Stock Synthesis Tutorial

CAPAM Spatial Assessment Models Workshop
Oct. 01, 2018, La Jolla, CA

From: Mark Maunder
To: Juan Valero
Subject: SS spatial models

Juan.

I have tried everyone to teach a SS course on the Monday morning of the CAPAM workshop. Spatial model, movement, and integrated tagging. **But nobody can do it**. Do you have experience and are you willing to do it?

Mark
IATTC

From: Juan Valero
To: Mark Maunder
Subject: Re: SS spatial models

Mark,

Yes, it should work. I have some materials and experience on spatial models and movement, less so re: use of integrated tagging in stock assessment models ... We should be further ahead on the spatial BET by then so that would be useful too.

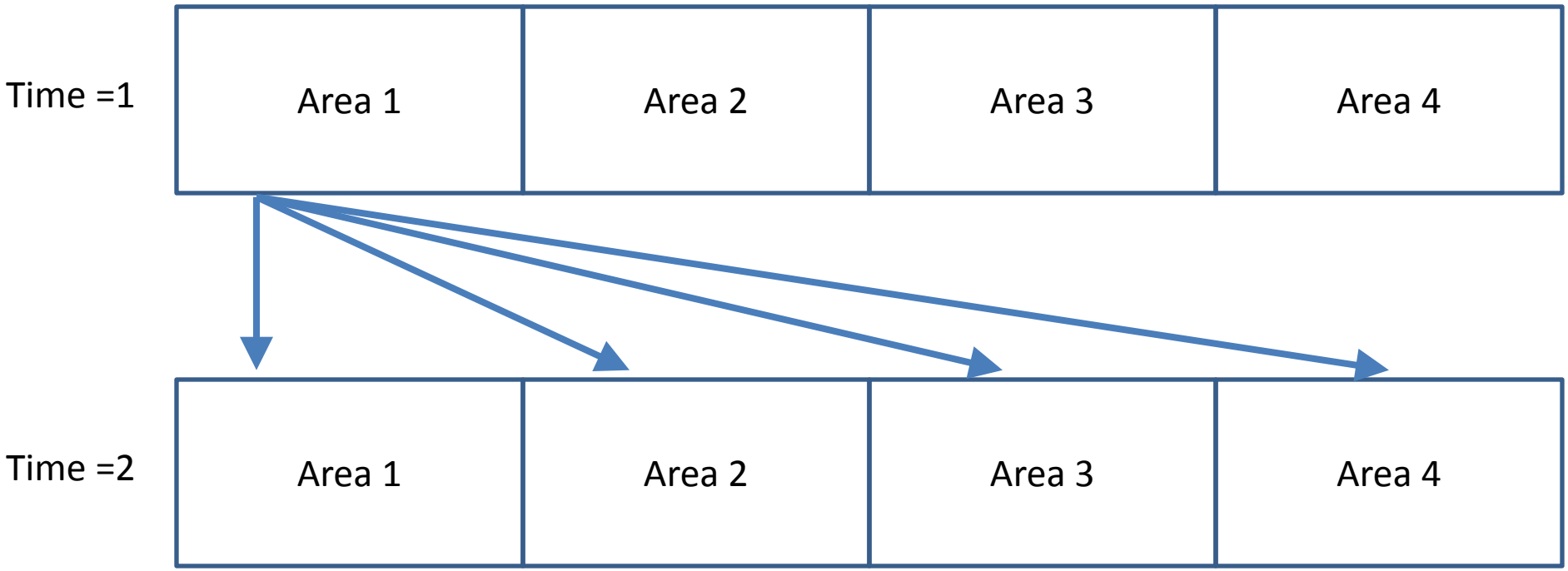
Juan

Stock Synthesis spatial options

- Any number of areas
  (limited by memory, speed, data…)
- Fleets are all area-specific
- Design matrix for movement between areas for each season, growth pattern
- Global recruitment partitioned to areas
- Uses generalized framework for parameters in SS (priors, time-varying options, etc.)

Movement in Stock Synthesis

- Box transfer with no explicit adjacency of areas, so fish can move from any area to any other area in each time step.



Movement in Stock Synthesis

- Two parameters per movement definition to allow separate rates for young (A) and old (B) fish, with ramp in between (linear in log space)
- For each source area the implicit movement parameter value is 0.0
- Exponentiated and scaled to sum to 1.0:

$$\text{rate}_i = e^{p_i} \Big/ \sum_{j=1}^{N} e^{p_j} \qquad p_i = \log\left(\frac{\text{rate}_i}{\text{rate}_1}\right) \text{ if } p_1 = 0$$

