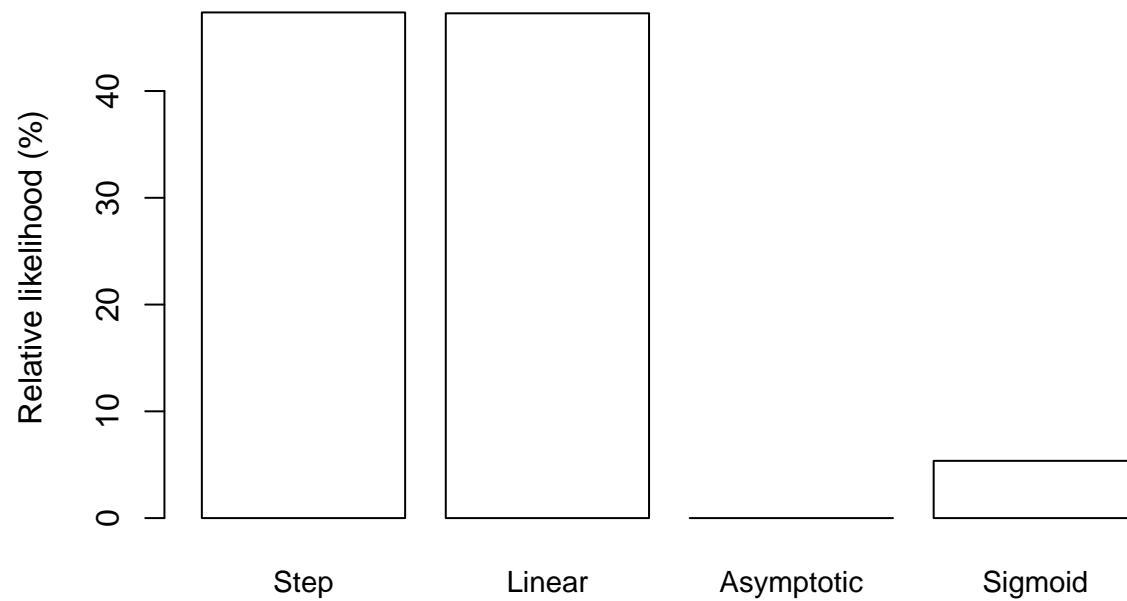
```
# LINEAR MODEL SELECTED - Likelihood = 55.7%
```

Naples

```
napl_biomass_annual <- time.model.fxn.new("napl", "annual")  
napl_biomass_continual <- time.model.fxn.new("napl", "continual")  
napl_annual_bacips_results <- biomass.pcbacips(napl_biomass_annual)
```



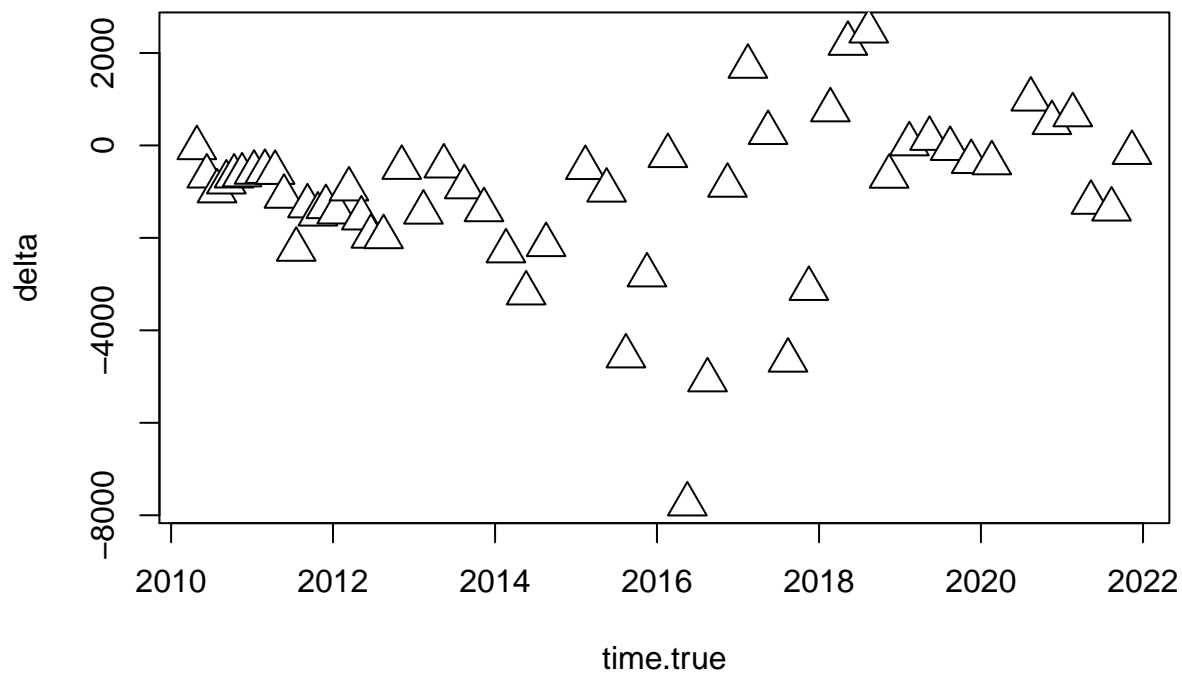
##		df	AIC	diff	RL	aicWeights
##	step.Model	3	1215.402	0.000000000	1.000000e+00	4.736108e+01
##	linear.Model	3	1215.405	0.003534701	9.982342e-01	4.727745e+01
##	asymptotic.Model	4	1255.979	40.577884239	1.543919e-09	7.312164e-08
##	sigmoid.Model	5	1219.759	4.357121509	1.132043e-01	5.361479e+00



