# Chapter 3

# Strategy

Estimate sustainability reference points for reef-associated carcharhinid shark species

1. Collect life history traits from stock assessments: density-independent survival rate, age structured maturity, age structured survival/mortality, age-structured fecundity, maximum age
2. Find equations describing ogives for natural mortality and maturity, also find priors
3. Model life history traits in python
4. Collect species-level attributes that may be related to productivity (species covariates)
5. Model the relationship between covariates and life history traits
   1. Take life history covariates and relate them to the terms in the maturity model, and then in the natural mortality model
6. Use above model to predict life history traits for data-limited species
7. Use predicted life-history traits to calculate â, and from there calculate target and limit reference points

Other:

* Check credibility of alpha-hat estimates against Pardo paper

**Notes on maturity:**

* If no age-structured values, use knife-edge maturity based on a50 value
* If no a50 value, can predict a50 if you know max age using method outlined in Frisk 2011

**Notes on natural mortality:**

* If no age-structured data, take single value and parcel it out into year-values using Chen-watanabe u-shaped (bathtub) function? Depends on knowing von-bertalanffy growth parameters k and t0 (Chen and Watanabe, 1989)
* If von-bertalanffy coefficients are unknown, can look to other simpler methods that depend only on maximum age, (Kenchington, 2014)
* See Manire & Gruber for natural morality of age 0 lemon sharks (survivorship = 0.39) (Manire and Gruber, 1993)
* See Purushottama 2017 for M of R. oligolinx
* Sen 2018 for M R. acutus

**Notes on fecundity:**

* Not as important to have age-structured fecundity. Dusky shark example in Brooks paper doesn’t have it. Just make sure fecundity is expressed as an annual value and only includes females. Where no estimate of male-female ratio assume 1:1

**Notes on density-independent survivorship**

This term is referred to in different ways in the Cortes and Brooks papers: b=S0= age 0 pup survival = slope at origin of stock-recruitment curve/density independent growth term

Difficult to find age 0 survival rates for sharks so for those that are missing, think about using alternate method from Pardo 2016. lαmat =b = S0 = (e-M) α mat so can figure out b from only age at maturity (a50) and instantaneous natural mortality

instead of survival to recruitment rate in Brooks ref point method?

Use this method to fill in missing values for S0? The updated model for estimating rmax includes juvenile survival which is derived from adult natural mortality M (Pardo et al., 2016). (Pardo et al., 2018)

# Models

## Model B – Maturity

How do life history traits covary with age structured maturity?

Where:

m = maturity

s = curve parameter (how flat/steep is the maturity ogive?)

a = age

a50 = age where 50% of population is mature (middle of curve)

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**Setting up model:**

- first you have a population of a50 values and a population of s values that (we assume) vary according to a normal distribution

Where:

G= mean value

∂ = standard deviation

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- Need to describe a50 in terms of covariates, and separately describe s in terms of covariates

- S covariates may have more to do with growth rather than reproduction (how quickly do you reach the size for reproduction) for example temperature or seasonality (maybe growth happens more suddenly in places with a short summer)

- a50 covariates more to do with reproduction rather than growth

Other model configuations:

* Could also set up a multivariate normal prior that connects S and a50 explicitly, maybe good idea because we know that these two parameters are correlated and they are also part of the same equation (rather than being two separately collected life history parameters). In this version all covariates influence both response variables, don’t have to assign covariates to s and a50 separately. Downside is that there are potentially covariates that influence s but not a50.
* Fixed effect model also an option – set up so that the a50 intercept doesn’t vary per stock. Allows you to see the changes in model fit more clearly but also potentially allows the model to be more driven by noise? Ask aaron. Mixed effect model (a50 intercept varies) acknowledges that there are differences between stocks that may not be accounted for in the chosen covariates. Fix effect model says that all variation must be described by covariates.

## Model Versions

**Model 1** – mixed effects model (slope of maturity curve changes for every stock)

A50 params: lmax, depth, k, interbirth interval, amax, litter size, offspring size, trophic level

S params: lmax, depth, k, interbirth, amax, litter size, offspring size, trophic level

Model takes forever to run (11hours). WAIC much lower for mixed effects than for fixed effects (model 2). Lots of the S parameters don’t make any difference at all, probably not necessary. Bad datapoints mostly in the middle of maturity ogives – probably a good thing as points in the middle should be driving the shape of the curve (as opposed to the points that are all on 0 and 1)

**Model 2** – fixed effects model (slope of maturity curve same for each stock, only intercept varies)

Same parameters as model 1, runs faster, fit is worse (higher WAIC), 2 model runs (see trace plots) give different results which is not good, caterpillars not as fuzzy, ‘bad’ datapoints (points driving change in fit because they don’t follow the slope as nicely as other points) are scattered throughout