Movement in Stock Synthesis

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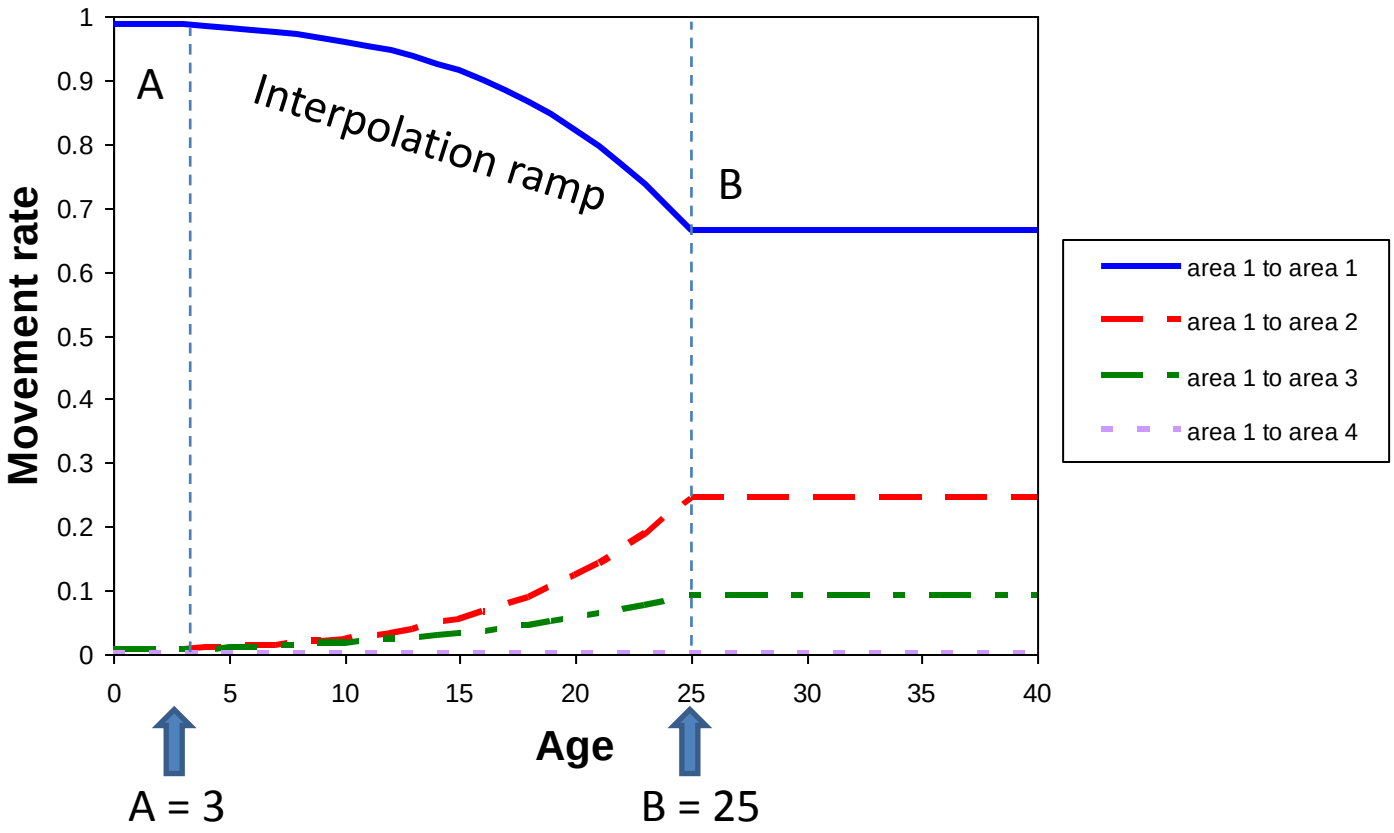


Movement and Areas in SS

- A fleet operates in only one area
  - but a fleet in one area can mirror a fleet in another area
- Movement at end of each season
  - fraction of fish in area A that move to area B
- The equilibrium calculator starts by distributing the total recruits to areas, settlement events, and morphs

Movement and Areas in SS (biology)

- Biology is assigned to morphs, not areas. So when fish move they retain same biological characteristics
  - it would be feasible to have area-specific M, but might be challenging to retrofit now
  - it would be feasible to have area-specific growth such that the mean size of fish in an area are weighted mean of the fish that stay in that area and the size of the fish entering that area. Lots of coding to do this, but seems feasible.

Movement and Areas in SS (tags)

- When a tag group is released in an area, p, at time, t, at age, a, they are distributed proportionally among all biology morphs according to the current distribution of morphs at that p, g, a,
- Then each p.g component of that tag group moves to other areas according to the movement parameters for that p,g; and in an area they experience F*selex and M along with their p,g group.

Recruitment

- Total global recruitment calculated from all areas, seasons, and growth patterns
- Recruits assigned to these divisions according to apportionment weights (estimated or fixed, constant or time-varying)
- Tranformation of apportionment weight parameters to fractions is equivalent to calculation used for movement rates.

Stock Synthesis DATA file setup

How many areas?

Area of each fleet?

TOP of DATA file

#Model Dimensions

⋮

#Fleet/Survey Setup

⋮

#Catch and Abundance Indices

⋮

#Discards

⋮

#Lenght Compositions

⋮

#Age Compositions

Stock Synthesis DATA file setup

How many areas

```
# TOP OF DATA file
1971 #_StartYr
2001 #_EndYr
1 #_Nseas
 12 #_months/season
2 #_Nsubseasons (even number, minimum is 2)
1 #_spawn_month
2 #_Ngenders
40 #_Nages=accumulator age
4 #_Nareas
:
:
:
```

Stock Synthesis DATA file setup

:
:
:

5 #_Nfleets (including surveys)

