

4. Summary and diagnostics

 offshore-wind.github.io/narwind/articles/model_summary.html

Preamble

This tutorial demonstrates how to inspect and summarize outputs from the agent-based model within the `narwind` R package.

Viewing data

Outputs from the `narw()` simulator can be viewed in the R console using the `print()` method. `print()` is part of a group of generic R functions that can be applied to various R objects and will behave differently depending on the type of object that is passed to them. Other generic functions include `plot()`, `summary()`, or `write()` (among others) – these are covered in later sections.

`print()` can also be called ‘implicitly’, that is, by simply typing the name of the relevant object in the R console and pressing `[Enter]` on the keyboard. The default behavior for objects returned by `narw()` is to give a tabular overview of the data from the first 5 days of the simulation, and for the first animal in each population cohort. For instance, to get a quick overview of the outputs from the `baseline_model` created in the previous tutorial, we can type:

```
model_base
```

Optional arguments allow users to override these default settings and display data for specific days, animals, and/or cohorts, as needed. The `print()` method has the following arguments:

Argument	Default value	Description
<code>obj</code>	-	Input model object returned by <code>narw()</code> .
<code>rowID</code>	<code>1:5</code>	Positive integer or vector of positive integers indicating which days of the simulation should be displayed. Defaults to the first first days.
<code>whale</code>	<code>1</code>	Positive integer indicating the individual for which data should be extracted. Only the first individual is included by default.
<code>cohort</code>	<code>1:6</code>	Positive integer or vector of positive integers indicating which cohorts should be considered. Defaults to all cohorts. Cohort identifiers are listed in an object called <code>cohorts</code> . Note that calves are included with their mothers (i.e., <code>cohort = 5</code>).

Given the above, the code below displays the first 5 days of the simulation for the fourth adult male.

```

print(model_base, rowID = 1:5, whale = 4, cohort = 3)
#>
#>
#>
#>
=====
=====
#> Adults (male)
#>
=====
=====
#>
#> -----
#> Locations
#> -----
#>
#>   whale day  date  easting northing region resid_m resid_sd please
#> 1:     4   1 01-10 740.5000 776.5000   GOM   20.4     1.1     0
#> 2:     4   2 02-10 738.0150 777.0969   GOM   20.4     1.1     0
#> 3:     4   3 03-10 740.6500 784.3279   GOM   20.4     1.1     0
#> 4:     4   4 04-10 741.8054 782.5409   GOM   20.4     1.1     0
#> 5:     4   5 05-10 741.6727 785.8434   GOM   20.4     1.1     0
#>
#> -----
#> Attributes
#> -----
#>   whale day cohort gsl seus alive      age      bc  length length_a
#> 1:     4   1      3   0   0      1 15.89359 0.3942573 13.34207 1362.755
#> 2:     4   2      3   0   0      1 15.89633 0.3944316 13.34221 1362.755
#> 3:     4   3      3   0   0      1 15.89907 0.3944270 13.34235 1362.755
#> 4:     4   4      3   0   0      1 15.90181 0.3945859 13.34248 1362.755
#> 5:     4   5      3   0   0      1 15.90455 0.3947831 13.34262 1362.755
#>   length_b length_c      mass leanmass  fatmass      mass_a  mass_b  mouth_r
#> 1:   -0.37   -0.18 28504.63 17266.47 11238.16 -4.834189 2.984353 0.1467477
#> 2:   -0.37   -0.18 28513.72 17267.01 11246.72 -4.834189 2.984353 0.1467477
#> 3:   -0.37   -0.18 28514.40 17267.55 11246.85 -4.834189 2.984353 0.1467477
#> 4:   -0.37   -0.18 28522.77 17268.08 11254.68 -4.834189 2.984353 0.1467477
#> 5:   -0.37   -0.18 28532.95 17268.62 11264.33 -4.834189 2.984353 0.1467477
#>   mouth_a  mouth_w abort starve died date_died p_surv
#> 1:   76.7 1.957917     0     0     0         0     1
#> 2:   76.7 1.957938     0     0     0         0     1
#> 3:   76.7 1.957958     0     0     0         0     1
#> 4:   76.7 1.957979     0     0     0         0     1
#> 5:   76.7 1.957999     0     0     0         0     1
#>
#> -----
#> Stressors
#> -----
#>
#>   whale day gear_risk is_entgl entgl_head entgl_sev entgl_d entgl_start
#> 1:     4   1         0         0         0         0         0
#> 2:     4   2         0         0         0         0         0
#> 3:     4   3         0         0         0         0         0
#> 4:     4   4         0         0         0         0         0
#> 5:     4   5         0         0         0         0         0
#>   entgl_end is_entgl_calf entgl_head_calf entgl_sev_calf entgl_d_calf

```

```

#> 1:      0      0      0      0      0
#> 2:      0      0      0      0      0
#> 3:      0      0      0      0      0
#> 4:      0      0      0      0      0
#> 5:      0      0      0      0      0
#>      entgl_start_calf entgl_end_calf strike_risk strike strike_calf noise_resp
#> 1:      0      0      0      0      0      0
#> 2:      0      0      0      0      0      0
#> 3:      0      0      0      0      0      0
#> 4:      0      0      0      0      0      0
#> 5:      0      0      0      0      0      0
#>      noise_lvl dB_thresh
#> 1:      0      0
#> 2:      0      0
#> 3:      0      0
#> 4:      0      0
#> 5:      0      0
#>
#> -----
#> Activity budgets
#> -----
#>
#>      whale day d_travel swimspeed      glide glide_feed glide_echelon t_travel
#> 1:      4   1 2.555656 0.8316983 0.09532139 0.3179245      0 0.8535601
#> 2:      4   2 7.696048 1.1538667 0.09290994 0.5119930      0 1.8527192
#> 3:      4   3 2.127993 0.5633504 0.08656162 0.3917774      0 1.0492746
#> 4:      4   4 3.305147 1.0732973 0.09643285 0.3520231      0 0.8553981
#> 5:      4   5 3.663948 1.1947665 0.08523470 0.2785317      0 0.8518512
#>      t_feed t_rest_nurse
#> 1: 16.19956      6.946884
#> 2: 15.56950      6.577784
#> 3: 16.66407      6.286659
#> 4: 15.86037      7.284232
#> 5: 15.63789      7.510257
#>
#> -----
#> Growth
#> -----
#>
#>      whale day delta_fat  EDlip EDpro lip_anab lip_catab perc_muscle
perc viscera
#> 1:      4   1 4.912263 39.539 23.64      0.8      0.8 0.5537975
0.2009494
#> 2:      4   2 8.559065 39.539 23.64      0.8      0.8 0.5537975
0.2009494
#> 3:      4   3 0.133245 39.539 23.64      0.8      0.8 0.5537975
0.2009494
#> 4:      4   4 7.833849 39.539 23.64      0.8      0.8 0.5537975
0.2009494
#> 5:      4   5 9.643540 39.539 23.64      0.8      0.8 0.5537975
0.2009494
#>      perc_bones
#> 1: 0.2452532
#> 2: 0.2452532
#> 3: 0.2452532
#> 4: 0.2452532

