

Rpath for Rocas Atoll Ecosystem

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Rpath is an implementation of the ecosystem model Ecopath with Ecosim (EwE; Christensen and Pauly 1992¹, Walters et al. 1997²). This vignette describes some of the basic functionality of the package using a fictional ecosystem, R Ecosystem. Any resemblance to an actual ecosystem is purely coincidental. To see the underlying mathematics please refer to Lucey et al. (in prep³).

Setting up Ecopath

Parameter file generation

Unlike the GUI based EwE software package, Rpath relies on a parameter input file. This file is actually a list of several different parameter files: model, diet, stanzas, and pedigree. Parameter files can be created outside of R and read in using the `read.rpath.params` function. This function will merge several different flat files into an R object of the list type. A preferred alternative is to generate the list file and populate it completely within R. The function `create.rpath.params` will generate an Rpath.param. This ensures that all of the correct columns are present in the parameter file.

The parameter file contains all of the information you would normally enter in the input data tabs in EwE. There are 2 necessary pieces of information to generate the parameter file: the group names and their corresponding type. The types are: living = 0, primary producer = 1, detritus = 2, and fleet = 3. If your model contains multi-stanza groups then you need 2 additional pieces of information: stanza group names (include NA for those groups not in a stanza) and the number of stanzas per stanza group.

```
#Groups and types for the R Ecosystem
```

```
groups <- c('Seabirds', "Negaprion brevirostris",  
           "Ginglymostoma cirratum", "Lutjanus jocu",  
           "Cephalopholis fulva", "Carangidae", "Acanthurus spp.",  
           "Stegastes rocasensis", "Thalassoma noronhanum",  
           "Abudefduf saxatilis", "Sparisoma spp.", "Melichthys niger",  
           "Kyphosus spp.", "Mulloidichthys martinicus",  
           "Holocentrus adscensionis", "Haemulidae", "Cryptobenthic reef fishes",  
           "Turtles", "Cephalopoda", "Panulirus spp.",  
           "Benthic macroinvertebrates", "Benthic microinvertebrates",  
           "Siderastrea stellata", "Zooplankton", "Phytoplankton", "Digenea simplex", "Other algal turf", "Detritus")  
  
types <- c(rep(0, 22), 0.8, 0, rep(1, 3), 2, 3)  
  
REco.params <- create.rpath.params(group = groups,  
                                   type = types, stgroup = NA)
```

```
#load basic input from my model EwE- Rocas Atoll  
basic_input <- read_csv("data/raw/basic_input.csv")  
#> Warning: Missing column names filled in: 'X1' [1]
```

¹Christensen and Pauly. 1992. ECOPATH II - a software for balancing steady-state models and calculating network characteristics. Ecological Modelling 61:169-85

²Walters et al. 1997. Structuring dynamic models of exploited ecosystems from trophic mass-balance assessments. Reviews of Fish Biology and Fisheries 7:1-34

³Lucey et al. in prep. Improving the EBFM toolbox with an alternative open source version of Ecopath with Ecosim

```
#> Parsed with column specification:
#> cols(
#>   X1 = col_double(),
#>   `Group name` = col_character(),
#>   `Hab area (proportion)` = col_double(),
#>   `Biomass in habitat area (t/km²)` = col_double(),
#>   `Production / biomass (/year)` = col_double(),
#>   `Consumption / biomass (/year)` = col_double(),
#>   `Ecotrophic Efficiency` = col_double(),
#>   `Other mortality` = col_double(),
#>   `Production / consumption` = col_double(),
#>   `Unassim. consumption` = col_double(),
#>   `Detritus import (t/km²/year)` = col_double()
#> )
#Filling columns a Biomass, PB and QB, Biomass accumulation parameters
biomass <- basic_input$`Biomass in habitat area (t/km²)`
REco.params$model[, Biomass := biomass]

pb <- c(5.4,0.264,0.566,0.524,1.3,1.163,0.96,1.74,1.67,1.22,1.02,1.32,0.73,1.92,1.24,1.07,2.73,0.29,6.4)
REco.params$model[, PB := pb]

qb <- c(76.5, 3.2, 3.1, 5.5, 6.7, 11.3, 10.9, 14.7, 14.1, 11.2, 6.2, 10, 27.5, 9.6,8.3, 11.6, 25.1, 2.3)
REco.params$model[, QB := qb]

ba<- c(0, 0, 0.558, -0.1378252, 0.1081793, 0.9327999, -0.08161397, -0.005367057, 0.004389316,
      -0.1343, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0)
REco.params$model[, BioAcc := ba]
#Set parameters for Unassimilation
REco.params$model[, Unassim := c(rep(0.2, 20), 0.4,0.4, 0.2,0.4, 0, 0, 0, 0,0)]
#EE for groups w/o biomass
REco.params$model[Group %in% 'Benthic macroinvertebrates', EE := 0.9]
REco.params$model[Group %in% 'Benthic microinvertebrates', EE := 0.85]
#Detrital Fate
REco.params$model[, Detritus := c(rep(1, 27), rep(0, 2))]
#
View(REco.params$model)
```

Note the use of the operator ‘:=’ to assign values. This is unique to data tables. Here are the rest of the columns for the model list

Table 1: Example of completed model list

Group	Type	Biomass	PB	QB	EE	ProdCons	BioAcc	Unassim	DetInput
Seabirds	0.0	0.020	5.400	76.50	NA	NA	0.0000000	0.2	NA
Negaprion brevirostris	0.0	0.170	0.264	3.20	NA	NA	0.0000000	0.2	NA
Ginglymostoma cirratum	0.0	1.800	0.566	3.10	NA	NA	0.5580000	0.2	NA
Lutjanus jocu	0.0	2.220	0.524	5.50	NA	NA	-0.1378252	0.2	NA
Cephalopholis fulva	0.0	0.200	1.300	6.70	NA	NA	0.1081793	0.2	NA
Carangidae	0.0	2.120	1.163	11.30	NA	NA	0.9327999	0.2	NA
Acanthurus spp.	0.0	9.860	0.960	10.90	NA	NA	-0.0816140	0.2	NA
Stegastes rocasensis	0.0	0.460	1.740	14.70	NA	NA	-0.0053671	0.2	NA
Thalassoma noronhanum	0.0	0.200	1.670	14.10	NA	NA	0.0043893	0.2	NA
Abudefduf saxatilis	0.0	0.990	1.220	11.20	NA	NA	0.0818163	0.2	NA