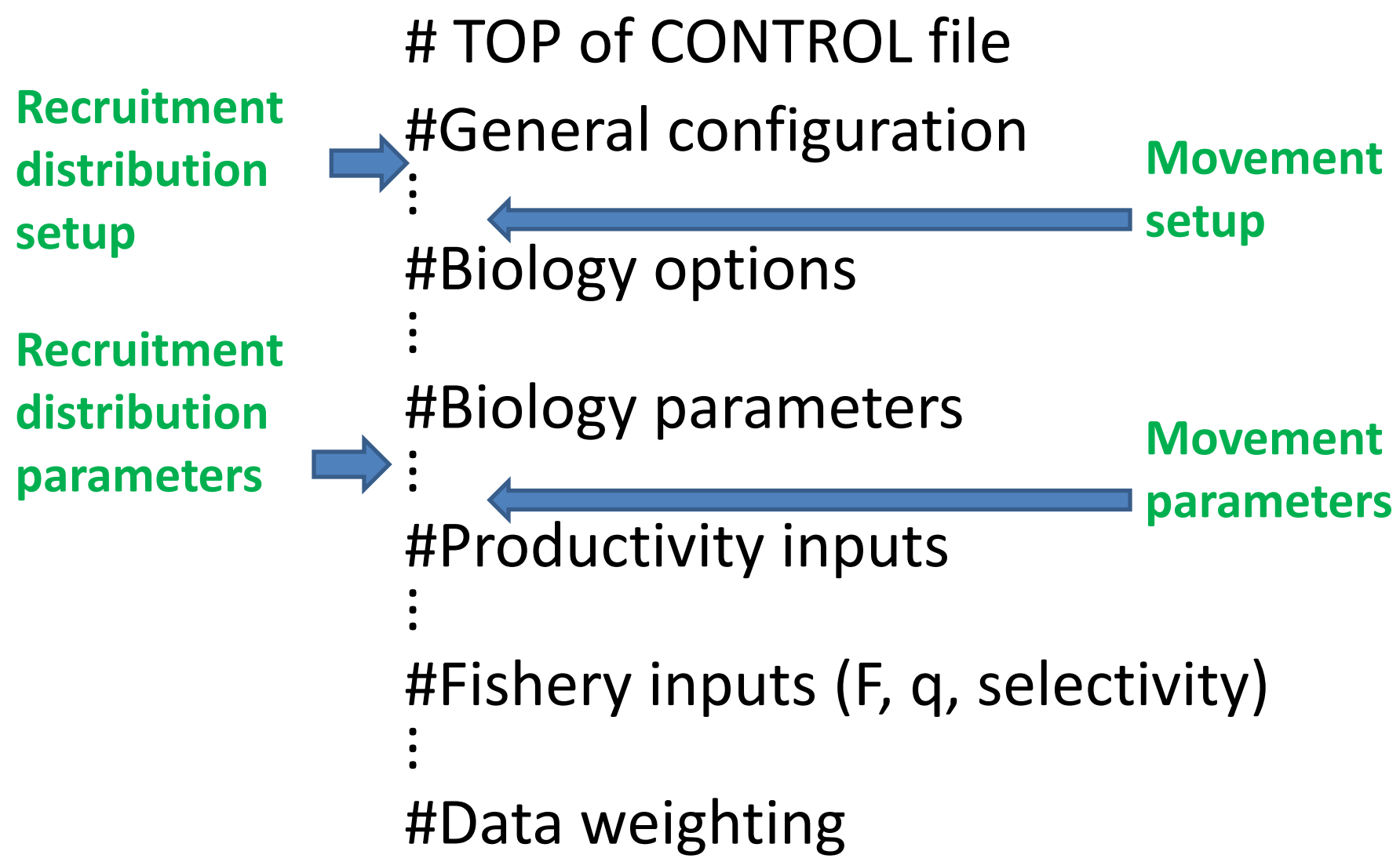
fleet.type fishery.time **area** catch.units catch_mult fleetname

1	-1	**1**	1	0	FISHERY1 # 1
1	-1	**2**	1	0	FISHERY2 # 2
1	-1	**3**	1	0	FISHERY3 # 3
3	1	**1**	2	0	SURVEY1 # 4
3	1	**2**	2	0	SURVEY2 # 5

:
:
:

Area of each fleet

Stock Synthesis CONTROL file setup



Stock Synthesis CONTROL file setup

Recruitment distribution setup

```
.
.
.
3 # recr_dist_method for parameters:  2=main effects for GP, Settle timing, Area;
          3=each Settle entity; 4=none, only when N_GP*Nsettle*pop==1
1 # not yet implemented; Future : Spawner-Recruitment: 1=global; 2=by area
4 #  number of recruitment settlement assignments
0 # unused option
#GPattern month  area  age (for each settlement assignment)
 1          1       1      0
 1          1       2      0
 1          1       3      0
 1          1       4      0
.
.
.
```

Stock Synthesis CONTROL file setup

Movement setup

```
:
:
:
2 #_N_movement_definitions
0 # first age that moves (real age at begin of season, not integer)
# seas,GP,source_area,dest_area,minage,maxage
    1    1    1              2              14        15
    1    1    3              4              14        15
.
:
:
```

Stock Synthesis CONTROL file setup

Recruitment distribution parameters

:
:

Bottom of Biology parameters

Recruitment Distribution

LO, HI, INIT, PR, PR.SD, PR.type PHASE env dev mnyr mxyr devPH Block Blk_Fxn

-5 5 0.5 0.2 0.5 1 -3 0 0 0 0 0 0 0 # RecrDist_GP_1_**area_1**_month_1

-5 5 0.2 0.2 0.5 1 3 0 1 1971 2001 4 0 0 # RecrDist_GP_1_**area_2**_month_1

-5 5 0.2 0.2 0.5 1 3 0 1 1971 2001 4 0 0 # RecrDist_GP_1_**area_3**_month_1

-5 5 0.2 0.2 0.5 1 3 0 1 1971 2001 4 0 0 # RecrDist_GP_1_**area_4**_month_1

:
:

Stock Synthesis CONTROL file setup

Movement parameters

:
:

Bottom of Biology parameters

Recruitment Distribution

LO, HI, INIT, PR, PR.SD, PR.type PHASE env dev mnyr mxyr devPH Block Blk_Fxn

-5 4 -1.8 0 0.05 1 -3 0 0 0 0 0.5 0 0 # MoveParm_A_seas_1_GP_1from_**1to_2**

-5 4 -7.0 0 0.05 1 -3 0 0 0 0 0.5 0 0 # MoveParm_B_seas_1_GP_1from_**1to_2**

-5 4 -1.8 0 0.05 1 -3 0 0 0 0 0.5 0 0 # MoveParm_A_seas_1_GP_1from_**3to_4**

-5 4 -7.0 0 0.05 1 -3 0 0 0 0 0.5 0 0 # MoveParm_B_seas_1_GP_1from_**3to_4**

:
:
:

