

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?

Initial pull and plotting of data: WCGBTS

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

```
## i Output will not be saved in dir because dir = NULL.
```

```
## i Pulling catch data for yelloweye rockfish.
```

```
## There are 374 positive tows across all years pulled.
```

```
## i There were 42 positive tows with non-satisfactory tow performance (e.g., no area swept estimate, no
```

```
##
```

```
## i There were 1 positive tows from stations that have been removed from the standard station list.
```

```
##
```

```
## There are 331 positive tows remaining across all years after standard  
## filtering.
```

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

```
## i Output will not be saved in dir because dir = NULL.
```

```
## i Pulling biological data for yelloweye rockfish.
```

```
## i There were 1167 biological samples pulled.
```

```
## i There were 117 biological samples with non-satisfactory tow performance (e.g., no area swept estimate,
```

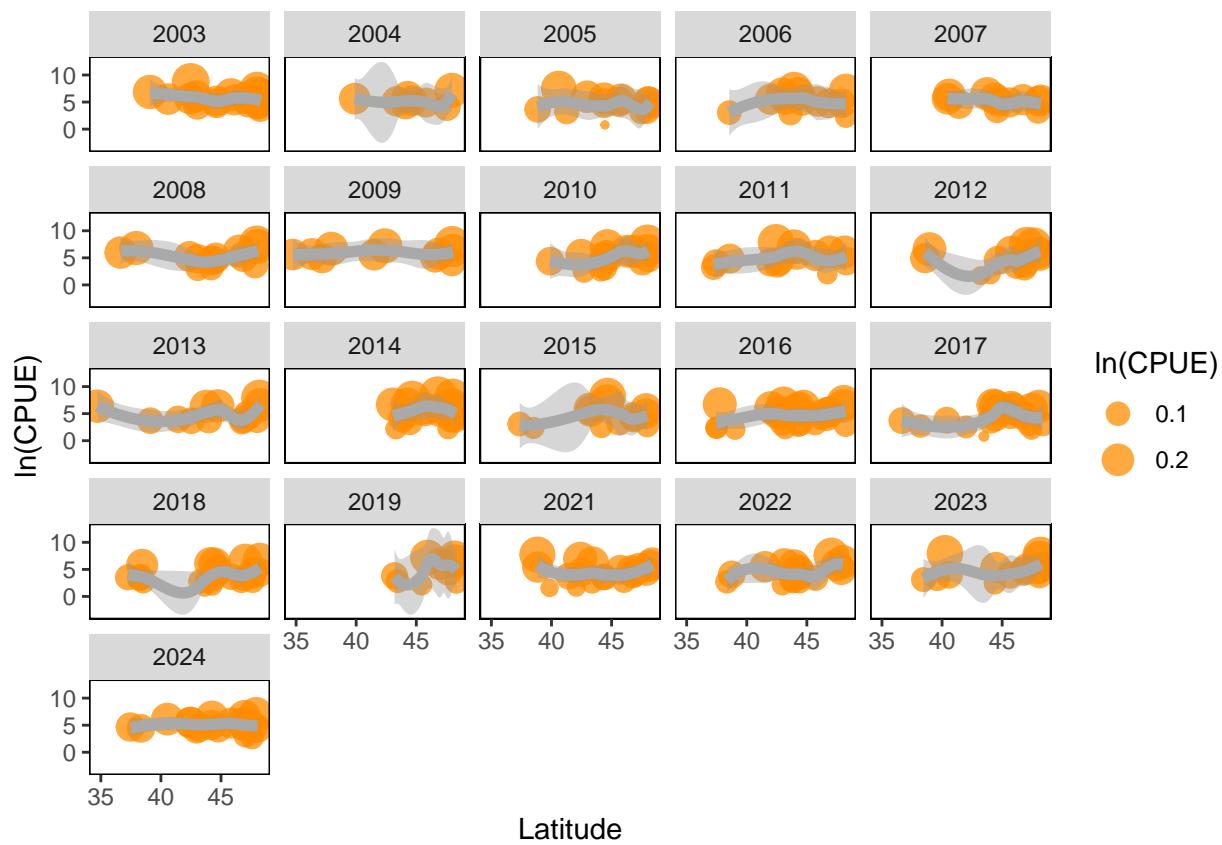
```
## i There were 1 biological samples from stations that have been removed from the standard station list
```

```
## i There were 1049 biological samples remaining after applying standard filtering.
```

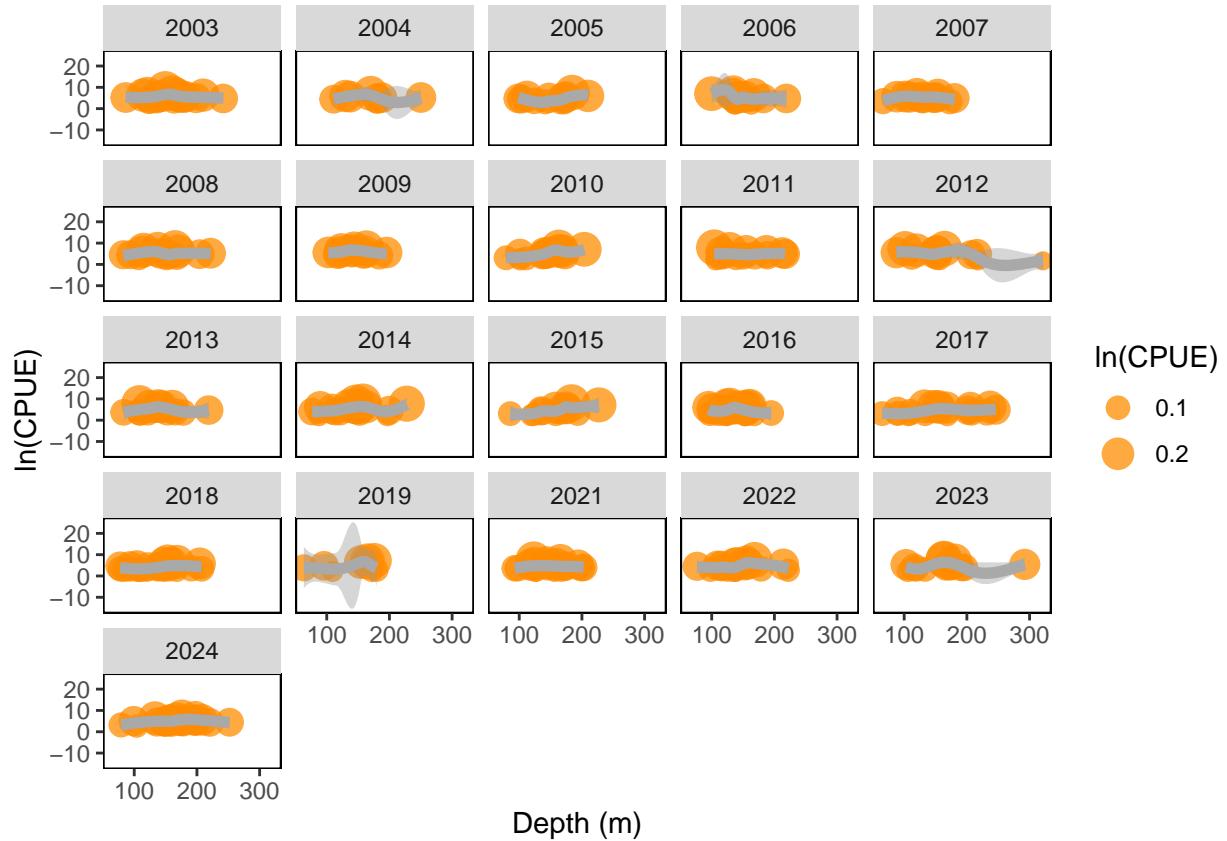
```
plot_cpue(  
  catch = catch)
```

```
## i Output will not be saved in dir because dir = NULL.
```

```
## 'geom_smooth()' using formula = 'y ~ x' 'geom_smooth()' using formula = 'y ~ x' 'geom_smooth()' using
```

