

# Build Table 1

Flexibility is a hidden axis of biomechanical diversity in fishes. J. Exp. Biol.

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```
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v purrr  0.3.5
## v tibble  3.1.8      v dplyr  1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v readr   2.1.3      v forcats 0.5.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

library(gt)
```

Formulas:

$$EI = \frac{CL}{\theta_{max}}$$

where  $C$  is the bending moment (N m),  $L$  is the length of the segment, and  $\theta_{max}$  is the bending angle. From Long (1998).

$\eta I$  should work the same way.

Graphs digitized with [<https://automeris.io/WebPlotDigitizer/>]

## Lamprey

Tytell, E. D., Carr, J. A., Danos, N., Wagenbach, C., Sullivan, C. M., Kiemel, T., Cowan, N. J. and Ankarali, M. M. (2018). Body stiffness and damping depend sensitively on the timing of muscle activation in lampreys. Integrative and Comparative Biology 58, 860–873.

```
lampreybenddata <- tribble(
  ~species, ~E.Pa, ~E.sd.Pa, ~I.mm4, ~I.sd.mm4, ~EI.Nm2, ~EI.sd.Nm2,
  'Ichthyomyzon unicuspis', 88e3, 67e3, 3256, 1741, 2.10e-4, 0.82e-4)

lampreydampdata <- tribble(
  ~eta.Pas, ~eta.sd.Pas, ~etaI.Nm2s, ~etaI.sd.Nm2s,
  224, 134, 6.1605e-07, 2.93036e-07)

lampreyprepdata <- tribble(
  ~tissue, ~location.L, ~location.desc, ~location.cat, ~Lseg.mm, ~Lbody.mm, ~freq.radps,
  'whole body', 0.55, 'midbody', 'mid', 17.6, 260, 2*pi)
```

```

lampreycurvedata <- tribble(
  ~curve.invm, ~angle.deg, ~angle.sd.deg, ~strain.pct, ~strain.sd.pct, ~N, ~method,
  4.4, NA, NA, 5.9, 0.8, 6, 'LAOB')

lampreydata <-
  bind_cols(lampreybenddata, lampreydampdata, lampreyprepdata, lampreycurvedata) |>
  mutate(frequency.cat = 'low',
         curve.cat = 'mid',
         cite = "Tytell et al. (2018)")

```

## Marlin intervertebral joints

Long, J. H. (1992). Stiffness and Damping Forces in the Intervertebral Joints of Blue Marlin (*Makaira nigricans*). *Journal of Experimental Biology*.

```
len.marlin.cm <- mean(c(88.0, 99.4, 116.7, 119.5, 122.8, 108.6))
```

### Joint 11

Stiffness is  $5.89 \pm 2$  N m rad<sup>-1</sup> at 3.3deg and  $7.31 \pm 2.57$  N m rad<sup>-1</sup> at 5.0deg (Table 1). Joint 11 is  $0.8 \pm 0.2$  cm long (mean  $\pm$  stdev, Table 2).

John reports values in N m / rad, which is  $C/\theta_{max}$ .

```

stiff.marlin.Nmprad <- c(5.89, 7.31)
ang.marlin.deg <- c(3.3, 5.0)
jointlen.marlin.cm <- 0.8

stiff.marlin.Nmprad.sd <- c(2.00, 2.57)
jointlen.marlin.cm.sd <- 0.2

stiff.marlin.err <- stiff.marlin.Nmprad.sd / stiff.marlin.Nmprad
jointlen.marlin.err <- jointlen.marlin.cm.sd / jointlen.marlin.cm

EI.marlin <- stiff.marlin.Nmprad * jointlen.marlin.cm/100
EI.err.marlin <- sqrt(stiff.marlin.err^2 + jointlen.marlin.err^2)
EI.sd.marlin <- EI.err.marlin * EI.marlin

```

The bending modulus ( $EI$ ) for marlin is 0.04712, 0.05848  $\pm$  0.0198688, 0.0252281 N m<sup>2</sup>.

```

damp.marlin.Nmsprad2 <- c(0.071, 0.082)
damp.marlin.Nmsprad2.sd <- c(0.022, 0.035)

damp.marlin.err <- damp.marlin.Nmsprad2.sd / damp.marlin.Nmsprad2

etaI.marlin <- damp.marlin.Nmsprad2 * jointlen.marlin.cm/100
etaI.err.marlin <- sqrt(damp.marlin.err^2 + jointlen.marlin.err^2)
etaI.sd.marlin <- etaI.err.marlin * etaI.marlin

```

```

width.marlin.cm <- 3.3
height.marlin.cm <- 2.4
width.marlin.sd.cm <- 0.5
height.marlin.sd.cm <- 0.4

width.marlin.err <- width.marlin.sd.cm / width.marlin.cm

```

```

height.marlin.err <- height.marlin.sd.cm / height.marlin.cm

I.marlin.m4 <- pi/4 * (width.marlin.cm/100/2)^3 * (height.marlin.cm/100/2)
I.marlin.err <- sqrt((3*width.marlin.err)^2 + height.marlin.err^2)
I.marlin.sd.m4 = I.marlin.err * I.marlin.m4

E.marlin <- EI.marlin / I.marlin.m4
E.marlin.sd <- sqrt(EI.err.marlin^2 + I.marlin.err^2) * E.marlin

eta.marlin <- etaI.marlin / I.marlin.m4
eta.marlin.sd <- sqrt(etaI.err.marlin^2 + I.marlin.err^2) * eta.marlin

marlindata <- bind_cols(
  tribble(
    ~species, ~E.Pa, ~E.sd.Pa, ~I.mm4, ~I.sd.mm4, ~EI.Nm2, ~EI.sd.Nm2,
    'Makaira nigricans', E.marlin[1], E.marlin.sd[1],
    I.marlin.m4 * 1000^4, I.marlin.sd.m4 * 1000^4,
    EI.marlin[1], EI.sd.marlin[1]
  ),
  tribble(
    ~eta.Pas, ~eta.sd.Pas, ~etaI.Nm2s, ~etaI.sd.Nm2s,
    eta.marlin[1], eta.marlin.sd[1],
    etaI.marlin[1], etaI.sd.marlin[1]
  ),
  tribble(~stiff.Nmprad, ~damp.Nmsprad2, ~torque.Nm,
    stiff.marlin.Nmprad[1], damp.marlin.Nmsprad2[1], NA),
  tribble(
    ~tissue, ~location.L, ~location.desc, ~location.cat, ~Lseg.mm, ~Lbody.mm, ~freq.radps,
    'intervertebral joint', NA, 'joint 11', 'mid', jointlen.marlin.cm*10, len.marlin.cm*10, 0),
  tribble(
    ~curve.invm, ~angle.deg, ~angle.sd.deg, ~strain.pct, ~strain.sd.pct, ~N, ~method,
    3.3*pi/180/(jointlen.marlin.cm/100), 3.3, 0, NA, NA, 6, 'dynamic bending'
  ),
  tribble(
    ~frequency.cat, ~curve.cat, ~dE.dloc, ~dE.dfreq, ~dE.dcurve, ~deta.dloc, ~deta.dfreq, ~deta.dcurve,
    '0', 'mid', 'inc', 'dec', 'inc', 'inc', 'dec', 'const', 'Long (1992)'
  )
)

```

```
marlindata
```

```

## # A tibble: 1 x 37
##   species      E.Pa E.sd.Pa I.mm4 I.sd~1 EI.Nm2 EI.sd~2 eta.Pas eta.s~3 etaI.~4
##   <chr>      <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Makaira ~ 1.11e6 714547. 42337. 20497. 0.0471 0.0199 13416. 8409. 5.68e-4
## # ... with 27 more variables: etaI.sd.Nm2s <dbl>, stiff.Nmprad <dbl>,
## #   damp.Nmsprad2 <dbl>, torque.Nm <lgl>, tissue <chr>, location.L <lgl>,
## #   location.desc <chr>, location.cat <chr>, Lseg.mm <dbl>, Lbody.mm <dbl>,
## #   freq.radps <dbl>, curve.invm <dbl>, angle.deg <dbl>, angle.sd.deg <dbl>,
## #   strain.pct <lgl>, strain.sd.pct <lgl>, N <dbl>, method <chr>,
## #   frequency.cat <chr>, curve.cat <chr>, dE.dloc <chr>, dE.dfreq <chr>,
## #   dE.dcurve <chr>, deta.dloc <chr>, deta.dfreq <chr>, deta.dcurve <chr>, ...

```

## Largemouth bass

Whole body. Long, J. H. and Nipper, K. S. (1996). The importance of body stiffness in undulatory propulsion. American Zoologist 36, 678–694.

```
stiff.bass.Nmprad <- 42.7
stiff.bass.se.Nmprad <- 0.57
N.bass <- 10 # number of trials. Only 1 individual
stiff.bass.sd.Nmprad <- stiff.bass.se.Nmprad * sqrt(N.bass)
stiff.bass.err <- stiff.bass.sd.Nmprad / stiff.bass.Nmprad

len.bass.cm <- 2.5

EI.bass <- stiff.bass.Nmprad * len.bass.cm/100
```

Measured from a dead specimen, at about 40% of length.

```
len.otherbass.mm <- 144
width.otherbass.mm <- 21.7
height.otherbass.mm <- 30.0

I.bass.L4 <- pi/4 * (width.otherbass.mm/len.otherbass.mm / 2)^3 *
  (height.otherbass.mm/len.otherbass.mm / 2)
```

Given the bass's length from the Long and Nipper paper, we can estimate the second moment of area

```
len.bass.cm <- 30
I.bass.mm4 <- I.bass.L4 * (len.bass.cm*10)^4

E.bass <- EI.bass / (I.bass.mm4 * (1/1000)^4)

bendloc.bass.L <- (0.39 + 0.47)/2
```

```
bassdata <- bind_cols(
  tribble(
    ~species, ~E.Pa, ~E.sd.Pa, ~I.mm4, ~I.sd.mm4, ~EI.Nm2, ~EI.sd.Nm2,
    'Micropterus salmoides', E.bass, NA, I.bass.mm4, NA, EI.bass, NA
  ),
  tribble(
    ~eta.Pas, ~eta.sd.Pas, ~etaI.Nm2s, ~etaI.sd.Nm2s,
    NA, NA, NA, NA
  ),
  tribble(
    ~tissue, ~location.L, ~location.desc, ~location.cat, ~Lseg.mm, ~Lbody.mm, ~freq.radps,
    'whole body', bendloc.bass.L, 'midbody', 'mid', 25, len.bass.cm*10, 2.6*2*pi,
  ),
  tribble(~stiff.Nmprad,
    stiff.bass.Nmprad),
  tribble(
    ~curve.invm, ~angle.deg, ~angle.sd.deg, ~strain.pct, ~strain.sd.pct, ~N, ~method,
    NA, 4.6, NA, NA, NA, 1, 'dynamic bending'
  ),
  tribble(
    ~frequency.cat, ~curve.cat, ~cite,
    'mid', 'mid', 'Long & Nipper (1996)'
  )
)
```

# Hagfish

Long, J. H., Koob-Emunds, M., Sinwell, B. and Koob, T. J. (2002). The notochord of hagfish *Myxine glutinosa*: visco-elastic properties and mechanical functions during steady swimming. *Journal of Experimental Biology* 205, 3819–3831.

```
hagfishbend <-  
  tribble(  
    ~curve.invm, ~EI.Nm2,  
    13.486005089058525, 0.00031577608142493643,  
    11.643765903307889, 0.0002974554707379135,  
    12.59033078880407, 0.0002974554707379135,  
    15.226463104325699, 0.00032900763358778627,  
  )  
  
hagfishbend$freq.radps <- 4*pi  
  
hagfishbend <-  
  hagfishbend |>  
  arrange(curve.invm) |>  
  mutate(curve.rnd = round(curve.invm, digits=1))  
  
hagfishbend
```

```
## # A tibble: 4 x 4  
##   curve.invm  EI.Nm2 freq.radps curve.rnd  
##       <dbl>   <dbl>      <dbl>    <dbl>  
## 1      11.6 0.000297      12.6      11.6  
## 2      12.6 0.000297      12.6      12.6  
## 3      13.5 0.000316      12.6      13.5  
## 4      15.2 0.000329      12.6      15.2
```

```
hagfishdamp <-  
  tribble(  
    ~curve.invm, ~etaI.Nm2s,  
    11.635443037974685, 0.0000033045356371490277,  
    12.587341772151898, 0.00000359611231101512,  
    13.48860759493671, 0.000004341252699784019,  
    15.220253164556961, 0.000003920086393088553  
  ) |>  
  mutate(curve.rnd = round(curve.invm, digits = 1))  
  
hagfishdata <-  
  hagfishbend |>  
  left_join(hagfishdamp, by = 'curve.rnd') |>  
  select(-starts_with('curve.invm')) |>  
  rename(curve.invm = curve.rnd)
```

```
width.hagfish.mm <- 12  
I.hagfish.mm4 <- 1053  
I.notochord.mm4 <- 62.8
```

```
hagfishdata <-  
  hagfishdata |>  
  mutate(species = 'Myxine glutinosa',  
         I.mm4 = I.hagfish.mm4) |>
```

```

mutate(E.Pa = EI.Nm2 / (I.mm4 * (1/1000)^4),
       tissue = 'whole body',
       location.L = 0.37,
       location.desc = 'midbody',
       location.cat = 'mid',
       Lseg.mm = 0.011 * 1000,
       Lbody.mm = 0.379 * 1000,
       angle.deg = curve.invm * Lseg.mm/1000 * 180/pi,
       strain.pct = curve.invm * width.hagfish.mm/1000 / 2 * 100,
       N = 4,
       method = 'dynamic bending') |>
mutate(frequency.cat = 'mid',
       curve.cat = c('low','mid','mid','high'))
hagfishdata

## # A tibble: 4 x 19
##      EI.Nm2 freq.ra~1 curve~2 etaI.~3 species I.mm4   E.Pa tissue locat~4 locat~5
##      <dbl>   <dbl>   <dbl>   <dbl> <chr>   <dbl>   <dbl> <chr>   <dbl> <chr>
## 1 0.000297    12.6    11.6 3.30e-6 Myxine~ 1053 2.82e5 whole~ 0.37 midbody
## 2 0.000297    12.6    12.6 3.60e-6 Myxine~ 1053 2.82e5 whole~ 0.37 midbody
## 3 0.000316    12.6    13.5 4.34e-6 Myxine~ 1053 3.00e5 whole~ 0.37 midbody
## 4 0.000329    12.6    15.2 3.92e-6 Myxine~ 1053 3.12e5 whole~ 0.37 midbody
## # ... with 9 more variables: location.cat <chr>, Lseg.mm <dbl>, Lbody.mm <dbl>,
## #   angle.deg <dbl>, strain.pct <dbl>, N <dbl>, method <chr>,
## #   frequency.cat <chr>, curve.cat <chr>, and abbreviated variable names
## #   1: freq.radps, 2: curve.invm, 3: etaI.Nm2s, 4: location.L, 5: location.desc

```

How much does stiffness change with curvature?

