Supporting Information

Large baleen and small toothed whales face greatest energetic consequences from sonar disturbance

Max F. Czapanskiy Matthew S. Savoca William T. Gough Paolo S. Segre
Danuta M. Wisniewska David E. Cade Jeremy A. Goldbogen

3/5/2020

Data

The sonar response energetic model uses three types of data: feeding rates, prey quality, and morphology. The feeding rate, morphology, and odontocete prey quality data were previously published by Goldbogen et al. (2019) doi:10.1126/science.aax9044. See supplement "Description of how rorqual prey resources were calculated" for description of rorqual prey quality data.

```
prey <- readRDS("prey_tbl.RDS")
feeding <- readRDS("feeding_tbl.RDS")
morphology <- readRDS("morpho_tbl.RDS")

cbf_palette <- c(
  # blue
  "Delphinidae and Phocoenidae" = rgb(0, 114, 178, maxColorValue = 255),
  # vermillion
  "Physeteridae and Ziphiidae" = rgb(213, 94, 0, maxColorValue = 255),
  # bluish green
  "Balaenopteridae" = rgb(0, 158, 115, maxColorValue = 255)
)

morphology %>%
  mutate(species = cell_spec(species, "latex", italic = TRUE)) %>%
  select(Species = species, Family = family, Clade = clade,
         `Length (m)` = length_m, `Mass (kg)` = mass_kg,
         Abbreviation = abbr) %>%
  kable("latex", booktabs = TRUE, escape = FALSE) %>%
  kable_styling(latex_options = c("scale_down"))
```

Species	Family	Clade	Length (m)	Mass (kg)	Abbreviation
Phocoena phocoena	Phocoenidae	Odontoceti	1.22	31	Pp
Grampus griseus	Delphinidae	Odontoceti	3.00	350	Gg
Mesoplodon densirostris	Ziphiidae	Odontoceti	4.10	860	Md
Globicephala macrorhynchus	Delphinidae	Odontoceti	4.30	980	Gma
Globicephala melas	Delphinidae	Odontoceti	5.00	1200	Gme
Ziphius cavirostris	Ziphiidae	Odontoceti	6.60	2900	Zc
Balaenoptera bonaerensis	Balaenopteridae	Mysticeti	7.80	6700	Bb
Physeter macrocephalus	Physeteridae	Odontoceti	11.00	15000	Pm
Megaptera novaeangliae	Balaenopteridae	Mysticeti	14.00	36000	Mn
Balaenoptera physalus	Balaenopteridae	Mysticeti	20.20	53000	Bp
Balaenoptera musculus	Balaenopteridae	Mysticeti	25.20	93000	Bm

For the model, feeding rate (r_f) and energy from prey per feeding event (E_p) distributions are empirical and lognormal, respectively. The following table combines the three data sources and provides quantile functions for r_f and E_p for each species.

```
# Creates a quantile function based on the log-mean and log-sd of each species'
#   prey distribution
prey_fun <- prey %>%
  mutate(q_Ep_kJ = map2(meanlnEp_lnkJ,
                        sdlnEp_lnkJ,
                        ~ function(p) qlnorm(p, .x, .y)))
# Creates an empirical quantile function for each species
feeding_fun <- feeding %>%
  group_by(species) %>%
  summarize(rf_h = list(rf_h)) %>%
  mutate(q_rf_h = map(rf_h, ~ function(p) quantile(.x, p)))
# Combines the three data sources
species_data <- morphology %>%
  left_join(prey_fun, by = "species") %>%
  left_join(feeding_fun, by = "species")
```

Baseline rate of energy acquisition

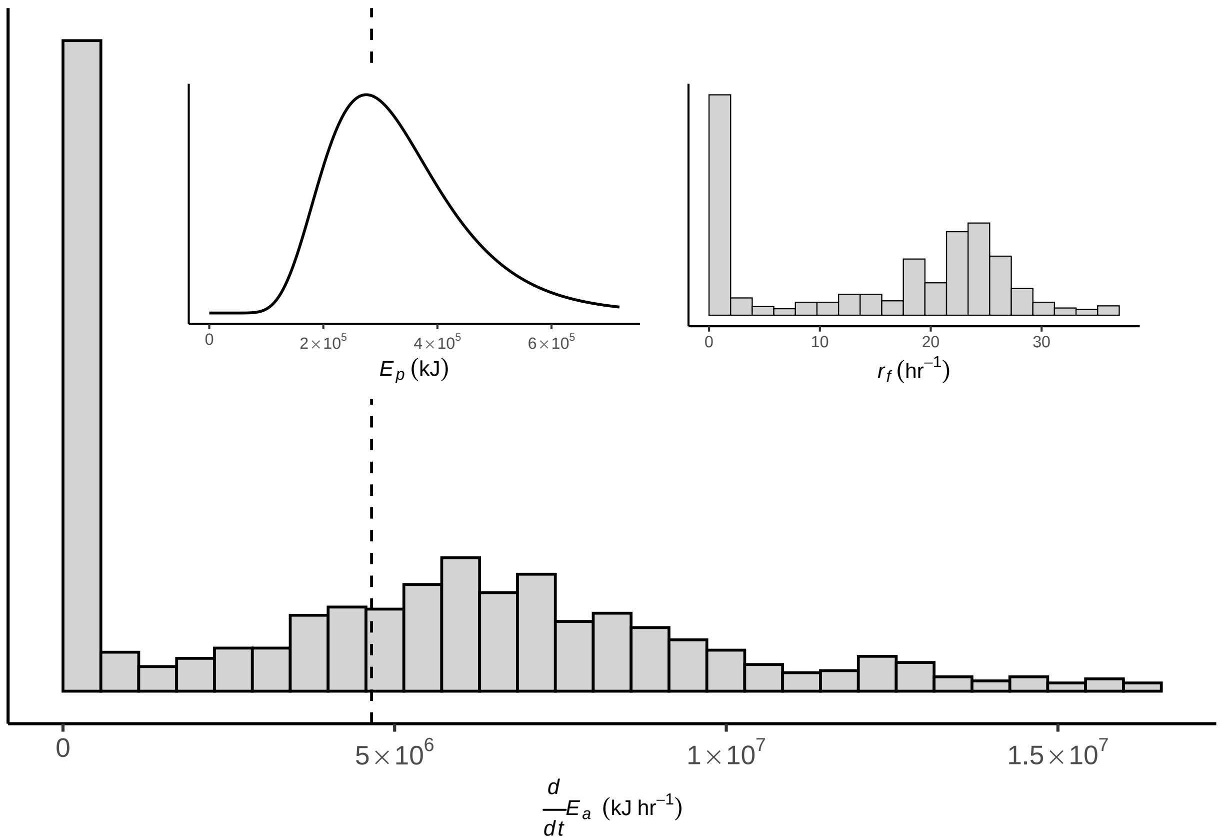
The baseline rate of energy acquisition ($\frac{d}{dt}E_a$) was modeled as the product of r_f and E_p. The resulting distribution for blue whales (*Balaenoptera musculus*) is presented in the main manuscript (Fig. 1). The distributions for all species are below.

```
# Adapted from https://stackoverflow.com/a/45867076
label_sci <- function(breaks) {
  ifelse(
    breaks == 0,
    "0",
    parse(text = gsub("[+]", "", gsub("e", " %*% 10^", scientific(breaks))))
  )
}

# Plot the lognormal distribution of energy from prey
Ep_plot <- function(q_Ep_kJ, meanlnEp_lnkJ, sdlnEp_lnkJ) {
  tibble(x = q_Ep_kJ(c(0.001, 0.99))) %>%
```

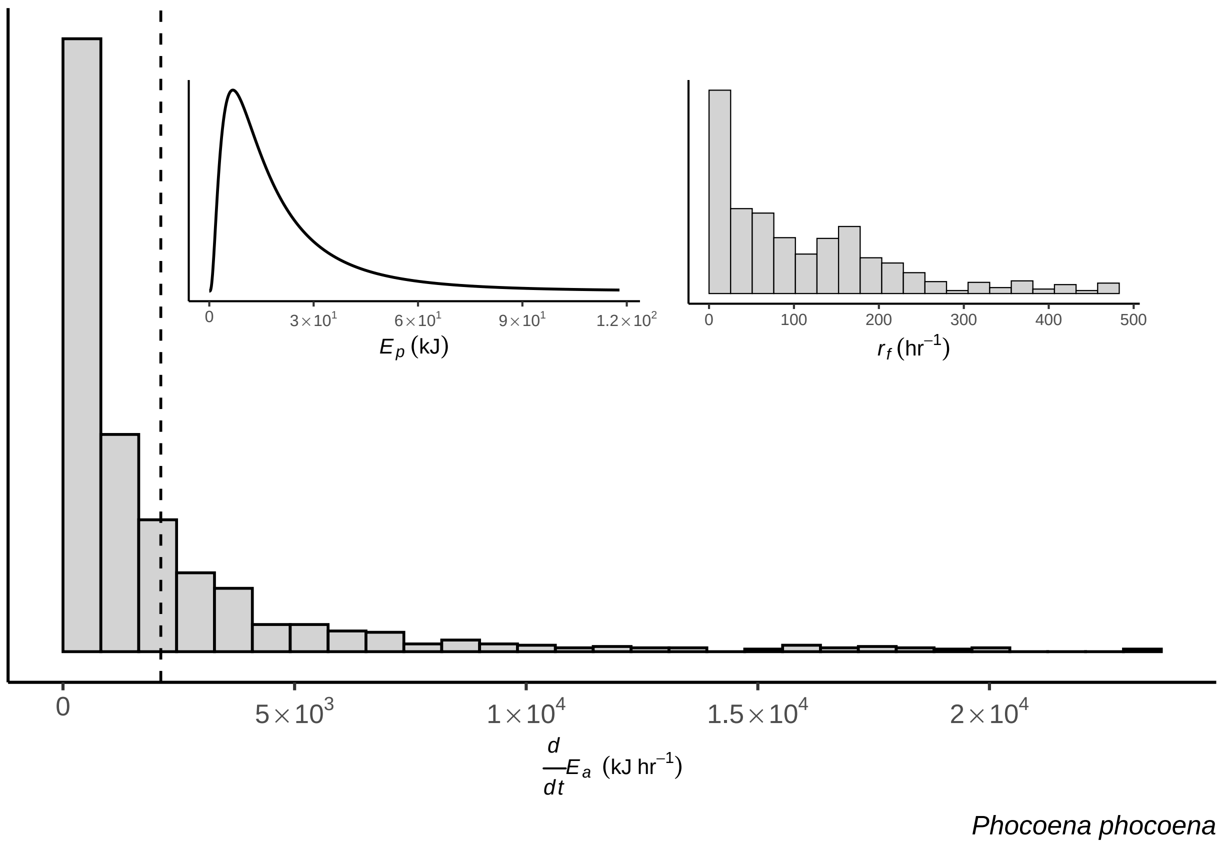
```
    ggplot(aes(x)) +
    stat_function(
      fun = dlnorm,
      args = list(meanlog = meanlnEp_lnkJ,
                  sdlog = sdlnEp_lnkJ),
      n = 1e3
    ) +
    expand_limits(x = 0) +
    scale_x_continuous(expression(italic(E[p]) ~ (kJ)),
                       labels = label_sci) +
    theme_classic(base_size = 8) +
    theme(axis.text.y = element_blank(),
          axis.ticks.y = element_blank(),
          axis.title.y = element_blank(),
          axis.title.x = element_text(size = 8))
}

# Plot the empirical distribution of feeding rates
rf_plot <- function(q_rf_h) {
  tibble(x = q_rf_h(seq(0, 1, length.out = 1000))) %>%
    ggplot(aes(x)) +
    geom_histogram(bins = 20,
                   boundary = 0,
                   fill = "light gray",
                   color = "black",
                   size = 0.2) +
    scale_x_continuous(expression(italic(r[f]) ~ ("hr"^{-1}))) +
    theme_classic(base_size = 8) +
    theme(axis.text.y = element_blank(),
          axis.ticks.y = element_blank(),
          axis.title.y = element_blank(),
          axis.title.x = element_text(size = 8))
}

# Plot the baseline rate of energy acquisition by sampling Ep and rf
ddtEa_plot <- function(species, q_Ep_kJ, q_rf_h, caption = TRUE) {
  ddtEa <- tibble(p_Ep = runif(1e3),
                  p_rf = runif(1e3)) %>%
    mutate(Ep = q_Ep_kJ(p_Ep),
           rf = q_rf_h(p_rf),
           ddtEa = Ep * rf)

  ddtEa_caption <- if (caption) {
    element_text(face = "italic")
  } else {
    element_blank()
  }

  ddtEa %>%
    filter(ddtEa < quantile(ddtEa, 0.99)) %>%
    ggplot(aes(ddtEa)) +
    geom_histogram(bins = 30,
                   boundary = 0,
```

```
                   fill = "light gray",
                   color = "black") +
    geom_vline(aes(xintercept = mean(ddtEa)),
               linetype = "dashed") +
    scale_x_continuous(expression(italic(frac(d, dt) * E[a]) ~~ ("kJ" ~ "hr"^{-1})),
                       labels = label_sci) +
    labs(caption = species) +
    theme_classic(base_size = 12) +
    theme(axis.text.y = element_blank(),
          axis.ticks.y = element_blank(),
          axis.title.y = element_blank(),
          axis.title.x = element_text(size = 8),
          plot.caption = ddtEa_caption)
}

# Combine plots (Ep and rf as insets in d/dt Ea)
arrange_ddtEa <- function(species, q_Ep_kJ, meanlnEp_lnkJ, sdlnEp_lnkJ, q_rf_h,
                          caption = TRUE, ...) {
  Ep <- Ep_plot(q_Ep_kJ, meanlnEp_lnkJ, sdlnEp_lnkJ)
  rf <- rf_plot(q_rf_h)
  ddtEa <- ddtEa_plot(species, q_Ep_kJ, q_rf_h, caption)

  # Figure out where the insets should go
  scales <- layer_scales(ddtEa)
  xlim <- scales$x$get_limits()
  ylim <- scales$y$get_limits()
  grid_to_data <- function(xmin, xmax, ymin, ymax) {
    c(xmin = xlim[1] + xmin * (xlim[2] - xlim[1]),
      xmax = xlim[1] + xmax * (xlim[2] - xlim[1]),
      ymin = ylim[1] + ymin * (ylim[2] - ylim[1]),
      ymax = ylim[1] + ymax * (ylim[2] - ylim[1]))
  }
  Ep_coord <- grid_to_data(0.1, 0.535, 0.45, 0.95)
  rf_coord <- grid_to_data(0.555, 0.99, 0.45, 0.95)
  ddtEa +
    annotation_custom(ggplotGrob(Ep),
                      xmin = Ep_coord["xmin"], xmax = Ep_coord["xmax"],
                      ymin = Ep_coord["ymin"], ymax = Ep_coord["ymax"]) +
    annotation_custom(ggplotGrob(rf),
                      xmin = rf_coord["xmin"], xmax = rf_coord["xmax"],
                      ymin = rf_coord["ymin"], ymax = rf_coord["ymax"])
}

# Figure 1 of main text
species_data %>%
  filter(abbr == "Bm") %>%
  pmap(arrange_ddtEa, caption = FALSE)
```

