

Comisión Interamericana del Atún Tropical  
Inter-American Tropical Tuna Commission



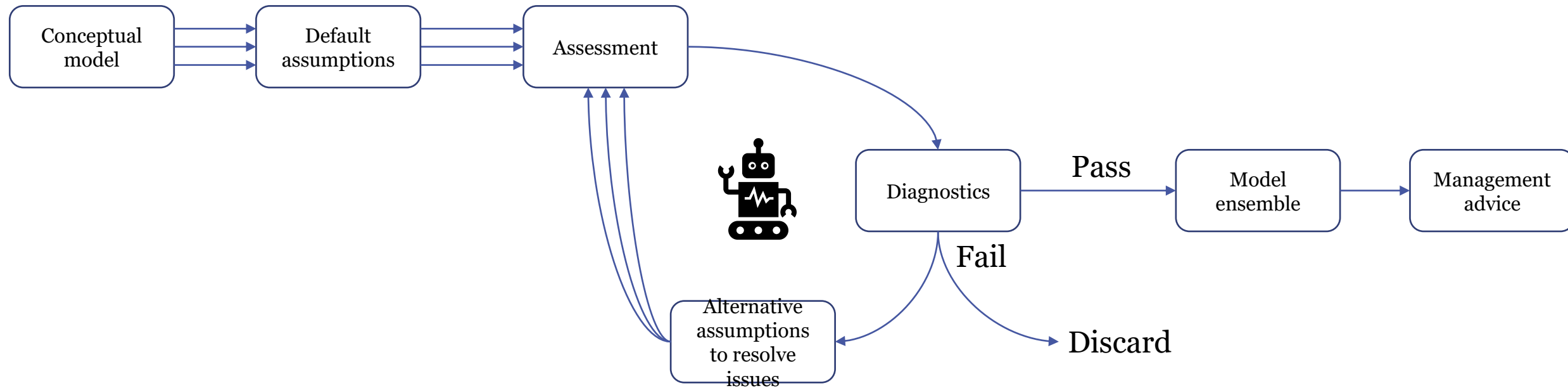
Model weighting and multimodel estimates

1st External review of modelling aspects in stock assessments of tropical tuna in the eastern Pacific Ocean  
6 - 10 Nov 2023 - Videoconference

# Key messages on model weighting

- Use diagnostics to fix models
- Only keep good models
- Use equal weight until a better approach is developed

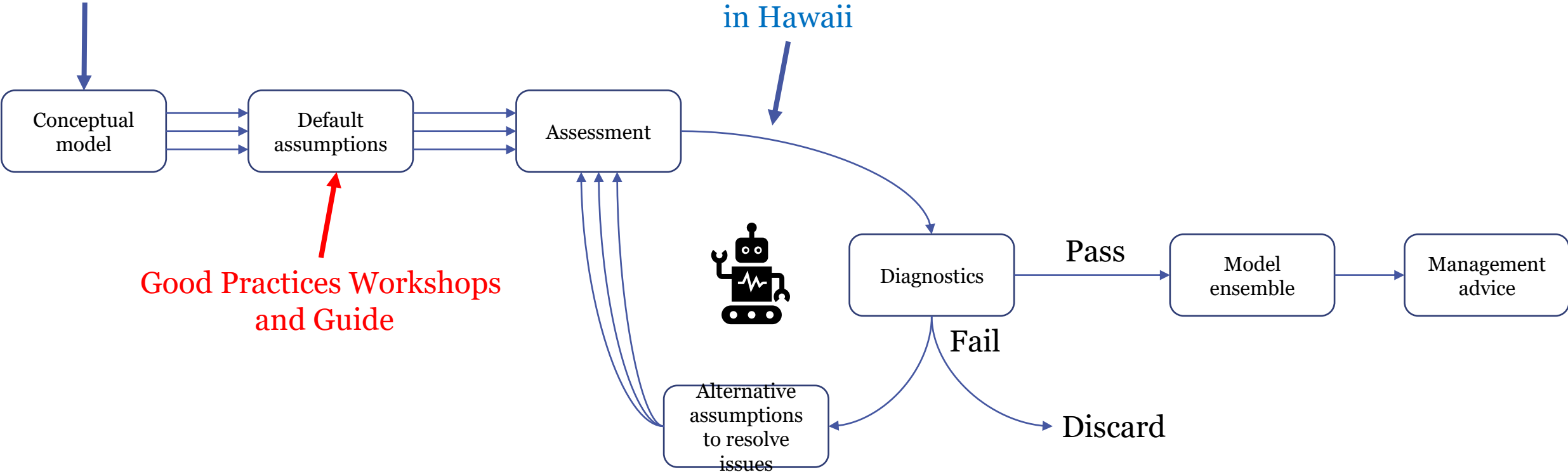
# Expert system to construct an ensemble of models for fisheries stock assessment