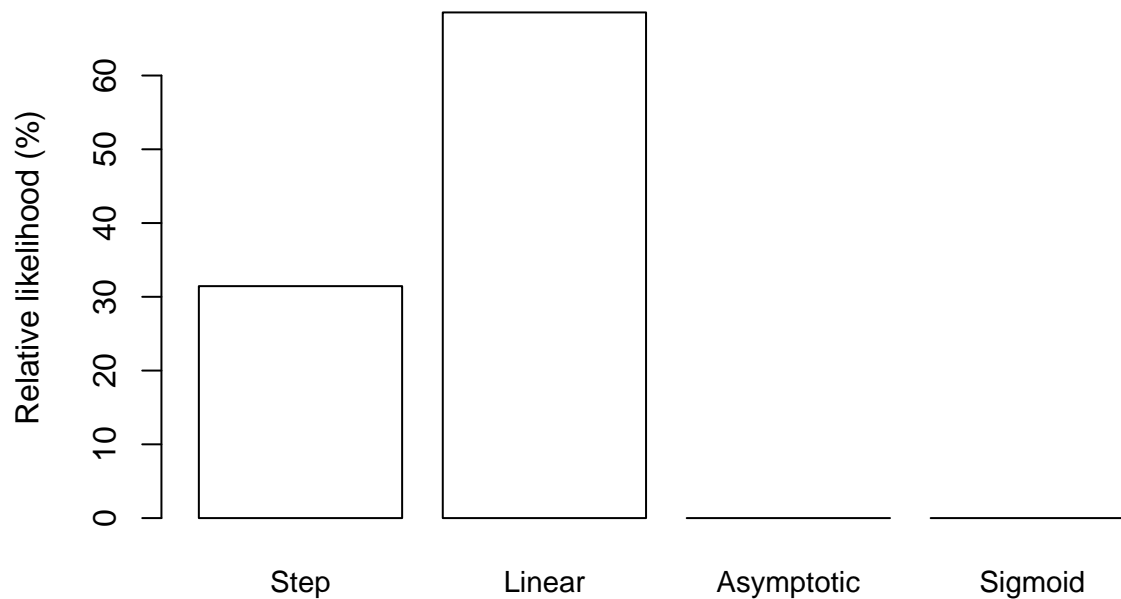
```
##
##
## STEP MODEL SELECTED - Likelihood = 47.4%
##
##
##          Df    Sum Sq Mean Sq F value Pr(>F)
## period      1    271285    271285     0.23  0.633
## Residuals   70  82733189   1181903
```

```
# STEP MODEL SELECTED - Likelihood = 47.4%
```

```
napl_continual_bacips_results <- biomass.pcbacips(napl_biomass_continual)
```



##	df	AIC	diff	RL	aicWeights
## step.Model	3	958.5830	1.558729	4.586974e-01	3.144569e+01
## linear.Model	3	957.0243	0.000000	1.000000e+00	6.855431e+01
## asymptotic.Model	4	1044.4511	87.426759	1.036383e-19	7.104856e-18
## sigmoid.Model	5	1029.7988	72.774530	1.574750e-16	1.079559e-14