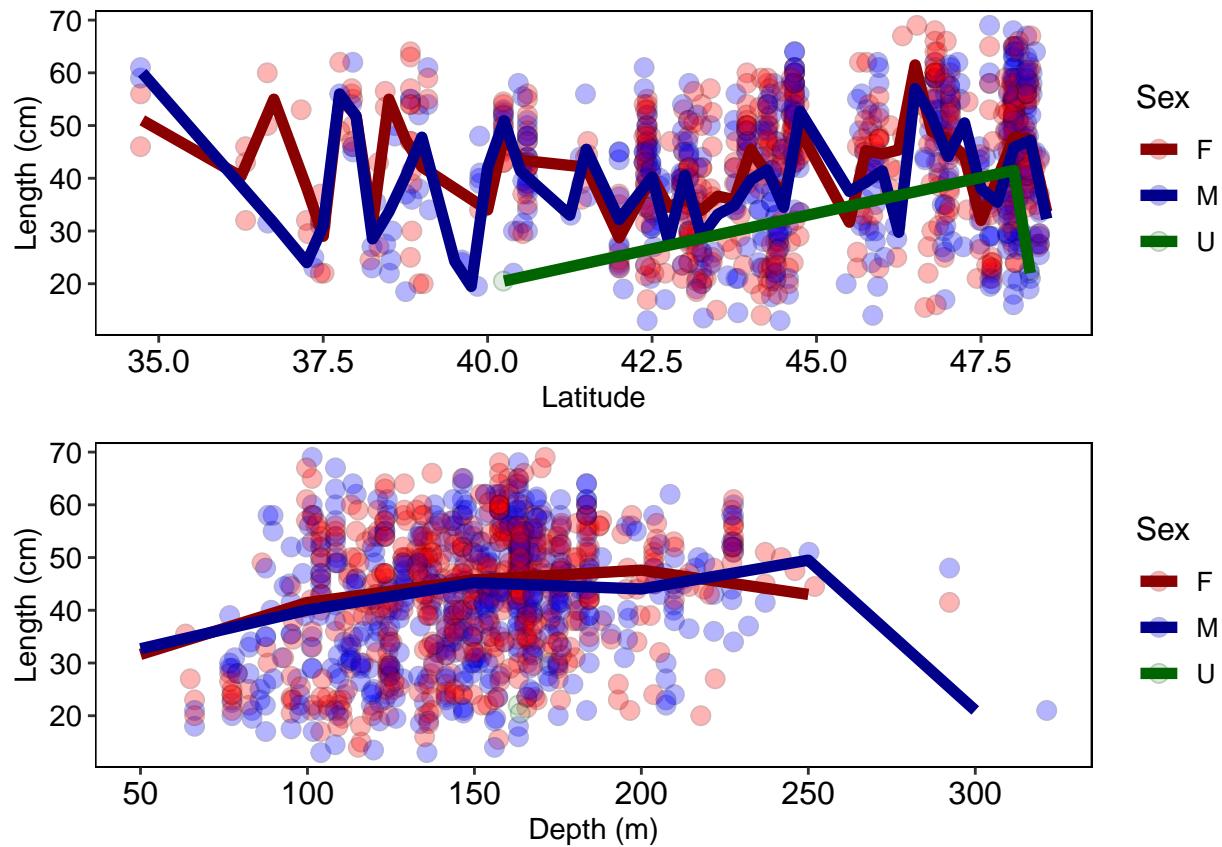


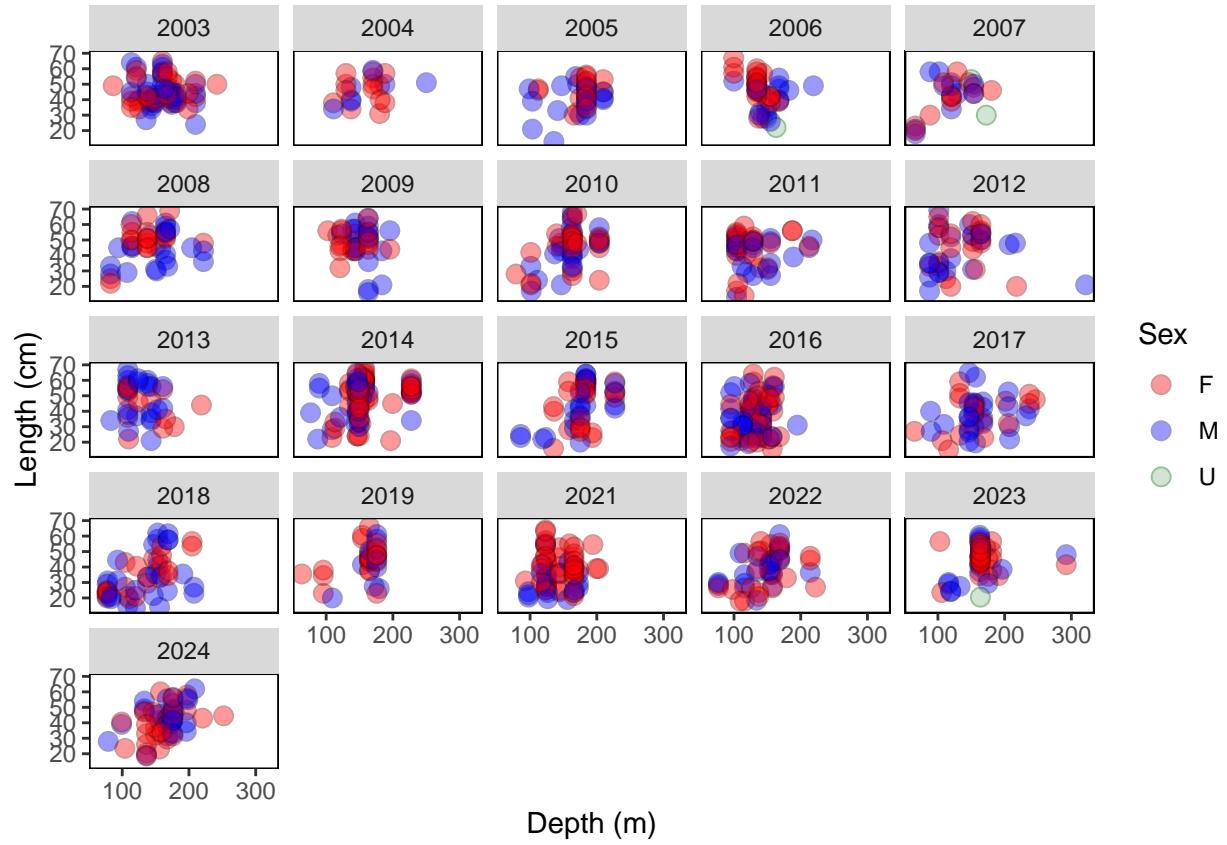
```
## `geom_smooth()` using formula = 'y ~ x'
```

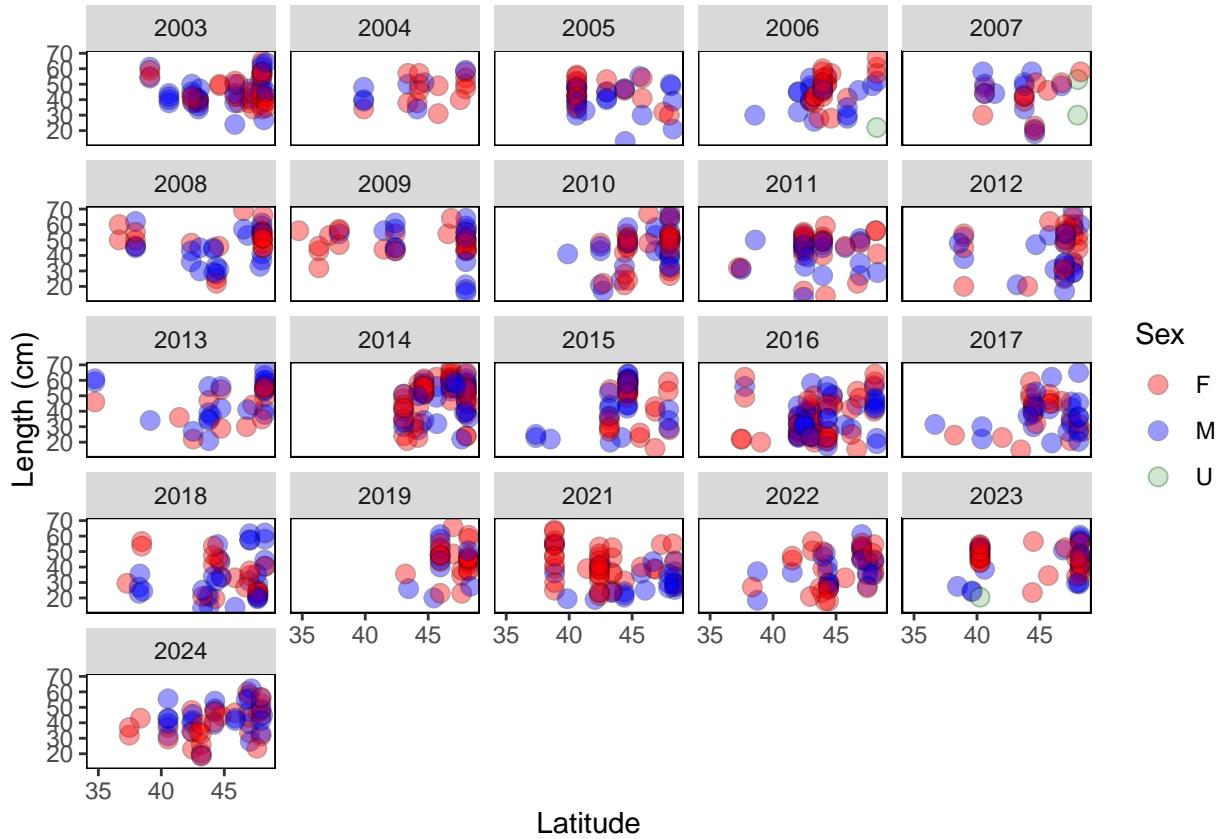


```
plot_bio_patterns(
  bio = bio,
  col_name = "Length_cm")
```

```
## i Output will not be saved in dir because dir = NULL.
```







```
wh_plot_proportion(
  data_catch = catch,
  data_bio = bio
)
```

```
## [1] "/Users/morgan/Documents/GitHub/Sebastes_ruberrimus_2025/Rcode/plots/presence-absence_by_depth.png"
## [2] "/Users/morgan/Documents/GitHub/Sebastes_ruberrimus_2025/Rcode/plots/presence-absence_by_latitude.png"
## [3] "/Users/morgan/Documents/GitHub/Sebastes_ruberrimus_2025/Rcode/plots/sex_by_depth.png"
## [4] "/Users/morgan/Documents/GitHub/Sebastes_ruberrimus_2025/Rcode/plots/sex_by_latitude.png"
```

Define the strata

```
WCGBTS_strata <- 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)
)
```

Calculate designed based index of abundance

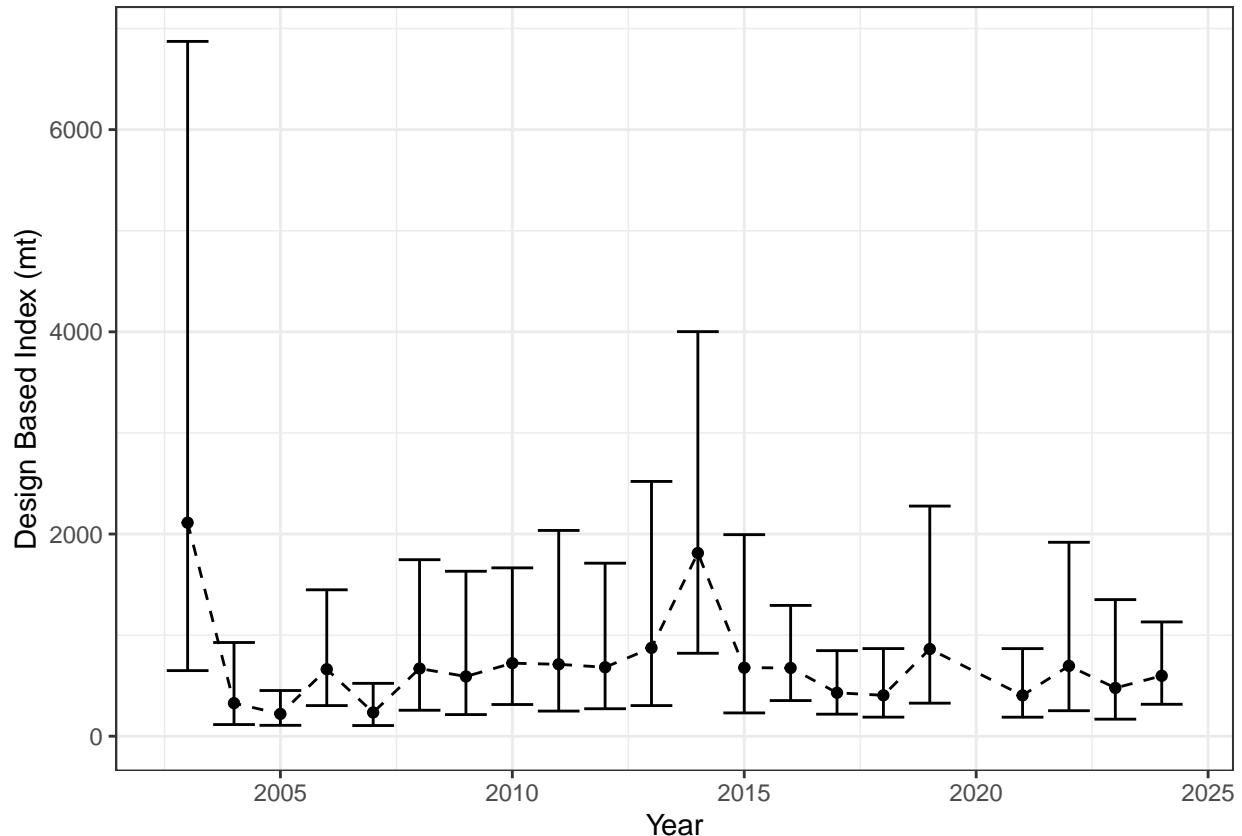
```
biomass = get_design_based(
  data = catch,
  strata = WCGBTS_strata)
```

```
## i Output will not be saved in dir because dir = NULL.  
## Joining with 'by = join_by(stratum)'
```