```

```

#> 5: 0.2452532
#>
#> -----
#> Energy balance
#> -----
#>
#>   whale day      E_tot      E_in      E_out
#> 1:      4      1 242.78246 706.1029 463.3204
#> 2:      4      2 423.02108 940.1171 517.0961
#> 3:      4      3  6.58547 479.3556 472.7701
#> 4:      4      4 387.17821 869.3136 482.1354
#> 5:      4      5 476.61991 951.7746 475.1547
#>
#> -----
#> Energy intake
#> -----
#>
#>   whale day feed preyconc   minprey      gape feedspeed captEff impedance
#> 1:      4      1      1 3.932587 0.4686015 2.521936 0.8316983 0.91575      0
#> 2:      4      2      1 3.932587 0.4686015 2.522014 1.1538667 0.91575      0
#> 3:      4      3      1 3.847692 0.4686015 2.522092 0.5633504 0.91575      0
#> 4:      4      4      1 3.847692 0.4686015 2.522170 1.0732973 0.91575      0
#> 5:      4      5      1 3.847692 0.4686015 2.522249 1.1947665 0.91575      0
#>   feed_effort eta_lwrBC eta_upprBC   targetBC      cop_mass      cop_kJ digestEff
#> 1:  0.3365457      10      30 0.3674076 0.001670151 0.02391922      0.94
#> 2:  0.3360340      10      30 0.3674076 0.001670151 0.02391922      0.94
#> 3:  0.3351153      10      30 0.3674076 0.001670151 0.02391922      0.94
#> 4:  0.3351396      10      30 0.3674076 0.001670151 0.02391922      0.94
#> 5:  0.3343043      10      30 0.3674076 0.001670151 0.02391922      0.94
#>   metabEff_juv metabEff_ad      E_cop
#> 1:  0.7403977      0.875 0.004762958
#> 2:  0.7403977      0.875 0.004762958
#> 3:  0.7403977      0.875 0.004762958
#> 4:  0.7403977      0.875 0.004762958
#> 5:  0.7403977      0.875 0.004762958
#>
#> -----
#> Energetic costs
#> -----
#>
#>   whale day      E_out      rmr      LC scalar_LC      stroke stroke_feed
#> 1:      4      1 463.3204 442.0439 13.12947      1 0.07724737 0.1687092
#> 2:      4      2 517.0961 442.0532 66.89951      1 0.13665451 0.1674238
#> 3:      4      3 472.7701 442.0626 22.56799      1 0.15996304 0.1622918
#> 4:      4      4 482.1354 442.0720 31.92769      1 0.15489603 0.1666031
#> 5:      4      5 475.1547 442.0813 24.94139      1 0.10646713 0.1722184
#>   E_growth
#> 1: 8.147064
#> 2: 8.143301
#> 3: 8.139539
#> 4: 8.135780
#> 5: 8.132021

```

Note 4.1: The `print()` method is only used for viewing data inside the R console. To export / save data on disk, use the `export()` method (see relevant tutorial).

Model summary and diagnostics

The `summary(.)` method provides a range of diagnostics that are helpful for assessing whether simulated whale behavior aligns with biological expectations. These relate to individual (1) health, (2) movements, (3) habitat use, (4) behavior (i.e., activity budgets), (5) stressor exposure, and (6) energy intake vs. expenditure (see Table 1 below).

The function takes the following arguments:

Argument	Default value	Description
<code>obj</code>	-	Model object of class <code>narwsim</code> , as returned by <code>narw(.)</code> .
<code>what</code>	"all"	Character string indicating which component(s) of the summary to display. Can be one of: "health", "movements", "habitat", "behavior", "stressors", "strike", "gear", "noise", "other", or "energy". See below for details. Defaults to "all" for a complete summary.
<code>relative</code>	FALSE	Logical. If <code>TRUE</code> , percentages are calculated relative to class totals. Defaults to <code>FALSE</code> .
<code>quintile</code>	TRUE	Logical. If <code>TRUE</code> , body condition plots (under the "health" section) are based on quintiles of the data.
<code>plot</code>	FALSE	Logical. If <code>TRUE</code> , plots are produced in addition to a text-based summary.
<code>whale</code>	1:nsim	Positive integer indicating the individual for which data should be extracted. By default, considers all <code>nsim</code> individuals.
<code>cohort</code>	1:6	Positive integer or vector of positive integers indicating which cohorts should be considered. Defaults to all cohorts. Cohort identifiers are listed in an object called <code>cohorts</code> .

As summaries tend to be long and dense, the `what` argument can be used to select subsets of data to show in the R console. The table below lists the information returned for each possible value of `what`.

Category	Component	Plots	Details
health	Mortality	No	Whale mortality by region, cohort, and cause of death (i.e., starvation vs. vessel strike) .

Category	Component	Plots	Details
	Pregnancy	No	Observed abortion rate in females that started the simulation in a pregnant state.
	Births	No	Mean (range) date of calving events.
	Body condition	Yes	Time series of individual body condition (expressed as relative fat mass), by cohort.
	Growth	Yes	Growth curves, by cohort.
movements	Locations	No	Breakdown of (daily) locations by cohort, region, and country (U.S. vs. Canada).
	Destinations	No	Comparison of assigned vs. realized migratory destinations both within and across cohorts. Migratory endpoints include the Southeastern United States calving grounds (SEUS) and Canadian feeding grounds in the Gulf of St Lawrence (GSL).
	Step lengths	Yes	Summary of daily movements, reported as mean (\pm SD, range) distances traveled per day, by cohort. Distributions of daily step lengths are also visualized by region and as a whole.
	Migration	No	Summary of yearly movements, reported as mean (\pm SD, range) total distance covered over the time span of the simulation, by cohort.
habitat	Occupancy	No	Cohort-specific summary of the numbers of animals visiting each region, and the number of regions visited by animals.
	Residency	No	Breakdown of days spent in each.

