

# nwfscSurvey Vignette

2025-01-23

Set up: The first set of code is for the Bottom trawl survey The second set of code is for the triennial survey

Questions: is this a two area model as in WA/OR + CA? or WA + OR only? Is California a whole different assessment model? If we are seeing catches in CA, what is the strata doing again?

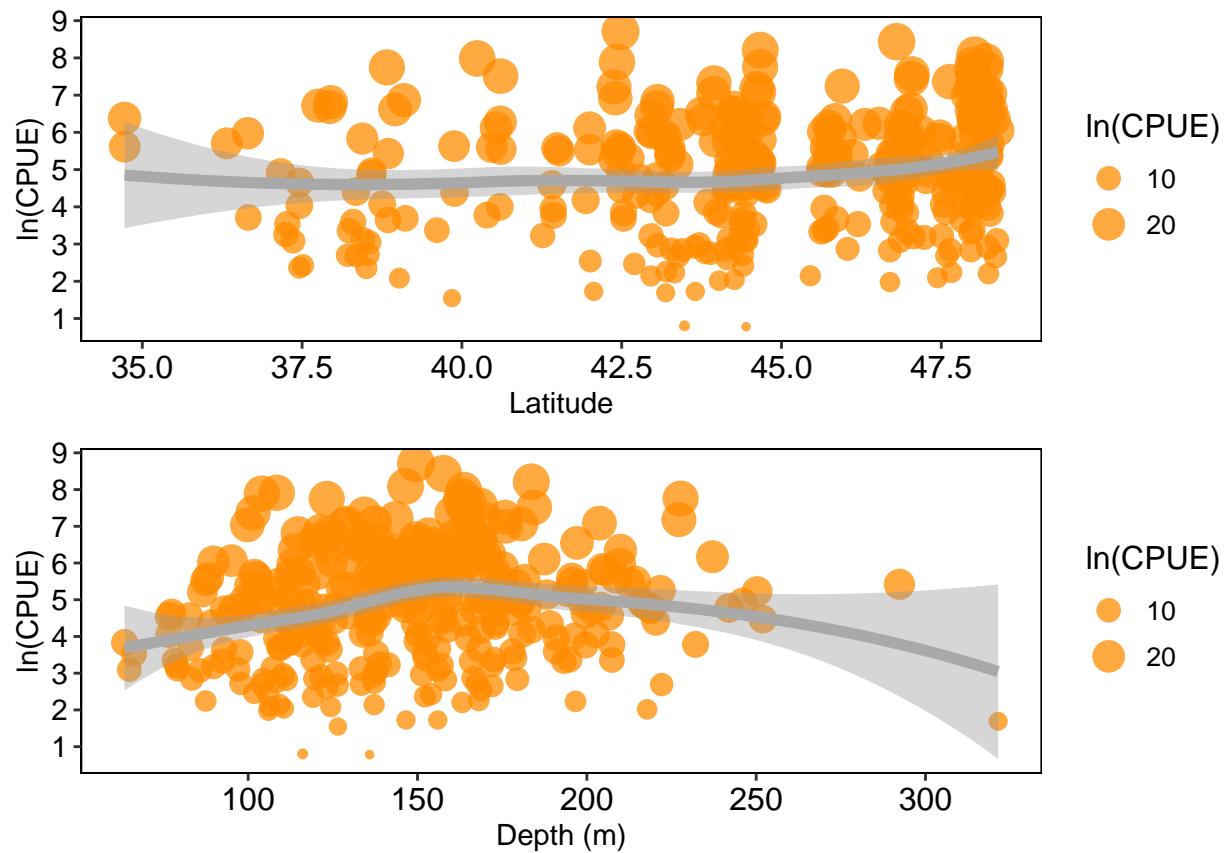
## NWFSC.Combo Data

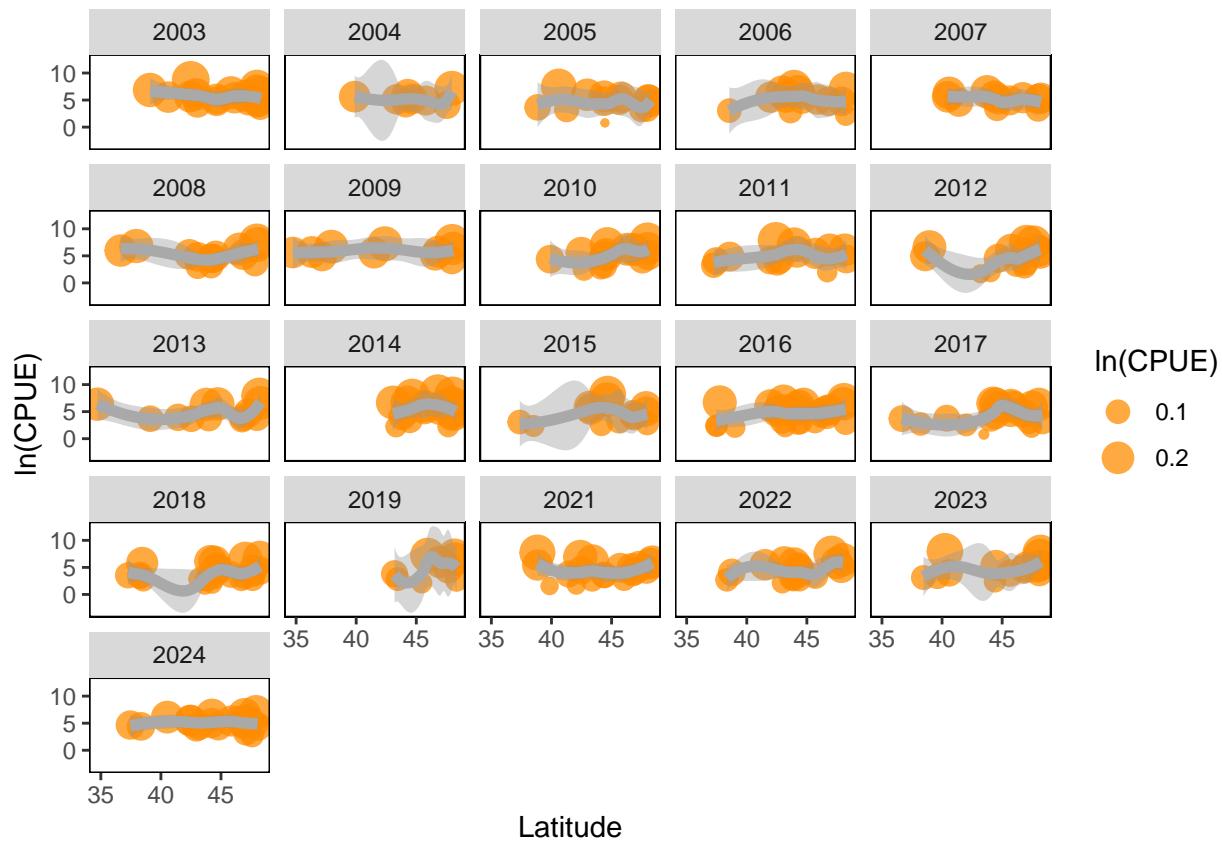
Initial pull and plotting of data: WCGBTS

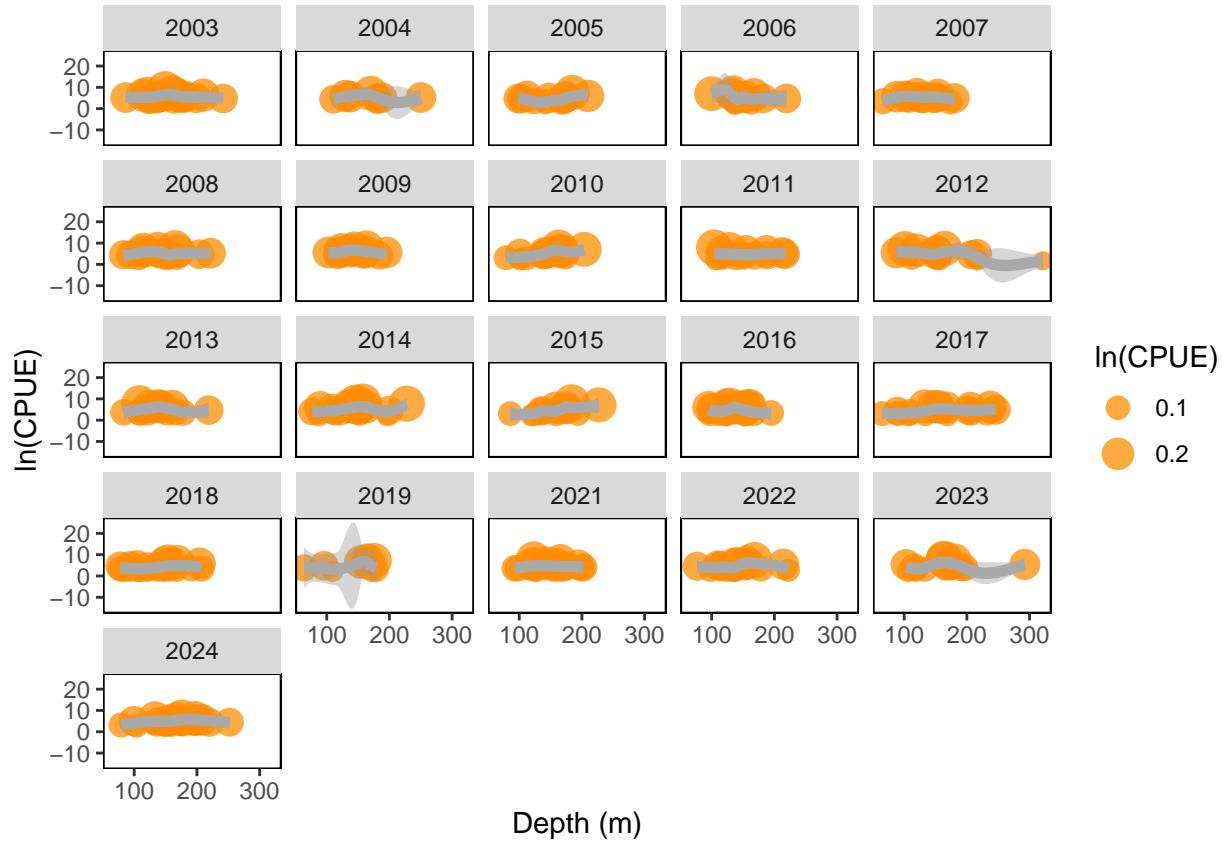
```
catch = pull_catch(
    common_name = "yelloweye rockfish",
    survey = "NWFSC.Combo")

bio = pull_bio(
    common_name = "yelloweye rockfish",
    survey = "NWFSC.Combo")

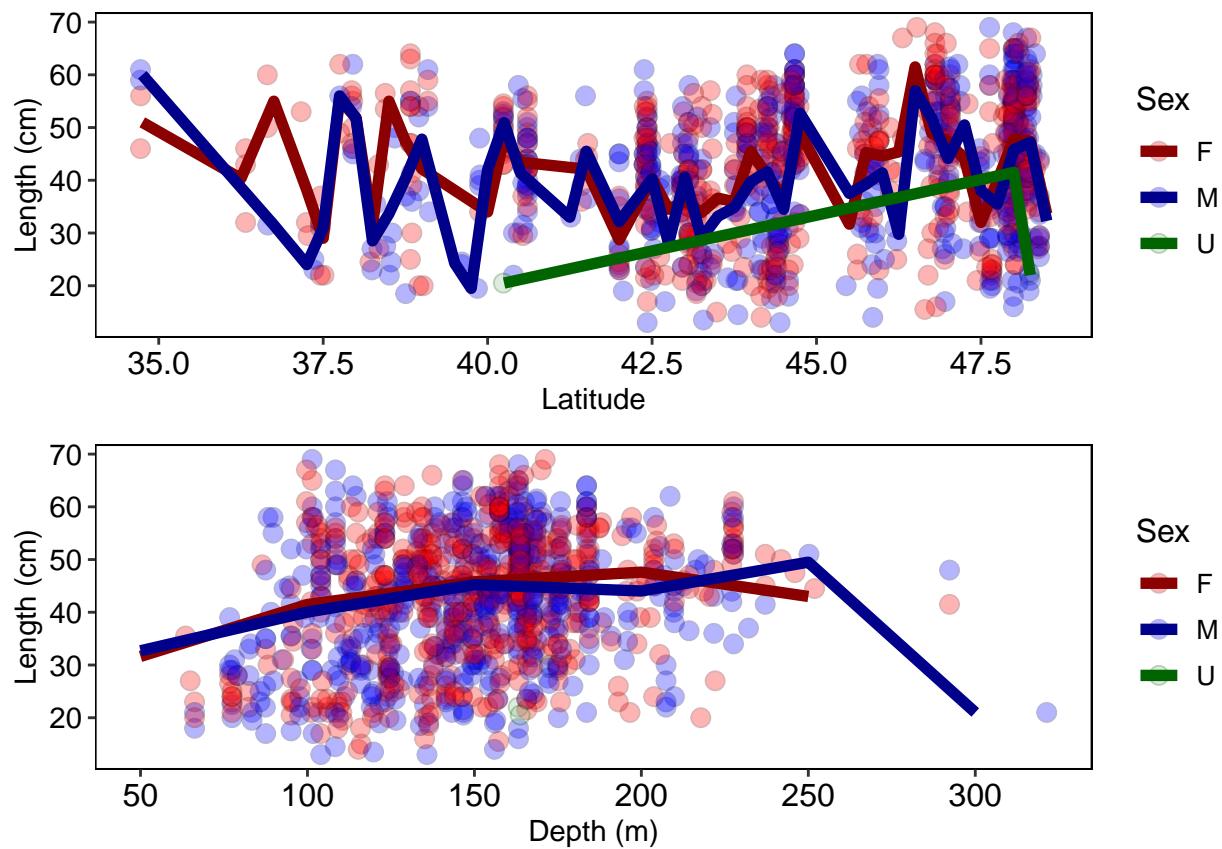
plot_cpue(
    catch = catch)
```