Group	Type	Biomass	PB	QB	EE	ProdCons	BioAcc	Unassim	DetInput
Sparisoma spp.	0.0	1.130	1.020	6.20	NA	NA	0.2839955	0.2	NA
Melichthys niger	0.0	0.270	1.320	10.00	NA	NA	0.1026000	0.2	NA
Kyphosus spp.	0.0	0.460	0.730	27.50	NA	NA	0.0000000	0.2	NA
Mulloidichthys martinicus	0.0	0.416	1.920	9.60	NA	NA	0.4368000	0.2	NA
Holocentrus adscensionis	0.0	2.118	1.240	8.30	NA	NA	0.9002874	0.2	NA
Haemulidae	0.0	0.962	1.070	11.60	NA	NA	0.0839298	0.2	NA
Cryptobenthic reef fishes	0.0	0.790	2.730	25.10	NA	NA	-0.1343000	0.2	NA
Turtles	0.0	0.022	0.290	2.35	NA	NA	0.0000000	0.2	NA
Cephalopoda	0.0	0.405	6.400	36.50	NA	NA	0.0000000	0.2	NA
Panulirus spp.	0.0	6.000	1.280	7.40	NA	NA	0.0000000	0.2	NA
Benthic macroinvertebrates	0.0	NA	3.800	10.00	0.90	NA	0.0000000	0.4	NA
Benthic microinvertebrates	0.0	NA	4.940	16.69	0.85	NA	0.0000000	0.4	NA
Siderastrea stellata	0.8	3.950	1.660	9.40	NA	NA	0.0000000	0.2	NA
Zooplankton	0.0	0.270	87.000	160.00	NA	NA	0.0000000	0.4	NA
Phytoplankton	1.0	0.150	109.500	NA	NA	NA	0.0000000	0.0	NA
Digenea simplex	1.0	352.730	274.000	NA	NA	NA	0.0000000	0.0	NA
Other algal turf	1.0	1458.750	323.000	NA	NA	NA	0.0000000	0.0	NA
Detritus	2.0	1.000	NA	NA	NA	NA	0.0000000	0.0	0
fleets	3.0	0.000	NA	NA	NA	NA	0.0000000	0.0	NA

###Diet Parameters

The data entered in the diet list is the same as the data entered in the diet composition tab in EwE. Just as within EwE, the columns represent the predators while the rows represent the prey. Individual diet components can be adjusted by specifying the prey in the ‘Group’ variable and assigning a value to the predator. For example, if you wanted to assign 10% of the seabird diet as ‘Other Groundfish’ you could do it like this: You can also assign the entire diet composition for a predator:

```
#load basic input from my model EwE- Rocas Atoll
diet_matrix <- read.csv("data/raw/diet_matrix_atoll_rocas.csv")
#remove lines 30 and 31
diet_matrix<- diet_matrix[c(-30,-31),]
#Convert columns X3,X5 and X6 class as numeric
diet_matrix$X3<- as.numeric(paste(diet_matrix$X3))
diet_matrix$X5<- as.numeric(paste(diet_matrix$X5))
diet_matrix$X6<- as.numeric(paste(diet_matrix$X6))
#diet sea birds
seabirds.diet<-diet_matrix$X1
REco.params$diet[, "Seabirds" := seabirds.diet]
#diet Negaprion brevirostris
Negaprion.diet<- diet_matrix$X2
REco.params$diet[, "Negaprion brevirostris" := Negaprion.diet]
#diet Ginglymostoma cirratum
Ginglymostoma.diet<- as.numeric(diet_matrix$X3)
REco.params$diet[, "Ginglymostoma cirratum" := Ginglymostoma.diet]
#diet Lutjanus jocu
Lutjanus_jocu.diet<- as.numeric(diet_matrix$X4)
REco.params$diet[, "Lutjanus jocu" := Lutjanus_jocu.diet]
#diet Cephalopholis fulva
Cephalopholis_fulva.diet<- as.numeric(diet_matrix$X5)
REco.params$diet[, "Cephalopholis fulva" := Cephalopholis_fulva.diet]
#diet Carangidae
```

```

Carangidae.diet<- as.numeric(diet_matrix$X6)
REco.params$diet[, "Carangidae" := Carangidae.diet]
#diet Acanthurus spp.
Acanthurus_spp.diet<- as.numeric(diet_matrix$X7)
REco.params$diet[, "Acanthurus spp." := Acanthurus_spp.diet]
#diet stegastes rocasensis
Stegastes_rocasensis.diet<- as.numeric(diet_matrix$X8)
REco.params$diet[, "Stegastes rocasensis" := Stegastes_rocasensis.diet]
#diet Thalassoma noronhanum
Thalassoma.diet<- as.numeric(diet_matrix$X9)
REco.params$diet[, "Thalassoma noronhanum" := Thalassoma.diet]
#diet Abudefduf saxatilis
Abudefduf.diet <- as.numeric(diet_matrix$X10)
REco.params$diet[, "Abudefduf saxatilis" := Abudefduf.diet]
#diet Sparisoma spp.
Sparisoma_spp.diet <- as.numeric(diet_matrix$X11)
REco.params$diet[, "Sparisoma spp." := Sparisoma_spp.diet]
#diet Melichthys niger
Melichthys_niger.diet <- as.numeric(diet_matrix$X12)
REco.params$diet[, "Melichthys niger" := Melichthys_niger.diet]
#diet Kyphosus spp.
Kyphosus_spp.diet <- as.numeric(diet_matrix$X13)
REco.params$diet[, "Kyphosus spp." := Kyphosus_spp.diet]
#diet Mulloidichthys martinicus
Mulloidichthys_martinicus.diet <- as.numeric(diet_matrix$X14)
REco.params$diet[, "Mulloidichthys martinicus" := Mulloidichthys_martinicus.diet]
#diet Holocentrus adscensionis
Holocentrus_adscensionis.diet <- as.numeric(diet_matrix$X15)
REco.params$diet[, "Holocentrus adscensionis" := Holocentrus_adscensionis.diet]
#diet Haemulidae
Haemulidae.diet <- as.numeric(diet_matrix$X16)
REco.params$diet[, "Haemulidae" := Haemulidae.diet]
#diet Cryptobenthic reef fishes
Cryptobenthic.diet <- as.numeric(diet_matrix$X17)
REco.params$diet[, "Cryptobenthic reef fishes" := Cryptobenthic.diet]
#diet Turtles
Turtles.diet <- as.numeric(diet_matrix$X18)
REco.params$diet[, "Turtles" := Turtles.diet]
#diet Cephalopoda
Cephalopoda.diet <- as.numeric(diet_matrix$X19)
REco.params$diet[, "Cephalopoda" := Cephalopoda.diet]
#diet Panulirus spp.
Panulirus_spp.diet <- as.numeric(diet_matrix$X20)
REco.params$diet[, "Panulirus spp." := Panulirus_spp.diet]

#diet Benthic macroinvertebrates
Benthic_macroinvertebrates.diet <- as.numeric(diet_matrix$X21)
REco.params$diet[, "Benthic macroinvertebrates" := Benthic_macroinvertebrates.diet]

#diet Benthic microinvertebrates
Benthic_microinvertebrates.diet <- as.numeric(diet_matrix$X22)
REco.params$diet[, "Benthic microinvertebrates" := Benthic_microinvertebrates.diet]