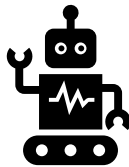
# Expert system to construct an ensemble of models for fisheries stock assessment

Carolina's work

Felipe Carvalho et al.  
in Hawaii



Good Practices Workshops  
and Guide



# Model weighting

- Data based approaches are not appropriate until we get the data weighting, process variation, and model misspecification sorted out
- Prediction methods are the standard
  - Management quantities are not observed
  - Predict index of adult abundance
  - Probably gives equal weight in many cases
- Need to have a good model to start with
- How to choose the alternative models

# More Issues

- Using data for parameter estimation uncertainty, but not model weighting
- How to deal with steepness
  - Can't be estimated
  - No information on its value
- How to include uncertainty in data
  - Uncertainty in Catch using MCBS
  - Alternative scenarios or data sets
- How to apply diagnostics to many models

# Model weighting Good Practices

- Start with the conceptual model and create a set of hypotheses about the population and the general structure of the model.
- Use the good practices to turn the hypotheses into alternative stock assessment models.
- Use diagnostics to either reject or fix the models.
- Equal weight should be the default, but if model weighting is desired, then perhaps hindcast a reliable index of abundance that is related to the management objectives (i.e., spawning biomass).
- The approach to diagnostics and model weighting should be set in advance and made transparent to avoid subjective judgements. List hypotheses that were not included because it was not practical to implement and test them (e.g., fine scale spatial models).
- Most model weighting is based on the hypotheses you choose to include, not what the diagnostics eliminate. Be realistic about the true uncertainty by including sufficient hypotheses. Use statistical methods (confounding) to run an efficient grid.

# Yellowfin tuna recruitment: multimodel estimates

48 model point estimates and uncertainty estimates ([SAC-11-07](#)) combined using relative weights ([SAC-11-INF-J](#))

the 95% confidence interval was computed using a normal approximation for each model, combined in a mixture of normal distributions with the mixing ratios equal to the model weights and finding the values for each year where the cumulative distribution function was equal to 0.025 and 0.975 for the lower and upper boundaries of the confidence interval (R function FindCI)