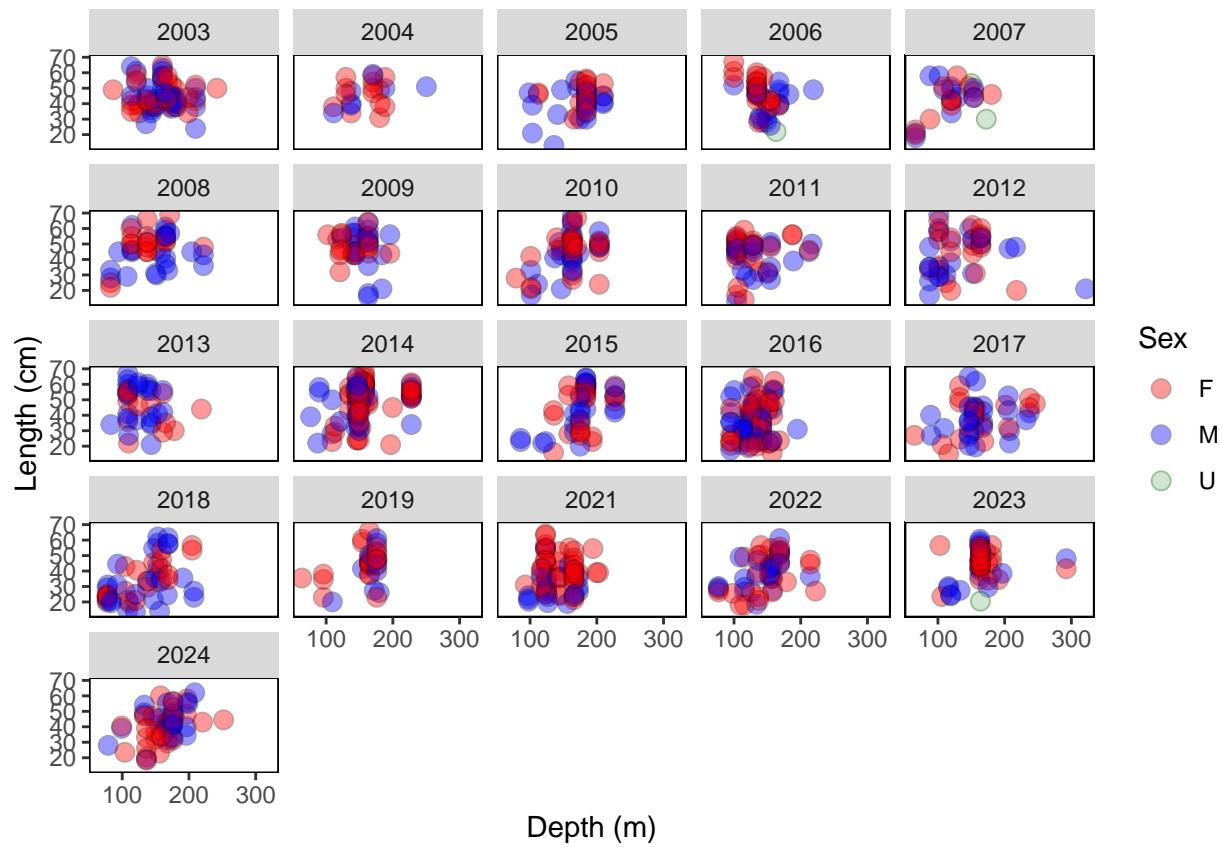


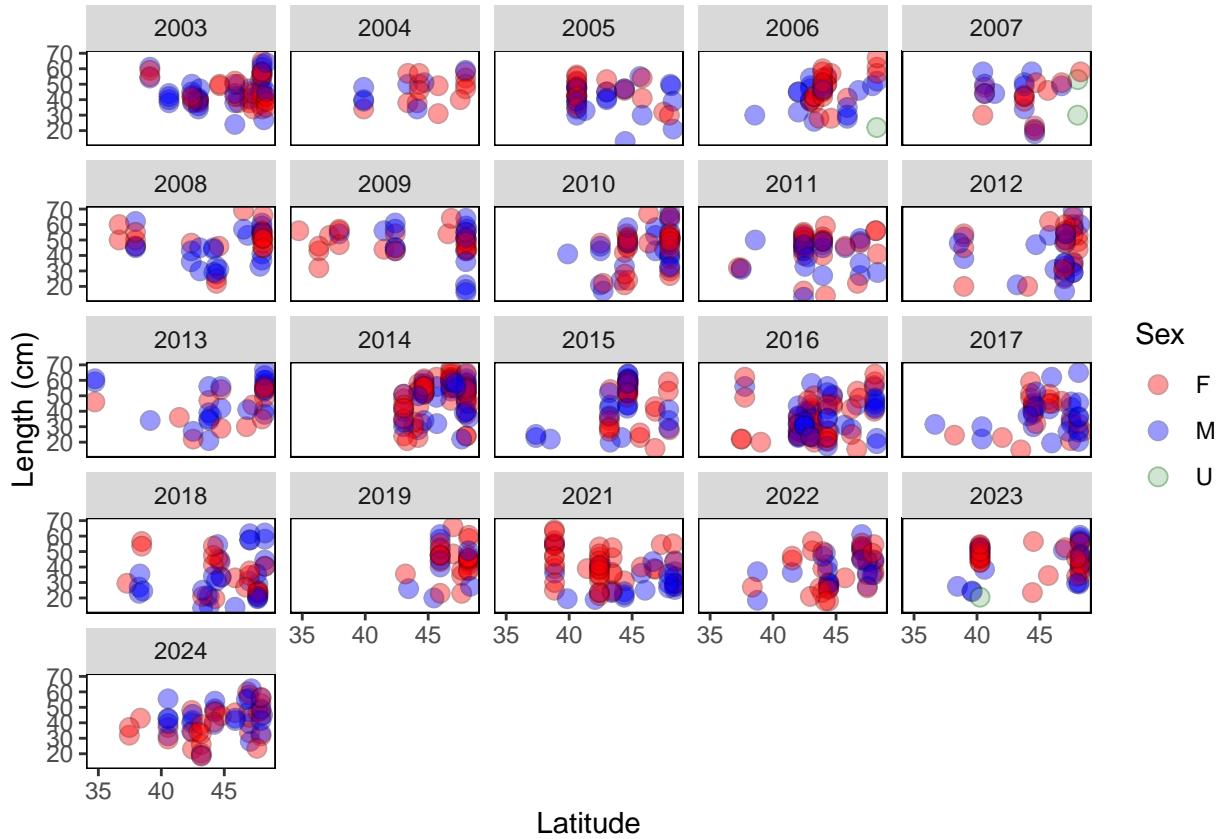




```
plot_bio_patterns(
  bio = bio,
  col_name = "Length_cm")
```







```

wh_plot_proportion(
  data_catch = catch,
  data_bio = bio
)

## [1] "C:/Users/elizabeth.gugliotti/Documents/github_repos/Sebastes_ruberimus_2025/Rcode/plots/presen"
## [2] "C:/Users/elizabeth.gugliotti/Documents/github_repos/Sebastes_ruberimus_2025/Rcode/plots/presen"
## [3] "C:/Users/elizabeth.gugliotti/Documents/github_repos/Sebastes_ruberimus_2025/Rcode/plots/sex_by"
## [4] "C:/Users/elizabeth.gugliotti/Documents/github_repos/Sebastes_ruberimus_2025/Rcode/plots/sex_by"

```

Calculate designed based index of abundance

```

WGBTStrata <- CreateStrataDF.fn(
  names = c("shallow_OR", "deep_OR", "shallow_WA", "deep_WA"),
  depths.shallow = c(55, 183, 55, 183),
  depths.deep = c(183, 350, 183, 350),
  lats.south = c(42, 42, 46, 46),
  lats.north = c(46, 46, 49, 49)
)

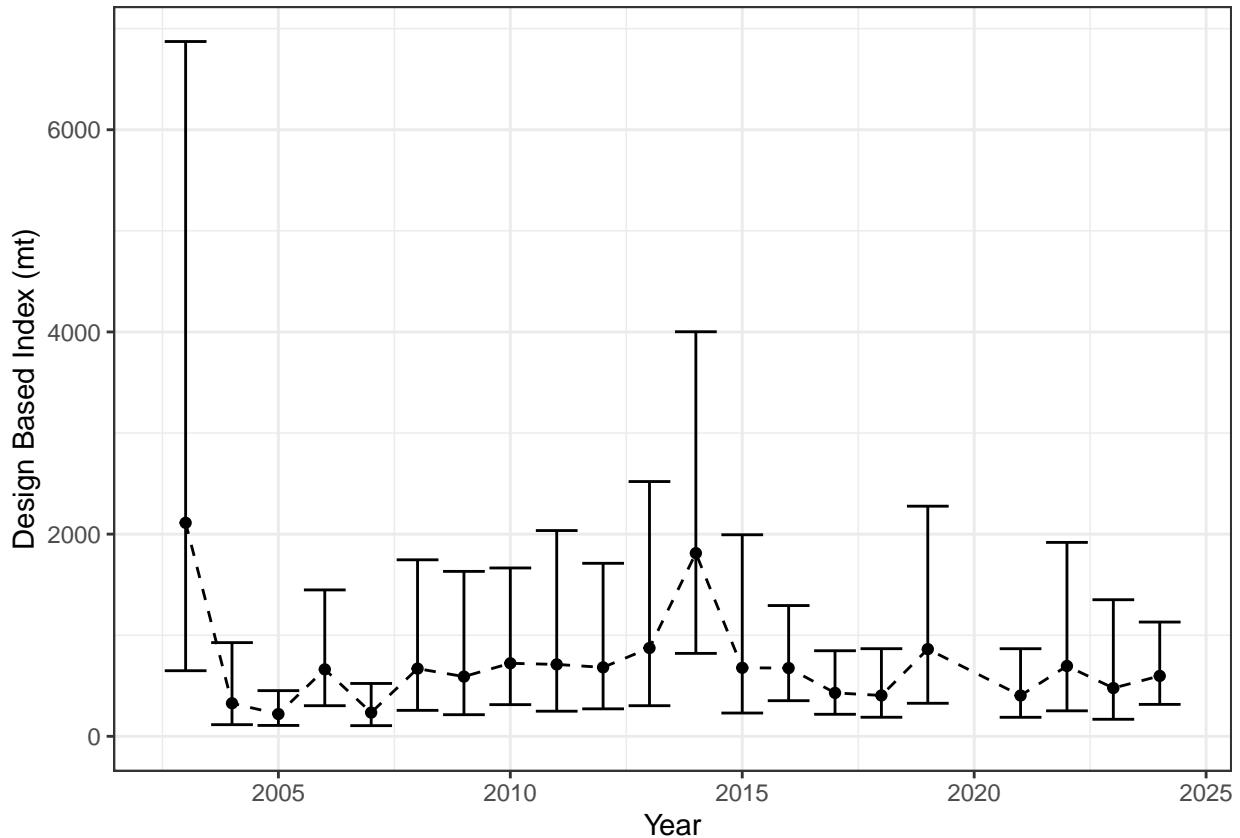
biomass = get_design_based(
  data = catch,
  strata = WGBTStrata,
  dir = file.path(dirname(getwd()), "Data", "NWFSC.Combo_and_Tri_design_based_indices"),
  printfolder = ""
)

## [1] TRUE