Simulation testing example making use of spatial options in Stock Synthesis

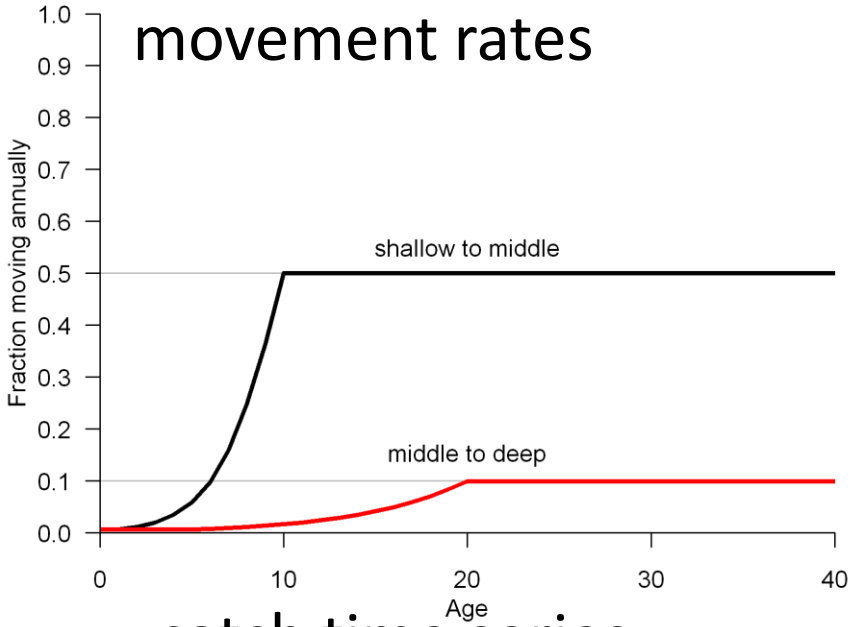
From Ian Taylor and Rick Methot

•Example: ontogenetic movement

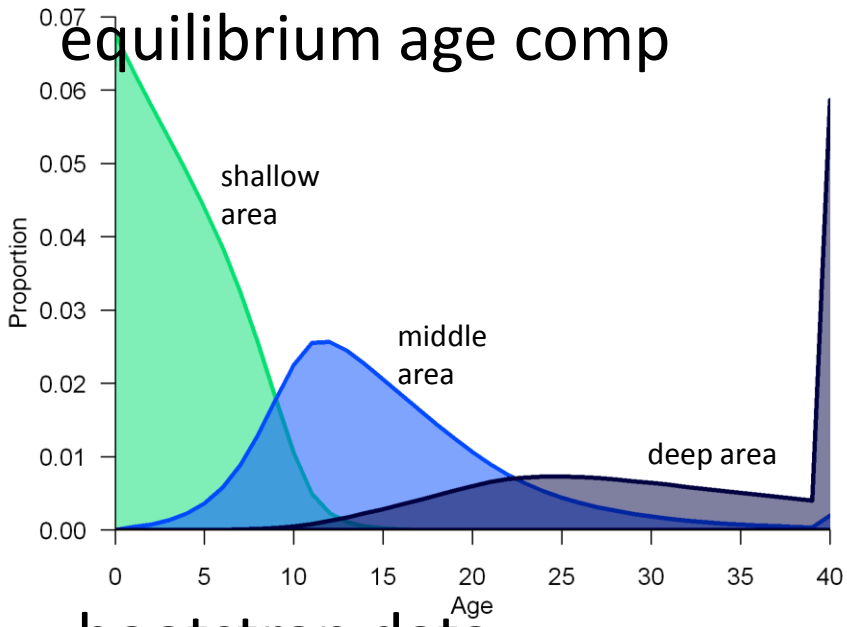
- Simulation study to test ability of single area model with separate fleets to approximate spatial shift
- Simulate using three spatial areas (shallow, middle, deep)
- Recruitment is to shallow area
- Age-based movement to deeper zones
- Apply single area models with different selectivities for each fleet
- Compare estimated parameters and quantities of interest to simulated values