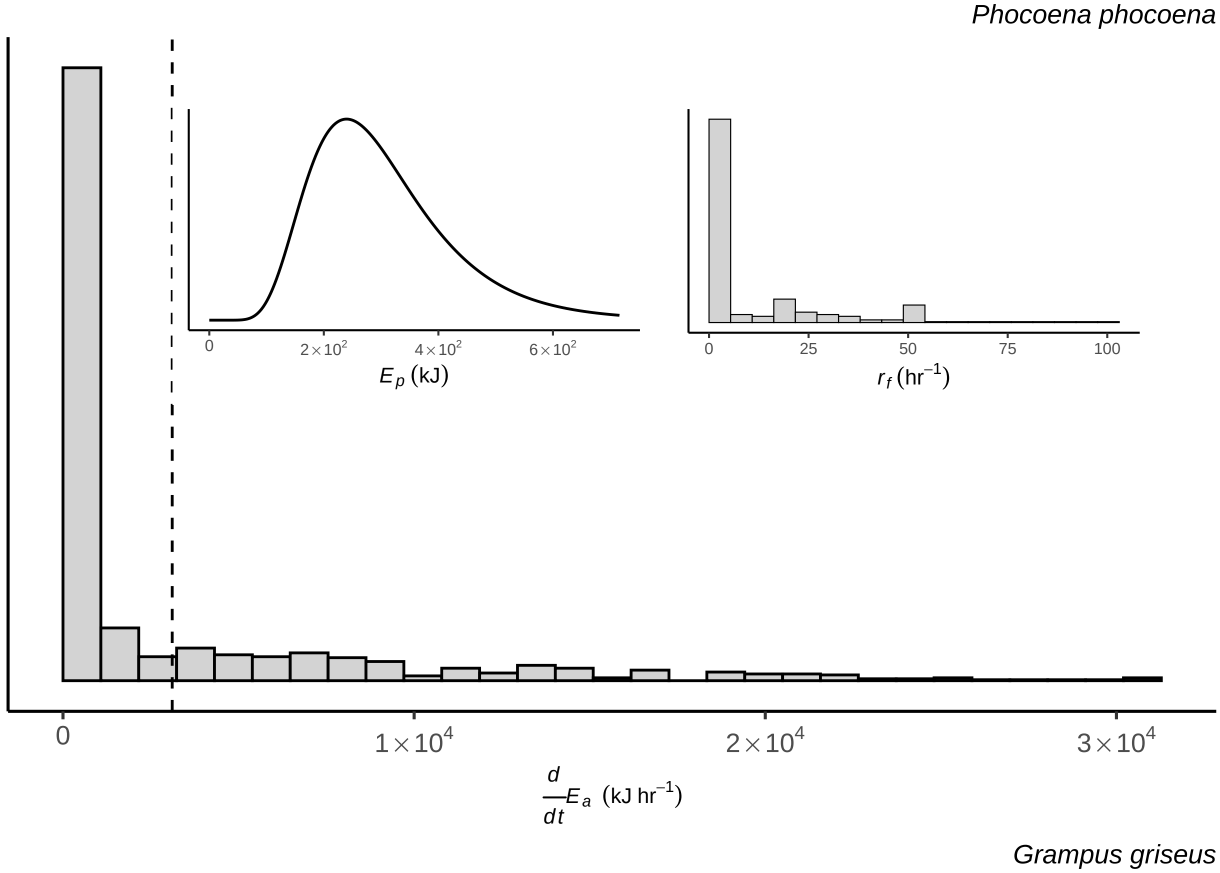
```
## [[1]]
```



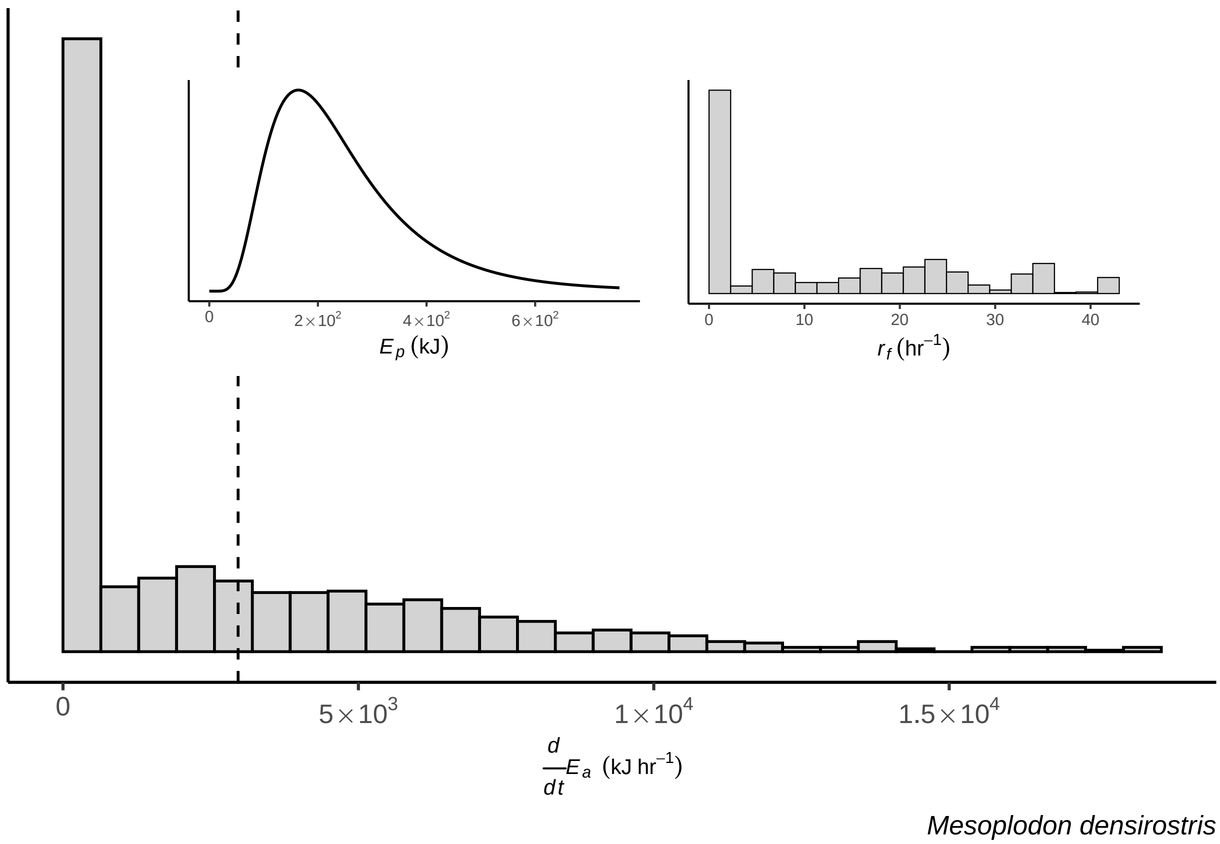

```
ddtEa_plots <- species_data %>%
  select(species, q_Ep_kJ, meanlnEp_lnkJ, sdlnEp_lnkJ, q_rf_h) %>%
  pmap(arrange_ddtEa)
walk(ddtEa_plots, print)
```



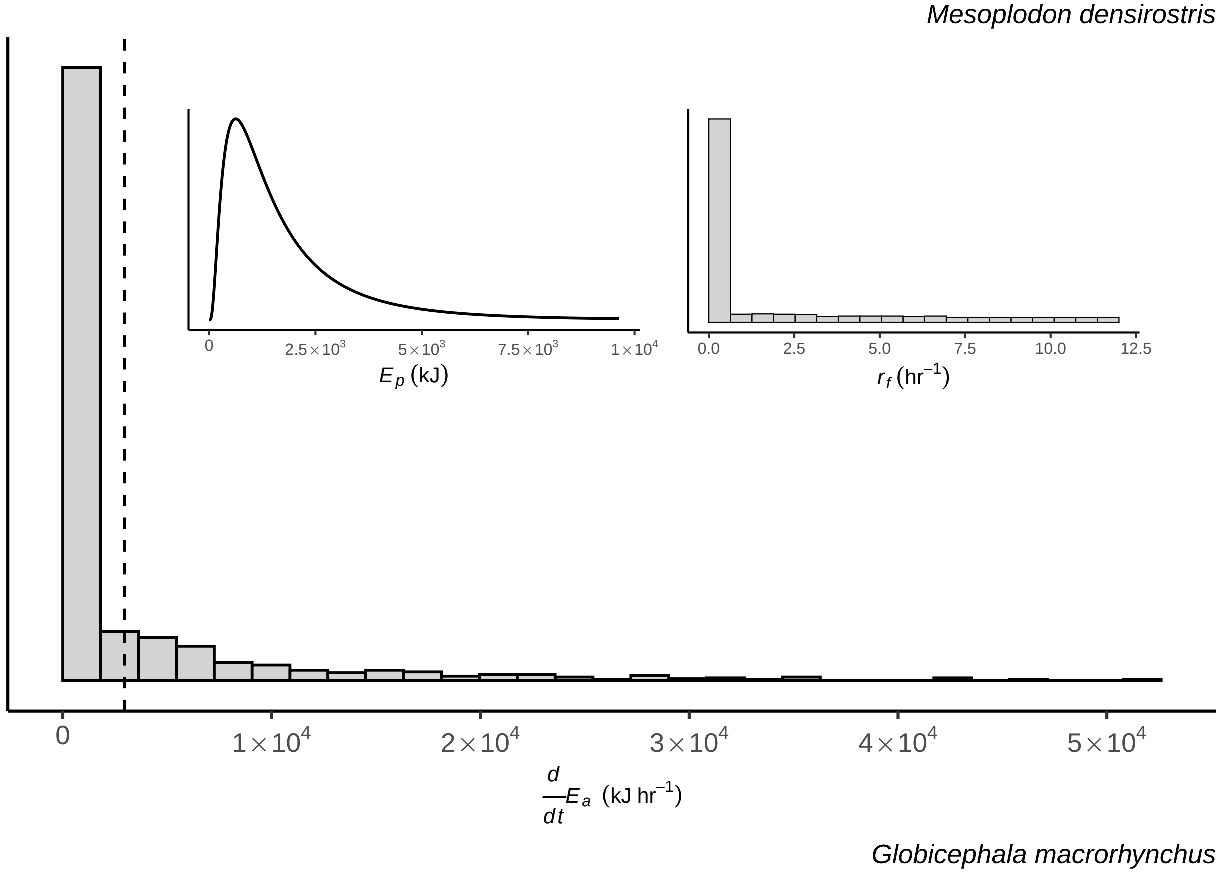
0
5×10^3
1×10^4
1.5×10^4
2×10^4
d/dt E_a (kJ hr^-1)
0
3×10^1
6×10^1
9×10^1
1.2×10^2
E_p (kJ)
0
100
200
300
400
500
r_f (hr^-1)
Phocoena phocoena