Category	Component	Plots	Details
behavior	Activity budgets	Yes	Mean (\pm SD) hours spent engaging in each of the four categories of behavior considered in the model (i.e., traveling, resting, nursing, and feeding), by region. A visual breakdown by region is also produced for each category of behavior.
stressors	Entanglements (gear)	Yes	Various summaries by cohort, including: entanglement rates, durations, severities, probabilities, and attachment sites along the body.
	Vessel strikes (strike)	No	Strike rates by cohort.
	Noise (noise)	No	Summary of mean (\pm SD, range) noise levels encountered, behavioral response thresholds, and numbers of days during which a response to pile-driving was observed.
	Other sources of mortality (other)	No	Summary of mortality from other sources, by cohort.
Energy	Energy budget	No	Mean (\pm SD, range) daily energy intake and expenditure (expressed in MJ/day), by cohort. Also reported are the mean (\pm SD, range) % time individuals are in energetic deficit (energy balance < 0) or surplus (energy balance > 0).

Similarly, the `cohort` argument can be used to only display data for specific population cohorts. This works based on a unique cohort ID number, which is an integer between 1 and 6. A list of cohort IDs is stored in the left-most column of an object called `cohorts`, as shown below:

```
cohorts
#>   id          name      class  abb  colour
#> 1:  0 Calves (male, female) Calves c(m,f)  black
#> 2:  1 Juveniles (male) Juveniles jv(m)  #104E8B
#> 3:  2 Juveniles (female) Juveniles jv(f)  #F69554
#> 4:  3 Adults (male) Adults ad(m)  #22BA9C
#> 5:  4 Adults (female, pregnant) Adults ad(f,p) #84375A
#> 6:  5 Adults (female, lactating) Adults ad(f,l) #EEB422
#> 7:  6 Adults (female, resting) Adults ad(f,r) #942F33
```


Based on this, the code below prints a complete summary (all categories of data listed in the above table) for the cohorts of lactating (ID = 5) females:

```

# Summary for adult females only
summary(model_base, cohort = 5)
#> -----
#> -----
#>
#>      NORTH ATLANTIC RIGHT WHALE (Eubalaena glacialis)
#>
#>          *** PCoMS MODEL SUMMARY ***
#>
#> -----
#> -----
#>
#> BOF: Bay of Fundy
#> CCB: Cape Cod Bay
#> CST: Cabot Strait
#> GMAN: Grand Manan Basin
#> GOM: Gulf of Maine and Georges Bank
#> GSL: Gulf of St Lawrence
#> MIDA: Mid-Atlantic
#> SCOS: Scotian Shelf
#> SEUS: Southeastern United States
#> SNE: Southern New England
#>
#> =====
#> SIMULATIONS
#> =====
#>
#> No. animals: 1,000
#>
#> Cohort(s)
#> -----
#> c(m,f): Calves (male, female)
#> ad(f,l): Adults (female, lactating)
#>
#> Simulation start: October
#>
#> =====
#> HEALTH
#> =====
#>
#> ++++++++ Mortality ++++++++
#>
#> cohort                alive                dead
#> -----
#> Adults (female, lactating)  92.1% (921)   7.9% (79)
#> Calves (male, female)      83.0% (830)  17.0% (170)
#>
#> ++++++++ Mortality (by source) ++++++++
#>
#> cohort    cause_death    N
#> -----
#> ad(f,l)   starve         3.9% (39)
#> ad(f,l)   strike         2.0% (20)
#> ad(f,l)   natural        2.0% (20)
#> c(m,f)    starve         6.9% (69)
#> c(m,f)    natural        2.9% (29)