```

hagfishdata |>
  transmute(dE = (E.Pa - E.Pa[1])/E.Pa[1])

## # A tibble: 4 x 1
##      dE
##      <dbl>
## 1 0
## 2 0
## 3 0.0616
## 4 0.106

hagfishdata <-
  hagfishdata |>
  summarize(across(where(is.numeric), ~mean(.x, na.rm = TRUE)),
            across(where(is.character), first)) |>
  mutate(dE.dcurve = 'const',
         dE.dfreq = 'inc',
         deta.dcurve = 'const',
         deta.dfreq = 'dec',
         cite = 'Long et al. (2002)')

```

## Striped bass

Szewciw, L., Zhu, D. and Barthelat, F. (2017). The nonlinear flexural response of a whole teleost fish: Contribution of scales and skin. *Journal of the Mechanical Behavior of Biomedical Materials*.

Digitized  $F = 0$  curve from Fig. 2.

```
striper1curve <-  
  tribble(~x.m, ~y.m,  
    0.009902396030554275, 0.13633295925683472,  
    0.01467813540510543, 0.14683866392343903,  
    0.02150062022589279, 0.1590545995822813,  
    0.028664229287719514, 0.17024439664578078,  
    0.038215708036821824, 0.18092926836871476,  
    0.048449435268002855, 0.18933383210199822,  
    0.06243552915061694, 0.20042590168022698,  
    0.07676274727427039, 0.20930281492565234,  
    0.09040771691584513, 0.2181797281710777,  
    0.10848730169093164, 0.22162733667923984,  
    0.12452014101978191, 0.22697520184544412,  
    0.1419174773127897, 0.22716522751124832,  
    0.15624469543644315, 0.22660057981857296,  
    0.17295978324737216, 0.22583504785061884,  
    0.19001599529934055, 0.22331042114779143,  
    0.20502546190507276, 0.22086723401602298,  
    0.21901155578768683, 0.21246267028273952,  
    0.23436214663445842, 0.20661530908070705,  
    0.2473248677939544, 0.19659824184045643,  
    0.25858196774825354, 0.18952928707253971,  
    0.26676894953319835, 0.1810595716824091  
  )  
  
striper1curve <-  
  striper1curve |>  
  mutate(d.m = sqrt((x.m - lag(x.m))^2 + (y.m - lag(y.m))^2),  
    d.m = replace_na(d.m, 0),  
    s.m = cumsum(d.m))  
  
striper1curve  
  
## # A tibble: 21 x 4  
##       x.m   y.m   d.m   s.m  
##   <dbl> <dbl> <dbl> <dbl>  
## 1 0.00990 0.136 0      0  
## 2 0.0147  0.147 0.0115 0.0115  
## 3 0.0215  0.159 0.0140 0.0255  
## 4 0.0287  0.170 0.0133 0.0388  
## 5 0.0382  0.181 0.0143 0.0532  
## 6 0.0484  0.189 0.0132 0.0664  
## 7 0.0624  0.200 0.0179 0.0842  
## 8 0.0768  0.209 0.0169 0.101  
## 9 0.0904  0.218 0.0163 0.117  
## 10 0.108  0.222 0.0184 0.136  
## # ... with 11 more rows  
  
Lseg.striper.m <-  
  striper1curve |>  
  tail(1) |>  
  pull(s.m)  
  
Lseg.striper.m
```

```
## [1] 0.3077993
```

```
striper1data <-  
  tribble(  
    ~curve.invmm, ~torque.Nmm, ~trial,  
    0.0063305509181969975, 2.173913043478251, 1,  
    0.00809348914858097, 81.30434782608677, 1,  
    0.009963272120200338, 379.56521739130426, 1,  
    0.010951585976627716, 793.478260869565, 1,  
    0.007131886477462439, 2.173913043478251, 2,  
    0.007746243739565946, 69.13043478260852, 2,  
    0.00908180300500835, 446.5217391304345, 2,  
    0.010016694490818032, 915.2173913043476, 2,  
    0.007585976627712856, 2.173913043478251, 3,  
    0.008707846410684478, 78.26086956521726, 3,  
    0.010550918196994996, 403.91304347826076, 3,  
    0.0118864774624374, 793.47826086956, 3  
  ) |>  
  mutate(species = 'striped bass',  
         location.mm = 180,  
         indiv = 1)
```

```
striper2data <-  
  tribble(  
    ~curve.invmm, ~torque.Nmm, ~trial,  
    0.006143790849673201, 0.8492569002123673, 1,  
    0.008183006535947711, 84.07643312101914, 1,  
    0.010640522875816991, 428.87473460721867, 1,  
    0.012235294117647056, 815.2866242038216, 1,  
    0.0073986928104575155, 3.8216560509554256, 2,  
    0.008993464052287582, 90.02123142250525, 2,  
    0.011241830065359476, 428.87473460721867, 2,  
    0.012758169934640521, 812.3142250530785, 2,  
    0.0073986928104575155, 3.8216560509554256, 3,  
    0.009803921568627449, 92.99363057324831, 3,  
    0.01184313725490196, 295.11677282377923, 3,  
    0.014326797385620912, 752.8662420382166, 3  
  ) |>  
  mutate(species = 'striped bass',  
         location.mm = 150,  
         indiv = 2)
```

```
striperdata <-  
  bind_rows(striper1data, striper2data)
```

```
striperdata
```

```
## # A tibble: 24 x 6
```

##	curve.invmm	torque.Nmm	trial	species	location.mm	indiv
##	<dbl>	<dbl>	<dbl>	<chr>	<dbl>	<dbl>
## 1	0.00633	2.17	1	striped bass	180	1
## 2	0.00809	81.3	1	striped bass	180	1
## 3	0.00996	380.	1	striped bass	180	1
## 4	0.0110	793.	1	striped bass	180	1



```
## 5      0.00713      2.17      2 striped bass      180      1
## 6      0.00775      69.1      2 striped bass      180      1
## 7      0.00908     447.      2 striped bass      180      1
## 8      0.0100     915.      2 striped bass      180      1
## 9      0.00759      2.17      3 striped bass      180      1
## 10     0.00871     78.3      3 striped bass      180      1
## # ... with 14 more rows
```

We want the tangent Young's modulus - the increase in torque due to an increase in curvature.

```
striperdata <-
  striperdata |>
  group_by(indiv, trial) |>
  arrange(indiv, trial, curve.invm) |>
  mutate(torque.Nm = torque.Nmm / 1000,
         curve.invm = (curve.invm + lag(curve.invm))/2 * 1000,
         EI.Nm2 = (torque.Nm - lag(torque.Nm)) / (curve.invm - lag(curve.invm)),
         I.mm4 = 4e6,
         E.Pa = EI.Nm2 / (I.mm4 * (1/1000)^4))
```

```
striperdata
```

```
## # A tibble: 24 x 11
## # Groups:   indiv, trial [6]
##   curve.invm torque~1 trial species locat~2 indiv torque~3 curve~4 EI.Nm2 I.mm4
##   <dbl> <dbl> <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 0.00633 2.17 1 stripe~ 180 1 0.00217 NA NA 4e6
## 2 0.00809 81.3 1 stripe~ 180 1 0.0813 7.21 NA 4e6
## 3 0.00996 380. 1 stripe~ 180 1 0.380 9.03 0.164 4e6
## 4 0.0110 793. 1 stripe~ 180 1 0.793 10.5 0.290 4e6
## 5 0.00713 2.17 2 stripe~ 180 1 0.00217 NA NA 4e6
## 6 0.00775 69.1 2 stripe~ 180 1 0.0691 7.44 NA 4e6
## 7 0.00908 447. 2 stripe~ 180 1 0.447 8.41 0.387 4e6
## 8 0.0100 915. 2 stripe~ 180 1 0.915 9.55 0.413 4e6
## 9 0.00759 2.17 3 stripe~ 180 1 0.00217 NA NA 4e6
## 10 0.00871 78.3 3 stripe~ 180 1 0.0783 8.15 NA 4e6
## # ... with 14 more rows, 1 more variable: E.Pa <dbl>, and abbreviated variable
## # names 1: torque.Nmm, 2: location.mm, 3: torque.Nm, 4: curve.invm
```

```
striperdata <-
  striperdata |>
  ungroup() |>
  filter(torque.Nmm > 100) |>
  summarize(across(c(EI.Nm2, I.mm4, E.Pa, location.mm, curve.invm, torque.Nm), list(mn=mean, sd=sd))) |>
  rename_with(~str_remove(.x, '_mn'), cols = contains('_mn')) |>
  rename_with(~str_replace(.x, '(.\\w+)\\.\\.\\.\\.\\.\\_sd', '\\1.sd\\.\\2'), cols = contains('_sd')) |>
  mutate(species = 'Morone saxatilis',
         tissue = 'whole body',
         Lseg.mm = Lseg.striper.m * 1000,
         Lbody.mm = 400,
         location.L = location.mm / Lbody.mm,
         location.desc = 'M',
         location.cat = 'mid',
         freq.radps = NA,
         frequency.cat = '0',
         curve.cat = 'high',
```

```

      dE.dcurve = 'inc',
      cite = 'Szewciw et al. 2017'
    ) |>
    select(-location.mm, -location.sd.mm)

striperdata <-
  striperdata |>
  select(any_of(colnames(marlindata)))

striperdata

## # A tibble: 1 x 20
##   species      E.Pa E.sd.Pa I.mm4 I.sd.~1 EI.Nm2 EI.sd~2 torqu~3 tissue locat~4
##   <chr>         <dbl>  <dbl> <dbl>  <dbl>  <dbl>   <dbl>  <dbl> <chr>   <dbl>
## 1 Morone sax~ 57001. 23521.  4e6      0  0.228  0.0941  0.605 whole~  0.412
## # ... with 10 more variables: location.desc <chr>, location.cat <chr>,
## #   Lseg.mm <dbl>, Lbody.mm <dbl>, freq.radps <lgl>, curve.invm <dbl>,
## #   frequency.cat <chr>, curve.cat <chr>, dE.dcurve <chr>, cite <chr>, and
## #   abbreviated variable names 1: I.sd.mm4, 2: EI.sd.Nm2, 3: torque.Nm,
## #   4: location.L

```

Seems low... Based on Fig. 2, radius of curvature at the highest point is  $\sim 0.07\text{m} = 14\text{ m}^{-1}$ , or  $70\text{mm} = 0.014\text{mm}^{-1}$ , which is consistent with their x axes in Fig 5.

## Eel

Long, J. H. (1998). Muscles, elastic energy, and the dynamics of body stiffness in swimming eels. *American Zoologist* 38, 771–792.

```

eelbodydata <-
  tribble(
    ~Lbody.mm, ~Lseg.mm, ~curve.invm, ~angle.deg, ~strain.pct, ~bodywidth.mm, ~bodyheight.mm, ~location.L
    210, 3.9, 38, 2.125*2, 3.81, 3.8, 8, 0.71,
    300, 7.5, 19.8, 1.417*3, 3.67, 8.6, 12.9, 0.69,
    330, 8.1, 18.3, 1.417*3, 3.84, 8.7, 14.9, 0.70,
  ) |>
  mutate(tissue = 'whole body',
         location.desc = 'mid-caudal',
         location.cat = 'mid',
         freq.radps = 3*2*pi,
         species = 'Anguilla rostrata') |>
  mutate(I.mm4 = pi/4 * (bodywidth.mm/2)^3 * (bodyheight.mm/2))

eelbodydata

```

```

## # A tibble: 3 x 14
##   Lbody~1 Lseg.mm curve~2 angle~3 strai~4 bodyw~5 bodyh~6 locat~7 tissue locat~8
##   <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <chr>  <chr>
## 1    210    3.9    38    4.25    3.81    3.8    8    whole~ mid-ca~
## 2    300    7.5   19.8    4.25    3.67    8.6   12.9  whole~ mid-ca~
## 3    330    8.1   18.3    4.25    3.84    8.7   14.9  whole~ mid-ca~
## # ... with 4 more variables: location.cat <chr>, freq.radps <dbl>,
## #   species <chr>, I.mm4 <dbl>, and abbreviated variable names 1: Lbody.mm,
## #   2: curve.invm, 3: angle.deg, 4: strain.pct, 5: bodywidth.mm,

```

## # 6: bodyheight.mm, 7: location.L, 8: location.desc

Data from Fig. 3A

```
eelbenddata <-
  tribble(
    ~beta.deg, ~EI.Nm2, ~tuple, ~val,
    0, 0.00016782608695652178, 0, 'mean',
    0, 0.00019739130434782623, 0, 'use',
    0.7224770642201861, 0.00013478260869565222, 0, 'lse',
    45.51605504587155, 0.00017652173913043482, 1, 'mean',
    44.79357798165137, 0.00020956521739130438, 1, 'use',
    44.79357798165137, 0.00014521739130434787, 1, 'lse',
    88.86467889908255, 0.0001695652173913044, 2, 'mean',
    89.58715596330273, 0.00019739130434782623, 2, 'use',
    89.58715596330273, 0.00014173913043478265, 2, 'lse',
    133.65825688073394, 0.00017478260869565232, 3, 'mean',
    134.38073394495413, 0.00020434782608695656, 3, 'use',
    134.38073394495413, 0.00014521739130434787, 3, 'lse',
    179.17431192660544, 0.00018521739130434786, 4, 'mean',
    179.17431192660544, 0.00021826086956521743, 4, 'use',
    179.17431192660544, 0.0001539130434782609, 4, 'lse',
    224.69036697247705, 0.00018521739130434786, 5, 'mean',
    223.96788990825686, 0.0002130434782608696, 5, 'use',
    224.69036697247705, 0.0001521739130434784, 5, 'lse',
    270.2064220183486, 0.00018000000000000004, 6, 'mean',
    270.2064220183486, 0.000211304347826087, 6, 'use',
    269.48394495412845, 0.00014695652173913048, 6, 'lse',
    315, 0.00018695652173913047, 7, 'mean',
    315, 0.00022173913043478264, 7, 'use',
    315, 0.0001521739130434784, 7, 'lse',
  )

eelbenddata <-
  eelbenddata |>
  select(-beta.deg) |>
  pivot_wider(names_from = val, values_from = EI.Nm2) |>
  rename(EI.Nm2 = mean) |>
  mutate(EI.sd.Nm2 = (use - lse)/2 * sqrt(6)) |>
  select(-use, -lse) |>
  mutate(w = 1/EI.sd.Nm2^2) |>
  summarize(EI.mn.Nm2 = sum(w*EI.Nm2) / sum(w),
    EI.sd.Nm2 = sum(w*EI.sd.Nm2) / sum(w))
```

Data from Fig. 4A. Units in the y axis are a typo

From Eq. 12:

$$c = \frac{M_0 \sin(\omega t)}{\omega \theta_0}$$

so that the units for  $c$  are

$$c \sim \frac{[Nm]}{[rad/s][rad]} = \left[ \frac{Nms}{rad^2} \right]$$

This means that  $c_{ext}$ , which is

$$c_{ext} = \frac{c}{L_t}$$

from Eq. 13 has units

$$c_{ext} \sim \left[ \frac{Ns}{rad^2} \right] = \left[ \frac{kg\ m}{s\ rad^2} \right]$$

and not  $[kg\ m\ rad^{-2}s^{-2}]$  as written in Fig. 4.

To convert  $c$  into  $\eta I$ , we use

$$\eta I_{ext} = c L_t = c_{ext} L_t^2$$