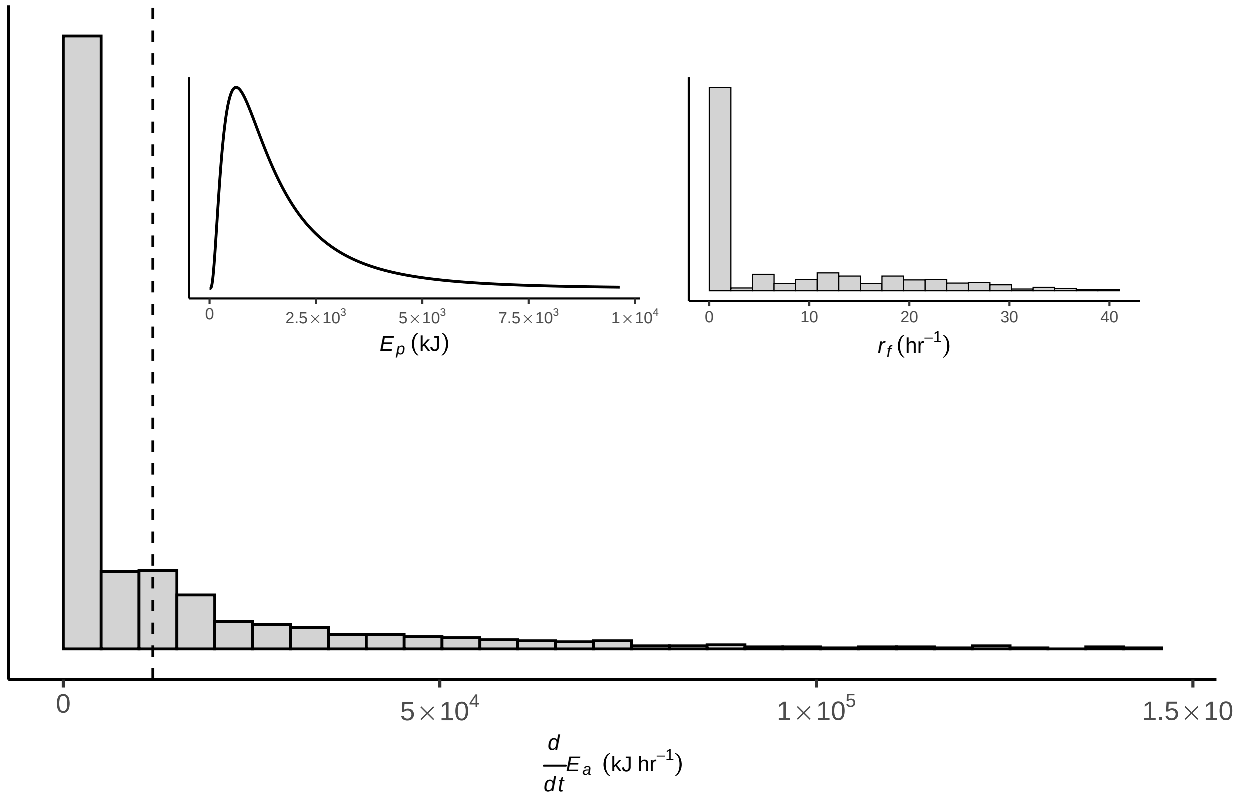
0
1×10^4
2×10^4
3×10^4
d/dt E_a (kJ hr^-1)
0
2×10^2
4×10^2
6×10^2
E_p (kJ)
0
25
50
75
100
r_f (hr^-1)
Grampus griseus



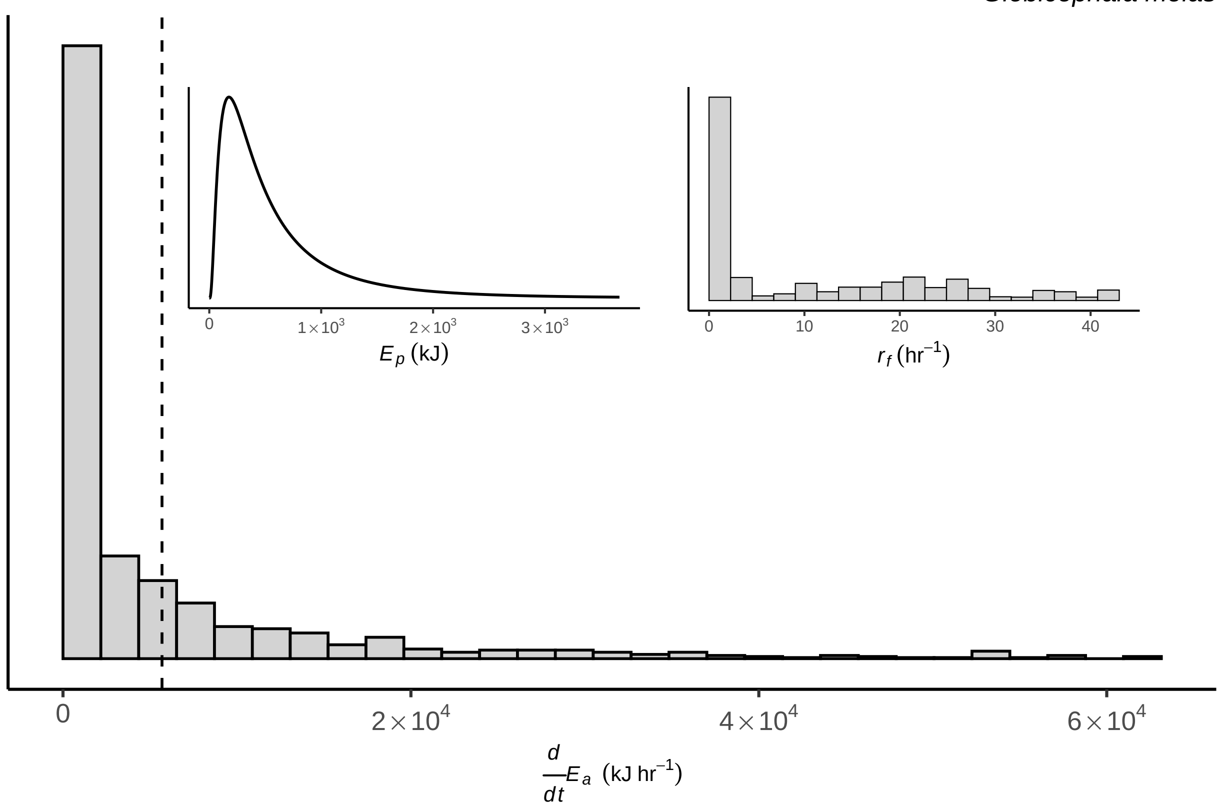
0
2×10^2
4×10^2
6×10^2
E_p (kJ)
0
10
20
30
40
r_f (hr^-1)
0
5×10^3
1×10^4
1.5×10^4
d/dt E_a (kJ hr^-1)
Mesoplodon densirostris



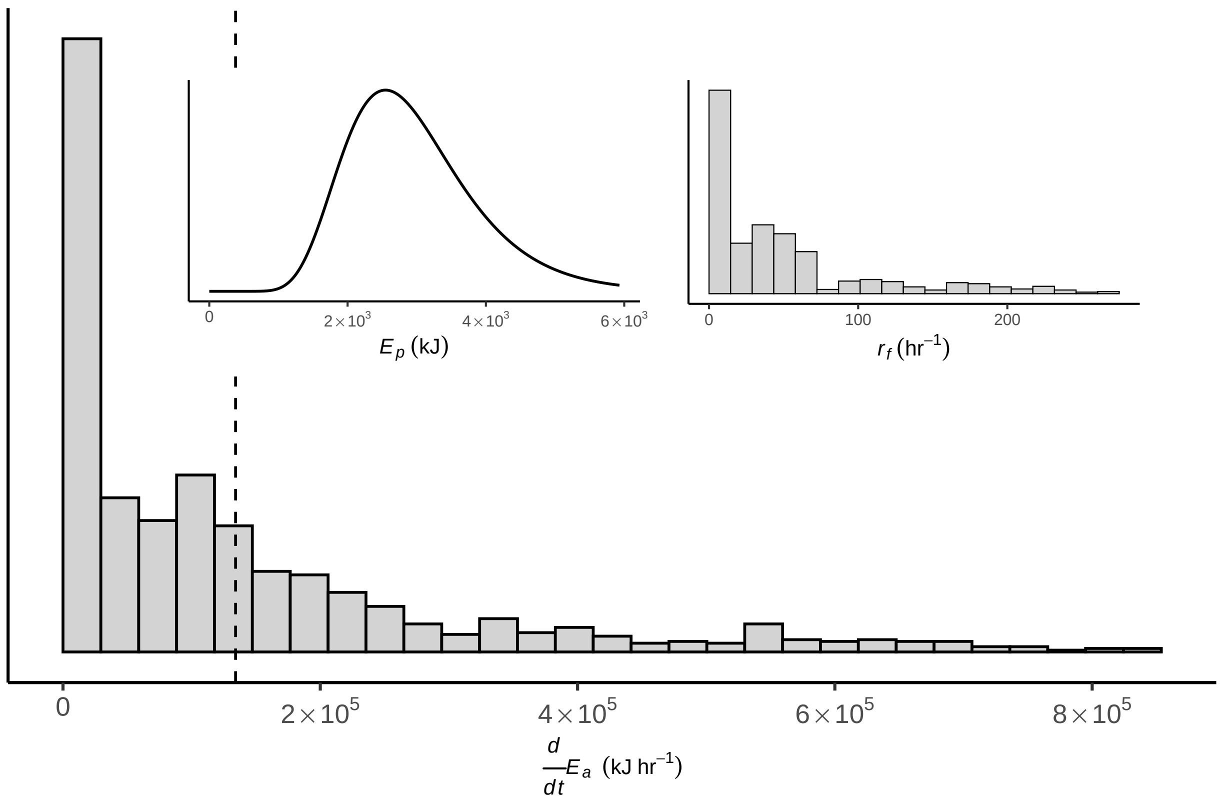
0
2.5×10^3
5×10^3
7.5×10^3
1×10^4
E_p (kJ)
0.0
2.5
5.0
7.5
10.0
12.5
r_f (hr^-1)
0
1×10^4
2×10^4
3×10^4
4×10^4
5×10^4
d/dt E_a (kJ hr^-1)
Globicephala macrorhynchus