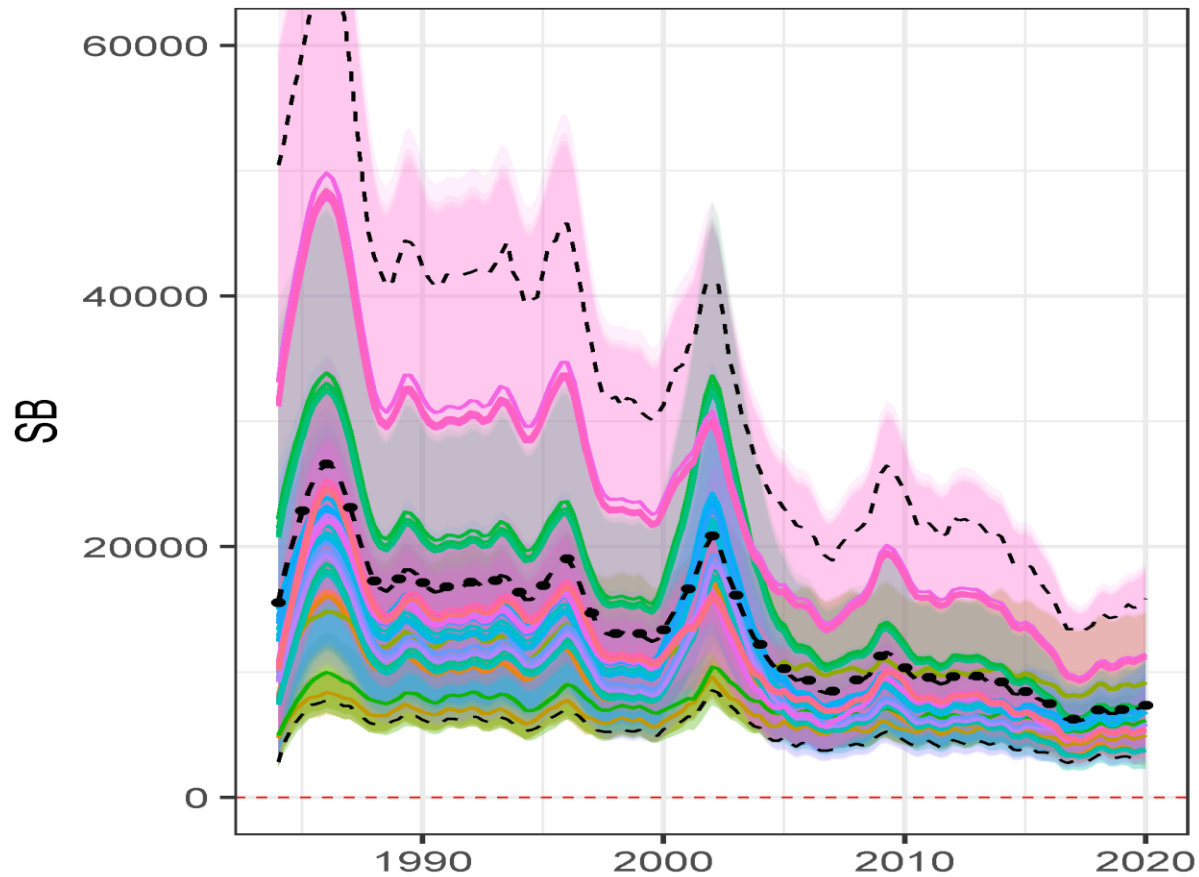


## Model

BASE 0.7	DS 0.7	TBE.GRO 0.7
BASE 0.8	DS 0.8	TBE.GRO 0.8
BASE 0.9	DS 0.9	TBE.GRO 0.9
BASE 1	DS 1	TBE.GRO 1
DDQ 0.7	GRO 0.7	TBM 0.7
DDQ 0.8	GRO 0.8	TBM 0.8
DDQ 0.9	GRO 0.9	TBM 0.9
DDQ 1	GRO 1	TBM 1
DDQ.DS 0.7	TBE 0.7	TBM.DS 0.7
DDQ.DS 0.8	TBE 0.8	TBM.DS 0.8
DDQ.DS 0.9	TBE 0.9	TBM.DS 0.9
DDQ.DS 1	TBE 1	TBM.DS 1
DDQ.GRO 0.7	TBE.DS 0.7	TBM.GRO 0.7
DDQ.GRO 0.8	TBE.DS 0.8	TBM.GRO 0.8
DDQ.GRO 0.9	TBE.DS 0.9	TBM.GRO 0.9
DDQ.GRO 1	TBE.DS 1	TBM.GRO 1