```
eeldampdata <-
  tribble(
    ~beta, ~cext, ~tuple, ~val,
    'Bar0', 0.0855855855855856, 0, 'mean',
    'Bar0', 0.11081081081081079, 0, 'use',
    'Bar0', 0.060360360360360354, 0, 'lse',
    'Bar1', 0.09189189189189195, 1, 'mean',
    'Bar1', 0.11921921921921919, 1, 'use',
    'Bar1', 0.06456456456456461, 1, 'lse',
    'Bar2', 0.10030030030030035, 2, 'mean',
    'Bar2', 0.12972972972972974, 2, 'use',
    'Bar2', 0.0687687687687688, 2, 'lse',
    'Bar3', 0.0792792792792793, 3, 'mean',
    'Bar3', 0.10030030030030035, 3, 'use',
    'Bar3', 0.060360360360360354, 3, 'lse',
    'Bar4', 0.0855855855855856, 4, 'mean',
    'Bar4', 0.11291291291291294, 4, 'use',
    'Bar4', 0.05825825825825831, 4, 'lse',
    'Bar5', 0.062462462462462565, 5, 'mean',
    'Bar5', 0.0876876876876877, 5, 'use',
    'Bar5', 0.03933933933933931, 5, 'lse',
  )

eeldampdata <-
  eeldampdata |>
  select(~beta) |>
  pivot_wider(names_from = val, values_from = cext) |>
  rename(cext = mean) |>
  mutate(cext.sd = (use - lse)/2 * sqrt(6)) |>
  select(~use, ~lse) |>
  mutate(w = 1/cext.sd^2) |>
  summarize(cext.mn = sum(w*cext) / sum(w),
            cext.sd = sum(w*cext.sd) / sum(w))

eelbodydata <-
  eelbodydata |>
  summarize(across(where(is.numeric), list(mn = mean, sd = sd)),
            across(where(is.character), first)) |>
  rename_with(.cols = contains('_mn') | contains('_sd'),
              ~str_replace(.x, '(.\\w+)\\.(.\\w+)_(mn|sd)', '\\1.\\3.\\2')) |>
  select(~freq.sd.radps) |>
  rename(freq.radps = freq.mn.radps)

eelbodydata

## # A tibble: 1 x 23
##   Lbody.mn.mm Lbody.sd~1 Lseg.~2 Lseg.~3 curve~4 curve~5 angle~6 angle~7 strai~8
```

```
##           <dbl>      <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1           280         62.4     6.5     2.27    25.4    11.0     4.25  5.77e-4    3.77
## # ... with 14 more variables: strain.sd.pct <dbl>, bodywidth.mn.mm <dbl>,
## #   bodywidth.sd.mm <dbl>, bodyheight.mn.mm <dbl>, bodyheight.sd.mm <dbl>,
## #   location.mn.L <dbl>, location.sd.L <dbl>, freq.radps <dbl>, I.mn.mm4 <dbl>,
## #   I.sd.mm4 <dbl>, tissue <chr>, location.desc <chr>, location.cat <chr>,
## #   species <chr>, and abbreviated variable names 1: Lbody.sd.mm,
## #   2: Lseg.mn.mm, 3: Lseg.sd.mm, 4: curve.mn.invm, 5: curve.sd.invm,
## #   6: angle.mn.deg, 7: angle.sd.deg, 8: strain.mn.pct
```

```
eeldata <-
  bind_cols(eelbodydata, eelbenddata, eeldampdata) |>
  mutate(N = 3,
         method = 'dynamic bending',
         I.m4 = I.mn.mm4 * (1/1000)^4,
         E.Pa = EI.mn.Nm2 / I.m4,
         E.sd.Pa = EI.sd.Nm2 / I.m4,
         etaI.mn.Nm2s = cext.mn * (Lseg.mn.mm/1000)^2,
         etaI.sd.Nm2s = cext.sd * (Lseg.mn.mm/1000)^2,
         eta.Pas = etaI.mn.Nm2s / I.m4,
         eta.sd.Pas = etaI.sd.Nm2s / I.m4,
         ) |>
  rename_with(.cols = contains('.mn'),
              ~str_remove(.x, '\\.mn')) |>
  mutate(frequency.cat = 'high',
         curve.cat = 'high',
         cite = 'Long (1998)')
```

```
eeldata |>
  summarize(E.cv.Pa = E.sd.Pa / E.Pa)
```

```
## # A tibble: 1 x 1
##   E.cv.Pa
##       <dbl>
## 1    0.428
```

```
eeldata <-
  eeldata |>
  select(any_of(colnames(marlindata)))
```

## Dogfish vertebral column

Porter, M. E., Ewoldt, R. H. and Long, J. H. (2016). Automatic control: the vertebral column of dogfish sharks behaves as a continuously variable transmission with smoothly shifting functions. *Journal of Experimental Biology* 219, 2908–2919.

```
dogfishstiff <- read_csv('stiffness data/Porter2016-Fig3A-EI1.csv')
```

```
## Rows: 42 Columns: 3
## -- Column specification -----
## Delimiter: ","
## dbl (3): frequency, curvature, EI1
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```

dogfishdamp <- read_csv('stiffness data/Porter2016-Fig4A-etaI1.csv')

## Rows: 48 Columns: 3
## -- Column specification -----
## Delimiter: ","
## dbl (3): frequency, curvature, etaI1
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

dogfishdata <-
  bind_rows(
    dogfishstiff |>
      mutate(param = 'EI1.Nm2') |>
      rename(value = EI1,
             curve.invm = curvature,
             frequency.Hz = frequency),

    dogfishdamp |>
      mutate(param = 'etaI1.Nm2s') |>
      rename(value = etaI1,
             curve.invm = curvature,
             frequency.Hz = frequency)
  ) |>
  mutate(curve.cat = case_when(curve.invm < 2 ~ 'low',
                               curve.invm > 4 ~ 'high',
                               TRUE ~ 'mid'))

dogfishcurves <-
  dogfishdata |>
  group_by(curve.cat) |>
  summarize(curve.invm = mean(curve.invm))

dogfishdatashort <-
  dogfishdata |>
  group_by(curve.cat, frequency.Hz, param) |>
  summarize(mn = mean(value),
            sd = sd(value)) |>
  left_join(dogfishcurves, by = 'curve.cat') |>
  pivot_wider(names_from = param,
              values_from = c(mn, sd)) |>
  rename_with(.cols = contains('sd'), ~str_replace(.x, 'sd_(\\w+).(\\w+)', '\\1.sd.\\2')) |>
  rename_with(.cols = contains('mn'), ~str_replace(.x, 'mn_(\\w+).(\\w+)', '\\1.\\2'))

## `summarise()` has grouped output by 'curve.cat', 'frequency.Hz'. You can
## override using the `.groups` argument.

dogfishdatashort

## # A tibble: 6 x 7
## # Groups:   curve.cat, frequency.Hz [6]
##   curve.cat frequency.Hz curve.invm   EI1.Nm2   etaI1.Nm2s EI1.sd.Nm2 etaI1.sd-1
##   <chr>         <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl>
## 1 high           0.25      4.52 0.0000694 0.00000707 0.0000329 2.10e-6
## 2 high           2        4.52 0.000127 0.000000524 0.0000362 1.64e-7
## 3 low            0.25      1.44 0.00000719 0.00000210 0.00000175 5.48e-7

```

```
## 4 low          2          1.44 0.0000187 0.000000280 0.00000319 6.73e-8
## 5 mid          0.25        3.01 0.0000385 0.00000457 0.0000278 1.59e-6
## 6 mid          2          3.01 0.0000739 0.000000530 0.0000458 2.94e-7
## # ... with abbreviated variable name 1: etaI1.sd.Nm2s
```

```
dogfishdatashort <-
dogfishdatashort |>
mutate(N = 3,
       species = 'Squalus acanthias',
       tissue = 'vertebral column',
       location.desc = 'precaudal',
       location.cat = 'post',
       method = 'LAOB',
       Lseg.mm = mean(62.72, 52.64, 53.12),
       Lbody.mm = mean(772, 740, 867),
       rseg.mm = mean(3.55, 2.95, 3.3),
       I.mm4 = pi/4 * rseg.mm^4,
       E.Pa = EI1.Nm2 / (I.mm4 * (1/1000)^4),
       E.sd.Pa = EI1.sd.Nm2 / (I.mm4 * (1/1000)^4),
       eta.Pas = etaI1.Nm2s / (I.mm4 * (1/1000)^4),
       eta.sd.Pas = etaI1.sd.Nm2s / (I.mm4 * (1/1000)^4)) |>
mutate(freq.radps = frequency.Hz * 2*pi,
       strain.pct = curve.invm * (rseg.mm / 1000) * 100) |>
rename(EI.Nm2 = EI1.Nm2,
       EI.sd.Nm2 = EI1.sd.Nm2,
       etaI.Nm2 = etaI1.Nm2s,
       etaI.sd.Nm2 = etaI1.sd.Nm2s) |>
mutate(frequency.cat = case_when(frequency.Hz < 1 ~ 'low',
                                frequency.Hz >= 2 ~ 'mid'))
```

```
dogfishdatashort
```

```
## # A tibble: 6 x 24
## # Groups:   curve.cat, frequency.Hz [6]
##   curve.cat frequ~1 curve~2 EI.Nm2 etaI.~3 EI.sd~4 etaI.~5 N species tissue
##   <chr>         <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl> <dbl> <chr>  <chr>
## 1 high         0.25     4.52 6.94e-5 7.07e-6 3.29e-5 2.10e-6 3 Squalu~ verte~
## 2 high         2         4.52 1.27e-4 5.24e-7 3.62e-5 1.64e-7 3 Squalu~ verte~
## 3 low          0.25     1.44 7.19e-6 2.10e-6 1.75e-6 5.48e-7 3 Squalu~ verte~
## 4 low          2         1.44 1.87e-5 2.80e-7 3.19e-6 6.73e-8 3 Squalu~ verte~
## 5 mid          0.25     3.01 3.85e-5 4.57e-6 2.78e-5 1.59e-6 3 Squalu~ verte~
## 6 mid          2         3.01 7.39e-5 5.30e-7 4.58e-5 2.94e-7 3 Squalu~ verte~
## # ... with 14 more variables: location.desc <chr>, location.cat <chr>,
## #   method <chr>, Lseg.mm <dbl>, Lbody.mm <dbl>, rseg.mm <dbl>, I.mm4 <dbl>,
## #   E.Pa <dbl>, E.sd.Pa <dbl>, eta.Pas <dbl>, eta.sd.Pas <dbl>,
## #   freq.radps <dbl>, strain.pct <dbl>, frequency.cat <chr>, and abbreviated
## #   variable names 1: frequency.Hz, 2: curve.invm, 3: etaI.Nm2, 4: EI.sd.Nm2,
## #   5: etaI.sd.Nm2
```

```
dogfishdatashort <-
dogfishdatashort |>
filter(curve.cat == 'mid' & frequency.cat == 'mid') |>
mutate(dE.dcurve = 'inc',
       dE.dfreq = 'inc',
       deta.dcurve = 'inc',
```

```
deta.dfreq = 'dec',
cite = 'Porter et al. (2016)')
```

```
dogfishdatashort <-
  dogfishdatashort |>
  ungroup() |>
  select(any_of(colnames(marlindata)))
```

## Kenaley skin measurements

Kenaley, C. P., Sanin, A., Ackerman, J., Yoo, J. and Alberts, A. (2018). Skin stiffness in ray-finned fishes: Contrasting material properties between species and body regions. *Journal of Morphology* 279, 1419–1430.