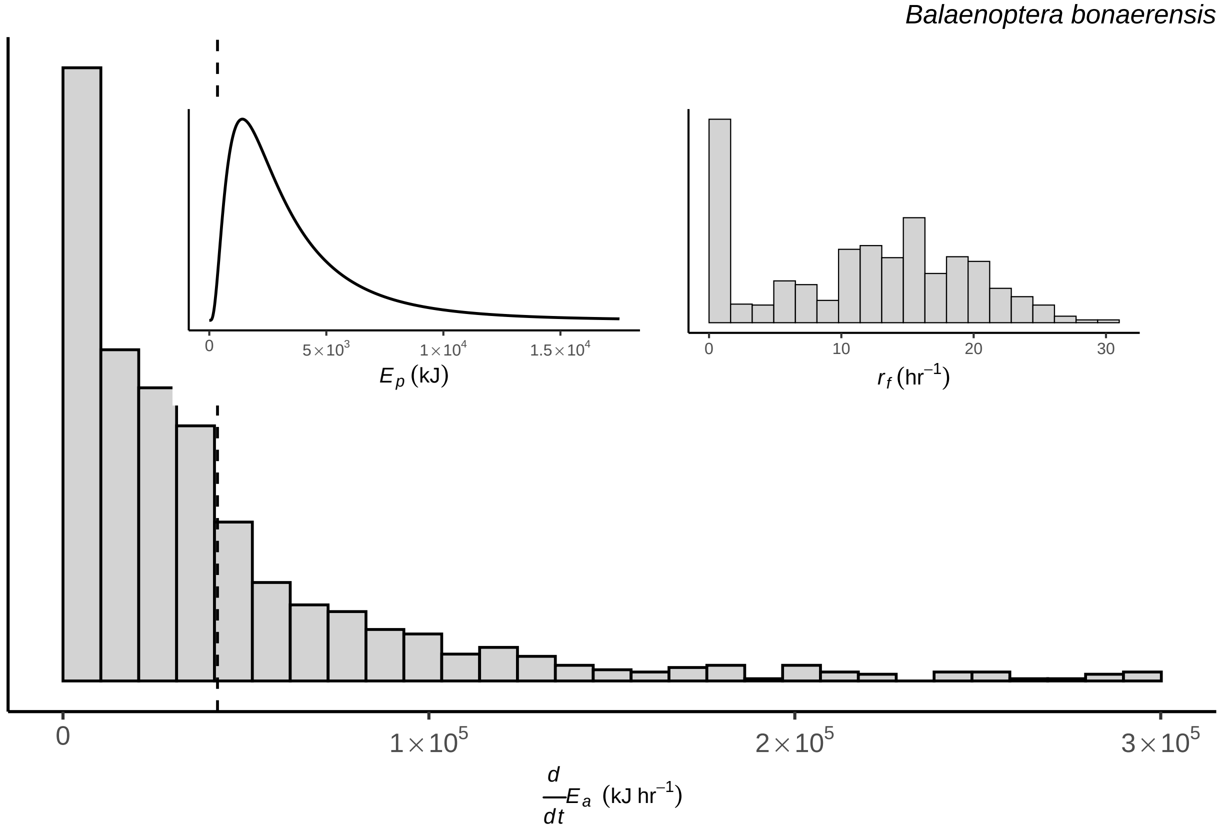
Globicephala melas



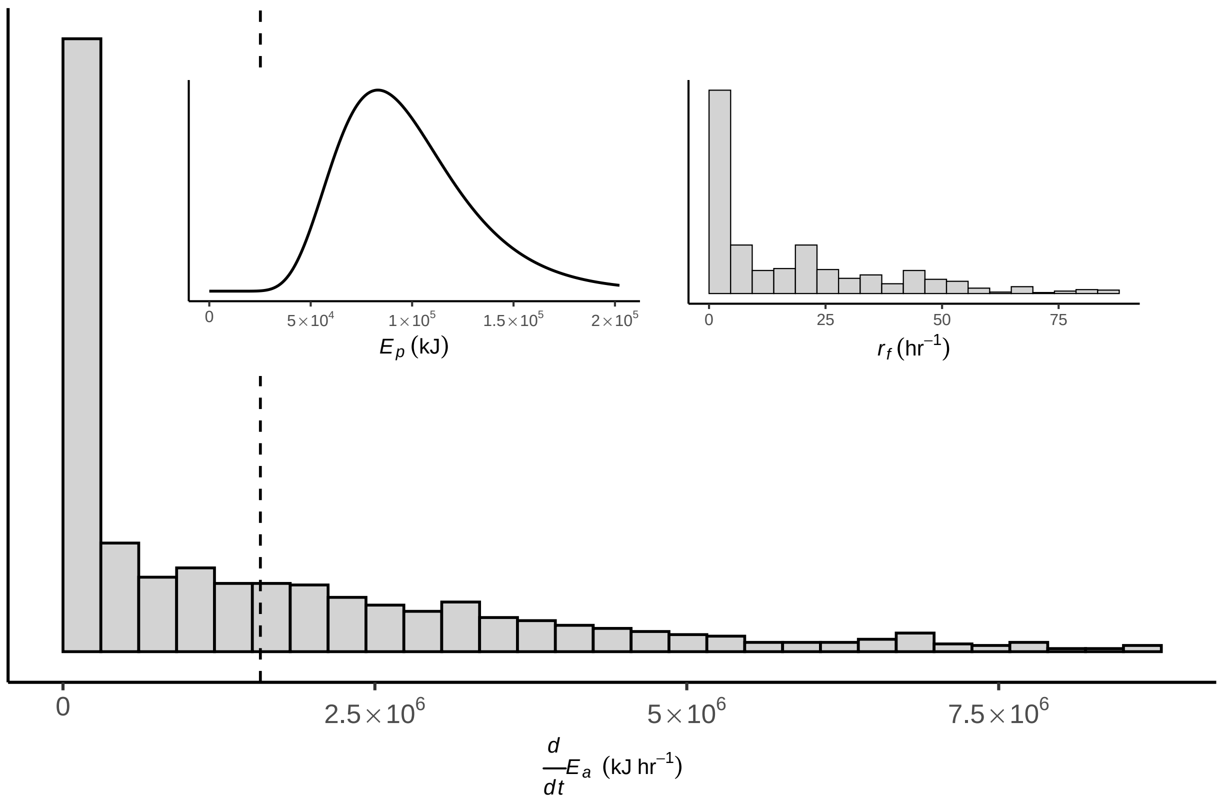
Ziphius cavirostris



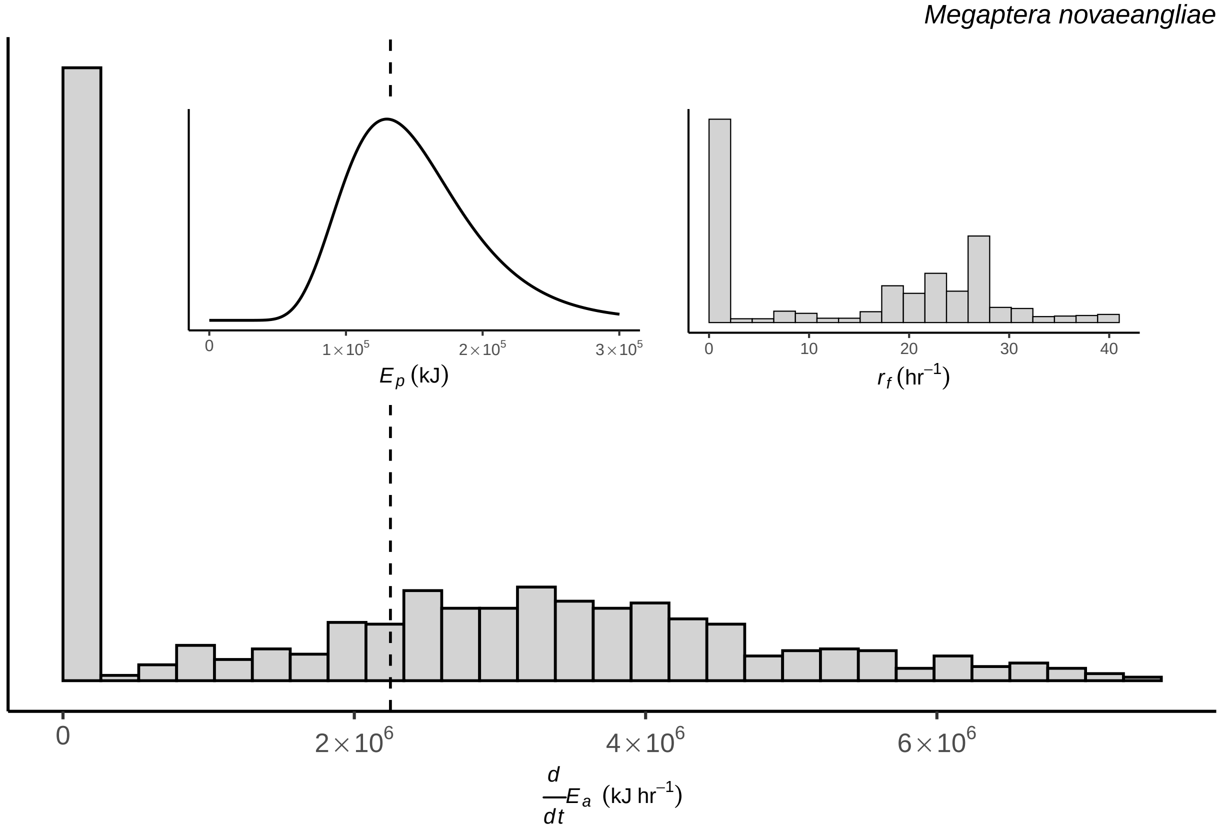
Balaenoptera bonaerensis



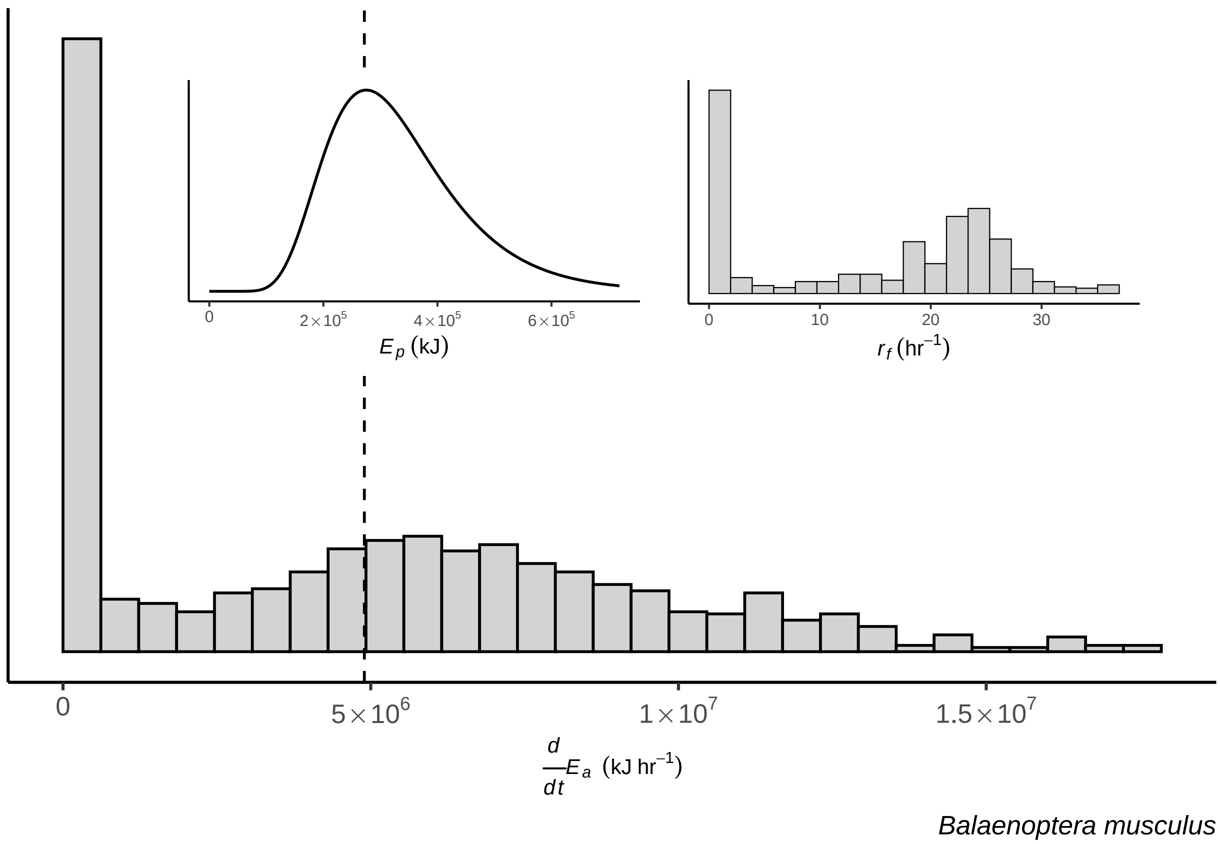
Physeter macrocephalus



Megaptera novaeangliae



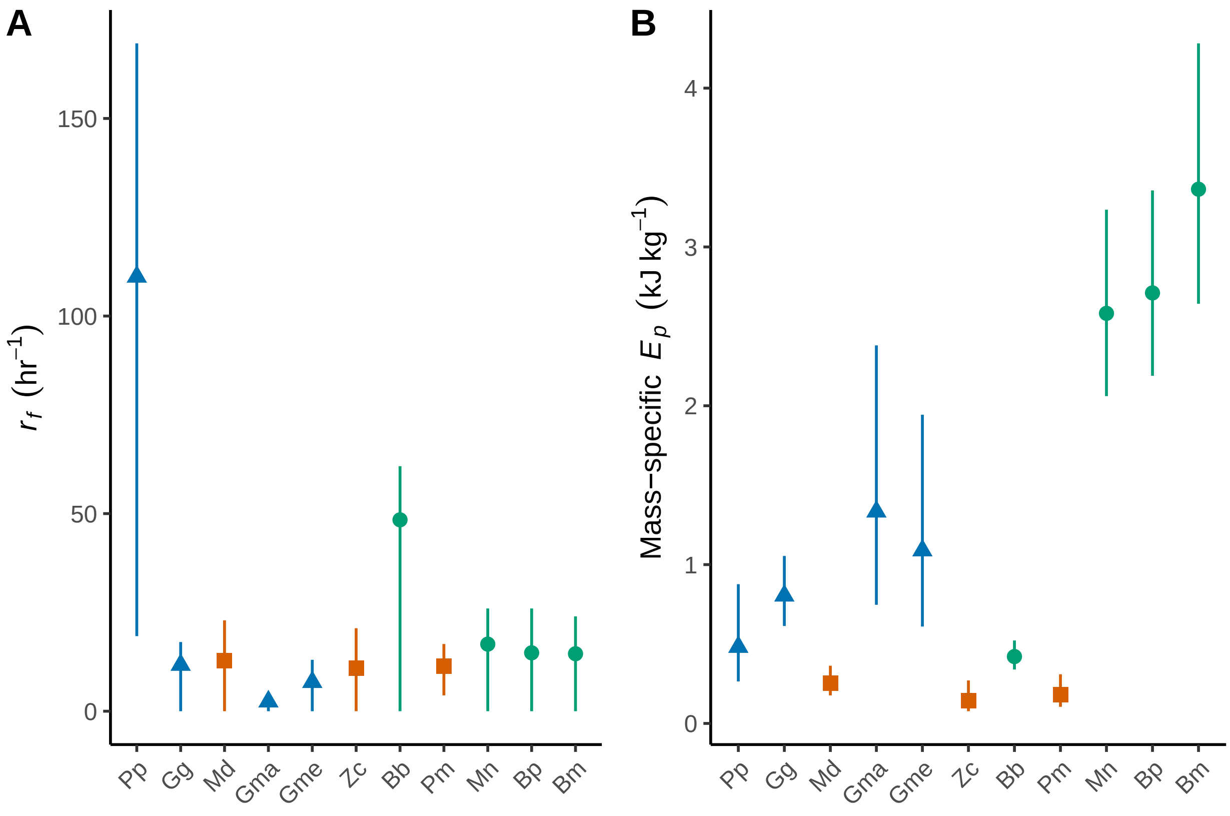
Balaenoptera physalus



r_f and mass-specific E_p across species (Figure 2 in main text).

```
fig2data <- species_data %>%
  mutate(
    rf_mean = map_dbl(rf_h, mean),
    rf_1q = map_dbl(rf_h, quantile, p = 0.25),
    rf_3q = map_dbl(rf_h, quantile, p = 0.75),
    Epmass_mean = exp(meanlnEp_lnkJ) / mass_kg,
    Epmass_1q = map2_dbl(meanlnEp_lnkJ, sdlnEp_lnkJ, ~ qlnorm(0.25, .x, .y)) / mass_kg,
    Epmass_3q = map2_dbl(meanlnEp_lnkJ, sdlnEp_lnkJ, ~ qlnorm(0.75, .x, .y)) / mass_kg,
    abbr = factor(abbr, levels = .$abbr)
  )
# Fig 2a
fig2a <- ggplot(fig2data, aes(abbr, rf_mean)) +
  geom_pointrange(aes(ymin = rf_1q, ymax = rf_3q,
                      color = group, shape = group)) +
  scale_color_manual(values = cbf_palette) +
  labs(x = "", y = expression(italic(r[f])~~(hr^{-1}))) +
  theme_classic() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        legend.position = "none")
# Fig 2b
fig2b <- ggplot(fig2data, aes(abbr, Epmass_mean)) +
  geom_pointrange(aes(ymin = Epmass_1q, ymax = Epmass_3q,
                      color = group, shape = group)) +
  scale_color_manual(values = cbf_palette) +
  labs(x = "", y = expression("Mass-specific"~~italic(E[p])~~(kJ~kg^{-1}))) +
```

```r
  theme_classic() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        legend.position = "none")
# Fig 2
plot_grid(fig2a, fig2b, labels = "AUTO")
```

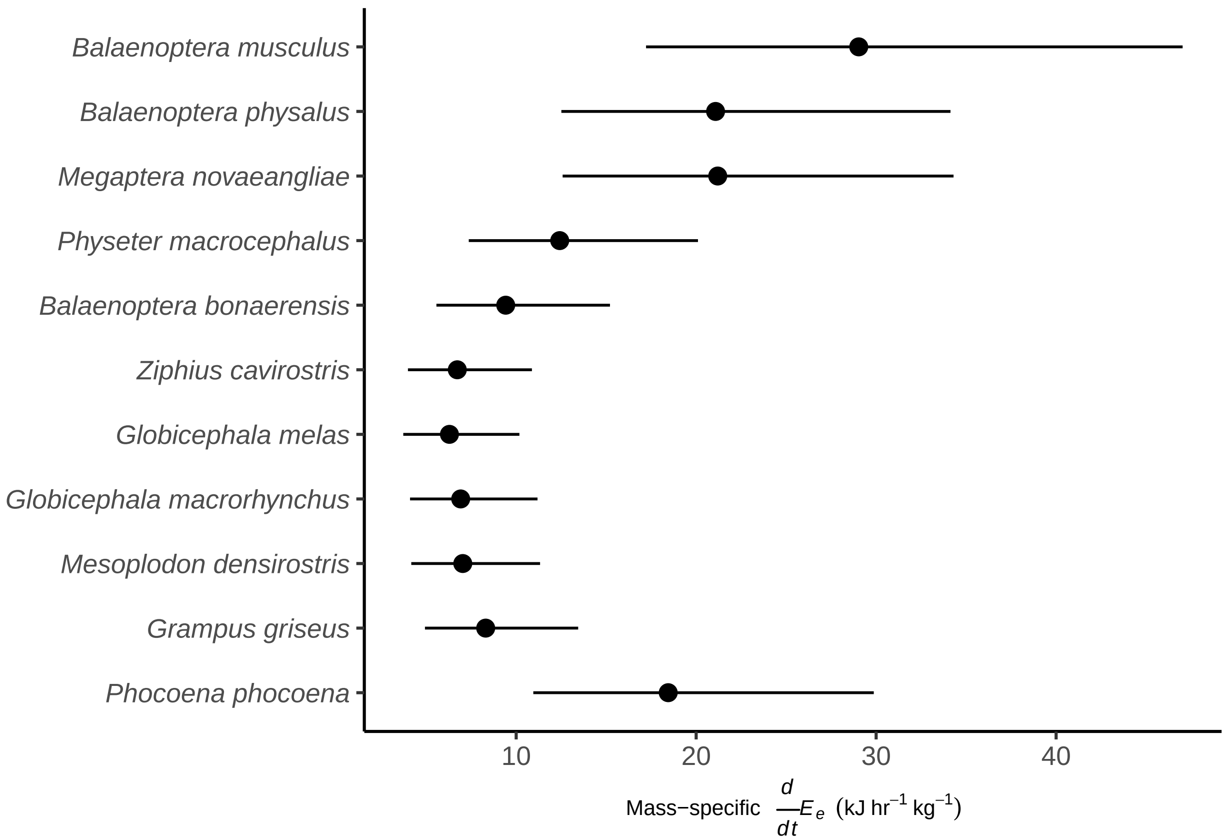


Energy expenditure due to elevated locomotion

Elevated locomotion is defined here as a speed increase (U_f) for a duration (t_f). The energetic cost associated with this behavior was modeled as the product of the increase in stroking frequency (Δf in Hz), the mass-specific locomotor cost (C_L in kJ stroke^{-1} kg^{-1}), and the individual's mass. To incorporate uncertainty, both Δf and C_L were treated as gamma distributed variables with a mean equal to the best estimate and a shape parameter of 4. The following figure shows the estimated increase in mass-specific energy expenditure when U_f is 5 m s^{-1}.