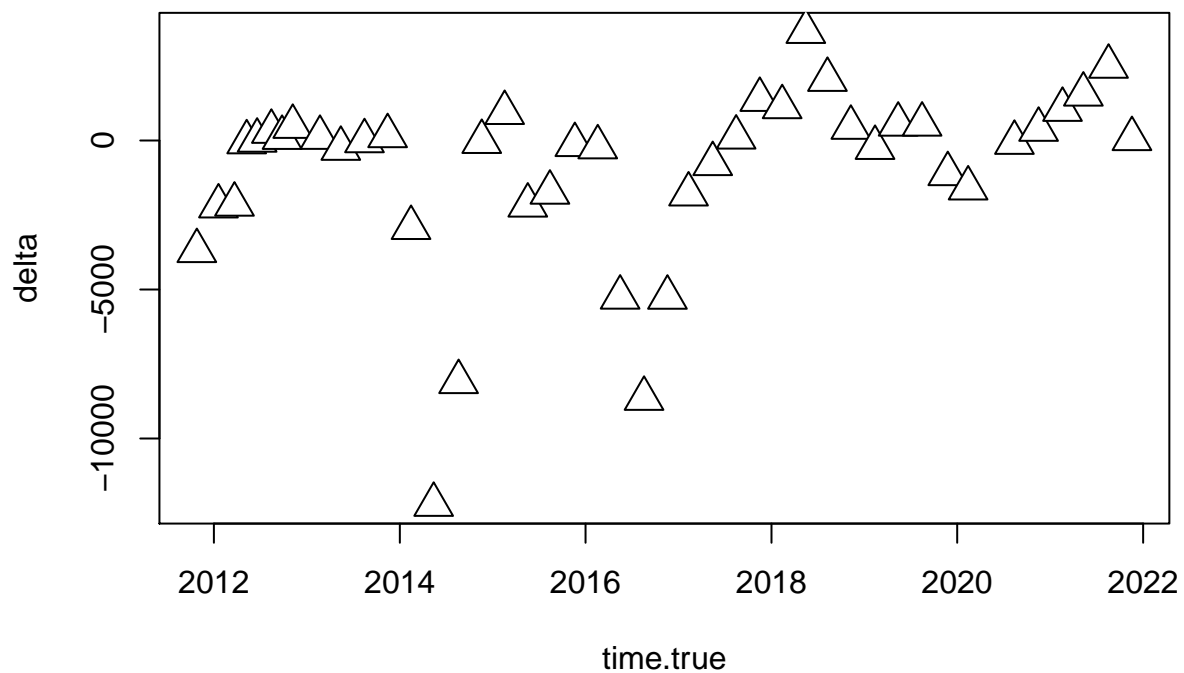


```
##
##
## LINEAR MODEL SELECTED - Likelihood = 68.6%
##
##
## Call:
## lm(formula = delta ~ time.model)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6280.3  -496.8   375.6   877.8  3106.0
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1481.38     266.14  -5.566 9.24e-07 ***
## time.model      93.66      33.99   2.756 0.00806 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1638 on 52 degrees of freedom
## Multiple R-squared:  0.1274, Adjusted R-squared:  0.1106
## F-statistic: 7.593 on 1 and 52 DF,  p-value: 0.008057
```

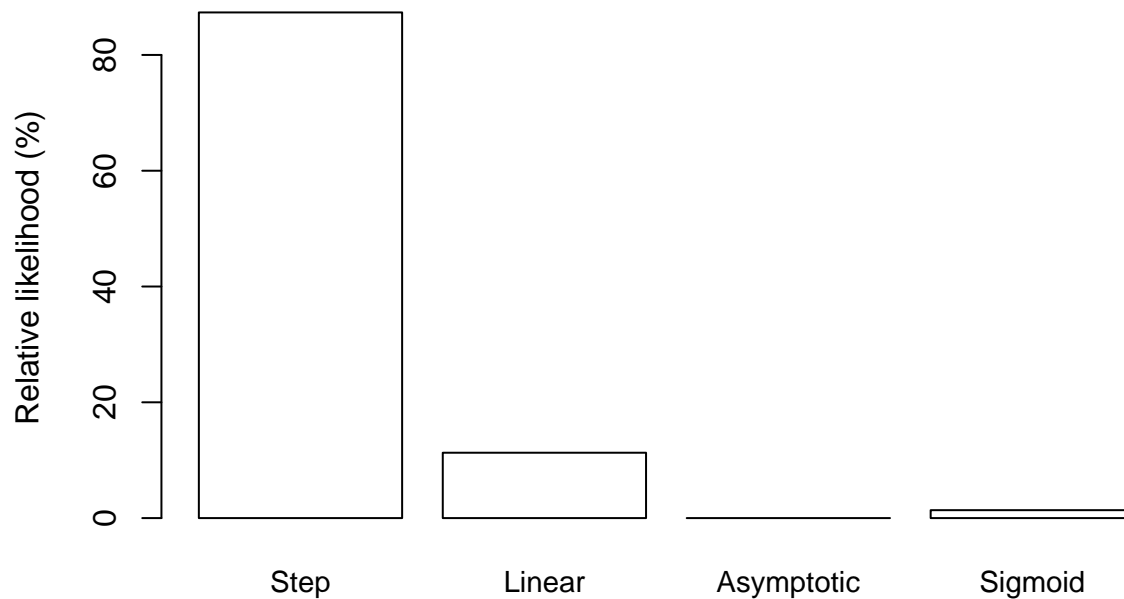
```
# LINEAR MODEL SELECTED - Likelihood = 68.6%
```

Isla Vista

```
ivee_biomass_annual <- time.model.fxn.new("ivee", "annual")  
ivee_annual_bacips_results <- biomass.pcbacips(ivee_biomass_annual)
```



##	df	AIC	diff	RL	aicWeights
## step.Model	3	805.8428	0.000000	1.000000e+00	8.734323e+01
## linear.Model	3	809.9346	4.091795	1.292641e-01	1.129035e+01
## asymptotic.Model	4	865.6674	59.824591	1.021540e-13	8.922457e-12
## sigmoid.Model	5	814.1581	8.315295	1.564432e-02	1.366425e+00

