Evaluating the Consequences of Misspecifying Population Structure within Spatially Explicit Stock Assessments?

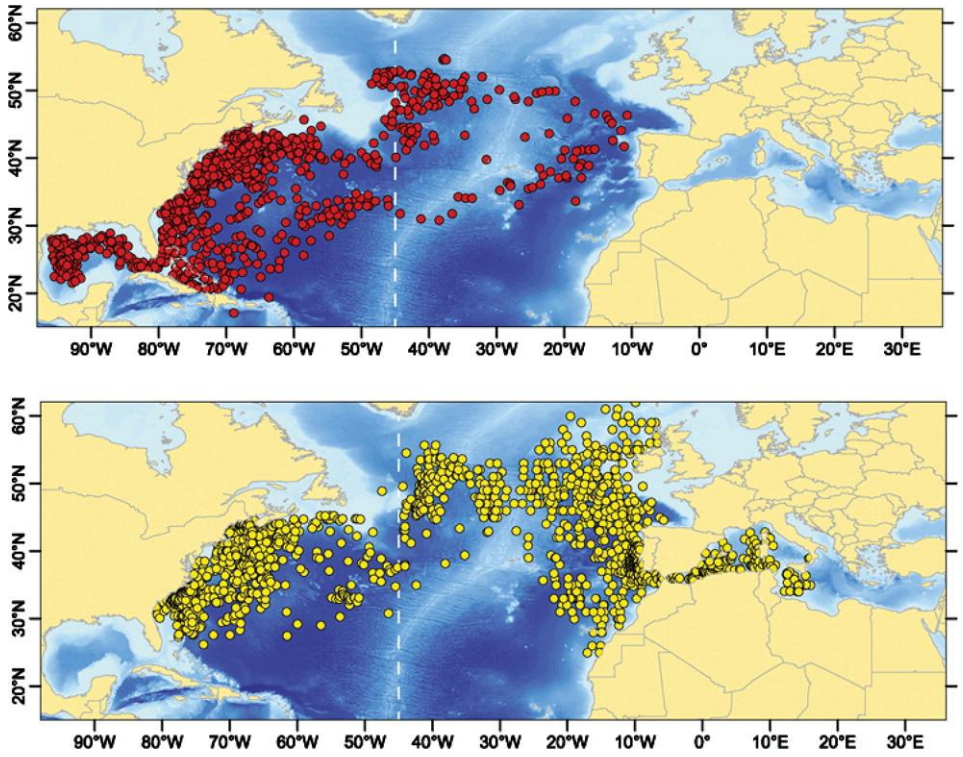
CAPAM - SWFSC
La Jolla, CA
Tues, Oct 2, 2018

Katelyn Bosley
NOAA Fisheries
Northwest Fisheries Science Center
Newport, Oregon, USA

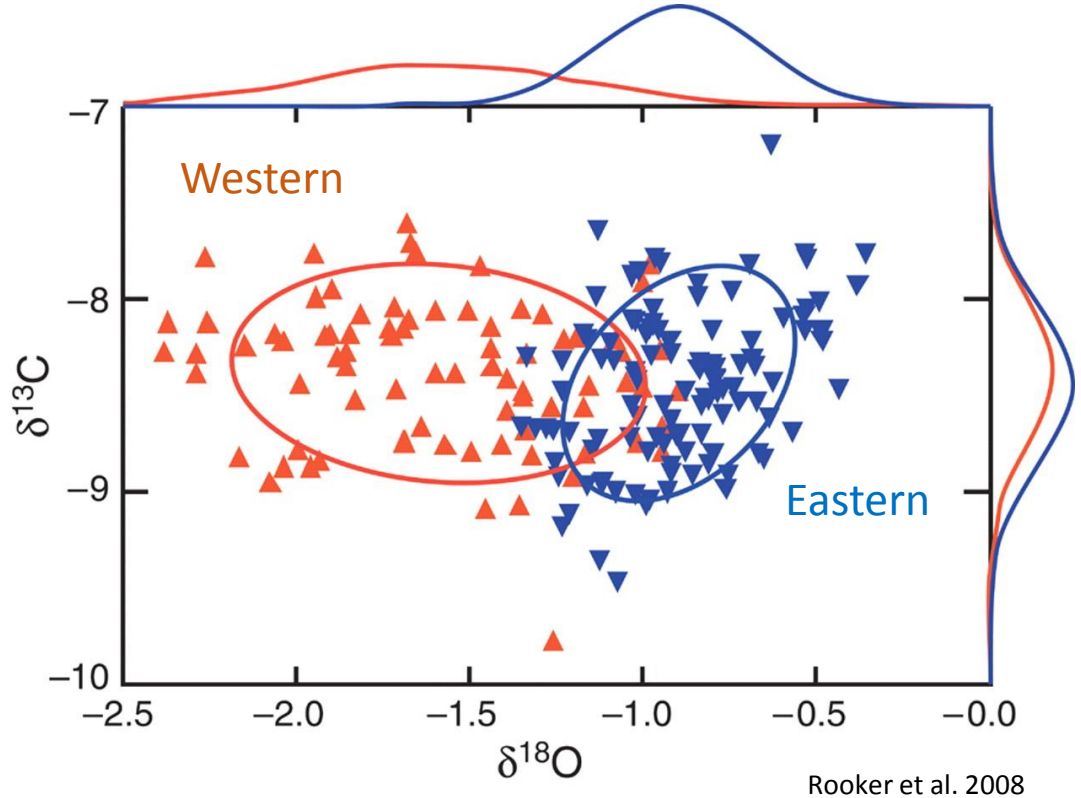
Sablefish (*Anoplopoma fimbria*)

Coauthors:
Daniel Goethel (NOAA-SEFSC)
Aaron Berger (NOAA-NWFSC)
Dana Hanselman (NOAA-AFSC)
Amy Schueller (NOAA-SEFSC)
Jonathan Deroba (NOAA-NEFSC)
Brian Langseth (NOAA-PIFSC)

- **Increasing evidence that marine species are spatially structured**
  - *Tagging-studies, morphometrics, genetic stock identification, etc.*

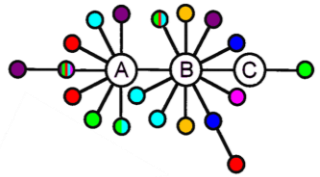


Rooker et al. 2007

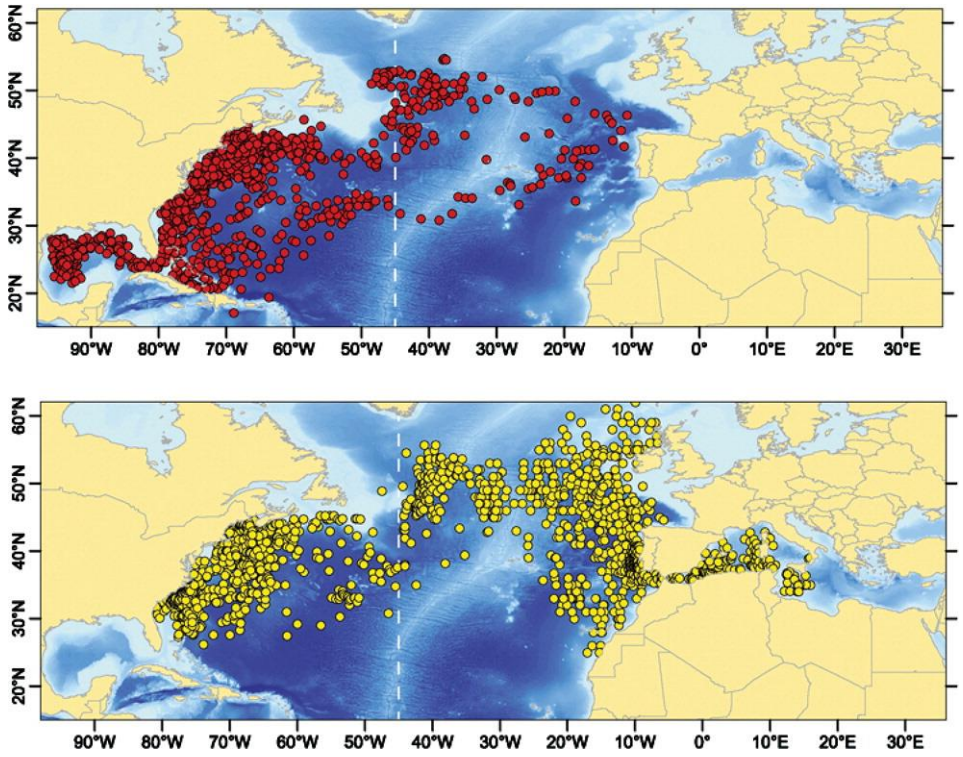


Rooker et al. 2008

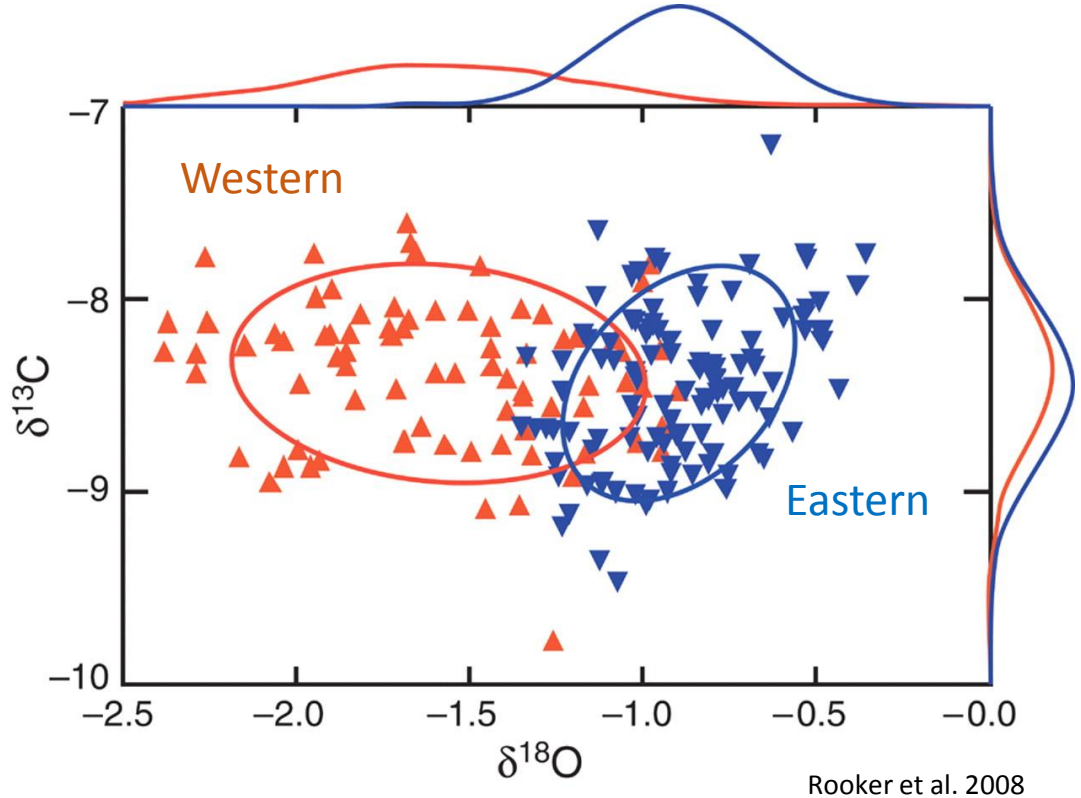
Atlantic bluefin tuna *(Thunnus thynnus)*



- When data suggest a spatially structured stock, what happens if the assumptions made within a stock assessment regarding stock structure are **WRONG**?

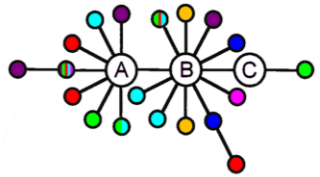


Rooker et al. 2007



Rooker et al. 2008

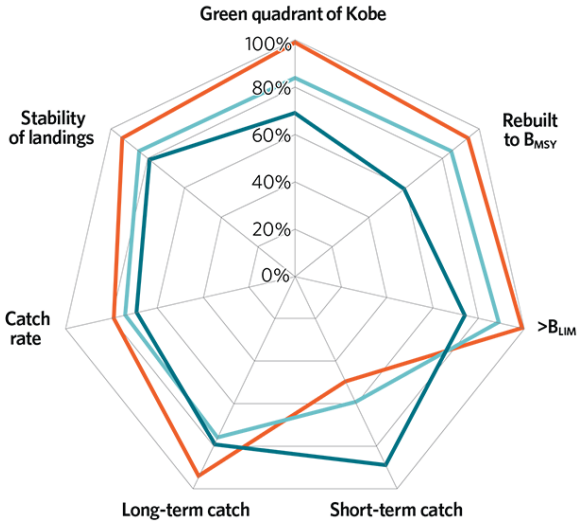
Atlantic bluefin tuna *(Thunnus thynnus)*



Spatial Processes And Stock Assessment Methods

PROJECT OBJECTIVE

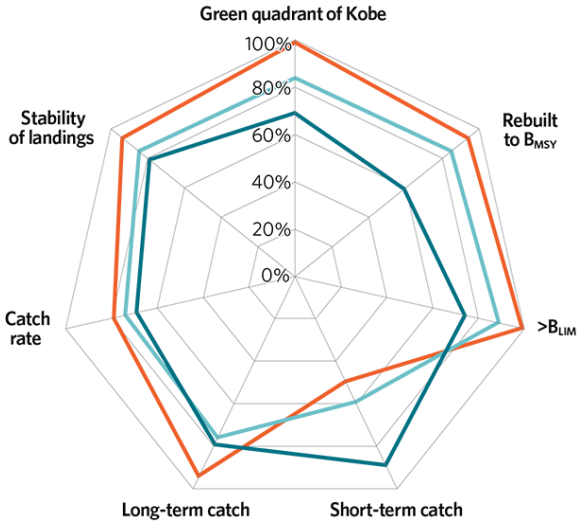
Evaluate and identify situations where accounting for spatial processes **improves the ability for management actions to achieve desired conservation and management goals**



Spatial
Processes
And
Stock
Assessment
Methods

PROJECT OBJECTIVE

Evaluate and identify situations where accounting for spatial processes **improves the ability for management actions to achieve desired conservation and management goals**



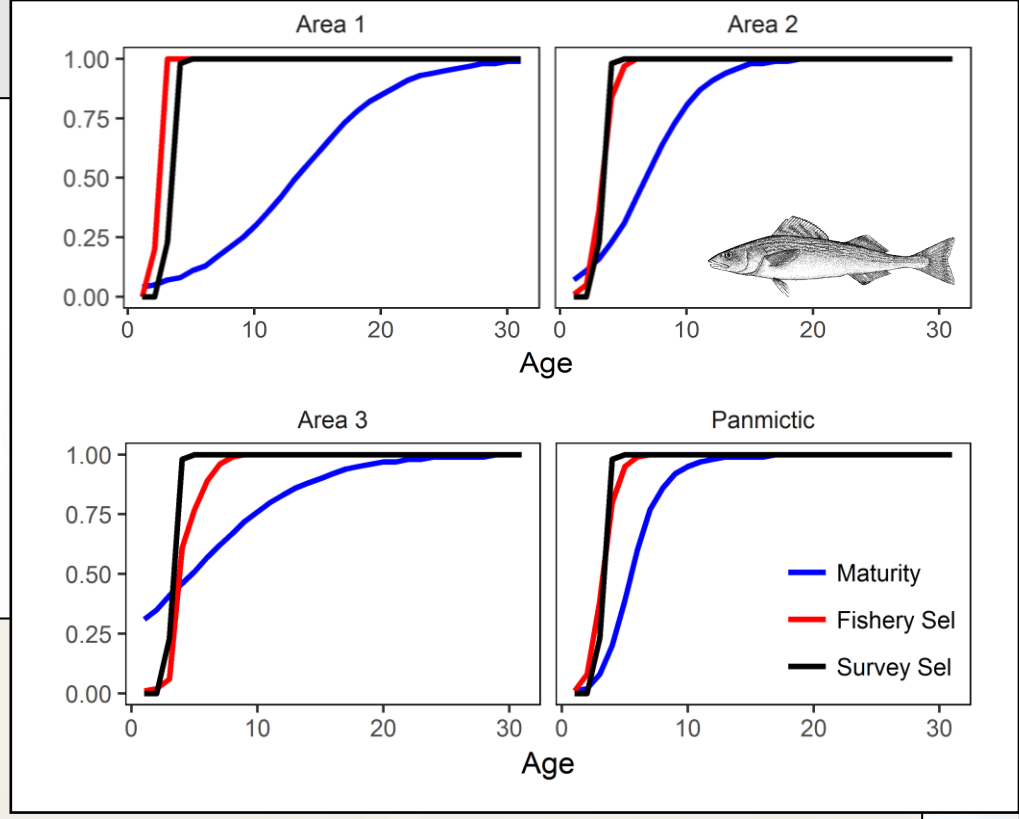
Many HYPOTHESES to explore

- Optimal spatial quota allocation
- **Misdiagnosis of population structure**
- Variation in life-history characteristics
- Reference points
- Data quality/quantity *(Goethel)*
- Management & regulations *(Berger)*

METHODS: TAG-INTEGRATED SIMULATION FRAMEWORK

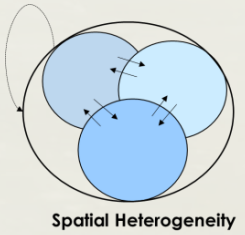
THE SPASAM MODELS ("The TIM")

- **Spatially-explicit, tag-integrated models**
- Simulation Model & Assessment Model
- HIGHLY flexible!!