Simulation model configuration

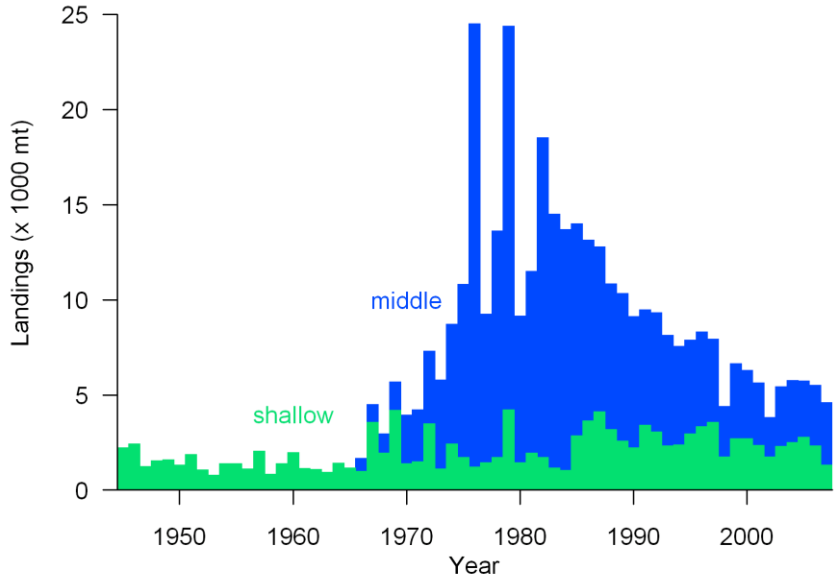
movement rates



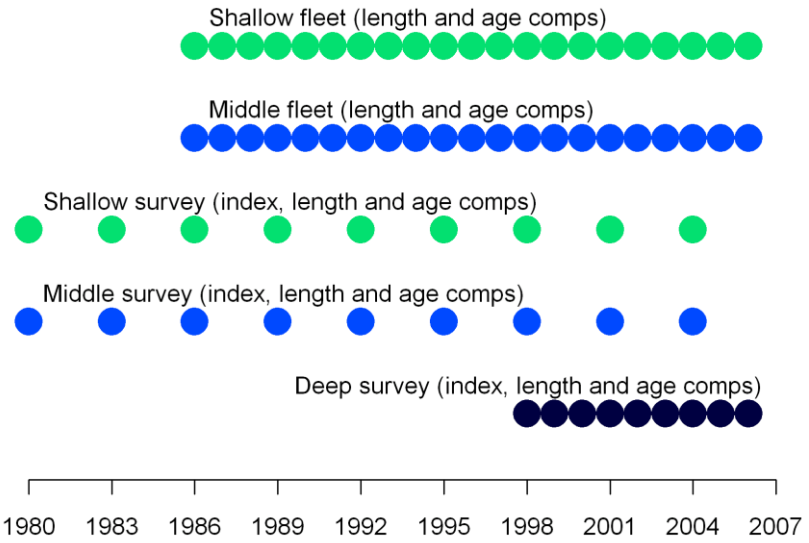
equilibrium age comp



catch time series



bootstrap data



Estimation model configuration

In all cases estimated parameters are

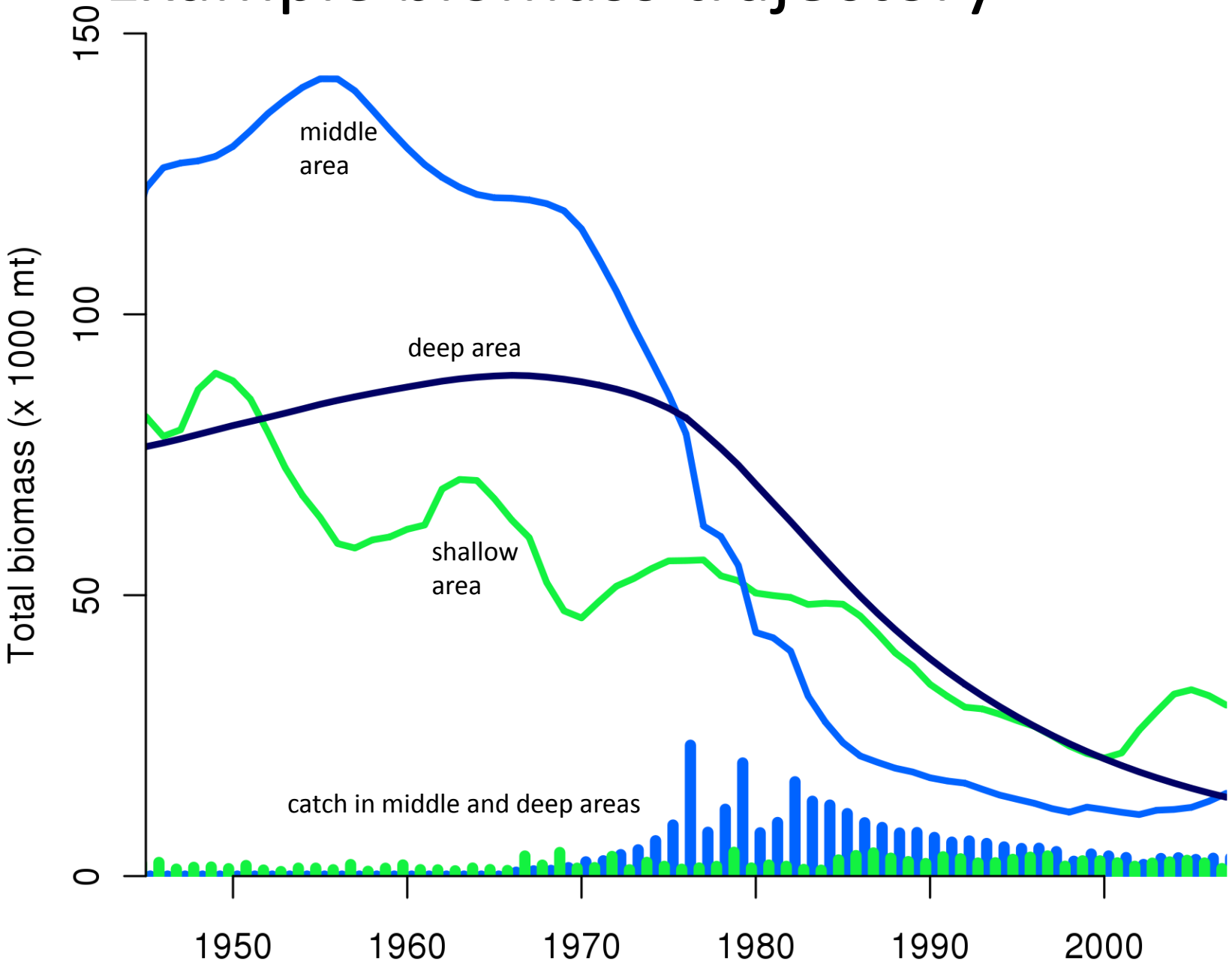
- selectivity for each fleet,
- initial biomass,
- recruitment deviations from 1970-2007

Fitting 3 area operating model to itself with logistic selectivity as a reference group