```

Plot coastwide

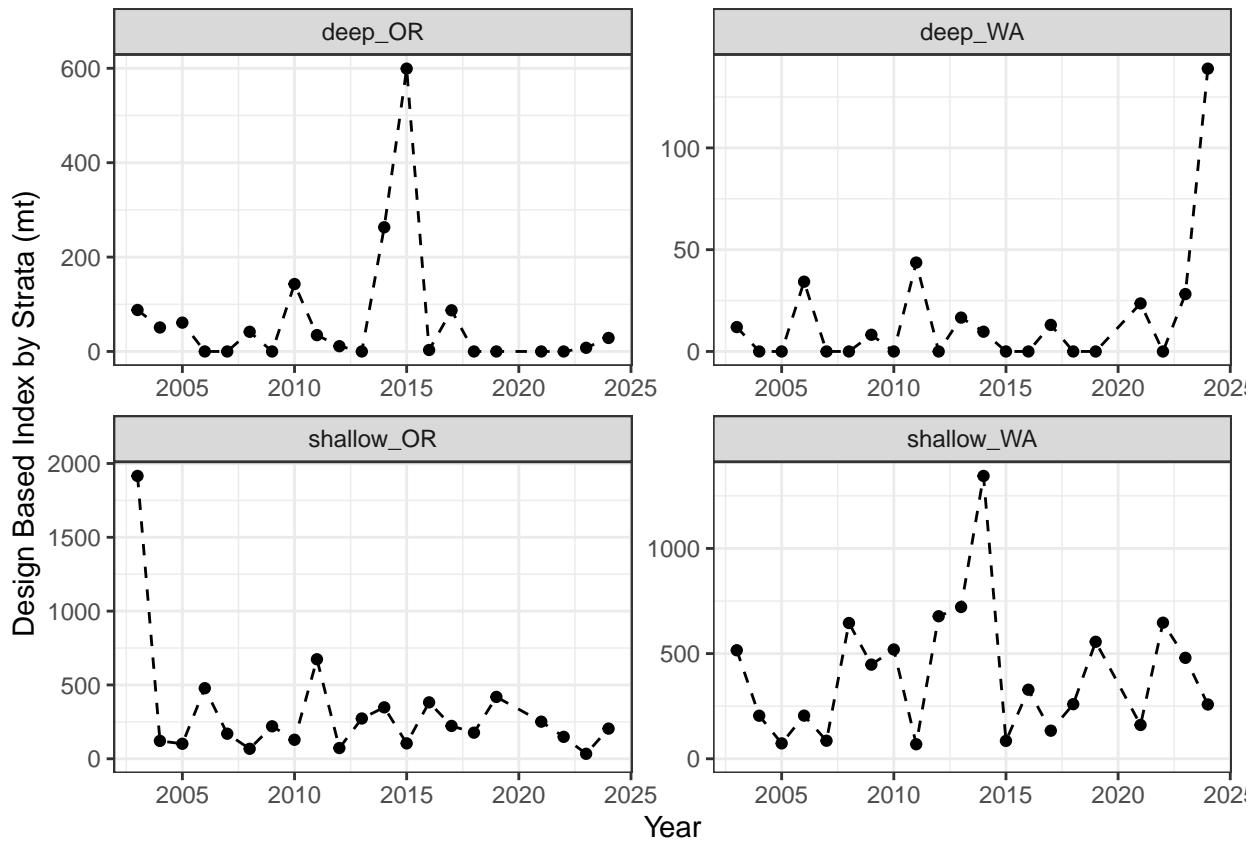
```
plot_index(  
  data = biomass,  
  plot = 1)
```



# that's only about a maximum of 200,500 fish.... very few...

Plot index for each strata

```
plot_index(  
  data = biomass,  
  plot = 2)
```

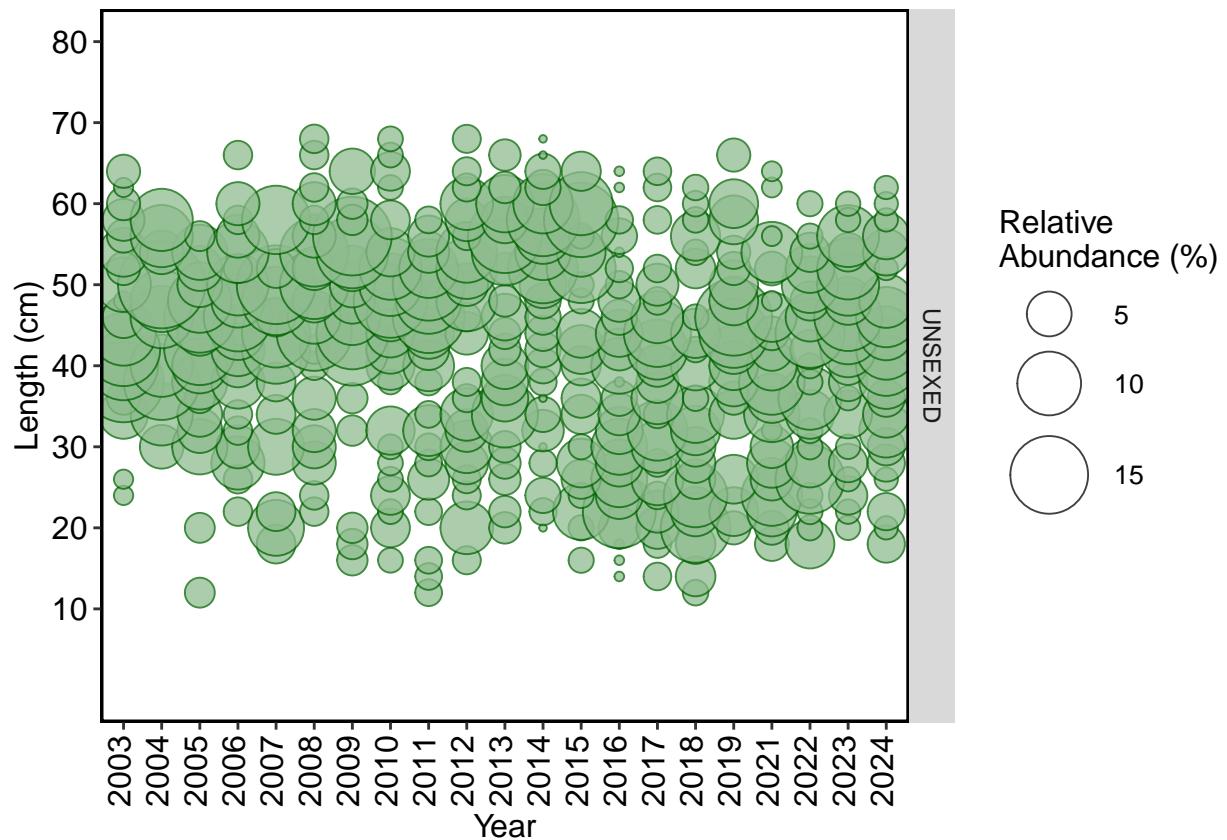


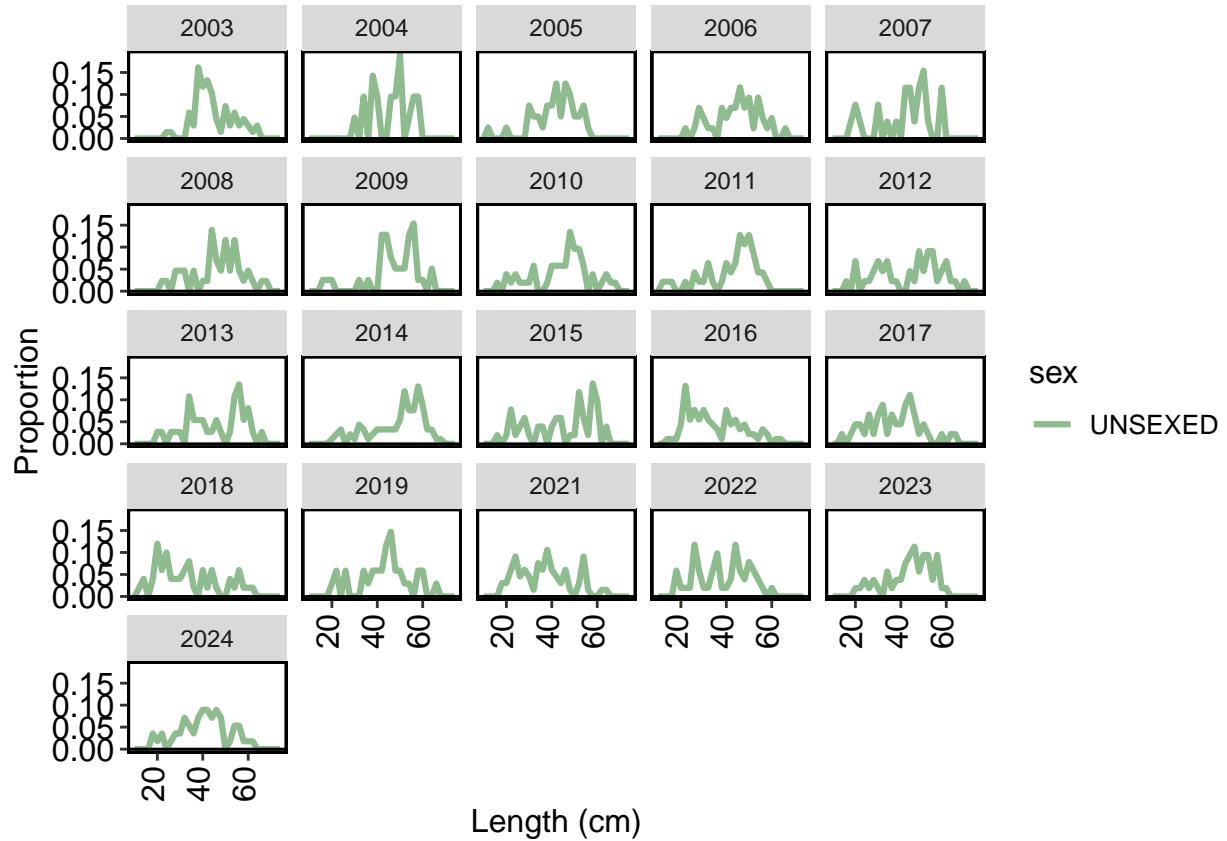
### Length composition data

```
# Expanded length comps are not used for the yelloweye assessment
# length_comps <- get_expanded_comps(
#   bio_data = bio,
#   catch_data = catch,
#   comp_bins = seq(10, 74, 2),
#   strata = WCBTS_strata,
#   comp_column_name = "length_cm",
#   output = "full_expansion_ss3_format",
#   two_sex_comps = FALSE, #single sex model
#   input_n_method = "stewart_hamel")
#
# plot_comps(
#   data = length_comps)

# Use raw length comps, you can tell this is what was used in the previous assessment because whole num
raw_length_comps <- get_raw_comps(
  data = bio,
  comp_bins = seq(10, 74, 2),
  comp_column_name = "length_cm",
  dir = getwd(),
  printfolder = "",
  two_sex_comps = FALSE) #single sex model
```

```
plot_comps(  
  data = raw_length_comps  
)
```