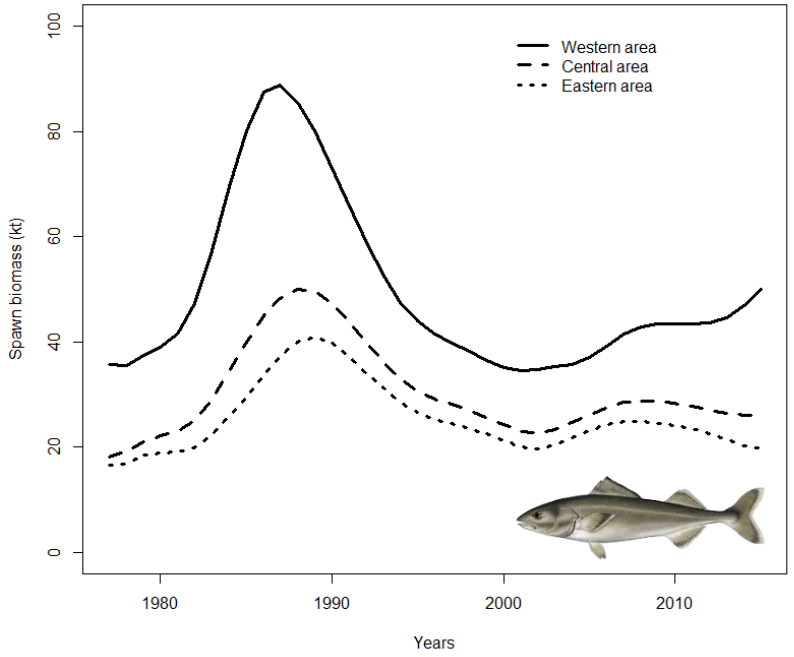


Model Features:

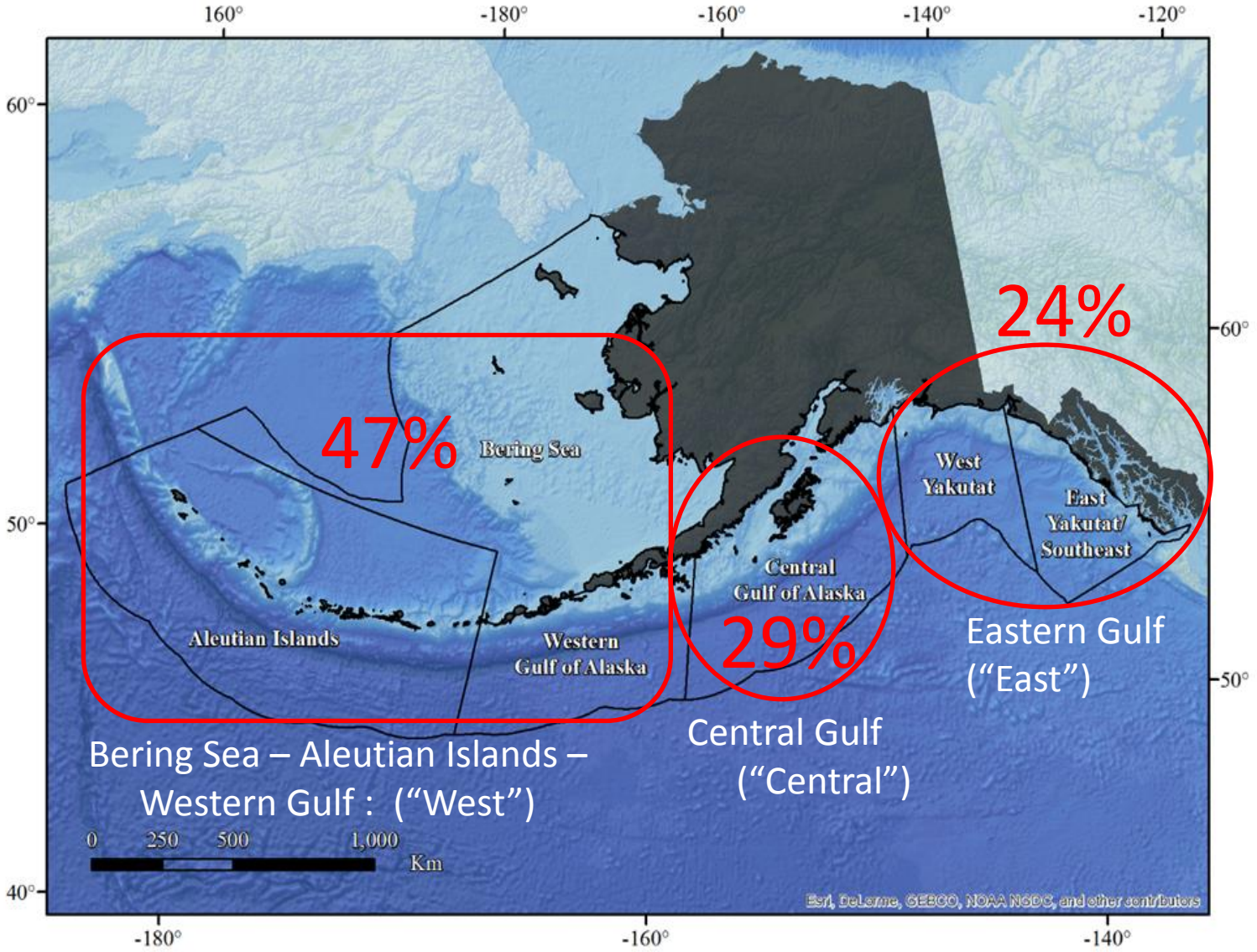
- Generalized, Age-structured
- Several population structures
- Allows for user to specify number of populations, regions, and fleets
- **Spatially-varying biological and fishery parameters**
  - *Recruitment, movement, maturity, growth, natural mortality, fishery selectivity*
- Stochastic and density-dependent parameterizations
- Simulates observed data with error



MODEL APPLICATION: OUR CASE STUDY



Fenske et al., in prep



40+ year time series of tagging data to inform movement

Plenty of evidence that suggests that a stock exhibits some degree of spatial heterogeneity & connectivity…now what?

Research questions:

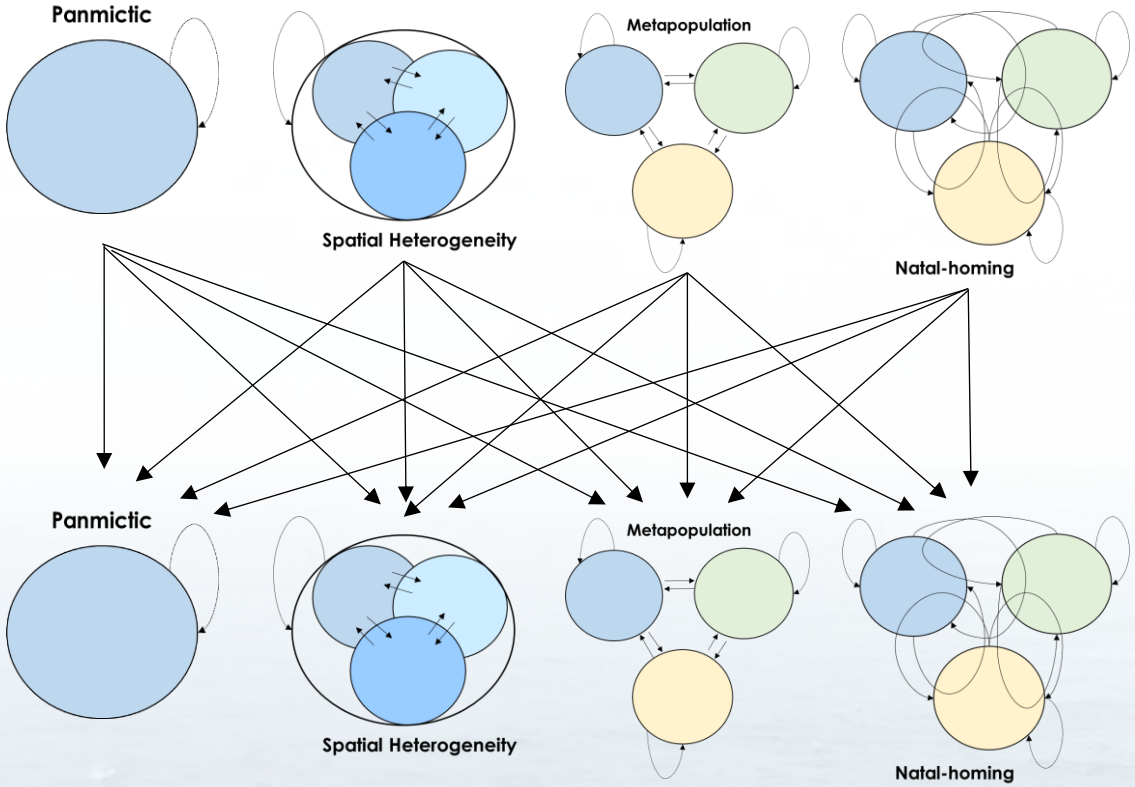
1) Can we obtain **improved estimates for stock productivity** by taking into account the spatial structure of spawning components and connectivity among them?

2) What are the **consequences of misdiagnosing the underlying population structure within a stock assessment**

   - Do wrong assumptions regarding population structure really matter when providing management advice?

MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

"True" population dynamics



Assumed population dynamics

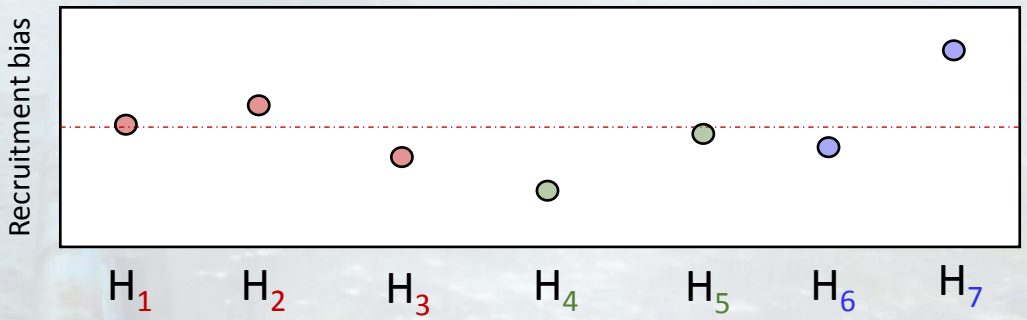
OUR APPROACH:

1) Simulate population dynamics for all spatial structures

- *Sablefish "like" parameters*

2) Conduct assessments when true underlying dynamics **match/mismatch** assumed

3) Compare performance of model in estimating parameters



MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

Model Details:

- Assume data rich
- Observed data are summed for panmictic assessment
- Model inputs are abundance weighted averages
- R_ave estimated
- Initial abundance assumed to be equilibrium unfished abundance-at-age
- Recruitment apportionment is estimated for multi-area models
- Age-invariant annual movement estimated

NO MOVEMENT

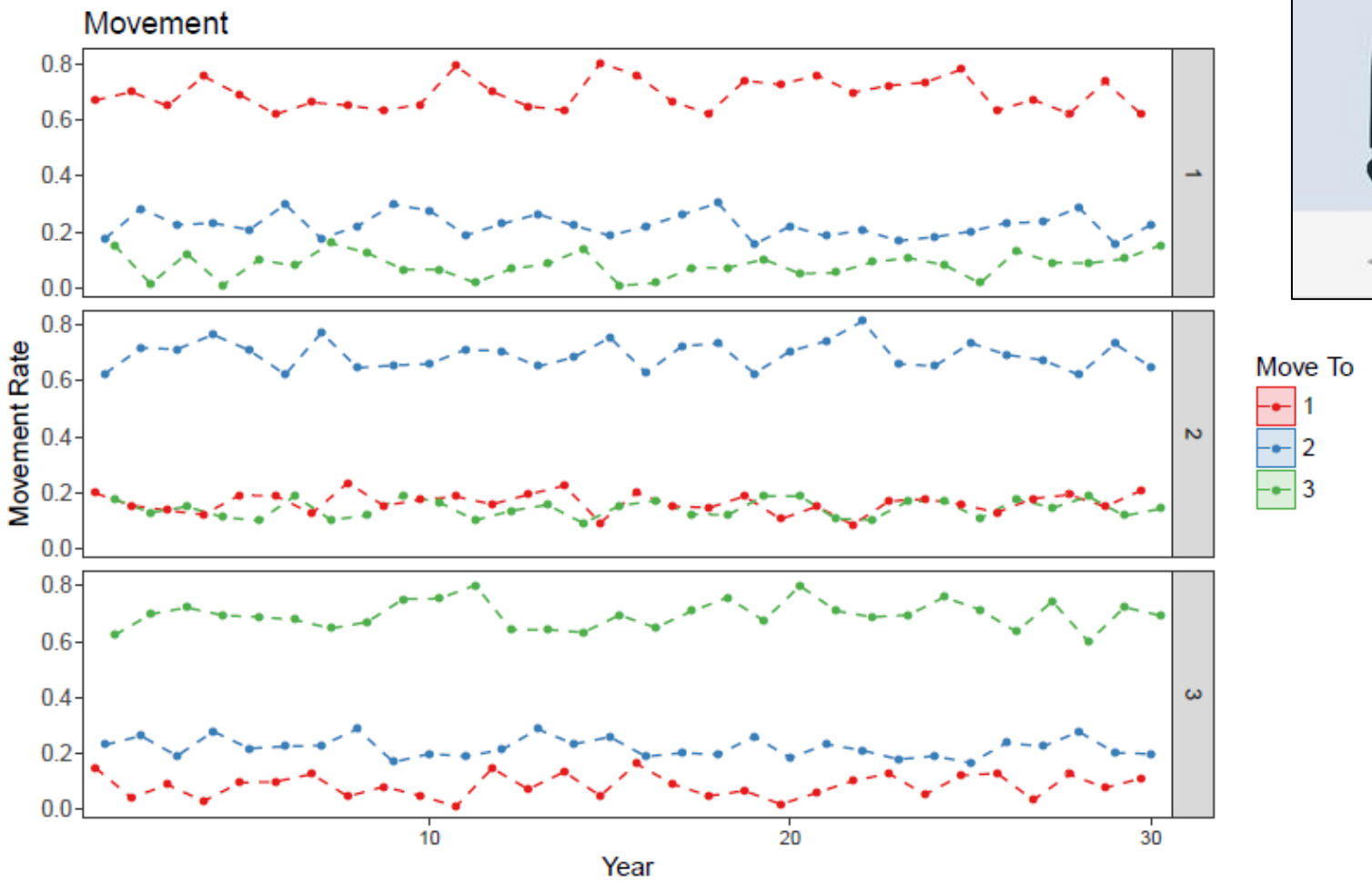
Simulation Model

Assessment Model

	Uniform	**Multiple Areas**	**Metapopulation**	**Natal Homing**
	Panmictic	Panmictic	Panmictic	Panmictic
		Fleet-as-Areas	Fleets-as-Areas	Fleets-as-Areas
	Uniform Multi-Area	Tag-Integrated Multi-Area	Tag-Integrated Multi-Area	Tag-Integrated Multi-Area
	Metapopulation	Tag-Integrated Metapopulation	Tag-Integrated Metapopulation	Tag-Integrated Metapopulation
	Natal Homing	Tag-Integrated Natal Homing	Tag-Integrated Natal Homing	Tag-Integrated Natal Homing

MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

- Age-invariant random movement patterns centered around a mean rate
- Varies by region
- Tag releases 1% of the abundance-at-age in each area



MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

Model Details:

- Assume data rich
- Observed data are summed for panmictic assessment
- Model inputs are abundance weighted averages
- R_ave estimated
- Initial abundance assumed to be equilibrium unfished abundance-at-age
- Recruitment apportionment is estimated for multi-area models
- Age-invariant annual movement estimated

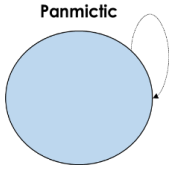
NO MOVEMENT

Simulation Model

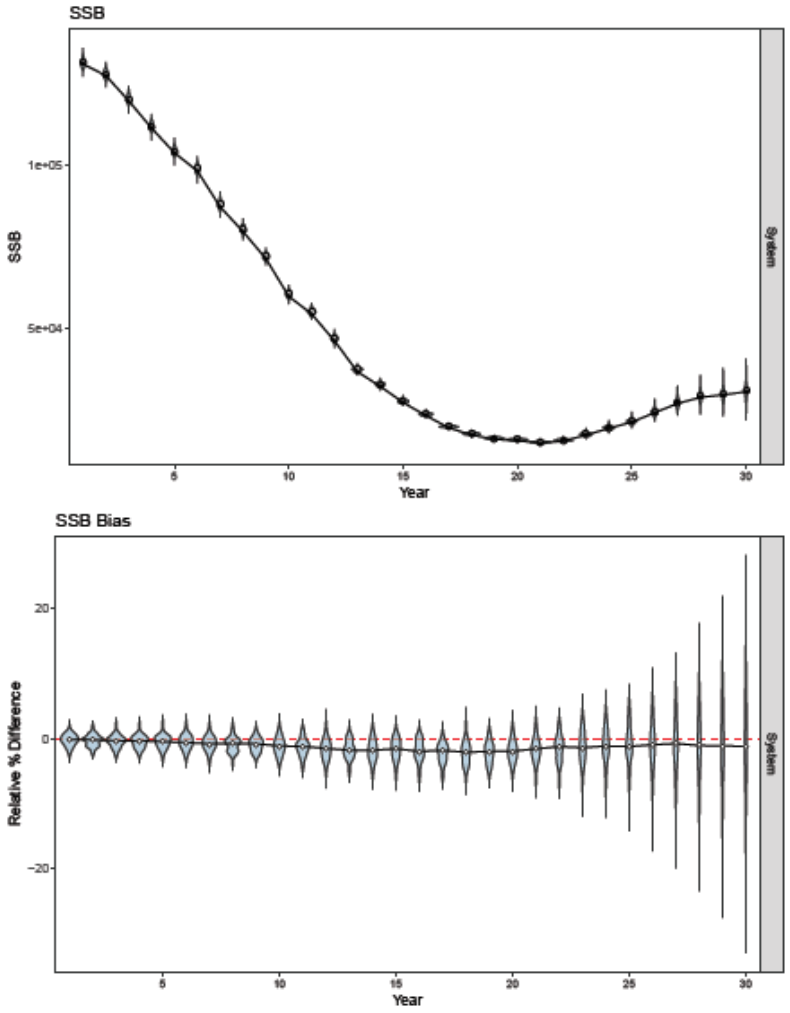
Assessment Model

	Uniform	Multiple Areas	Metapopulation	Natal Homing
	Panmictic	Panmictic	Panmictic	Panmictic
		Fleet-as-Areas	Fleets-as-Areas	Fleets-as-Areas
	Uniform Multi-Area	Tag-Integrated Multi-Area	Tag-Integrated Multi-Area	Tag-Integrated Multi-Area
	Metapopulation	Tag-Integrated Metapopulation	Tag-Integrated Metapopulation	Tag-Integrated Metapopulation
	Natal Homing	Tag-Integrated Natal Homing	Tag-Integrated Natal Homing	Tag-Integrated Natal Homing

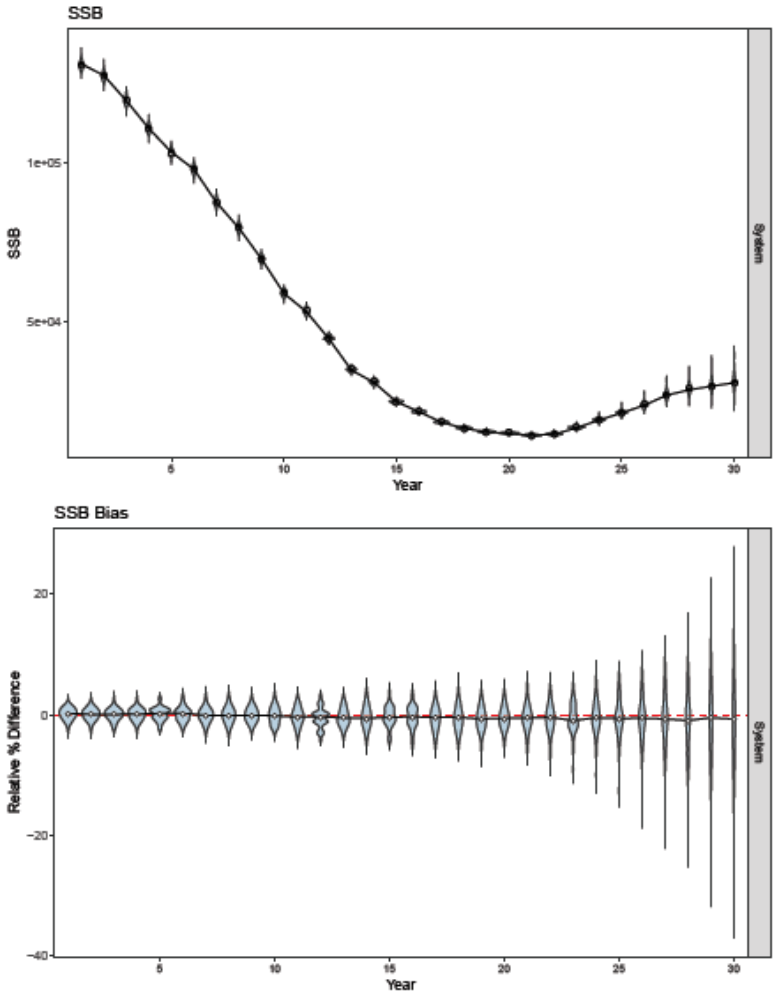
Spawning Stock Biomass



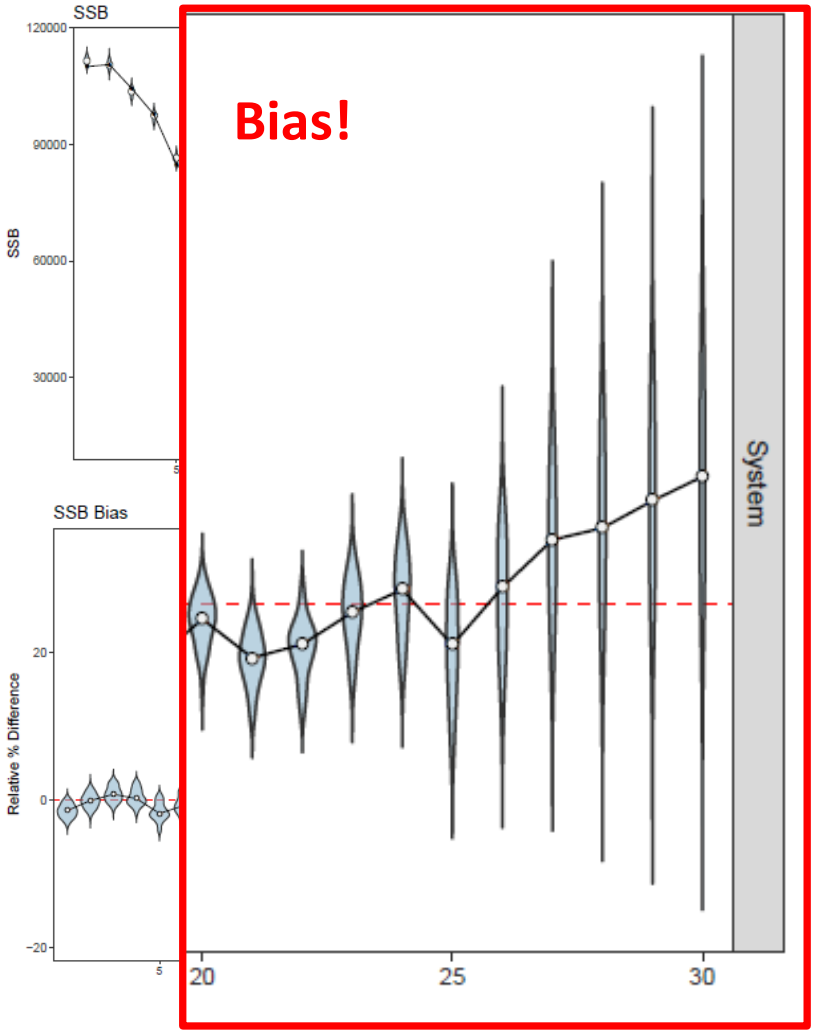
Uniform



Multiple Areas



Metapopulation



MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

Model Details:

- Assume data rich
- Observed data are summed for panmictic assessment
- Model inputs are abundance weighted averages
- R_ave estimated
- Initial abundance assumed to be equilibrium unfished abundance-at-age
- Recruitment apportionment is estimated for multi-area models
- Age-invariant annual movement estimated

NO MOVEMENT

Simulation Model

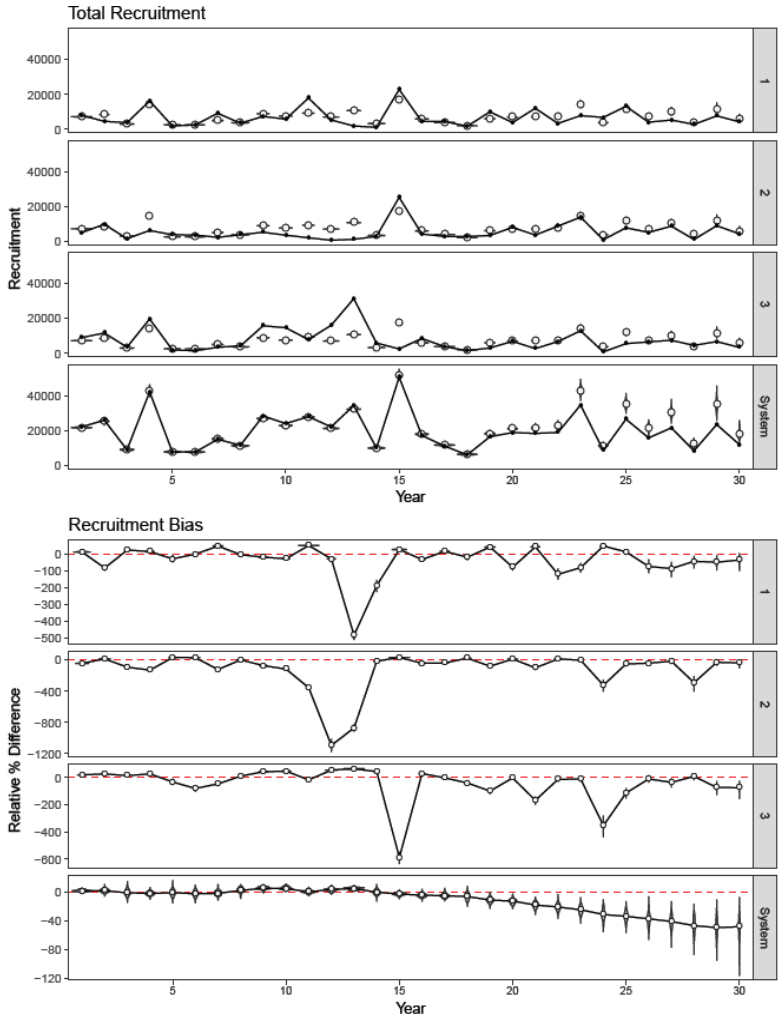
Assessment Model

	Uniform	**Multiple Areas**	**Metapopulation**	**Natal Homing**
	Panmictic	Panmictic	Panmictic	Panmictic
		Fleet-as-areas	Fleets-as-Areas	Fleets-as-Areas
	Uniform Multi-Area	Tag-Integrated Multi-Area	Tag-Integrated Multi-Area	Tag-Integrated Multi-Area
	Metapopulation	Tag-Integrated Metapopulation	Tag-Integrated Metapopulation	Tag-Integrated Metapopulation
	Natal Homing	Tag-Integrated Natal Homing	Tag-Integrated Natal Homing	Tag-Integrated Natal Homing

MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

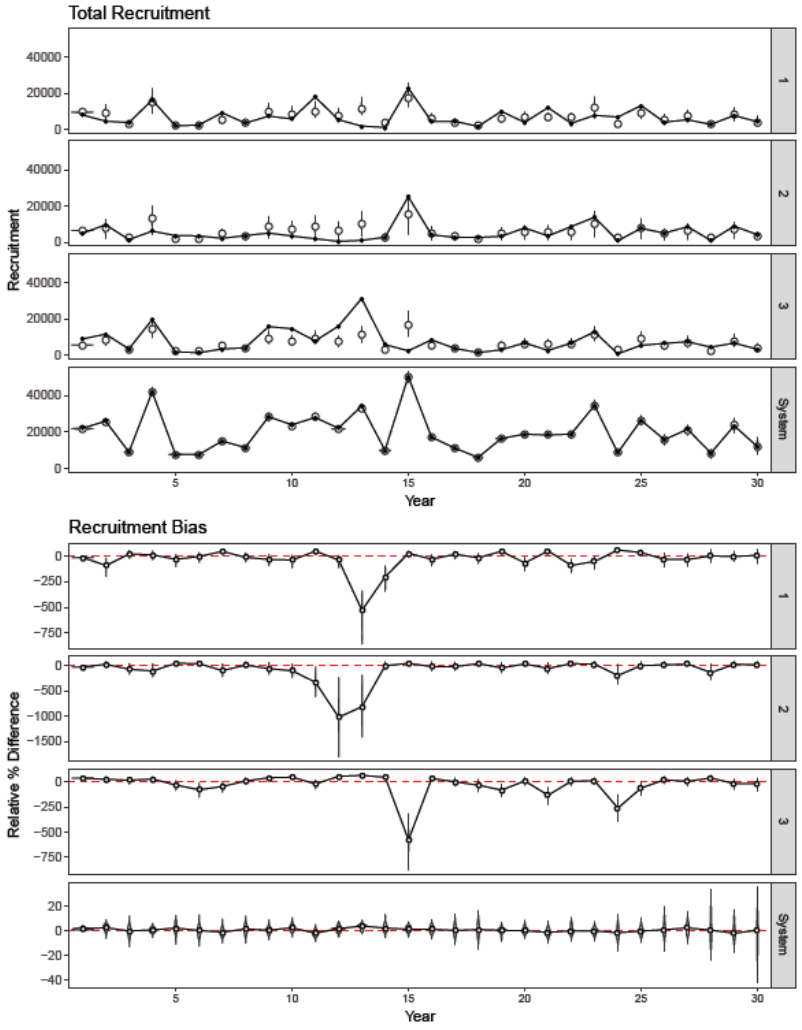
Recruitment Estimation

Fleets-as-Areas

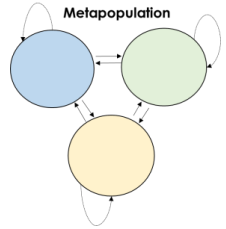


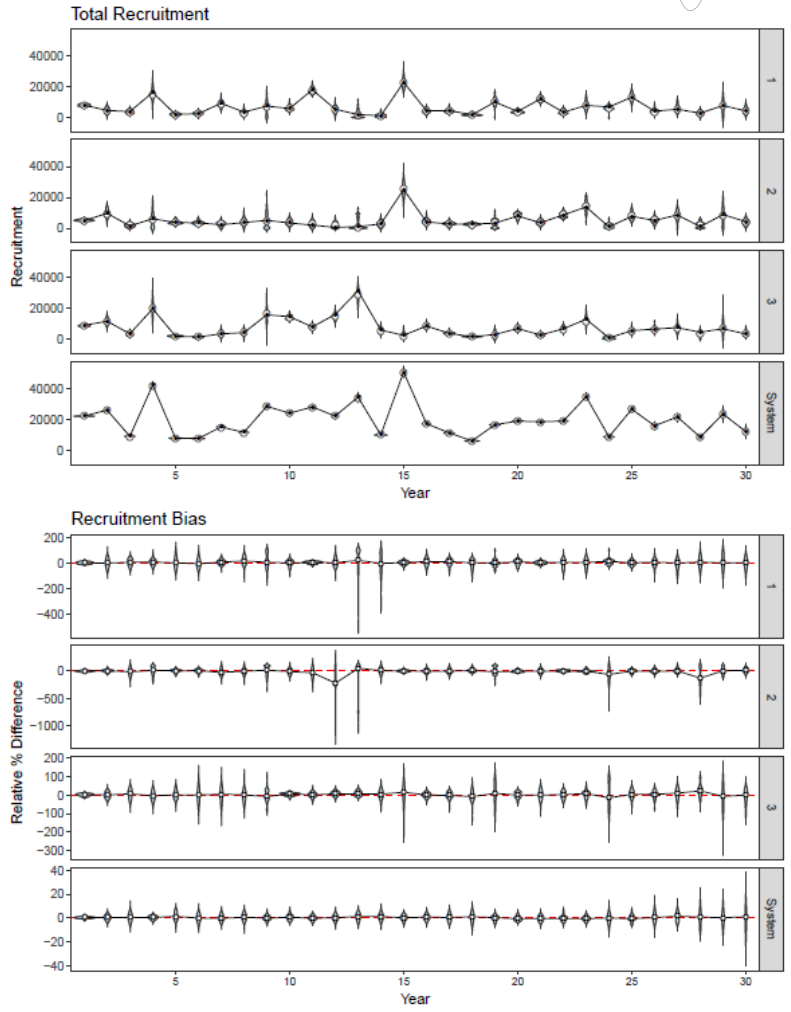
Multiple Areas

54% convergence

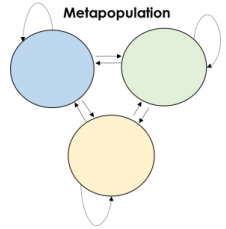


Metapopulation

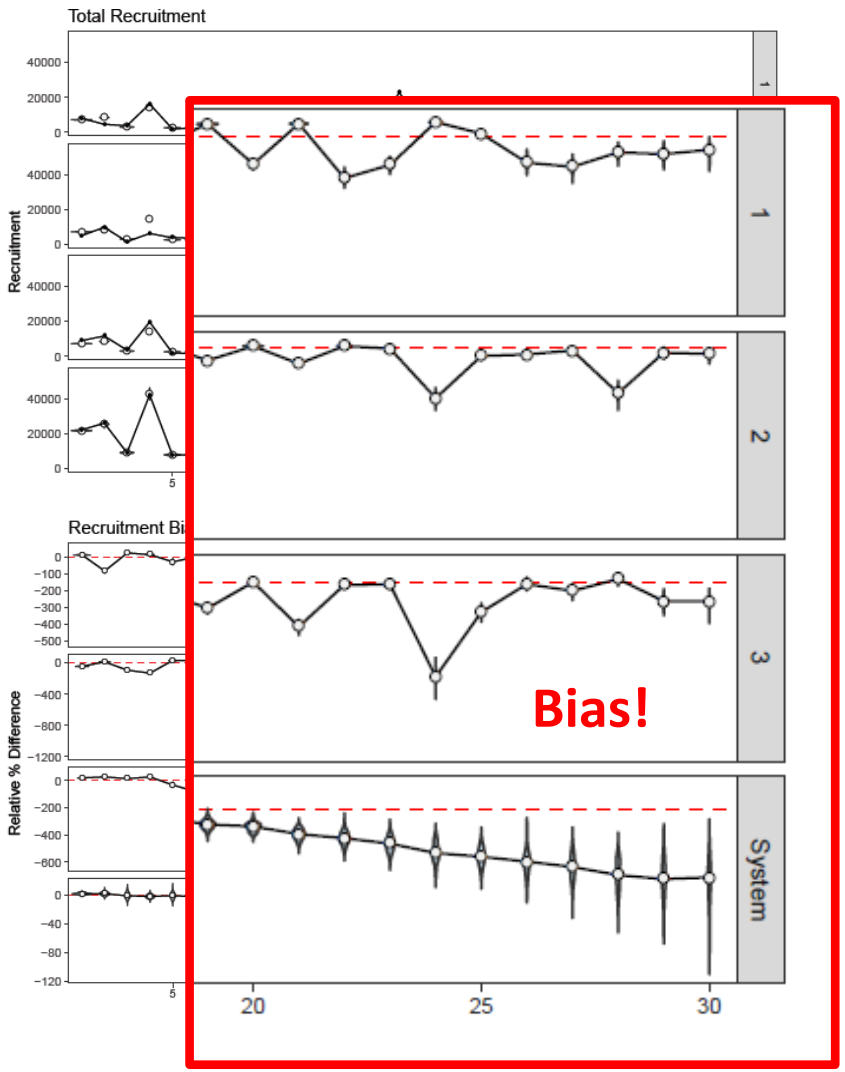




Recruitment Estimation

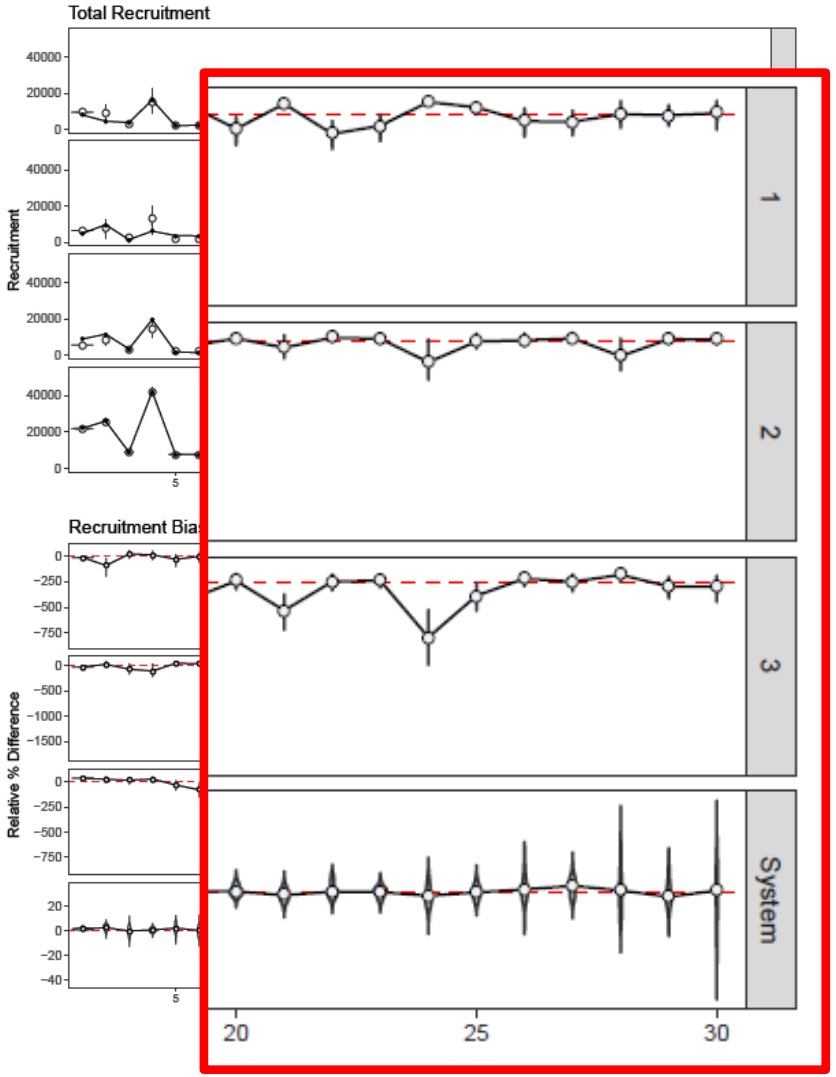


Fleets-as-Areas

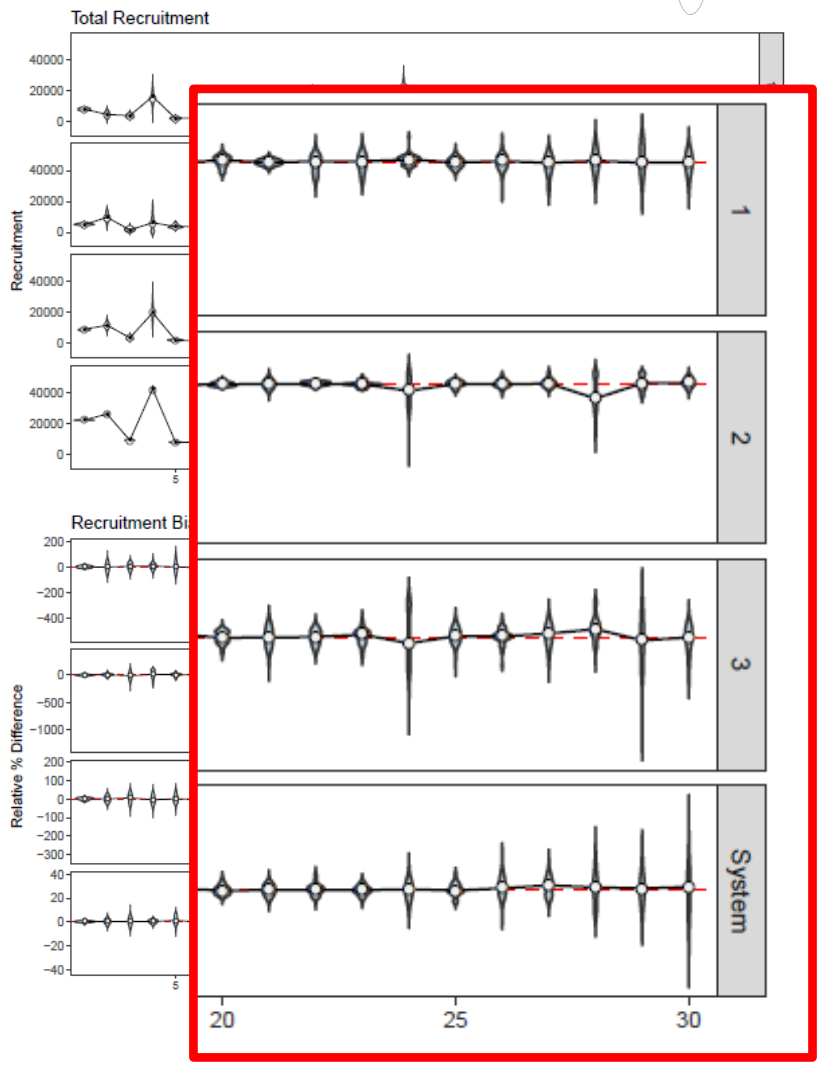


Multiple Areas

54% convergence



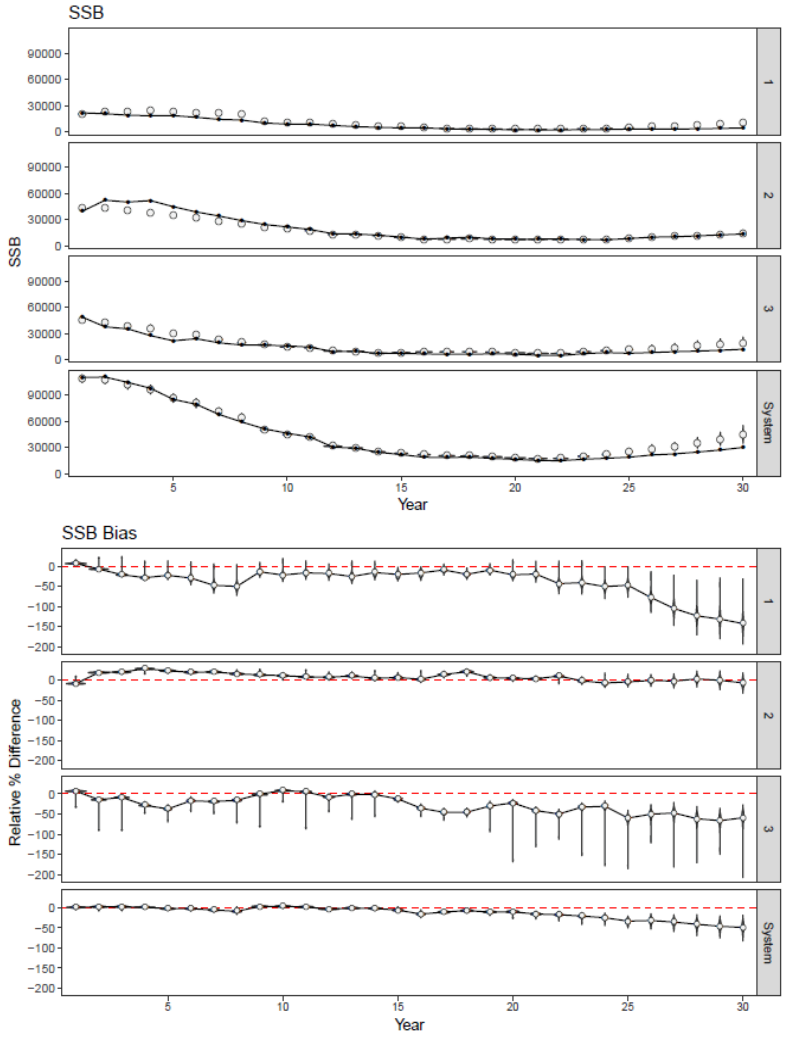
Metapopulation



MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

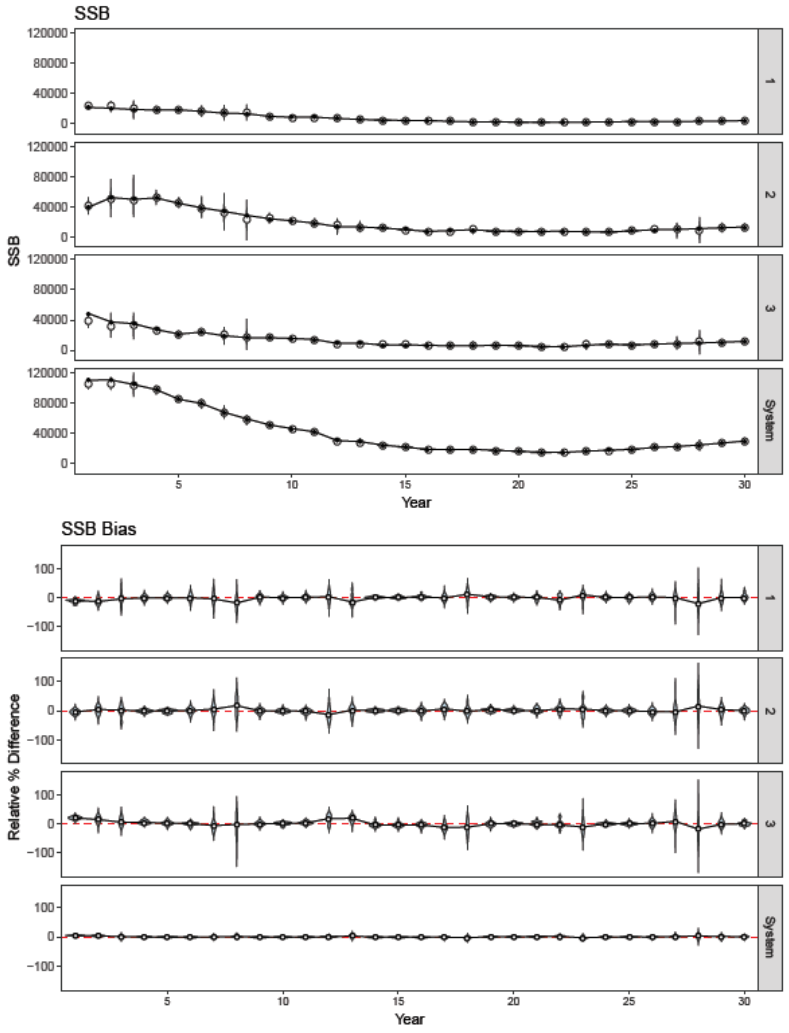
Spawning Stock Biomass

Fleets-as-Areas

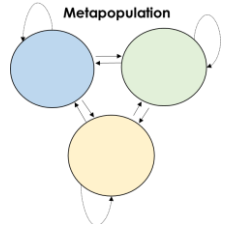


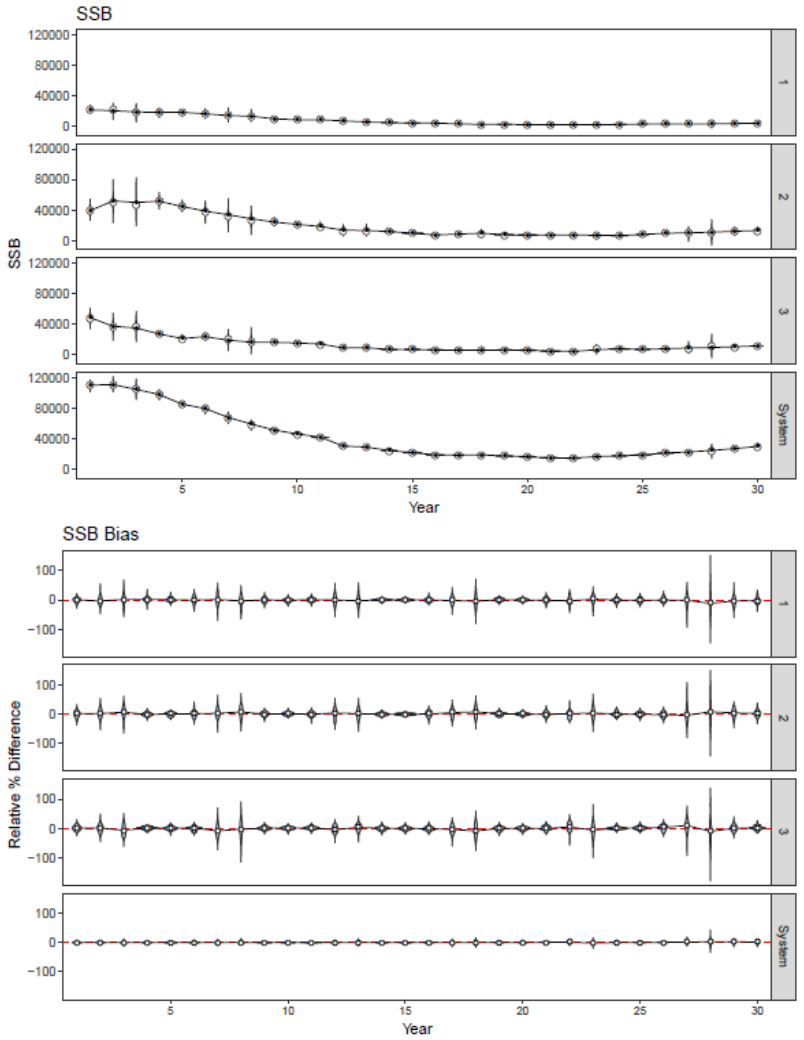
Multiple Areas

54% convergence



Metapopulation

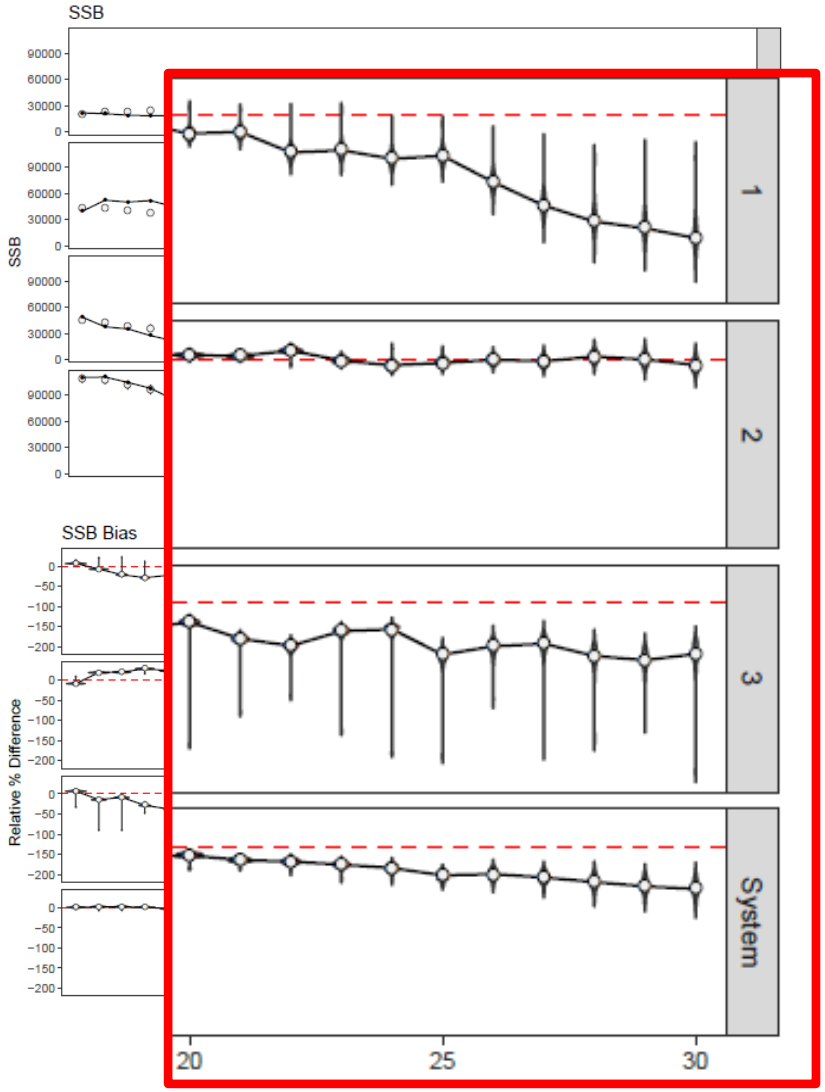




MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

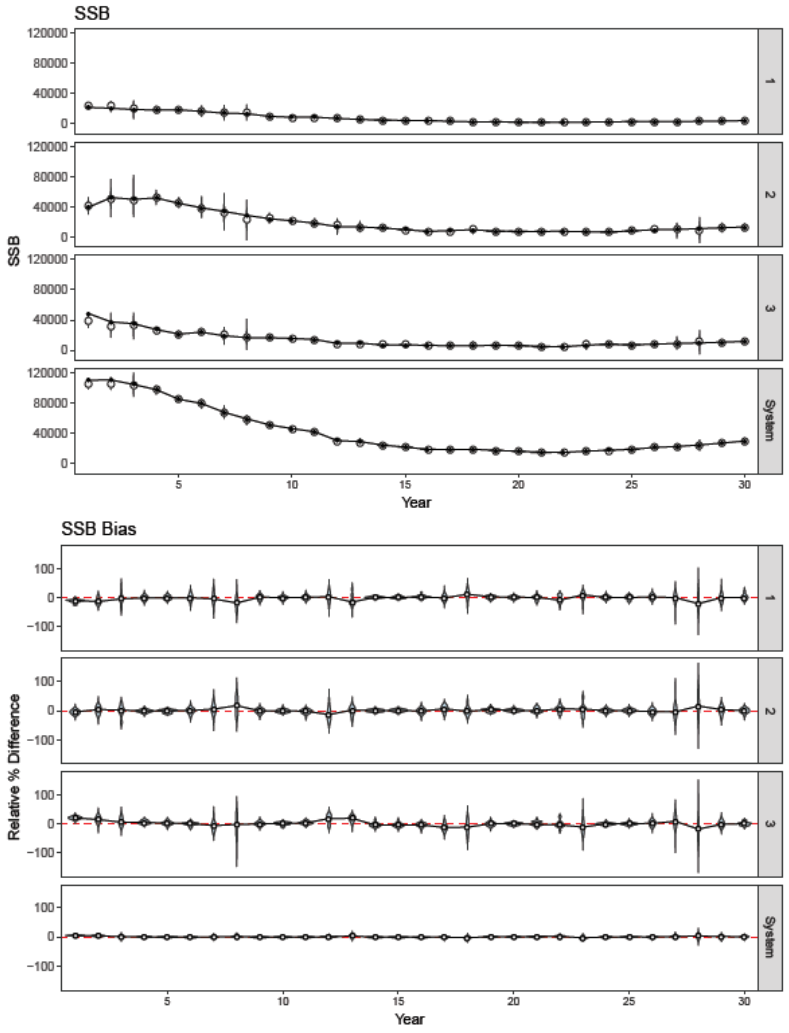
Spawning Stock Biomass

Fleets-as-Areas

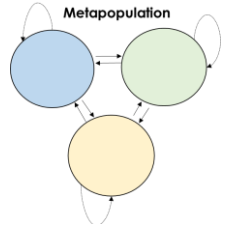


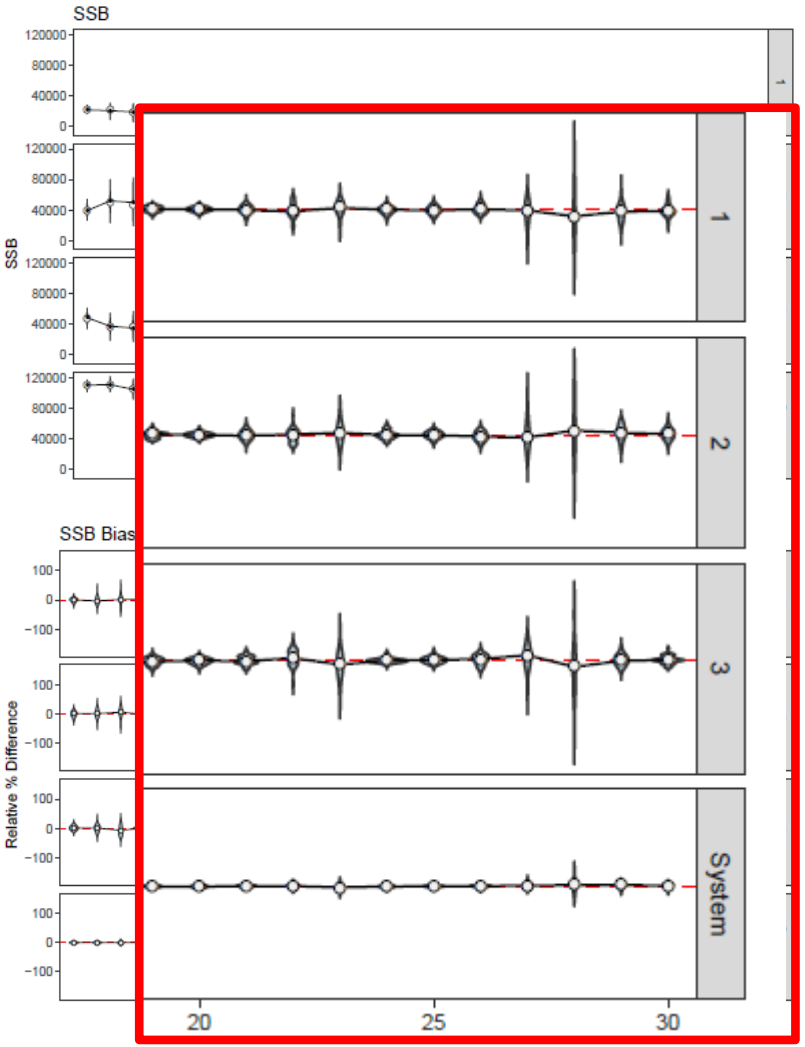
Multiple Areas

54% convergence

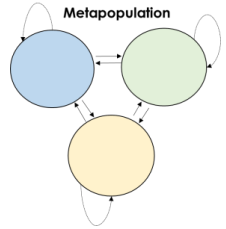


Metapopulation

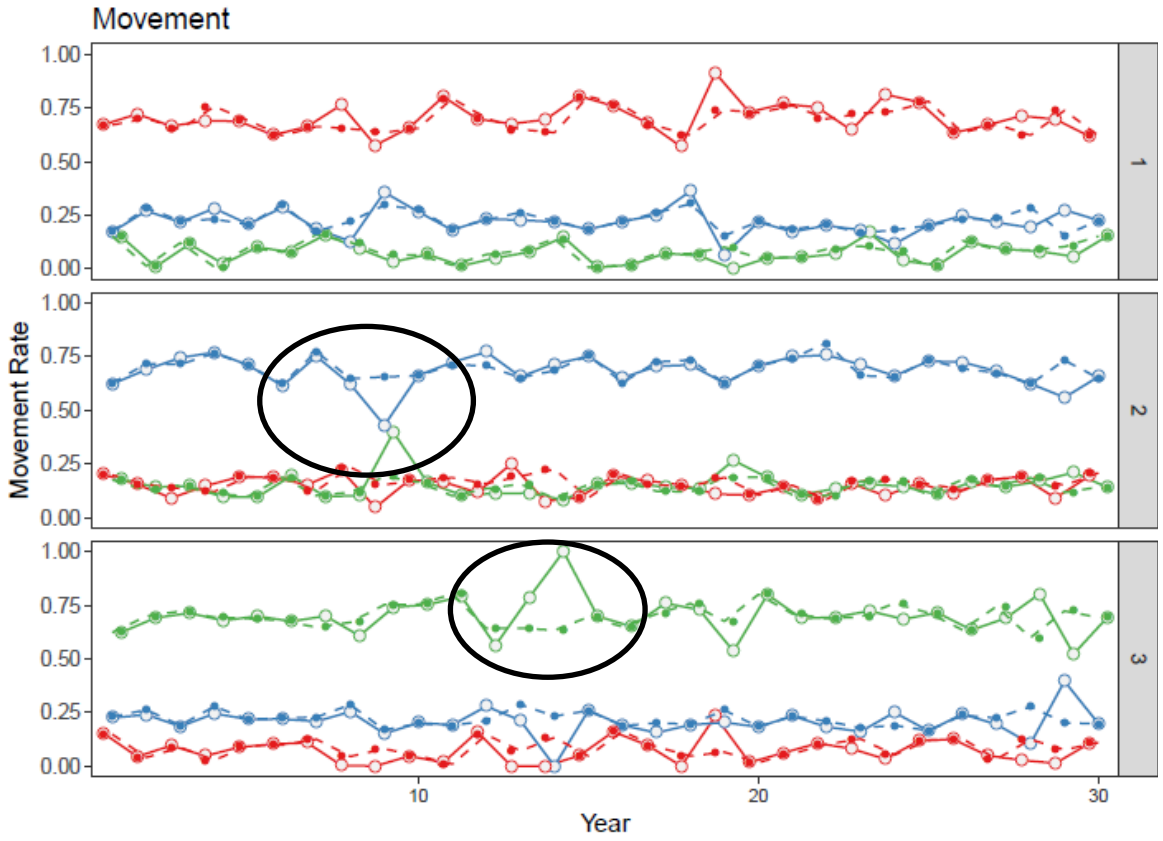




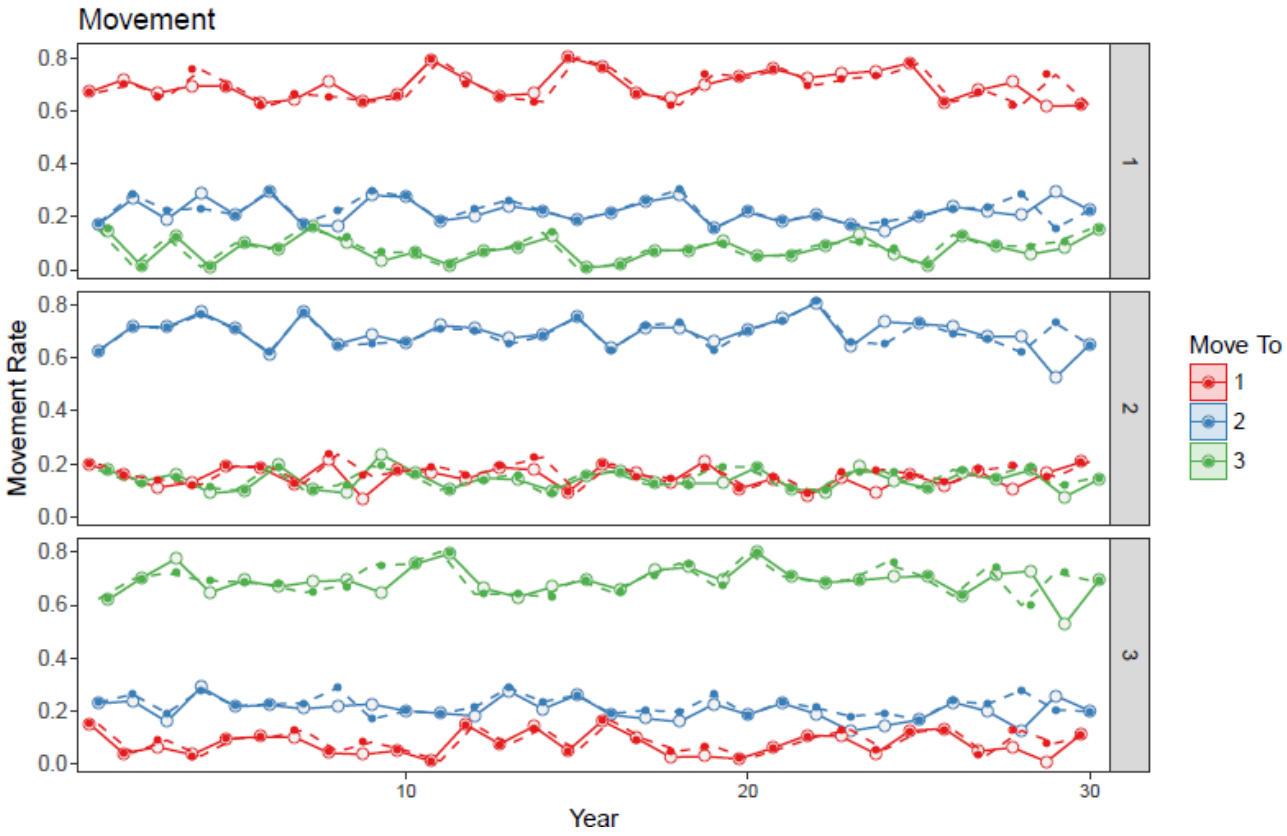
Movement Estimation



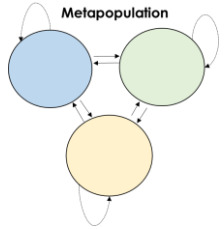
Multiple Areas



Metapopulation

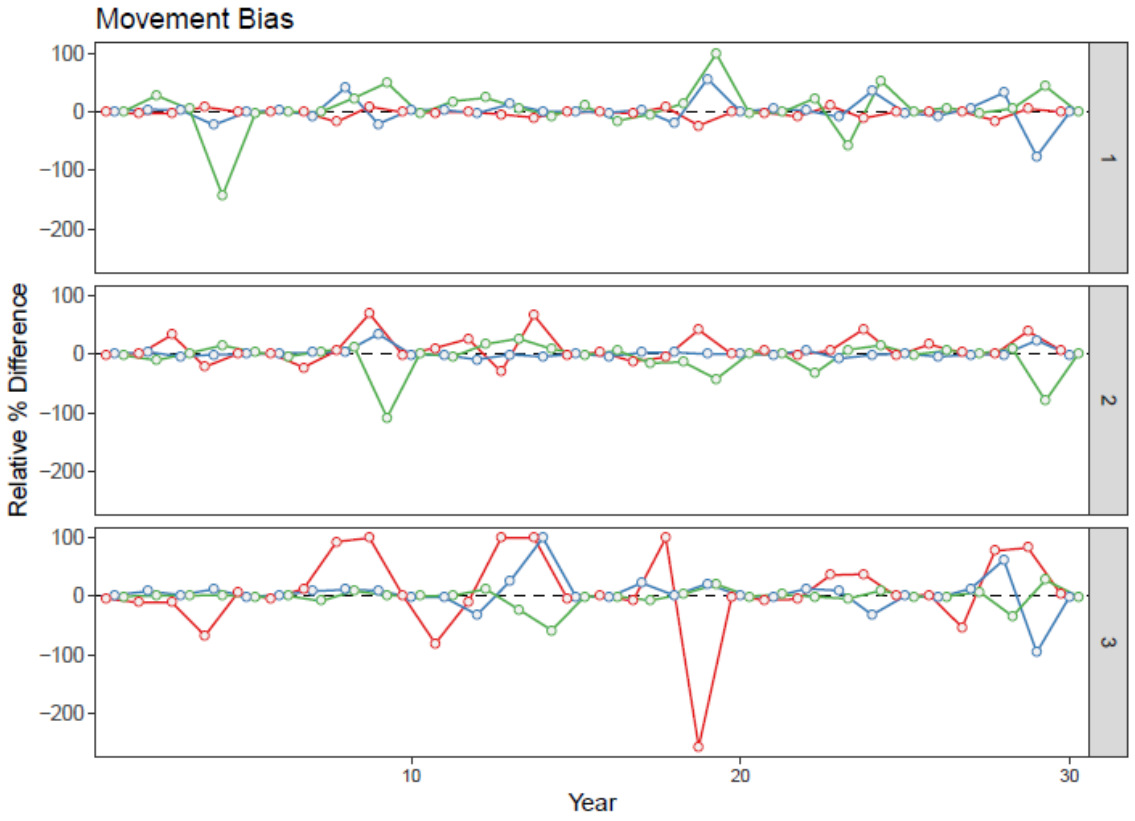


Movement Estimation

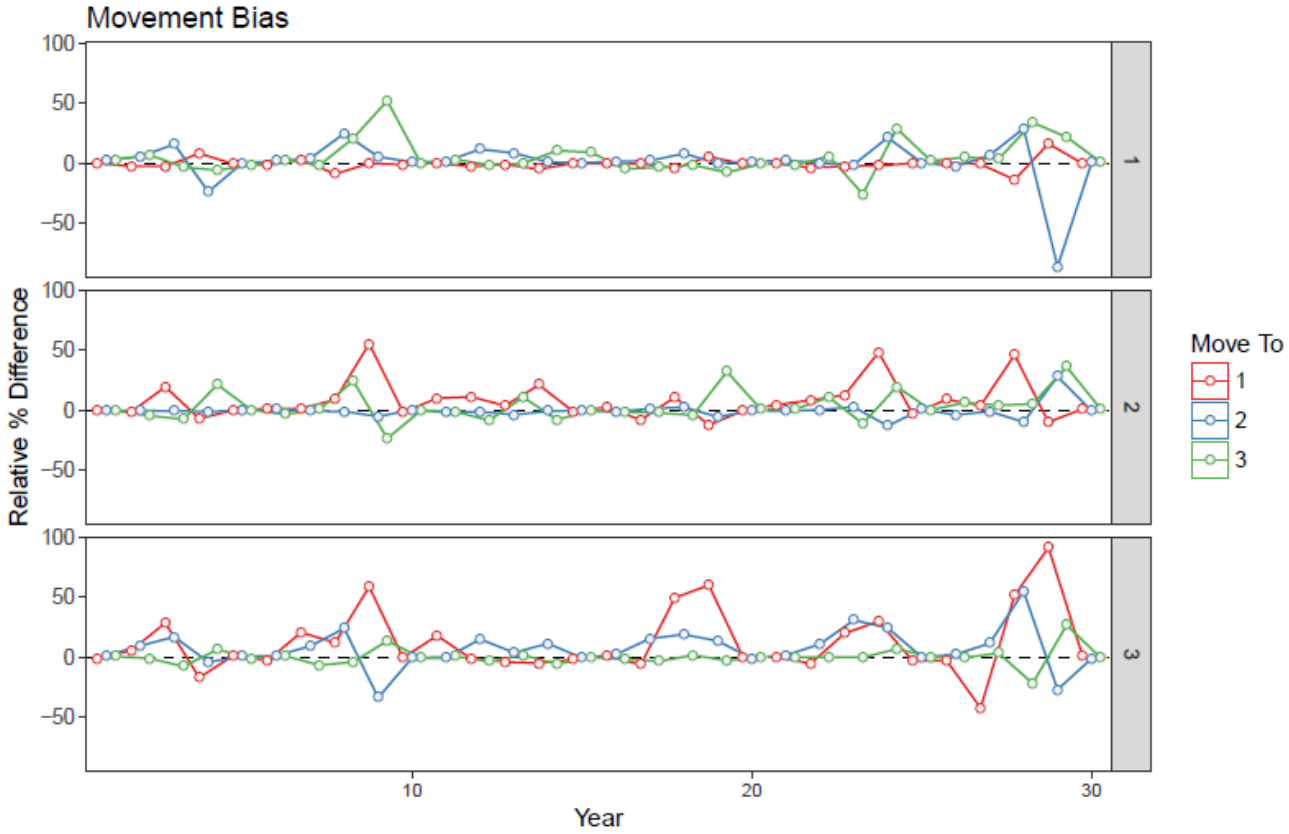


Greater precision when the TRUE and ASSUMED population structures MATCH

Multiple Areas



Metapopulation



~~Conclusions:~~ Looks like…