Plot coastwide

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

```
## i Output will not be saved in dir because dir = NULL.
```

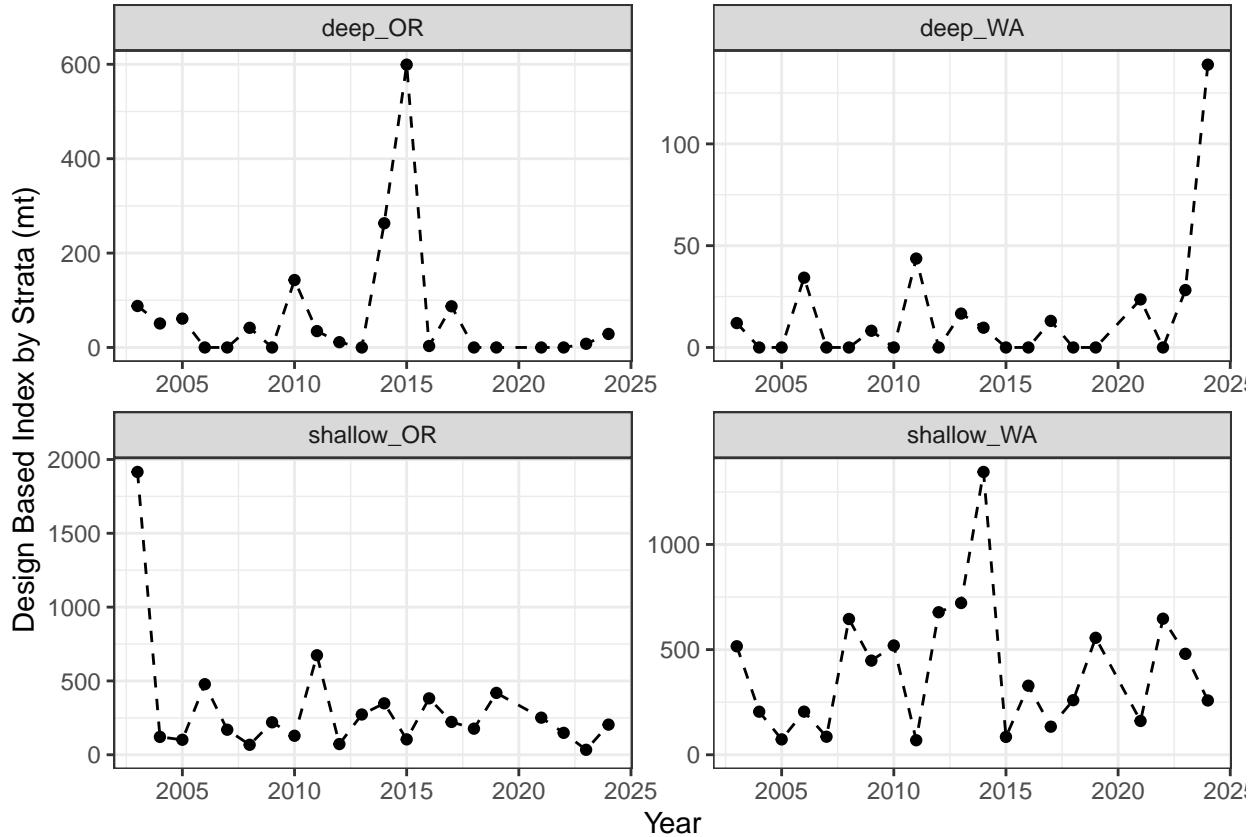


```
# that's only about a maximum of 200,500 fish.... very few...
```

Plot index for each strata

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

```
## i Output will not be saved in dir because dir = NULL.
```



Length composition data

```
length_comps <- get_expanded_comps(
  bio_data = bio,
  catch_data = catch,
  comp_bins = seq(10, 74, 2),
  strata = WCGBTS_strata,
  comp_column_name = "length_cm",
  output = "full_expansion_ss3_format",
  two_sex_comps = FALSE, #single sex model
  input_n_method = "stewart_hamel")

## i Output will not be saved in dir because dir = NULL.

## i There are 0% of records that are less than the minimum composition bin. These
##   fish will be added to the minimum bin.

## i There are 0% of records that are greater than the maximum composition bin.
##   These fish will be added to the maximum bin.

## i There are 1 tows where fish were observed but not sampled.
## These tows comprise 0.4 percent of the total catch numbers.
## Only measured fished in the bio_data file are used for composition expansions.

## i There were 165 biological samples removed out of 1049 after filtering for strata.
```

```

## Joining with 'by = join_by(year, bin)'
## i Output will not be saved in dir because dir = NULL.
## Sample size will be calculated based on stewart_hamel.
## The unique samples by tow for shelfrock is 2.43.

```

```

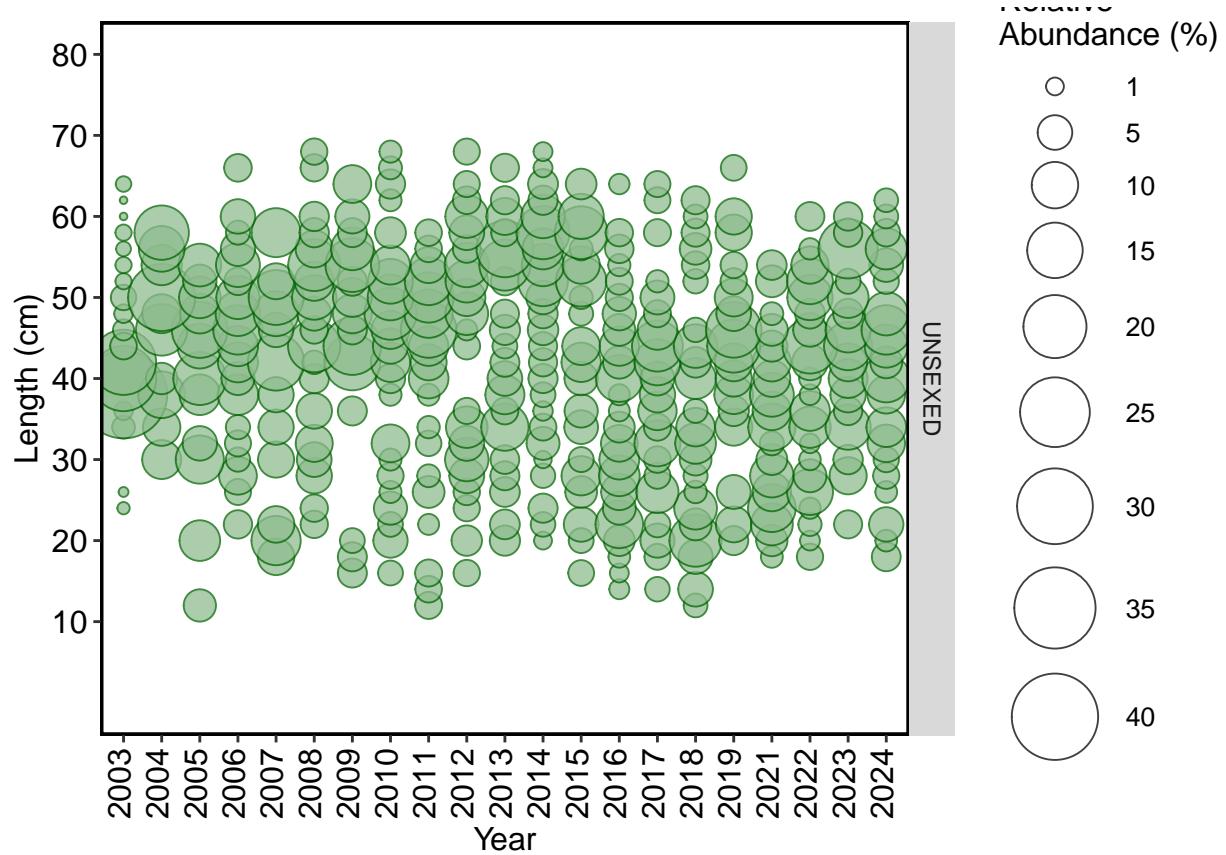
plot_comps(
  data = length_comps)