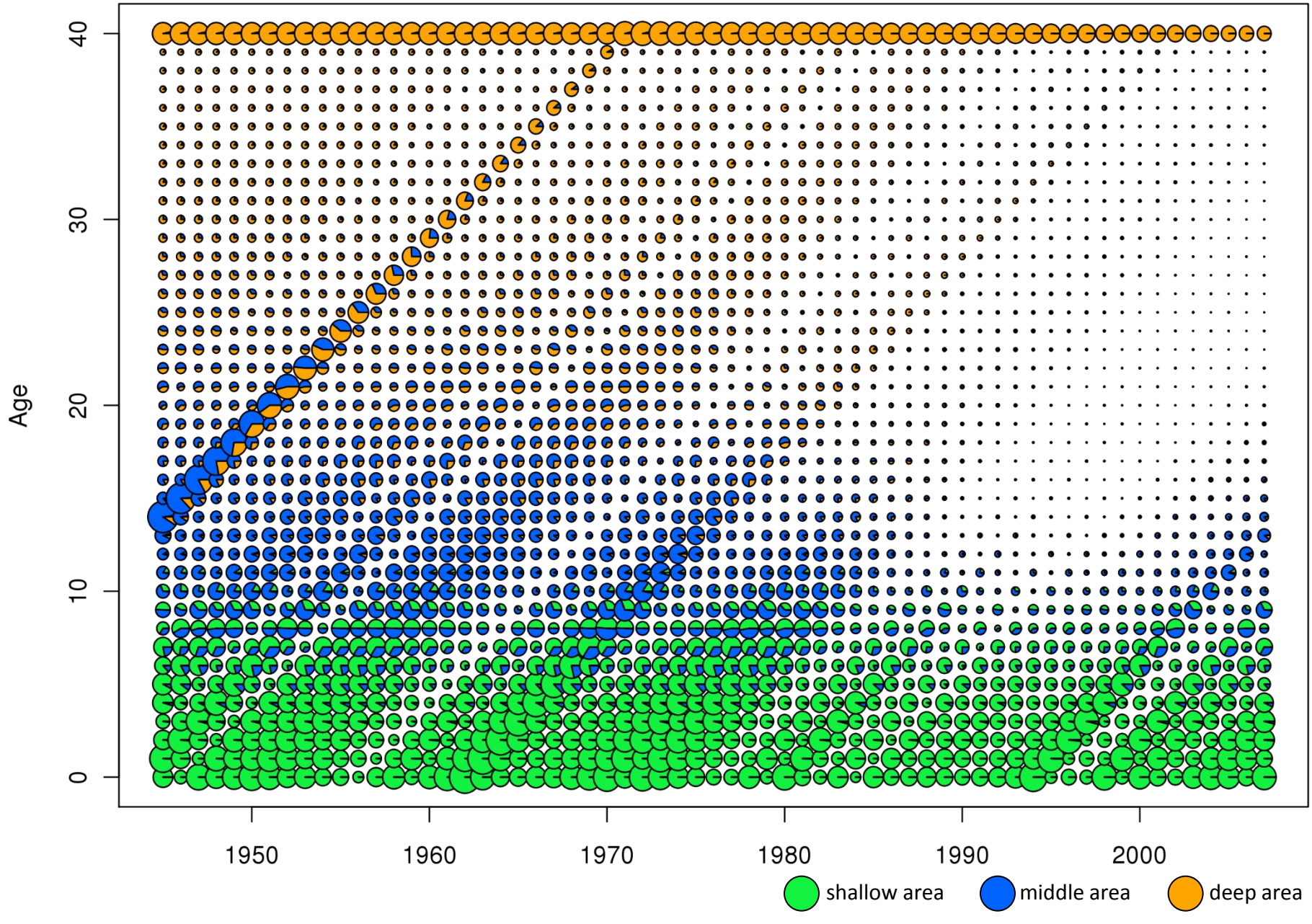
Fitting 1 area model with three selectivity arrangements:

- Length-based (double-normal)
- Age-based (double-normal)
- Both length- and age-based (all double-normal)