```r
# Predict the change in fluking frequency (deltaff) and mass-specific locomotor
# costs (CL)
U_cruise_ms <- 1.5
U_flight_ms <- 5
# Change in fluking frequency in strokes per hour
ff_fun <- function(U, L, La = 0.2, St = 0.3) {
  St * U / L / La * 3600
}
# Mass-specific locomotor cost in kJ / kg / stroke
CL_fun <- function(m) (1.46 + 0.0005 * m) / 1000

# Estimate the quantile of mass-specific ddtEe (product of two gammas)
```

```r
q_ddtEe <- function(p, deltaff_shape, deltaff_scale, CL_shape, CL_scale) {
  pmap_dbl(
    list(deltaff_shape, deltaff_scale, CL_shape, CL_scale),
    function(deltaff_shape, deltaff_scale, CL_shape, CL_scale) {
      tibble(
        deltaff = rgamma(1e6, shape = deltaff_shape, scale = deltaff_scale),
        CL = rgamma(1e6, shape = CL_shape, scale = CL_scale)
      ) %>%
        mutate(ddtEe = deltaff * CL) %>%
        pull(ddtEe) %>%
        quantile(p)
    })
}

# Plot median and IQR of mass-specific ddtEe
species_data %>%
  mutate(
    ff_cruise = ff_fun(U_cruise_ms, length_m),
    ff_flight = ff_fun(U_flight_ms, length_m),
    mean_deltaff = ff_flight - ff_cruise,
    deltaff_shape = 4,
    deltaff_scale = mean_deltaff / deltaff_shape,
    mean_CL = CL_fun(mass_kg),
    CL_shape = 4,
    CL_scale = mean_CL / CL_shape,
    ddtEe_1q = q_ddtEe(0.25, deltaff_shape, deltaff_scale, CL_shape, CL_scale),
    ddtEe_med = q_ddtEe(0.5, deltaff_shape, deltaff_scale, CL_shape, CL_scale),
    ddtEe_3q = q_ddtEe(0.75, deltaff_shape, deltaff_scale, CL_shape, CL_scale),
    species = factor(species, levels = species[order(length_m)])
  ) %>%
  ggplot(aes(x = species, y = ddtEe_med)) +
  geom_pointrange(aes(ymin = ddtEe_1q, ymax = ddtEe_3q)) +
  coord_flip() +
  labs(y = expression("Mass-specific " ~~ italic(frac(d, dt) * E[e]) ~~ ("kJ" ~ "hr"^{-1} ~ "kg"^{-1})))
  theme_classic(base_size = 12) +
  theme(axis.text.y = element_text(face = "italic"),
        axis.title.x = element_text(size = 8),
        axis.title.y = element_blank())
```



Sensitivity analysis

We tested the model's sensitivity to energy acquisition (E_p, r_f) and expenditure (Δf, C_L) parameters in two behavioral scenarios. The scenarios were chosen to emphasize increased energy expenditure (t_d = 1 hour, t_f = 0.5 hours, U_f = 5 m s^{-1}) or lost consumption (t_d = 4 hours, t_f = 0.25 hours, U_f = 3.5 m s^{-1}).