```

```

## i Output will not be saved in dir because dir = NULL.

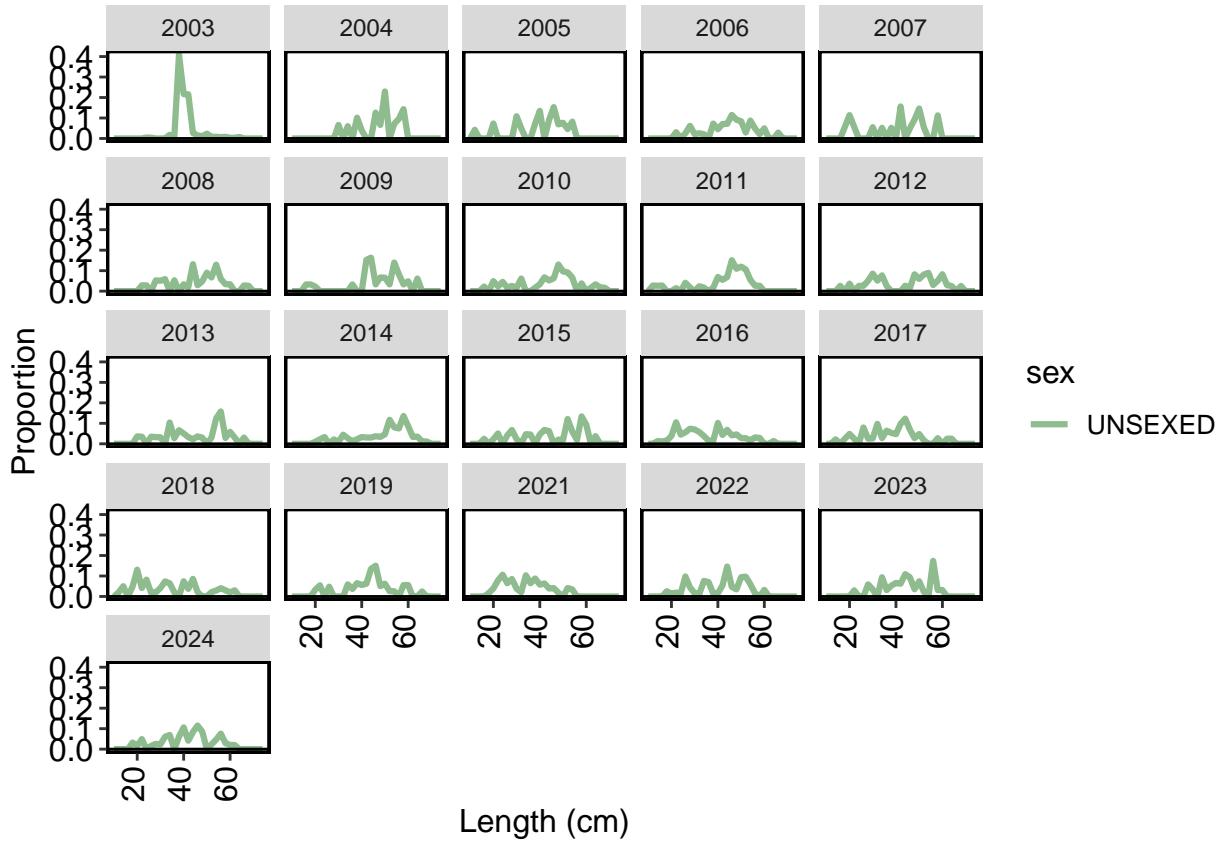
```



```

## Warning: No shared levels found between 'names(values)' of the manual scale and the
## data's fill values.

```



```
raw_length_comps <- get_raw_comps(
  data = bio,
  comp_bins = seq(10, 74, 2),
  comp_column_name = "length_cm",
  two_sex_comps = FALSE) #single sex model

## i Output will not be saved in dir because dir = NULL.
## i Output will not be saved in dir because dir = NULL.
## Sample size will be calculated based on stewart_hamel.The unique samples by tow for shelfrock is 2.4
```

Marginal age composition data

```
age_comps <- get_expanded_comps(
  bio_data = bio,
  catch_data = catch,
  comp_bins = 0:65,
  strata = WCGBTStrata,
  comp_column_name = "age",
  output = "full_expansion_ss3_format",
  two_sex_comps = FALSE, #single sex model
  input_n_method = "stewart_hamel")
```

```
## i Output will not be saved in dir because dir = NULL.

## i There are 0% of records that are less than the minimum composition bin. These
##   fish will be added to the minimum bin.
```

```

## i There are 2.2% of records that are greater than the maximum composition bin.
## These fish will be added to the maximum bin.

## i There are 133 tows where fish were observed but not sampled.
## These tows comprise 32.7 percent of the total catch numbers.
## Only measured fishes in the bio_data file are used for composition expansions.

## i There were 98 biological samples removed out of 683 after filtering for strata.

## Joining with 'by = join_by(year, bin)'
## i Output will not be saved in dir because dir = NULL.
## Sample size will be calculated based on stewart_hamel.
## The unique samples by tow for shelfrock is 2.43.

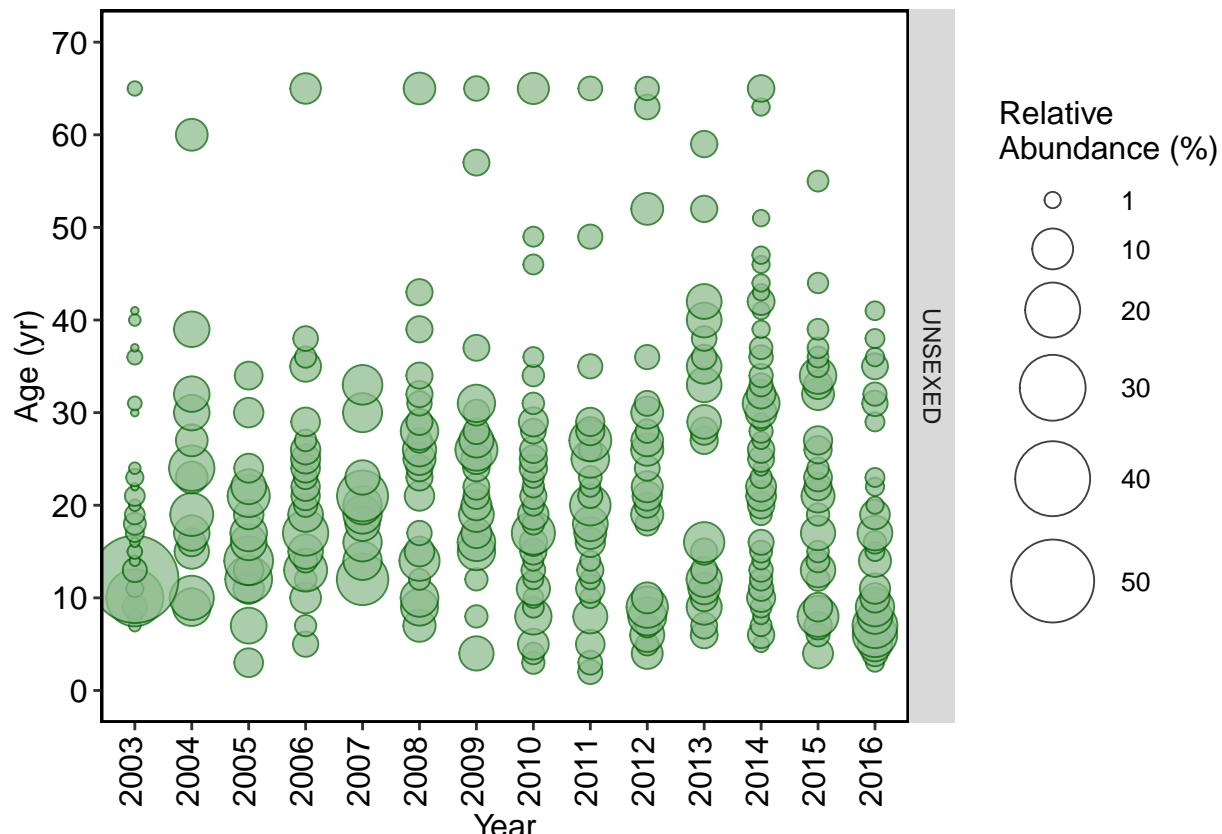
plot_comps(
  data = age_comps)

```

```

## i Output will not be saved in dir because dir = NULL.

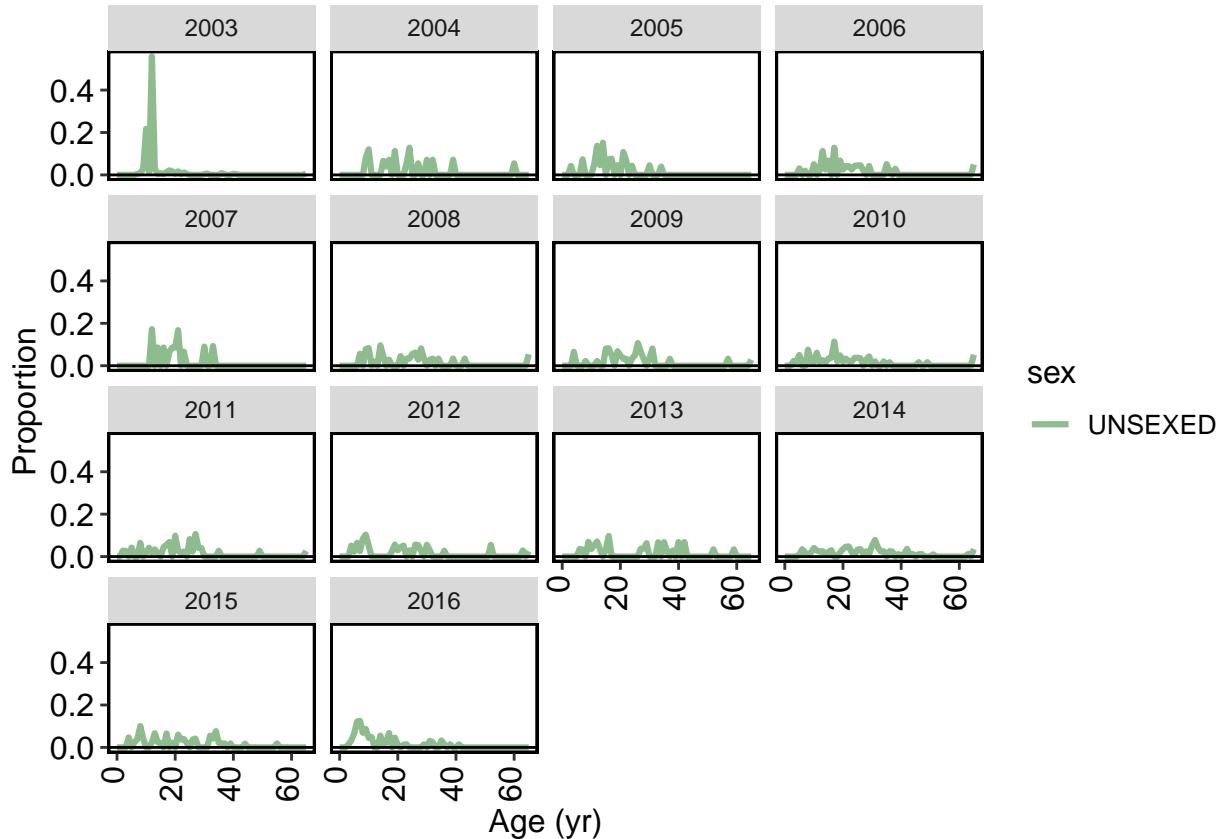
```



```

## Warning: No shared levels found between 'names(values)' of the manual scale and the
## data's fill values.