**Model 3** – also called maturity\_model\_habitat, mixed effects model same as 1 except with categorical habitat variable. Seems to work with habitat written in as a dummy variable, but I can’t get habitat to work as an index variable (aaron says this is preferable)

**Model 4** – same as model 1 except with litter size and offspring size relative to maternal body size. Intent is to make sure I’m looking at differences between species, not within species. Turns out it doesn’t make any meaningful difference to model results

**Model 5** – same as model 2 except with litter size and offspring size relative to maternal body size. Model results are pretty much the same

**Model 6** – same as model 2 but with only a50 parameters. Fixed effects models (6&7) have more bad data points than mixed effects models (8&9). WAIC values higher for both 6&7 compared to 8&9. runs faster than model 7.

**Model 7** – same as model 2 but s parameters only. Without a50 parameters, none of the s parameters have an effect on maturity

**Model 8** – same as model 1 but a50 parameters only. WAIC values lower again for both mixed effects models compared to fixed effects models. This one ran much longer than model 9 (4 hrs vs 9 hrs)

**Model 9** – same as model 1 but s params only. Without a50 parameters, none of the s parameters have an effect on maturity.

After running models 1-9, decided to make following parameter changes: a50 = amax, depth, habitat, interbirth interval, lmax, offspring size, trophic level, litter size. S= k, trophic level, amax, habitat.

**Maturity\_model\_depth** – ran mixed effects model with different depth measurements to see which one is better. Max\_depth turns out has the strongest effect on maturity. Average depth is ok, and min\_Depth is a poor predictor.

**Maturity\_model\_habitat** – simplified mixed effects model with categorical variable for habitat. Figured out how to run it as a dummy variable but not as indicator variable

Maturity\_model\_habitat2 – simplified mixed effects model with categorical variable for habitat. Finally runs properly with habitat as indicator variable. Trace = 5

**Models 10 & 11** – models compare fully parameterised model with a version where most of the s params are stripped out. both mixed effects models. Both use depth max and the not relative versions of litter size and offspring size. Trophic has smaller effect in model 11 (stripped out) compared to model 10. K has slighter stronger effect for model 11 vs model 10. WAIC values very close but slightly better for model 11. Decided to move forward with model 11.

Trace for model 11 is saved as trace3

**Models 12** **& 15**- both mixed effects models. same as models 10& 11 but with temperature and habitat added (habitat as indicator variable as in habitat2). Depth ave. Model 12 has all covariates dumped in. Model 15 has some stripped out based on results from previous runs.

Model 10 has better looking trace plots than model 12 – something about adding habitat or temp is making the 2 model runs more inconsistent with each other. Effect size density is much wigglier, not centred around a single value.

Temperature has a slightly -ive effect on a50 in model 12, and no effect in model 15. Slightly negative effect in the full model as well for S, and no effect for the stripped out model. Doesn’t really seem worth keeping for mixed-effects models except that it’s one of the few variables I can find consistently for all of the prediction species.

Habitat has basically no effect on a50 except for reef species. Realised that’s probably because 90% of the sharks in the input dataset are reef-associated. Not enough variation in input to produce a sensible relationship. Aaron recommends taking this out.

Other a50 params: Offspring size effect same as models 10&11, but slightly smaller. K same. Amax same. Trophic same. Effect on litter in model 12 smaller than in model 10. In model 15 slightly larger than model 11. Depth same as 10&11 (clearly positive). Interbirth interval stronger effect in stripped model.

Other S params: Offsz same as models 10&11. Interbirth interval same. K still has strong effect, slightly bigger for stripped model (15). No effect of Amax in either model. Was small effect in model 10. No effect of Litter size. Trophic has slightly negative effect on S, same as 10&11. Depth slight positive in full model. Maybe put back in?

Model 12 trace = 8

Model 15 trace = 7

**Model 13** - fixed effects model (like model 5) but with same covariates as model 15. Trace=6. Fit is much worse than the mixed effects models, ogives don’t follow raw data at all for some species. Effects of covariates are much more certain than in mixed effects model – almost no error bars.

S: Trophic no effect, Amax very slightly negative, K effect smaller than mixed models, temperature no effect,

A50: Interbirth strongly positive, same for depth, litter size, Amax, Offspring size, Trophic and Lmax slightly negative (opposite of mixed models). Temperature clearly positive (opposite of model 12)

In general a50 effects clearer and stronger in fixed effects model, and S effects weaker. Is it possible to run a model which is mixed effect for S and fixed effect for a50?