```

```

#diet Siderastrea stellata
Siderastrea_stellata.diet <- c(0, 0, 0, 0, 0, 0, 0, 0,
                             0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
                             0, 1, 0, 0, 0, 0, 0, 0)

REco.params$diet[, "Siderastrea stellata" := Siderastrea_stellata.diet]

#diet Zooplankton
Zooplankton.diet <- as.numeric(diet_matrix$X24)
REco.params$diet[, "Zooplankton" := Zooplankton.diet]
View(REco.params$diet)

```

Group	Seabirds	Negaprion brevirostris	Ginglymostoma cirratum	Lutjanus jocu	Cephalopholis
Seabirds	0.00	0.00	0.00	0.00	
Negaprion brevirostris	0.00	0.00	0.00	0.00	
Ginglymostoma cirratum	0.00	0.00	0.00	0.00	
Lutjanus jocu	0.00	0.01	0.01	0.01	
Cephalopholis fulva	0.00	0.10	0.00	0.00	
Carangidae	0.07	0.06	0.00	0.00	
Acanthurus spp.	0.05	0.20	0.01	0.05	
Stegastes rocasensis	0.00	0.05	0.00	0.02	
Thalassoma noronhanum	0.00	0.00	0.00	0.00	
Abudefduf saxatilis	0.00	0.00	0.00	0.01	
Sparisoma spp.	0.00	0.05	0.00	0.00	
Melichthys niger	0.00	0.04	0.00	0.00	
Kyphosus spp.	0.00	0.05	0.00	0.00	
Mulloidichthys martinicus	0.00	0.02	0.00	0.00	
Holocentrus adscensionis	0.00	0.04	0.01	0.04	
Haemulidae	0.03	0.05	0.00	0.03	
Cryptobenthic reef fishes	0.03	0.08	0.00	0.01	
Turtles	0.00	0.01	0.00	0.00	
Cephalopoda	0.05	0.05	0.10	0.03	
Panulirus spp.	0.00	0.00	0.35	0.00	
Benthic macroinvertebrates	0.12	0.03	0.29	0.39	
Benthic microinvertebrates	0.10	0.01	0.15	0.31	
Siderastrea stellata	0.00	0.00	0.00	0.00	
Zooplankton	0.00	0.00	0.00	0.00	
Phytoplankton	0.00	0.00	0.00	0.00	
Digenea simplex	0.00	0.00	0.00	0.00	
Other algal turf	0.00	0.00	0.00	0.00	
Detritus	0.00	0.00	0.00	0.00	
Import	0.55	0.14	0.08	0.10	