```



```
raw_age_comps <- get_raw_comps(
  data = bio,
  comp_bins = 0:65,
  comp_column_name = "age",
  two_sex_comps = FALSE) #single sex model
```

```
## i Output will not be saved in dir because dir = NULL.
## i Output will not be saved in dir because dir = NULL.
## Sample size will be calculated based on stewart_hamel.The unique samples by tow for shelfrock is 2.40
```

Conditional age-at-length data

```
caal <- SurveyAgeAtLen.fn(
  datAL = bio,
  datTows = catch,
  strat.df = WCGBTS_strata,
  lgthBins = seq(10, 74, 2),
  ageBins = 0:65)
```

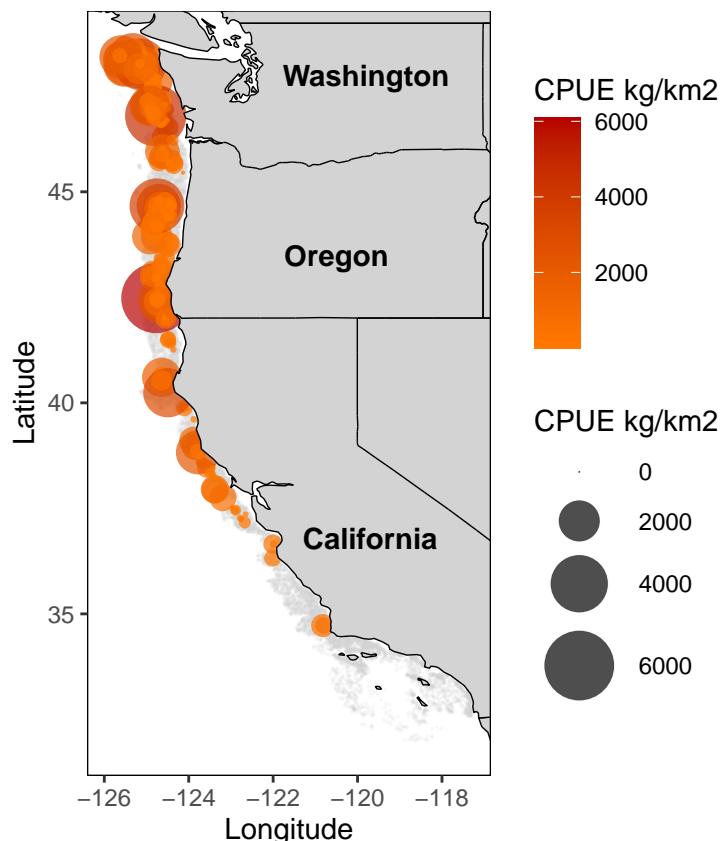
```
## i Output will not be saved in dir because dir = NULL.

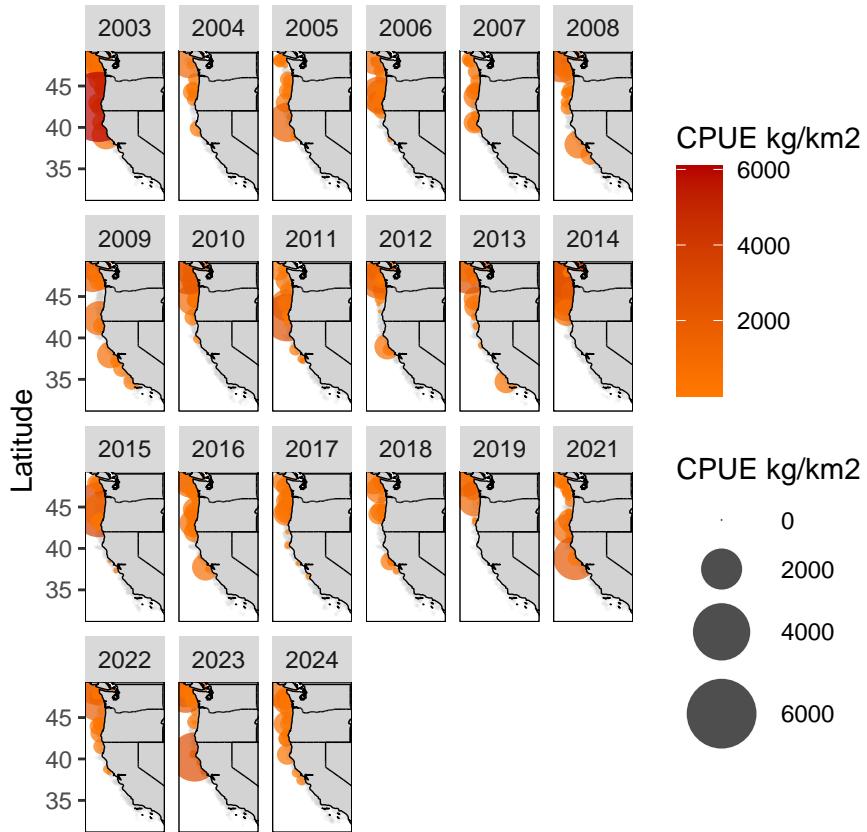
## There are 683 records kept out of 1049 records after removing missing records.
##
## Effective sample size is based on number of fish.
```

```
##  
##  
## Using raw numbers of age-at-length  
##  
##  
## Directory not specified and csv will not be written.
```

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

```
## i Output will not be saved in dir because dir = NULL.
```





Initial pull and plotting of data: Triennial

```
catchT = pull_catch(
  common_name = "yelloweye rockfish",
  survey = "Triennial")
```

```
## i Output will not be saved in dir because dir = NULL.
```

```
## i Pulling catch data for yelloweye rockfish.
```

```
## There are 211 positive tows across all years pulled.
## i There were 31 positive tows with non-satisfactory tow performance (e.g., no area swept estimate, no
## i There were 7 positive tows that were determined to be water hauls (net not on the bottom).
## 
## There are 173 positive tows remaining across all years after standard
## filtering.
```

```
#this is creating a list, just use $age_data
bioT = pull_bio(
  common_name = "yelloweye rockfish",
  survey = "Triennial")
```

```
## i Output will not be saved in dir because dir = NULL.
```

```

## i Pulling biological data for yelloweye rockfish.
## i There were 152 age/otolith samples pulled.
## i There were 36 age/otolith samples with non-satisfactory tow performance (e.g., no area swept estimate)
## i There were 224 length samples pulled.
## i There were 27 length samples with non-satisfactory tow performance (e.g., no area swept estimate, no
## i Triennial & AFSC Slope data returned as a list: bio$length_data and bio$age_data
## i There were 197 lengths and 116 ages samples remaining after applying standard filtering.

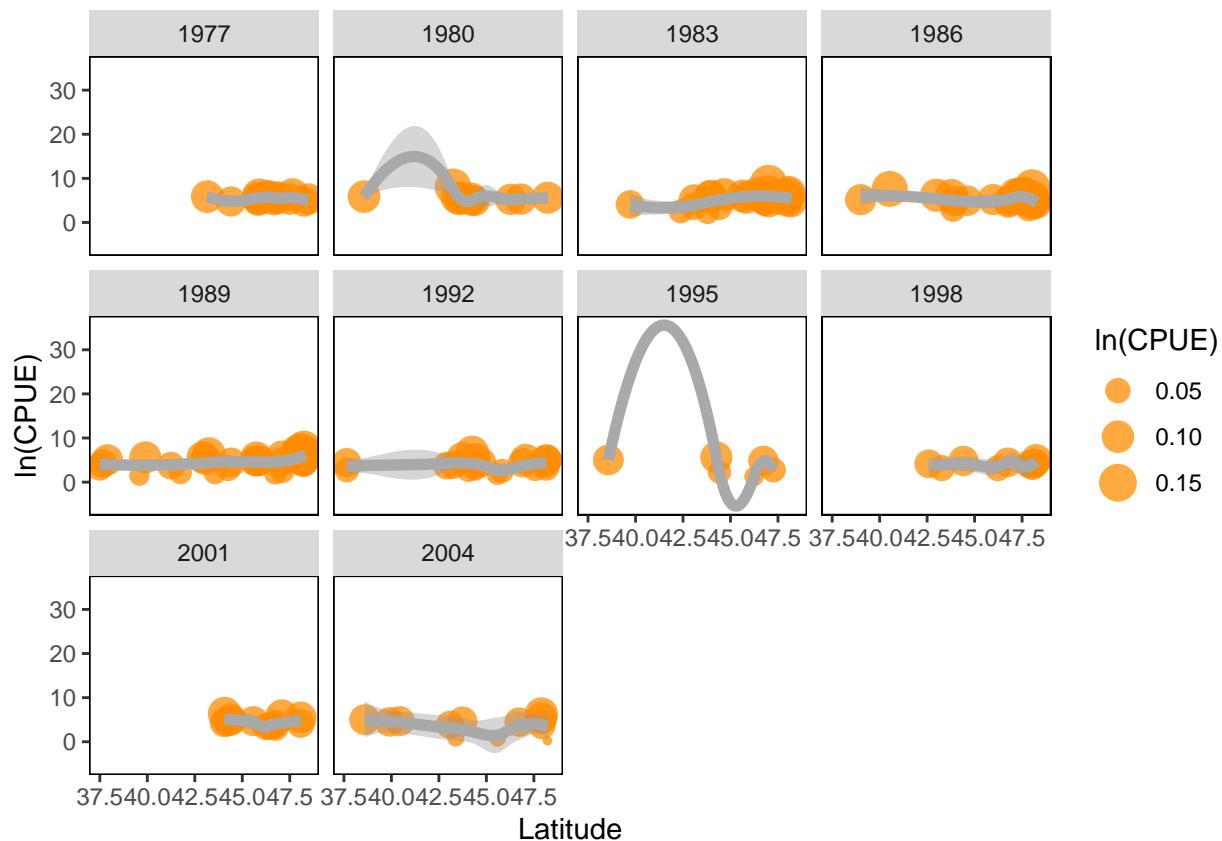
bioTtest <- bioT$age_data #this is the same number of variables as bio from the WGBTS
bioT <- bioTtest

plot_cpue(
  catch = catchT)

## i Output will not be saved in dir because dir = NULL.
## 'geom_smooth()' using formula = 'y ~ x' 'geom_smooth()' using formula = 'y ~ x' 'geom_smooth()' using

## Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning
## -Inf