```

```

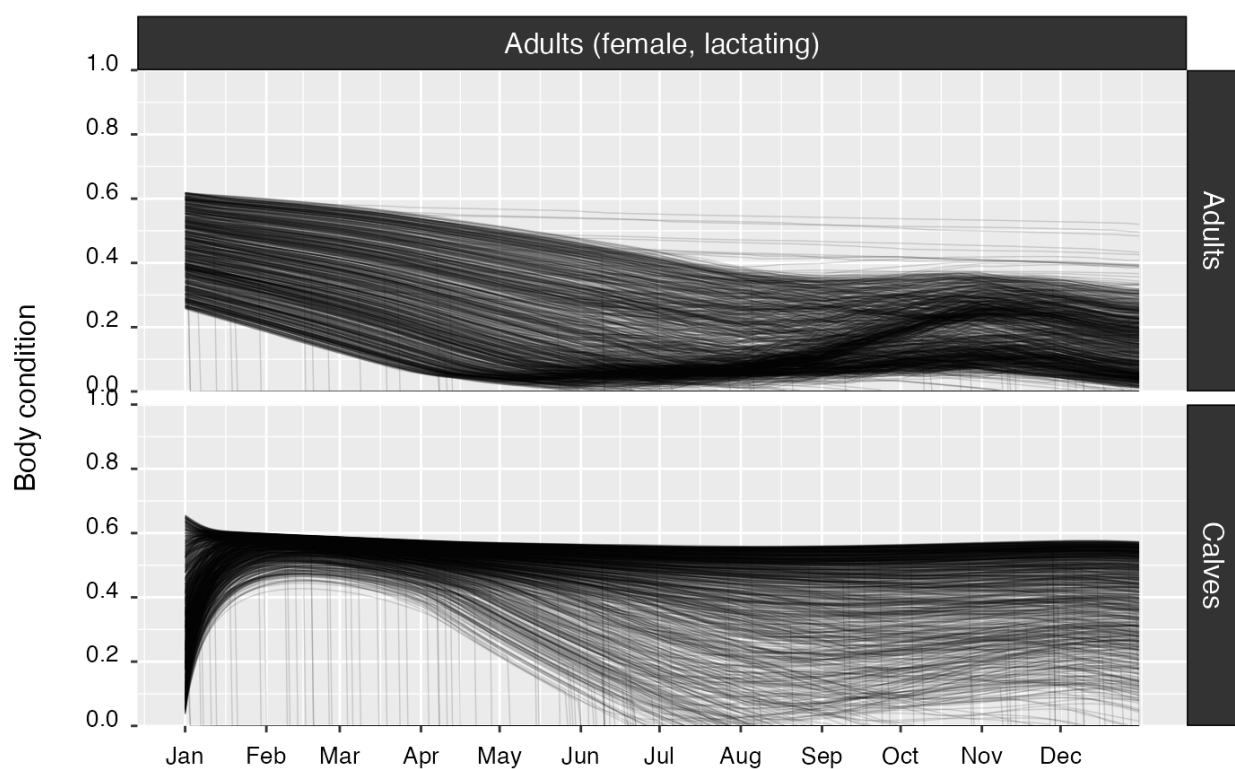
#> c(m,f)    starve (female)    2.5% (25)
#> c(m,f)    natural (female)   1.9% (19)
#> c(m,f)    strike (female)    1.8% (18)
#> c(m,f)    strike              1.0% (10)
#>
#> ++++++ Mortality (by region) ++++++
#>
#> region      cause_death      ad(f,l)      c(m,f)
#> -----
#> CST         natural          0.1% (1)    0.1% (1)
#> GOM         natural          0.6% (6)    0.8% (8)
#> GSL         natural          0.3% (3)    0.3% (3)
#> MIDA        natural          0.1% (1)    0.1% (1)
#> SCOS        natural          0.2% (2)    0.1% (1)
#> SEUS        natural          0.4% (4)    0.9% (9)
#> SNE         natural          0.3% (3)    0.6% (6)
#>
#>
#> region      cause_death      ad(f,l)      c(m,f)
#> -----
#> CST         natural (female)  0.0% (0)    0.1% (1)
#> GOM         natural (female)  0.0% (0)    0.6% (6)
#> GSL         natural (female)  0.0% (0)    0.3% (3)
#> MIDA        natural (female)  0.0% (0)    0.1% (1)
#> SCOS        natural (female)  0.0% (0)    0.2% (2)
#> SEUS        natural (female)  0.0% (0)    0.4% (4)
#> SNE         natural (female)  0.0% (0)    0.2% (2)
#>
#>
#> region      cause_death      ad(f,l)      c(m,f)
#> -----
#> CCB         starve           0.1% (1)    0.0% (0)
#> CST         starve           1.0% (10)   1.0% (10)
#> GOM         starve           0.5% (5)    2.1% (21)
#> GSL         starve           0.3% (3)    0.6% (6)
#> MIDA        starve           0.0% (0)    0.1% (1)
#> SCOS        starve           1.0% (10)   2.6% (26)
#> SNE         starve           1.0% (10)   0.5% (5)
#>
#>
#> region      cause_death      ad(f,l)      c(m,f)
#> -----
#> CST         starve (female)   0.0% (0)    0.4% (4)
#> GOM         starve (female)   0.0% (0)    0.5% (5)
#> SCOS        starve (female)   0.0% (0)    0.9% (9)
#> SNE         starve (female)   0.0% (0)    0.7% (7)
#>
#>
#> region      cause_death      ad(f,l)      c(m,f)
#> -----
#> CST         strike           0.1% (1)    0.0% (0)
#> GOM         strike           0.2% (2)    0.1% (1)
#> GSL         strike           0.1% (1)    0.2% (2)
#> MIDA        strike           0.4% (4)    0.1% (1)
#> SEUS        strike           0.8% (8)    0.3% (3)
#> SNE         strike           0.4% (4)    0.3% (3)

```

```

#>
#>
#> region      cause_death      ad(f,l)      c(m,f)
#> -----
#> CST        strike (female)  0.0% (0)    0.1% (1)
#> GOM        strike (female)  0.0% (0)    0.2% (2)
#> GSL        strike (female)  0.0% (0)    0.1% (1)
#> MIDA       strike (female)  0.0% (0)    0.4% (4)
#> SEUS       strike (female)  0.0% (0)    0.8% (8)
#> SNE        strike (female)  0.0% (0)    0.2% (2)
#>
#>
#> ++++++++ Births ++++++++
#>
#> No. births: 1000 (100%)
#> DOB: 1 Jan

```

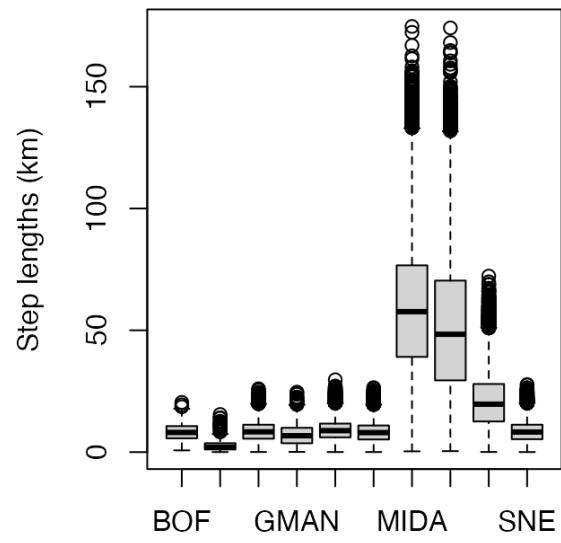
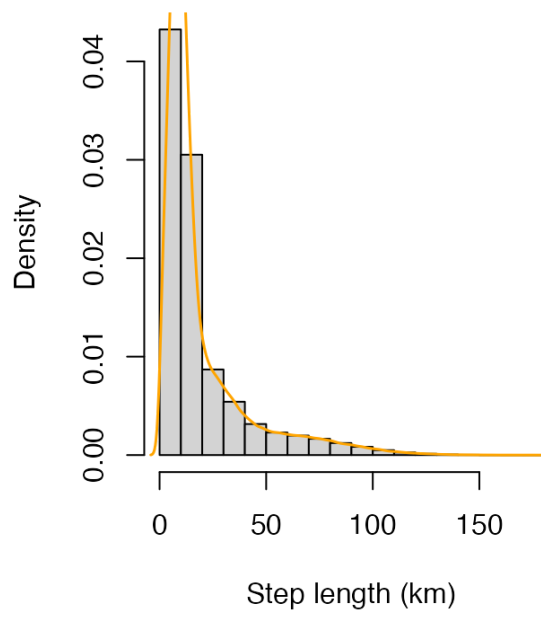


```

#>
#> =====
#> MOVEMENTS (km)
#> =====