Running Ecopath

After creating the parameter object, running ecopath in R is relatively straightforward. It is just the function `rpath` supplied with the parameter object. Additionally, you can supply an ecosystem name for the output.

```
REco <- rpath(REco.params, eco.name = 'Rpath Rocas Atoll marine food web ')
REco
#> Rpath model: Rpath Rocas Atoll marine food web
#> Model Area: 1
#> Status: Unbalanced!
#> The following groups have EE > 1:
#> [1] "Zooplankton"
#>
#>
#>      Group type      TL      Biomass      PB      QB
#> 1      Seabirds  0.0 3.472713  0.02000  5.400 76.50
#> 2  Negaprion brevirostris  0.0 3.523583  0.17000  0.264  3.20
#> 3  Ginglymostoma cirratum  0.0 3.473124  1.80000  0.566  3.10
#> 4      Lutjanus jocu  0.0 3.275414  2.22000  0.524  5.50
#> 5  Cephalopholis fulva  0.0 3.244684  0.20000  1.300  6.70
#> 6      Carangidae  0.0 3.022266  2.12000  1.163 11.30
#> 7      Acanthurus spp.  0.0 2.101010  9.86000  0.960 10.90
#> 8  Stegastes rocasensis  0.0 2.030303  0.46000  1.740 14.70
#> 9  Thalassoma noronhanum  0.0 2.378044  0.20000  1.670 14.10
#> 10  Abudefduf saxatilis  0.0 2.335578  0.99000  1.220 11.20
#> 11      Sparisoma spp.  0.0 2.202020  1.13000  1.020  6.20
#> 12  Melichthys niger  0.0 2.251010  0.27000  1.320 10.00
#> 13      Kyphosus spp.  0.0 2.020202  0.46000  0.730 27.50
#> 14  Mulloidichthys martinicus  0.0 3.073392  0.41600  1.920  9.60
#> 15  Holocentrus adscensionis  0.0 3.188224  2.11800  1.240  8.30
#> 16      Haemulidae  0.0 3.085646  0.96200  1.070 11.60
#> 17  Cryptobenthic reef fishes  0.0 2.375385  0.79000  2.730 25.10
#> 18      Turtles  0.0 2.804811  0.02200  0.290  2.35
#> 19      Cephalopoda  0.0 3.188729  0.40500  6.400 36.50
#> 20      Panulirus spp.  0.0 2.606592  6.00000  1.280  7.40
#> 21  Benthic macroinvertebrates  0.0 2.265284 16.70264  3.800 10.00
#> 22  Benthic microinvertebrates  0.0 2.010101 25.19172  4.940 16.69
#> 23  Siderastrea stellata  0.8 1.400000  3.95000  1.660  9.40
#> 24      Zooplankton  0.0 2.000000  0.27000  87.000 160.00
#> 25      Phytoplankton  1.0 1.000000  0.15000 109.500  0.00
#> 26      Digenea simplex  1.0 1.000000 352.73000 274.000  0.00
#> 27  Other algal turf  1.0 1.000000 1458.75000 323.000  0.00
#> 28      Detritus  2.0 1.000000  1.00000 568025.904  0.00
#> 29      fleets  3.0 1.000000  0.00000  0.000  0.00
#>
#>      EE      GE Removals
#> 1  0.000000e+00 0.07058824  0
#> 2  0.000000e+00 0.08250000  0
#> 3  5.477032e-01 0.18258065  0
#> 4  5.064542e-02 0.09527273  0
#> 5  6.253050e-01 0.19402985  0
#> 6  4.350086e-01 0.10292035  0
#> 7  2.234603e-01 0.08807339  0
#> 8  3.993415e-01 0.11836735  0
#> 9  8.908662e-01 0.11843972  0
#> 10 3.782715e-01 0.10892857  0
#> 11 2.699944e-01 0.16451613  0
#> 12 3.489338e-01 0.13200000  0
#> 13 8.100060e-02 0.02654545  0
#> 14 5.604968e-01 0.20000000  0
```

```
#> 15 6.648114e-01 0.14939759 0
#> 16 5.344491e-01 0.09224138 0
#> 17 2.090138e-01 0.10876494 0
#> 18 8.526646e-01 0.12340426 0
#> 19 7.724633e-01 0.17534247 0
#> 20 2.542969e-01 0.17297297 0
#> 21 9.000000e-01 0.38000000 0
#> 22 8.500000e-01 0.29598562 0
#> 23 2.130218e-13 0.17659574 0
#> 24 1.896153e+00 0.54375000 0
#> 25 9.169102e-01 0.00000000 0
#> 26 5.362570e-04 0.00000000 0
#> 27 2.176546e-04 0.00000000 0
#> 28 9.720597e-04 0.00000000 0
#> 29 0.000000e+00 0.00000000 0
```