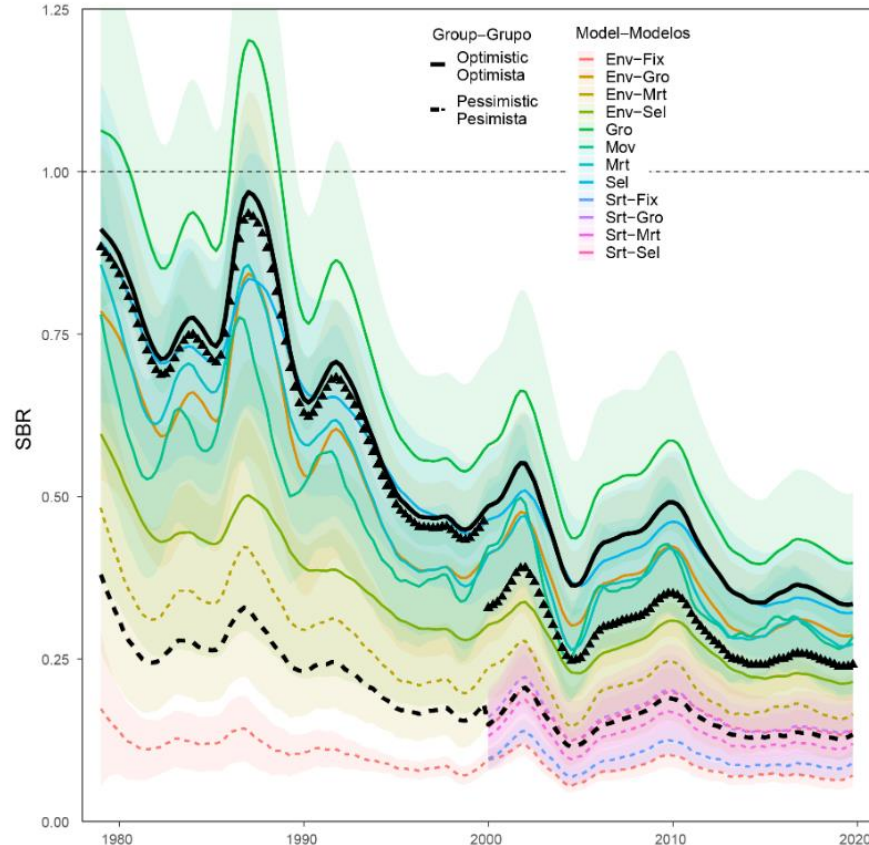
# Yellowfin tuna Spawning potential



## Model

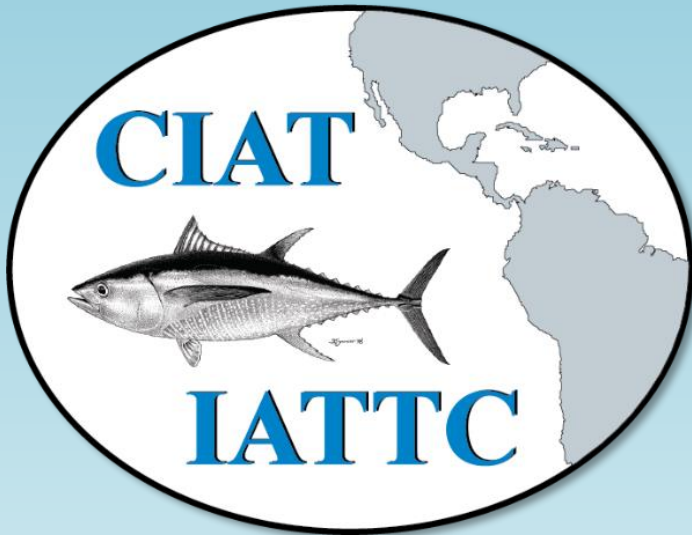
- |             |            |             |
|-------------|------------|-------------|
| BASE 0.7    | DS 0.7     | TBE.GRO 0.7 |
| BASE 0.8    | DS 0.8     | TBE.GRO 0.8 |
| BASE 0.9    | DS 0.9     | TBE.GRO 0.9 |
| BASE 1      | DS 1       | TBE.GRO 1   |
| DDQ 0.7     | GRO 0.7    | TBM 0.7     |
| DDQ 0.8     | GRO 0.8    | TBM 0.8     |
| DDQ 0.9     | GRO 0.9    | TBM 0.9     |
| DDQ 1       | GRO 1      | TBM 1       |
| DDQ.DS 0.7  | TBE 0.7    | TBM.DS 0.7  |
| DDQ.DS 0.8  | TBE 0.8    | TBM.DS 0.8  |
| DDQ.DS 0.9  | TBE 0.9    | TBM.DS 0.9  |
| DDQ.DS 1    | TBE 1      | TBM.DS 1    |
| DDQ.GRO 0.7 | TBE.DS 0.7 | TBM.GRO 0.7 |
| DDQ.GRO 0.8 | TBE.DS 0.8 | TBM.GRO 0.8 |
| DDQ.GRO 0.9 | TBE.DS 0.9 | TBM.GRO 0.9 |
| DDQ.GRO 1   | TBE.DS 1   | TBM.GRO 1   |