```

Adults (female, lactating)



```

#>
#> ++++++++ Migratory destinations (by cohort) ++++++++
#>
#> cohort      SEUS    reach_not    reach
#> -----
#> ad(f,l)    0        0.0% (0)    94.6% (946)
#> ad(f,l)    1        0.0% (0)    100.0% (1000)
#>
#>
#> cohort      GSL     reach_not      reach
#> -----
#> ad(f,l)    0        105.1% (1051)    13.6% (136)
#> ad(f,l)    1         4.8% (48)      71.1% (711)
#>
#> ++++++++ Migratory destinations (all individuals) ++++++++
#>
#> SEUS    reach_not    reach
#> -----
#> 0        0.0% (0)    94.6% (946)
#> 1        0.0% (0)    100.0% (1000)
#>
#>
#> GSL     reach_not      reach
#> -----
#> 0        105.1% (1051)    13.6% (136)
#> 1         4.8% (48)      71.1% (711)
#>
#> ++++++++ Step lengths and migration distances ++++++++
#>
#> cohort      step                      migration
#> -----
#> ad(f,l)    18.9 (±20.9) [0-174.7]    8,521 (±1,065) [1,684-12,424]
#>
#> =====
#> HABITAT USE
#> =====
#>
#> region      ad(f,l)
#> -----
#> BOF         0.1% (382)
#> CCB         0.1% (231)
#> CST         4.7% (20741)
#> GMAN        0.8% (3588)
#> GOM        21.4% (95008)
#> GSL         9.3% (41381)
#> MIDA        8.5% (37839)
#> SCOS        7.4% (33052)
#> SEUS       23.6% (104960)
#> SNE        24.1% (106925)
#>
#>
#> country      ad(f,l)
#> -----
#> Canada      22.3% (99144)
#> U.S.        77.7% (344963)
#>

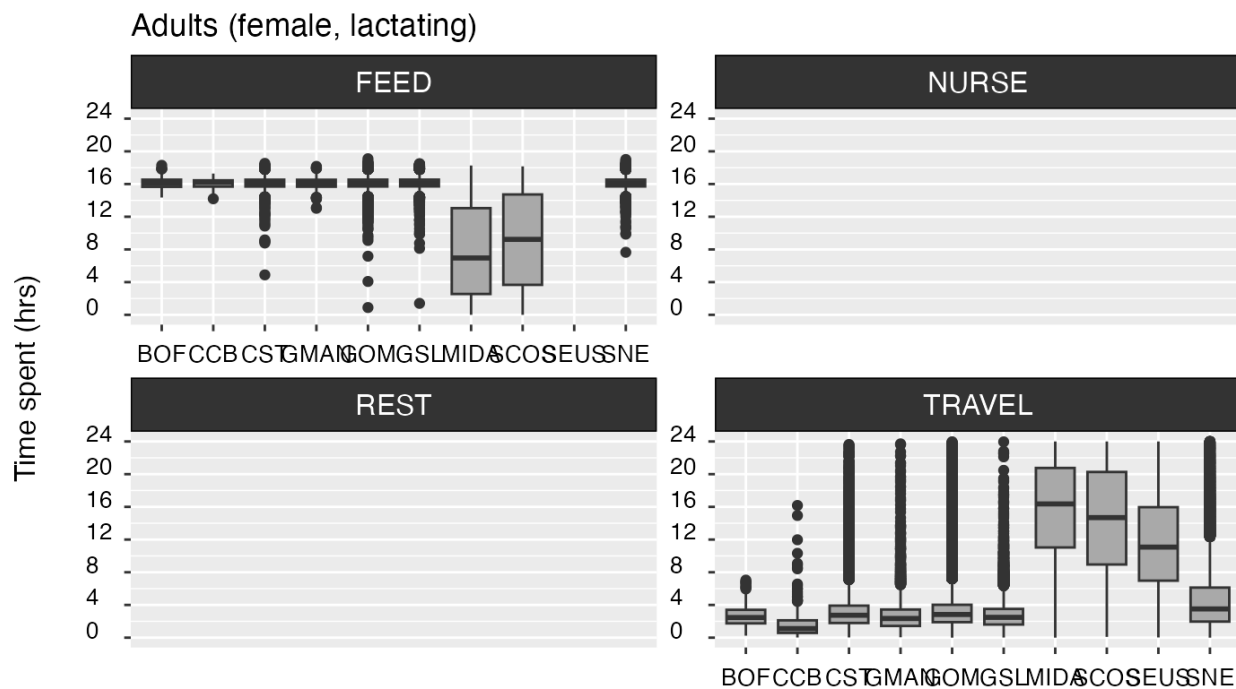
```

```

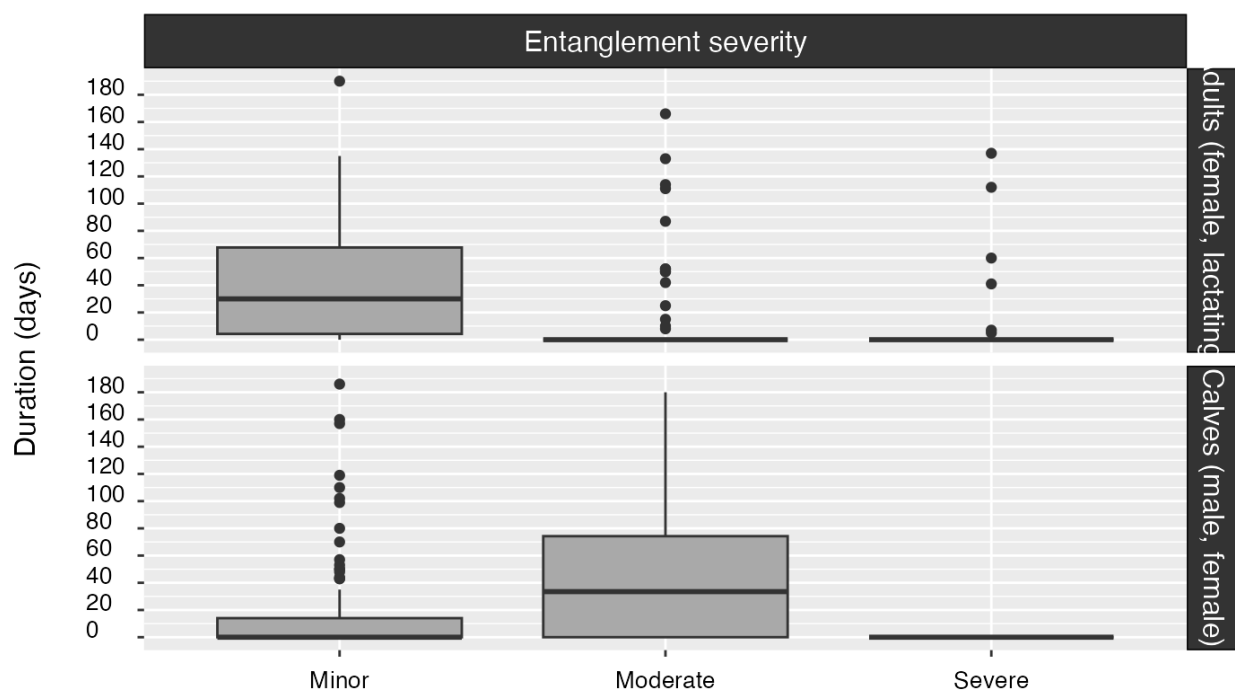
#> ++++++ Number of animals visiting each region (N = 1000) ++++++
#>
#> region    ad(f,l)
#> -----
#> BOF      2.8% (28)
#> CCB      0.8% (8)
#> CST      55.2% (552)
#> GMAN     12.7% (127)
#> GOM      98.2% (982)
#> GSL      42.5% (425)
#> MIDA     100% (1000)
#> SCOS     94.7% (947)
#> SEUS     100% (1000)
#> SNE      100% (1000)
#>
#> ++++++ Days spent in each region ++++++
#>
#> region    ad(f,l)
#> -----
#> BOF      13.6 ( $\pm 11.9$ ) [1-63]
#> CCB      28.9 ( $\pm 43.2$ ) [1-111]
#> CST      37.6 ( $\pm 15.5$ ) [1-143]
#> GMAN     28.3 ( $\pm 19.1$ ) [1-95]
#> GOM      96.7 ( $\pm 50.7$ ) [3-237]
#> GSL      97.4 ( $\pm 41.6$ ) [1-195]
#> MIDA     37.8 ( $\pm 10.5$ ) [13-128]
#> SCOS     34.9 ( $\pm 19.5$ ) [1-109]
#> SEUS     105.6 ( $\pm 14.6$ ) [66-150]
#> SNE      106.9 ( $\pm 36.3$ ) [29-315]
#>
#> ++++++ Total number of regions visited ++++++
#>
#> No.regions  ad(f,l)
#> -----
#>           3  1.8% (18)
#>           4  3.3% (33)
#>           5 30.1% (301)
#>           6 17.5% (175)
#>           7 45.8% (458)
#>           8  1.3% (13)
#>           9  0.2% (2)
#>
#> =====
#> ACTIVITY BUDGETS
#> =====
#>
#> ++++++ Adults (female, lactating) ++++++
#>
#> region    travel (hrs)    rest/nurse (hrs)    feed (hrs)
#> -----
#> SNE      4.69 ( $\pm 4.05$ )    12.42 ( $\pm 6.89$ )    16.12 ( $\pm 0.63$ )
#> MIDA     15.5 ( $\pm 6.03$ )    7.67 ( $\pm 6.15$ )    7.81 ( $\pm 5.54$ )
#> SEUS     11.6 ( $\pm 5.8$ )     12.4 ( $\pm 5.8$ )      0 ( $\pm 0$ )
#> GOM      3.29 ( $\pm 2.36$ )    6.5 ( $\pm 4.58$ )     16.11 ( $\pm 0.63$ )
#> SCOS     14.33 ( $\pm 6.48$ )    1.3 ( $\pm 3.22$ )      9 ( $\pm 5.6$ )
#> CST      3.19 ( $\pm 2.35$ )    7.31 ( $\pm 5.56$ )    16.11 ( $\pm 0.65$ )