The output object from `rpath` is an S3 object type called 'Rpath'. Rpath objects are a list of parameters from the mass balance. However, the `print` function will display the same information as the "Basic Estimates" tab from EwE. You will also notice that the `print` function will display whether the model is balanced or not. If the model was not balanced, it would list the groups that are not balanced. Rpath has the same constraint that all DC's should equal one. Rpath only gives errors if you run the `check.rpath.params()` function. You can also display the mortalities associated with each group by supplying the argument `morts = T` to the `print` function.

```
print(REco, morts = T)
#> Rpath model: Rpath Rocas Atoll marine food web
#> Model Area: 1
#>      Status: Unbalanced!
#> The following groups have EE > 1:
#> [1] "Zooplankton"
#>
#>      Group type      PB      MO
#> 1      Seabirds 0.0    5.400 5.400000e+00
#> 2 Negaprion brevirostris 0.0    0.264 2.640000e-01
#> 3 Ginglymostoma cirratum 0.0    0.566 2.560000e-01
#> 4 Lutjanus jocu 0.0    0.524 4.974618e-01
#> 5 Cephalopholis fulva 0.0    1.300 4.871035e-01
#> 6 Carangidae 0.0    1.163 6.570850e-01
#> 7 Acanthurus spp. 0.0    0.960 7.454781e-01
#> 8 Stegastes rocasensis 0.0    1.740 1.045146e+00
#> 9 Thalassoma noronhanum 0.0    1.670 1.822534e-01
#> 10 Abudefduf saxatilis 0.0    1.220 7.585088e-01
#> 11 Sparisoma spp. 0.0    1.020 7.446058e-01
#> 12 Melichthys niger 0.0    1.320 8.594074e-01
#> 13 Kyphosus spp. 0.0    0.730 6.708696e-01
#> 14 Mulloidichthys martinicus 0.0    1.920 8.438462e-01
#> 15 Holocentrus adscensionis 0.0    1.240 4.156339e-01
#> 16 Haemulidae 0.0    1.070 4.981395e-01
#> 17 Cryptobenthic reef fishes 0.0    2.730 2.159392e+00
#> 18 Turtles 0.0    0.290 4.272727e-02
#> 19 Cephalopoda 0.0    6.400 1.456235e+00
#> 20 Panulirus spp. 0.0    1.280 9.545000e-01
#> 21 Benthic macroinvertebrates 0.0    3.800 3.800000e-01
#> 22 Benthic microinvertebrates 0.0    4.940 7.410000e-01
```



```

#> 23      Siderastrea stellata 0.8      1.660 1.660000e+00
#> 24      Zooplankton 0.0      87.000 -7.796530e+01
#> 25      Phytoplankton 1.0     109.500 9.098333e+00
#> 26      Digenea simplex 1.0     274.000 2.738531e+02
#> 27      Other algal turf 1.0     323.000 3.229297e+02
#> 28      Detritus 2.0 568025.904 9.720597e-04
#>      Fmort[1:ngroup, ] M2.Seabirds M2.Negaprion brevirostris
#> 1      0 0.000000000 0.000000000
#> 2      0 0.000000000 0.000000000
#> 3      0 0.000000000 0.000000000
#> 4      0 0.000000000 0.0024504505
#> 5      0 0.000000000 0.2720000000
#> 6      0 0.050518868 0.0153962264
#> 7      0 0.007758621 0.0110344828
#> 8      0 0.000000000 0.0591304348
#> 9      0 0.000000000 0.000000000
#> 10     0 0.000000000 0.000000000
#> 11     0 0.000000000 0.0240707965
#> 12     0 0.000000000 0.0805925926
#> 13     0 0.000000000 0.0591304348
#> 14     0 0.000000000 0.0261538462
#> 15     0 0.000000000 0.0102738432
#> 16     0 0.047713098 0.0282744283
#> 17     0 0.058101266 0.0550886076
#> 18     0 0.000000000 0.2472727273
#> 19     0 0.188888889 0.0671604938
#> 20     0 0.000000000 0.000000000
#> 21     0 0.010992277 0.0009770913
#> 22     0 0.006073425 0.0002159440
#> 23     0 0.000000000 0.000000000
#> 24     0 0.000000000 0.000000000
#> 25     0 0.000000000 0.000000000
#> 26     0 0.000000000 0.000000000
#> 27     0 0.000000000 0.000000000
#> 28     0 0.000000000 0.000000000
#>      M2.Ginglymostoma cirratum M2.Lutjanus jocu M2.Cephalopholis fulva
#> 1      0.000000000 0.00000000 0.000000000
#> 2      0.000000000 0.00000000 0.000000000
#> 3      0.000000000 0.00000000 0.000000000
#> 4      0.025135135 0.05500000 0.006036036
#> 5      0.000000000 0.00000000 0.000000000
#> 6      0.000000000 0.00000000 0.000000000
#> 7      0.005659229 0.06191684 0.014949290
#> 8      0.000000000 0.53086957 0.116521739
#> 9      0.000000000 0.00000000 0.268000000
#> 10     0.000000000 0.12333333 0.013535354
#> 11     0.000000000 0.00000000 0.000000000
#> 12     0.000000000 0.00000000 0.000000000
#> 13     0.000000000 0.00000000 0.000000000
#> 14     0.000000000 0.00000000 0.000000000
#> 15     0.026345609 0.23059490 0.018980170
#> 16     0.000000000 0.38076923 0.027858628
#> 17     0.000000000 0.15455696 0.169620253

```


#> 18	0.000000000	0.000000000	0.000000000
#> 19	1.377777778	0.904444444	0.033086420
#> 20	0.325500000	0.000000000	0.000000000
#> 21	0.096882915	0.28509872	0.028079401
#> 22	0.033225205	0.15025176	0.010106496
#> 23	0.000000000	0.000000000	0.000000000
#> 24	0.000000000	0.000000000	0.000000000
#> 25	0.000000000	0.000000000	0.000000000
#> 26	0.000000000	0.000000000	0.000000000
#> 27	0.000000000	0.000000000	0.000000000
#> 28	0.000000000	0.000000000	0.000000000
#>	M2.Carangidae	M2.Acanthurus spp.	M2.Stegastes rocasensis
#> 1	0.0000000	0.000000000	0.000000000
#> 2	0.0000000	0.000000000	0.000000000
#> 3	0.0000000	0.000000000	0.000000000
#> 4	0.0000000	0.000000000	0.000000000
#> 5	0.0000000	0.000000000	0.000000000
#> 6	0.0000000	0.000000000	0.000000000
#> 7	0.1214807	0.000000000	0.000000000
#> 8	0.0000000	0.000000000	0.000000000
#> 9	1.1978000	0.000000000	0.000000000
#> 10	0.2419798	0.000000000	0.000000000
#> 11	0.0000000	0.000000000	0.000000000
#> 12	0.0000000	0.000000000	0.000000000
#> 13	0.0000000	0.000000000	0.000000000
#> 14	0.0000000	0.000000000	0.000000000
#> 15	0.1131067	0.000000000	0.000000000
#> 16	0.0000000	0.000000000	0.000000000
#> 17	0.3032405	0.000000000	0.000000000
#> 18	0.0000000	0.000000000	0.000000000
#> 19	2.3660247	0.000000000	0.000000000
#> 20	0.0000000	0.000000000	0.000000000
#> 21	0.2725103	0.000000000	0.000000000
#> 22	0.3803790	0.42662434	0.008052647
#> 23	0.0000000	0.000000000	0.000000000
#> 24	5.3235556	0.000000000	0.000000000
#> 25	0.0000000	0.000000000	0.000000000
#> 26	0.0000000	0.06093839	0.001917047
#> 27	0.0000000	0.02947016	0.002734931
#> 28	2.6351600	32.24220000	1.893360000
#>	M2.Thalassoma noronhanum	M2.Abudedefduf saxatilis	M2.Sparisoma spp.
#> 1	0.000000000	0.000000000	0.000000000
#> 2	0.000000000	0.000000000	0.000000000
#> 3	0.000000000	0.000000000	0.000000000
#> 4	0.000000000	0.000000000	0.000000000
#> 5	0.000000000	0.000000000	0.000000000
#> 6	0.000000000	0.000000000	0.000000000
#> 7	0.000000000	0.000000000	0.000000000
#> 8	0.000000000	0.000000000	0.000000000
#> 9	0.000000000	0.000000000	0.000000000
#> 10	0.000000000	0.000000000	0.000000000
#> 11	0.000000000	0.000000000	0.000000000
#> 12	0.000000000	0.000000000	0.000000000