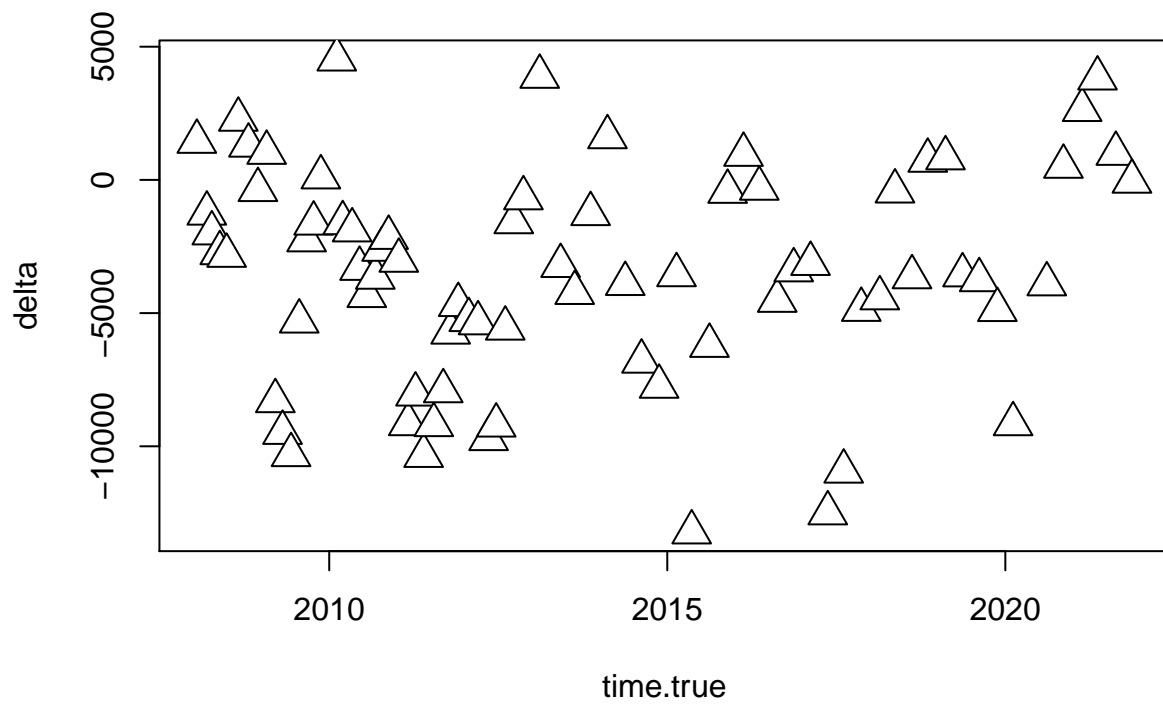


```
##
##
## STEP MODEL SELECTED - Likelihood = 87.3%
##
##
##           Df      Sum Sq  Mean Sq F value   Pr(>F)
## period      1 84089740 84089740    11.6 0.00149 **
## Residuals  41 297227446  7249450
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

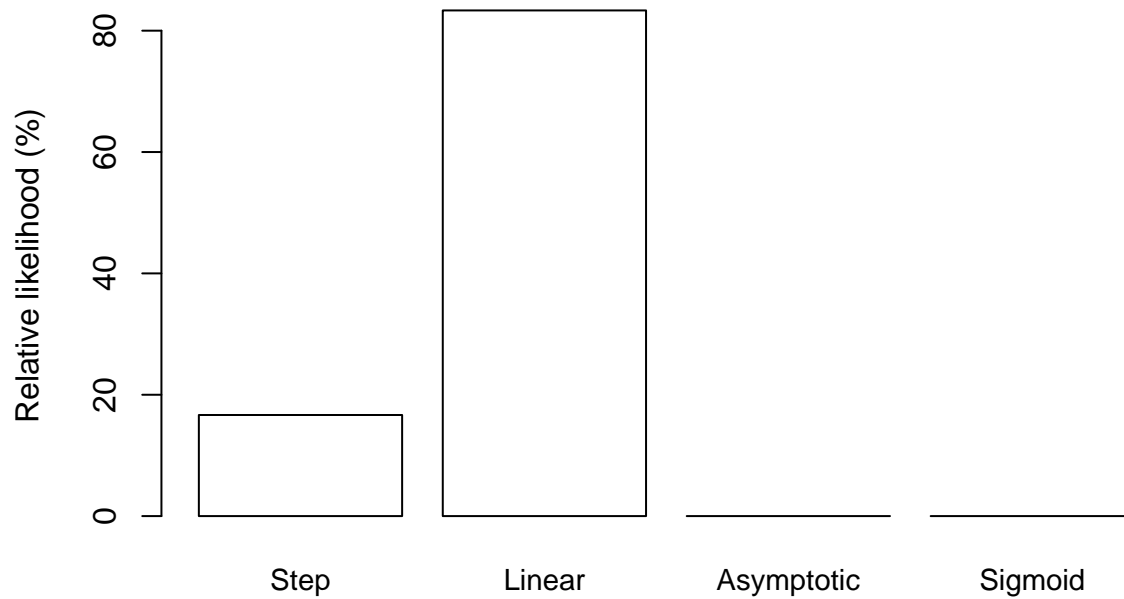
```
# STEP MODEL SELECTED - Likelihood = 87.3%
```

Mohawk