```

```
#> GSL      2.69 (±1.57)    5.76 (±3.39)    16.12 (±0.64)
#> GMAN     2.8 (±2.36)     9.21 (±7.02)    16.1 (±0.61)
#> BOF      2.66 (±1.31)    5.34 (±1.93)    16.13 (±0.63)
#> CCB      1.82 (±2.24)    19.13 (±6.84)   16.05 (±0.66)
```



```
#>
#> =====
#> STRESSORS
#> =====
```




```

#>
#> ++++++ Entanglements ++++++
#>
#> entangled    rate
#> -----
#> no           90.1% (1802)
#> yes          9.9% (198)
#>
#>
#> position     rate
#> -----
#> body         55.6% (110)
#> head         43.4% (86)
#> head         1% (2)
#>
#>
#> cohort      not entangled    entangled
#> -----
#> ad(f,l)     89.8% (898)      10.2% (102)
#> c(m,f)      90.4% (904)      9.6% (96)
#>
#>
#> cohort      No. events per animal    p(entangled)
#> -----
#> ad(f,l)     1.04 ( $\pm 0.2$ ) [1-2]      0 ( $\pm 0.002$ ) [0-0.272]
#> c(m,f)      1.03 ( $\pm 0.18$ ) [1-2]      NA
#>
#>
#> cohort      minor          moderate    severe
#> -----
#> ad(f,l)     8.3% (83)      1.4% (14)    0.6% (6)
#> c(m,f)      3.0% (30)      6.6% (66)    0.0% (0)
#>
#>
#> cohort      minor (days)      moderate (days)    severe (days)
#> -----
#> ad(f,l)     48 ( $\pm 36$ ) [1-190]    65 ( $\pm 49$ ) [8-166]    60 ( $\pm 54$ ) [5-137]
#> c(m,f)      56 ( $\pm 50$ ) [1-186]    64 ( $\pm 43$ ) [1-180]    0 ( $\pm 0$ ) [0-0]
#>
#>
#> ++++++ Vessel strikes ++++++
#>
#> strike      rate
#> -----
#> no          197.0% (1970)
#> yes         3.0% (30)
#>
#>
#> cohort      not struck    struck
#> -----
#> ad(f,l)     98.0% (980)    2.0% (20)
#> c(m,f)      99.0% (990)    1.0% (10)
#>
#>
#> cohort      p(strike)
#> -----