**Models 14 –** same as model 11 except that covariates are mean-centred rather than 0-centred. Need this to make output for prediction script because effect sizes need to be on the same scale as the raw data in order to calculate predicted values for a50 and s

Trace = 4

**Models 16 & 17:** 16 = mixed effects, uses depth ave, litter & offspring (not relative); habitat removed from previous run. comparable to model 12. 17= fixed effects model, all same covariates as 16. comparable to 15. Changed prior for a50 to 0-30 because some recorded carcharhinids mature at 1

Traces: 16=12, 17=13

**Models 18 & 19 =** prediction models. Data transformed in the same way as mat14 for use to predict new ogives. 18=mixed effects. 19=fixed effects. Same covariates as 16 & 17.

**Models 20 & 21:** Models to test two different versions of the fixed effect model with different priors. Maybe priors for mixed effects model don’t make sense for fixed effect. Changed prior for a50 from uniform to normal, S from uniform to exponential

Rhat values for 21 are closer to 1 than for model 20

WAIC lower for 20 vs 21, original priors model has closer fit

Model fit in predicted vs observed looks the same

Effect sizes are mostly the same

Traces: 20= 14, 21=15

Aaron says… fixed effects model clearly worse performing because fit is so bad – model does not allow s and a50 to vary per stock and therefore does not capture variability from unobserved sources (only captures variability from the covariates which we know don’t tell the whole story). Effect sizes are small because of this restriction on variation per stock. Also fixed effects model is bad for prediction, again because it’s not allowed to vary per stock. Since the effect sizes are really small, this restricts the range of predicted a50 and s values which is bad. Also doesn’t build in variability from unobserved sources, which is why the predicted curves are so awful. Dump it!

**Models 22 & 23:** same as model 16 except ga50 is moved to end of model spec. mixed effects, no habitats. All continuous variables dumped back into 22 because Aaron says removing variables with a small effect size is frequentist garbage (except for linf because it’s the same thing as lmax). Habitats not in because there isn’t enough data from species that are not reef-associated. Model 23 has all covariates except the ones that are harder to find for understudied species: K,linf, amax. See if can still predict ogives without these.

Model completely failed to fit. Don’t do this again.

Traces = 16,17

Tried same model with sharpnose and spadenose removed because a50 < 1 maybe is the reason the model is fucked up. Model still failed to converge, so the problem was with the code as well as the new data.

**Models 24 & 25** – prediction model versions of models 22&23. Abandoned bc 23 & 22 failed

**Models 26 & 27** – same as models 22 & 23 except with ga50 and gS moved back to the way they were in model 16. Tried with additional ogives (mostly short-lived sharpnoses) and model did not converge. Could be something with the code but I suspect its either a problem with the additional covariates or with the new data. Lmat not the problem as tried running without lmat and model did not converge

Tried same models again with spadenose and R. oligolinx ogives removed. Model converges now 😊 New ogives were either a problem because they mature too quickly for the ogives to be properly characterised by annual data (3 datapoints does not a curve make); or (Aaron says) because values that are too close to 0 fuck up the model, something to do with conversion of values to log-odds scale and how the numbers are too big

Also tried model 26 with R. acutus, R. oligolinx and S. laticaudus recorded with mat values for ages 0.25, 0.5, 0.75, 1.25 etc. found out that R. oligolinx was recorded incorrectly in the first run – mat value for age 0 was recorded as mat value for age 1. Fixed errors and model does converge but doesn’t perform as well as without the new stocks. Some R hat values >1.2. waic value is for some reason better than it was without the new stocks (-3520 vs -3320)

**Models 28 & 29:** prediction model versions of 26 & 27. Prediction models for some reason do converge even though mdoels 27 and 26 don’t. something to do with the transformation of the covariates? Model specifications are exactly the same.

**Models 30:** mixed effects model without sharpnose stocks, with all covariates besides habitat included (even the repro ones on S). Runs properly but doesn’t converge.

**Model 31**: mixed effects model without sharpnoses, only includes covariates with a50 and s if says to in model param doc (if evidence in literature to support). No habitats because of data limitations. Converges beautifully. R values all 1. WAIC -3364 (best so far!)