```
mohk_biomass_annual <- time.model.fxn.new("mohk", "annual")
mohk_biomass_continual <- time.model.fxn.new("mohk", "continual")
mohk_annual_bacips_results <- biomass.pcbacips(mohk_biomass_annual)
```

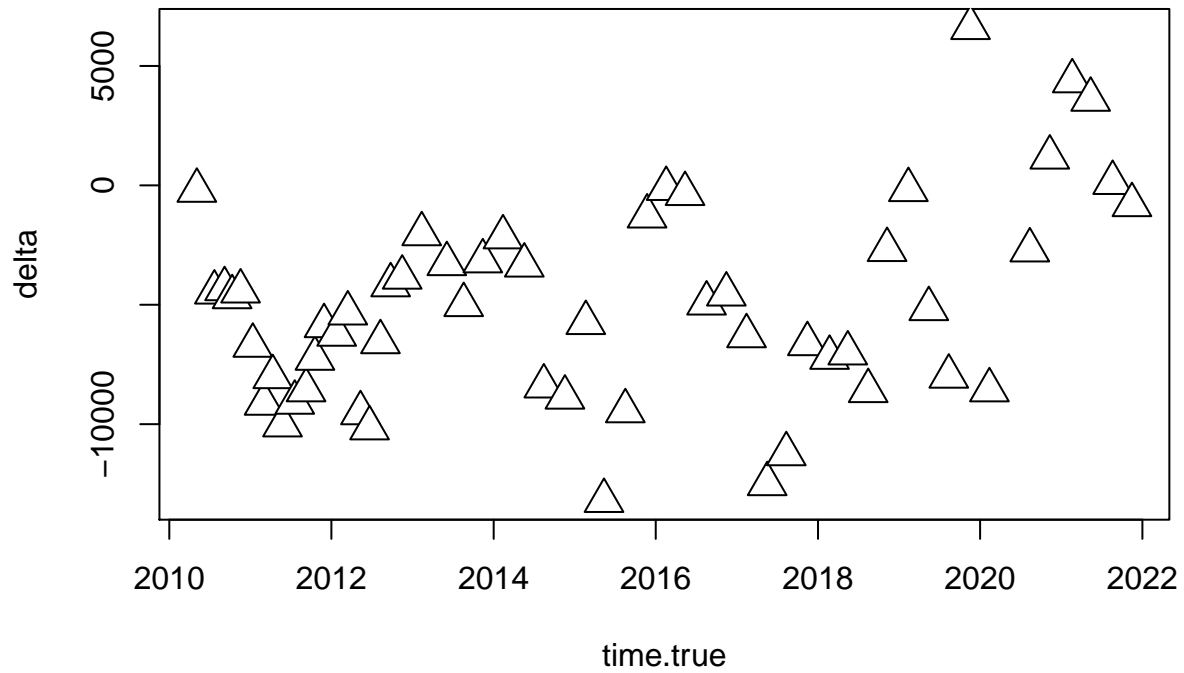
##		df	AIC	diff	RL	aicWeights
##	step.Model	3	1441.855	3.219425	1.999451e-01	1.666286e+01
##	linear.Model	3	1438.636	0.000000	1.000000e+00	8.333714e+01
##	asymptotic.Model	4	1560.416	121.779929	3.596040e-27	2.996837e-25
##	sigmoid.Model	5	1548.649	110.013886	1.290590e-24	1.075541e-22



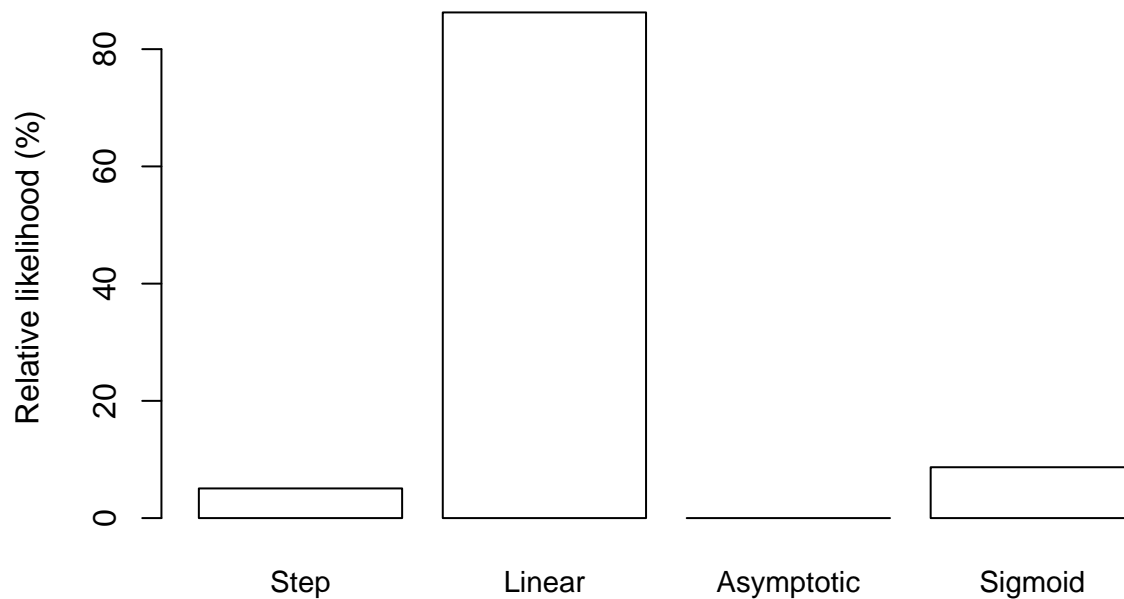
```
##
##
## LINEAR MODEL SELECTED - Likelihood = 83.3%
##
##
## Call:
## lm(formula = delta ~ time.model)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -9349.9 -2222.8   345.9  2611.8  8400.6
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -3875.6      481.3  -8.052 1.22e-11 ***
## time.model     497.1      211.0   2.356  0.0212 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3914 on 72 degrees of freedom
## Multiple R-squared:  0.07155,    Adjusted R-squared:  0.05866
## F-statistic: 5.549 on 1 and 72 DF,  p-value: 0.02122
```

