TS simulations - ZooScatR

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```
#tidyverse for cleaner code
library(tidyr)
library(dplyr)
library(purrr)
#apply with progress
library(pbapply)

#plotting
library(ggplot2)

#special libraries
library(ZooScatR)

#pdf stuff
library(kableExtra)
library(knitr)

#define if simulations should be multithreadded. THis will run the simulations in parallel using with #
runParallel = TRUE
if (runParallel == TRUE){
  library(foreach)
  library(doParallel)

  registerDoParallel(parallel::detectCores()-1)
}
#force running a new simulation, even if an RDS file with simualtions is available
force=TRUE
#set working dir
setwd('C:\\Users\\sven\\Documents\\Zonar\\DVM\\sim\\')
```

A priori assumptions

We assume copepods, euphausiids, appendicularians and chaetognaths to be the dominant species groups. For diverse Calanus groups, cheatognaths and euphausiids, we can use literature values to populate the model. I couldn't find any values for appendicularians, so I used values for fish larvae here as an approximation.

Model definition

Let's start by loading some standard values for the model:

```
#number of simulations
nsim = 100
#location of the standard parameter file contained within the package
fname <- paste0(system.file(package="ZooScatR"),"/extdata/configs/config_0.dat")
# read the parameters file
para = ZooScatR::read_para(fname)
#set the soundspeed in the surrounding sea water
misc <- list(cw=1500)
#let's set the start and end frequencies
f0=200 #eill bepara$simu$var0
f1=1000 #will be para$simu$var1
#number of output frequencies
nf=801 #will be para$simu$n
```

For the parameter distributions a gamma, normal or uniform dsitribution were used.
For gamma distributions a density function with a shape s and a rate a was defined as:

$$f_\Gamma(x) = \frac{1}{s^a \Gamma(a) x^{a-1} e^{-\frac{x}{s}}}$$

where $\Gamma(a)$ is defined as [@milne-thomson_handbook_1972]:

$$\Gamma(a) = \int_0^\infty t^{a-1} e^{-t} dt$$

Normal distributions were computed with standard deviation σ and mean μ with a density given by [@johnson_continuous_1995]:

$$f_N(x) = \frac{1}{\sqrt{2\pi}\sigma e^{-\frac{(x-\mu)^2}{2\sigma^2}}}$$

A summary of the settings is defined in table 1.

For euphausiids a bimodal truncated normal distribution was used.