# Bigeye tuna spawning biomass: multimodel estimates



**FIGURE D-5.** Comparison of spawning biomass estimates for bigeye tuna in the eastern Pacific Ocean from the twelve reference models (only the estimates that correspond to steepness = 1.0 are shown). The shaded areas represent the 95% confidence intervals and the two black lines represent the combined estimates across the two groups of reference models. Black triangles mark the combined estimates across all reference models.

- A set of models composed the benchmark assessment for bigeye tuna ([SAC-11-06](#)). All models were used to produce management advice by combining them using relative weights ([SAC-11-INF-F](#)).
- In the case of BET the management quantities presented a bimodal probability distribution, therefore we provide the estimates of the pessimistic and optimistic models here, as the average will not represent the population state (see explanation here: [SAC-11-08](#)) In addition, some models are long-term, and others are short term, starting in the year 2000. Therefore, the combined estimates are provided from year 2000 on, which is the start of the period all models have in common.
- For each set of models (pessimistic set and optimistic set), the multimodel inference was based on the weighted average of the estimates and the 95% confidence intervals was computed using a normal approximation for each model, combined in a mixture of normal distributions with the mixing ratios equal to the model weights and finding the values for each year where the cumulative distribution function was equal to 0.025 and 0.975 (function FindCI)



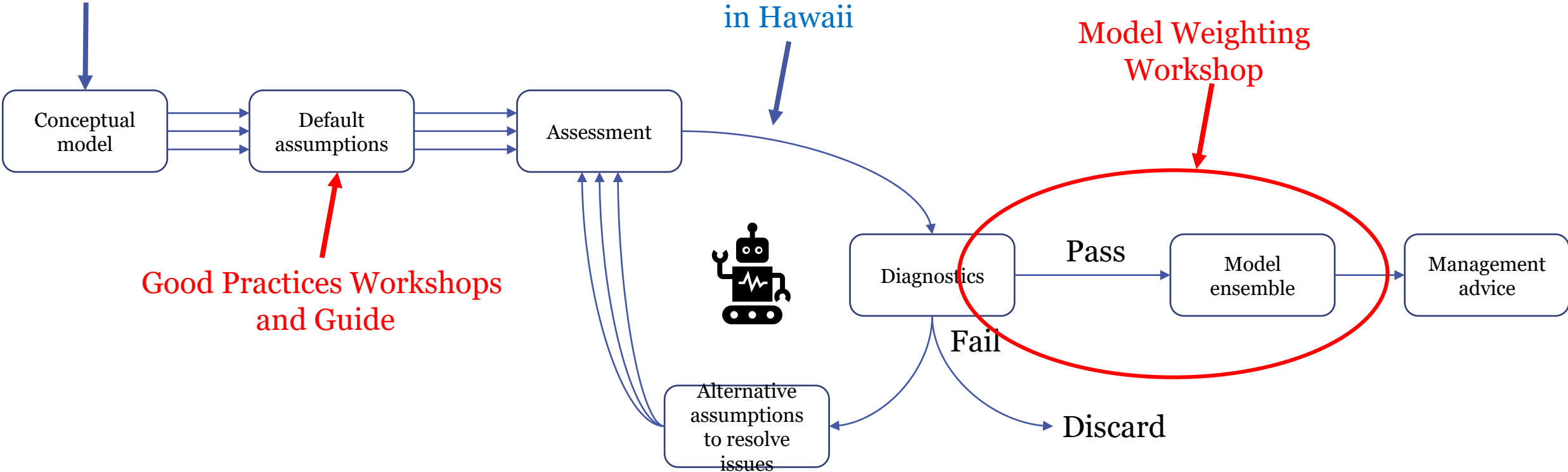
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# Key message and issues