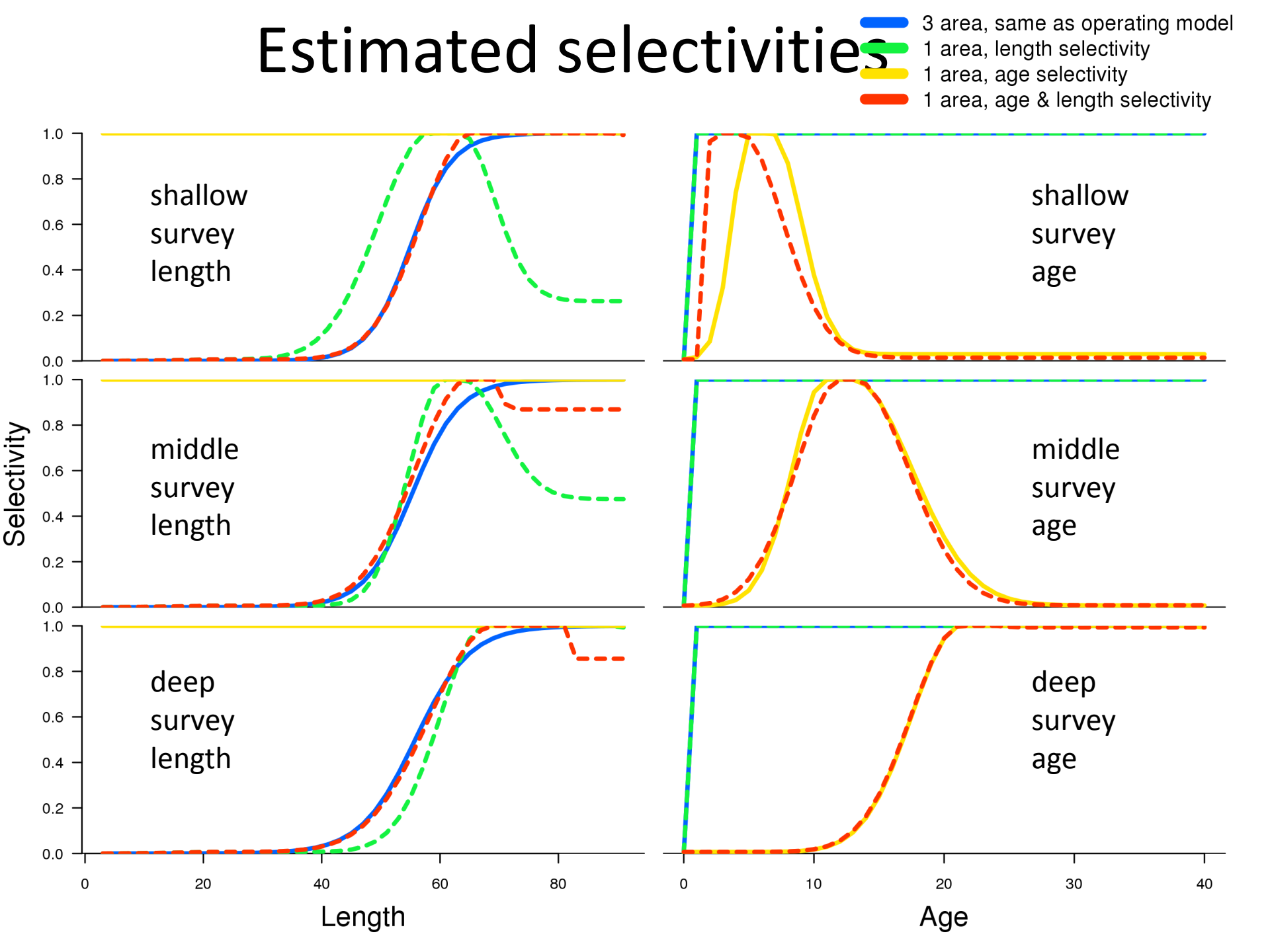
Example biomass trajectory



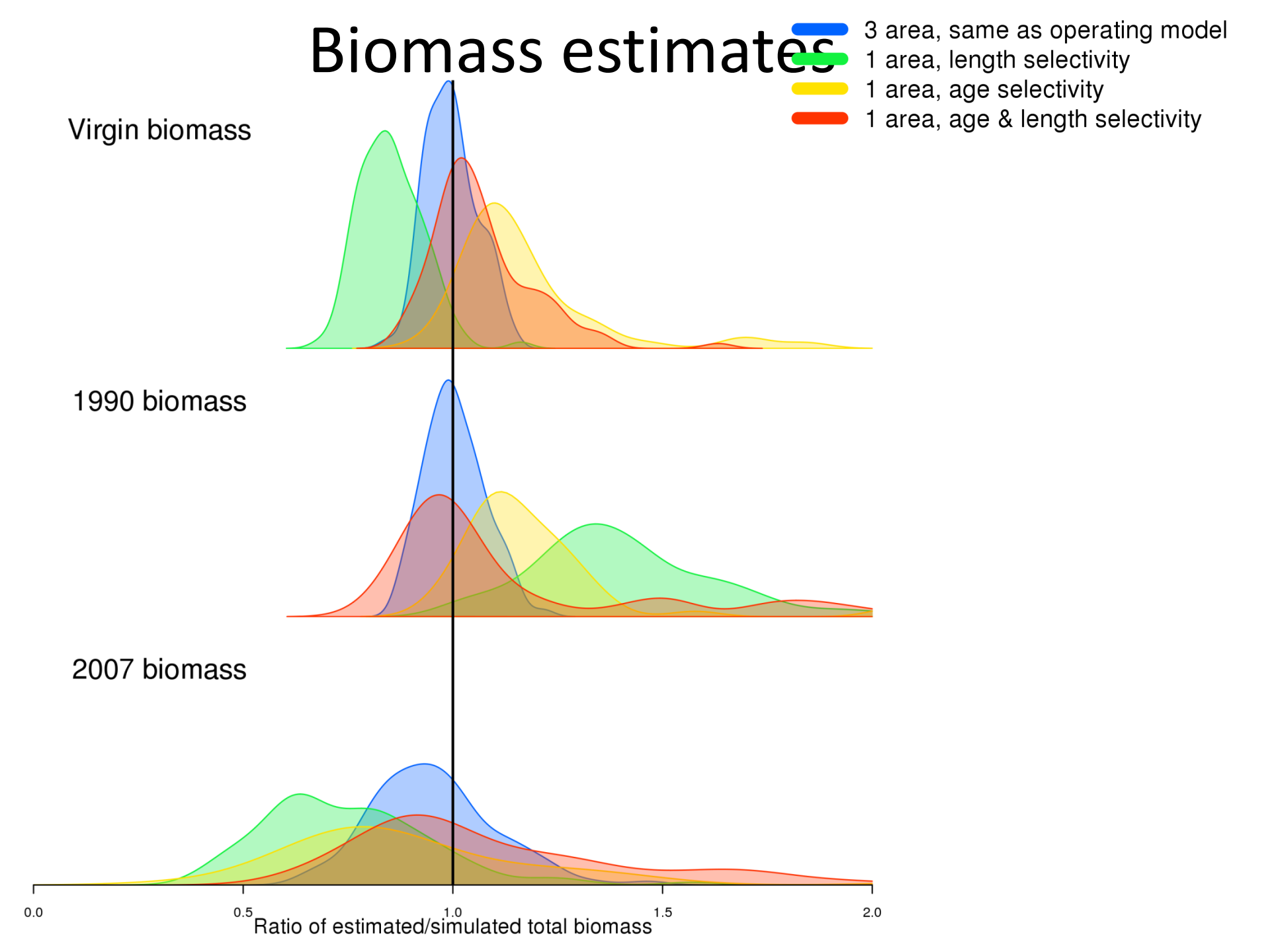
Example simulation: numbers at age



Estimated selectivities

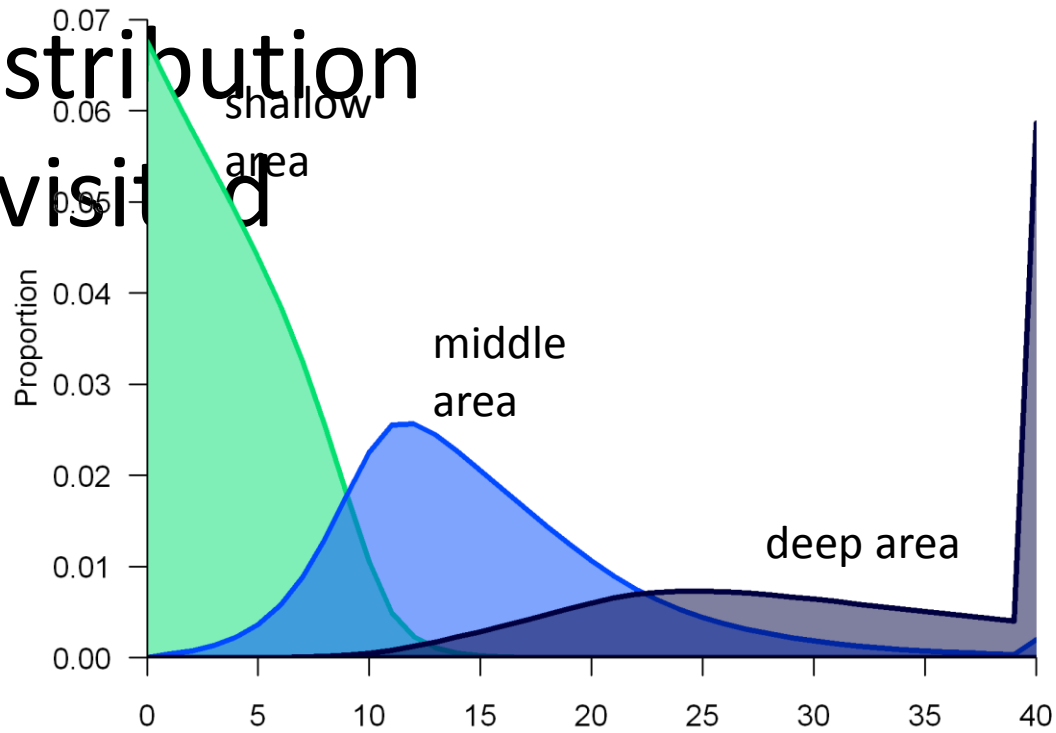


Biomass estimates

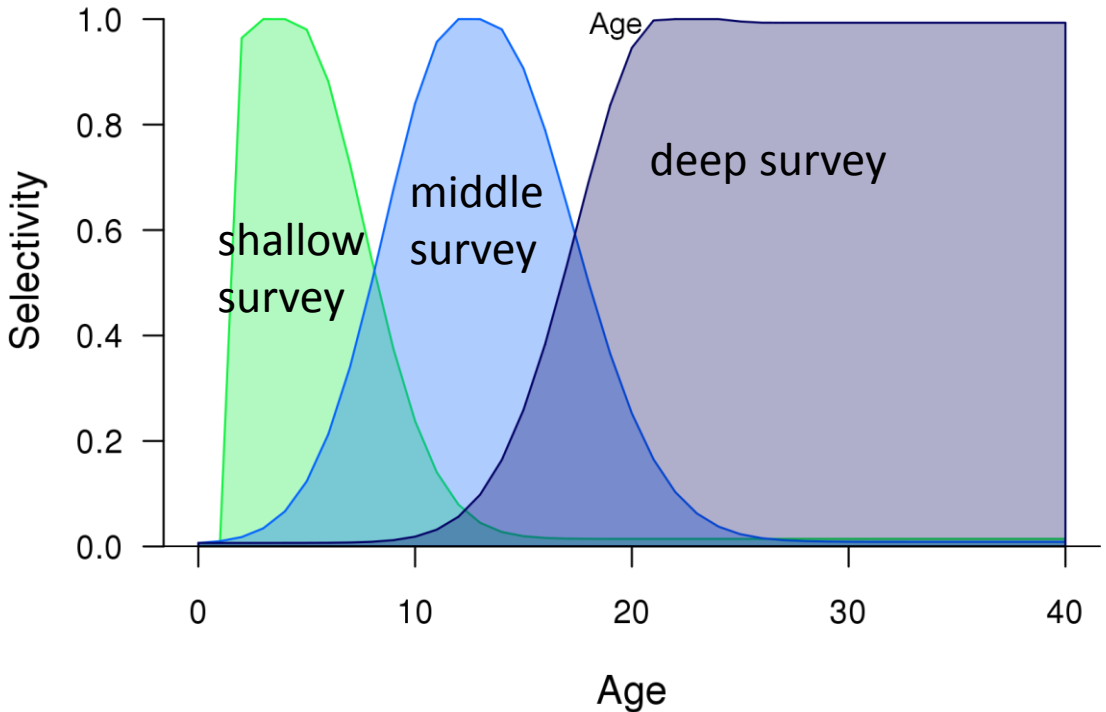


Age distribution revisited

Age distribution by area from unfished equilibrium population in 3-area simulation



Median estimated age-based selectivity from 1-area model with age- and length-based selectivity



Simulation model conclusions

- Single area model with only length- or age-based selectivity does not perform well.
- Single area model with selectivity as dome-shaped functions of both length and age shows less bias, but high variability.
- Spatial model which matches generating model performs well.