```
pm = data.frame(species=c('copepod','Euphausiids1','Euphausiids2','Chaetognaths','Appendicularians'),
  L_dist=c('gamma', 'truncated normal','truncated normal', 'gamma','gamma'),
  L_shape=c(7, 3,20, 3, 4),
  L_rate=c(4, 3,4,4, 4),
  L_a_dist =c('normal'),
  L_a_mean = c(2.8, 10.5, 10.5, 17.15, 4),
  L_a_sd = c(0.2,.2,1,3,1),
  g_dist = 'uniform',
  g_min = c(1.015,1.009,1.009,1.03, 0.979),
  g_max = c(1.025,1.016,1.016,1.04, 0.999),
  h_dist='uniform',
  h_min = c(1.027,1.019,1.019,1.025,1.016),
  h_max = c(1.030,1.029,1.029,1.035,1.018),
  theta_dist='uniform',
  theta_mean = c(0,20,20,0,0),
  theta_sd = c(30,20,20,30,20),
  rho_l=c(100,100,100,100,100),
  taper=c(4,5,5,2,2)
)
```

species	L_dist	L_shape	L_rate	L_a_dist	L_a_mean	L_a_sd
copepod	gamma	7	4	normal	2.80	0.2
Euphausiids1	truncated normal	3	3	normal	10.50	0.2
Euphausiids2	truncated normal	20	4	normal	10.50	1.0
Chaetognaths	gamma	3	4	normal	17.15	3.0
Appendicularians	gamma	4	4	normal	4.00	1.0

species	g_dist	g_min	g_max	h_dist	h_min	h_max
copepod	uniform	1.015	1.025	uniform	1.027	1.030
Euphausiids1	uniform	1.009	1.016	uniform	1.019	1.029
Euphausiids2	uniform	1.009	1.016	uniform	1.019	1.029
Chaetognaths	uniform	1.030	1.040	uniform	1.025	1.035
Appendicularians	uniform	0.979	0.999	uniform	1.016	1.018

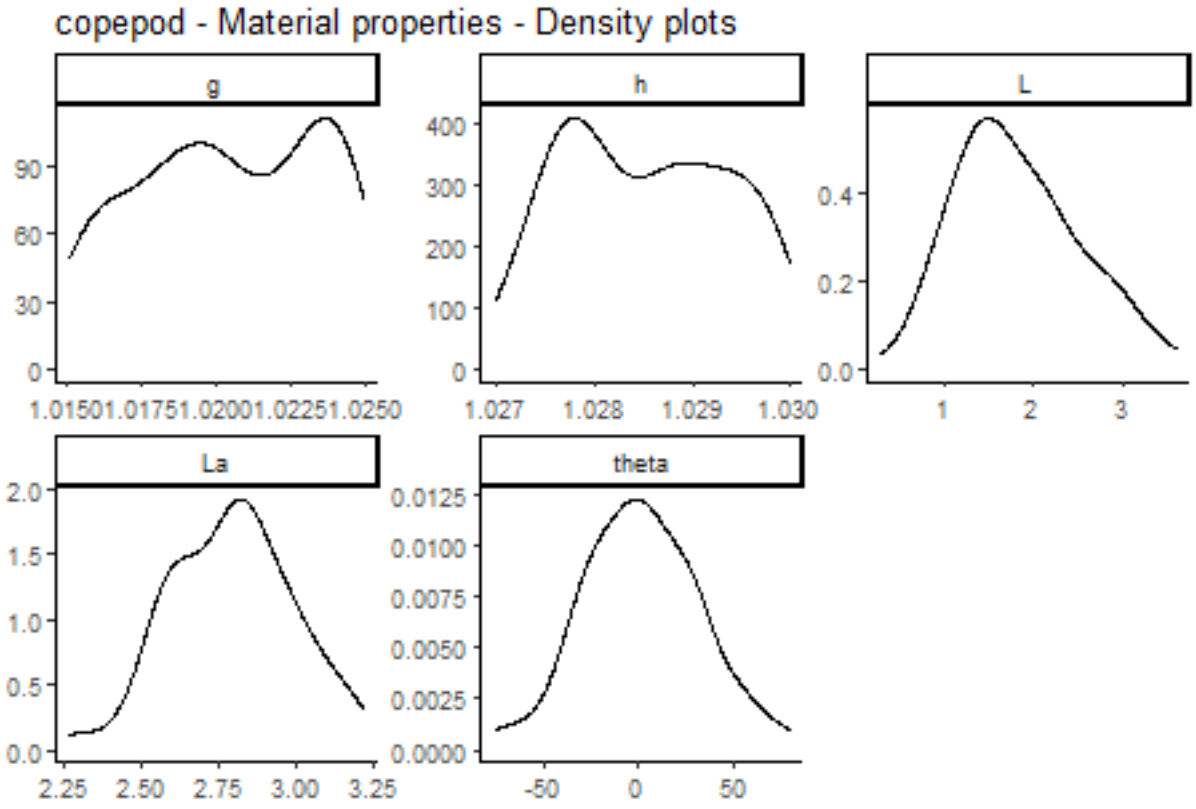
species	theta_dist	theta_mean	theta_sd	rho_l	taper
copepod	uniform	0	30	100	4
Euphausiids1	uniform	20	20	100	5
Euphausiids2	uniform	20	20	100	5
Chaetognaths	uniform	0	30	100	2
Appendicularians	uniform	0	20	100	2

Define the Model parameters

Now that we have lists of settings we can set those in the parameter files for each species group.

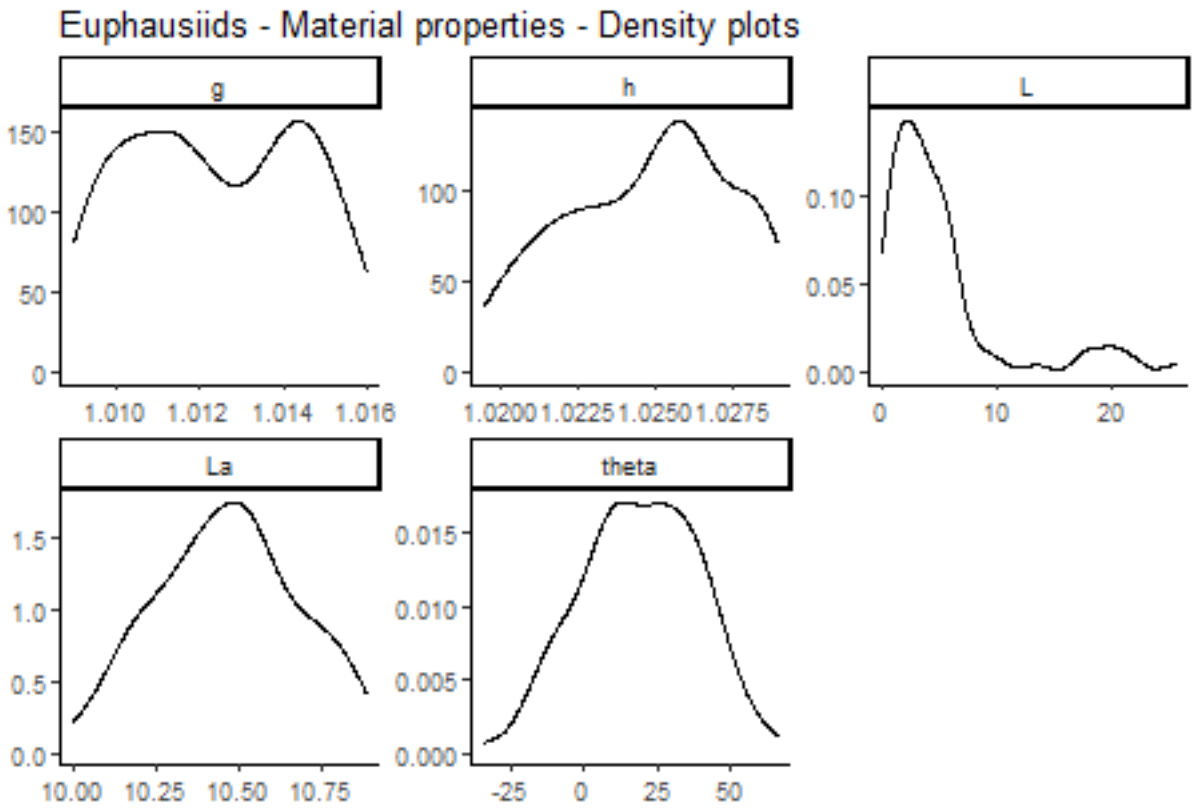
```
##############################################################################
#create a get_para funciton
get_para <- function(pm,spec,fn=-1){
#length distribution - this is made up...
if(spec=='Euphausiids'){
  pmsel = pm%>%filter(species=='Euphausiids1')
  L = c(abs(rnorm(9*nsim/10,3,3)), rnorm(1*nsim/10, 20,4))
  }else{
  pmsel = pm%>%filter(species==spec)
  L = rgamma(nsim,shape=pmsel$L_shape,rate=pmsel$L_rate)
  }
  cp = data.frame(species=spec,
  L=L,
  La=rnorm(nsim, pmsel$L_a_mean, pmsel$L_a_sd),
  g=runif(nsim, pmsel$g_min, pmsel$g_max),
  h=runif(nsim, pmsel$h_min, pmsel$h_max),
  taper=pmsel$taper,
  rhol=pmsel$rho_l,
  pf=fn,
  theta=rnorm(nsim, pmsel$theta_mean, pmsel$theta_sd))
```