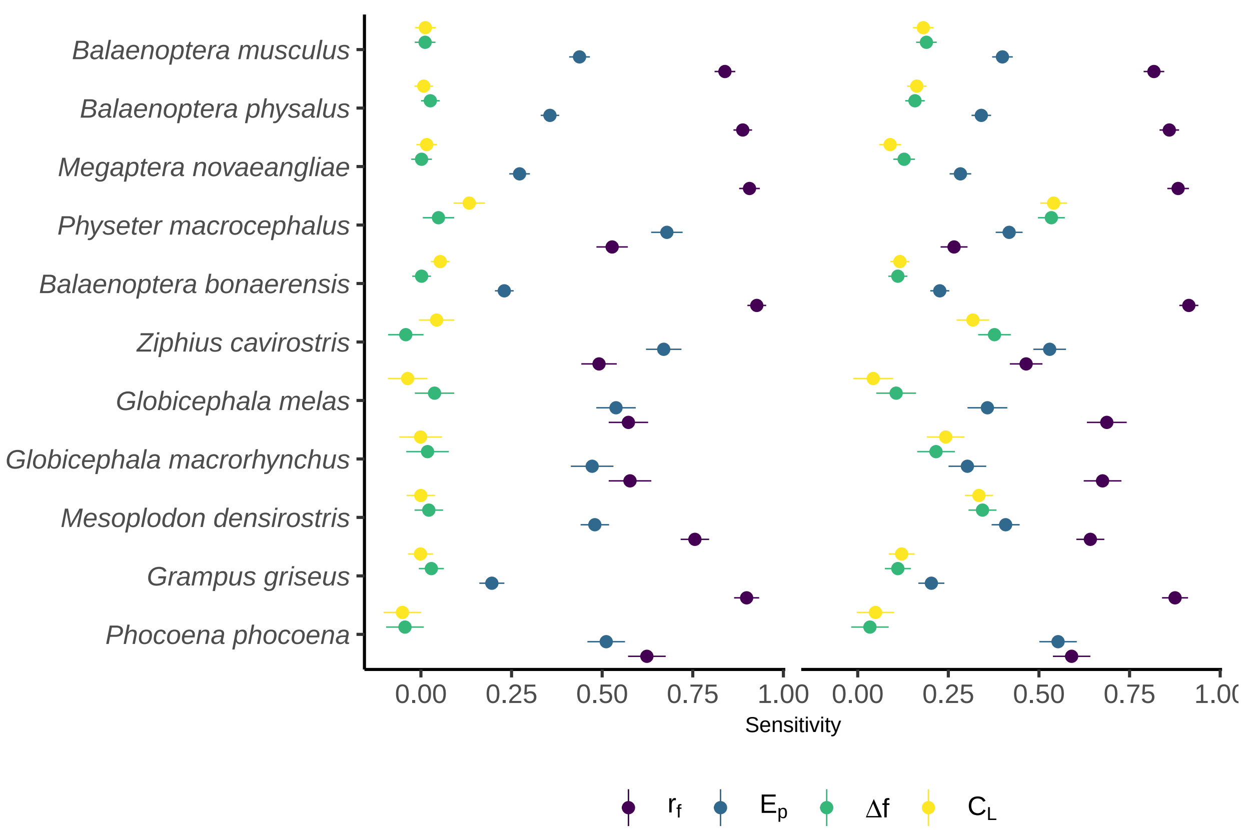
```
# Energetic cost of sonar exposure
Esonar_fun <- function(td_hr, tf_hr, rf, Ep, delta_ff, CL, mass) {
  ddtEa <- Ep * rf # kJ * hr-1 = kJ hr-1
  ddtEe <- delta_ff * CL * mass # strokes hr-1 * kJ kg-1 stroke-1 * kg = kJ hr-1
  ddtEa * td_hr + ddtEe * tf_hr # kJ hr-1 * hr + kJ hr-1 * hr = kJ
}
# Run a scenario
run_scenario <- function(species, scenario,
                         td_hr, tf_hr, Uf_ms,
                         q_rf_h, meanlnEp_lnkJ, sdlnEp_lnkJ,
                         length_m, mass_kg, ...) {
  shape_arg <- 4
  delta_ff <- ff_fun(Uf_ms, length_m) - ff_fun(1.5, length_m)
  CL <- CL_fun(mass_kg)

  # Parameter list
  param <- c("rf_h", "Ep_kJ", "delta_ff", "CL")
  # Quantile functions
  q <- list(rf_h = q_rf_h,
            Ep_kJ = qlnorm,
```

```r
            delta_ff = qgamma,
            CL = qgamma)
  # Parameter arguments
  q_arg <- list(
    rf_h = list(),
    Ep_kJ = list(meanlog = meanlnEp_lnkJ,
                 sdlog = sdlnEp_lnkJ),
    delta_ff = list(shape = shape_arg, scale = delta_ff / shape_arg),
    CL = list(shape = shape_arg, scale = CL / shape_arg)
  )
  # Generate Latin hypercube samples and run model
  pse::LHS(model = NULL, param, 5e2, q, q_arg)$data %>%
    mutate(
      esonar_kJ = Esonar_fun(td_hr, tf_hr, rf_h, Ep_kJ, delta_ff, CL, mass_kg)
    ) %>%
    {cbind(tibble(species, scenario, td_hr, tf_hr, Uf_ms), .)}
}

# Run both behavioral scenarios
sensitivity_tbl <-
  tribble(~scenario,     ~td_hr, ~tf_hr, ~Uf_ms,
          "flight",      1,      0.5,    5,
          "consumption", 4,      0.25,   3.5) %>%
  crossing(species_data) %>%
  pmap_dfr(run_scenario)
```

Model sensitivity to each parameter was quantified as the coefficient in the linear model $z(E) \sim z(r_f) + z(E_p) + z(\Delta f) + z(C_L)$ where $z()$ is the z-score. Results by guild are presented in the main text (Fig. 3). The following are the results for each species.

```r
# Normalize parameters by z-score
zscore <- function(x) (x - mean(x)) / sd(x)
sensitivity_coef <- sensitivity_tbl %>%
  group_by(species, scenario) %>%
  mutate_at(vars(esonar_kJ, rf_h, Ep_kJ, delta_ff, CL), zscore) %>%
  group_modify(function(data, keys) {
    # Fit linear model
    esonar_lm <- lm(esonar_kJ ~ rf_h + Ep_kJ + delta_ff + CL, data = data)
    # Extract coefficients and confidence intervals
    esonar_coef <- coef(esonar_lm)
    esonar_ci <- as_tibble(confint(esonar_lm, level = 0.95),
                           rownames = "param")
    colnames(esonar_ci)[2:3] <- c("ci_min", "ci_max")

    cbind(esonar_coef, esonar_ci) %>%
      select(param, esonar_coef, ci_min, ci_max) %>%
      # drop intercept
      slice(-1)
  }) %>%
  ungroup() %>%
  mutate(
    param = factor(
      param,
      levels = c("rf_h", "Ep_kJ", "delta_ff", "CL"),
```

```r
      labels = c("r[f]", "E[p]", "Delta*f", "C[L]")
    ),
    species = factor(
      species,
      levels = species_data$species[order(species_data$length_m)]
    )
  )

# Plot sensitivity coefficients and confidence intervals for all species
param_lbls <- parse(text = levels(sensitivity_coef$param))
ggplot(sensitivity_coef, aes(species, esonar_coef, color = param)) +
  geom_pointrange(aes(ymin = ci_min, ymax = ci_max),
                  position = position_dodge(1),
                  size = 0.25) +
  scale_color_viridis_d(labels = param_lbls) +
  coord_flip() +
  facet_wrap(~ scenario) +
  labs(y = "Sensitivity") +
  theme_classic(base_size = 12) +
  theme(axis.text.y = element_text(face = "italic"),
        axis.title.x = element_text(size = 8),
        axis.title.y = element_blank(),
        legend.position = "bottom",
        legend.text = element_text(hjust = 0),
        legend.title = element_blank(),
        strip.background = element_blank(),
        strip.text = element_blank())
```



```r
# Sensitivity coefficients and CIs by guid
sensitivity_guilds <- sensitivity_tbl %>%
  left_join(select(species_data, species, group), by = "species") %>%
  mutate(group = factor(group,
                        levels = c("Balaenopteridae",
                                   "Physeteridae and Ziphiidae",
                                   "Delphinidae and Phocoenidae"))) %>%
  group_by(group, scenario) %>%
  mutate_at(vars(esonar_kJ, rf_h, Ep_kJ, delta_ff, CL), zscore) %>%
  group_modify(function(data, keys) {
    # Fit linear model
    esonar_lm <- lm(esonar_kJ ~ rf_h + Ep_kJ + delta_ff + CL, data = data)
    # Extract coefficients and confidence intervals
    esonar_coef <- coef(esonar_lm)
    esonar_ci <- as_tibble(confint(esonar_lm, level = 0.95),
                           rownames = "param")
    colnames(esonar_ci)[2:3] <- c("ci_min", "ci_max")

    cbind(esonar_coef, esonar_ci) %>%
      select(param, esonar_coef, ci_min, ci_max) %>%
      # drop intercept
      slice(-1)
  }) %>%
  ungroup() %>%
  mutate(
    param = factor(
      param,
      levels = c("rf_h", "Ep_kJ", "delta_ff", "CL"),
      labels = sprintf("italic(%s)",
                       c("r[f]", "E[p]", "Delta*f", "C[L]"))
    )
  )
fig3 <- sensitivity_guilds %>%
  group_by(scenario) %>%
  group_map(
    function(data, ...) {
      ggplot(data,
             aes(x = param, y = esonar_coef,
                 ymin = ci_min, ymax = ci_max,
                 color = group)) +
        geom_pointrange(position = position_dodge(0.6),
                        size = 1,
                        fatten = 0.75) +
        coord_flip() +
        scale_x_discrete(
          labels = parse(text = levels(sensitivity_guilds$param))
        ) +
        scale_y_continuous(
          "Sensitivity",
          breaks = seq(0, 1, by = 0.2),
          labels = seq(0, 1, by = 0.2)
        ) +
        scale_color_manual(values = cbf_palette) +
```

```r
        expand_limits(y = c(0, 1)) +
        theme_classic(base_size = 18) +
        theme(axis.title.y = element_blank(),
              legend.position = "none",
              strip.background = element_blank())
    }
  ) %>%
  plot_grid(plotlist = ., labels = "AUTO")

# Table of sensitivity coefficients and CIs
abbr_binom <- function(binom) {
  paste(str_sub(binom, 1, 1),
        str_extract(binom, " .*"),
        sep = ".")
}
coef_tbl <- sensitivity_coef %>%
  mutate(abbr = abbr_binom(species),
         esonar_fmt = sprintf("%0.2f (%0.2f - %0.2f)",
                              esonar_coef, ci_min, ci_max),
         species = as.character(species)) %>%
  left_join(select(species_data, species, length_m), by = "species") %>%
  arrange(length_m) %>%
  select(scenario, abbr, param, esonar_fmt) %>%
  pivot_wider(names_from = param, values_from = esonar_fmt) %>%
  arrange(scenario) %>%
  select(-scenario)
colnames(coef_tbl) <- c("", "$r_f$", "$E_p$", "$\\Delta f$", "$C_L$")

coef_tbl %>%
  kable("latex", booktabs = TRUE, escape = FALSE) %>%
  kable_styling(latex_options = c("scale_down")) %>%
  row_spec(0, align = "c") %>%
  pack_rows("Lost consumption scenario", 1, 11) %>%
  pack_rows("Increased expenditure scenario", 12, 22)
```