- Incorrect assumptions of population structure and movement may not lead to biased estimates in productivity **IF** the true and assumed recruitment dynamics match *(i.e. a single stock recruit function vs multiple),* but this may not be true of all scenarios…these results are PRELIMINARY

- **Precision** in estimation of MOVEMENT greatly improves when true and assumed population structures match

- If metapopulation dynamics are suspected, it may be beneficial to assume a spatial model with connectivity

Technical Challenges

- High dimensional arrays (7D arrays!)
- HUGE number of parameters with complex models
- **Computation time!!!** *0.2 min to 1+ hour each sim*
- Operating model parameterizations – some result in poor estimation
- Initialization of 'equilibrium' dynamics
- Low convergence rate with mismatched dynamics

CENTER FOR GENOME RESEARCH & BIOCOMPUTING

NEXT STEPS:

- Apply the model!
- Number of papers planned using the SPASAM framework
- Finish the natal homing component of the models

Acknowledgements

- Kari Fenske (NOAA-AFSC)
- Jim Miller (NOAA-NWFSC)
- Hatfield Marine Science Center

Funding sources

- NOAA Office of Science and technology
- National Research Council
- Stock Assessment Analytical Methods RFP

The National Academies of SCIENCES ENGINEERING MEDICINE

```
}
}
UNCTION get_vitals
/POSSIBLE ADDITIONS:
 //random walk in apportionment or random to give time-varying
 //switch for input recruitment devs by year to recreate a given population
R_ave=ln_R_ave; ///this is annoying...//a quick fix

 for (int p=1;p<=npops;p++)
  {
   for (int j=1;j<=npops;j++)
    {
     for (int r=1;r<=nregions(j);r++)
     {
      for (int y=1;y<=nyrs;y++)
       {
       for (int a=1;a<=nages;a++)
        {
         for (int z=1;z<=nfleets(j);z++)