```



```

## 'geom_smooth()' using formula = 'y ~ x'

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : pseudoinverse used at 161.34

```

```

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : neighborhood radius 29.335

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : reciprocal condition number 5.2867e-17

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric = parametric,
## : There are other near singularities as well. 841

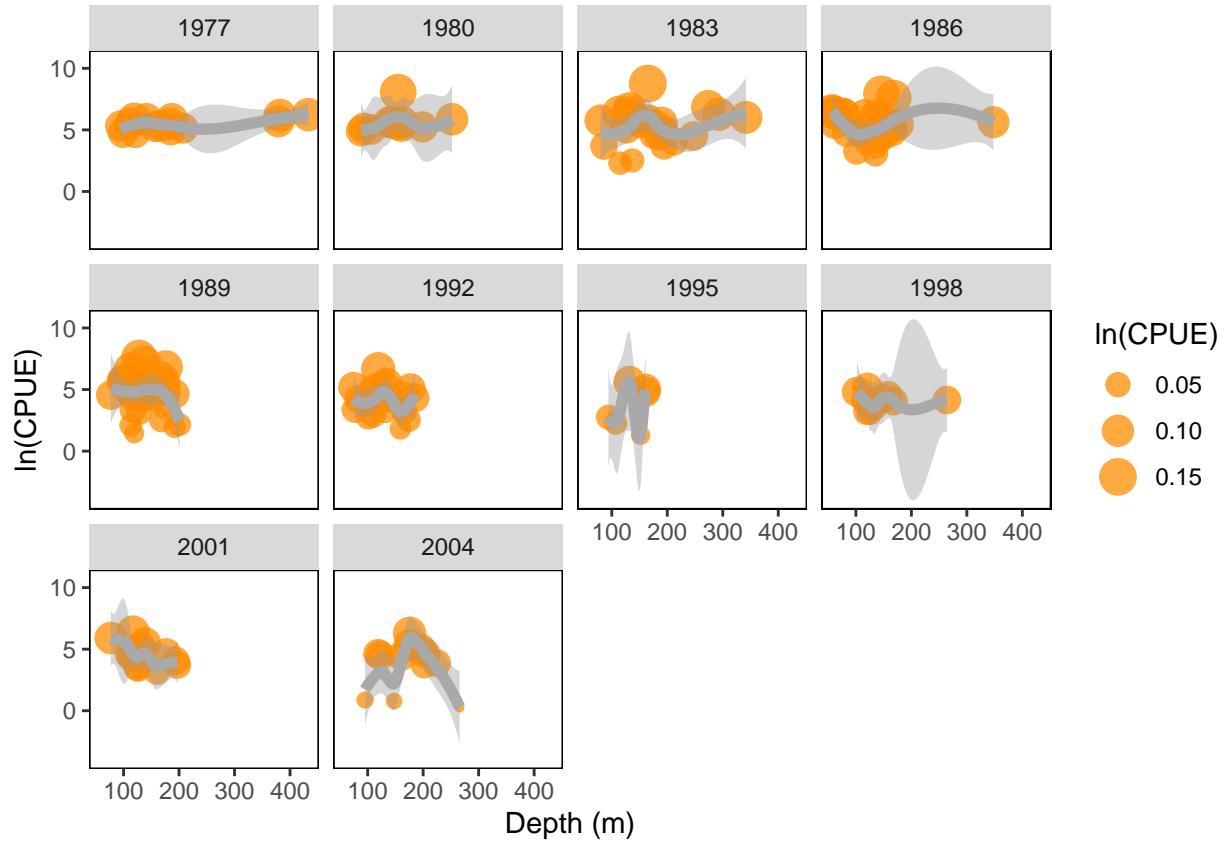
## Warning in predLoess(object$y, object$x, newx = if (is.null(newdata)) object$x
## else if (is.data.frame(newdata))
## as.matrix(model.frame(delete.response(terms(object))), : pseudoinverse used at
## 161.34

## Warning in predLoess(object$y, object$x, newx = if (is.null(newdata)) object$x
## else if (is.data.frame(newdata))
## as.matrix(model.frame(delete.response(terms(object))), : neighborhood radius
## 29.335

## Warning in predLoess(object$y, object$x, newx = if (is.null(newdata)) object$x
## else if (is.data.frame(newdata))
## as.matrix(model.frame(delete.response(terms(object))), : reciprocal condition
## number 5.2867e-17

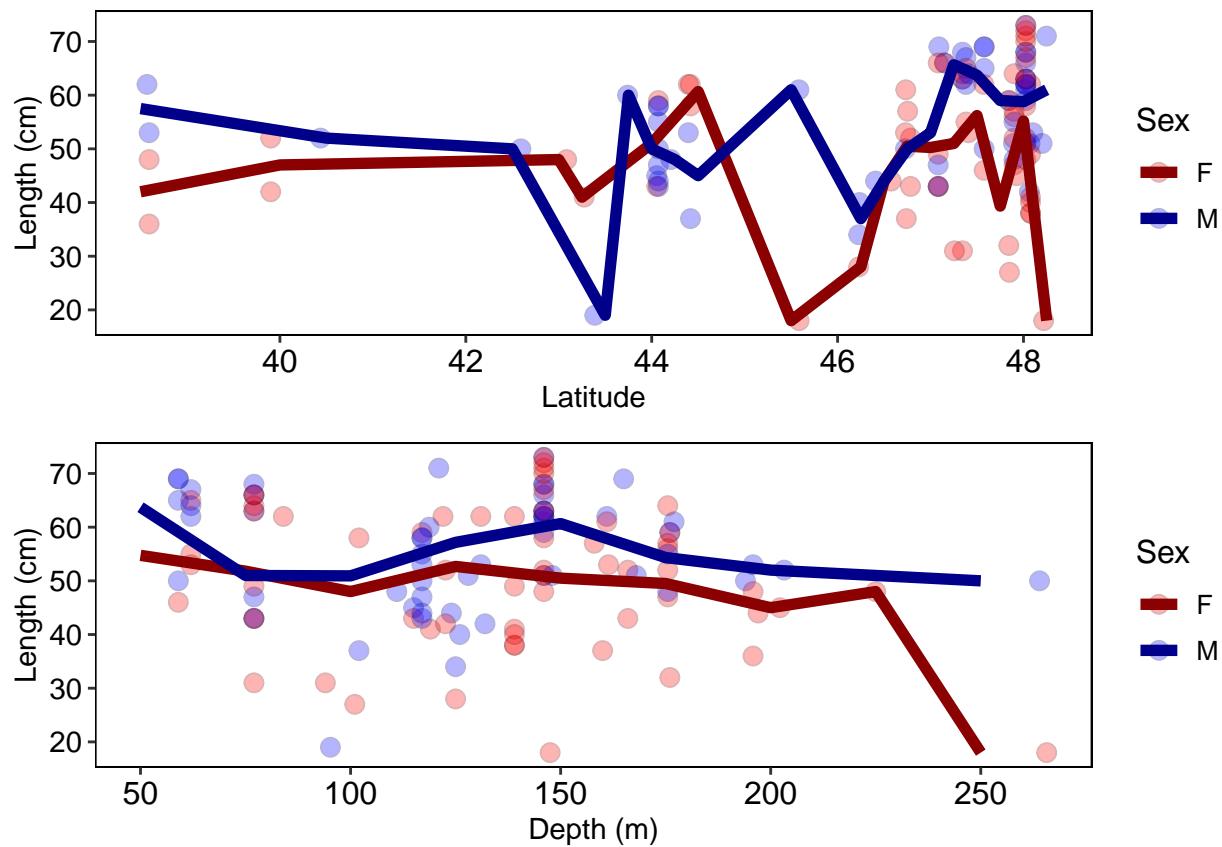
## Warning in predLoess(object$y, object$x, newx = if (is.null(newdata)) object$x
## else if (is.data.frame(newdata))
## as.matrix(model.frame(delete.response(terms(object))), : There are other near
## singularities as well. 841

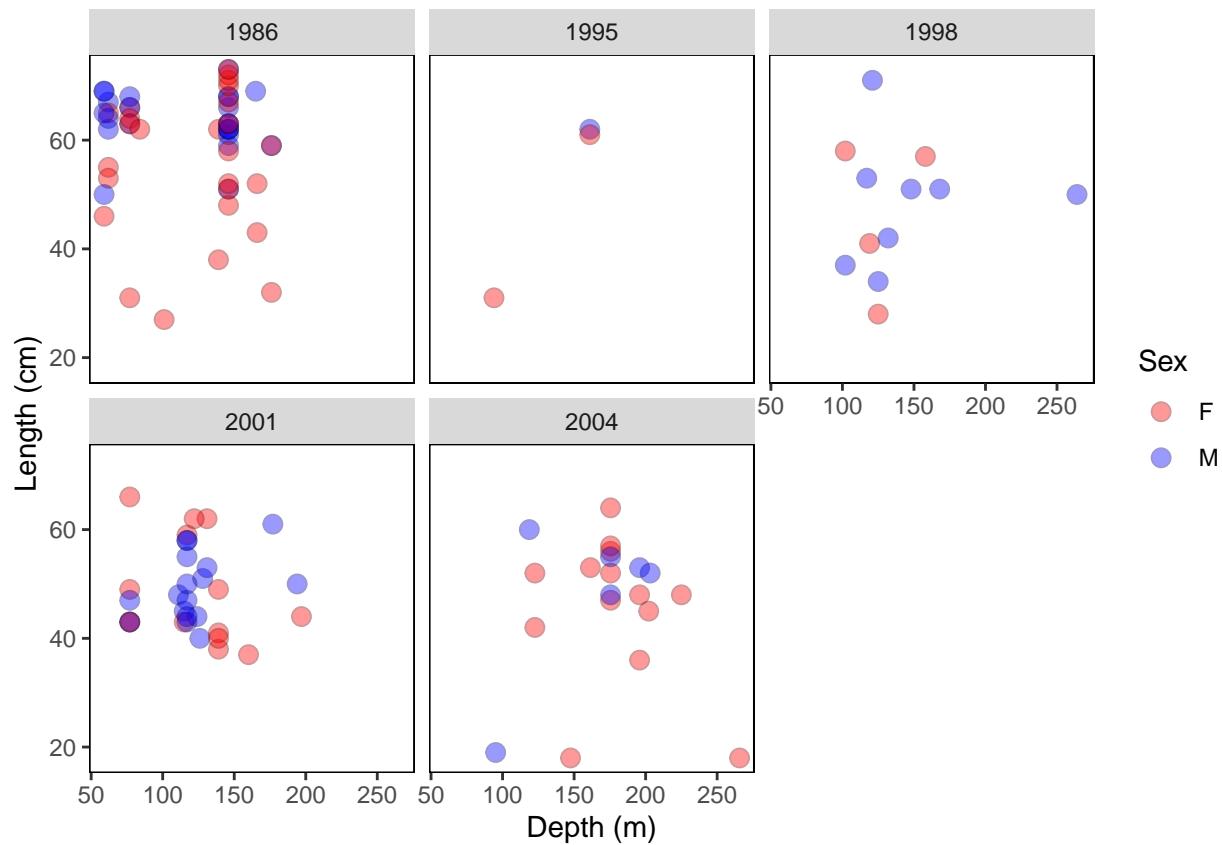
```