```
# LINEAR MODEL SELECTED - Likelihood = 64%
```

```
mohk_continual_bacips_results <- biomass.pcbacips(mohk_biomass_continual)
```



##		df	AIC	diff	RL	aicWeights
##	step.Model	3	1064.057	5.673147	5.862620e-02	5.057451e+00
##	linear.Model	3	1058.384	0.000000	1.000000e+00	8.626605e+01
##	asymptotic.Model	4	1204.408	146.023941	1.955708e-32	1.687112e-30
##	sigmoid.Model	5	1062.978	4.593635	1.005784e-01	8.676502e+00

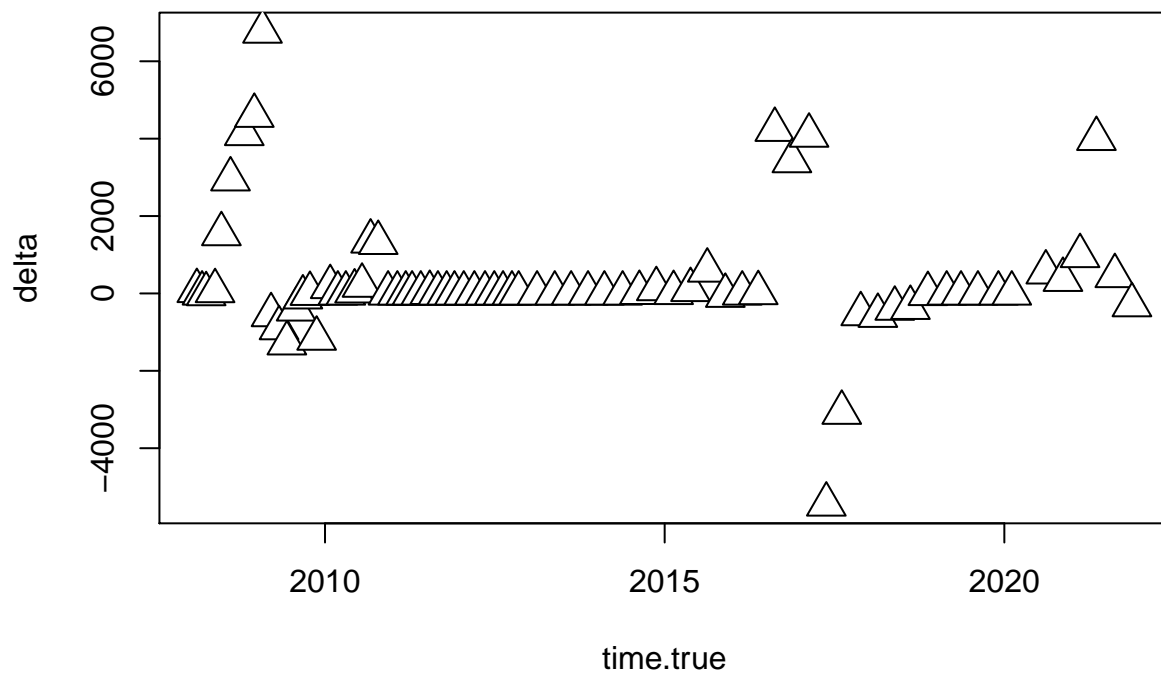