```
  cdf = gather(cp,'var','value',-species,-taper, -rhol,-pf)
  subtit <- c('L' = "Length~(mm)",
  'La' = "L/a",
  'g' ="Density~contrast~g",
  'h' = 'Sound~speed~contrast~h',
  'theta' = 'Angle~theta~(degree)' )
  p <- ggplot(data=cdf, aes(x=value))+
  geom_density()+
  facet_wrap(.~var, scales='free')+#, labeller =labeller(var= as_labeller(subtit, label_parsed)))+
  theme_classic()+
  ggtitle(paste(spec,'- Material properties - Density plots'))+
  xlab('')+ylab('')
  return(list(cp,p))
}
#####################################################################
#set copepod settings
#fn = paste0(system.file(package="ZooScatR"),"/extdata/profiles/copepod0.dat")
fn = 'cop0.sat'
cout = get_para(pm, 'copepod', fn)
cdf = cout[[1]]
cout[[2]]
```



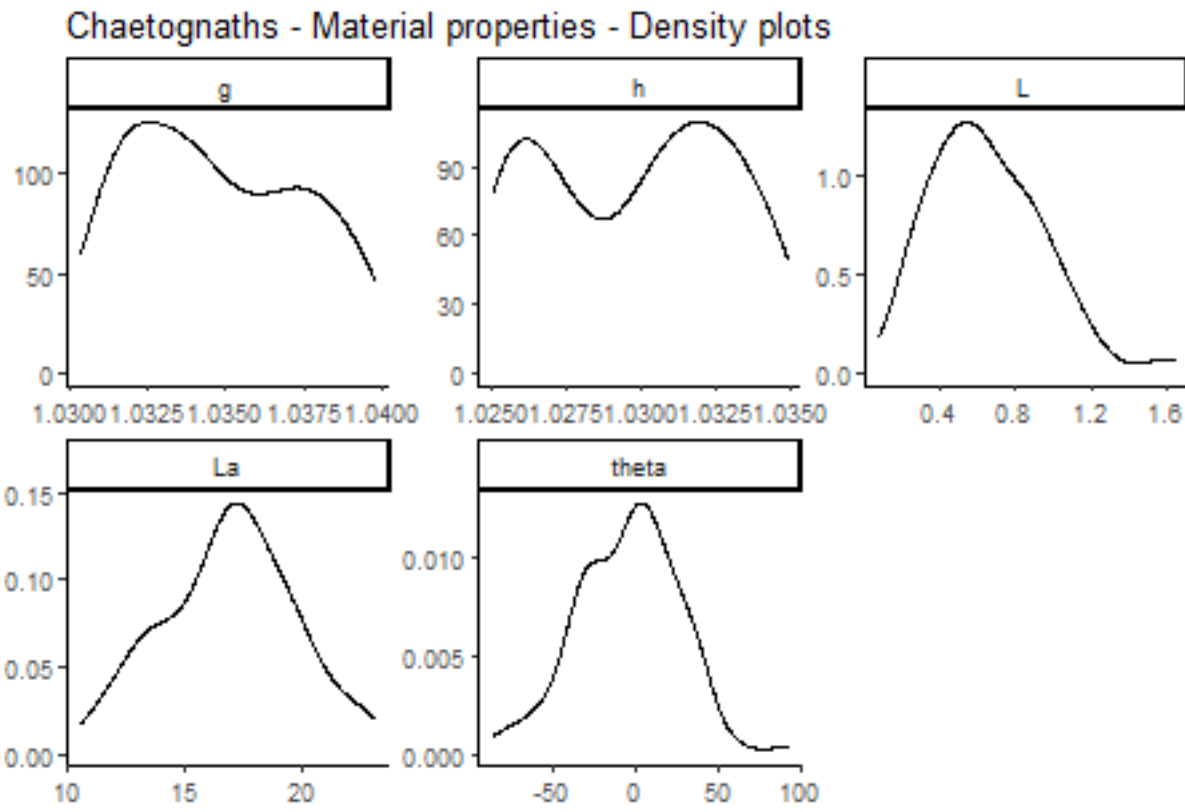
Copepods