```
skindata <- read_csv('stiffness data/Kenaley2018-Fig4.csv') |>
  mutate(E.Pa = E.MPa * 1e6)
```

```
## Rows: 27 Columns: 4
## -- Column specification -----
## Delimiter: ","
## chr (2): species, location.desc
## dbl (2): strain.pct, E.MPa
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Lengths (by personal communication with Chris Kenaley)

coho salmon: 55, 64, 67, 68, 71 cm pompano: 26, 29, 29, 30, 32 cm red snapper: 26, 26, 27, 27, 28 cm

He lists skin segments as having height and width. Width is along the length of the body and is the same as the testing axis, so we'll use that.

```
nskin <-
  tribble(
    ~species, ~N, ~Lbody.mm, ~Lseg.mm,
    'coho', 5, mean(c(55, 64, 67, 68, 71))*10, 50,
    'pompano', 5, mean(c(26, 29, 29, 30, 32))*10, (20+35)/2,
    'snapper', 5, mean(c(26, 26, 27, 27, 28))*10, (20+35)/2,
  )
```

```
skindata <-
  skindata |>
  left_join(nskin, by = 'species') |>
  mutate(frequency.cat = '0',
         curve.cat = 'high')
```

```
skindata
```

```
## # A tibble: 27 x 10
##   species location~1 strai~2 E.MPa   E.Pa     N Lbody~3 Lseg.mm frequ~4 curve~5
##   <chr>    <chr>         <dbl> <dbl>  <dbl> <dbl>  <dbl>  <dbl>  <chr>    <chr>
## 1 coho    anterior         5  1.14 1.14e6  5    650    50  0    high
## 2 coho    anterior        10  1.63 1.63e6  5    650    50  0    high
## 3 coho    anterior        15  2.21 2.21e6  5    650    50  0    high
## 4 coho    midlateral        5  1.04 1.04e6  5    650    50  0    high
## 5 coho    midlateral       10  1.58 1.58e6  5    650    50  0    high
```



```
## 6 coho      midlateral      15  2.24 2.24e6      5      650      50  0      high
## 7 coho      posterior       5  2.57 2.57e6      5      650      50  0      high
## 8 coho      posterior      10  4.88 4.88e6      5      650      50  0      high
## 9 coho      posterior      15  7.01 7.01e6      5      650      50  0      high
## 10 pompano anterior        5  2.70 2.70e6      5      292      27.5 0      high
## # ... with 17 more rows, and abbreviated variable names 1: location.desc,
## # 2: strain.pct, 3: Lbody.mm, 4: frequency.cat, 5: curve.cat
```

Fig 2 shows the approximate locations of the body positions. It looks more or less to scale, so we'll use that to estimate the locations.

```
skinloc <- read_csv('stiffness data/Kenaley2018-Fig2.csv')

## Rows: 15 Columns: 4
## -- Column specification -----
## Delimiter: ","
## chr (2): species, point
## dbl (2): x, y
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

skinloc <-
  skinloc |>
  group_by(species) |>
  summarize(L = x[2] - x[1],
            anterior = (x[3] - x[1])/L,
            midlateral = (x[4] - x[1])/L,
            posterior = (x[5] - x[1])/L) |>
  select(-L) |>
  ungroup() |>
  pivot_longer(cols = c(anterior, midlateral, posterior),
               names_to = 'location.desc',
               values_to = 'location.L') |>
  mutate(location.cat = case_when(location.desc == 'anterior' ~ 'ant',
                                  location.desc == 'midlateral' ~ 'mid',
                                  location.desc == 'posterior' ~ 'post'))

skindata <-
  left_join(skindata, skinloc, by = c('species', 'location.desc'))
```

```
skinloc

## # A tibble: 9 x 4
##   species location.desc location.L location.cat
##   <chr>   <chr>         <dbl> <chr>
## 1 coho   anterior         0.304 ant
## 2 coho   midlateral       0.559 mid
## 3 coho   posterior       0.787 post
## 4 pompano anterior     0.356 ant
## 5 pompano midlateral   0.536 mid
## 6 pompano posterior   0.711 post
## 7 snapper anterior     0.398 ant
## 8 snapper midlateral   0.605 mid
## 9 snapper posterior   0.768 post
```

Kenaley reports that the maximum strain was 20% at a strain rate of  $0.3L/s = 30\%/sec$ . If that's a constant

stretching rate, it then should take  $20/30 \text{ sec} = 0.66 \text{ sec}$ . Ignoring the relaxation period (5sec long; Fig 3), that corresponds to a cycle period of 1.333sec or a frequency of  $1/1.3333$  (Kenaley pers comm).

```
skindata <-
  skindata |>
  mutate(tissue = 'skin',
         freq.radps = 1/1.33333 * 2*pi,
         method = 'tensile',
         species = case_when(species == 'coho' ~ 'Oncorhynchus kisutch',
                             species == 'snapper' ~ 'Lutjanus campechanus',
                             species == 'pompano' ~ 'Trachinotus carolinus'),
         frequency.cat = 'low') |>
  ungroup() |>
  select(any_of(colnames(marlindata)))

skindata <-
  skindata |>
  filter(location.cat == 'mid' & strain.pct == 10) |>
  mutate(dE.dloc = 'inc',
         dE.dcurve = 'inc',
         cite = 'Kenaley et al. (2018)')
```

## Gar

Long, J. H., Hale, M. E., McHenry, M. J. and Westneat, M. W. (1996). Functions of fish skin: Flexural stiffness and steady swimming of longnose gar *Lepisosteus osseus*. *Journal of Experimental Biology* 199, 2139–2151.

Neutral zone curvature. Fig 4B

```
gardata <- tribble(
  ~curve.neutral.invm, ~curve.neutral.sem.invm, ~EI.Nm2, ~EI.sem.Nm2, ~freq.radps,
  10.32, 11.055 - 10.325, 0.0649, 0.0827-0.0649, 1*2*pi
) |>
  mutate(N = 3,
         Lbody.mm = mean(c(640, 640, 710)),
         curve.invm = curve.neutral.invm + 10,
         curve.cat = 'mid',
         EI.sd.Nm2 = EI.sem.Nm2 * sqrt(N))
```

Fig. 4A:

```
garmomvcurve <- tribble(
  ~curve.invm, ~moment.Nm,
  12.6, 0.00123,
  15.8, 0.00362,
  18.5, 0.00731,
  20.8, 0.0111,
  22.7, 0.0146,
  24.4, 0.0197,
  26.1, 0.0235,
  27.7, 0.0279,
  28.8, 0.0312,
  29.4, 0.0332
)
```

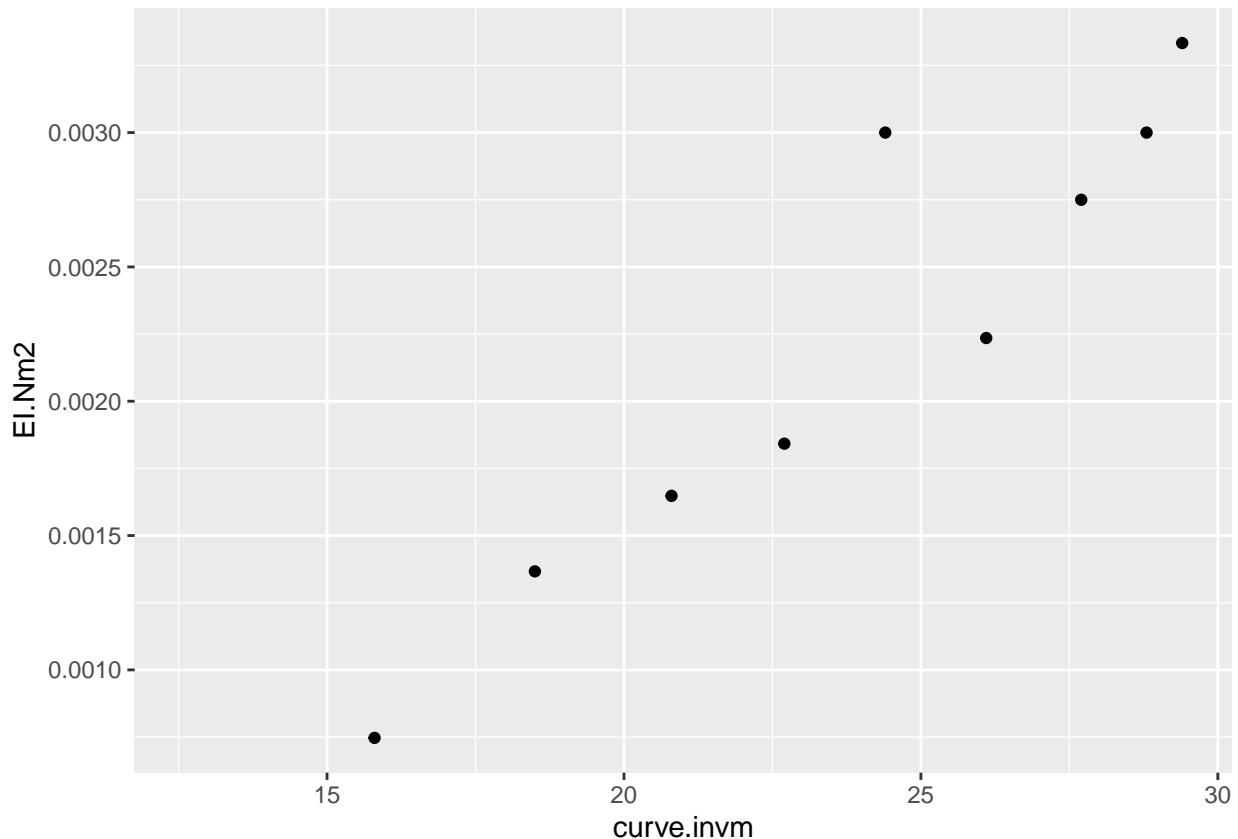
Long shows bending moment  $M$  vs curvature  $\kappa$ , which increases. But does  $EI$  change with curvature?

$$EI = \frac{M}{\kappa}$$

Here, we'll use the slope of the curve, as Long does.

```
garmomvcurve |>
  mutate(EI.Nm2 = (moment.Nm - lag(moment.Nm)) / (curve.invm - lag(curve.invm))) |>
  ggplot(aes(x = curve.invm, y = EI.Nm2)) +
  geom_point()
```

```
## Warning: Removed 1 rows containing missing values (`geom_point()`).
```



Stiffness increases with increasing curvature.

Shape of another gar, from John Long.

```
garshape <-
  tribble(~Lbody.mm, ~height.mm, ~width.mm,
    880, 60, 45) |>
  mutate(height.L = height.mm / Lbody.mm,
    width.L = width.mm / Lbody.mm) |>
  select(-Lbody.mm)
```

```
gardata <-
  bind_cols(gardata, garshape) |>
  mutate(I.mm4 = pi/4 * (width.L/2 * Lbody.mm)^3 * (height.L*Lbody.mm/2),
    E.Pa = EI.Nm2 / (I.mm4 * (1/1000)^4),
    E.sd.Nm2 = EI.sd.Nm2 / (I.mm4 * (1/1000)^4)) |>
  mutate(species = 'Lepisosteus osseus',
```

```

    tissue = 'whole body',
    method = 'bending',
    strain.pct = curve.invm * (width.L/2 * Lbody.mm / 1000),
    frequency.cat = 'low',
    location.cat = 'post',
    cite = 'Long et al. (1996)'
  ) |>
  select(any_of(colnames(marlindata)))

```

gardata

```

## # A tibble: 1 x 16
##   species      E.Pa  I.mm4 EI.Nm2 EI.sd~1 tissue locat~2 Lbody~3 freq.~4 curve~5
##   <chr>      <dbl> <dbl> <dbl> <dbl> <chr> <chr>      <dbl> <dbl> <dbl>
## 1 Lepisoste~ 7.49e5 86647. 0.0649 0.0308 whole~ post      663.    6.28    20.3
## # ... with 6 more variables: strain.pct <dbl>, N <dbl>, method <chr>,
## #   frequency.cat <chr>, curve.cat <chr>, cite <chr>, and abbreviated variable
## #   names 1: EI.sd.Nm2, 2: location.cat, 3: Lbody.mm, 4: freq.radps,
## #   5: curve.invm

```

## Bass intervertebral joints

Nowroozi, B. N. and Brainerd, E. L. (2012). Regional variation in the mechanical properties of the vertebral column during lateral bending in *Morone saxatilis*. *Journal of the Royal Society, Interface / the Royal Society* 9, 2667–2679.

Nowroozi, B. N., Harper, C. J., De Kegel, B., Adriaens, D. and Brainerd, E. L. (2012). Regional variation in morphology of vertebral centra and intervertebral joints in striped bass, *Morone saxatilis*. *Journal of Morphology* 273, 441–452.

Data from Fig. 4A and 8D. We assume in Fig 8D that we're again looking at example data from individual 01.

```

bass2.ivj.morph <- read_csv('stiffness data/Nowroozi 2012 IVJ morphology.csv') |>
  mutate(len.ivj.L = len.ivj.mm / Lbody.mm,
         I.L4 = I.mm4 / (Lbody.mm^4)) |>
  select(-contains('mm'))

```

```

## Rows: 23 Columns: 4
## -- Column specification -----
## Delimiter: ","
## dbl (4): vertebra, I.mm4, len.ivj.mm, Lbody.mm
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

```

bass2.ivj.morph

```

## # A tibble: 23 x 3
##   vertebra len.ivj.L      I.L4
##   <dbl>      <dbl>      <dbl>
## 1       1    0.00481 4.96e-10
## 2       2    0.00549 5.15e-10
## 3       3    0.00585 5.22e-10
## 4       4    0.00499 5.32e-10
## 5       5    0.00534 5.41e-10

```

```
## 6      6      0.00478 5.40e-10
## 7      7      0.00599 5.32e-10
## 8      8      0.00569 5.19e-10
## 9      9      0.00448 5.22e-10
## 10     10     0.00464 5.23e-10
## # ... with 13 more rows
```

Data from Tables 2 and 3.

```
bass2.ivj.mech <- read_csv('stiffness data/Nowroozi 2012 IVJ mechanics.csv')
```

```
## Rows: 18 Columns: 6
## -- Column specification -----
## Delimiter: ","
## chr (1): location.desc
## dbl (5): angle.deg, freq.Hz, stiff.Nmprad, stiff.sd.Nmprad, vertebra
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Lengths from the Nowroozi 2012 mechanics paper.

```
bass2.len.cm <- mean(c(31.75, 32.64, 34.29, 36.07, 38.10))
```

```
bass2.ivj.mech <-
  bass2.ivj.mech |>
  left_join(bass2.ivj.morph, by = 'vertebra') |>
  mutate(Lbody.mm = bass2.len.cm * 10,
         len.ivj.mm = len.ivj.L * Lbody.mm,
         I.mm4 = I.L4 * Lbody.mm^4) |>
  mutate(EI.Nm2 = stiff.Nmprad * len.ivj.mm/1000,
         EI.sd.Nm2 = stiff.sd.Nmprad * len.ivj.mm/1000,
         E.Pa = EI.Nm2 / (I.mm4 * (1/1000)^4),
         E.sd.Pa = EI.sd.Nm2 / (I.mm4 * (1/1000)^4),
         ) |>
  mutate(species = 'Morone saxatilis',
         tissue = 'intervertebral joint',
         method = 'dynamic bending',
         freq.radps = freq.Hz*2*pi,
         Lseg.mm = len.ivj.mm,
         N = 5) |>
  mutate(location.cat = case_when(location.desc == 'CV' ~ 'ant',
                                   location.desc == 'AB' ~ 'mid',
                                   location.desc == 'CD' ~ 'post'),
         frequency.cat = case_when(freq.Hz == 2 ~ 'low',
                                    freq.Hz == 5 ~ 'mid',
                                    freq.Hz == 7 ~ 'high'),
         curve.cat = case_when(angle.deg == 10 ~ 'mid',
                                angle.deg == 15 ~ 'high'))
```

```
bass2.ivj.mech
```

```
## # A tibble: 18 x 24
##   angle.deg freq.Hz location~1 stiff~2 stiff~3 verte~4 len.i~5 I.L4 Lbody~6
##   <dbl> <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 10 2 CV 0.05 0.01 3 0.00585 5.22e-10 346.
## 2 10 2 AB 0.11 0.03 9 0.00448 5.22e-10 346.
```