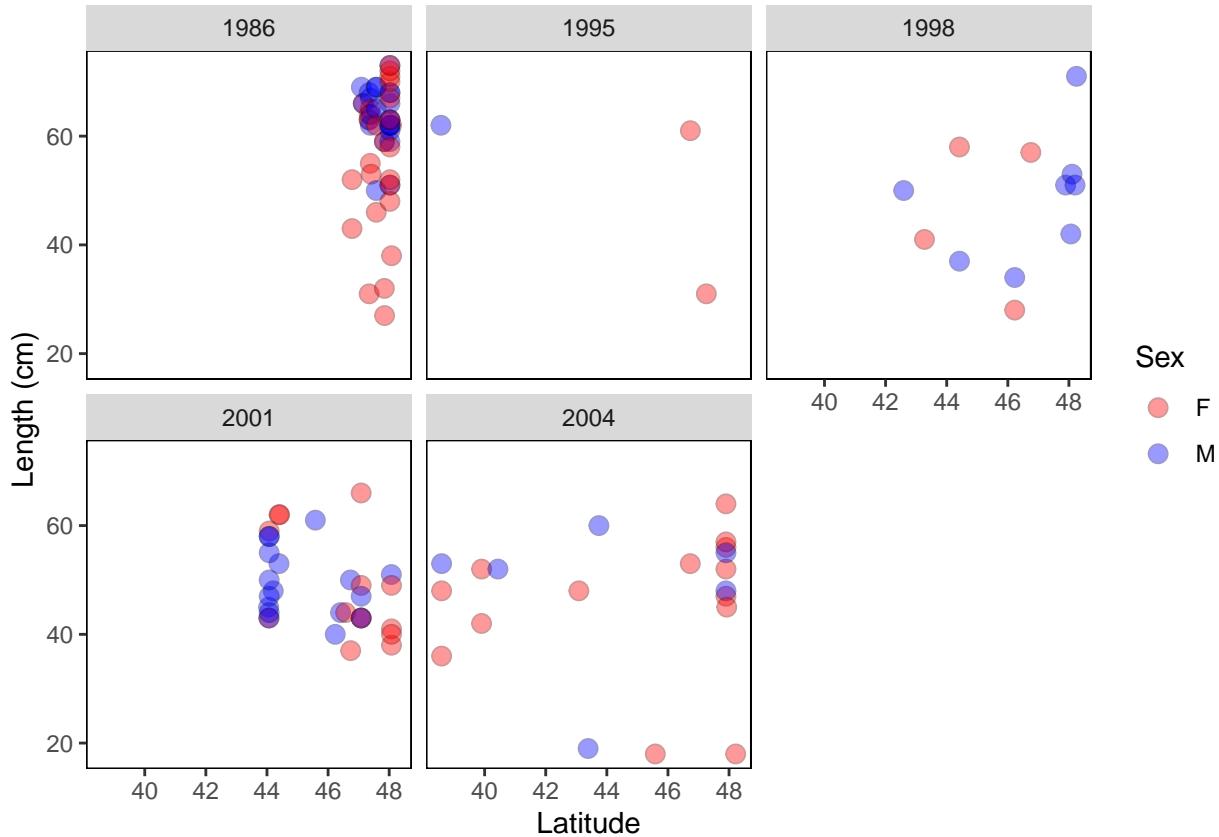


```
plot_bio_patterns(
  bio = bioT,
  col_name = "Length_cm")
```

```
## i Output will not be saved in dir because dir = NULL.
```







```
wh_plot_proportion(
  data_catch = catchT,
  data_bio = bioT
)
```

```
## [1] "/Users/morgan/Documents/GitHub/Sebastes_ruberrimus_2025/Rcode/plots/presence-absence_by_depth.png"
## [2] "/Users/morgan/Documents/GitHub/Sebastes_ruberrimus_2025/Rcode/plots/presence-absence_by_latitude.png"
## [3] "/Users/morgan/Documents/GitHub/Sebastes_ruberrimus_2025/Rcode/plots/sex_by_depth.png"
## [4] "/Users/morgan/Documents/GitHub/Sebastes_ruberrimus_2025/Rcode/plots/sex_by_latitude.png"
```

Define the strata

```
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))
```

Calculate designed based index of abundance

```
biomassT = get_design_based(
  data = catchT,
  strata = Triennial_strata)
```

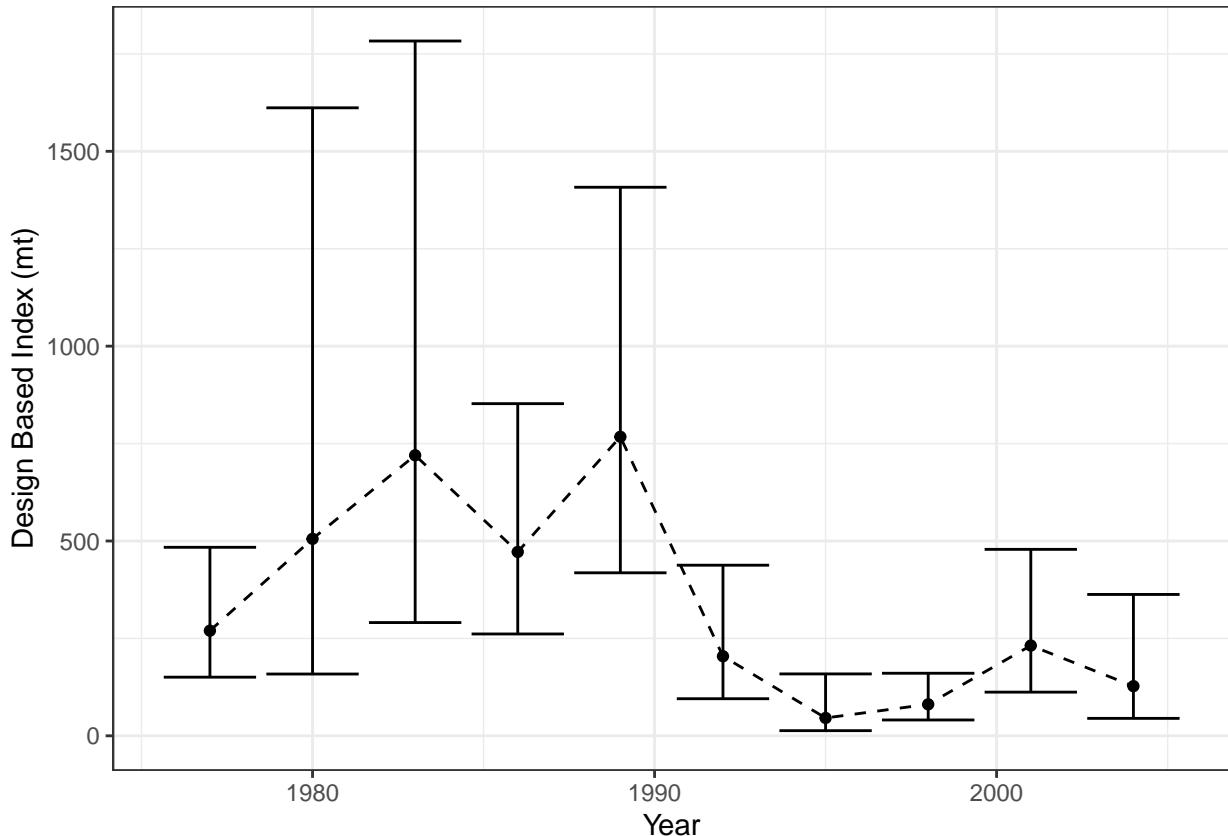
```
## i Output will not be saved in dir because dir = NULL.
```

```
## Joining with 'by = join_by(stratum)'
```

Plot coastwide

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

```
## i Output will not be saved in dir because dir = NULL.
```