#> 13	0.0000000000	0.0000000000	0.0000000000
#> 14	0.0000000000	0.0000000000	0.0000000000
#> 15	0.0000000000	0.0000000000	0.0000000000
#> 16	0.0000000000	0.0000000000	0.0000000000
#> 17	0.0000000000	0.0000000000	0.0000000000
#> 18	0.0000000000	0.0000000000	0.0000000000
#> 19	0.0000000000	0.0000000000	0.0000000000
#> 20	0.0000000000	0.0000000000	0.0000000000
#> 21	0.0168835633	0.0000000000	0.0000000000
#> 22	0.0167912328	0.088028931	0.055621455
#> 23	0.0000000000	0.0000000000	0.0000000000
#> 24	1.0444444444	4.106666667	0.0000000000
#> 25	0.0000000000	7.392000000	0.0000000000
#> 26	0.0003997392	0.0000000000	0.003972444
#> 27	0.0007732648	0.003040411	0.001440823
#> 28	0.5640000000	1.108800000	2.101800000
M2.Melichthys niger M2.Kyphosus spp. M2.Mulloidichthys martinicus			
#> 1	0.0000000000	0.0000000000	0.00000000
#> 2	0.0000000000	0.0000000000	0.00000000
#> 3	0.0000000000	0.0000000000	0.00000000
#> 4	0.0000000000	0.0000000000	0.00000000
#> 5	0.0000000000	0.0000000000	0.00000000
#> 6	0.0000000000	0.0000000000	0.00000000
#> 7	0.0000000000	0.0000000000	0.00000000
#> 8	0.0000000000	0.0000000000	0.00000000
#> 9	0.0000000000	0.0000000000	0.00000000
#> 10	0.0000000000	0.0000000000	0.00000000
#> 11	0.0000000000	0.0000000000	0.00000000
#> 12	0.0000000000	0.0000000000	0.00000000
#> 13	0.0000000000	0.0000000000	0.00000000
#> 14	0.0000000000	0.0000000000	0.00000000
#> 15	0.0000000000	0.0000000000	0.00000000
#> 16	0.0000000000	0.0000000000	0.00000000
#> 17	0.0000000000	0.0000000000	0.00000000
#> 18	0.0000000000	0.0000000000	0.00000000
#> 19	0.0000000000	0.0000000000	0.00000000
#> 20	0.0000000000	0.0000000000	0.00000000
#> 21	0.0000000000	0.0000000000	0.0597750
#> 22	0.010717808	0.0100429832	0.1109698
#> 23	0.0000000000	0.0000000000	0.00000000
#> 24	1.5000000000	0.0000000000	0.7395556
#> 25	0.0000000000	0.0000000000	0.00000000
#> 26	0.000765458	0.0315595498	0.00000000
#> 27	0.001110540	0.0008671808	0.00000000
#> 28	0.1350000000	0.0000000000	0.00000000
M2.Holocentrus adscensionis M2.Haemulidae M2.Cryptobenthic reef fishes			
#> 1	0.00000000	0.00000000	0.0000000000
#> 2	0.00000000	0.00000000	0.0000000000
#> 3	0.00000000	0.00000000	0.0000000000
#> 4	0.00000000	0.00000000	0.0000000000
#> 5	0.00000000	0.00000000	0.0000000000
#> 6	0.00000000	0.00000000	0.0000000000
#> 7	0.00000000	0.00000000	0.0000000000

#> 8	0.0000000	0.0000000	0.000000000
#> 9	0.0000000	0.0000000	0.000000000
#> 10	0.0000000	0.0000000	0.000000000
#> 11	0.0000000	0.0000000	0.000000000
#> 12	0.0000000	0.0000000	0.000000000
#> 13	0.0000000	0.0000000	0.000000000
#> 14	0.0000000	0.0000000	0.000000000
#> 15	0.0000000	0.0000000	0.000000000
#> 16	0.0000000	0.0000000	0.000000000
#> 17	0.0000000	0.0000000	0.000000000
#> 18	0.0000000	0.0000000	0.000000000
#> 19	0.0000000	0.0000000	0.000000000
#> 20	0.0000000	0.0000000	0.000000000
#> 21	0.7367448	0.2004330	0.059358897
#> 22	0.1744561	0.2657826	0.165295992
#> 23	0.0000000	0.0000000	0.000000000
#> 24	3.2554444	4.1330370	7.344074074
#> 25	0.0000000	0.0000000	6.609666667
#> 26	0.0000000	0.0000000	0.000000000
#> 27	0.0000000	0.0000000	0.002038972
#> 28	0.0000000	0.0000000	8.724760000
#>	M2.Turtles M2.Cephalopoda M2.Panulirus spp.		
#> 1	0.000000e+00	0.000000	0.00000000
#> 2	0.000000e+00	0.000000	0.00000000
#> 3	0.000000e+00	0.000000	0.00000000
#> 4	0.000000e+00	0.000000	0.00000000
#> 5	0.000000e+00	0.000000	0.00000000
#> 6	0.000000e+00	0.000000	0.00000000
#> 7	0.000000e+00	0.000000	0.00000000
#> 8	0.000000e+00	0.000000	0.00000000
#> 9	0.000000e+00	0.000000	0.00000000
#> 10	0.000000e+00	0.000000	0.00000000
#> 11	0.000000e+00	0.000000	0.00000000
#> 12	0.000000e+00	0.000000	0.00000000
#> 13	0.000000e+00	0.000000	0.00000000
#> 14	0.000000e+00	0.000000	0.00000000
#> 15	0.000000e+00	0.000000	0.00000000
#> 16	0.000000e+00	0.000000	0.00000000
#> 17	0.000000e+00	0.000000	0.00000000
#> 18	0.000000e+00	0.000000	0.00000000
#> 19	6.382716e-03	0.000000	0.00000000
#> 20	0.000000e+00	0.000000	0.00000000
#> 21	1.083362e-03	0.619528	0.5316526
#> 22	5.130654e-04	0.176040	0.6168694
#> 23	0.000000e+00	0.000000	0.00000000
#> 24	0.000000e+00	0.000000	0.00000000
#> 25	0.000000e+00	0.000000	0.00000000
#> 26	2.931421e-05	0.000000	0.00000000
#> 27	3.544130e-06	0.000000	0.00000000
#> 28	2.585000e-03	0.000000	19.9800000
#>	M2.Benthic macroinvertebrates M2.Benthic microinvertebrates		
#> 1	0.00000000		0.00000000
#> 2	0.00000000		0.00000000