```
## 3      10      2 CD      0.02  0.006      20 0.00367 4.20e-10 346.
## 4      10      5 CV      0.06  0.023      3 0.00585 5.22e-10 346.
## 5      10      5 AB      0.11  0.06       9 0.00448 5.22e-10 346.
## 6      10      5 CD      0.03  0.01      20 0.00367 4.20e-10 346.
## 7      10      7 CV      0.06  0.04       3 0.00585 5.22e-10 346.
## 8      10      7 AB      0.09  0.006      9 0.00448 5.22e-10 346.
## 9      10      7 CD      0.02  0.006      20 0.00367 4.20e-10 346.
## 10     15      2 CV      0.16  0.07       3 0.00585 5.22e-10 346.
## 11     15      2 AB      0.28  0.075      9 0.00448 5.22e-10 346.
## 12     15      2 CD      0.08  0.036      20 0.00367 4.20e-10 346.
## 13     15      5 CV      0.17  0.071      3 0.00585 5.22e-10 346.
## 14     15      5 AB      0.27  0.075      9 0.00448 5.22e-10 346.
## 15     15      5 CD      0.07  0.041      20 0.00367 4.20e-10 346.
## 16     15      7 CV      0.12  0.06       3 0.00585 5.22e-10 346.
## 17     15      7 AB      0.21  0.78       9 0.00448 5.22e-10 346.
## 18     15      7 CD      0.05  0.036      20 0.00367 4.20e-10 346.
## # ... with 15 more variables: len.ivj.mm <dbl>, I.mm4 <dbl>, EI.Nm2 <dbl>,
## #   EI.sd.Nm2 <dbl>, E.Pa <dbl>, E.sd.Pa <dbl>, species <chr>, tissue <chr>,
## #   method <chr>, freq.radps <dbl>, Lseg.mm <dbl>, N <dbl>, location.cat <chr>,
## #   frequency.cat <chr>, curve.cat <chr>, and abbreviated variable names
## #   1: location.desc, 2: stiff.Nmprad, 3: stiff.sd.Nmprad, 4: vertebra,
## #   5: len.ivj.L, 6: Lbody.mm
```

Nowroozi reports no significant effect of frequency on stiffness. Angular stiffness (Nm/rad) goes up from 10deg bending to 15deg. EI is angular stiffness multiplied by the distance between the clamps (which is constant), so the same effect is true for bending modulus or Young's modulus

```
bass2.ivj.mech <-
  bass2.ivj.mech |>
  filter(location.cat == 'mid' & frequency.cat == 'mid' & curve.cat == 'mid') |>
  mutate(dE.dloc = 'incdec',
         dE.dfreq = 'const',
         dE.dcurve = 'inc',
         cite = 'Nowroozi & Brainerd (2012)')
```

```
bass2.ivj.mech
```

```
## # A tibble: 1 x 28
##   angle.deg freq.Hz location.~1 stiff~2 stiff~3 verte~4 len.i~5   I.L4 Lbody~6
##   <dbl>    <dbl> <chr>          <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
## 1      10      5 AB          0.11   0.06    9 0.00448 5.22e-10 346.
## # ... with 19 more variables: len.ivj.mm <dbl>, I.mm4 <dbl>, EI.Nm2 <dbl>,
## #   EI.sd.Nm2 <dbl>, E.Pa <dbl>, E.sd.Pa <dbl>, species <chr>, tissue <chr>,
## #   method <chr>, freq.radps <dbl>, Lseg.mm <dbl>, N <dbl>, location.cat <chr>,
## #   frequency.cat <chr>, curve.cat <chr>, dE.dloc <chr>, dE.dfreq <chr>,
## #   dE.dcurve <chr>, cite <chr>, and abbreviated variable names
## #   1: location.desc, 2: stiff.Nmprad, 3: stiff.sd.Nmprad, 4: vertebra,
## #   5: len.ivj.L, 6: Lbody.mm
```

```
bass2.ivj.mech <-
  bass2.ivj.mech |>
  select(any_of(colnames(marlindata)))
```

## Crucian carp

Zhou, M., Yin, X. and Tong, B. (2011). An experimental investigation into electromyography, constitutive relationship and morphology of crucian carp for biomechanical “digital fish.” Sci. China Phys. Mech. Astron. 54, 966–977.

```
carp.bend.data <- read_csv('stiffness data/Zhou 2011 carp.csv') |>
  pivot_wider(names_from = param, values_from = k.Nmprad) |>
  rename(stiff.Nmprad = mn,
         stiff.sd.Nmprad = sd) |>
  mutate(location.L = location.pct / 100) |>
  select(-tuple, -location.pct)

## Rows: 30 Columns: 6
## -- Column specification -----
## Delimiter: ","
## chr (2): location.desc, param
## dbl (4): individual, location.pct, k.Nmprad, tuple
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

carp.bend.data
```

```
## # A tibble: 15 x 5
##   individual location.desc stiff.Nmprad stiff.sd.Nmprad location.L
##   <dbl> <chr> <dbl> <dbl> <dbl>
## 1      1 1 forebody 0.088 0.088 0.316
## 2      2 2 forebody 0.149 0.197 0.316
## 3      3 3 forebody 0.169 0.185 0.316
## 4      4 4 forebody 0.163 0.167 0.316
## 5      5 5 forebody 0.135 0.163 0.316
## 6      1 1 midbody 0.077 0.077 0.476
## 7      2 2 midbody 0.077 0.092 0.476
## 8      3 3 midbody 0.073 0.081 0.476
## 9      4 4 midbody 0.074 0.086 0.476
## 10     5 5 midbody 0.055 0.06 0.476
## 11     1 1 afterbody 0.061 0.061 0.632
## 12     2 2 afterbody 0.071 0.08 0.632
## 13     3 3 afterbody 0.069 0.081 0.632
## 14     4 4 afterbody 0.067 0.081 0.632
## 15     5 5 afterbody 0.095 0.13 0.632
```

They don't include the length between the clamps in the paper. If Fig. 8 is to scale, then the distance between the clamps is defined as below.

```
L.carp.pix = 412 - 268
Lseg.carp.pix = 354 - 331
Lseg.carp.L = Lseg.carp.pix / L.carp.pix

carp.bend.data <-
  carp.bend.data |>
  mutate(Lseg.L = Lseg.carp.L,
         Lbody.mm = 190,
         Lseg.mm = Lseg.L*Lbody.mm,
         angle.deg = 5.77,
         freq.Hz = 2) |>
```

```

mutate(EI.Nm2 = stiff.Nmprad * Lseg.mm / 1000,
       EI.sd.Nm2 = stiff.sd.Nmprad * Lseg.mm / 1000,
       curve.invm = angle.deg * pi/180 / (Lseg.mm/1000))

carp.bend.data

## # A tibble: 15 x 13
##   individual location~1 stiff~2 stiff~3 locat~4 Lseg.L Lbody~5 Lseg.mm angle~6
##   <dbl> <chr>          <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
## 1      1 forebody      0.088  0.088  0.316  0.160    190   30.3   5.77
## 2      2 forebody      0.149  0.197  0.316  0.160    190   30.3   5.77
## 3      3 forebody      0.169  0.185  0.316  0.160    190   30.3   5.77
## 4      4 forebody      0.163  0.167  0.316  0.160    190   30.3   5.77
## 5      5 forebody      0.135  0.163  0.316  0.160    190   30.3   5.77
## 6      1 midbody       0.077  0.077  0.476  0.160    190   30.3   5.77
## 7      2 midbody       0.077  0.092  0.476  0.160    190   30.3   5.77
## 8      3 midbody       0.073  0.081  0.476  0.160    190   30.3   5.77
## 9      4 midbody       0.074  0.086  0.476  0.160    190   30.3   5.77
## 10     5 midbody       0.055  0.06   0.476  0.160    190   30.3   5.77
## 11     1 afterbody     0.061  0.061  0.632  0.160    190   30.3   5.77
## 12     2 afterbody     0.071  0.08   0.632  0.160    190   30.3   5.77
## 13     3 afterbody     0.069  0.081  0.632  0.160    190   30.3   5.77
## 14     4 afterbody     0.067  0.081  0.632  0.160    190   30.3   5.77
## 15     5 afterbody     0.095  0.13   0.632  0.160    190   30.3   5.77
## # ... with 4 more variables: freq.Hz <dbl>, EI.Nm2 <dbl>, EI.sd.Nm2 <dbl>,
## #   curve.invm <dbl>, and abbreviated variable names 1: location.desc,
## #   2: stiff.Nmprad, 3: stiff.sd.Nmprad, 4: location.L, 5: Lbody.mm,
## #   6: angle.deg

```

Digitizing width and height from Fig. 16

```

L.carp.Fig16.pix <- 680 - 39
x0.carp.Fig16.pix <- 39

carp.width = tribble(
  ~x, ~y.left,
  126.441, 60.169,
  197.946, 48.833,
  283.403, 48.833,
  385.428, 66.273,
  451.701, 77.609,
)
carp.width.right <- tribble(
  ~x, ~y,
  122.081, 147.370,
  204.922, 149.986,
  291.251, 147.370,
  388.916, 135.161,
  456.933, 124.697,
)

carp.width <-
  carp.width |>
  mutate(x = x - x0.carp.Fig16.pix)

```



```

carp.width.right <-
  carp.width.right |>
  mutate(x = x - x0.carp.Fig16.pix)

xyright <- approx(carp.width.right$x, carp.width.right$y, xout = carp.width$x)
carp.width <-
  carp.width |>
  mutate(y.right = xyright$y,
         location.L = x / L.carp.Fig16.pix,
         width.L = (y.right - y.left) / L.carp.Fig16.pix)

xywidth <- with(carp.width,
               approx(location.L, width.L, c(0.316, 0.476, 0.632))) |>
  as_tibble() |>
  rename(location.L = x,
         width.L = y)

carp.width <-
  carp.width |>
  bind_rows(xywidth)

carp.height <- tribble(
  ~x, ~z.dorsal,
  0.117, 0.089,
  0.263, 0.174,
  0.456, 0.193,
  0.660, 0.143,
  0.776, 0.096,
)

carp.height.ventral <- tribble(
  ~x, ~z,
  0.117, -0.079,
  0.271, -0.144,
  0.454, -0.157,
  0.668, -0.140,
  0.785, -0.092,
)

xyventral <- with(carp.height.ventral,
                 approx(x, z, xout = carp.height$x))

carp.height <-
  carp.height |>
  mutate(z.ventral = xyventral$y,
         height.L = z.dorsal - z.ventral) |>
  rename(location.L = x)

xyheight <- with(carp.height,
                approx(location.L, height.L, c(0.316, 0.476, 0.632))) |>
  as_tibble() |>
  rename(location.L = x,
         height.L = y)

```

```
carp.height <-
  carp.height |>
  bind_rows(xyheight)
```

Assume an oval cross section and estimate second moment of area.

```
carp.shape <-
  inner_join(carp.width, carp.height, by = 'location.L') |>
  select(contains('.L', ignore.case = FALSE)) |>
  mutate(location.desc = c('forebody', 'midbody', 'afterbody')) |>
  mutate(I.L4 = pi/4 * (width.L / 2)^3 * (height.L / 2))
```

```
carp.shape
```

```
## # A tibble: 3 x 5
##   location.L width.L height.L location.desc      I.L4
##   <dbl>    <dbl>    <dbl> <chr>          <dbl>
## 1    0.316    0.156    0.324 forebody      0.0000601
## 2    0.476    0.127    0.343 midbody       0.0000343
## 3    0.632    0.0785   0.293 afterbody   0.00000696
```

```
carp.bend.data <-
  carp.bend.data |>
  left_join(carp.shape, by = 'location.desc') |>
  select(-location.L.y) |>
  rename(location.L = location.L.x) |>
  group_by(location.desc) |>
  mutate(w = 1/stiff.sd.Nmprad^2) |>
  summarize(stiff.Nmprad = sum(stiff.Nmprad * w) / sum(w),
            across(c(location.L, I.L4, Lseg.L, Lbody.mm, Lseg.mm, angle.deg, curve.invm, freq.Hz, width
                      first)) |>
mutate(EI.Nm2 = stiff.Nmprad * Lseg.mm / 1000,
      I.mm4 = I.L4 * Lbody.mm^4,
      E.Pa = EI.Nm2 / (I.mm4 * (1/1000)^4)) |>
  ungroup() |>
  mutate(species = 'Carassius auratus',
         tissue = 'whole body',
         method = 'dynamic bending',
         freq.radps = freq.Hz * 2*pi
         ) |>
  mutate(curve.cat = 'low',
         frequency.cat = 'mid',
         location.cat = case_when(location.desc == 'afterbody' ~ 'post',
                                   location.desc == 'midbody' ~ 'mid',
                                   location.desc == 'forebody' ~ 'ant'),
         cite = 'Zhou et al. (2011)') |>
  select(any_of(colnames(marlindata)))
```

```
carp.bend.data
```

```
## # A tibble: 3 x 18
##   species      E.Pa  I.mm4  EI.Nm2 stiff-1 tissue locat-2 locat-3 locat-4 Lseg.mm
##   <chr>      <dbl> <dbl>   <dbl>   <dbl> <chr>   <dbl> <chr>   <chr>   <dbl>
## 1 Carassiu~ 2.28e5  9074. 0.00207 0.0682 whole~ 0.632 afterb~ post    30.3
## 2 Carassiu~ 4.67e4 78371. 0.00366 0.121  whole~ 0.316 forebo~ ant     30.3
## 3 Carassiu~ 4.66e4 44731. 0.00208 0.0686 whole~ 0.476 midbody mid     30.3
```

```
## # ... with 8 more variables: Lbody.mm <dbl>, freq.radps <dbl>,
## #   curve.invm <dbl>, angle.deg <dbl>, method <chr>, frequency.cat <chr>,
## #   curve.cat <chr>, cite <chr>, and abbreviated variable names
## #   1: stiff.Nmprad, 2: location.L, 3: location.desc, 4: location.cat
```

Based on Fig. 10. Fig. 10A shows that force changes little with increasing frequency. The moment is the force multiplied by a constant moment arm. Fig. 10B shows that force increases linearly with angle. Torque is force multiplied by a constant, and then the angular stiffness (moment / angle) is thus approximately constant.

```
carp.bend.data <- carp.bend.data |>
  mutate(dE.dloc = 'dec',
         dE.dfreq = 'const',
         dE.dcurve = 'const') |>
  filter(location.cat == 'mid')
```

```
carp.tensile.data <- tribble(
  ~tissue, ~Lbody.mm, ~Lbody.sd.mm, ~E.MPa, ~E.sd.MPa, ~Lseg.mm, ~N, ~strain.pct,
  'muscle', 186.3, 7.2, 1.10, 0.84, 10, 4, 6.2,
  'skin', 186.3, 7.2, 1.82, 0.68, 10, 4, 14.7,
) |>
  mutate(species = 'Carassius auratus',
         method = 'tensile')
```

```
carp.tensile.data <-
  carp.tensile.data |>
  mutate(width.L = max(carp.shape$width.L),
         curve.invm = strain.pct/100 / (width.L/2*Lbody.mm/1000),
         E.Pa = E.MPa * 1e6,
         E.sd.Pa = E.sd.MPa * 1e6) |>
  mutate(frequency.cat = '0',
         curve.cat = 'mid',
         location.cat = 'mid',
         cite = 'Zhou et al. (2011)') |>
  select(any_of(colnames(marlindata)))
```

## Fish acellular rib bone

Horton, J. M. and Summers, A. P. (2009). The material properties of acellular bone in a teleost fish. *Journal of Experimental Biology* 212, 1413–1420.