```
##
##
## LINEAR MODEL SELECTED - Likelihood = 86.3%
##
##
## Call:
## lm(formula = delta ~ time.model)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7124.7 -2645.4  -163.8   2169.0   8865.2
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -6083.3      523.4  -11.623 3.38e-16 ***
## time.model     635.4      135.6    4.685 1.99e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3507 on 53 degrees of freedom
## Multiple R-squared:  0.2928, Adjusted R-squared:  0.2795
## F-statistic: 21.95 on 1 and 53 DF,  p-value: 1.991e-05
```

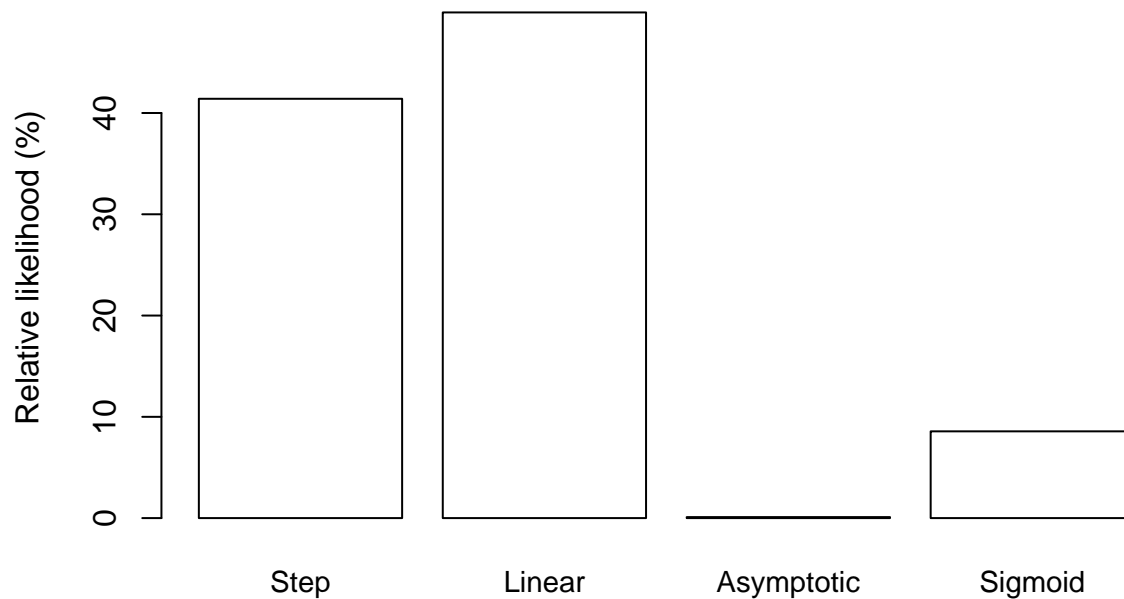
```
# LINEAR MODEL SELECTED - Likelihood = 86.3%
```

Carpinteria