```
fn = paste0(system.file(package="ZooScatR"),"/extdata/profiles/euphaus0.dat")
eout = get_para(pm, 'Euphausiids',fn)
edf = eout[[1]]
eout[[2]]
```



Euphausiids

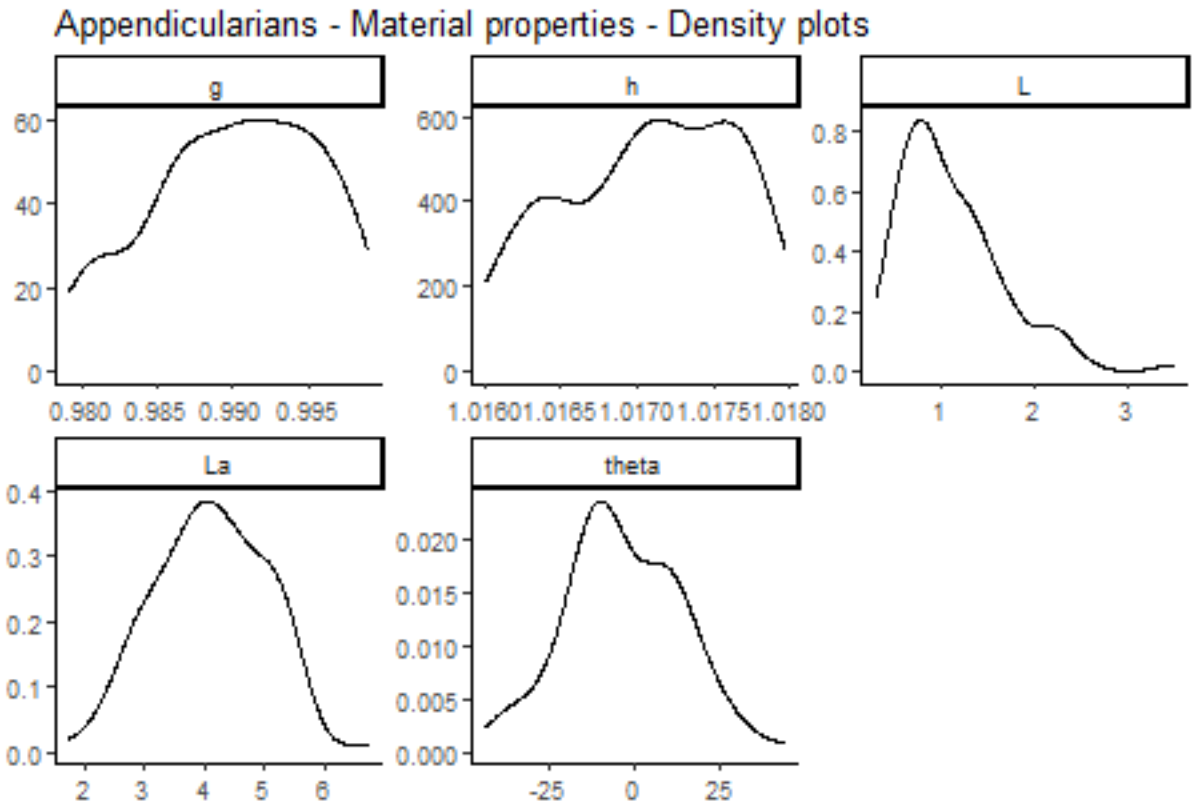
```
fn = 'chaeto0.sat'
chout = get_para(pm, 'Chaetognaths',fn)
chdf = chout[[1]]
chout[[2]]
```



Chaetognaths

Appendicularians