**Model 32**: same as 30 except von-bertalanffy and age-based params are removed. To see if can describe ogvies without these hard to find parameters. Runs ok but doesn’t converge. Some rhat values higher than 1.7

# Data

Data come from stock assessments and from papers

* Initial data collection stage just looked at stock assessments because more likely to have maturity, fecundity and natural mortality in one document
* Second data collection stage looking at papers with more specific focus

## Stock Assessments

Gulf of Mexico blacktip shark (Carcharhinus limbatus, Carcharhinidae) stock assessment (NMFS 2012

NMFS (2012). Southeast Data, Assessment and Review (SEDAR) 29: Stock assessment report—Gulf of Mexico blacktip shark. North Charleston, SC, USA. Retrieved from http://sedarweb.org/docs/sar/ S29\_GOM%20blacktip%20report\_SAR\_final.pdf

Stock assessments in Cortes & Brooks 2018

Stock assessment from Brooks 2010

### Stocks in Simpfendorder & Dulvy 2017

65 stock assessments. Reefs sharks include…

**Sustainable and with management:** Northern Aus Australian Blacktip, Gulf of Mexico Blacktip, Gulf of Mexico Bonnethead, NW Atlantic finetooth,

**Sustainable, no management:** Queensland pigeye, Queensland spinner, Queensland spottail,

**Rebuilding**: Western Australia Dusky, WA Sandbar, NW Atlantic sandbar,

**Not sustainable**: Queensland Australian Blacktip, NW Atlantic Blacknose, NW Atlantic Blacktip, India Blacktip, NW Atlantic Dusky, NW Atlantic scalloped hammerhead

AU 2015 – has von Bertalanffy growth parameters for 23 stocks

Stocks in Clarke & Hoyle 2014

Harry et al 2016

Barker & Schleussel 2005 – bayesian production modelling

Brooks et al 2010 has biological parameters for dusky sharks

### Dulvy et al 2008

Life history parameters for 21 pelagic sharks

### Cortes et al 2006 Stock Assessment for Dusky

US Atlantic sharks are managed under the Fishery Management Plan for Atlantic Tunas, Swordfish and Sharks HMSFMP

## Life History Covariates

**Covariates:**

* Temperature preference and coastal vs open ocean (Simpfendorfer et al., 2002)
* Use of nursery areas (carcharhinids using nursery areas tend to have slower growth rates) see (Branstetter, 1990)
* Length at maturity, total length, species growth rate k (von Bertalanffy parameter), intrinsic rate of increase r, age at 50 maturity a50, maximum age, (Frisk 2011, Hutchings 2012)
* Fecundity
* Genus (relatedness)- is this a nuisance variable?
* From Beukhof dataset: habitat, feeding mode, body shape, offspring size, spawning type

**Sources:**

Dusky – Compagno 1984, Musick 1993, Musick & Colvocoresses 1986, Castro 1993, Natanson 1995 from Cortes 2006

Hutchings et al 2012

Longline data from Hansell et al 2018

Robbins 2006 see for white-tip and grey reef sharks in australia

**Notes on data collection:**

Data is included in the master table preferentially by source. Highest priority inclusion status = data from peer-reviewed papers or fisheries management documents e.g. stock assessments. 2nd tier is data from Beukhof dataset. 3rd tier is data from FishBase.

## Equations

**From Cortes 2006 (catch-free age structured model):**

Eq. 3.4 and 3.5

Where

S0=age 0 pup survival

R0=net reproductive rate (recruitment)

lx=survivorship ogive

mx=maturity ogive

n=max lifespan

α=maximum lifetime reproduction per female (density independent) – same as â in Brooks 2010

f(ma)=maturity as a function of age

k=slope of logistic maturity curve

a95=age when 95% of population is mature

a50=age when 50% of population is mature/median age at maturity

z = steepness (ratio of recruitment at 20% of virgin biomass to recruitment at virgin biomass)

**Beverton-Holt eq. from Brooks et al 2010**

Where

Ma =maturity at age

fa =fecundity at age

Mj = natural mortality at age

R =age at recruitment=1

b=S0= age 0 pup survival = slope at origin of stock-recruitment curve/density independent growth term

a = density dependent growth term

â=maximum lifetime reproductive rate at low density

h=steepness=slope of stock-recruit function at 20% biomass

S = stock fecundity

R = recruitment

**From Cortes & Brooks 2018:**

Where

M=natural mortality (average from age 1 to age max)

Bmer=biomass corresponding to maximum excess recruitment

B0=virgin biomass

s=slope factor for logistic maturity ogive

a=age

a50=age when 50% of population is mature/median age at maturity

**From Myers 1999:**

Paper models steepness and maximum annual reproduction from >700 stock-recruitment series (Ram database).

Where:

â=maximum lifetime reproductive rate at low density

ã = maximum annual reproductive rate at low density

α = slope at origin of stock-recruit curve (same as b in Brooks 2010)

SPRf=0 = spawners per recruit @ zero fishing mortality (same as Φ from Brooks paper)

ps = adult survival rate