#> 3	0.00000000		0.00000000
#> 4	0.00000000		0.00000000
#> 5	0.00000000		0.00000000
#> 6	0.00000000		0.00000000
#> 7	0.00000000		0.00000000
#> 8	0.00000000		0.00000000
#> 9	0.00000000		0.00000000
#> 10	0.00000000		0.00000000
#> 11	0.00000000		0.00000000
#> 12	0.00000000		0.00000000
#> 13	0.00000000		0.00000000
#> 14	0.00000000		0.00000000
#> 15	0.00000000		0.00000000
#> 16	0.00000000		0.00000000
#> 17	0.00000000		0.00000000
#> 18	0.00000000		0.00000000
#> 19	0.00000000		0.00000000
#> 20	0.00000000		0.00000000
#> 21	0.50000000		0.00000000
#> 22	1.32604179		0.16690000
#> 23	0.00000000		0.00000000
#> 24	0.00000000		0.00000000
#> 25	0.00000000		0.00000000
#> 26	0.04735247		0.00000000
#> 27	0.00000000		0.02882261
#> 28	108.56712928		374.20029613
#>	M2.Siderastrea stellata M2.Zooplankton M2.Phytoplankton		
#> 1	0.0000	0.0	0
#> 2	0.0000	0.0	0
#> 3	0.0000	0.0	0
#> 4	0.0000	0.0	0
#> 5	0.0000	0.0	0
#> 6	0.0000	0.0	0
#> 7	0.0000	0.0	0
#> 8	0.0000	0.0	0
#> 9	0.0000	0.0	0
#> 10	0.0000	0.0	0
#> 11	0.0000	0.0	0
#> 12	0.0000	0.0	0
#> 13	0.0000	0.0	0
#> 14	0.0000	0.0	0
#> 15	0.0000	0.0	0
#> 16	0.0000	0.0	0
#> 17	0.0000	0.0	0
#> 18	0.0000	0.0	0
#> 19	0.0000	0.0	0
#> 20	0.0000	0.0	0
#> 21	0.0000	0.0	0
#> 22	0.0000	0.0	0
#> 23	0.0000	0.0	0
#> 24	137.5185	0.0	0
#> 25	0.0000	86.4	0
#> 26	0.0000	0.0	0

```

#> 27          0.0000          0.0          0
#> 28          0.0000          0.0          0
#>   M2.Digenea simplex M2.Other algal turf
#> 1          0          0
#> 2          0          0
#> 3          0          0
#> 4          0          0
#> 5          0          0
#> 6          0          0
#> 7          0          0
#> 8          0          0
#> 9          0          0
#> 10         0          0
#> 11         0          0
#> 12         0          0
#> 13         0          0
#> 14         0          0
#> 15         0          0
#> 16         0          0
#> 17         0          0
#> 18         0          0
#> 19         0          0
#> 20         0          0
#> 21         0          0
#> 22         0          0
#> 23         0          0
#> 24         0          0
#> 25         0          0
#> 26         0          0
#> 27         0          0
#> 28         0          0
check.rpath.params(REco.params)
#> Warning in check.rpath.params(REco.params): fleets is a fleet and should not have a biomass...set to
#> Warning in check.rpath.params(REco.params): fleets are fleets and should not have a BioAcc...set to
#> Warning in check.rpath.params(REco.params): fleets are fleets and should not have an Unassim...set t
#> Warning in check.rpath.params(REco.params): Negaprion brevirostris sum,
#> 0.99 is not 1...check DC or proportion of primary production
#> Warning in check.rpath.params(REco.params): Cephalopholis fulva sum, 0.99
#> is not 1...check DC or proportion of primary production
#> Warning in check.rpath.params(REco.params): Siderastrea stellata sum, 1 is
#> not 1...check DC or proportion of primary production
#> Rpath parameter file needs attention!

```

Note that if you wish to save the `print` output you need to use the function `write.rpath`. This function will also accept the argument `'morts = T'`.

The generic function `summary` will display some summary statistics on the model as well as a list of attributes you can access. To access any of the other attributes simply use the standard list notation.