          {
           weight_population(j,r,y,a)=input_weight(j,r,a);
           weight_catch(j,r,y,a)=input_catch_weight(j,r,a);

           if(maturity_switch_equil==0) // for SPR calculations when maturity across areas is equal or if want a straight ave
            {
             if(SSB type==1) //fecundity based SSB
              {
               ave_mat_temp(j,a,r)=prop_fem(j,r)*fecundity(j,r,a)*maturity(j,r,a);//rearranging for summing
               ave_mat(j,a) = sum(ave_mat_temp(j,a))/nregions(j); //average maturity across regions
               wt_mat_mult(j,y,a)=ave_mat(j,a);//for SPR calcs
              }
             if(SSB_type==2) //weight based SSB
              {
               ave_mat_temp(j,a,r)=prop_fem(j,r)*weight_population(j,r,y,a)*maturity(j,r,a);//rearranging for summing
               ave_mat(j,a) = sum(ave_mat_temp(j,a))/nregions(j); //average maturity across region
               wt_mat_mult(j,y,a)=ave_mat(j,a);//for SPR calcs
              }
            }
           if(maturity_switch_equil==1)
            {// calculates the weighted average matruity based on equilibrium apportionment of SSB
             if(SSB_type==1) //fecundity based SSB
              {
               ave_mat_temp(j,a,r)=prop_fem(j,r)*fecundity(j,r,a)*maturity(j,r,a)*equil_ssb_apport
               ave_mat(j,a) = sum(ave_mat_temp(j,a))/nregions(j); //average
               wt_mat_mult(j,y,a)=ave_mat(j,a);//for SPR calcs
```

Development models can be found at…

https://github.com/KatelynBosley/SPASAM

Photo credits:

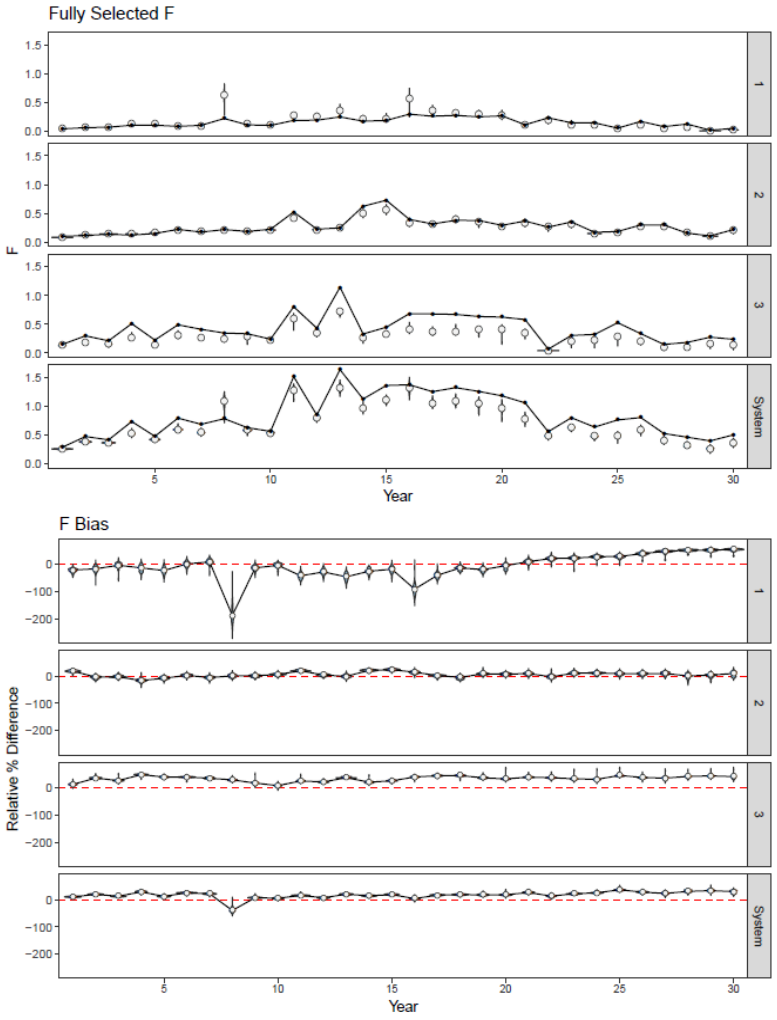
http://pacificrichresources.com/site/assets/files/1417/black_cod.jpg
http://www.alaskabroker.com/listings/sablequota.html