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

#### Marginal age composition data

```
# Expanded age comps are not used in the yelloweye assessment
# age_comps <- get_expanded_comps(
#   bio_data = bio,
#   catch_data = catch,
#   comp_bins = 0:65,
#   strata = WGBTTS_strata,
#   comp_column_name = "age",
#   output = "full_expansion_ss3_format",
#   two_sex_comps = FALSE, #single sex model
#   input_n_method = "stewart_hamel")
#
# plot_comps(
#   data = age_comps)

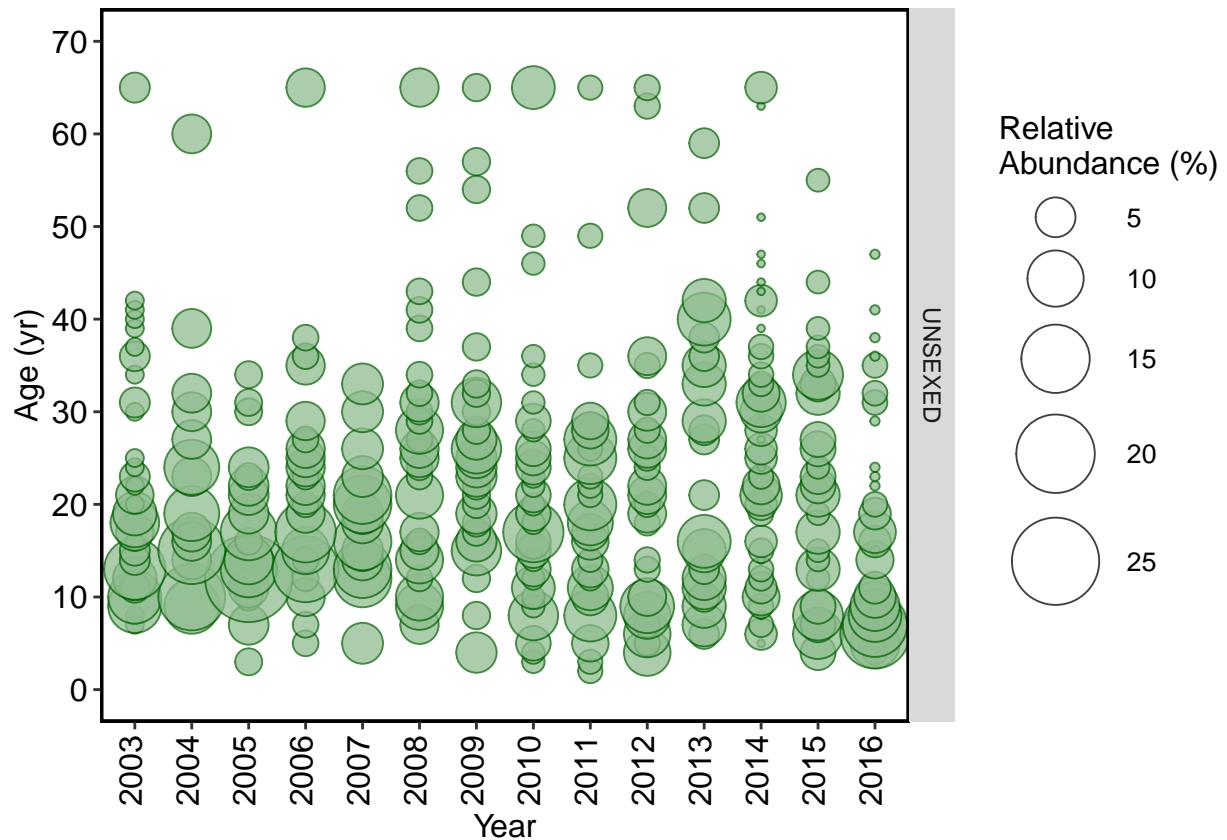
raw_age_comps <- get_raw_comps(
  data = bio,
  comp_bins = 0:65,
```

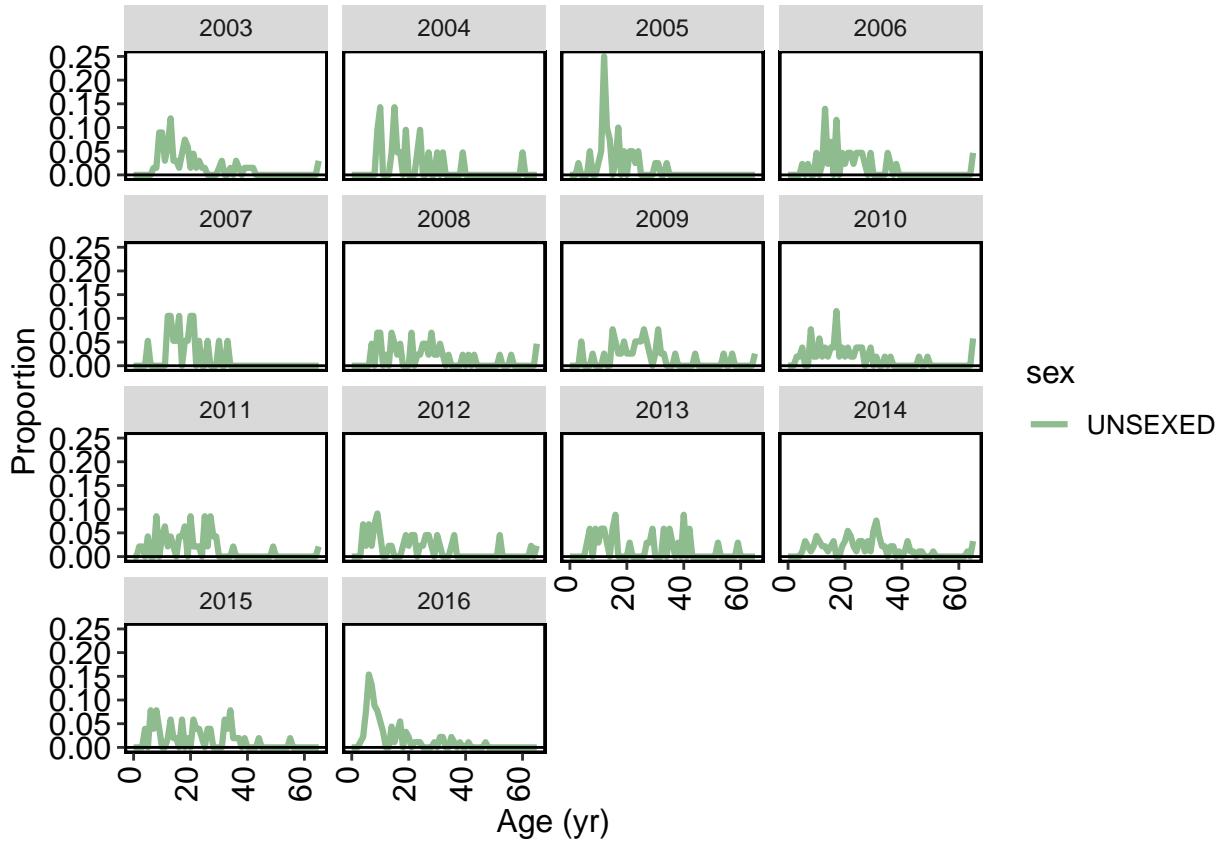
```

comp_column_name = "age",
dir = getwd(),
printfolder = "",
two_sex_comps = FALSE) #single sex model

plot_comps(
  data = raw_age_comps)

```



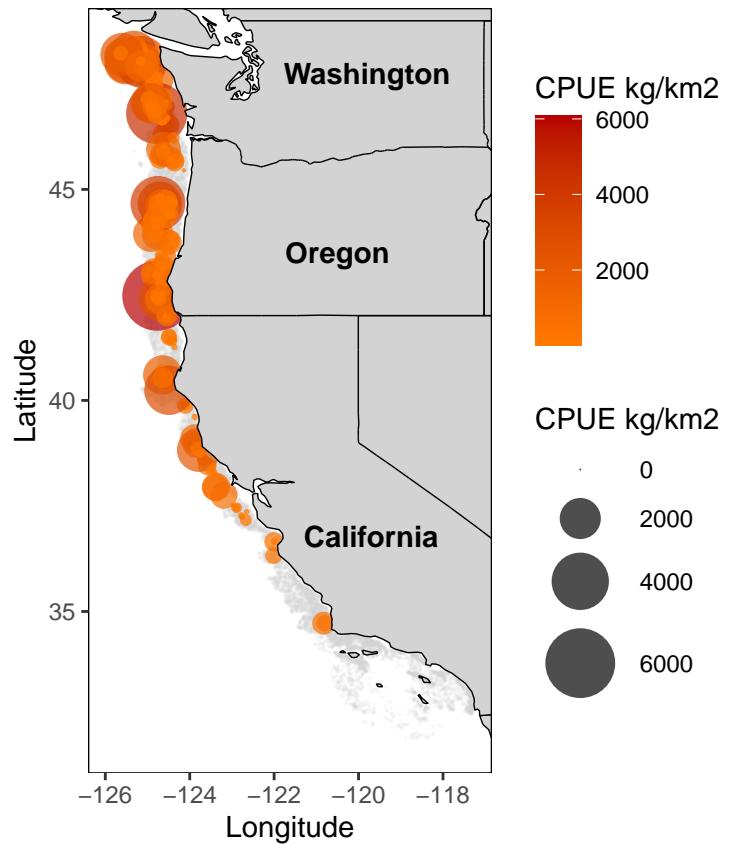


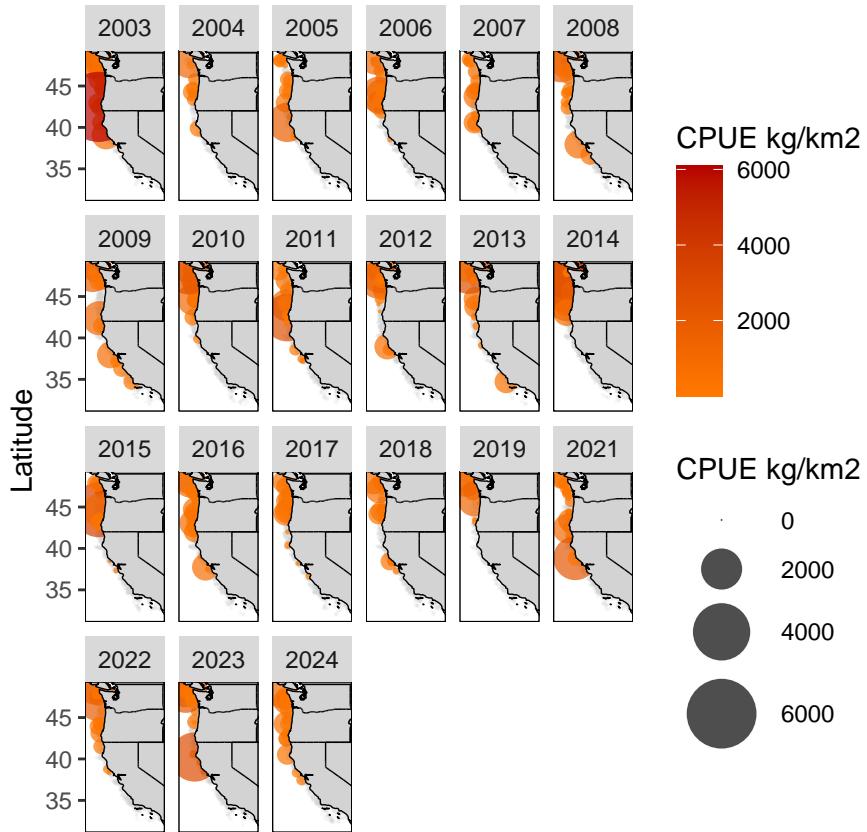
```
## [1] TRUE
## [1] TRUE
## [1] TRUE
## [1] TRUE
```