```

```

#> ad(f,l)    2.88e-05 (±7.1e-05) [0-0.0037253]
#>
#>
#> ++++++++ Other sources of mortality ++++++++
#>
#> mortality    rate
#> -----
#> alive        97.5% (1950)
#> dead         2.5% (50)
#>
#>
#> cohort      alive          dead
#> -----
#> ad(f,l)     98.0% (980)    2.0% (20)
#> c(m,f)      97.0% (970)    3.0% (30)
#>
#>
#> ++++++++ Pile-driving noise ++++++++
#>
#> cohort      noise level          response threshold          response
Duration (days)
#> -----
#> ad(f,l)     63.427 (±32.422) [0-80]    119.4 (±64.3) [0-199.9]    0.0% (0)    0
(±0) [0-0]
#>
#> =====
#> ENERGY BUDGETS (MJ per day)
#> =====
#>
#> cohort      Energy_intake          Energy_expenditure
#> -----
#> ad(f,l)     734.1 (±1,340.7) [0-15,091.8]    1,938.8 (±813.6) [428.1-7,276.8]
#> c(m,f)      1,309.1 (±627.2) [0-3,381.6]    519.7 (±134.8) [241.9-2,046.9]
#>
#>
#> cohort      Deficit          Surplus
#> -----
#> ad(f,l)     81.2% (±9.7) [54.9-100]    18.8% (±9.7) [0-45.1]
#> c(m,f)      16.2% (±18) [0.3-61.3]    83.8% (±18) [38.7-99.7]

```

Plotting model outputs

Several plots can be obtained from the outputs of the agent-based model – all are produced using the `plot(.)` method, which takes the following arguments:

Argument	Default value	Description
<code>obj</code>	-	Model object of class <code>narwsim</code> , as returned by <code>narw(.)</code> .
<code>what</code>	"map"	Character string indicating which plots to return.

Argument	Default value	Description
<code>whale</code>	<code>1:nsim</code>	Positive integer or vector of integers indicating the individual(s) for which data should be extracted. By default, the function plots tracks for all <code>nsim</code> simulated animals.
<code>cohort</code>	<code>1:6</code>	Positive integer or vector of positive integers indicating which cohorts should be considered. Defaults to all cohorts. Cohort identifiers are listed in an object called <code>cohorts</code> .
<code>web</code>	<code>FALSE</code>	Logical. Whether to produce static maps (<code>FALSE</code>) or interactive, web-based maps (<code>TRUE</code>).
<code>nL</code>	<code>100</code>	Positive integer. Number of tracks to plot (when <code>what = "map"</code>) or number of draws to plot from the Bayesian posterior distribution of survival, health, and gestation models (when <code>what = "pred"</code>). In the former case, this argument should be kept < 100 to minimize memory usage and avoid lengthy run times.
<code>lwd</code>	<code>0.2</code>	Numeric value. Thickness of the lines used to illustrate movement tracks.
<code>alpha</code>	<code>0.7</code>	Numeric value between 0 and 1. Level of transparency of the tracks.

Plot type

By default, a call to `plot(.)` will automatically generate maps of simulated whale tracks, with labels indicating the locations of births (in green, if relevant) and deaths (color-coded by cause of mortality). This behavior is controlled by the `what` argument, which is preset to `"map"`. `what` may also be set to `"pred"` to visualize how survival and body condition are predicted to vary as a function of individual health (see next Tutorial 5).