```
ribdata <- read_csv('stiffness data/Horton2009-bone.csv')
```

```
## Rows: 12 Columns: 4
## -- Column specification -----
## Delimiter: ","
## dbl (4): rib, I.mm4, E.GPa, EI
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
ribdata <-
  ribdata |>
  mutate(species = 'Myoxocephalus polyacanthocephalus',
         tissue = 'bone (acellular rib)',
         method = '3-point bending',
```

```

    freq.radps = 0,
    location.desc = str_c('rib ', rib),
    N = 6,
    Lbody.mm = mean(c(285, 375)),
    Lseg.mm = 10,
    frequency.cat = '0',
    curve.cat = 'high',
    location.cat = 'mid') |>
mutate(E.Pa = E.GPa * 1e9,
       #EI.Nm2 = E.Pa * I.mm4 * (1/1000)^4,
       EI.Nm2 = EI * 1e-3)

ribdata

```

```

## # A tibble: 12 x 17
##   rib  I.mm4 E.GPa  EI species      tissue method freq.~1 locat~2    N
##   <dbl>  <dbl> <dbl>  <dbl> <chr>      <chr>  <chr>    <dbl> <chr>    <dbl>
## 1     1  0.125   3.70 0.310 Myoxocephalus~ bone ~ 3-poi~    0 rib 1      6
## 2     2  0.0591  5.49 0.307 Myoxocephalus~ bone ~ 3-poi~    0 rib 2      6
## 3     3  0.0474  6.36 0.279 Myoxocephalus~ bone ~ 3-poi~    0 rib 3      6
## 4     4  0.0305  6.60 0.193 Myoxocephalus~ bone ~ 3-poi~    0 rib 4      6
## 5     5  0.0188  8.40 0.131 Myoxocephalus~ bone ~ 3-poi~    0 rib 5      6
## 6     6  0.0162  6.30 0.0856 Myoxocephalus~ bone ~ 3-poi~    0 rib 6      6
## 7     7  0.0208  6.85 0.138 Myoxocephalus~ bone ~ 3-poi~    0 rib 7      6
## 8     8  0.0162  7.22 0.0990 Myoxocephalus~ bone ~ 3-poi~    0 rib 8      6
## 9     9  0.0143  5.68 0.0789 Myoxocephalus~ bone ~ 3-poi~    0 rib 9      6
## 10    10  0.0104  5.49 0.0487 Myoxocephalus~ bone ~ 3-poi~    0 rib 10     6
## 11    11  0.00519  8.15 0.0386 Myoxocephalus~ bone ~ 3-poi~    0 rib 11     6
## 12    12  0.00519  7.41 0.0302 Myoxocephalus~ bone ~ 3-poi~    0 rib 12     6
## # ... with 7 more variables: Lbody.mm <dbl>, Lseg.mm <dbl>,
## #   frequency.cat <chr>, curve.cat <chr>, location.cat <chr>, E.Pa <dbl>,
## #   EI.Nm2 <dbl>, and abbreviated variable names 1: freq.radps,
## #   2: location.desc

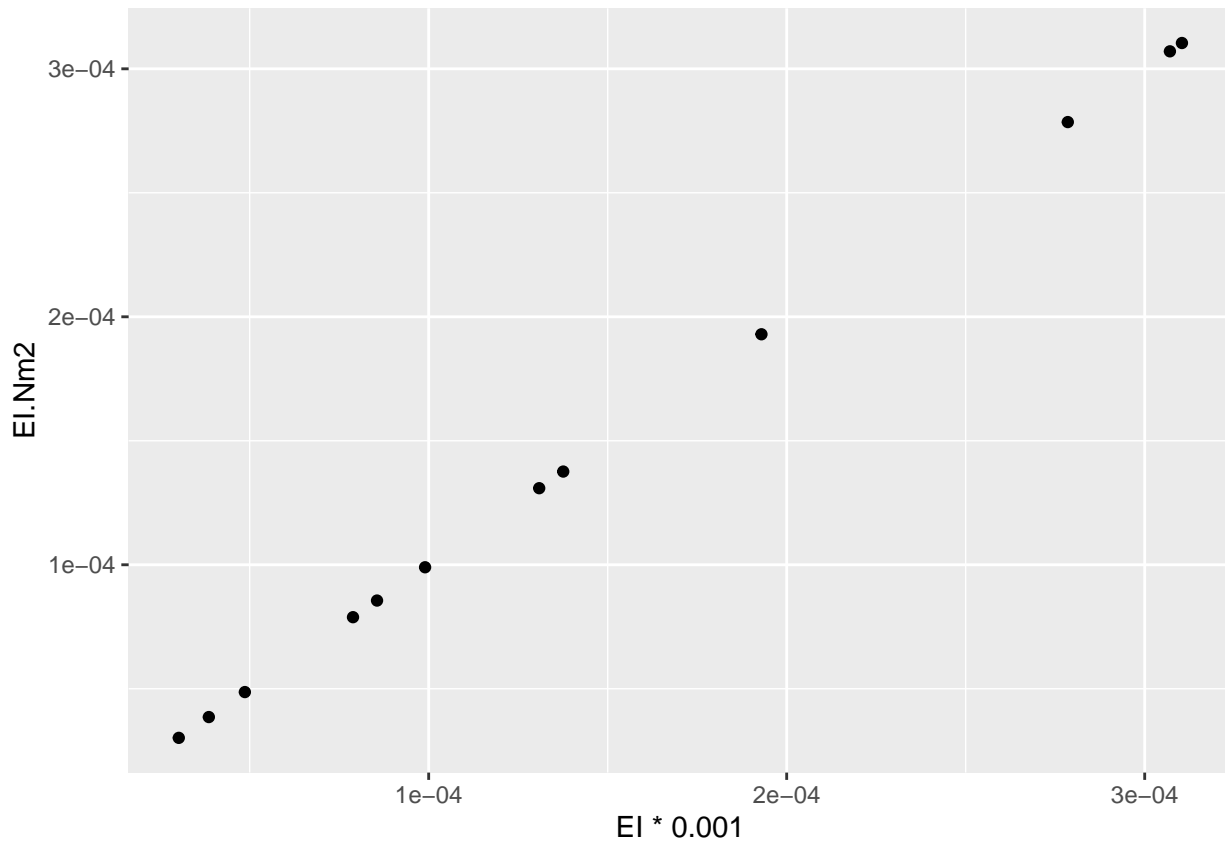
```

It's not clear what Horton means by EI. They don't give units. It looks like it's probably in  $\text{N m}^2 * 1e-3$

```

ribdata |>
  ggplot(aes(EI * 1e-3, EI.Nm2)) +
  geom_point()

```



```
ribdata <-
  ribdata |>
  summarize(across(where(is.numeric), ~mean(.x, na.rm = TRUE)),
            across(where(is.character), first)) |>
  mutate(cite = 'Horton & Summers (2009)') |>
  select(any_of(colnames(marlindata)))
```

```
ribdata <-
  ribdata |>
  mutate(dE.dloc = 'const')
```

## Eel skin

Hebrank, M. R. (1980). Mechanical properties and locomotor functions of eel skin. The Biological Bulletin 158, 58–68.

Lengths are given as a range from 41 to 64cm, so we take the midpoint.

```
# columns
# species, E.Pa, E.sd.Pa, I.mm4, I.sd.mm4, EI.Nm2, EI.sd.Nm2, eta.Pas, eta.sd.Pas, etaI.Nm2s, etaI.sd.Nm2s
# tissue, location.L, location.desc, location.cat, Lseg.mm, Lbody.mm, freq.radps, curve.invm, angle.deg
# angle.sd.deg, strain.pct, strain.sd.pct, N, method, frequency.cat, curve.cat, cite

eelskindata <- tibble(
  species = 'Anguilla rostrata',
  tissue = 'skin',
  E.Pa = c(3.54e6, 1.47e7),
  E.sd.Pa = c(2.52e6, 1.28e7),
```

```

Lseg.mm = -30,
Lbody.mm = mean(c(410, 640)),
location.desc = c('midbody (long)', 'midbody (hoop)'),
location.cat = c('mid', 'mid'),
strain.pct = -c(40, 20),
method = 'tensile',
N = 10,
cite = 'Hebrank (1980)'
)

eelskindata

## # A tibble: 2 x 12
##   species   tissue   E.Pa E.sd.Pa Lseg.mm Lbody~1 locat~2 locat~3 strai~4 method
##   <chr>     <chr>   <dbl> <dbl>   <dbl>   <dbl> <chr>   <chr>     <dbl> <chr>
## 1 Anguilla~ skin    3.54e6 2.52e6   -30     525 midbod~ mid      -40 tensi~
## 2 Anguilla~ skin    1.47e7 1.28e7   -30     525 midbod~ mid      -20 tensi~
## # ... with 2 more variables: N <dbl>, cite <chr>, and abbreviated variable
## #   names 1: Lbody.mm, 2: location.desc, 3: location.cat, 4: strain.pct

danoseelskindata <- tibble(
  species = 'Anguilla rostrata',
  tissue = 'skin',
  E.Pa = c(7.68e6, 12.10e6, 6.20e6, 9.45e6),
  indiv = c(1, 1, 2, 2),
  Lbody.mm = c(340, 340, 450, 450),
  Lseg.mm = 10,
  strain.rate.Lps = c(0.25, 1.8, 0.25, 1.8),
  N = 2,
  method = 'tensile',
  location.L = c(0.167, 0.167, 0.176, 0.176),
  cite = 'Danos (2005)'
)

danoseelskindata <-
  danoseelskindata |>
  group_by(strain.rate.Lps) |>
  summarize(across(c(E.Pa, Lbody.mm), mean),
    across(c(species, tissue, Lseg.mm, N, method, location.L, cite), first))

danoseelskindata

## # A tibble: 2 x 10
##   strain.rate~1 E.Pa Lbody~2 species tissue Lseg.mm   N method locat~3 cite
##           <dbl> <dbl>   <dbl> <chr>   <chr>   <dbl> <dbl> <chr>   <dbl> <chr>
## 1           0.25 6.94e6   395 Anguil~ skin     10     2 tensi~  0.167 Dano~
## 2           1.8 1.08e7   395 Anguil~ skin     10     2 tensi~  0.167 Dano~
## # ... with abbreviated variable names 1: strain.rate.Lps, 2: Lbody.mm,
## #   3: location.L

danoseelskindata <-
  danoseelskindata |>
  filter(strain.rate.Lps == 0.25)

```

## Hebrank and Hebrank 1986

Norfolk spot and skipjack tuna

Hebrank, M. R. and Hebrank, J. H. (1986). The mechanics of fish skin: Lack of an “external tendon” role in two teleosts. The Biological Bulletin 171, 236–247.

Lengths are given as ranges. 16 to 21cm for spots and 44 to 50cm for skipjacks.

```
spotskindata <- tibble(
  species = 'Leiostomus xanthurus',
  tissue = 'skin',
  E.Pa = c(2.41e6, 1.64e7),
  E.sd.Pa = c(2.26e6, 0.63e7),
  Lbody.mm = mean(c(160, 210)),
  Lseg.mm = -30,
  location.desc = c('midbody (long)', 'midbody (hoop)'),
  location.cat = c('mid', 'mid'),
  strain.pct = -c(12, 4),
  method = 'tensile',
  N = 5,
  cite = 'Hebrank & Hebrank (1986)'
)

skipjackskindata <- tibble(
  species = 'Katsuwonus pelamis',
  tissue = 'skin',
  E.Pa = c(6.92e6, 6.02e7),
  E.sd.Pa = c(4.25e6, 5.44e7),
  Lbody.mm = mean(c(440, 500)),
  Lseg.mm = -30,
  location.desc = c('midbody (long)', 'midbody (hoop)'),
  location.cat = c('mid', 'mid'),
  strain.pct = -c(14, 4),
  method = 'tensile',
  N = 4,
  cite = 'Hebrank & Hebrank (1986)'
)

HHskindata <-
  bind_rows(spotskindata, skipjackskindata)
```

## Clark et al 2016

Clark, A. J., Crawford, C. H., King, B. D., Demas, A. M. and Uyeno, T. A. (2016). Material Properties of Hagfish Skin, with Insights into Knotting Behaviors. Biological Bulletin 230, 243–256.

```
# columns
# species, E.Pa, E.sd.Pa, I.mm4, I.sd.mm4, EI.Nm2, EI.sd.Nm2, eta.Pas, eta.sd.Pas, etaI.Nm2s, etaI.sd.Nm2s
# tissue, location.L, location.desc, location.cat, Lseg.mm, Lbody.mm, freq.radps, curve.inum, angle.deg
# angle.sd.deg, strain.pct, strain.sd.pct, N, method, frequency.cat, curve.cat, cite

hagfishskin <- tibble(
  E.Pa = c(38.5e6, 52.6e6, 24.0e6, 31.3e6),
  E.sem.Pa = c(5.82e6, 8.36e6, 3.48e6, 5.18e6),
```

```

loc = c('H', 'T', 'H', 'T'),
dir = c('long','long', 'circ','circ'),
N = 5,
common.name = 'Hagfish',
)

gunnelskin <- tibble(
  E.Pa = c(13.3e6, 28.2e6, 41.8e6, 49.5e6),
  E.sem.Pa = c(1.3e6, 8.85e6, 2.67e6, 4.85e6),
  loc = c('H', 'T', 'H', 'T'),
  dir = c('long','long', 'circ','circ'),
  N = 4,
  common.name = 'Gunnel',
)

lampreyskin <- tibble(
  E.Pa = c(22.8e6, 21.1e6),
  E.sem.Pa = c(9.37e6, 2.82e6),
  loc = c('H', 'T'),
  dir = c('long','long'),
  N = 5,
  common.name = 'Lamprey',
)

clarkdata <-
  bind_rows(hagfishskin, gunnelskin, lampreyskin)

clarkdata <-
  clarkdata |>
  mutate(E.sd.Pa = E.sem.Pa * sqrt(N)) |>
  mutate(species = case_when(common.name == 'Hagfish' ~ 'Eptatretus stoutii',
                             common.name == 'Gunnel' ~ 'Apodichthys flavidus',
                             common.name == 'Lamprey' ~ 'Petromyzon marinus'),
         location.desc = case_when(loc == 'H' ~ 'ant',
                                    loc == 'T' ~ 'post'),
         location.L = case_when(loc == 'H' ~ 25,
                                 loc == 'T' ~ 75),
         location.cat = case_when(loc == 'H' ~ 'ant',
                                   loc == 'T' ~ 'mid'),
         location.desc = str_c(location.desc, '(', dir, ')'),
         Lseg.mm = 17,
         tissue = 'skin',
         method = 'tensile',
         cite = 'Clark et al. (2016)')

clarkdata <-
  clarkdata |>
  filter(location.cat == 'mid' & str_detect(location.desc, 'long'))

```

## Striped bass skin

Szewciw, L. and Barthelat, F. (2017). Mechanical properties of striped bass fish skin: Evidence of an extendon function of the stratum compactum. *Journal of the Mechanical Behavior of Biomedical Materials*



73, 28–37.