#### Conditional age-at-length data

```
caal <- SurveyAgeAtLen.fn(
  datAL = bio,
  datTows = catch,
  strat.df = WCGBT_S_strata,
  lgthBins = seq(10, 74, 2),
  ageBins = 0:65,
  dir = file.path(dirname(getwd()), "Data", "NWFSC.Combo_CAAAL"),
  printfolder = "")
```

```
PlotMap.fn(
  dat = catch)
```





### Weight-Length Relationship

```
# Ian said we can just use the nwfsc.combo data and don't need to filter by the same latitudes as the i
wt_len_est <- estimate_weight_length(
  bio,
  col_length = "Length_cm",
  col_weight = "Weight_kg",
  verbose = FALSE
)

wt_len_est

##      sex median_intercept           SD          A          B
## 1 female    7.027898e-06 0.11126214 7.071533e-06 3.254269
## 2 male     7.328479e-06 0.09047821 7.358537e-06 3.233642
## 3 all      7.094611e-06 0.10339147 7.132633e-06 3.247382

plot_weight_length(
  bio,
  dir = getwd(),
  estimates = wt_len_est,
  col_length = "length_cm",
  col_weight = "weight_kg",
  two_sex = FALSE,
  add_save_name = NULL,
  height = 7,
```

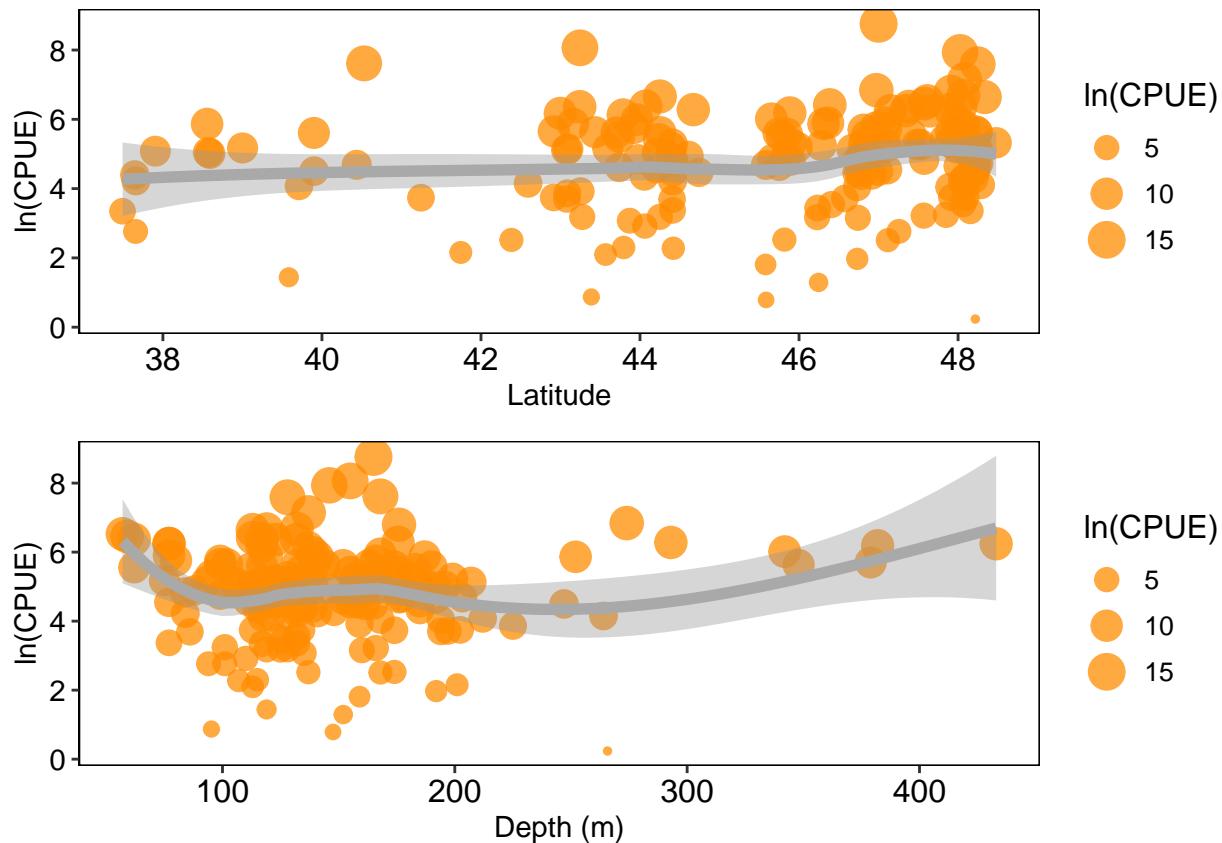
```
width = 7,  
dpi = 300  
)
```

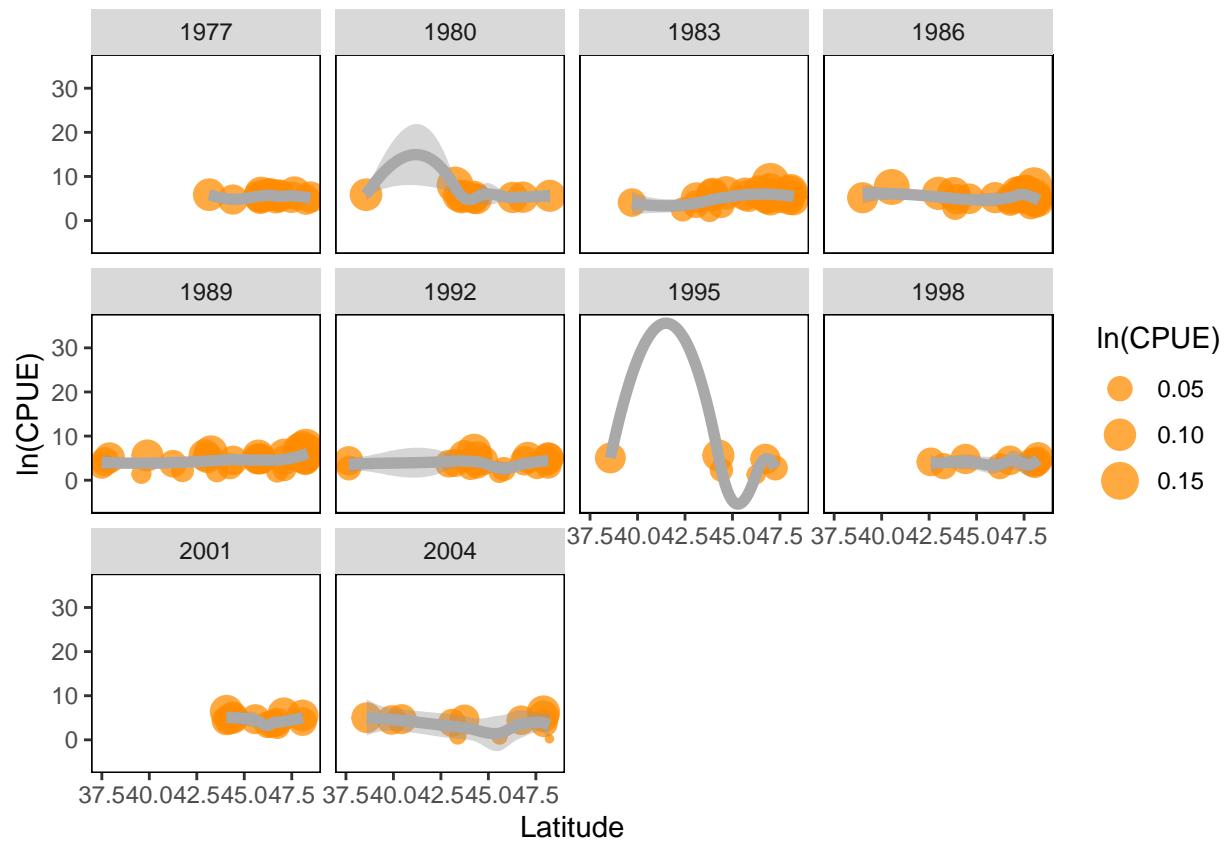
```