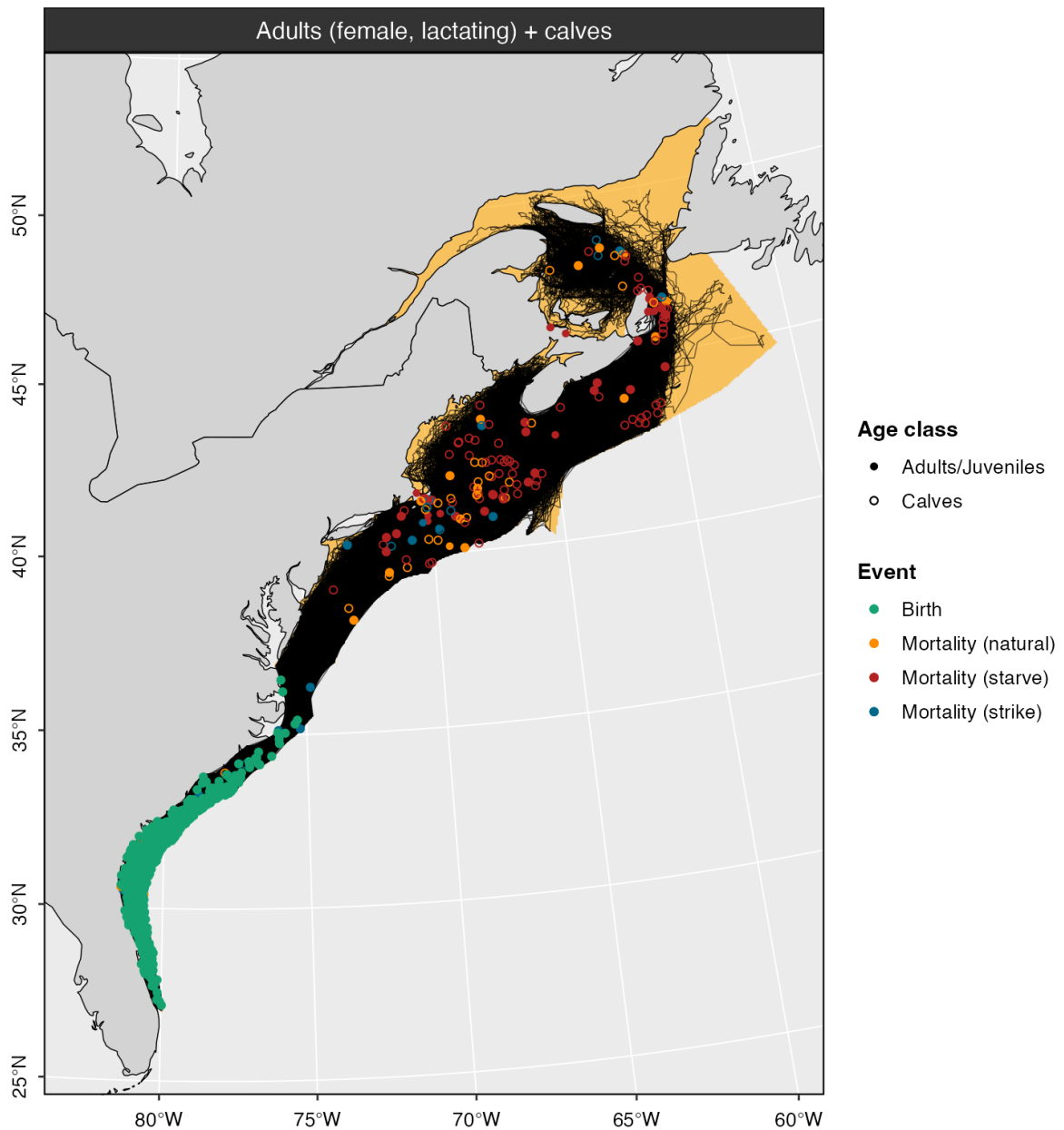
Number of tracks

The number of tracks shown is limited to a maximum of `nL = 100` to improve legibility and ensure that the code runs smoothly. We recommend against modifying this default setting, unless absolutely necessary (i.e., fewer/more tracks can be displayed by decreasing or increasing value passed to the `nL` argument).

Subsets of data

Similarly to the other methods described in preceding sections, the `cohort` and `whale` arguments can be used to display data for particular cohorts and/or individuals of interest.

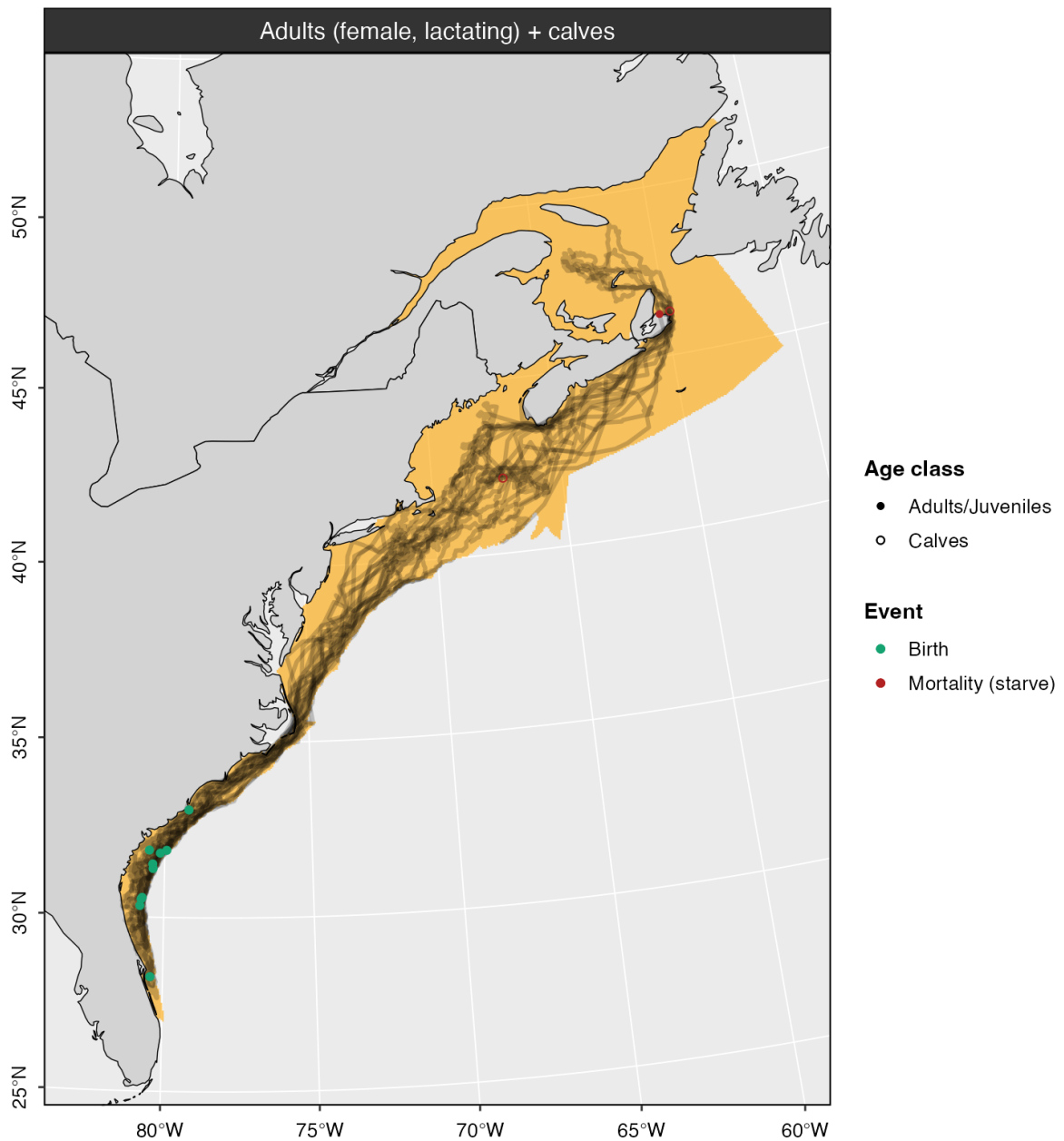
```
plot(model_base, cohort = 5)
#> Warning in plot.narwsim(model_base, cohort = 5): Plotting only the first 100
#> tracks
```



Plot aesthetics

The thickness and transparency of track lines can be changed via the `lwd` and `alpha` arguments, respectively. Lower values of `lwd` produce thinner lines, and lower values of `alpha` increase transparency.

```
plot(model_base, cohort = 5, whale = 1:10, alpha = 0.2, lwd = 1)
```



Interactive maps

Lastly, when **web** is set to **TRUE**, interactive web-based maps are produced using the **ggplotly** R package. These can be zoomed and panned using the mouse cursor to get a closer look at specific areas of interest. The location (easting, northing) and ID of each animal are displayed upon mouse hover.