	r_f	E_p	Δf	C_L
Lost consumption scenario				
P. phocoena	0.62 (0.57 - 0.68)	0.51 (0.46 - 0.56)	-0.04 (-0.10 - 0.01)	-0.05 (-0.10 - 0.00)
G. griseus	0.90 (0.86 - 0.93)	0.20 (0.16 - 0.23)	0.03 (-0.01 - 0.06)	-0.00 (-0.04 - 0.03)
M. densirostris	0.76 (0.72 - 0.80)	0.48 (0.44 - 0.52)	0.02 (-0.02 - 0.06)	-0.00 (-0.04 - 0.04)
G. macrorhynchus	0.58 (0.52 - 0.64)	0.47 (0.41 - 0.53)	0.02 (-0.04 - 0.08)	-0.00 (-0.06 - 0.06)
G. melas	0.57 (0.52 - 0.63)	0.54 (0.48 - 0.59)	0.04 (-0.02 - 0.09)	-0.04 (-0.09 - 0.02)
Z. cavirostris	0.49 (0.44 - 0.54)	0.67 (0.62 - 0.72)	-0.04 (-0.09 - 0.01)	0.04 (-0.01 - 0.09)
B. bonaerensis	0.93 (0.90 - 0.95)	0.23 (0.20 - 0.26)	0.00 (-0.02 - 0.03)	0.05 (0.03 - 0.08)
P. macrocephalus	0.53 (0.48 - 0.57)	0.68 (0.64 - 0.72)	0.05 (0.01 - 0.09)	0.13 (0.09 - 0.18)
M. novaeangliae	0.91 (0.88 - 0.93)	0.27 (0.24 - 0.30)	0.00 (-0.03 - 0.03)	0.02 (-0.01 - 0.04)
B. physalus	0.89 (0.86 - 0.91)	0.36 (0.33 - 0.38)	0.03 (0.00 - 0.05)	0.01 (-0.02 - 0.03)
B. musculus	0.84 (0.81 - 0.87)	0.44 (0.41 - 0.47)	0.01 (-0.02 - 0.04)	0.01 (-0.02 - 0.04)
Increased expenditure scenario				
P. phocoena	0.59 (0.54 - 0.64)	0.55 (0.50 - 0.60)	0.03 (-0.02 - 0.09)	0.05 (-0.00 - 0.10)
G. griseus	0.88 (0.84 - 0.91)	0.20 (0.17 - 0.24)	0.11 (0.07 - 0.15)	0.12 (0.09 - 0.16)
M. densirostris	0.64 (0.60 - 0.68)	0.41 (0.37 - 0.45)	0.34 (0.31 - 0.38)	0.33 (0.30 - 0.37)
G. macrorhynchus	0.68 (0.62 - 0.73)	0.30 (0.25 - 0.35)	0.22 (0.16 - 0.27)	0.24 (0.19 - 0.29)
G. melas	0.69 (0.63 - 0.74)	0.36 (0.30 - 0.41)	0.11 (0.05 - 0.16)	0.04 (-0.01 - 0.10)
Z. cavirostris	0.46 (0.42 - 0.51)	0.53 (0.48 - 0.57)	0.38 (0.33 - 0.42)	0.32 (0.27 - 0.36)
B. bonaerensis	0.91 (0.89 - 0.94)	0.23 (0.20 - 0.25)	0.11 (0.08 - 0.14)	0.12 (0.09 - 0.14)
P. macrocephalus	0.27 (0.23 - 0.30)	0.42 (0.38 - 0.45)	0.53 (0.50 - 0.57)	0.54 (0.50 - 0.58)
M. novaeangliae	0.88 (0.85 - 0.91)	0.28 (0.25 - 0.31)	0.13 (0.10 - 0.16)	0.09 (0.06 - 0.12)
B. physalus	0.86 (0.83 - 0.89)	0.34 (0.31 - 0.37)	0.16 (0.13 - 0.18)	0.16 (0.14 - 0.19)
B. musculus	0.82 (0.79 - 0.85)	0.40 (0.37 - 0.43)	0.19 (0.16 - 0.22)	0.18 (0.15 - 0.21)

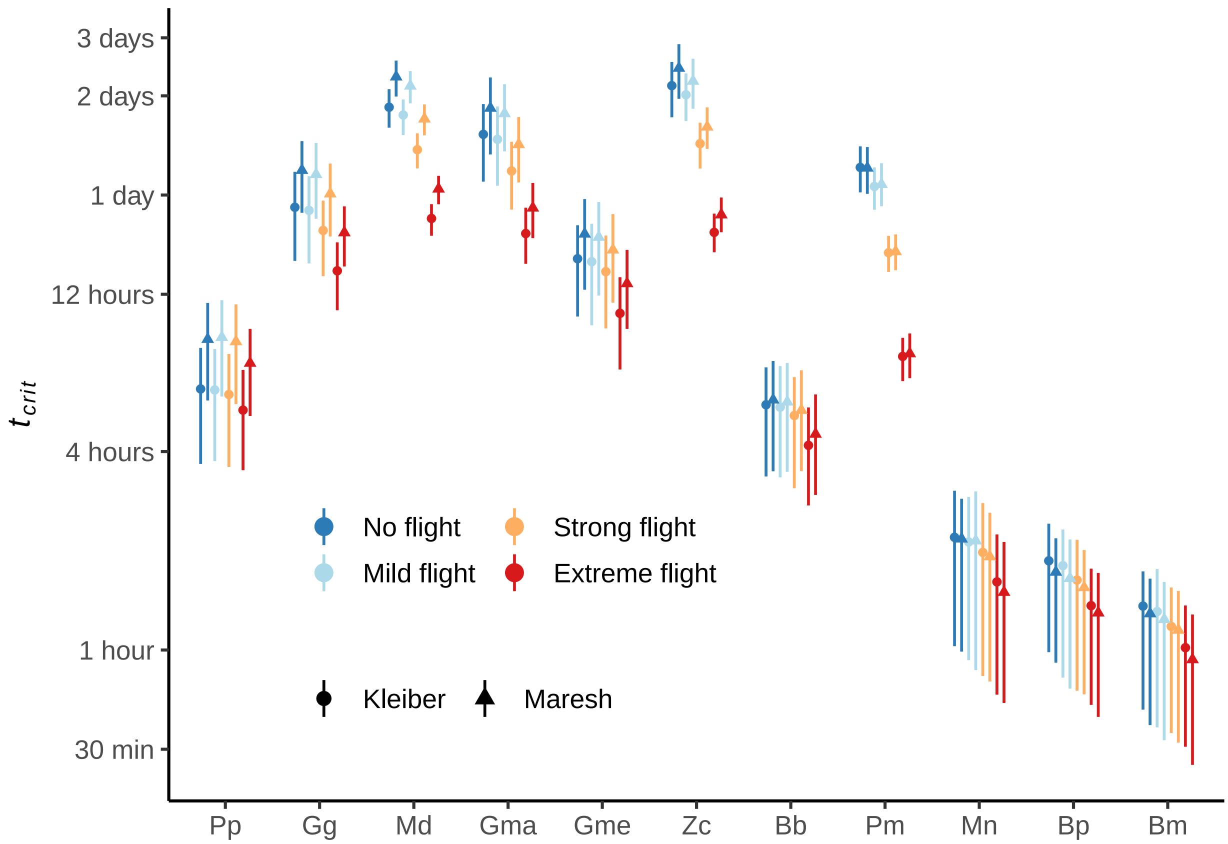
Critical cessation threshold

Cross-species comparisons of energetic costs are complicated by the range of body sizes across cetaceans. In absolute terms, a loss of 10,000 kJ would be extreme for a harbor porpoise but likely insubstantial to a blue whale. To account for these differences, we used metabolic scaling to approximately estimate the daily energy budget for each species and modeled the duration of a feeding cessation that would exceed the daily energy budget (t_{crit}). The results presented in the main text (Fig. 4) are for metabolic scaling according to Kleiber (1975) and Maresh (2014) and an FMR:BMR ratio (β) of 3. For comparison, the following calculations include β of 2.5 and 5.

```r
# Estimate FMR from mass and beta (Kleiber and Maresh curves)
fmr_fun <- function(mass, beta, bmr) {
  daily_bmr <- if (bmr == "Kleiber") {
    293.1 * mass ^ 0.75
  } else if (bmr == "Maresh") {
    581 * mass ^ 0.68
  } else {
    stop("Unspecified BMR calculation")
  }
  beta * daily_bmr
}

# Estimate tcrit once
tcrit_fun <- function(Uf_ms, tf_hr, beta, bmr, mass_kg, length_m,
                      rf_h, meanlnEp_lnkJ, sdlnEp_lnkJ, ...) {
  # Mean delta_ff and CL
```

```r
  delta_ff <- ff_fun(Uf_ms, length_m) - ff_fun(1.5, length_m)
  CL <- CL_fun(mass_kg)

  # Simulate 14 days of feeding cessation and find the fmr crossing-point
  fmr <- fmr_fun(mass_kg, beta, bmr)
  cumulative_Esonar <- tibble(hour = seq(1, 14 * 24)) %>%
    mutate(
      rf = sample(rf_h, nrow(.), replace = TRUE),
      Ep = rlnorm(nrow(.), meanlog = meanlnEp_lnkJ, sdlog = sdlnEp_lnkJ),
      delta_ff = rgamma(nrow(.), shape = 4, scale = delta_ff / 4),
      CL = rgamma(nrow(.), shape = 4, scale = CL / 4),
      Esonar = Esonar_fun(td_hr = 1, tf_hr, rf, Ep, delta_ff, CL, mass_kg),
      cum_Esonar = cumsum(Esonar)
    )

  approx(x = c(0, cumulative_Esonar$cum_Esonar),
         y = c(0, cumulative_Esonar$hour),
         xout = fmr,
         ties = mean)$y
}

# Flight scenarios for tcrit calculations
tcrit_tbl <- tribble(
  ~scenario,         ~tf_hr,  ~Uf_ms,
  "no_flight",       0,       1.5,
  "mild_flight",     5 / 60,  2.5,
  "strong_flight",   15 / 60, 3.5,
  "extreme_flight", 30 / 60, 5
  ) %>%
  mutate(scenario = factor(scenario,
                           levels = c("no_flight",
                                      "mild_flight",
                                      "strong_flight",
                                      "extreme_flight"),
                           labels = c("No flight",
                                      "Mild flight",
                                      "Strong flight",
                                      "Extreme flight"))) %>%
  # Estimate tcrit for all scenarios 1000 times
  crossing(species_data,
           beta = c(2.5, 3, 5),
           bmr = factor(c("Kleiber", "Maresh")),
           i = 1:1000) %>%
  mutate(tcrit = pmap_dbl(., tcrit_fun))

# Summarize tcrit results
tcrit_summ <- tcrit_tbl %>%
  group_by(abbr, scenario, bmr, beta) %>%
  summarize(tcrit_mean = mean(tcrit),
            tcrit_1q = quantile(tcrit, 0.25),
            tcrit_3q = quantile(tcrit, 0.75)) %>%
  ungroup() %>%
  mutate(abbr = factor(abbr, levels = species_data$abbr))
```

```r
# Figure 4 from main text
filter(tcrit_summ, beta == 3) %>%
  ggplot(aes(abbr,
             tcrit_mean,
             color = scenario,
             shape = bmr)) +
  geom_pointrange(aes(ymin = tcrit_1q,
                      ymax = tcrit_3q),
                  fatten = 2,
                  position = position_dodge(width = 0.6)) +
  # scale_x_discrete(labels = morphologies$abbr) +
  scale_y_continuous(
    expression(italic(t[crit])),
    breaks = c(0.5, 1, 4, 12, 24, 48, 72),
    minor_breaks = NULL,
    labels = c("30 min", "1 hour", "4 hours", "12 hours",
               "1 day", "2 days", "3 days"),
    trans = "log2"
  ) +
  scale_color_brewer(palette = "RdYlBu", direction = -1) +
  labs(y = "Feeding cessation") +
  theme_classic(base_size = 12) +
  theme(axis.title.x = element_blank(),
        legend.box.margin = margin(),
        legend.justification = c(0, 0),
        legend.position = c(0.11, 0.08),
        legend.title = element_blank()) +
  guides(color = guide_legend(ncol = 2), shape = guide_legend(ncol = 2))
```




```r
# Table of tcrit results
tcrit_table <- tcrit_summ %>%
  mutate(tcrit_fmt = sprintf("%.3g (%.3g - %.3g)",
                             tcrit_mean, tcrit_1q, tcrit_3q)) %>%
  select(-(tcrit_mean:tcrit_3q)) %>%
  pivot_wider(names_from = c("bmr", "beta"), values_from = tcrit_fmt)
colnames(tcrit_table) <- c(
  "", "",
  "$t_{crit} (hr), \\beta = 2.5$",
  "$t_{crit} (hr), \\beta = 3$",
  "$t_{crit} (hr), \\beta = 5$",
  "$t_{crit} (hr), \\beta = 2.5$",
  "$t_{crit} (hr), \\beta = 3$",
  "$t_{crit} (hr), \\beta = 5$"
)
kable(tcrit_table, "latex", booktabs = TRUE, escape = FALSE) %>%
  kable_styling(latex_options = c("scale_down")) %>%
  add_header_above(c(" " = 2, "Kleiber" = 3, "Maresh" = 3)) %>%
  collapse_rows(columns = 1, latex_hline = "major", valign = "top")
```