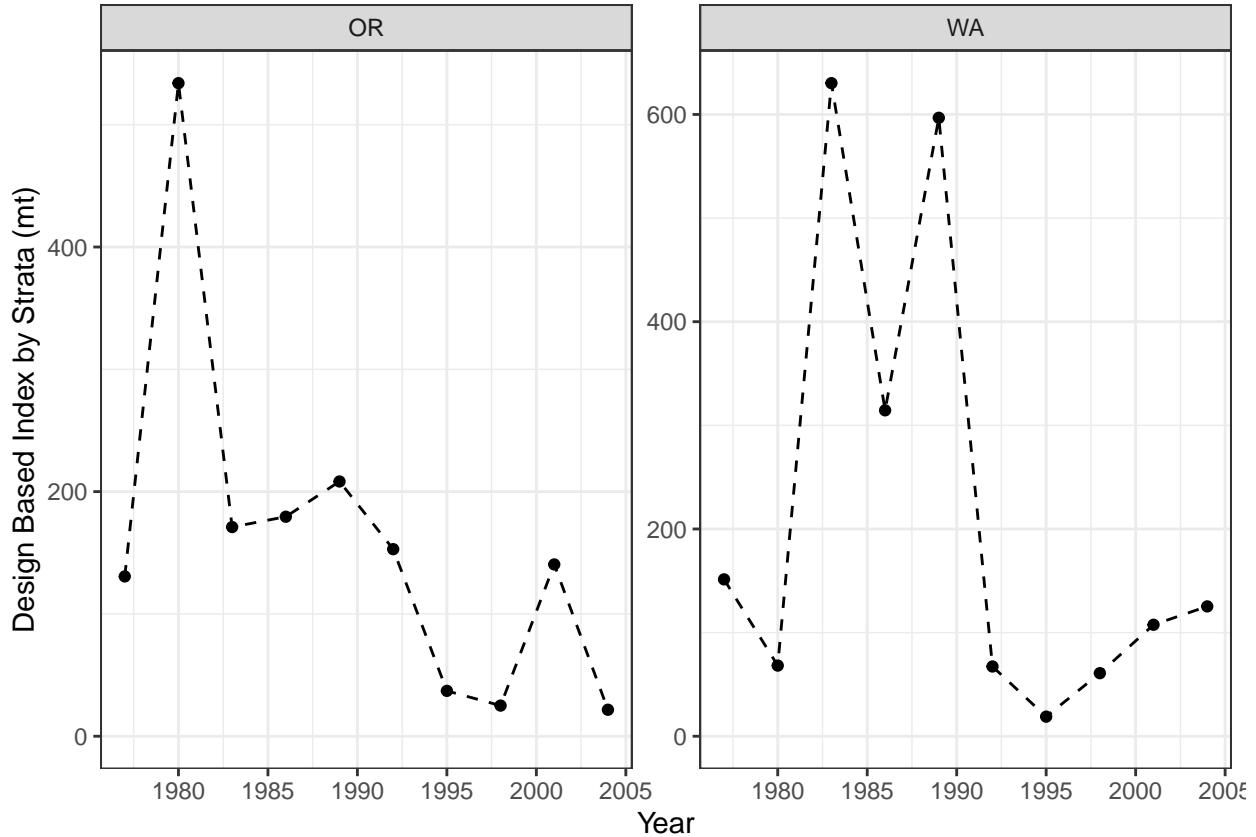


```
# not a lot of fish...
```

Plot index for each strata

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

```
## i Output will not be saved in dir because dir = NULL.
```



Length composition data

```
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")

## i Output will not be saved in dir because dir = NULL.

## i There are 0% of records that are less than the minimum composition bin. These
##   fish will be added to the minimum bin.

## i There are 0% of records that are greater than the maximum composition bin.
##   These fish will be added to the maximum bin.

## i There are 122 tows where fish were observed but not sampled.
## These tows comprise 77.4 percent of the total catch numbers.
## Only measured fished in the bio_data file are used for composition expansions.

## i There were 7 biological samples removed out of 116 after filtering for strata.
```

```

## Joining with 'by = join_by(year, bin)'
## i Output will not be saved in dir because dir = NULL.
## Sample size will be calculated based on stewart_hamel.
## The unique samples by tow for shelfrock is 2.43.

```

```

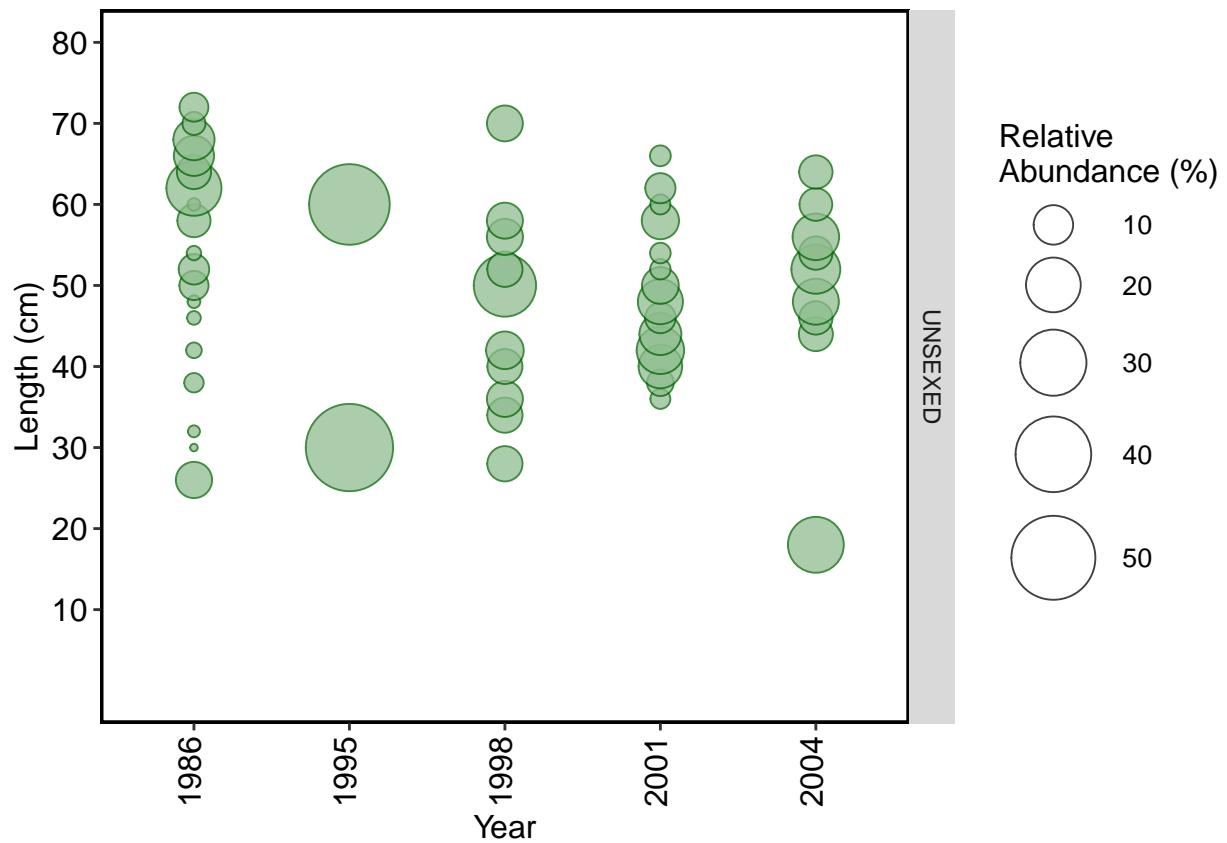
plot_comps(
  data = length_compsT)

```

```

## i Output will not be saved in dir because dir = NULL.

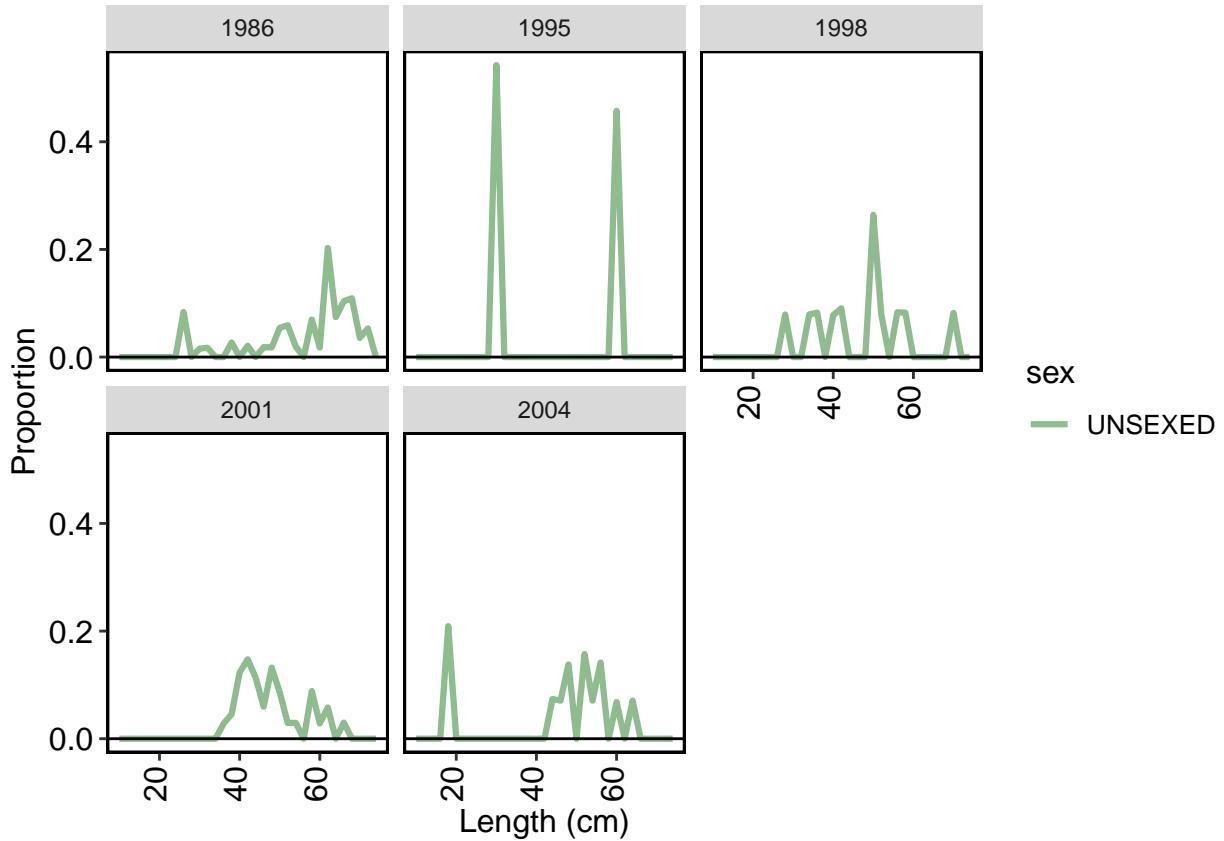
```



```

## Warning: No shared levels found between 'names(values)' of the manual scale and the
## data's fill values.

```



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

```
## i Output will not be saved in dir because dir = NULL.
## i Output will not be saved in dir because dir = NULL.
## Sample size will be calculated based on stewart_hamel.The unique samples by tow for shelfrock is 2.4
```

Marginal age composition data

```
#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
```

Conditional age-at-length data

```
#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)
```

```
## i Output will not be saved in dir because dir = NULL.
```