Spanish  
English



# Yellowfin tuna recruitment: multimodel estimates

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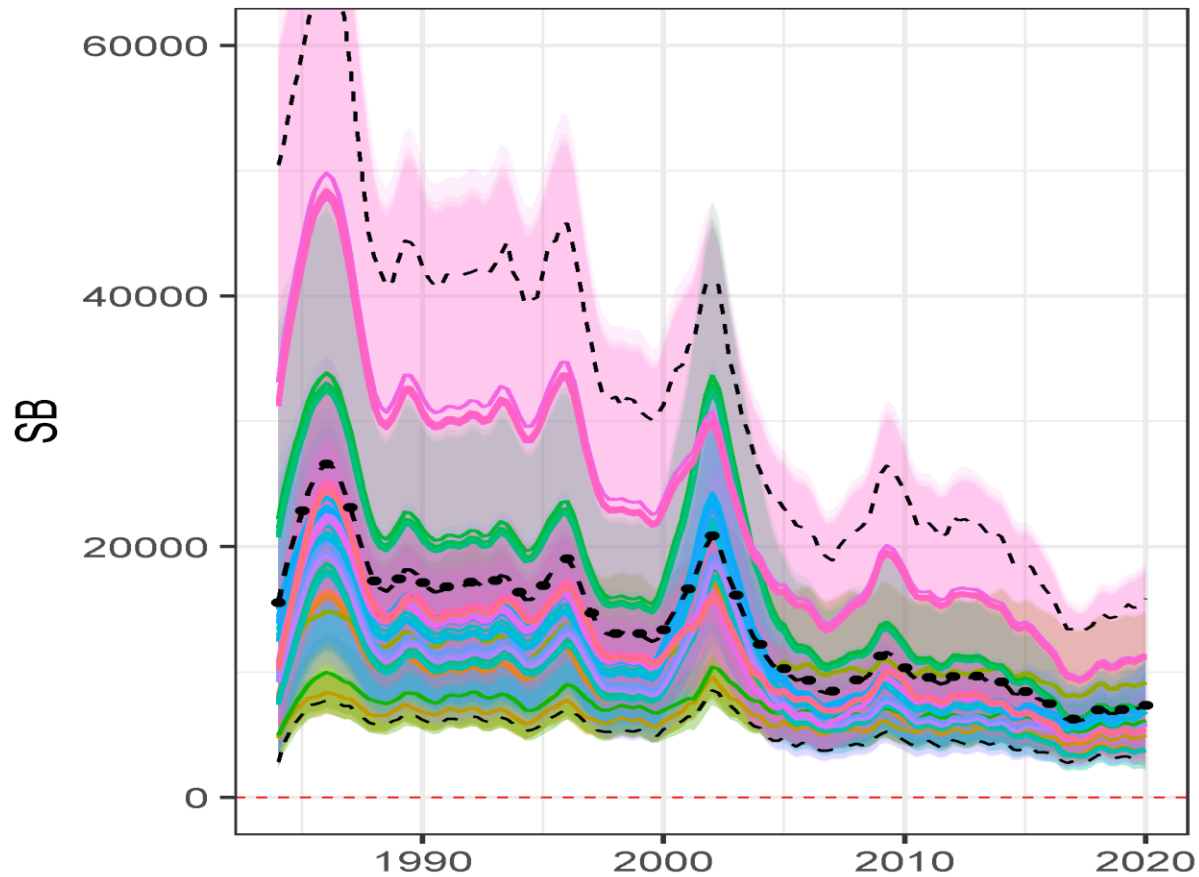
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## Model