```
fn = 'app0.sat'
apout = get_para(pm, 'Appendicularians',fn)
apdf = apout[[1]]
apout[[2]]
```



Run the model

Now we can combine all the settings and prepare to run the simulations:

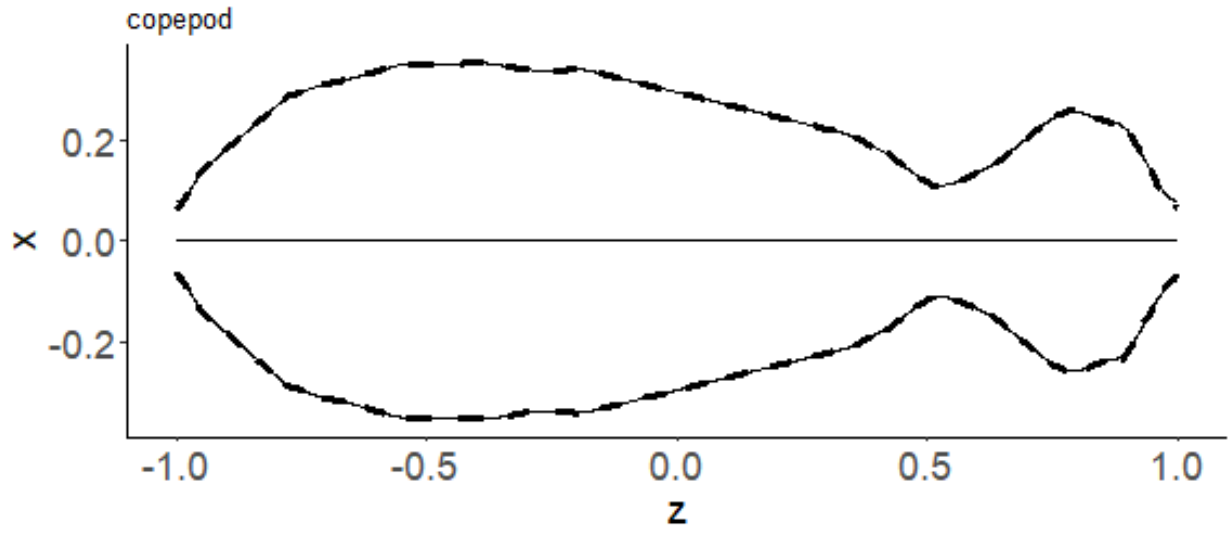
```
setdf = do.call('rbind',list(cdf,edf,chdf,apdf))
set_para <- function(i, shape=FALSE, setdf=setdf){
  para = ZooScatR::read_para(fname)
  #set the soundspeed in the surrounding sea water
  #misc <- list(cw=1500)
  #let's set the start and end frequencies
  para$simu$var0=f0
  para$simu$var1=f1
  #number of output frequencies
  para$simu$n=nf
  para$shape$L = setdf$L[i]
  para$shape$L_a = setdf$La[i]
  para$phy$g0 = setdf$g[i]
  para$phy$h0 = setdf$h[i]
  para$shape$order = setdf$taper[i]
  para$shape$rho_L = setdf$rhol[i]
  para$shape$prof_name = setdf$pf[i]
  para$orient$angm = setdf$theta[i]