## [1] TRUE
```

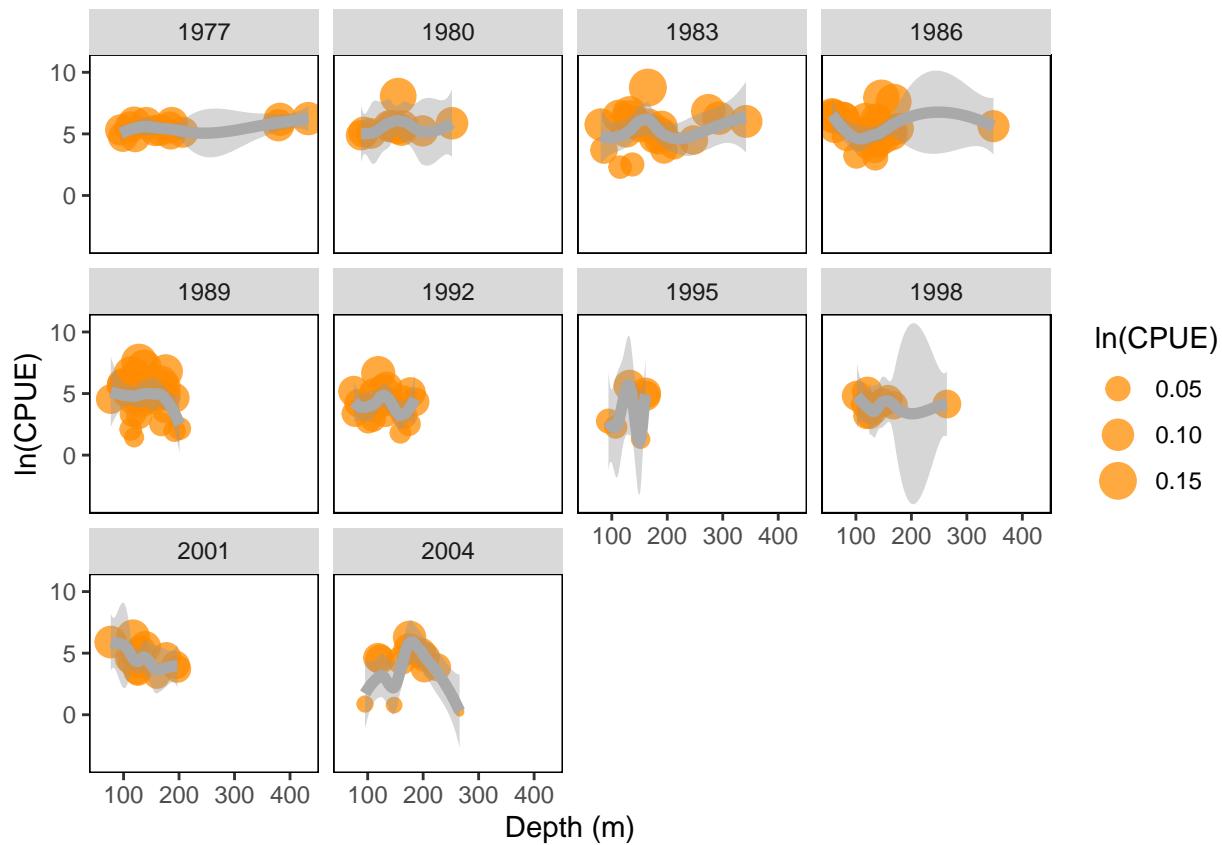
## Triennial Data

Initial pull and plotting of data: Triennial

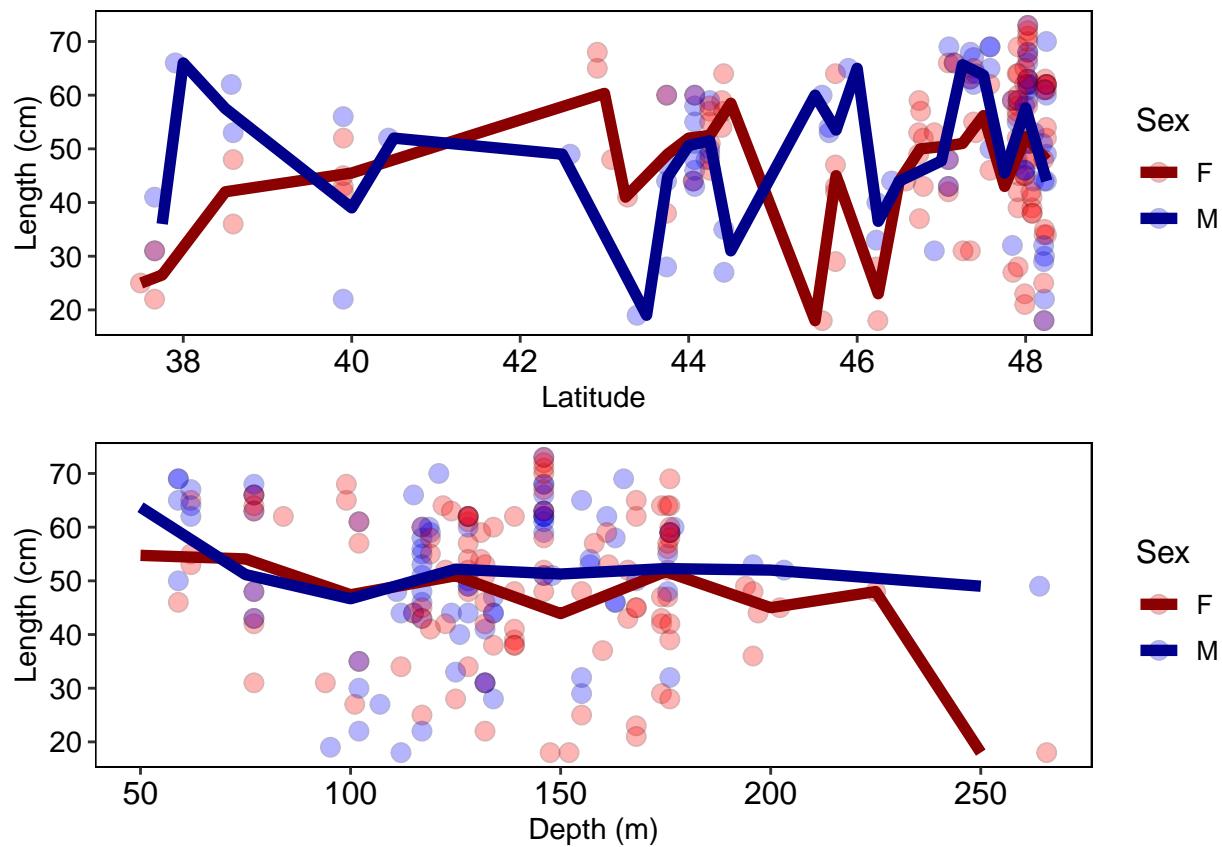
```
catchT = pull_catch(  
  common_name = "yelloweye rockfish",  
  survey = "Triennial")  
  
#this is creating a list, just use $age_data  
bioT = pull_bio(  
  common_name = "yelloweye rockfish",  
  survey = "Triennial")  
  
bioT <- bioT$length_data # Ian said to use length data  
  
plot_cpue(  
  catch = catchT)
```

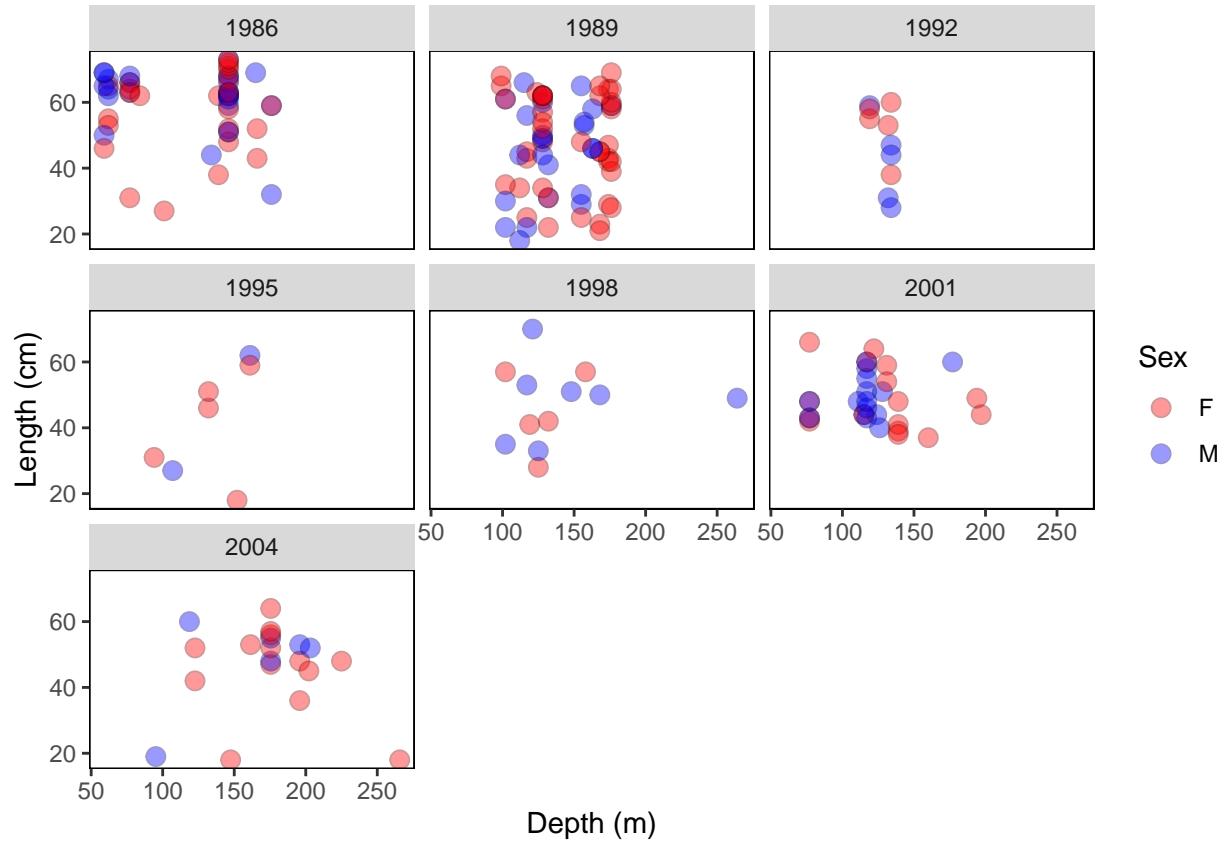


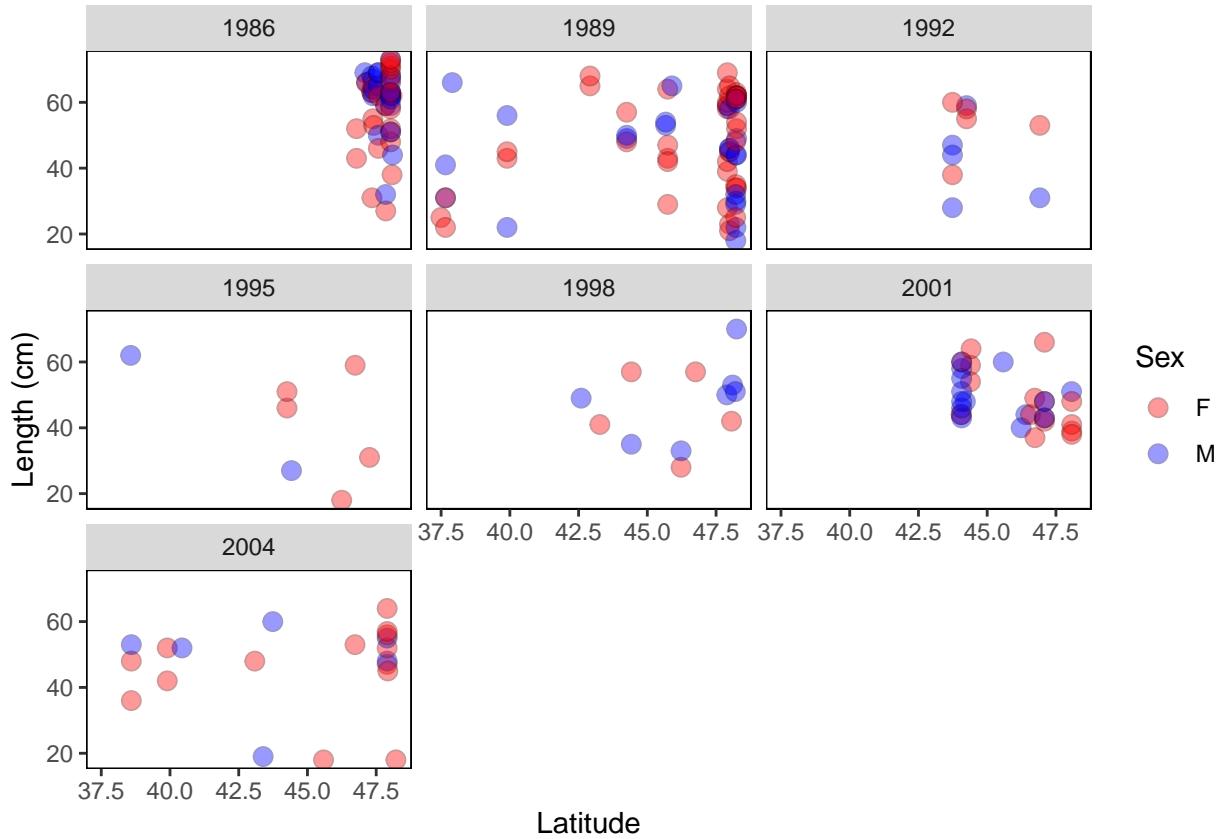




```
plot_bio_patterns(
  bio = bioT,
  col_name = "Length_cm")
```







```

wh_plot_proportion(
  data_catch = catchT,
  data_bio = bioT
)

## [1] "C:/Users/elizabeth.gugliotti/Documents/github_repos/Sebastes_ruberrimus_2025/Rcode/plots/presen"
## [2] "C:/Users/elizabeth.gugliotti/Documents/github_repos/Sebastes_ruberrimus_2025/Rcode/plots/presen"
## [3] "C:/Users/elizabeth.gugliotti/Documents/github_repos/Sebastes_ruberrimus_2025/Rcode/plots/sex_by"
## [4] "C:/Users/elizabeth.gugliotti/Documents/github_repos/Sebastes_ruberrimus_2025/Rcode/plots/sex_by"