BASE 0.7	DS 0.7	TBE.GRO 0.7
BASE 0.8	DS 0.8	TBE.GRO 0.8
BASE 0.9	DS 0.9	TBE.GRO 0.9
BASE 1	DS 1	TBE.GRO 1
DDQ 0.7	GRO 0.7	TBM 0.7
DDQ 0.8	GRO 0.8	TBM 0.8
DDQ 0.9	GRO 0.9	TBM 0.9
DDQ 1	GRO 1	TBM 1
DDQ.DS 0.7	TBE 0.7	TBM.DS 0.7
DDQ.DS 0.8	TBE 0.8	TBM.DS 0.8
DDQ.DS 0.9	TBE 0.9	TBM.DS 0.9
DDQ.DS 1	TBE 1	TBM.DS 1
DDQ.GRO 0.7	TBE.DS 0.7	TBM.GRO 0.7
DDQ.GRO 0.8	TBE.DS 0.8	TBM.GRO 0.8
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DDQ.GRO 1	TBE.DS 1	TBM.GRO 1

# Yellowfin tuna Spawning potential

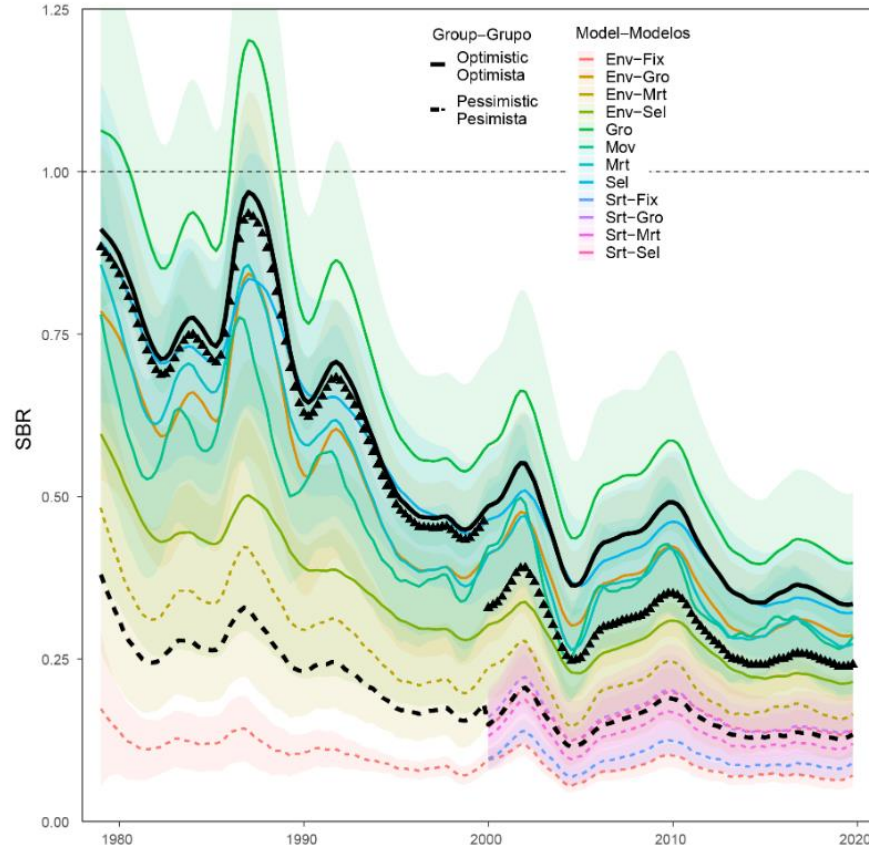


## Model

- |             |            |             |
|-------------|------------|-------------|
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| DDQ 0.9     | GRO 0.9    | TBM 0.9     |
| DDQ 1       | GRO 1      | TBM 1       |
| DDQ.DS 0.7  | TBE 0.7    | TBM.DS 0.7  |
| DDQ.DS 0.8  | TBE 0.8    | TBM.DS 0.8  |
| DDQ.DS 0.9  | TBE 0.9    | TBM.DS 0.9  |
| DDQ.DS 1    | TBE 1      | TBM.DS 1    |
| DDQ.GRO 0.7 | TBE.DS 0.7 | TBM.GRO 0.7 |
| DDQ.GRO 0.8 | TBE.DS 0.8 | TBM.GRO 0.8 |
| DDQ.GRO 0.9 | TBE.DS 0.9 | TBM.GRO 0.9 |
| DDQ.GRO 1   | TBE.DS 1   | TBM.GRO 1   |



# Bigeye tuna spawning biomass: multimodel estimates



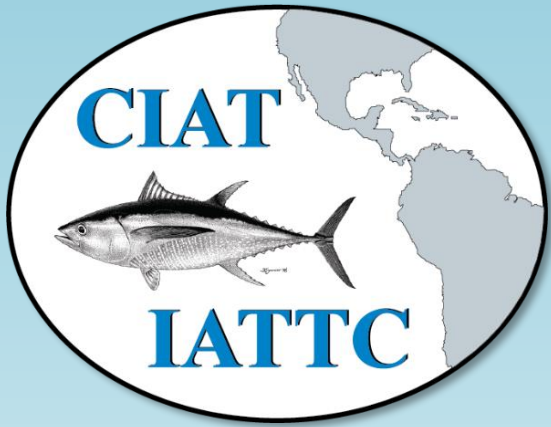