  if(shape==FALSE){
    res = ZooScatR::bscat(para=para, misc=misc) #Target strength vs Frequency
```

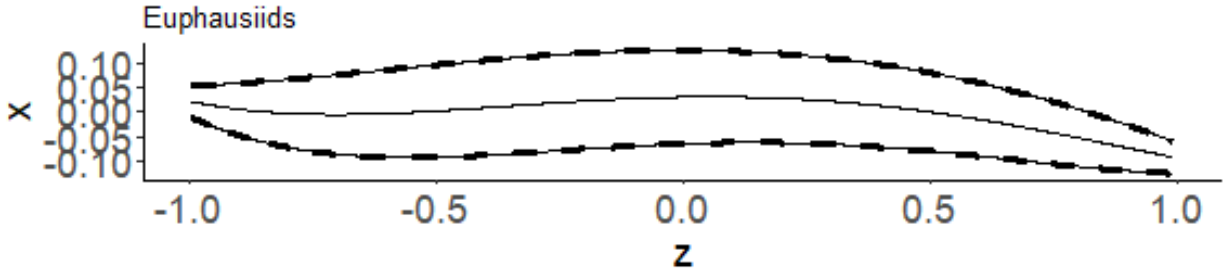
```
    tmp=data.frame(TS=res$y,
    freq=seq(f0,f1, length.out = nf),
    L=para$shape$L,
    la=para$shape$L_a,
    g=para$phy$g0,
    h=para$phy$h0,
    orient=para$orient$angm,
    spec=setdf$species[i])
    return(tmp)