```

Calculate designed based index of abundance

```

Triennial_strata = CreateStrataDF.fn(names=c("OR", "WA"),
                                      depths.shallow = c(55, 55),
                                      depths.deep    = c(350, 350),
                                      lats.south     = c(42, 46),
                                      lats.north     = c(46, 49))

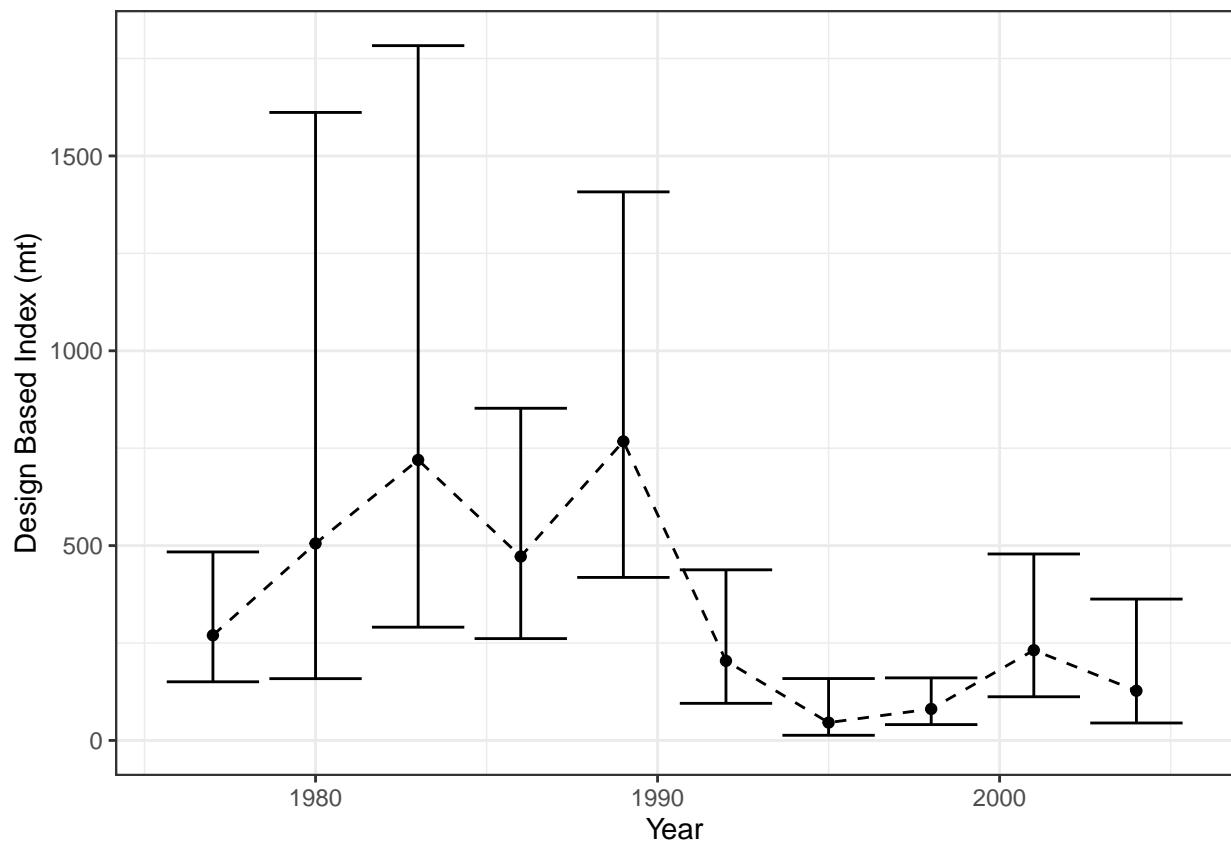
biomassT = get_design_based(
  data = catchT,
  strata = Triennial_strata,
  dir = file.path(dirname(getwd()), "Data", "NWFSC.Combo_and_Tri_design_based_indices"),
  printfolder = "")

```

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

Plot coastwide

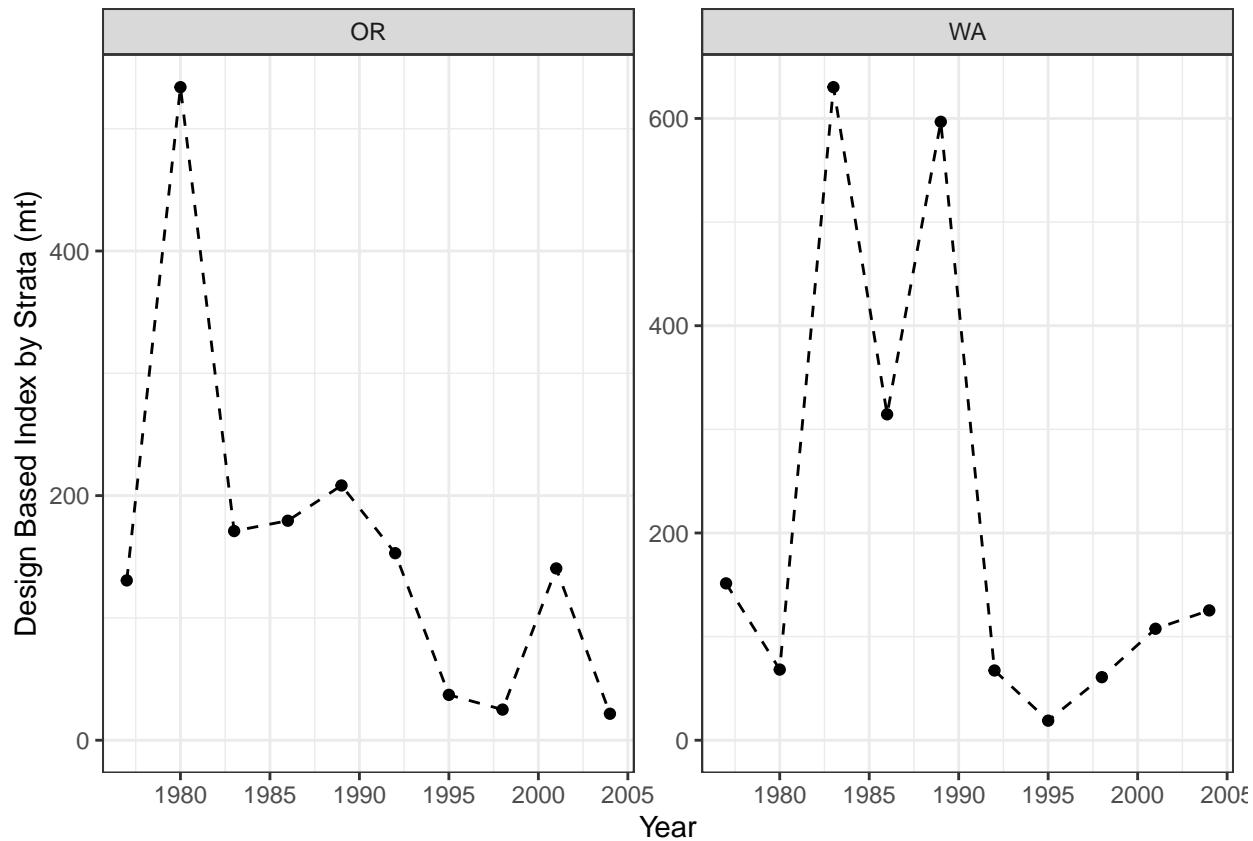
```
plot_index(  
  data = biomassT,  
  plot = 1)
```



```
# not a lot of fish...
```

Plot index for each strata

```
plot_index(  
  data = biomassT,  
  plot = 2)
```



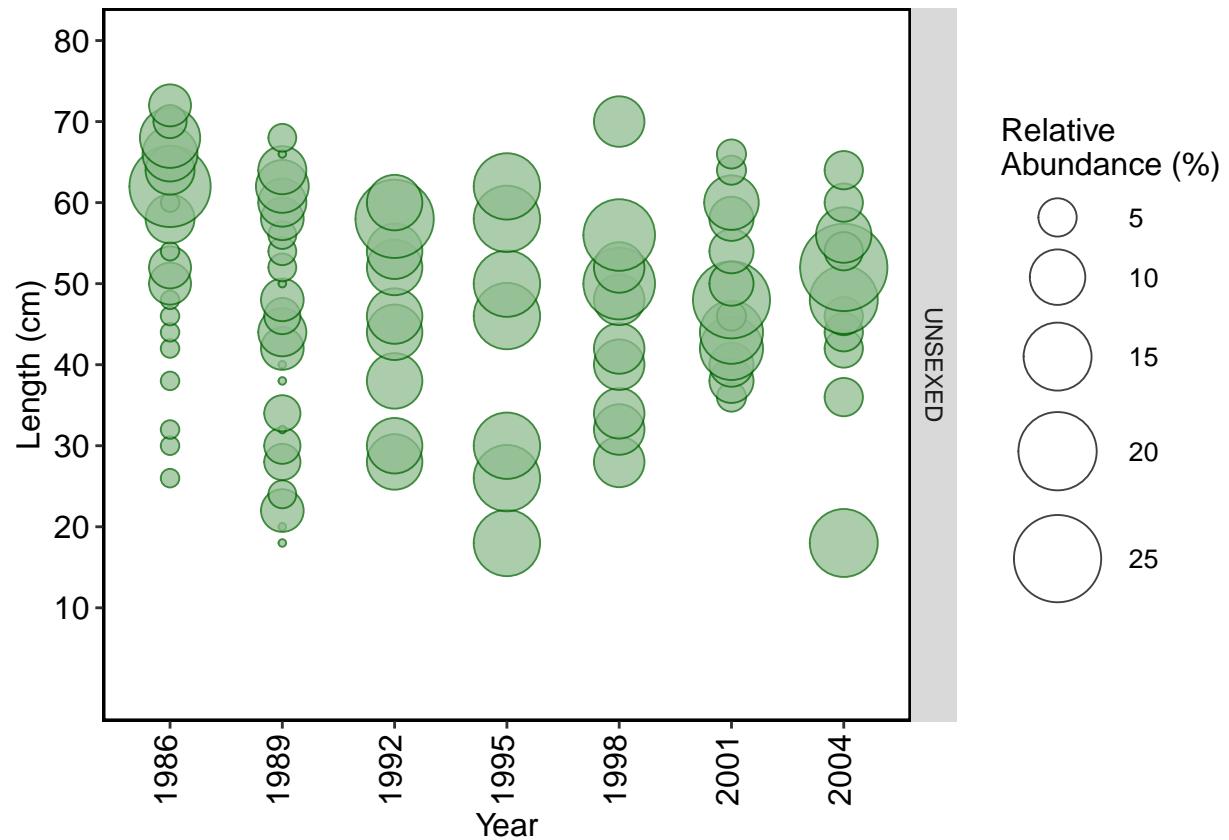
### Length composition data

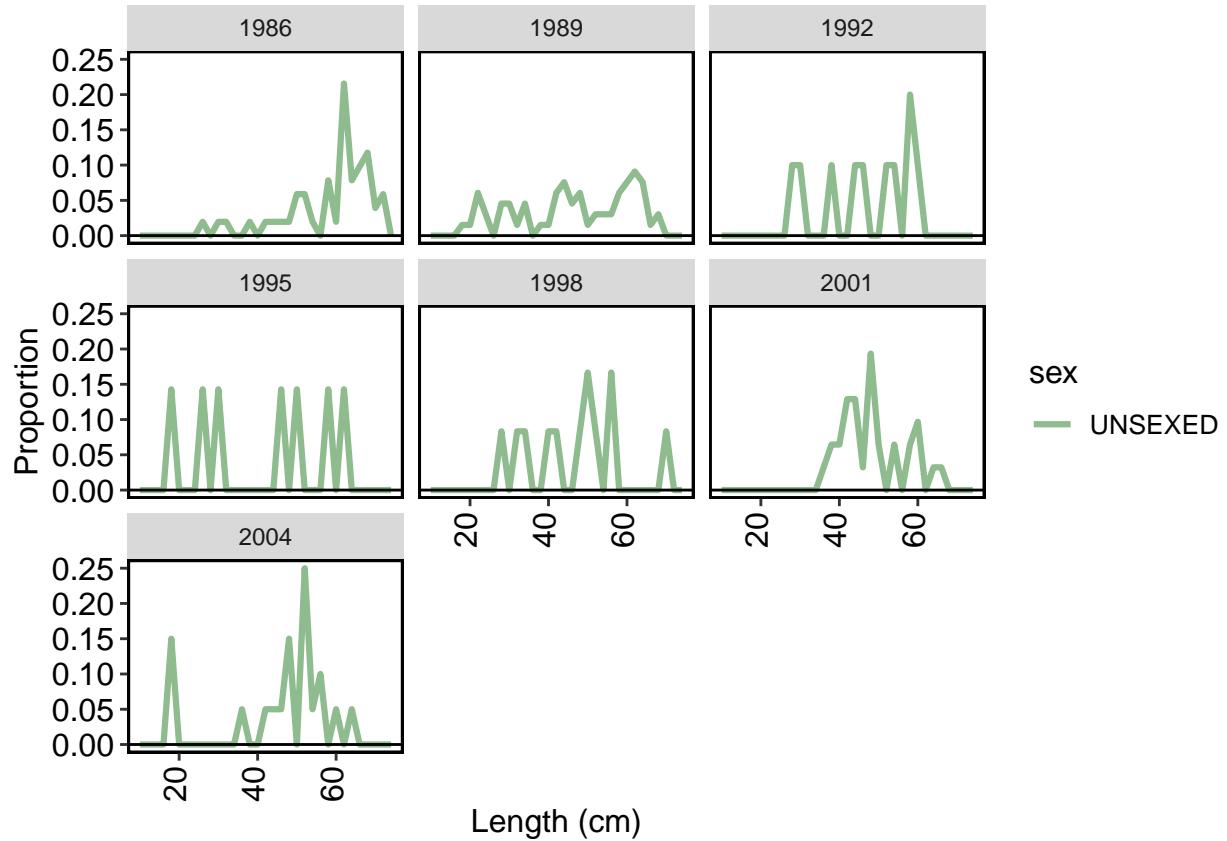
```
# Expanded length comps are not used for the yelloweye assessment
# length_compsT <- get_expanded_comps(
#   bio_data = bioT,
#   catch_data = catchT,
#   comp_bins = seq(10, 74, 2),
#   strata = Triennial_strata,
#   comp_column_name = "length_cm",
#   output = "full_expansion_ss3_format",
#   two_sex_comps = FALSE, #single sex model
#   input_n_method = "stewart_hamel")
#
# plot_comps(
#   data = length_compsT)

raw_length_compsT <- get_raw_comps(
  data = bioT,
  comp_bins = seq(10, 74, 2),
  comp_column_name = "length_cm",
  dir = getwd(),
  printfolder = "",
  two_sex_comps = FALSE) #single sex model

plot_comps(
```

```
data = raw_length_compsT)
```