NOAA NATIONAL OCEANIC AND ATMOSPHERIC ADMINISTRATION U.S. DEPARTMENT OF COMMERCE

MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

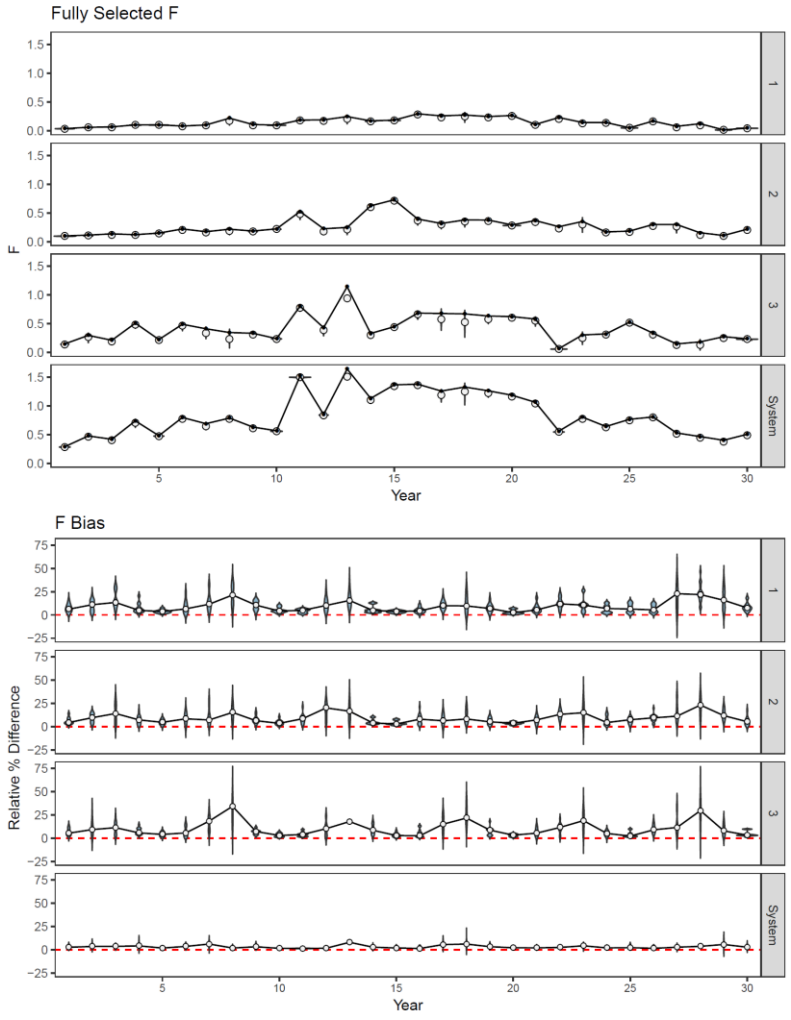
Fishing Mortality

Fleets-as-Areas

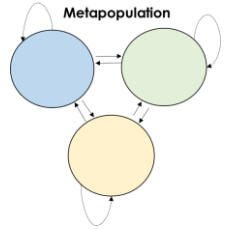


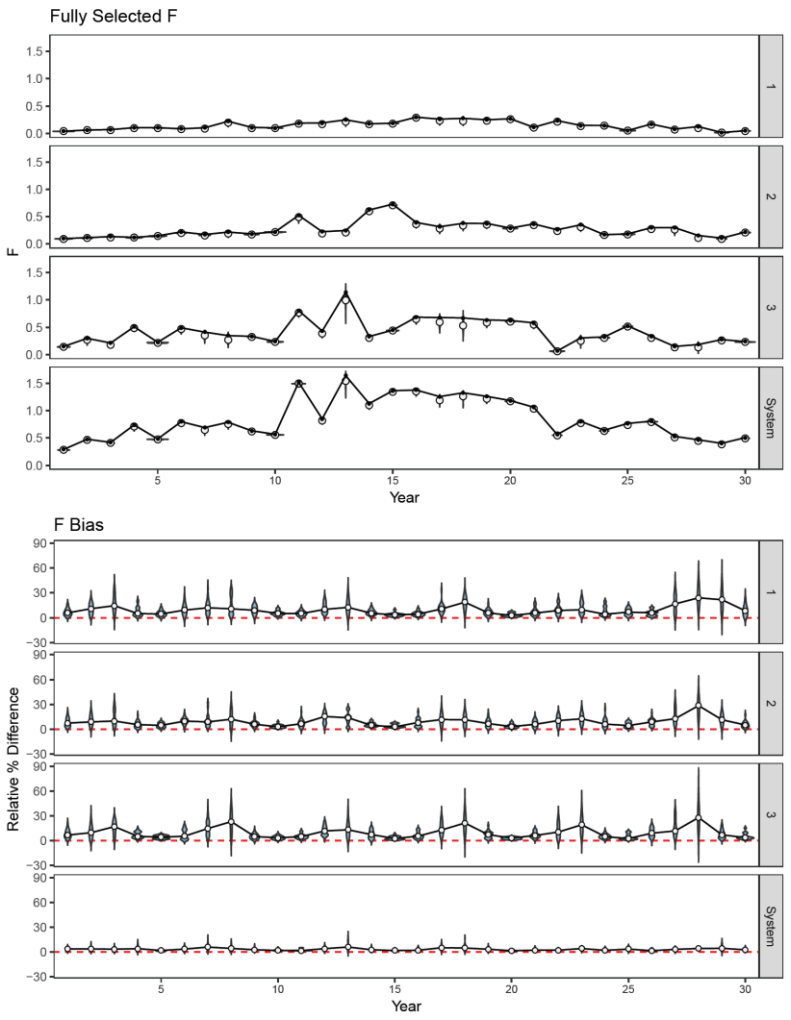
Multiple Areas

54% convergence



Metapopulation

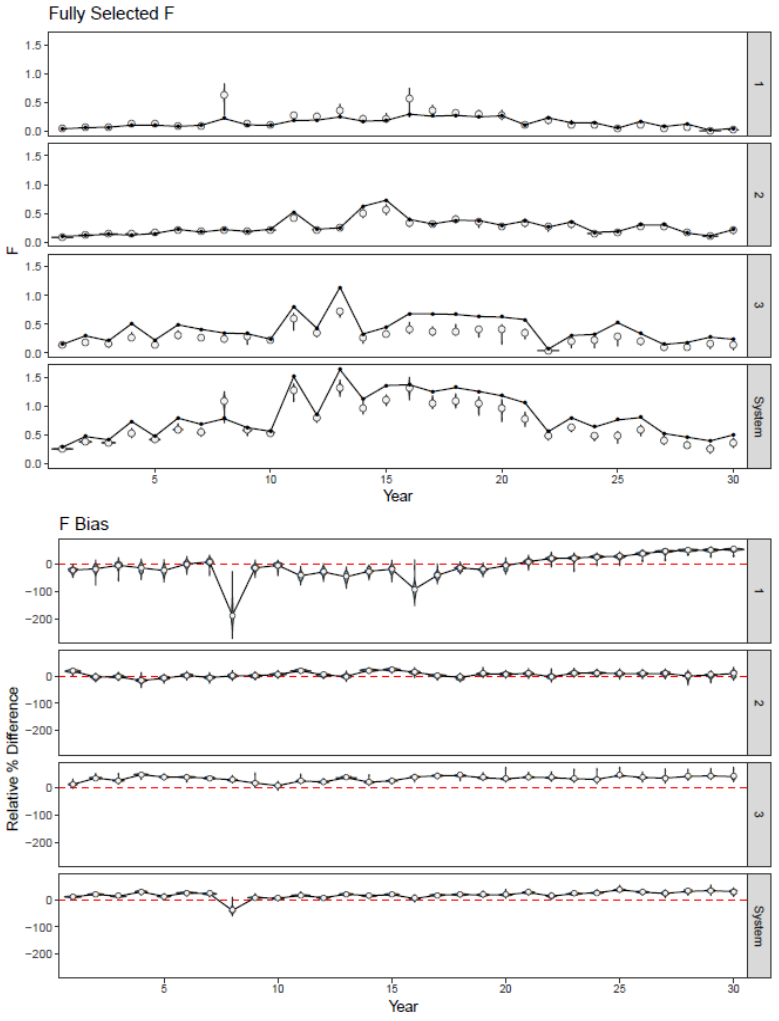




MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

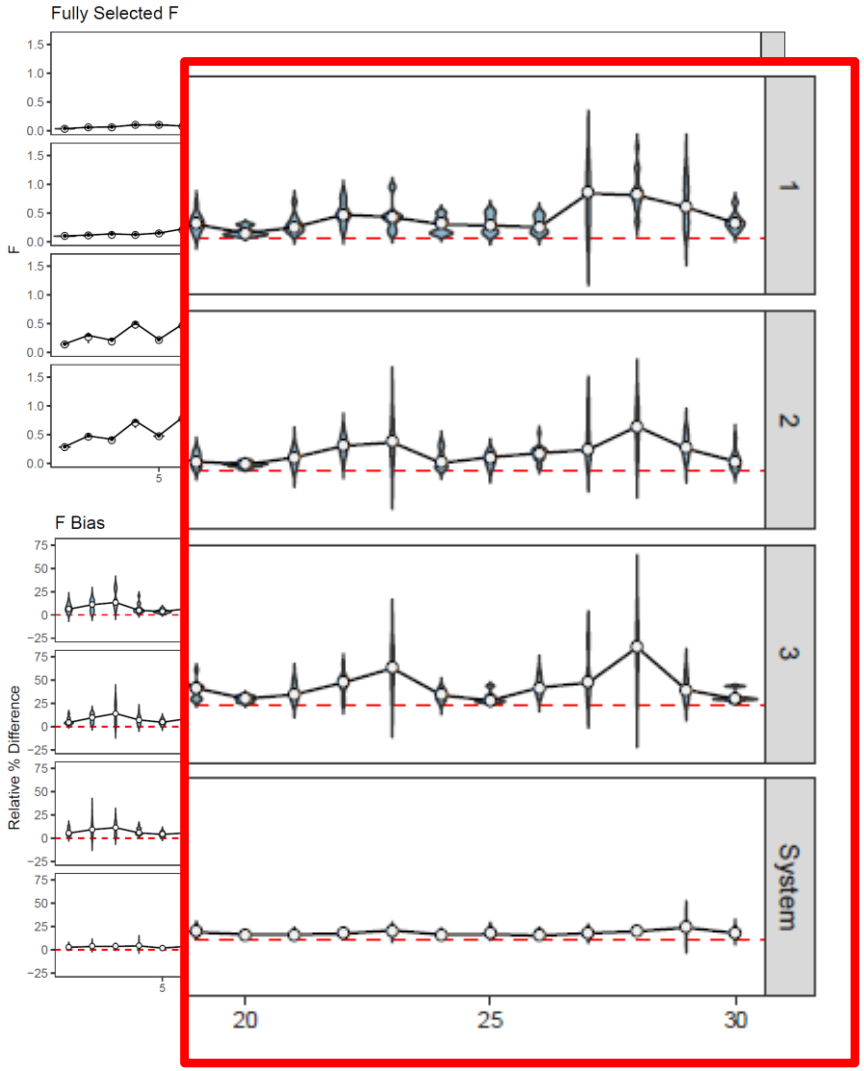
Fishing Mortality

Fleets-as-Areas

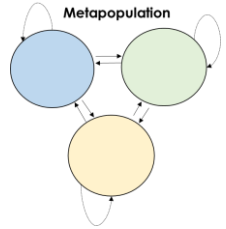


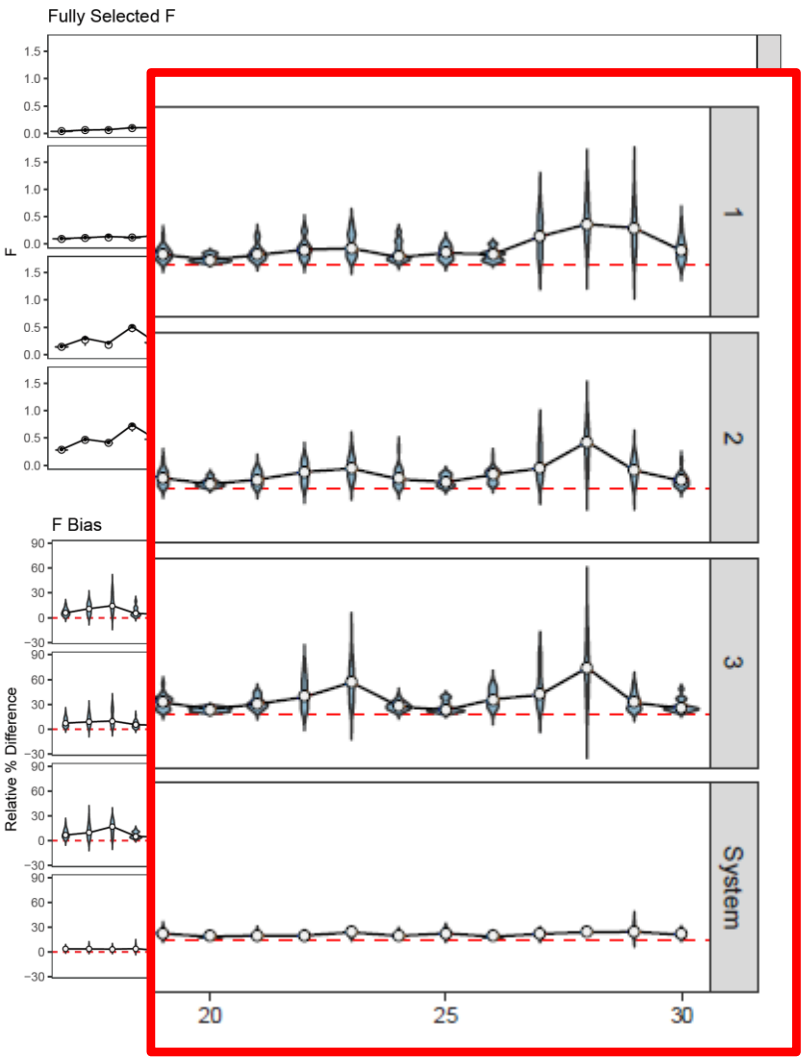
Multiple Areas

54% convergence



Metapopulation





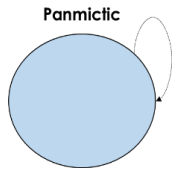
Estimation Model Specifics

Population dynamics equations are identical to Operating Model

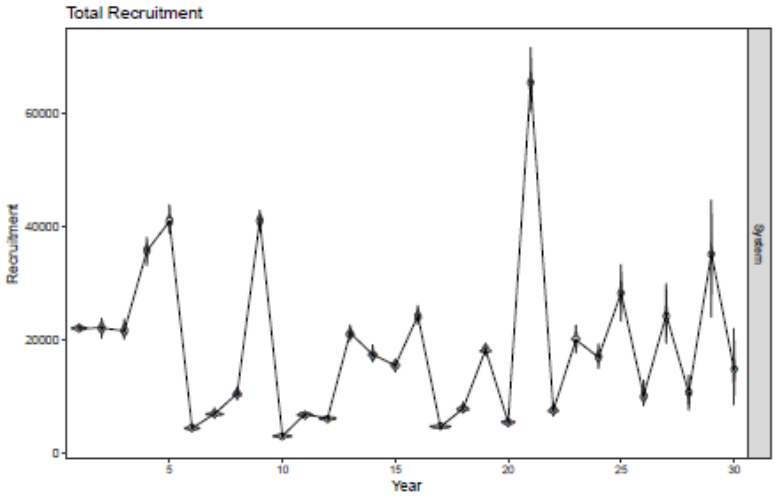
ESTIMATED PARAMETERS
R0/R average
Recruit deviations/apportionment
Initial Abundance
Fishery Selectivity
Survey Selectivity
Catchability (q)
Fishing Mortality
Movement
Tag Reporting Rate
Mortality

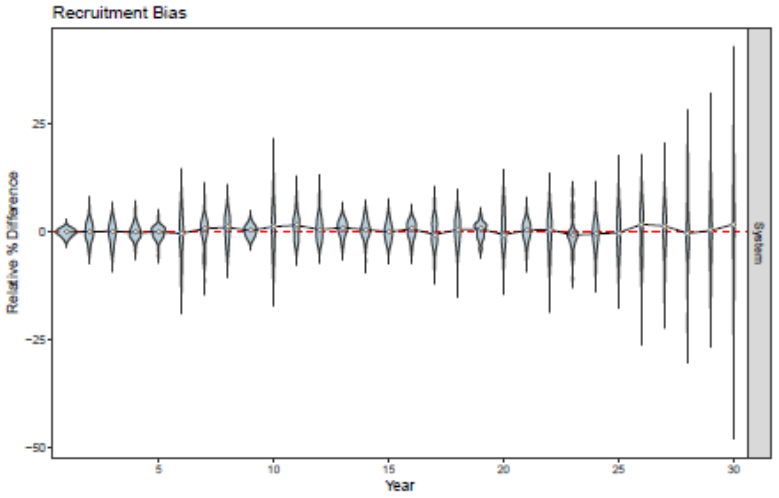
- **Generalized spatially explicit**
  - *Populations/Regions/Fleets*
- **Fit to observed data with error**
  - *Age composition, indices, tag recoveries*
- **Incorporates process error**
  - *Recruitment, movement, population structure*
- **Multiple movement parameterizations**
  - *Constant, time-varying, age-based*