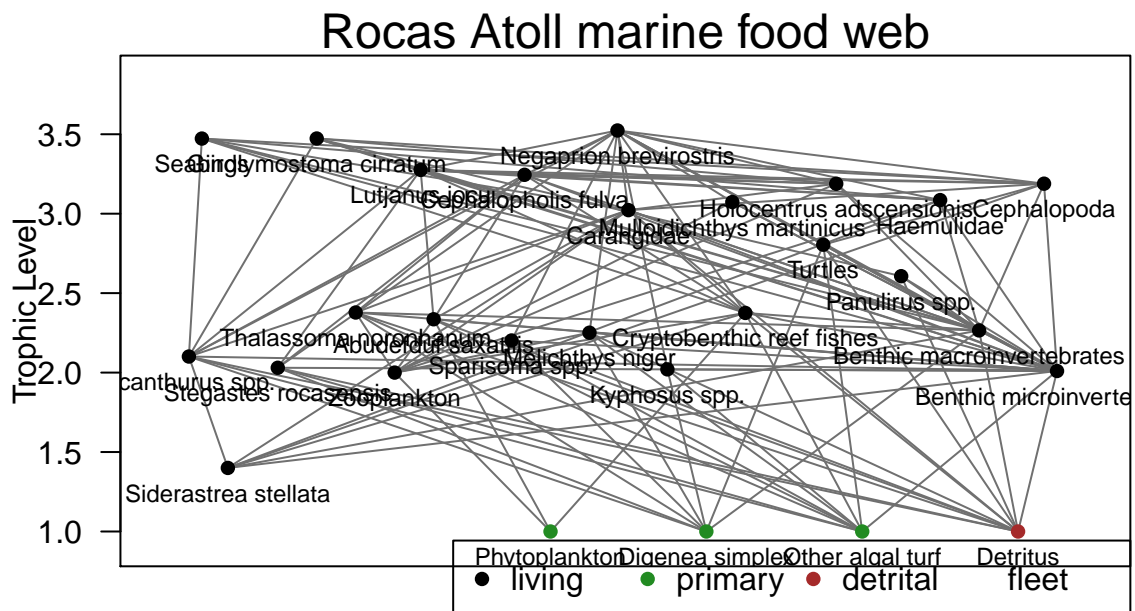
```

summary(REco)
#> Rpath model: Rpath Rocas Atoll marine food web
#>   Status: Unbalanced!
#> The following groups have EE > 1:
#> [1] "Zooplankton"

```

```
#>
#>
#> Summary Statistics:
#>   Num.Groups Num.Living Num.Detritus Num.Fleets TotBiomass TotCatch
#> 1          29          27           1           1  72.77735         0
#>
#> Rpath model also includes:
#> [1] "NUM_GROUPS" "NUM_LIVING" "NUM_DEAD" "NUM_GEARS" "Group"
#> [6] "type"       "TL"       "BB"       "PB"       "QB"
#> [11] "EE"        "BA"        "GS"        "GE"        "DC"
#> [16] "DetFate"    "Catch"     "Discards"
REco$TL
#> [1] 3.472713 3.523583 3.473124 3.275414 3.244684 3.022266 2.101010
#> [8] 2.030303 2.378044 2.335578 2.202020 2.251010 2.020202 3.073392
#> [15] 3.188224 3.085646 2.375385 2.804811 3.188729 2.606592 2.265284
#> [22] 2.010101 1.400000 2.000000 1.000000 1.000000 1.000000 1.000000
#> [29] 1.000000
```

```
p <- webplot(REco, line.col = "gray44", eco.name = "Rocas Atoll marine food web", labels = T, label.pos
```



```
p
#> $xlog
#> [1] FALSE
#>
#> $ylog
```

```
#> [1] FALSE
#>
#> $adj
#> [1] 0.5
#>
#> $ann
#> [1] TRUE
#>
#> $ask
#> [1] FALSE
#>
#> $bg
#> [1] "transparent"
#>
#> $bty
#> [1] "o"
#>
#> $cex
#> [1] 1
#>
#> $cex.axis
#> [1] 1
#>
#> $cex.lab
#> [1] 1
#>
#> $cex.main
#> [1] 1.2
#>
#> $cex.sub
#> [1] 1
#>
#> $col
#> [1] "black"
#>
#> $col.axis
#> [1] "black"
#>
#> $col.lab
#> [1] "black"
#>
#> $col.main
#> [1] "black"
#>
#> $col.sub
#> [1] "black"
#>
#> $crt
#> [1] 0
#>
#> $err
#> [1] 0
#>
```



```
#> $family
#> [1] ""
#>
#> $fg
#> [1] "black"
#>
#> $fig
#> [1] 0 1 0 1
#>
#> $fin
#> [1] 6.5 4.5
#>
#> $font
#> [1] 1
#>
#> $font.axis
#> [1] 1
#>
#> $font.lab
#> [1] 1
#>
#> $font.main
#> [1] 2
#>
#> $font.sub
#> [1] 1
#>
#> $lab
#> [1] 5 5 7
#>
#> $las
#> [1] 0
#>
#> $lend
#> [1] "round"
#>
#> $lheight
#> [1] 1
#>
#> $ljoin
#> [1] "round"
#>
#> $lmitre
#> [1] 10
#>
#> $lty
#> [1] "solid"
#>
#> $lwd
#> [1] 1
#>
#> $mai
#> [1] 1.02 0.82 0.82 0.42
```

```

#>
#> $mar
#> [1] 5.1 4.1 4.1 2.1
#>
#> $mex
#> [1] 1
#>
#> $mfcol
#> [1] 1 1
#>
#> $mfg
#> [1] 1 1 1 1
#>
#> $mfrow
#> [1] 1 1
#>
#> $mgp
#> [1] 3 1 0
#>
#> $mkh
#> [1] 0.001
#>
#> $new
#> [1] TRUE
#>
#> $oma
#> [1] 0 0 0 0
#>
#> $omd
#> [1] 0 1 0 1
#>
#> $omi
#> [1] 0 0 0 0
#>
#> $pch
#> [1] 1
#>
#> $pin
#> [1] 5.26 2.66
#>
#> $plt
#> [1] 0.09538462 0.90461538 0.20444444 0.79555556
#>
#> $ps
#> [1] 12
#>
#> $pty
#> [1] "m"
#>
#> $sma
#> [1] 1
#>
#> $srt

```

```

#> [1] 0
#>
#> $tck
#> [1] NA
#>
#> $tcl
#> [1] -0.5
#>
#> $usr
#> [1] -0.0400000  1.0400000  0.7809624  3.9949787
#>
#> $xaxp
#> [1] 0 1 5
#>
#> $xaxs
#> [1] "r"
#>
#> $xaxt
#> [1] "s"
#>
#> $xpd
#> [1] FALSE
#>
#> $yaxp
#> [1] 0 1 5
#>
#> $yaxs
#> [1] "r"
#>
#> $yaxt
#> [1] "s"
#>
#> $ylbias
#> [1] 0.2

```