		Kleiber			Maresh		
		$t_{crit}(hr), \beta = 2.5$	$t_{crit}(hr), \beta = 3$	$t_{crit}(hr), \beta = 5$	$t_{crit}(hr), \beta = 2.5$	$t_{crit}(hr), \beta = 3$	$t_{crit}(hr), \beta = 5$
Bb	No flight	4.86 (2.83 - 6.47)	5.55 (3.36 - 7.2)	8.57 (5.82 - 10.7)	4.93 (2.77 - 6.46)	5.74 (3.49 - 7.53)	9.17 (6.26 - 11.8)
	Mild flight	4.64 (2.65 - 6.17)	5.45 (3.34 - 7.27)	8.18 (5.29 - 10.5)	4.92 (2.86 - 6.59)	5.66 (3.47 - 7.43)	8.67 (5.86 - 11.2)
	Strong flight	4.27 (2.51 - 5.75)	5.14 (3.1 - 6.73)	7.74 (5.36 - 9.61)	4.52 (2.78 - 6)	5.34 (3.49 - 7.06)	8.42 (5.88 - 10.7)
	Extreme flight	3.57 (2.21 - 4.76)	4.18 (2.75 - 5.44)	6.6 (4.76 - 8.18)	3.76 (2.37 - 4.99)	4.52 (2.95 - 5.96)	6.99 (4.97 - 8.7)
Bm	No flight	1.18 (0.56 - 1.53)	1.36 (0.659 - 1.73)	1.99 (1.13 - 2.51)	1.13 (0.502 - 1.47)	1.29 (0.592 - 1.65)	1.82 (1 - 2.29)
	Mild flight	1.16 (0.475 - 1.53)	1.31 (0.583 - 1.76)	1.98 (0.969 - 2.66)	1.12 (0.431 - 1.54)	1.24 (0.533 - 1.61)	1.85 (0.9 - 2.39)
	Strong flight	1.08 (0.469 - 1.45)	1.18 (0.56 - 1.55)	1.74 (0.934 - 2.21)	0.978 (0.432 - 1.32)	1.15 (0.524 - 1.51)	1.71 (0.897 - 2.22)
	Extreme flight	0.895 (0.424 - 1.26)	1.02 (0.509 - 1.36)	1.44 (0.83 - 1.88)	0.797 (0.372 - 1.13)	0.936 (0.448 - 1.28)	1.33 (0.742 - 1.7)
Bp	No flight	1.6 (0.794 - 2.07)	1.86 (0.985 - 2.42)	2.86 (1.66 - 3.66)	1.52 (0.719 - 1.97)	1.72 (0.915 - 2.18)	2.63 (1.47 - 3.3)
	Mild flight	1.5 (0.671 - 1.99)	1.8 (0.825 - 2.32)	2.75 (1.52 - 3.56)	1.51 (0.621 - 2.07)	1.65 (0.764 - 2.17)	2.47 (1.35 - 3.24)
	Strong flight	1.42 (0.653 - 1.88)	1.63 (0.752 - 2.16)	2.55 (1.43 - 3.32)	1.32 (0.589 - 1.69)	1.55 (0.734 - 2.01)	2.37 (1.27 - 3.07)
	Extreme flight	1.17 (0.576 - 1.53)	1.36 (0.682 - 1.76)	1.98 (1.15 - 2.47)	1.15 (0.529 - 1.49)	1.3 (0.627 - 1.71)	1.96 (1.14 - 2.48)
Gg	No flight	19 (13 - 24)	22 (15.2 - 28.2)	35.9 (27.3 - 42.9)	23.7 (16.8 - 29.8)	28.5 (21.2 - 35)	46.2 (36.3 - 55.6)
	Mild flight	18.2 (12 - 23)	21.6 (14.9 - 27.4)	34.3 (26.2 - 41.3)	23.4 (16.8 - 28.9)	27.7 (20.3 - 34.5)	44.2 (35.1 - 52.5)
	Strong flight	16 (11.4 - 20.4)	18.7 (13.6 - 23.1)	30.6 (24.1 - 36.6)	20.9 (15.1 - 26.1)	24.2 (18 - 29.9)	39.1 (30.8 - 46.5)
	Extreme flight	11.9 (8.65 - 14.8)	14.1 (10.7 - 17.3)	23.3 (18.7 - 27.4)	15.5 (11.9 - 19)	18.5 (14.6 - 22.2)	29.9 (25 - 34.7)
Gma	No flight	30.6 (21.8 - 39.1)	36.7 (26.4 - 45.3)	59.9 (45.9 - 72.2)	37.3 (27 - 46.8)	44.1 (31.9 - 54.6)	71.9 (57.9 - 85.9)
	Mild flight	30.1 (21.7 - 37.3)	35.4 (25.6 - 44.6)	57.2 (44.4 - 69.8)	35.3 (25.5 - 43.7)	42.4 (32.6 - 52.1)	67.9 (54.8 - 80.7)
	Strong flight	23.9 (17.7 - 30)	28.4 (21.7 - 34.8)	46.5 (37.6 - 55)	29.5 (22.4 - 36.3)	34.2 (26.2 - 41.4)	56.1 (46.2 - 65.1)
	Extreme flight	15.3 (12.3 - 18.4)	18.3 (14.8 - 22)	29.8 (25 - 34.9)	18.6 (15.3 - 22.2)	21.9 (17.8 - 26.1)	36.5 (31.3 - 42)
Gme	No flight	13.2 (8.46 - 17.3)	15.4 (10.3 - 19.4)	23.7 (17.2 - 30)	15.3 (9.77 - 20)	18.3 (12.4 - 23.3)	27.9 (20.4 - 34.6)
	Mild flight	12.3 (7.63 - 16.4)	15.1 (9.66 - 19.6)	23.7 (16.7 - 29.9)	15.1 (9.85 - 19.5)	17.9 (11.9 - 22.9)	27.3 (20.1 - 33.9)
	Strong flight	11.9 (7.64 - 15.4)	14.1 (9.45 - 18.1)	21.1 (15.6 - 26.3)	13.6 (9.22 - 17.6)	16.4 (11.3 - 21)	25.5 (19.1 - 31.2)
	Extreme flight	9.61 (6.68 - 12.2)	10.5 (7.1 - 13.5)	17.5 (13.5 - 21.4)	11 (7.69 - 14)	12.9 (9.42 - 16.4)	20.6 (15.9 - 25.3)
Md	No flight	36.9 (31.8 - 41.8)	44.3 (38.4 - 50.3)	73.2 (65.5 - 81.1)	45.5 (39.2 - 51.3)	54.8 (47.8 - 61.4)	89.4 (81.4 - 98.1)
	Mild flight	34.7 (30 - 39.3)	42 (36.5 - 46.8)	69.5 (62 - 76.8)	42.7 (36.8 - 48.2)	51.4 (45.6 - 57.1)	85.2 (76.7 - 93)
	Strong flight	27.7 (24 - 31.2)	33 (28.9 - 36.9)	54.8 (49.7 - 59.8)	34.3 (30.3 - 38.3)	40.9 (36.5 - 45.2)	67.3 (61.7 - 72.8)
	Extreme flight	16.8 (14.7 - 18.8)	20.4 (18.1 - 22.5)	33.5 (30.5 - 36.2)	21.1 (18.8 - 23.3)	25.1 (22.5 - 27.4)	41.4 (38.3 - 44.7)
Mn	No flight	2 (0.877 - 2.74)	2.2 (1.03 - 3.04)	3.16 (1.61 - 4.16)	1.89 (0.869 - 2.51)	2.17 (0.989 - 2.88)	2.95 (1.49 - 4)
	Mild flight	1.95 (0.774 - 2.69)	2.13 (0.932 - 2.91)	3.11 (1.51 - 4.31)	1.84 (0.679 - 2.45)	2.15 (0.869 - 3.03)	2.97 (1.49 - 4.1)
	Strong flight	1.78 (0.782 - 2.45)	1.98 (0.834 - 2.79)	2.92 (1.5 - 4.02)	1.77 (0.678 - 2.37)	1.92 (0.802 - 2.61)	2.74 (1.37 - 3.77)
	Extreme flight	1.41 (0.601 - 2.01)	1.61 (0.732 - 2.24)	2.35 (1.34 - 3.14)	1.38 (0.605 - 2.02)	1.5 (0.691 - 2.13)	2.19 (1.18 - 2.98)
Pm	No flight	24.4 (19.9 - 28.7)	29.1 (24.5 - 33.7)	47.6 (41.5 - 53.9)	24.6 (19.9 - 28.9)	29 (24.2 - 33.6)	48.2 (42 - 54.3)
	Mild flight	21.4 (17.9 - 25.1)	25.5 (21.7 - 29.1)	42.5 (37.6 - 47.5)	21.6 (17.9 - 25.1)	25.9 (22.2 - 30)	42.8 (38 - 47.3)
	Strong flight	13.5 (11.6 - 15.5)	16 (14 - 18)	26.6 (23.7 - 29.4)	13.7 (11.8 - 15.5)	16.2 (14.2 - 18.2)	27 (24.1 - 30)
	Extreme flight	6.52 (5.39 - 7.59)	7.78 (6.54 - 8.85)	12.8 (11.3 - 14.3)	6.58 (5.45 - 7.63)	7.93 (6.68 - 9.13)	13 (11.4 - 14.4)
Pp	No flight	5.6 (3.39 - 7.38)	6.19 (3.67 - 8.25)	9.27 (6.07 - 12.1)	7.69 (4.83 - 10.2)	8.77 (5.72 - 11.3)	13.9 (9.73 - 17.7)
	Mild flight	5.29 (3.21 - 7.07)	6.15 (3.74 - 8.19)	9.49 (6.21 - 12.4)	7.34 (4.61 - 9.56)	8.89 (5.87 - 11.5)	13.8 (9.54 - 17.8)
	Strong flight	5.1 (3.03 - 6.82)	5.96 (3.59 - 7.91)	8.94 (5.94 - 11.7)	7.32 (4.53 - 9.67)	8.63 (5.57 - 11.2)	13.4 (9.64 - 17.2)
	Extreme flight	4.42 (2.7 - 5.95)	5.34 (3.51 - 7.07)	8.01 (5.59 - 10.4)	6.35 (4.13 - 8.26)	7.42 (5.13 - 9.42)	12 (8.78 - 15.1)
Zc	No flight	43.6 (34.6 - 52.2)	51.5 (41.3 - 60.8)	85.5 (71.5 - 97.7)	49.4 (39.6 - 58.8)	58.2 (47 - 68.9)	95.5 (82 - 108)
	Mild flight	40.4 (32.3 - 48.5)	48.4 (40.2 - 56.2)	77.7 (66.2 - 88.5)	45.6 (37.4 - 53.4)	53.2 (43.9 - 62.2)	88.3 (76.4 - 101)
	Strong flight	28.9 (24 - 33.7)	34.4 (28.9 - 39.8)	56.7 (49.9 - 63.6)	32.6 (27.1 - 38.2)	38.6 (33.1 - 44.3)	63.4 (55.8 - 71.6)
	Extreme flight	15.6 (13.3 - 17.9)	18.5 (16.1 - 21.1)	30.9 (27.5 - 34.5)	17.6 (15.3 - 20)	20.9 (18.5 - 23.6)	34.7 (31.6 - 38.2)