  }else{
    p = buildpos(para)
    p = p$plot
    p = p+coord_equal()
    p = p+ggtitle(setdf$species[i])
    print(p)
    return(p)
  }
}
```

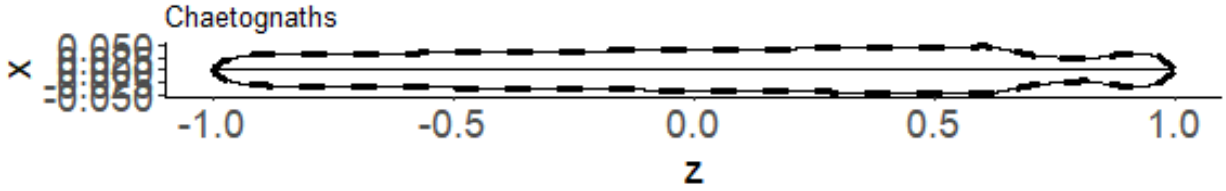
Model input shapes

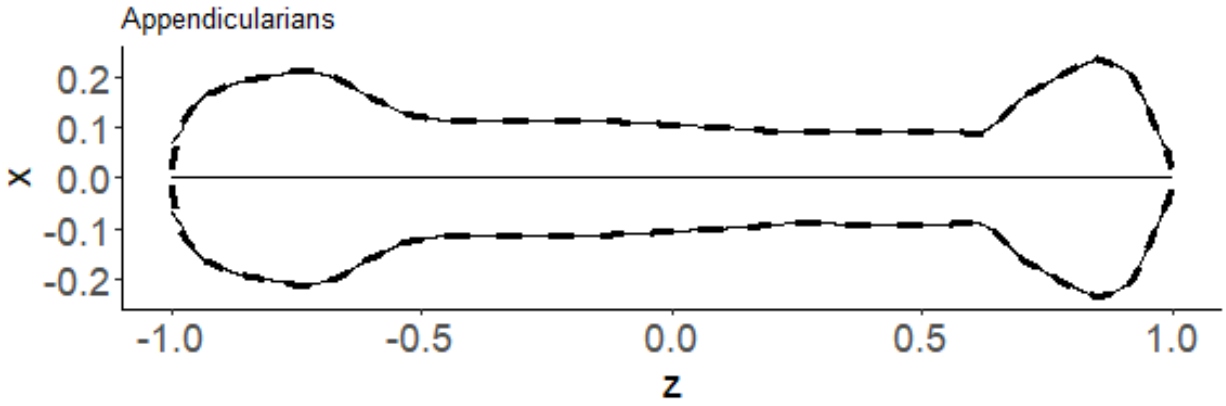
First let's have a look at the selected shapes:

```
specp = setdf%>%group_by(species)%>%filter(row_number()==1)
for(i in 1:length(specp$species)){set_para(i,shape=TRUE, setdf=specp)}
```




Euphausiids
x
0.10
0.05
0.00
-0.05
-0.10
-1.0
-0.5
0.0
0.5
1.0
z


Chaetognaths
x
-1.0
-0.5
0.0
0.5
1.0
z



Now we can run the simulations:

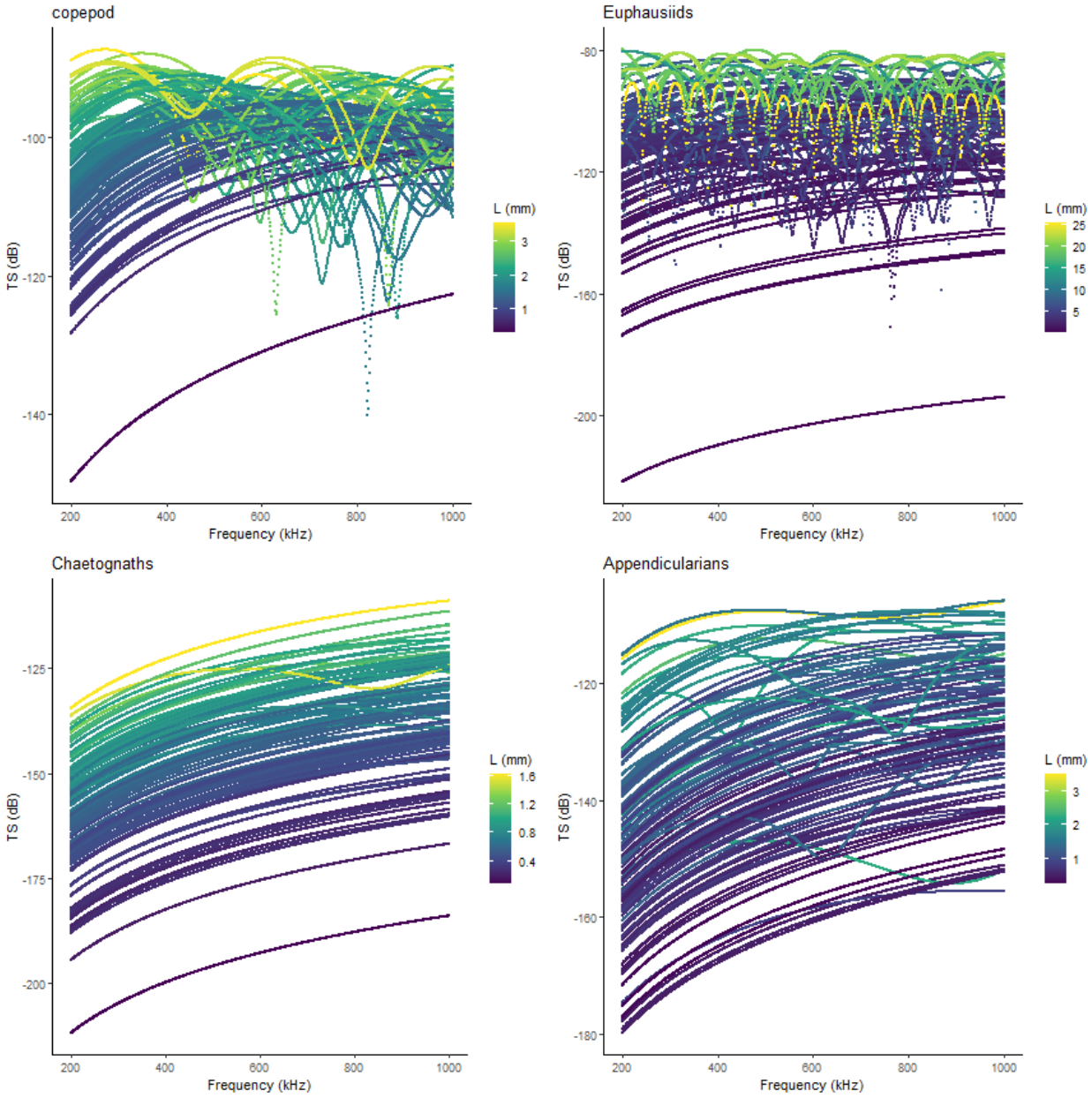
```
if(force ==FALSE & file.exists('sim2.RDS')){
  message(Sys.time(), ': Found simulations...Using old simulaitons...')
  sim = readRDS('sim2.RDS')
}else{
message(Sys.time(),': Running simulations...')
if(runParallel == TRUE){
sim = foreach(i=1:length(setdf$L), .combine=rbind) %dopar% {set_para(i, shape=FALSE,setdf=setdf)}
}else{
sim = do.call('rbind',
pbapply(matrix(1:length(setdf$L)),1,function(i){set_para(i, shape=FALSE,setdf=setdf)})
)
}
message(Sys.time(),': Running simulations completed!')
saveRDS(sim, file='sim2.RDS', compress=TRUE)
}
```

Let's have a look at the results.

Let's plot TS grouped by species vs Length:

```
plot_func <- function(sim, name='L (mm)', var='L', y='TS',x='freq', title) {
  ggplot(data = sim, aes_string(x = x, y = y, col = var)) +
    geom_point(size=0.01) +
    scale_colour_viridis_c(name=name)+
    ggtitle(title)+
    xlab('Frequency (kHz)')+
    ylab('TS (dB)')+
    theme_classic()
}
pL <- function(sim,spec){plot_func(sim, name='L (mm)', var='L', y='TS',x='freq', spec)}

sim_tmp <- sim %>%
```

```
  group_by(spec) %>%
  nest() %>%
  mutate(plots = map2(data, spec, pL))
pL = gridExtra::grid.arrange(grobs = sim_tmp$plots)
```



To have a look at the overall distribution, we can also look at 2D density plots:

```
pL <- function(sim, title){
  ggplot(data=sim, aes(x=freq, y=TS))+
    geom_density2d_filled()+
    #facet_wrap(.~spec, scales='free')+
    scale_x_continuous(expand=c(0,0))+
    scale_y_continuous(expand=c(0,0))+
```

```
    ggtitle(title)+
    theme_classic()
}


sim_tmp <- sim %>%
  group_by(spec) %>%
  nest() %>%
  mutate(plots = map2(data, spec, pL))
pL = gridExtra::grid.arrange(grobs = sim_tmp$plots)
```