```
striperskindata <- tibble(  
  Lseg.mm = 50,  
  E.Pa = c(152, 441, 532, 129, 112, 245),  
  strain.stiff.frac = c(0.17, 0.11, 0.09, 0.09, 0.15, 0.12),  
  strain.frac = -c(0.2, 0.22, 0.12, 0.2, 0.22, 0.12),  
  location.desc = c('AD', 'MD', 'PD', 'AV', 'MV', 'PV'),  
  point = c('A', 'M', 'P', 'A', 'M', 'P'),  
  N = 3,  
  location.cat = if_else(point == 'M', 'mid', NA_character_),  
  method = 'tensile',  
  cite = 'Szewciw (2017)'  
)
```

Locations from Fig 4A

```
striperloc <- tribble(  
  ~point, ~x, ~y,  
  'snout', 15, 133,  
  'tail', 493, 102,  
  'A', 189, 109,  
  'M', 254, 110,  
  'P', 316, 109,  
)  
  
striperlen1 <- with(striperloc, x[2] - x[1])  
striperloc <-  
  striperloc |>  
  mutate(location.L = (x - x[1]) / striperlen1)  
  
striperskindata <-  
  striperskindata |>  
  left_join(striperloc, by = 'point') |>  
  select(-c(point, x, y)) |>  
  mutate(strain.pct = strain.frac * 100)  
  
striperskindata <-  
  striperskindata |>  
  filter(location.cat == 'mid' & str_detect(location.desc, 'D')) |>  
  mutate(tissue = 'skin',  
         species = 'Morone saxatilis')
```

## Fin rays: Aiello et al 2018

Aiello, B. R., Hardy, A. R., Cherian, C., Olsen, A. M., Ahn, S. E., Hale, M. E. and Westneat, M. W. (2018). The relationship between pectoral fin ray stiffness and swimming behavior in Labridae: insights into design, performance and ecology. The Journal of experimental biology 221, jeb163360.

```
aiellofinraydata <- read_csv('stiffness data/Aiello2018_Table1.csv')
```

```
## Rows: 19 Columns: 14  
## -- Column specification -----  
## Delimiter: ","  
## chr (2): Species, Indiv
```

```
## dbl (12): Proximal, LE.Middle, LE.Distal, LE.Proximal, M1.Middle, M1.Distal,...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
aiellofinraydata <-
  aiellofinraydata |>
  filter(Indiv %in% c('Mean', 's.d.)) |>
  mutate(Indiv = case_when(Indiv == 'Mean' ~ 'mn',
                           Indiv == 's.d.' ~ 'sd')) |>
  pivot_wider(names_from = Indiv,
              values_from = c(Proximal:TE.Distal)) |>
  pivot_longer(!Species, names_to = c('location.desc', '.value'),
              names_pattern = '(.+)_ (mn|sd)') |>
  mutate(EI.Nm2 = mn * 1e-6,
         EI.sd.Nm2 = sd * 1e-6) |>
  select(-mn, -sd)
```

```
# columns
```

```
# species, E.Pa, E.sd.Pa, I.mm4, I.sd.mm4, EI.Nm2, EI.sd.Nm2, eta.Pas, eta.sd.Pas, etaI.Nm2s, etaI.sd.Nm2s,
# tissue, location.L, location.desc, location.cat, Lseg.mm, Lbody.mm, freq.radps, curve.invm, angle.deg,
# angle.sd.deg, strain.pct, strain.sd.pct, N, method, frequency.cat, curve.cat, cite
```

```
Gomphosusfinrays <- tibble(
  species = 'Gomphosus varius',
  N = 7,
  m.g = 22.44,
)
```

```
Halichoeresfinrays <- tibble(
  species = 'Halichoeres bivittatus',
  N = 8,
  m.g = 22.03,
)
```

```
aiellofinraydata <-
  aiellofinraydata |>
  rename(species = Species) |>
  left_join(bind_rows(Gomphosusfinrays, Halichoeresfinrays), by = c('species')) |>
  mutate(method = '3-point bending',
         tissue = 'fin (pectoral)',
         curve.invm = -0.35,
         cite = 'Aiello et al. (2018)')
```

```
aiellofinraydata <-
  aiellofinraydata |>
  filter(location.desc == 'M1.Middle') |>
  mutate(location.desc = 'pectoral')
```

## Bluegill pectoral fin rays

Alben, S., Madden, P. G. A. and Lauder, G. V. (2007). The mechanics of active fin-shape control in ray-finned fishes. *Journal of The Royal Society Interface* 4, 243–256.

Not clear if we can derive a bulk EI from their results.

## Yellow perch fin rays

Taft, N. K., Taft, B. N., Henck, H. and Mehner, T. (2018). Variation in flexural stiffness of the lepidotrichia within and among the soft fins of yellow perch under different preservation techniques. *J Morphol* 279, 1045–1057.

```
perchfinrays <- read_csv('stiffness data/Taft2018Fig6.csv')

## Rows: 29 Columns: 3
## -- Column specification -----
## Delimiter: ","
## chr (1): Fin
## dbl (2): RayLength.mm, EI.Nmm2
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

No values for I reported, though they do discuss that they estimated it.

```
perchfinrays <-
  perchfinrays |>
  mutate(Lseg.mm = RayLength.mm,
         EI.Nm2 = EI.Nmm2 * (1/1000)^2,
         location.desc = str_c(Fin, ' fin'),
         tissue = str_c('fin (', Fin, ')')) |>
  group_by(tissue, location.desc) |>
  summarize(across(c(Lseg.mm, EI.Nm2), ~ mean(.x, na.rm = TRUE))) |>
  mutate(species = 'Perca flavescens',
         method = '3-point bending',
         N = 11,
         Lbody.mm = 183,
         cite = 'Taft et al. (2018)')
```

```
## `summarise()` has grouped output by 'tissue'. You can override using the
## `.groups` argument.
```

```
perchfinrays

## # A tibble: 5 x 9
## # Groups:   tissue [5]
##   tissue      location~1 Lseg.mm EI.Nm2 species method      N Lbody~2 cite
##   <chr>      <chr>      <dbl> <dbl> <chr>  <chr>  <dbl>  <dbl> <chr>
## 1 fin (Anal)    Anal fin    18.4 7.33e-7 Perca ~ 3-poi~ 11    183 Taft~
## 2 fin (Caudal)  Caudal f~  28.3 1.10e-6 Perca ~ 3-poi~ 11    183 Taft~
## 3 fin (Dorsal soft) Dorsal s~  17.5 4.26e-7 Perca ~ 3-poi~ 11    183 Taft~
## 4 fin (Pectoral) Pectoral~  20.9 1.54e-7 Perca ~ 3-poi~ 11    183 Taft~
## 5 fin (Pelvic)  Pelvic f~  26.3 2.95e-6 Perca ~ 3-poi~ 11    183 Taft~
## # ... with abbreviated variable names 1: location.desc, 2: Lbody.mm
```

## Zebrafish caudal fin

Puri, S., Aegerter-Wilmsen, T., Jaźwińska, A. and Aegerter, C. M. (2017). In-vivo quantification of mechanical properties of caudal fins in adult zebrafish. *The Journal of Experimental Biology* jeb.171777.

```

zebrafishfinEI <- read_csv('stiffness data/Puri2018Fig2C.csv')

## Rows: 30 Columns: 3
## -- Column specification -----
## Delimiter: ","
## chr (1): fish
## dbl (2): beamlen.mm, EI.Nm2
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
zebrafishfinI <- read_csv('stiffness data/Puri2018FigS5B.csv')

## Rows: 12 Columns: 2
## -- Column specification -----
## Delimiter: ","
## dbl (2): beamlen.mm, I.m4
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
zebrafishfinE <- read_csv('stiffness data/Puri2018FigS5C.csv')

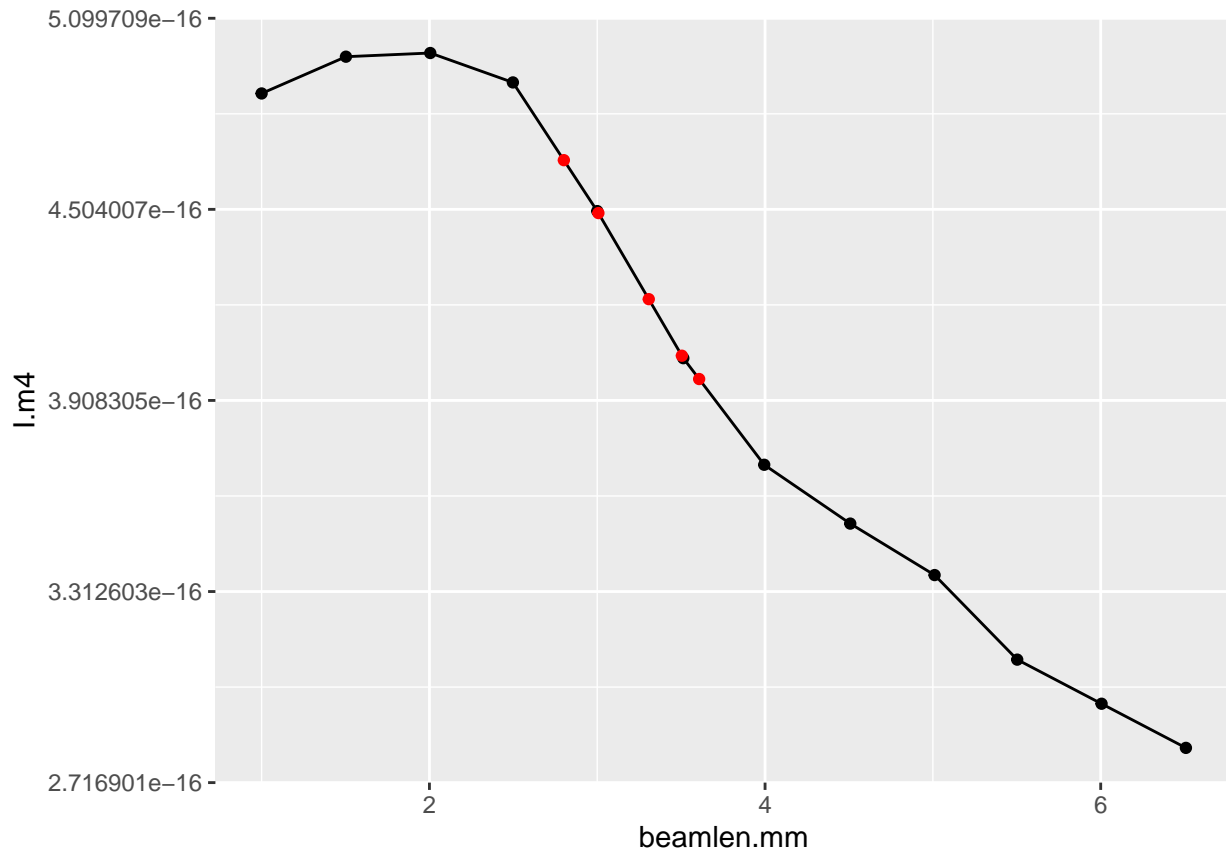
## Rows: 30 Columns: 3
## -- Column specification -----
## Delimiter: ","
## chr (1): fish
## dbl (2): beamlen.mm, E.MPa
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
zebrafishfinEI <-
  zebrafishfinEI |>
  group_by(fish) |>
  summarize(beamlen.mm = beamlen.mm[which.max(EI.Nm2)],
            EI.Nm2 = max(EI.Nm2))

Ivals <- with(zebrafishfinI, approx(beamlen.mm, I.m4, xout = zebrafishfinEI$beamlen.mm))

zebrafishfinI |>
  ggplot(aes(x = beamlen.mm, y = I.m4)) +
  geom_point() +
  geom_line() +
  geom_point(data = as.tibble(Ivals), aes(x = x, y = y), color = 'red')

## Warning: `as.tibble()` was deprecated in tibble 2.0.0.
## i Please use `as_tibble()` instead.
## i The signature and semantics have changed, see `?as_tibble`.