```
carp_biomass_annual <- time.model.fxn.new("carp", "annual")
carp_biomass_continual <- time.model.fxn.new("carp", "continual")
carp_annual_bacips_results <- biomass.pcbacips(carp_biomass_annual)
```



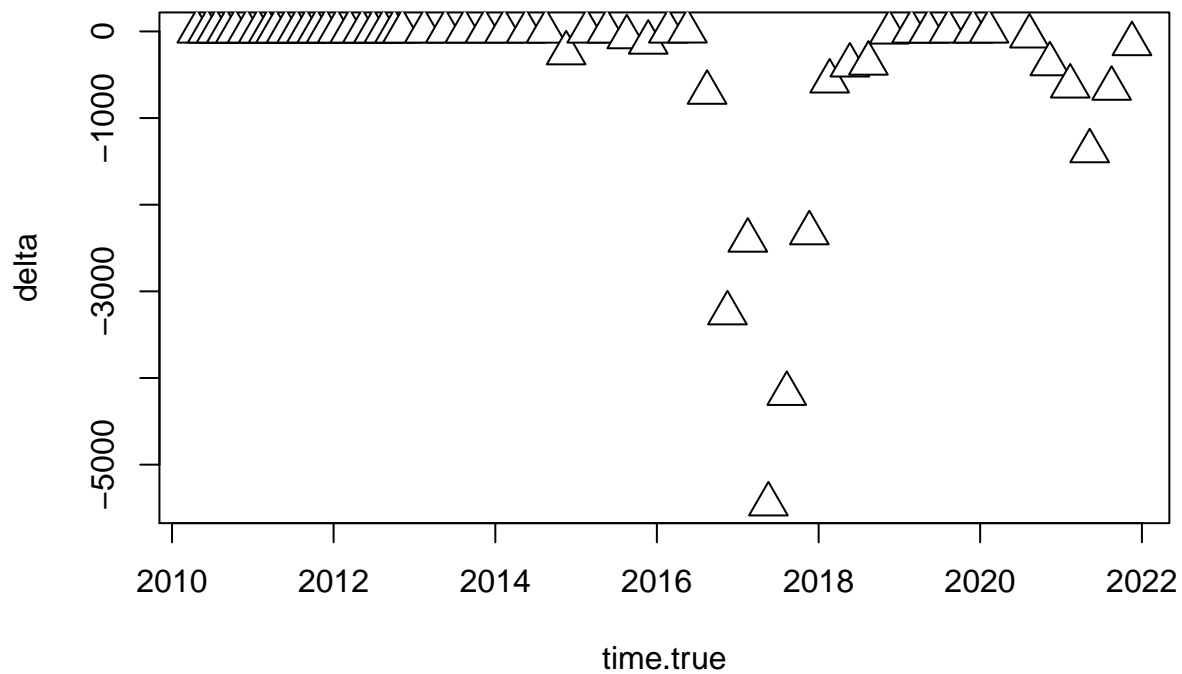
##		df	AIC	diff	RL	aicWeights
##	step.Model	3	1311.338	0.374493	0.829239290	41.40468449
##	linear.Model	3	1310.963	0.000000	1.000000000	49.93092463
##	asymptotic.Model	4	1323.431	12.467199	0.001962376	0.09798325
##	sigmoid.Model	5	1314.489	3.525584	0.171565171	8.56640763



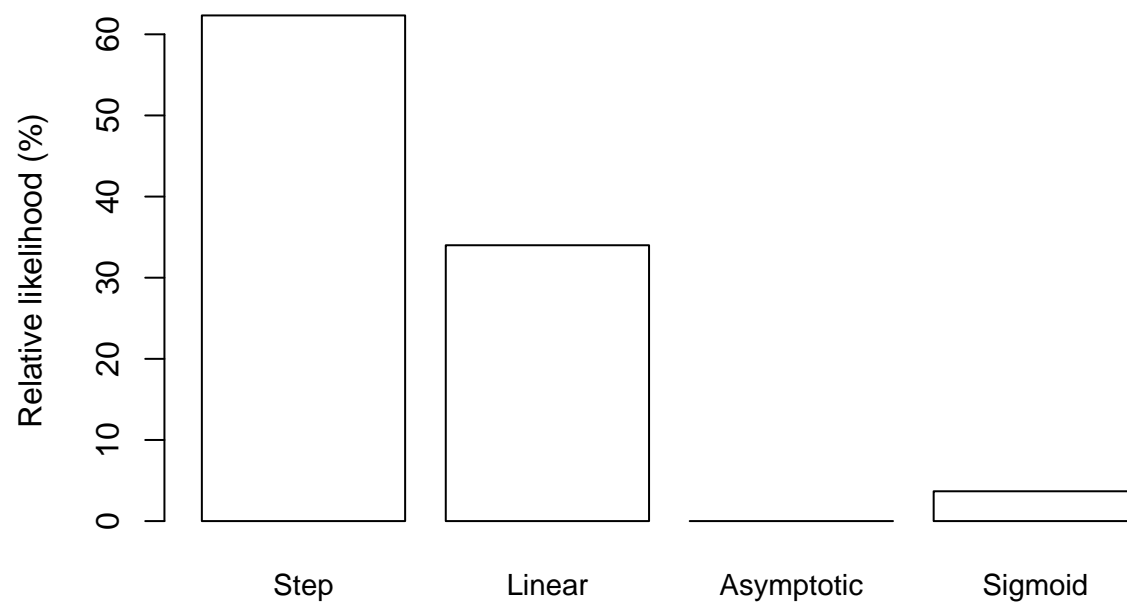
```
##
##
## LINEAR MODEL SELECTED - Likelihood = 49.9%
##
##
## Call:
## lm(formula = delta ~ time.model)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5767.2  -403.9  -314.9  -250.1   6453.9
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    314.92     207.91   1.515   0.134
## time.model      33.97      56.14   0.605   0.547
##
## Residual standard error: 1652 on 72 degrees of freedom
## Multiple R-squared:  0.005059,    Adjusted R-squared:  -0.00876
## F-statistic: 0.3661 on 1 and 72 DF,  p-value: 0.547
```

```
# LINEAR MODEL SELECTED - Likelihood = 49.9%
```

```
carp_continual_bacips_results <- biomass.pcbacips(carp_biomass_continual)
```



##		df	AIC	diff	RL	aicWeights
##	step.Model	3	944.8180	0.000000	1.000000e+00	6.232675e+01
##	linear.Model	3	946.0302	1.212157	5.454859e-01	3.399837e+01
##	asymptotic.Model	4	975.6151	30.797116	2.053484e-07	1.279870e-05
##	sigmoid.Model	5	950.4798	5.661747	5.896131e-02	3.674867e+00



```
##
##
## STEP MODEL SELECTED - Likelihood = 62.3%
##
##
##          Df    Sum Sq Mean Sq F value Pr(>F)
## period     1  1360261  1360261    1.183   0.282
## Residuals  54 62074144  1149521
```

```
# STEP MODEL SELECTED - Likelihood = 62.3%
```