**FIGURE D-5.** Comparison of spawning biomass estimates for bigeye tuna in the eastern Pacific Ocean from the twelve reference models (only the estimates that correspond to steepness = 1.0 are shown). The shaded areas represent the 95% confidence intervals and the two black lines represent the combined estimates across the two groups of reference models. Black triangles mark the combined estimates across all reference models.

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# FindCI

```
FindCI<-function(Mean_vec,STD_vec,Weight_vec,Lower=0,Upper=20000)
{
#####
getCumP<-function(x,Quant=0.975)
{
n<-length(Weight_vec)
tmp<-0
for(i in 1:n)
tmp<- tmp+Weight_vec[i]*pnorm(x, log.p = FALSE,mean=Mean_vec[i], sd=STD_vec[i])
tmp<- (Quant-tmp)^2
return(tmp)
}
#####
f<-getCumP
UP<- optimize(f, lower=Lower, upper=Upper)

getCumP<-function(x,Quant=0.025)
{
n<-length(Weight_vec)
tmp<-0
for(i in 1:n)
tmp<- tmp+Weight_vec[i]*pnorm(x, log.p = FALSE,mean=Mean_vec[i], sd=STD_vec[i])
tmp<- (Quant-tmp)^2
return(tmp)
}
#####
f<-getCumP
LO<-optimize(f, lower=Lower, upper=Upper)
CI<-c(LO$minimum,UP$minimum)
return(CI)
}
```



Preguntas -Questions