```



```
zebrafishfinE <-
  zebrafishfinE |>
  left_join(zebrafishfinEI, by = 'fish') |>
  rename(beamlen.mm = beamlen.mm.x,
         beamlen.mm.max = beamlen.mm.y) |>
  select(-EI.Nm2) |>
  group_by(fish) |>
  summarize(E.max.MPa = approx(x = beamlen.mm, y = E.MPa, xout = beamlen.mm.max[1])$y)
```

```
zebrafishfin <-
  as_tibble(Ivals) |>
  rename(beamlen.mm = x,
         I.m4 = y) |>
  right_join(zebrafishfinEI, by = c('beamlen.mm')) |>
  right_join(zebrafishfinE, by = 'fish')
```

```
zebrafishfin
```

```
## # A tibble: 5 x 5
##   beamlen.mm    I.m4 fish      EI.Nm2 E.max.MPa
##   <dbl>      <dbl> <chr>      <dbl>    <dbl>
## 1      3.50 4.05e-16 fish11 0.00000000204    4.84
## 2      3.01 4.49e-16 fish12 0.00000000437    9.61
## 3      3.31 4.22e-16 fish13 0.0000000042     9.67
## 4      3.61 3.98e-16 fish4   0.00000000415    7.26
## 5      2.80 4.66e-16 fish5   0.00000000356    8.54
```

```
# columns
# species, E.Pa, E.sd.Pa, I.mm4, I.sd.mm4, EI.Nm2, EI.sd.Nm2, eta.Pas, eta.sd.Pas, etaI.Nm2s, etaI.sd.Nm2s
# tissue, location.L, location.desc, location.cat, Lseg.mm, Lbody.mm, freq.radps, curve.inum, angle.deg
# angle.sd.deg, strain.pct, strain.sd.pct, N, method, frequency.cat, curve.cat, cite

zebrafishfin <-
  zebrafishfin |>
  ungroup() |>
  summarize(across(c(beamlen.mm, I.m4, EI.Nm2, E.max.MPa), c(mn = mean, sd = sd)),
    N = n()) |>
  rename(Lseg.mm = beamlen.mm_mn,
    Lseg.sd.mm = beamlen.mm_sd,
    I.m4 = I.m4_mn,
    I.sd.m4 = I.m4_sd,
    EI.Nm2 = EI.Nm2_mn,
    EI.sd.Nm2 = EI.Nm2_sd) |>
  mutate(E.Pa = E.max.MPa_mn * 1e6,
    E.sd.Pa = E.max.MPa_sd * 1e6) |>
  select(-c(E.max.MPa_mn, E.max.MPa_sd)) |>
  mutate(species = 'Danio rerio',
    method = 'static bending',
    tissue = 'fin',
    location.desc = 'caudal',
    cite = 'Puri et al. (2018)')
```

```
zebrafishfin
```

```
## # A tibble: 1 x 14
##   Lseg.mm Lseg.sd.mm   I.m4 I.sd.m4   EI.Nm2 EI.sd.Nm2   N   E.Pa E.sd.Pa
##   <dbl>   <dbl>   <dbl> <dbl>   <dbl> <dbl> <int> <dbl> <dbl>
## 1    3.25    0.338 4.28e-16 2.91e-17 3.66e-9 9.58e-10    5 7.98e6 2.01e6
## # ... with 5 more variables: species <chr>, method <chr>, tissue <chr>,
## #   location.desc <chr>, cite <chr>, and abbreviated variable name 1: EI.sd.Nm2
```

## Compile results

```
alldata <- bind_rows(hagfishdata, lampreydata, eeldata, bassdata, striperdata, marlindata,
  dogfishdatashort, skindata, gardata, bass2.ivj.mech, carp.tensile.data, carp.bend.data,
  ribdata, eelskindata, danoseelskindata, HHskindata, clarkdata, striperskindata,
  zebrafishfin, aiellofinraydata, perchfinrays)
```

```
tab <-
  alldata |>
  mutate(EI.NL2 = EI.Nm2 / (Lbody.mm/1000)^2,
    I.L4 = I.mm4 / (Lbody.mm/1000)^4) |>
  relocate(species, tissue, E.Pa, eta.Pas) |>
  group_by(species, tissue, frequency.cat, location.cat, curve.cat) |>
  summarize(across(where(is.numeric), mean),
    across(where(is.character), first)) |>
  mutate(freq.Hz = freq.radps / (2*pi),
    location.L = if_else(location.L > 1, location.L / 100, location.L)) |>
  mutate(tissue = case_when(str_detect(tissue, 'fin') ~ 'fin',
    str_detect(tissue, 'vert') ~ 'vertebral column',
    TRUE ~ tissue),
```

```

    tissue = factor(tissue),
    tissue = fct_relevel(tissue, 'whole body')) |>
  arrange(tissue, species)

## `summarise()` has grouped output by 'species', 'tissue', 'frequency.cat',
## 'location.cat'. You can override using the `.groups` argument.

tab

## # A tibble: 32 x 52
## # Groups:   species, tissue, frequency.cat, location.cat [28]
##   species      tissue frequ~1 locat~2 curve~3 E.Pa eta.Pas EI.Nm2 freq.~4
##   <chr>         <fct> <chr>   <chr>   <chr>   <dbl> <dbl>   <dbl> <dbl>
## 1 Anguilla rost~ whole~ high   mid     high   5.89e5 11518. 1.78e-4 18.8
## 2 Carassius aur~ whole~ mid     mid     low    4.66e4 NA      2.08e-3 12.6
## 3 Ichthyomyzon ~ whole~ low     mid     mid     8.8 e4 224    2.1 e-4 6.28
## 4 Lepisosteus o~ whole~ low     post    mid     7.49e5 NA      6.49e-2 6.28
## 5 Micropterus s~ whole~ mid     mid     mid     3.77e6 NA      1.07e+0 16.3
## 6 Morone saxati~ whole~ 0       mid     high   5.70e4 NA      2.28e-1 NA
## 7 Myxine glutin~ whole~ mid     mid     low    2.94e5 NA      3.10e-4 12.6
## 8 Anguilla rost~ skin   <NA>    mid     <NA>    9.12e6 NA      NA      NA
## 9 Anguilla rost~ skin   <NA>    <NA>    <NA>    6.94e6 NA      NA      NA
## 10 Apodichthys f~ skin   <NA>    mid     <NA>    2.82e7 NA      NA      NA
## # ... with 22 more rows, 43 more variables: curve.invm <dbl>, etaI.Nm2s <dbl>,
## # I.mm4 <dbl>, location.L <dbl>, Lseg.mm <dbl>, Lbody.mm <dbl>,
## # angle.deg <dbl>, strain.pct <dbl>, N <dbl>, E.sd.Pa <dbl>, I.sd.mm4 <dbl>,
## # EI.sd.Nm2 <dbl>, eta.sd.Pas <dbl>, etaI.sd.Nm2s <dbl>, angle.sd.deg <dbl>,
## # strain.sd.pct <dbl>, stiff.Nmprad <dbl>, torque.Nm <dbl>,
## # damp.Nmsprad2 <dbl>, strain.rate.Lps <dbl>, E.sem.Pa <dbl>,
## # strain.stiff.frac <dbl>, strain.frac <dbl>, Lseg.sd.mm <dbl>, ...

build_measurements <- function(df) {
  meas = tibble(measurement = rep(NA_character_, nrow(df)),
    value = rep(NA_real_, nrow(df)),
    units = rep(NA_character_, nrow(df)))
  for (i in seq(1, nrow(df))) {
    if (!is.na(df$torque.Nm[i])) {
      meas$measurement[i] = '\tau ='
      meas$value[i] = df$torque.Nm[i]
      meas$units[i] = 'N m'
    } else if (!is.na(df$stiff.Nmprad[i])) {
      meas$measurement[i] = 'k ='
      meas$value[i] = df$stiff.Nmprad[i]
      meas$units[i] = 'N m rad^{-1}'
    } else if (!is.na(df$EI.Nm2[i])) {
      meas$measurement[i] = 'EI ='
      meas$value[i] = df$EI.Nm2[i]
      meas$units[i] = 'N m^2'
    }
  }
  bind_cols(df, meas)
}

citenum <-
  tab |>

```

```

group_by(tissue, species, cite) |>
summarize(cite = first(cite)) |>
ungroup() |>
arrange(tissue, species) |>
distinct(cite) |>
mutate(citenum = seq(1, n()))

```

## `summarise()` has grouped output by 'tissue', 'species'. You can override using  
## the `.groups` argument.

```

suffix_formatter <- function(x, n_sigfig = 2,
                             breaks = c(1e-9, 1e-6, 1e-3, 1, 1000, 1e6, 1e9),
                             labels = c('n', 'u', 'm', '', 'k', 'M', 'G'),
                             div = c(1e-9, 1e-6, 1e-3, 1, 1000, 1e6, 1e9)) {

  print(x)
  fmt = rep_along(x, '')
  for (j in seq_along(x)) {
    if (is.na(x[j])) {
      val <- NA
      suf <- ''
    }
    else if (x[j] < breaks[1]) {
      val <- x[j] / div[1]
      suf <- labels[1]
    } else {
      for (i in seq(length(breaks), 1, by=-1)) {
        if (x[j] >= breaks[i]) {
          val <- x[j] / div[i]
          suf <- labels[i]
          break
        }
      }
    }

    fmt[j] <- paste0(signif(val, digits = n_sigfig), suf)
  }

  fmt
}

```

```

displaytab <-
  tab |>
  ungroup() |>
  left_join(citenum, by = "cite") |>
  mutate(location.pct = location.L * 100) |>
  mutate(location.desc = str_remove(location.desc, ' fin')) |>
  build_measurements() |>
  ungroup() |>
  mutate(across(contains('dE.'),
    ~case_when(.x == 'inc' ~ '+',
               .x == 'dec' ~ '-',
               .x == 'const' ~ '=',
               .x == 'incdec' ~ '+-')) |>

```



```

select(tissue, species, location.desc, location.L, E.Pa, EI.NL2, contains('dE.'), eta.Pas,
      #curve.invm, strain.pct, angle.deg,
      I.L4,
      #measurement, value, units,
      Lbody.mm, N, method, citenum) |>
arrange(tissue, species) |>
group_by(tissue) |>
gt() |>
sub_missing(missing_text = '') |>
fmt(columns = c(E.Pa, eta.Pas, EI.NL2),
     fns = \(num) suffix_formatter(num, n_sigfig = 2)) |>
fmt_scientific(columns = c(I.L4)) |>
# fmt_scientific(columns = c(value)) |>
fmt_percent(columns = c(location.L), decimals = 0) |>
# fmt_percent(columns = c(strain.pct), decimals = 1, scale_values = FALSE) |>
# fmt_number(c(curve.invm, angle.deg), decimals = 1) |>
fmt_number(Lbody.mm, decimals = 0) |>
cols_label(tissue = 'Tissue',
           species = 'Species',
           location.desc = '',
           location.L = '',
           E.Pa = md('E (Pa)'),
           EI.NL2 = md('EI (N L2)'),
           dE.dcurve = 'curvature +',
           dE.dfreq = 'frequency +',
           dE.dloc = 'location post',
           eta.Pas = md('eta (Pa s)'),
           # curve.invm = 'Curvature (m^-1)',
           # strain.pct = 'Strain',
           # angle.deg = 'Angle (o)',
           I.L4 = 'I (L^4)',
           # measurement = '',
           # value = '',
           # units = '',
           Lbody.mm = 'Body length (mm)',
           method = 'Method',
           citenum = '')
# tab_spanner('Change in E when',
#             columns = contains('dE.')) |>
# tab_spanner('Original measurement',
#             columns = c(measurement, value, units))

displaytab

```

```

## [1] 5.885226e+05 4.656678e+04 8.800000e+04 7.490131e+05 3.765845e+06
## [6] 5.700140e+04 2.943245e+05 9.120000e+06 6.940000e+06 2.820000e+07
## [11] 1.820000e+06 5.260000e+07 3.356000e+07 9.405000e+06 4.653578e+06
## [16] 4.410000e+02 1.575359e+06 2.110000e+07 8.405425e+06 1.100000e+06
## [21] 7.983861e+06 NA NA NA NA
## [26] NA NA NA 1.112967e+06 2.286617e+07
## [31] 5.923329e+05 6.471193e+09
## [1] 11518.343 NA 224.000 NA NA NA NA
## [8] NA NA NA NA NA NA NA
## [15] NA NA NA NA NA NA NA

```

```

## [22]      NA      NA      NA      NA      NA      NA      NA
## [29] 13416.072      NA 4249.306      NA
## [1] 2.266880e-03 5.769987e-02 3.106509e-03 1.474963e-01 1.186111e+01
## [6] 1.425035e+00 2.157627e-03      NA      NA      NA
## [11]      NA      NA      NA      NA      NA
## [16]      NA      NA      NA      NA      NA
## [21]      NA      NA      NA 2.188807e-05 3.285627e-05
## [26] 1.271455e-05 4.597117e-06 8.798716e-05 3.953895e-02 1.425690e-03
## [31] 1.239751e-04 1.330161e-03

```

Species	E (Pa)	EI (N L2)	curvature +	frequency +	location
whole body					
Anguilla rostrata		mid-caudal	70%	590k	2.3m
Carassius auratus		midbody	48%	47k	58m =
Ichthyomyzon unicuspis		midbody	55%	88k	3.1m =
Lepisosteus osseus				750k	150m
Micropterus salmoides		midbody	43%	3.8M	12
Morone saxatilis		M	41%	57k	1.4 +
Myxine glutinosa		midbody	37%	290k	2.2m = +
skin					
Anguilla rostrata		midbody (long)		9.1M	
Anguilla rostrata			17%	6.9M	
Apodichthys flavidus		post (long)	75%	28M	
Carassius auratus				1.8M	
Eptatretus stoutii		post (long)	75%	53M	
Katsuwonus pelamis		midbody (long)		34M	
Leiostomus xanthurus		midbody (long)		9.4M	
Lutjanus campechanus		midlateral	61%	4.7M	+ +
Morone saxatilis		MD	50%	440	
Oncorhynchus kisutch		midlateral	56%	1.6M	+ +
Petromyzon marinus		post (long)	75%	21M	
Trachinotus carolinus		midlateral	54%	8.4M	+ +
muscle					
Carassius auratus				1.1M	
fin					
Danio rerio		caudal		8M	
Gomphosus varius		pectoral			
Halichoeres bivittatus		pectoral			
Perca flavescens		Anal		22u	
Perca flavescens		Caudal		33u	
Perca flavescens		Dorsal soft		13u	
Perca flavescens		Pectoral		4.6u	
Perca flavescens		Pelvic		88u	
vertebral column					
Makaira nigricans		joint 11	1.1M	40m	+ - +
Morone saxatilis		AB	23M	1.4m	+ = +-
Squalus acanthias		precaudal	590k	120u	+ +
bone (acellular rib)					
Myoxocephalus polyacanthocephalus		rib 1	6.5G	1.3m	=

```
gtsave(displaytab, 'mehtable2.docx')
```

```
## [1] 5.885226e+05 4.656678e+04 8.800000e+04 7.490131e+05 3.765845e+06
## [6] 5.700140e+04 2.943245e+05 9.120000e+06 6.940000e+06 2.820000e+07
## [11] 1.820000e+06 5.260000e+07 3.356000e+07 9.405000e+06 4.653578e+06
## [16] 4.410000e+02 1.575359e+06 2.110000e+07 8.405425e+06 1.100000e+06
## [21] 7.983861e+06 NA NA NA NA
## [26] NA NA NA 1.112967e+06 2.286617e+07
## [31] 5.923329e+05 6.471193e+09
## [1] 11518.343 NA 224.000 NA NA NA NA
## [8] NA NA NA NA NA NA NA
## [15] NA NA NA NA NA NA NA
## [22] NA NA NA NA NA NA NA
## [29] 13416.072 NA 4249.306 NA
## [1] 2.266880e-03 5.769987e-02 3.106509e-03 1.474963e-01 1.186111e+01
## [6] 1.425035e+00 2.157627e-03 NA NA NA
## [11] NA NA NA NA NA
## [16] NA NA NA NA NA
## [21] NA NA NA 2.188807e-05 3.285627e-05
## [26] 1.271455e-05 4.597117e-06 8.798716e-05 3.953895e-02 1.425690e-03
## [31] 1.239751e-04 1.330161e-03
```

```
note <-
  citenum |>
  mutate(note = str_c(citenum, cite, sep = ' '))

do.call(paste, c(sep = '; ', as.list(note$note)))
```

```
## [1] "1 Long (1998); 2 Zhou et al. (2011); 3 Tytell et al. (2018); 4 Long et al. (1996); 5 Long & Nipr"
```