Recruitment Estimation

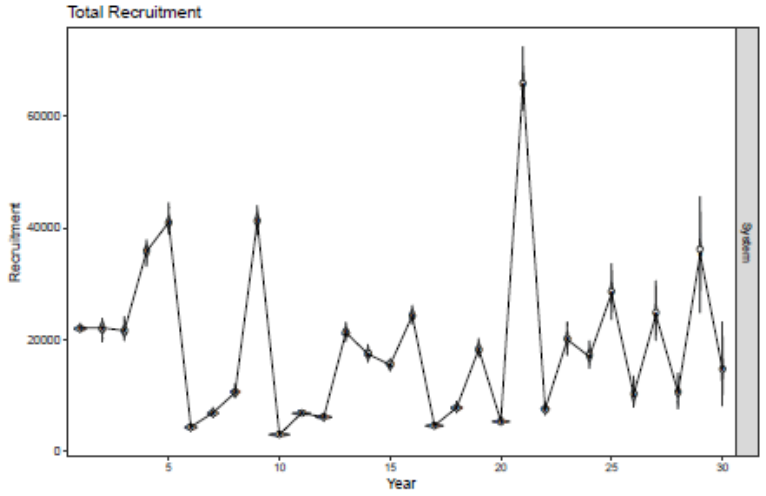


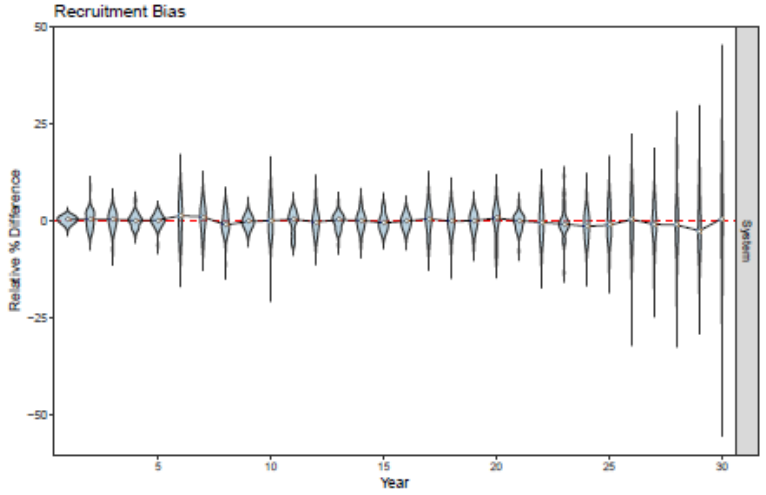
Uniform



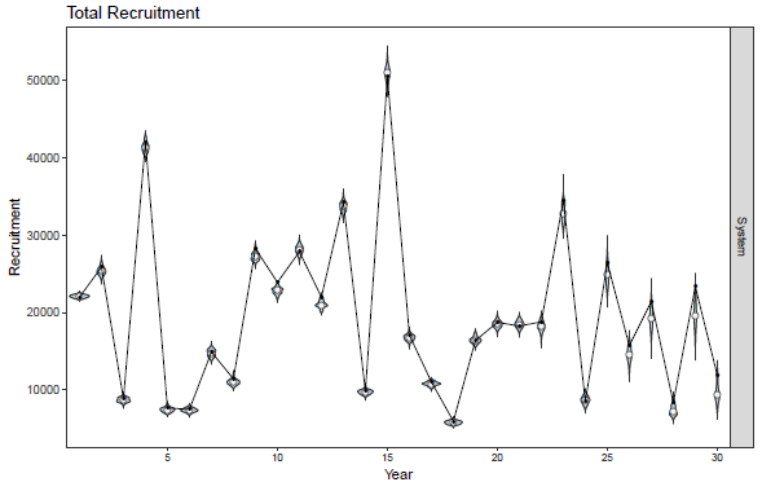


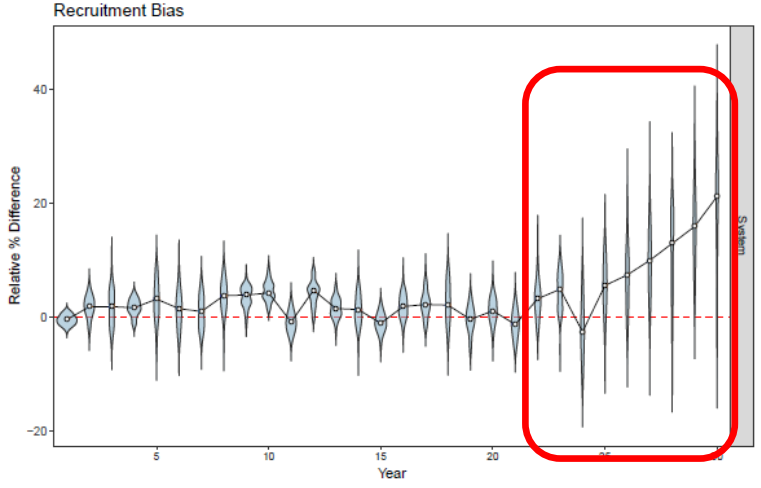
Multiple Areas





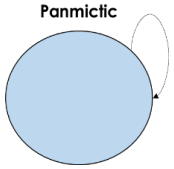
Metapopulation



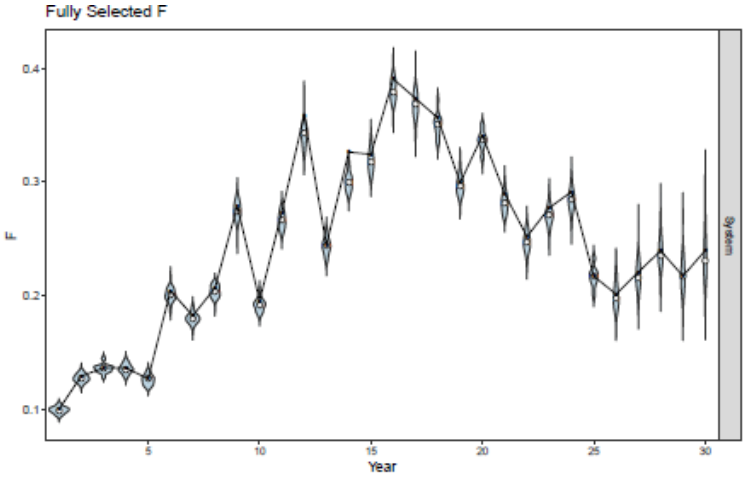


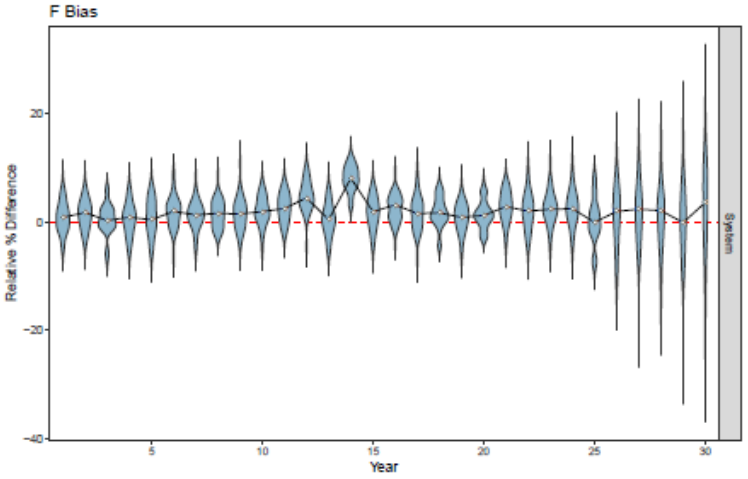
MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

Fishing Mortality

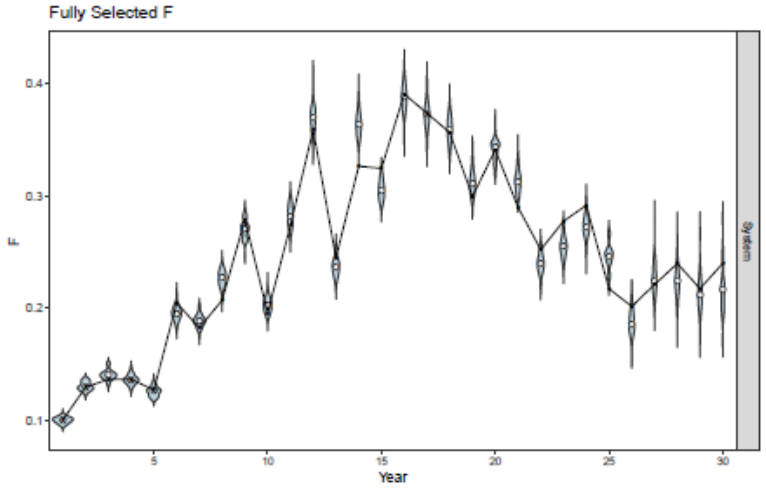


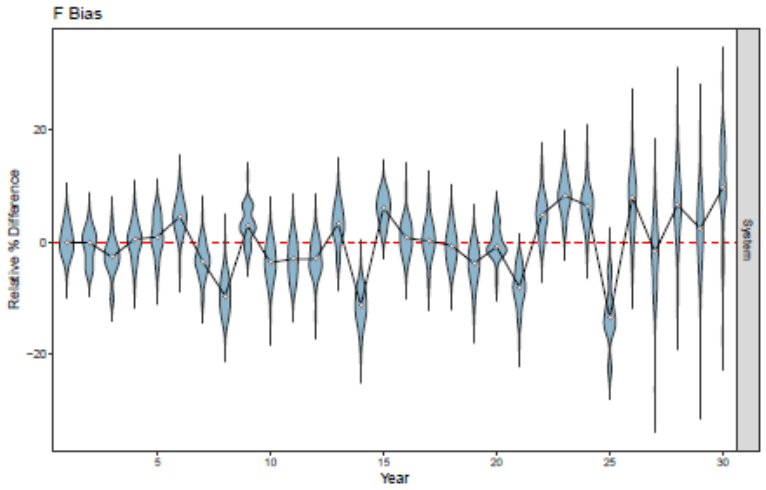
Uniform



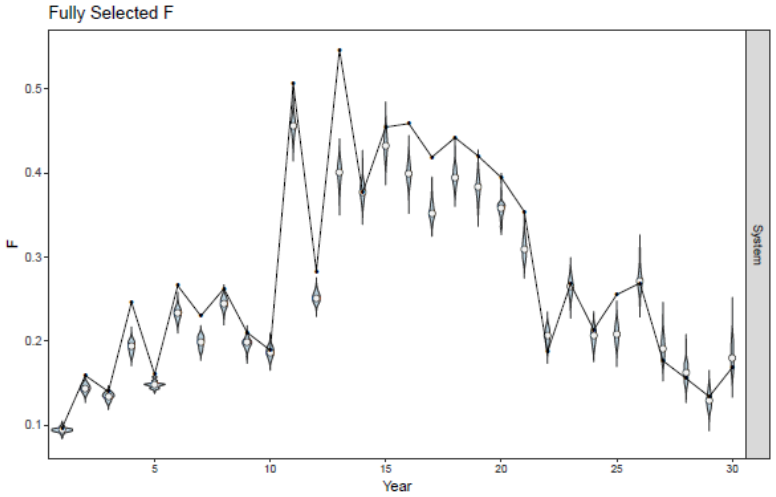


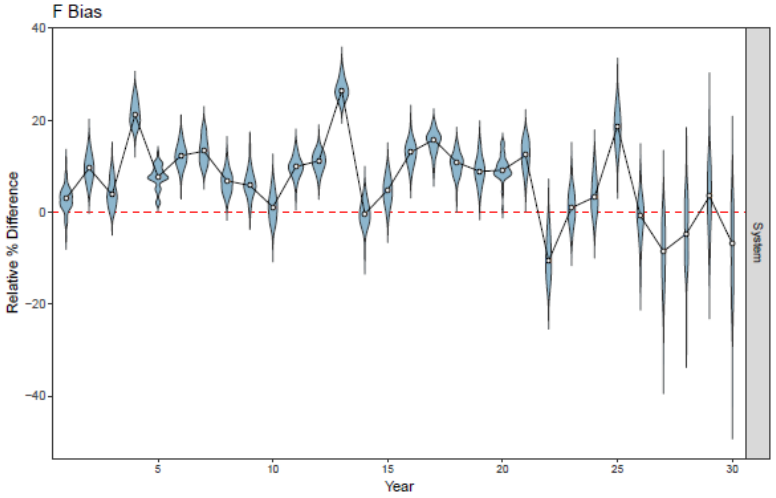
Multiple Areas





Metapopulation



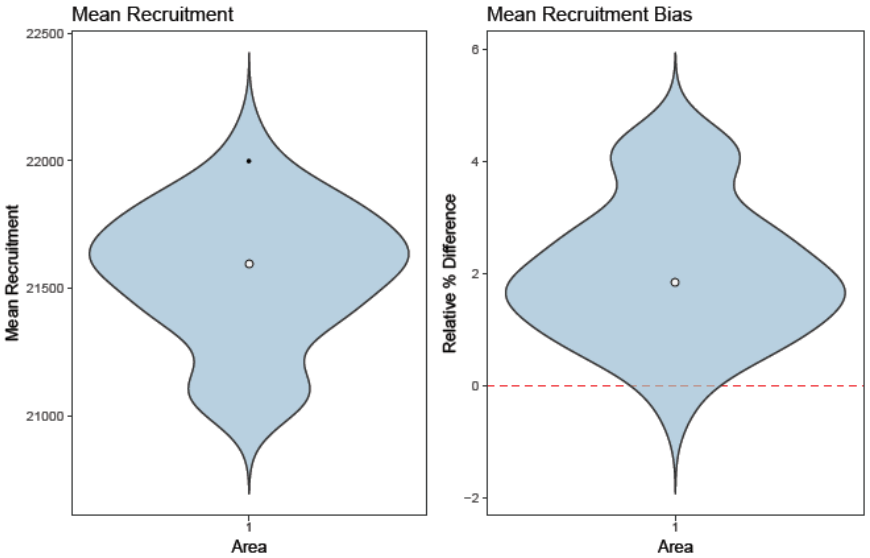


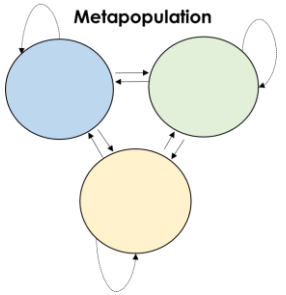
MODEL APPLICATION: MODEL MISSPECIFICATION EXPERIMENT

Recruitment Average *(R0)*

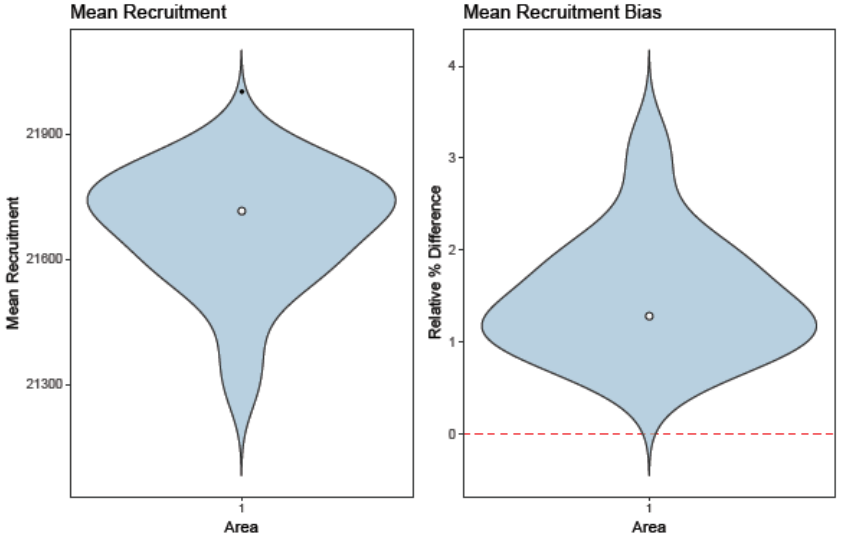
Panmictic

Fleets-as-Areas

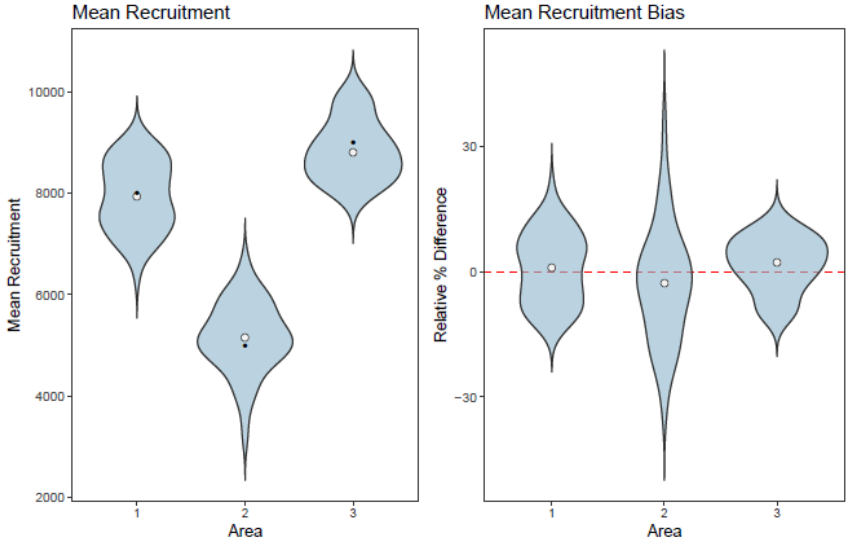




Multiple Areas



Metapopulation



NOAA Sablefish Tagging Program

Annual longline survey (June-August)

- T-bar anchor tags on ~1500-3500 sablefish per year (**5%** of catch); Bering Sea and Aleutian Islands in alternating years, Gulf of Alaska every year
- Tagging time series early 1970s – present (**40+years!**)
- ~370,000+ tagged fish released to date
- Recaptured through survey and fishery (**33,000+ recoveries**); 650-750/year
- Also some satellite tagging occurs on large (80+ cm) fish for special projects

Gold Standard for the application of spatial models