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

No marginal age composition data for triennial survey

```
#no age data from Triennial survey?

#age_compsT <- get_expanded_comps(
#  bio_data = bioT,
#  catch_data = catchT,
#  comp_bins = 0:65,
#  strata = Triennial_strata,
#  comp_column_name = "age",
#  output = "full_expansion_ss3_format",
#  two_sex_comps = FALSE, #single sex model
#  input_n_method = "stewart_hamel")

#plot_comps(
#  data = age_compsT)

#raw_age_compsT <- get_raw_comps(
#  data = bioT,
```

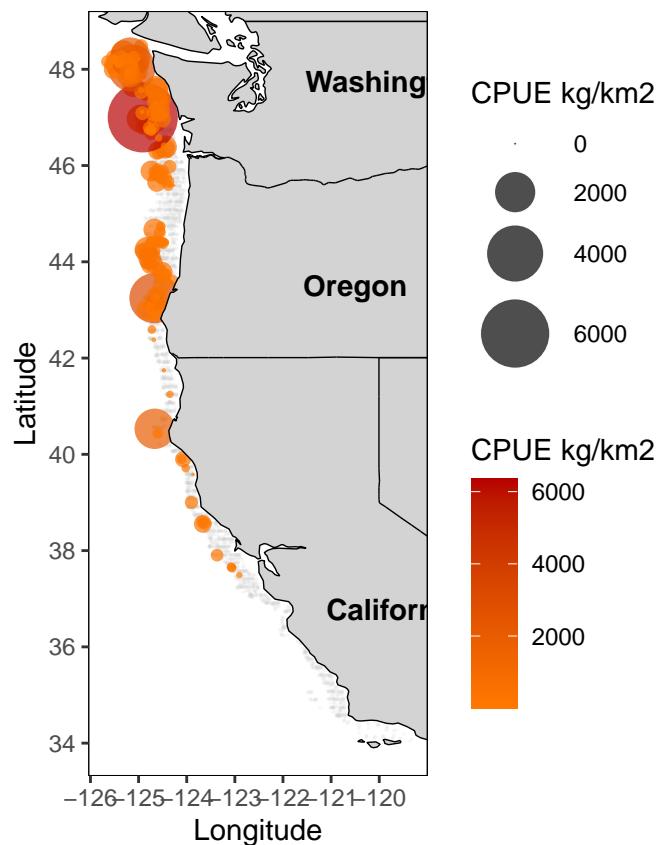
```
#     comp_bins = 0:65,
#     comp_column_name = "age",
#     two_sex_comps = FALSE) #single sex model
```

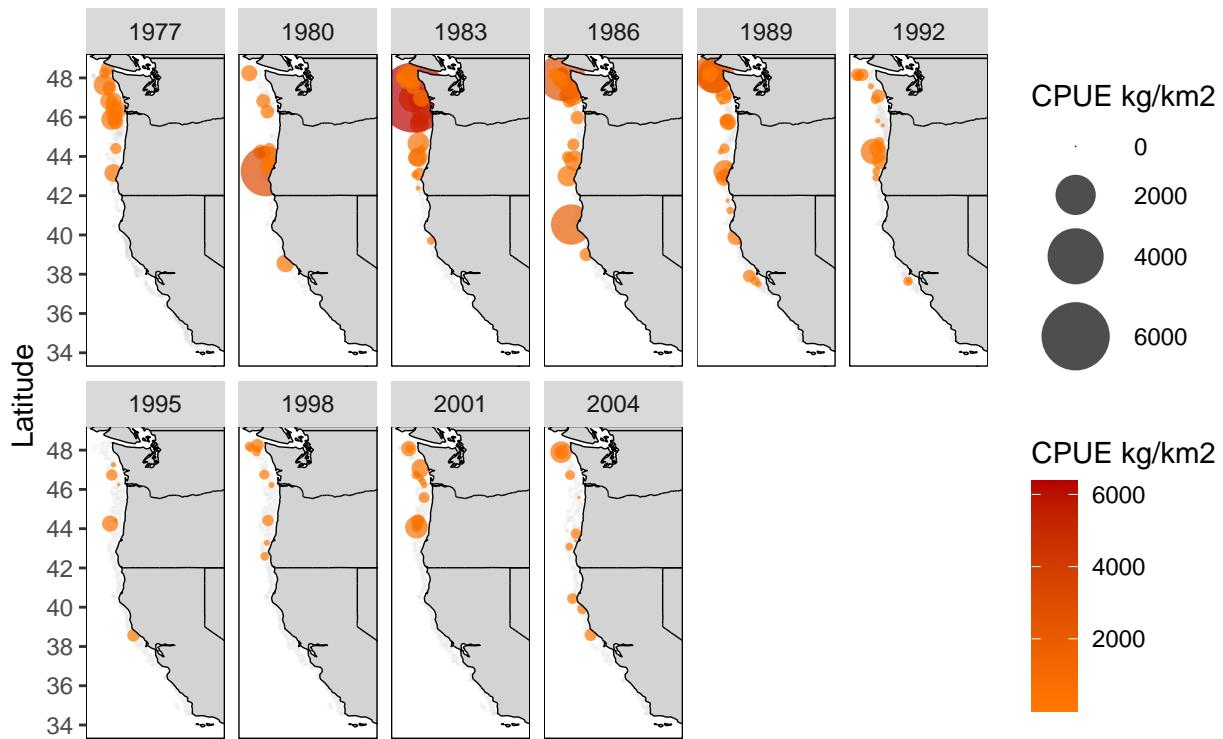
No conditional age-at-length data for triennial survey

```
#no age data from Triennial survey?

#caalT <- SurveyAgeAtLen.fn(
#  datAL = bioT,
#  datTows = catchT,
#  strat.df = Triennial_strata,
#  lgthBins = seq(10, 74, 2),
#  ageBins = 0:65)

PlotMap.fn(
  dat = catchT)
```





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

## WCGOP Fisheries Discards

```
gemm_data <- pull_gemm("yelloweye rockfish",
                        dir = file.path(dirname(getwd()), "Data"),
                        verbose = TRUE)
```

```
head(gemm_data, n = 20)
```

	cv	grouping	sector	species
## 29	NA	Yelloweye rockfish	At-Sea Hake CP	Yelloweye Rockfish
## 166	NA	Yelloweye rockfish	At-Sea Hake MCSV	Yelloweye Rockfish
## 239	NA	Yelloweye rockfish	California Recreational	Yelloweye Rockfish
## 371	NA	Yelloweye rockfish	CS - Bottom Trawl	Yelloweye Rockfish
## 639	NA	Yelloweye rockfish	CS EM - Bottom Trawl	Yelloweye Rockfish
## 804	NA	Yelloweye rockfish	CS EM - Pot	Yelloweye Rockfish
## 933	NA	Yelloweye rockfish	Incidental	Yelloweye Rockfish
## 1226	0.2010	Yelloweye rockfish	LE Sablefish - Hook & Line	Yelloweye Rockfish
## 1313	0.7071	Yelloweye rockfish	LE Sablefish - Pot	Yelloweye Rockfish
## 1393	NA	Yelloweye rockfish	Midwater Hake	Yelloweye Rockfish
## 1451	NA	Yelloweye rockfish	Midwater Rockfish	Yelloweye Rockfish
## 1648	0.1962	Yelloweye rockfish	Nearshore	Yelloweye Rockfish
## 1953	0.4029	Yelloweye rockfish	OA Fixed Gear - Hook & Line	Yelloweye Rockfish
## 2064	NA	Yelloweye rockfish	Oregon Recreational	Yelloweye Rockfish
## 2297	NA	Yelloweye rockfish	Research	Yelloweye Rockfish

	NA Yelloweye rockfish	Tribal Shoreside Yelloweye Rockfish
## 2411	NA Yelloweye rockfish	Washington Recreational Yelloweye Rockfish
## 2449	NA Yelloweye rockfish	California Recreational Yelloweye Rockfish
## 2734	NA Yelloweye rockfish	CS - Bottom Trawl Yelloweye Rockfish
## 2828	NA Yelloweye rockfish	CS EM - Bottom Trawl Yelloweye Rockfish
## 3133	NA Yelloweye rockfish	
	total_discard_and_landings_mt	total_discard_mt
## 29	0.008090189	0.008090189
## 166	0.005692350	0.001974691
## 239	23.110335868	22.226033249
## 371	0.331968730	0.032594694
## 639	0.079833076	0.0000000000
## 804	0.000907194	0.0000000000
## 933	0.056699628	0.0000000000
## 1226	4.959751182	4.957029600
## 1313	0.013064238	0.005353089
## 1393	0.009554114	0.000028577
## 1451	0.013154508	0.000000195
## 1648	3.823393417	3.823393417
## 1953	4.541011780	4.536022212
## 2064	15.252869152	15.002164320
## 2297	2.547652171	0.0000000000
## 2411	8.510387372	0.0000000000
## 2449	6.134381586	5.936130949
## 2734	11.444385043	10.392699488
## 2828	0.736515570	0.013035885
## 3133	0.027669418	0.0000000000
	total_discard_with_mort_rates_applied_and_landings_mt	
## 29		0.008090189
## 166		0.005692350
## 239		9.588233406
## 371		0.331968730
## 639		0.079833076
## 804		0.000907194
## 933		0.056699628
## 1226		4.959751182
## 1313		0.013064238
## 1393		0.009554114
## 1451		0.013154508
## 1648		1.785947257
## 1953		4.541011780
## 2064		3.903488643
## 2297		2.547652171
## 2411		8.510387372
## 2449		0.198250637
## 2734		3.801367438
## 2828		0.736515570
## 3133		0.027669418
	total_discard_with_mort_rates_applied_mt	total_landings_mt type year
## 29	0.008090189	0.000000000 groundfish 2023
## 166	0.001974691	0.003717658 groundfish 2023
## 239	8.703930788	0.884302619 groundfish 2023
## 371	0.032594694	0.299374036 groundfish 2023
## 639	0.000000000	0.079833076 groundfish 2023
## 804	0.000000000	0.000907194 groundfish 2023

## 933	0.000000000	0.056699628 groundfish 2023
## 1226	4.957029600	0.002721582 groundfish 2023
## 1313	0.005353089	0.007711149 groundfish 2023
## 1393	0.000028577	0.009525538 groundfish 2023
## 1451	0.000000195	0.013154314 groundfish 2023
## 1648	1.785947257	0.000000000 groundfish 2023
## 1953	4.536022212	0.004989567 groundfish 2023
## 2064	3.652783811	0.250704832 groundfish 2023
## 2297	0.000000000	0.000000000 groundfish 2023
## 2411	0.000000000	8.510387372 groundfish 2023
## 2449	0.000000000	0.198250637 groundfish 2023
## 2734	2.749681884	1.051685555 groundfish 2022
## 2828	0.013035885	0.723479685 groundfish 2022
## 3133	0.000000000	0.027669418 groundfish 2022